EMORY COLLEGE OF ARTS AND SCIENCES | Undergraduate Research Programs

Summer 2021 Symposium

ABSTRACT BOOK

August 5, 2021
9:00 PM to 5:00 PM EST

Abstracts Organized by Alphabetical Order by Presenter's Last Name

Oral Presentation Links

Session	Session Time	Zoom Link
1	9:00 AM to 10:30 AM EST	https://emory.zoom.us/j/92988928818
2	9:00 AM to 10:30 AM EST	https://emory.zoom.us/j/95175906316
3	10:30 AM to 12:00 PM EST	https://emory.zoom.us/j/95598055387
4	12:00 PM to 1:30 PM EST	https://emory.zoom.us/j/99643683271
5	12:00 PM to 1:30 PM EST	https://emory.zoom.us/j/99538389212
6	1:30 to 3:00 PM EST	https://emory.zoom.us/j/95175843929
7	3:00 PM to 4:30 PM EST	https://emory.zoom.us/j/97807604820

Poster Presention Link

https://spatial.chat/s/EmorySummerSymposium

Oral Presentation Schedule

Presenter	Session Time	Oral Session	Presenter Order
Hui Qi Loo	9:00 AM to 10:30 AM	1	1 of 5
Gabriele Kim	9:00 AM to 10:30 AM	1	2 of 5
Abigal Stamper	9:00 AM to 10:30 AM	1	3 of 5
Jhillika Trisal	9:00 AM to 10:30 AM	1	4 of 5
Emil Zhang	9:00 AM to 10:30 AM	1	5 of 5
Bowei Deng	9:00 AM to 10:30 AM	2	1 of 5
Clio Hancock	9:00 AM to 10:30 AM	2	2 of 5
Emma Hendrickson	9:00 AM to 10:30 AM	2	3 of 5
Da Young Lee	9:00 AM to 10:30 AM	2	4 of 5
Sneh Patel	9:00 AM to 10:30 AM	2	5 of 5
Leah Bader	10:30 AM to 12:00 PM	3	1 of 6
Sophia Bereaud	10:30 AM to 12:00 PM	3	2 of 6
Kirsten Gillette	10:30 AM to 12:00 PM	3	3 of 6
Yujia Hao	10:30 AM to 12:00 PM	3	4 of 6
Annie Li	10:30 AM to 12:00 PM	3	5 of 6
Zitong Su	10:30 AM to 12:00 PM	3	6 of 6
Alex Ceballos	12:00 PM to 1:30 PM	4	1 of 5
Sawyer Gray	12:00 PM to 1:30 PM	4	2 of 5
Rahil Mahmood	12:00 PM to 1:30 PM	4	3 of 5
Kayla Salehian	12:00 PM to 1:30 PM	4	4 of 5
Sophie Vo	12:00 PM to 1:30 PM	4	5 of 5
Rakeyah Ahsan	12:00 PM to 1:30 PM	5	1 of 6
Adway Gopakumar	12:00 PM to 1:30 PM	5	2 of 6
Shreya Reddy	12:00 PM to 1:30 PM	5	3 of 6
Alexander Wesley	12:00 PM to 1:30 PM	5	4 of 6
Sophia Xu	12:00 PM to 1:30 PM	5	5 of 6
Grace Zhou	12:00 PM to 1:30 PM	5	6 of 6
Sarah Abraham	1:30 PM to 3:00 PM	6	1 of 6
Kwame Armah	1:30 PM to 3:00 PM	6	2 of 6
Mingee Chung	1:30 PM to 3:00 PM	6	3 of 6
Young Lin	1:30 PM to 3:00 PM	6	4 of 6
Richard Nwakamma	1:30 PM to 3:00 PM	6	5 of 6
Seung Won (Jenna) Shin	1:30 PM to 3:00 PM	6	6 of 6
Anna (Qinyan) Cai	3:00 PM to 4:30 PM	7	1 of 6
Joyce Li	3:00 PM to 4:30 PM	7	2 of 6
Timethius Terrell	3:00 PM to 4:30 PM	7	3 of 6
Elie York	3:00 PM to 4:30 PM	7	4 of 6
Hollis Zeng	3:00 PM to 4:30 PM	7	5 of 6
Jiajin (Molina) Zhang	3:00 PM to 4:30 PM	7	6 of 6

Poster Presentation Schedule

Presenter	Presentation Time	Poster Room	Poster Number
Jennifer Bae	9:00 AM to 9:50 AM	1 A	1
Aastha Bansal	9:00 AM to 9:50 AM	1 A	2
Yuyang Bian	9:00 AM to 9:50 AM	1 A	3
Ammar Dharani	9:00 AM to 9:50 AM	1 A	4
Anna Ecanow	9:00 AM to 9:50 AM	1 B	5
Rebecca Gibbons	9:00 AM to 9:50 AM	1 B	6
Ashlynn Gray	9:00 AM to 9:50 AM	1 B	7
Alexa McGrath	9:00 AM to 9:50 AM	1 B	7
Eliza Grenci	9:00 AM to 9:50 AM	1 B	8
Emily Kim	9:00 AM to 9:50 AM	1 C	9
Megan Lagerquist	9:00 AM to 9:50 AM	1 C	10
Shivani Lam	9:00 AM to 9:50 AM	1 C	11
Jason Lett	9:00 AM to 9:50 AM	1 C	12
Joyce Liu	9:00 AM to 9:50 AM	1 D	13
Trisha Minocha	9:00 AM to 9:50 AM	1 D	14
Anusha Panjwani	9:00 AM to 9:50 AM	1 D	15
Se Hyeon Park	9:00 AM to 9:50 AM	1 D	16
Esther Pincate	9:00 AM to 9:50 AM	1 E	17
Justin Powell	9:00 AM to 9:50 AM	1 E	18
Alexis Roberson	9:00 AM to 9:50 AM	1 E	19
Alex Rojas	9:00 AM to 9:50 AM	1 E	20
Alexandra Slusarenko	9:00 AM to 9:50 AM	1 F	21
Serena Song	9:00 AM to 9:50 AM	1 F	22
Joseph Song	9:00 AM to 9:50 AM	1 F	23
Kris Stallings	9:00 AM to 9:50 AM	1 F	24
Kristina Trifonova	9:00 AM to 9:50 AM	1 G	25
Amanda Wolf	9:00 AM to 9:50 AM	1 G	26
Aya Youssef	9:00 AM to 9:50 AM	1 G	27
Nithin Bagal	10:00 AM to 10:50 AM	2 A	1
Tara Balu	10:00 AM to 10:50 AM	2 A	2
Microl Chen	10:00 AM to 10:50 AM	2 A	3
Christy Daniel	10:00 AM to 10:50 AM	2 A	4
Maria Dhinojwala	10:00 AM to 10:50 AM	2 B	5
Sarah Hancock	10:00 AM to 10:50 AM	2 B	6
Kashari Henry	10:00 AM to 10:50 AM	2 B	7
Shiyeon Kim	10:00 AM to 10:50 AM	2 B	8
Lindsey Lang	10:00 AM to 10:50 AM	2 C	9
Priscilla Lin	10:00 AM to 10:50 AM	2 C	10

Presenter	Presentation Time	Poster Room	Poster Number
Amaya Martin	10:00 AM to 10:50 AM	2 C	11
Abhijay Mudigonda	10:00 AM to 10:50 AM	2 C	12
Ishika Mukherjee	10:00 AM to 10:50 AM	2 D	13
Jenika Packiaraj	10:00 AM to 10:50 AM	2 D	14
Charles Qi	10:00 AM to 10:50 AM	2 D	15
Claire Qu	10:00 AM to 10:50 AM	2 D	16
Michael Sau	10:00 AM to 10:50 AM	2 E	17
Wenyi Shao	10:00 AM to 10:50 AM	2 E	18
Hannah Soloff	10:00 AM to 10:50 AM	2 E	19
Sayli Sonsurkar	10:00 AM to 10:50 AM	2 E	20
Elijah Sterling	10:00 AM to 10:50 AM	2 F	21
Jiarui Tang	10:00 AM to 10:50 AM	2 F	22
Foje Tendoh	10:00 AM to 10:50 AM	2 F	23
Sarah Thomas	10:00 AM to 10:50 AM	2 F	24
Crystal Wang	10:00 AM to 10:50 AM	2 G	25
Joanna Yu	10:00 AM to 10:50 AM	2 G	26
Yiran Zhang	10:00 AM to 10:50 AM	2 G	27
George Abreu	11:00 AM to 11:50 AM	3 A	1
Catharine Anderson	11:00 AM to 11:50 AM	3 A	2
Nikea Banks	11:00 AM to 11:50 AM	3 A	3
Eduardo Barquet Arrambide	11:00 AM to 11:50 AM	3 A	4
Manish Bhatta	11:00 AM to 11:50 AM	3 B	5
Isabella Cavagna	11:00 AM to 11:50 AM	3 B	6
Dheep Dalamal	11:00 AM to 11:50 AM	3 B	7
Antonio Gao	11:00 AM to 11:50 AM	3 B	8
Ryan Gibbons	11:00 AM to 11:50 AM	3 C	9
Brittney Haney	11:00 AM to 11:50 AM	3 C	10
Cora Hirst	11:00 AM to 11:50 AM	3 C	11
Kennedy Humphrey	11:00 AM to 11:50 AM	3 C	12
Sarah Kim	11:00 AM to 11:50 AM	3 D	13
Christopher Kozuch	11:00 AM to 11:50 AM	3 D	14
Frances Lee	11:00 AM to 11:50 AM	3 D	15
Carolyn Ma	11:00 AM to 11:50 AM	3 D	16
Alejandro McDonald	11:00 AM to 11:50 AM	3 E	17
Kylie Measimer	11:00 AM to 11:50 AM	3 E	18
Noyonika Parulekar	11:00 AM to 11:50 AM	3 E	19
Aneri Patel	11:00 AM to 11:50 AM	3 E	20
Bhavana Pavuluri	11:00 AM to 11:50 AM	3 F	21
Destini Renard	11:00 AM to 11:50 AM	3 F	22

Presenter	Presentation Time	Poster Room	Poster Number
Varun Saxena	11:00 AM to 11:50 AM	3 F	23
Akash Shanmugam	11:00 AM to 11:50 AM	3 F	24
Yishen (Angela) Shen	11:00 AM to 11:50 AM	3 G	25
SARA USECHE DE ABREU	11:00 AM to 11:50 AM	3 G	26
Mellisa Xie	11:00 AM to 11:50 AM	3 G	27
Julie Zhu	11:00 AM to 11:50 AM	3 G	28
Aniket Adhikari	12:00 PM to 12:50 PM	4 A	1
Marina Albuquerque	12:00 PM to 12:50 PM	4 A	2
William Ball	12:00 PM to 12:50 PM	4 A	3
Johnny Bui	12:00 PM to 12:50 PM	4 A	4
Jonathan Cho	12:00 PM to 12:50 PM	4 B	5
Sina Djafari Rouhani	12:00 PM to 12:50 PM	4 B	6
Julia Francois	12:00 PM to 12:50 PM	4 B	7
Michelle Garrison	12:00 PM to 12:50 PM	4 B	8
Julia Gonzalez	12:00 PM to 12:50 PM	4 C	9
Maddie Hasson	12:00 PM to 12:50 PM	4 C	10
Dustin Hoffman	12:00 PM to 12:50 PM	4 C	11
Tiffany Hung	12:00 PM to 12:50 PM	4 C	12
Semin Kang	12:00 PM to 12:50 PM	4 D	13
Uswa Khan	12:00 PM to 12:50 PM	4 D	14
Nitya Koduri	12:00 PM to 12:50 PM	4 D	15
Saad Maan	12:00 PM to 12:50 PM	4 D	16
Calen MacDonald	12:00 PM to 12:50 PM	4 E	17
Sejal Murthy	12:00 PM to 12:50 PM	4 E	18
Jasmine Ng	12:00 PM to 12:50 PM	4 E	19
Nicole Petit	12:00 PM to 12:50 PM	4 E	20
Tsian Ramrattan	12:00 PM to 12:50 PM	4 F	21
Nicole Sarette	12:00 PM to 12:50 PM	4 F	22
Colin Song	12:00 PM to 12:50 PM	4 F	23
Christy Song	12:00 PM to 12:50 PM	4 F	24
Nathan Trinkl	12:00 PM to 12:50 PM	4 G	25
Natali Vera Pimentel	12:00 PM to 12:50 PM	4 G	26
Tianyi Xu	12:00 PM to 12:50 PM	4 G	27
Patrick Czabala	12:00 PM to 12:50 PM	4 G	28
Lauren Anshen	1:00 PM to 1:50 PM	5 A	1
Danielle Orloff	1:00 PM to 1:50 PM	5 A	1
Kathryn Barr	1:00 PM to 1:50 PM	5 A	2
Xavier Bell	1:00 PM to 1:50 PM	5 A	3
Matthew Buxton	1:00 PM to 1:50 PM	5 A	4

Presenter	Presentation Time	Poster Room	Poster Number
Allison Cartee	1:00 PM to 1:50 PM	5 B	5
Zirui Chen	1:00 PM to 1:50 PM	5 B	6
Dabin Cho	1:00 PM to 1:50 PM	5 B	7
Layla Dhabaan	1:00 PM to 1:50 PM	5 B	8
Michael Hendrix	1:00 PM to 1:50 PM	5 C	9
Afsha Hossain	1:00 PM to 1:50 PM	5 C	10
Asha Hurreh	1:00 PM to 1:50 PM	5 C	11
Sonia Karkare	1:00 PM to 1:50 PM	5 C	12
Brandon Kassouf	1:00 PM to 1:50 PM	5 D	13
Jeffrey Ling	1:00 PM to 1:50 PM	5 D	14
Zachary Lorson	1:00 PM to 1:50 PM	5 D	15
Andrea Mancia	1:00 PM to 1:50 PM	5 D	16
Danielle Mangabat	1:00 PM to 1:50 PM	5 E	17
Jasleen Narula	1:00 PM to 1:50 PM	5 E	18
Michella Obialor	1:00 PM to 1:50 PM	5 E	19
Qian Qian	1:00 PM to 1:50 PM	5 E	20
Adrian Rivera	1:00 PM to 1:50 PM	5 F	21
Bethany Scheel	1:00 PM to 1:50 PM	5 F	22
Patrick Shen	1:00 PM to 1:50 PM	5 F	23
Ethan Shi	1:00 PM to 1:50 PM	5 F	24
Rhea Tumminkatti	1:00 PM to 1:50 PM	5 G	25
Ashwin Ujre	1:00 PM to 1:50 PM	5 G	26
Aditi Vellore	1:00 PM to 1:50 PM	5 G	27
Xaviera Villarino	1:00 PM to 1:50 PM	5 G	28
Delvonae Beckles	2:00 PM to 2:50 PM	6 A	1
Swagata Datta	2:00 PM to 2:50 PM	6 A	2
Jake Diamond	2:00 PM to 2:50 PM	6 A	3
Janissa Fuentes	2:00 PM to 2:50 PM	6 A	4
Valeria Gomez	2:00 PM to 2:50 PM	6 B	5
Paige Hewitt	2:00 PM to 2:50 PM	6 B	6
Sophia Hwang	2:00 PM to 2:50 PM	6 B	7
Amrutha Kotlure	2:00 PM to 2:50 PM	6 B	8
Danbi Lim	2:00 PM to 2:50 PM	6 C	9
Nicole Lulkin	2:00 PM to 2:50 PM	6 C	10
Caroline McCormack	2:00 PM to 2:50 PM	6 C	11
Rahul Nalluri	2:00 PM to 2:50 PM	6 C	12
Andrew Pahnke	2:00 PM to 2:50 PM	6 D	13
Diana Pineda	2:00 PM to 2:50 PM	6 D	14
Siyan Pu	2:00 PM to 2:50 PM	6 D	15

Presenter	Presentation Time	Poster Room	Poster Number
Sophia Shahin	2:00 PM to 2:50 PM	6 D	16
Camille Simmons	2:00 PM to 2:50 PM	6 E	17
Nate Smyth	2:00 PM to 2:50 PM	6 E	18
Ally Su	2:00 PM to 2:50 PM	6 E	20
Claudia Wahoski	2:00 PM to 2:50 PM	6 F	21
Anthony Wang	2:00 PM to 2:50 PM	6 F	22
Alaina Waters	2:00 PM to 2:50 PM	6 F	23
Jack Wessell	2:00 PM to 2:50 PM	6 F	24
Ashley Williams	2:00 PM to 2:50 PM	6 G	25
Chloe Yang	2:00 PM to 2:50 PM	6 G	26
Chris Yang	2:00 PM to 2:50 PM	6 G	27
Victor You	2:00 PM to 2:50 PM	6 G	28
Yasmeen Ahmed	3:00 PM to 3:50 PM	7 A	1
Reina Ambrocio	3:00 PM to 3:50 PM	7 A	2
Ali Ashraf	3:00 PM to 3:50 PM	7 A	3
Cherice Chan	3:00 PM to 3:50 PM	7 A	4
Victor Chen	3:00 PM to 3:50 PM	7 B	5
Chavis Ferguson	3:00 PM to 3:50 PM	7 B	6
Paige Gallagher	3:00 PM to 3:50 PM	7 B	7
Matowacipi Horse	3:00 PM to 3:50 PM	7 B	8
Bahaa Kazzi	3:00 PM to 3:50 PM	7 C	9
Samia Khan	3:00 PM to 3:50 PM	7 C	10
Zee Kwong	3:00 PM to 3:50 PM	7 C	11
Annabelle Marko	3:00 PM to 3:50 PM	7 C	12
Rachel Patterson	3:00 PM to 3:50 PM	7 C	12
Mira Rajani	3:00 PM to 3:50 PM	7 C	12
Elena Mishkovsky	3:00 PM to 3:50 PM	7 D	13
Arshiya Namazi	3:00 PM to 3:50 PM	7 D	14
Idalis Ramos Correa	3:00 PM to 3:50 PM	7 D	15
Nicholas Skelley	3:00 PM to 3:50 PM	7 D	16
Kiara Vazquez Narvaez	3:00 PM to 3:50 PM	7 E	17
Nevin Walia	3:00 PM to 3:50 PM	7 E	18
Andrew Wei	3:00 PM to 3:50 PM	7 E	19
Jack Wolfram	3:00 PM to 3:50 PM	7 E	20
Jared Druss	3:00 PM to 3:50 PM	7 F	21
Aaron Wozniak	3:00 PM to 3:50 PM	7 F	21
Alizabeth York	3:00 PM to 3:50 PM	7 F	22
Ana Zaalishvili	3:00 PM to 3:50 PM	7 F	23
Jedidiah Zhu	3:00 PM to 3:50 PM	7 F	24

Presenter	Presentation Time	Poster Room	Poster Number
Cindy Amaya Lopez	4:00 PM to 4:50 PM	8 A	1
Joseph Ambarian	4:00 PM to 4:50 PM	8 A	2
Andrea Anchondo	4:00 PM to 4:50 PM	8 A	3
Sophia Boraschi Umana	4:00 PM to 4:50 PM	8 A	4
Linda Chen	4:00 PM to 4:50 PM	8 B	5
Jianze Chen	4:00 PM to 4:50 PM	8 B	6
Griffin Davis	4:00 PM to 4:50 PM	8 B	7
Pranavi Dulam	4:00 PM to 4:50 PM	8 B	8
Maylynn Hu	4:00 PM to 4:50 PM	8 C	9
Sabina Iqbal	4:00 PM to 4:50 PM	8 C	10
Ruth Korder	4:00 PM to 4:50 PM	8 C	11
Sam Lee	4:00 PM to 4:50 PM	8 C	12
Carl Li	4:00 PM to 4:50 PM	8 D	13
Sandy Su-Ting Lin	4:00 PM to 4:50 PM	8 D	14
Rohan Singh	4:00 PM to 4:50 PM	8 D	14
Rhiannon Moore	4:00 PM to 4:50 PM	8 D	15
Ruth Nelson	4:00 PM to 4:50 PM	8 D	16
Niki Patel	4:00 PM to 4:50 PM	8 E	17
Siri Peddineni	4:00 PM to 4:50 PM	8 E	18
Alvaro Perez	4:00 PM to 4:50 PM	8 E	19
George Poppitz	4:00 PM to 4:50 PM	8 E	20
Josh Riembauer	4:00 PM to 4:50 PM	8 F	21
Annie Shen	4:00 PM to 4:50 PM	8 F	22
Samuel Shih	4:00 PM to 4:50 PM	8 F	23
Maxwell Su	4:00 PM to 4:50 PM	8 F	24
Nandish Vora	4:00 PM to 4:50 PM	8 G	25
Lennox Xu	4:00 PM to 4:50 PM	8 G	26
Ella Zhao	4:00 PM to 4:50 PM	8 G	27

Investigation of Phospholipid-Mimicking Small Molecule Modulators of Liver Receptor Homolog-1

Abraham, Sarah; Cato, Michael; Flynn, Autumn; Johnson, Alyssa; D'Agostino, Emma ; Jui, Nathan; Ortlund, Eric

Presenter/s: Sarah Abraham
Emory Faculty Mentor: Eric Ortlund

Liver receptor homolog-1 (LRH-1; NR5A2) is a nuclear receptor that modulates expression of genes that regulate bile acid biosynthesis, lipid homeostasis, and cell proliferation. LRH-1 also has key roles in steroidogenesis in the intestine, making it an attractive target for treatment of disease states characterized by intestinal inflammation. Though LRH-1 is activated by phospholipids (PLs), more potent synthetic agonists have been developed. However, most synthetic agonists bind and activate the receptor through residues distinct from those contacted by PLs. To better imitate agonizing PLs, the synthetic agonist “10CA” was developed, which includes a polar “tail” that targets residues at the mouth of the pocket contacted by PLs. To explore how different modifications contacting this site impact activation of the receptor, we synthesized and investigated a series of 10CA isosteres with various functional groups. Analysis of compound mediated activation and stabilization of LRH-1 reveal that modifications to the tail promote drastically different activation states of the receptor. Additionally, molecular dynamics simulations reveal different allostery driven by isosteres and parent compound 10CA. Overall, our work demonstrates the effects of differential contact of the mouth the LRH-1 binding pocket and provides us with useful tools for studying LRH-1 in the context of intestinal biology.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 6
Presentation/Poster Number: 1 of 6
Presentation Time: 1:30 PM to 3:00 PM
Presentation Link: https://emory.zoom.us/j/95175843929

The impact of COVID-19 on South Korea’s CO2 levels.

Abreu, George; Saikawa, Eri

Presenter/s: George Abreu
Emory Faculty Mentor: Eri Saikawa

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 3 A
Presentation/Poster Number: 1
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

LCMT-1's effects on Regulation of Hematopoietic Stem Cell Proliferation:

Adhikari, Aniket; Tam, Duncan; Pallas, David

Presenter/s: Aniket Adhikari
Emory Faculty Mentor: David Pallas

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 A
Presentation/Poster Number: 1
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

How Do Children Learn and Acquire Rules?

Rochat, Philippe; Agarwal, Nikita; Ahmed, Yasmeen

Presenter/s: Yasmeen Ahmed
Emory Faculty Mentor: Philippe Rochat

In the past century, a great deal of research has been focused on the moral and cognitive development of humans, starting from birth and progressing into adulthood. Dating back to the 1920s, famous psychologist Jean Piaget's theories and research sparked an emphasis on the education of children and their development. Piaget focused on the progression of rule learning in children through storytelling: he theorized that from ages five to nine, children view morality and rules as absolute, unchanging, and made by an authority figure; he called this heteronomous morality. From ages nine and onward, children begin to construct their own morality and understand that people both make rules and can change rules; Piaget called this autonomous morality. With this understanding of morality and cognition in children, other psychologists like Freud, Kohlberg, Skinner, and Turiel built their own theories. Our research is able to replicate a similar study and build on the understanding of how children begin to construct their own understanding of morality and rules. We will have children ages three to seven play a virtual game with a point system, and part of the game will involve stealing as a way to acquire points. We will have two trials of the game. In the first trial, we will not explicitly tell the children that stealing is allowed, but it will still be a part of the game as a way to acquire points. In the other trial, we will instruct the children that they are allowed to steal to gain more points in the game. This game will involve elements of rule learning while testing children's morality by implementing the aspect of "stealing," which is traditionally viewed as being immoral.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 7 A
Presentation/Poster Number: 1
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Planar cell polarity is impaired in human nasal polyps

Ahsan, Rakeyah; Koval, Michael; Smith, Prestina; Gowrishankar, Ram

Presenter/s: Rakeyah Ahsan
Emory Faculty Mentor: Michael Koval

Around 4% of the population suffers froßm nasal polyps (NPs), teardrop-like growths that block nasal passages and lead to breathing problems. In more severe cases of recurrent NPs, the polyps are surgically removed every two to three years which is a painful process. Chronic inflammation of epithelial nasal tissue has been linked to recurrent NPs. We were interested in examining the planar cell polarity (PCP) signaling pathway which controls cell polarization and orientation. Past RT-qPCR analysis has shown decreased mRNA expression of PCP genes in NPs. It is currently unknown whether changes in PCP mRNA result in differences in protein expression and localization within the cell. Given this we examined PCP protein expression and localization in NPs compared with healthy nasal epithelial cells. PCP proteins proved difficult to analyze by western blot and so we first tested different blocking agents for the ability to enable analysis of specific PCP protein bands. For most PCP proteins (DVL2, VANGL1, FZD6) a blocking agent based on milk proteins gave the most reproducible results. Other PCP proteins were better analyzed using a bovine serum albumin (BSA) based blocking reagent. We are currently determining whether the levels of PCP protein correlate with differences in mRNA levels observed between NPs and normal nasal epithelial cells. We are also examining whether PCP proteins are properly localized to the plasma membrane in in NPs or whether they are mislocalized within the cell. Uncovering whether PCP pathways are disrupted in NPs will help understand the disease and discover new therapeutics.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 5
Presentation/Poster Number: 1 of 6
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99538389212

Empathy in Health Professionals: How its Components Relate to Burnout

Albuquerque, Marina; Jimenez, Marta; Fullarton, Catherine

Presenter/s: Marina Albuquerque
Emory Faculty Mentor: Marta Jimenez

This project analyzes how the different components of empathy are associated with burnout in health professionals. The way health professionals relate to patients requires them to do a kind of interpersonal emotional labor that can be enriching, but it can also negatively affect their propensity for experiencing burnout. In fact, I found that most research supports a negative correlation between empathy and burnout. That is, health professionals experiencing higher empathy tend to experience less burnout [1-3]. However, there is some evidence that too much affective empathy can lead to "compassion fatigue", or caregiver burnout [4]. How could high levels of empathy lead to burnout (i.e. compassion fatigue) in some cases while protecting from burnout in others?

To answer this question, I look at the Interpersonal Reactivity Index conceptualization of empathy and the Maslach Burnout Inventory [5-6]. The Interpersonal Reactivity Index defines empathy through two main components: a cognitive component, which typically takes the form of perspective-taking; and an affective component, which can be either (1) other-oriented empathic concern, or (2) self-oriented personal distress. Interestingly, researchers found that high scores both in perspective-taking (cognitive empathy) and empathic concern (other-oriented affective empathy) are protective from burnout [7].

To explain how empathy can contribute to avoiding burnout, I appeal to Halpern's model of "clinical empathy," which emphasizes the importance of engaged curiosity (practiced through perspective-taking) and emotional attunement (manifested through empathic concern) for a successful clinical practice [8-9]. With the skills of clinical empathy, health professionals are able to derive meaning from their work, experiencing more "compassion satisfaction" and less personal distress, and thus avoiding burnout [7]. Future research should further explore how different empathic skills can be trained in order to improve health professionals' wellbeing.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 4 A
Presentation/Poster Number: 2
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The crystallization of Guanosine 5'-triphosphate (GTP) cyclohydrolase-IB (GCYH-IB) bounded to inhibitors Dehydrocostus lactone (DHL) and β-lapachone to gain crystallographic structures

Amaya Lopez, Cindy; McWhorter, Kirklin; Davis, Katherine M.

Presenter/s: Cindy Amaya Lopez
Emory Faculty Mentor: Katherine Davis

In many human pathogens, the prokaryotic-specific, zinc-dependent enzyme Guanosine 5'-triphosphate (GTP) cyclohydrolase-IB (GCYH-IB; encoded by the fole2 gene), a class of GCYH-I, is the only enzyme present to catalyze the first step of the folate pathway. This fact makes GCYH-IB a perfect target for antibiotics; we are studying dehydrocostus lactone (DHL) and β-lapachone. Previous structural and enzymatic studies on GCYH-IB from N. gonorrhoeae showed it is structurally distinct from GCYH-I. GCYH-IB is a bimodular, homotetrameric enzyme activated by various divalent cations, and its active site differs in the helical insertions and deletions near the interface. Our study aims to gain structures of the inhibitors bound to the enzyme's active site to complement the experimental data collected by our collaborators with GCYH-IB from B. thailandensis. Previous inhibitors have been proposed and co-crystallized with GCYH-IB from N. gonorrhoeae, but our solution data for DHL and β-lapachone suggest the latter inhibitors are preferable. From our initial crystal screens and optimization trays, FolE2 is particular about its environmental condition for crystallization, yielding non-diffracting crystals in one or two conditions. Therefore, FolE2 was lysine methylated to improve the success rate of crystallization by widening the range of conditions FolE2 crystallized in. After modification, FolE2's crystallization was more successful than previous attempts and was further optimized for crystal growth. This resulted in the crystal formation evolving from walnut-shaped crystals (less desirable) to rod-shaped and plate-shaped crystals (more desirable). These crystals were prepared and looped for x-ray crystallography at Sector 23 of the Advanced Photon Source at Argonne National Labs. Once the structures of the enzyme with the inhibitors DHL and β-lapachone are solved, the results will be published with the solution experiments, providing a new option to combat pathogens with this enzyme, and the first structure of GCYH-IB from B. thailandensis.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 A
Presentation/Poster Number: 1
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Crystallizing Coenzyme Q-bound Class II Dihydroorotate Dehydrogenase for Crystallographic Analysis

Ambarian, Joseph; Horwitz, Samantha; Davis, Katherine

Presenter/s: Joseph Ambarian
Emory Faculty Mentor: Katherine Davis

Several autoimmune diseases, infectious diseases, and fenretinide-mediated cancers use the pyrimidine metabolic pathway to proliferate. The fourth step of pyrimidine metabolism is catalyzed by dihydroorotate dehydrogenase (DHODH), an enzyme that oxidizes dihydroorotate. Humans express Class II DHODH, which requires a coenzyme Q (CoQ) ligand to function. If explored further, Class II DHODH inhibitors could serve as potential pharmaceuticals, as they obstruct pyrimidine metabolism and halt disease proliferation. Our collaborators found that two quinolones produced by Burkholderia thailandensis each competitively displaced CoQ, inhibiting Class II DHODH. Our group had previously visualized the two DHODH/quinolone complexes through X-ray crystallography and affirmed our collaborators' findings. However, no high-resolution structures of the DHODH/CoQ complex have been solved. Visualizing CoQ bound to DHODH would complement our past findings on DHODH inhibition and improve our understanding of the interactions that potential pharmaceuticals could target. This project consisted of crystallizing the complex and performing X-ray crystallography to solve a structure. Class II DHODH was heterologously expressed with Escherichia coli. DHODH was crystallized by hanging drop in 1.6 M sodium malonate at pH 7.1, 23% PEG3350 in 25 mM sodium phosphate buffer, 100 mM EDTA, and 10% glycerol. DHODH crystalized in solution, and CoQ was added to the solution afterwards. To improve the likelihood that CoQ would be bound to DHODH in the crystals, we also crystallized them together in the same condition. Crystals containing the ligand were sent to the Advanced Photon Source in Argonne National Laboratory in hopes of providing the first high-resolution structures of CoQ bound to DHODH.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 A
Presentation/Poster Number: 2
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Assessing oncohistone impact on biological pathways using S. cerevisiae model

Ambrocio, Reina; Corbett, Anita; Lemon, Laramie

Presenter/s: Reina Ambrocio
Emory Faculty Mentor: Anita Corbett

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 A
Presentation/Poster Number: 2
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Isolation and Cloning of Influenza A Virus segments using DNA transfection

Anchondo, Andrea; Lowen, Anice; Lee, Chung-Young Lee

Presenter/s: Andrea Anchondo
Emory Faculty Mentor: Anice Lowen

`The focus of the Lowen Lab is the reassortment of influenza A virus, more specifically to study the gradual process of antigenic drift as well as the roles of pre-existing immunity and genetic compatibility. To further research IAV there is a need to have readily available Influenza A Virus TX.50.2021 plasmid samples. I was tasked to use a DNA transfection system in order to first rescue the infectious influenza A virus from previously cloned cDNA with the goal on cloning each individual eight segments of IAV. This plasmid-based expression system functions by inserting cDNA between the RNA polymerase I promoter and terminator sequences and lastly tailed by an RNA polymerase II promoter and a polyadenylation site. The approach in which I took began in the form of plasmid transformation, this step is to introduce the initial foreign plasmid into the given DH5a E. coli strain bacteria cell. The bacteria will then amplify the introduced plasmid, essentially growing it. The next step was putting this plasmid transformation though an isolation process called Midi Prep. Through this procedure bacterial lysates are cleared by centrifugation, the DNA is in turn concentrated for further use. The next step is key in terms of the objective, restriction enzyme digestion, here the purified nucleic acid is cleaved in the necessary sites using the restriction enzyme BSMBI-V2. Using a GelRed Nucleic Acid Gel Stain, the bands were reviews at their weight in kb, the correct size for the eight segments are then sliced out of the gel. Ligation Transformation is the next procedure in which the desired DNA vector is introduced to our previously cloned segments. These samples then go through a final step of purification by the Spin Miniprep. Using DNA transfection, all eight segments of IAV are cloned and available for further research by the Lowen Lab.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 A
Presentation/Poster Number: 3
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating the Effects of Point Mutations on Influenza Fusion Peptide Insertion into Model Membrane Liposomes

Anderson, Catharine; Prokopik, Alexia; Dyer, Brian

Presenter/s: Catharine Anderson
Emory Faculty Mentor: Brian Dyer

The first 20-25 residues of influenza hemagglutinin (HA), known as the fusion peptide (FP), are critical for fusion of the viral and endosomal membranes during viral infection. Although HA is prone to mutation, these FP are highly conserved among serotypes. Even conservative substitutions have been shown to significantly alter the peptide's conformational ensemble and abolish fusogenicity. Equilibrium fluorescence and CD spectroscopy are used here to study the effects of different point mutations on fusion peptide insertion into vesicles. G1V, G8A, G16A, and W14A variants are examined in addition to the WT peptide. Insertion is initiated by heating DPPC (1,2-dipalmitoyl-sn-glycero-3-phosphocholine) lipid vesicles above the gel-to-liquid phase transition temperature of DPPC. The G8A and G16A variants appear to partially insert at lower temperatures than WT, more noticeably for G8A. These variants likely sample open conformations to a greater degree than the WT peptide, which mainly adopts a tight helical hairpin structure, and it has been proposed that the open conformation is critical for insertion. The W14A and G1V variants appear to insert similarly to the WT, but more shallowly. Fusion peptide insertion appears to be irreversible, possibly due to aggregation of the peptides at higher temperatures. With the equilibrium fluorescence signals characterized, time-resolved temperature-jump fluorescence spectroscopy could be used to visualize the timescale of insertion for each FP variant. Resolving the temporal and spatial details of FP insertion could eventually provide a way to target all influenza serotypes.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 3 A
Presentation/Poster Number: 2
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating the presence of premature ovarian insufficiency in a galactose-1-phosphate uridylyltransferase-null rat model of classic galactosemia

Anshen, Lauren; Orloff, Danielle; Judith Fridovich-Keil

Presenter/s: Lauren Anshen and Danielle Orloff
Emory Faculty Mentor: Judith Fridovich-Keil

Classic galactosemia (CG) is a genetic disorder that results from a lack of galactose-1-phosphate uridylyltransferase (GALT), an enzyme essential for the efficient metabolism of galactose via the Leloir pathway. Detection of the disease in newborns and immediate restriction of galactose consumption can avert the acute and often-times lethal symptoms characteristic of CG. However, a majority of patients still encounter galactosemia-associated complications long-term. Premature ovarian insufficiency (POI), for instance, affects 80-90% of girls and women with CG. Our objective in this study was to determine whether the females in our GALT-null rat model of the disease exhibited ovarian insufficiency. To evaluate this, vaginal smears with saline were obtained daily from wild type and GALT-null female rats. The samples were placed on glass slides, stained with hexamethyl pararosaniline chloride, and observed under a light microscope to establish the stage of the estrous cycle based on the cell types present. If a female rat was in the proestrus phase, based on the presence of mostly nucleated epithelial cells, it was paired with a male overnight for breeding. Insemination was confirmed by obtaining a vaginal smear the next day, placing it on a glass slide, staining it with Giemsa stain, and recognizing sperm under a light microscope. We observed no difference in the length of the estrous cycle between wild-type and GALT-null female rats. Moreover, the differences in length of gestation and number of pups delivered among wild-type and GALT-null rats did not differ significantly ($p=0.08$ and $p=0.55$). This suggests that if GALT-null female rats experience POI, it is subtle and does not impact reproductive ability, at least during the age range included in our study (2-7 months). Future studies could analyze age and follicle cell development in females of our GALT-null rat model to further assess their ovarian function.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 A
Presentation/Poster Number: 1
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Hygiene Hypothesis & Neoplastic T-cell Activation in Acute Lymphoblastic Leukemia

Armah, Kwame; Hamilton, Jamie; Henry, Curtis Ph.D.

Presenter/s: Kwame Armah
Emory Faculty Mentor: Curtis Henry

Introduction: The Hygiene Hypothesis posits that we live in a society that is becoming devoid of adequate pathogen exposure. Thus, our immune system becomes limited in its ability to identify pathogens and we succumb to higher rates of infection. Studies have shown that higher rates of carcinogenesis is correlated with immune disorders. Cell mediated immunity is mediated by T-cells (TC), and relies both on potent naive and memory TC responses to foreign antigens when encountered (e.g. bacterial or viral). However, cancers do not evolve from exogenous sources, rather, it manifests via mutations in our genome. Therefore, the lack of “foreign” antigens creates opportunities for immune evasion. Despite having extensive knowledge of pathogen-induced immunity, our understanding of cancer immunology is lacking. In this study, we hypothesized that pathogenic exposure is protective against leukemia development resulting from the non-specific killing of cancer cells by pathogen-specific TC. Mechanistically, we posit that “cross recognition” is mediated by the pro-apoptotic CD95/CD95L pathway.

Methods: Part 1. To define the surface expression of FasL on malignant relative to non-transformed B-cells (BC). Flow Cytometry (FC): To determine the surface expression of FasL on murine and human B-ALL cells. FC and Lionheart (live cell imaging): To determine how the CD95 pathway contributes to TC-mediated killing of B-ALL cells. Part 2. To determine how vaccinations against viral infections impact B-ALL pathogenicity using murine models. LCMV Experiments: Mice will be injected with LCMV to elicit anti-viral TC-mediated immunity. Vaccinated mice will be transplanted with B-ALL cells and survival will be monitored. We will determine the role of FAS/FASL in TC-mediated protection by treating mice with αFAS blocking antibody.

Results: We have confirmed that human B-ALL cells express CD95L but not CD95 on their cell surface.

Conclusions: Human B-ALL cells express CD95L which could be targeted by TC.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 6
Presentation/Poster Number: 2 of 6
Presentation Time: 1:30 PM to 3:00 PM
Presentation Link: https://emory.zoom.us/j/95175843929

Analyzing the Role of LCMT-1 in Granulocytes Using a Conditional LCMT-1 Knockout Mouse Model

Ashraf, Ali; Tam, Duncan; Pallas, David

Presenter/s: Ali Ashraf
Emory Faculty Mentor: David Pallas

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 A
Presentation/Poster Number: 3
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Global Trends of Populism and the Middle East

Bader, Leah; Emily, Dr. Gade

Presenter/s: Leah Bader
Emory Faculty Mentor: Emily Gade

Populist nationalism has been on the rise globally over the past 5 years, with political, economic, and cultural causes and impacts. The MENA region has a history of populism, but hasn't seen the same resurgence in populist nationalism we've seen in the US and UK. Why do certain countries turn towards populism at particular moments, while others eschew it? This study explores the rise in populism--or lack there of-- in the MENA region and the factors that make it more likely. I evaluate this question with a statistical analysis of contemporary populism in the Middle East in relation to factors that drive populism such as citizen perception of democratic power, foreign involvement, migration policy, large economic inequality, and strong ethnic divides in states. Populism has ties to societal shifts away from modern values such as political pluralism and globalism, and has been found to contribute to the erosion of democracy. The results of this study will be integral in understanding modern political trends in economic policy and international engagement in the Middle East as well as projecting the role that populist politics will play in the region.

Research Discipline: Social Sciences
Presentation Type: Oral Presentation

Session: 3
Presentation/Poster Number: 1 of 6
Presentation Time: 10:30 AM to 12:00 PM
Presentation Link: https://emory.zoom.us/j/95598055387

The importance of cholesterol metabolism in adipose-resident regulatory T cell maintenance in metabolic diseases

Bae, Jennifer; Elkins, Cody; Sivasami, Pulav; Li, Chaoran

Presenter/s: Jennifer Bae
Emory Faculty Mentor: Chaoran Li

Diet-induced obesity is associated with increased visceral adipose tissue (VAT) inflammation and reduction in anti-inflammatory VAT-resident regulatory T cells (Tregs). The reduction in these VAT Tregs is associated with symptoms of metabolic diseases, such as insulin resistance in type 2 diabetes. It has been shown that VAT Tregs exhibit down regulation of genes involved in cholesterol homeostasis under high fat diet (HFD) conditions. However, the importance of this specific pathway and the reason for VAT-Treg reduction under HFD conditions are still largely unknown. We hypothesize that knocking down this pathway through ablating SREBP2 (encoded by Srebf2 gene), the master regulator of cholesterol biosynthesis and uptake, would ultimately result in reduced VAT Treg levels in the adipose tissue. To test this hypothesis, we used a competitive transfer assay for assessing the role SREBP2 in Tregs in vivo. We first isolated Tregs from the secondary lymphoid organs of donor mice and utilized CRISPR/Cas9 technology to knock down SREBP2. We then mixed SREBP2 deficient Tregs and control cells in a 1:1 ratio before transferring them into recipient mice. 10 weeks following the transfer, we used flow cytometry to assess the accumulation of donor-derived cells in the adipose tissue and spleen of the recipient mice. Our data showed that ablation of SREBP2 significantly impaired VAT-, but not splenic donor-derived Treg accumulation. These results uncover an important role of the cholesterol homeostasis pathway in controlling VAT Treg accumulation and suggest that the disruption of this pathway during obesity might be a potential mechanism underlying the reduction of VAT Tregs.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 A
Presentation/Poster Number: 1
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Crystallization of [4Fe-4S] Dependent Enzyme YYDG

Bagal, Nithin; Blue, Tamra; Davis, Katherine

Presenter/s: Nithin Bagal
Emory Faculty Mentor: Katherine Davis

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 A
Presentation/Poster Number: 1
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Assessing Potential Cytoplasmic Decay Process Errors caused by RNA Exosome Mutations and Their Role in Producing RNA Exosomopathies Using a Yeast Mutant Model

Ball, William; Sterrett, Maria; Corbett, Anita

Presenter/s: William Ball
Emory Faculty Mentor: Anita Corbett

The RNA exosome is a conserved molecular machine found in almost all eukaryotes and is involved in RNA degradation. RNA exosomopathies are a particular group of tissue-specific diseases related to mutations of the RNA exosome. One aspect of the RNA exosome is its role in the cytoplasmic decay of mRNA. While previous research has focused on the nuclear decay of mRNA, this project focused on the RNA exosomes' role in non-stop mRNA cytoplasmic decay- degradation of mRNA lacking a stop codon needed to stop protein production. Two experiments were conducted to establish whether mutations of the RNA exosome affect its role in the cytoplasmic decay of mRNA that could then eventually leads to the RNA exosomopathy symptoms exhibited by humans. The first experiment was designed to indirectly determine cytoplasmic decays' role by measuring the growth of 3 different sets of mutant-wild type yeast cells transformed with a his3 nonstop reporter mRNA on different media at varying temperatures. The second experiment focused on developing the framework for directly measuring any potential impact mutant RNA exosomes would have by performing a western blot to determine the presence of proteins produced from nonstop mRNA transcripts. Indirectly measuring the cytoplasmic decay process through cell growth indicated that the mutant exosomes may not affect the cytoplasmic decay pathway, as it did not affect the breakdown of the nonstop mRNA transcript required for growth in environments without histidine. Future experiments will apply the proposed framework to the 3 sets of mutant-wild type yeast cells and may also extend to the RNA exosomes' role in nonsense-mediated and no-go mRNA decay. Understanding the mechanisms of how different mutations of the components of the RNA exosome cause symptoms in humans could lead to potential treatments of these illnesses in the future.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 A
Presentation/Poster Number: 3
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Determining the Streptomycin resistance of honeybee gut bacteria found in strawberry and apple fields

Balu, Tara; Avila-Segura, Laura

Presenter/s: Tara Balu
Emory Faculty Mentor: Laura Avila-Segura

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 A
Presentation/Poster Number: 2
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Framing Shadows: Analyzing the visual narratives of a forgotten population in America

Wallace-Sanders, Kimberly; Banks, Nikea.

Presenter/s: Nikea Banks
Emory Faculty Mentor: Kimberly Wallace-Sanders

Abstract not available.

Research Discipline: Humanities
Presentation Type: Poster Presentation

Session: 3 A
Presentation/Poster Number: 3
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Response Time is Not a More Sensitive Metric than Raw Score on the Boston Naming Test in Medial Temporal Lobe Epilepsy

Bansal, Aastha; Hewitt, Kelsey C.; Drane, Daniel L.

Presenter/s: Aastha Bansal
Emory Faculty Mentor: Daniel Drane

Visual naming of man-made objects, typically using the quantitative score of the Boston Naming Test (BNT), is a central metric for evaluating function of epilepsy surgical candidates and post-surgical cognitive outcome. However, evidence from related patient cohorts suggest response time (RT) may be a more sensitive metric. Therefore, we examined whether BNT RT is superior to raw score for confirming seizure lateralization and post-surgical decline with regards to type of surgical procedure [open resection (OR) versus stereotactic laser amygdalohippocampotomy (SLAH)]. We examined patients with medial temporal lobe (MTL) epilepsy determined through presurgical evaluation at Emory University (37 left MTL, 43 right MTL), along with 16 healthy controls. We used one-way ANOVA analyses to determine if RT distinguished between groups. We classified individual post-surgical BNT performance using reliable change indices, and compared proportion of decline for each metric by surgery type and side using Fischer's exact tests. The left MTL group performed significantly worse than the right MTL and control groups on presurgical BNT raw score [F(2, 96)=10.1, p<.001], while right MTL and controls did not significantly differ from one another. Left and right MTL cases performed worse than controls on RT, but did not differ from one another [F(2, 96)=5.3, p=.007]. Post-surgically, no right MTL cases declined on raw score. However, left OR cases showed a greater rate of decline on BNT raw score than left SLAH cases (55.45% versus 4.76%) and all right MTL cases (p<.001). Surgical groups did not differ from one another on change in BNT RT (p=.685). BNT response time is not a more sensitive metric than raw score for confirming presurgical seizure lateralization and post-surgical decline. This may confirm that the BNT should primarily focus on raw score and is deserving of further exploration of potential intervening causes, such as medications.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 A
Presentation/Poster Number: 2
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Developing Surgical Protocol for Implantation of Arrays to Measure Single Motor Unit EMG Recordings

Barquet Arrambide, Eduardo; Chung, Bryce; Sober, Sam

Presenter/s: Eduardo Barquet Arrambide
Emory Faculty Mentor: Sam Sober

In order to better understand how the brain controls complex motor behaviors, the ability to measure muscle activity (electromyograms, EMG) is essential as they are the output of the motor system. When developing a method to implant a recording device it is important that the recording devices can record single motor unit EMG data without being susceptible to in vivo deterioration over time. Another key factor is that the device is flexible so that it can record EMG during behavior with minimal interference from movement artifacts. The goal of this project is to develop an implantation method that can later be used by various researchers to study various neural diseases in vivo.

Using a high density flexible multielectrode array made of a flexible polymer, multiple single motor units are recorded in an awake mouse on a running wheel. The implantable device has 32 contacts across four arrays with 8 contacts that span subcutaneously along a mouse's forelimb. The arrays can be sutured both superficially or intramuscularly to maintain physical contact with the desired locus of the muscle.

The procedure was developed to maximize the welfare of the animal, the quality of the EMG signal, and the duration of the electrodes implanted within the animal. Impedance measurements were taken to analyze the progression of the implantation. After in vivo recordings, the arrays were recovered to study their condition.

This surgical protocol and implantation of these devices allows for the recordings of single motor unit EMG data. With this method, various motor diseases, such as dystonia, can be studied at a functional circuit level. This also opens the door for similar studies to occur with other model systems as the surgical protocols and devices can be modified to have a similar use in different species.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 A
Presentation/Poster Number: 4
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effects of Various Farming Techniques on the Degradation of DDT using Gas Chromatography- tandem Mass Spectrometry

Barr, Kathryn; Saikawa, Eri; Barr, Dana; Panuwet, Prinn

Presenter/s: Kathryn Barr
Emory Faculty Mentor: Eri Saikawa

p,p'-Dichlorodiphenyltrichloroethane (DDT) was a popular pesticide in the mid 20th century for commercial crop and livestock production. DDT remains in the environment for decades as either the original compound or its dechlorinated environmental metabolites p,p'-dichlorodiphenyldichloroethylene (DDE) and p,p'-dichlorodiphenyldichloroethane (DDD) which can bioaccumulate and translocate. Many studies have correlated these compounds (collectively referred to as DDX) with human health and environmental effects. DDX are xenobiotics that can disturb endocrine function resulting in infertility, pre-mature births, delayed sexual development, and other hormone-mediated effects in wildlife. Several studies have reported that the rate of degradation of DDT into its metabolites is affected by various farming techniques like tillage, irrigation techniques, and fertilizers. Historical cotton farm soils likely have more DDX residue than the other soils because cotton farming uses 16% of all the insecticides, including historical use of DDT, worldwide. Georgia has been one of the major producers of cotton since the 19th century, thus is likely to have high levels of DDX. Therefore, in this study, we aimed to determine if different farming techniques affect the decomposition of DDT in north Georgia farms that historically grew cotton. In this study, several Walton County farms were sampled for soil. The history of the land was recorded, and the soil levels of DDX were measured using gas chromatography-tandem mass spectrometry. Preliminary data demonstrate measurable levels of DDX in cotton farm soils with highly irrigated soils having slightly lower levels. Levels of DDE ranged from 45-132 pg/g with a median value of 97 pg/g with a 100% frequency of detection. DDT was less frequently detected but the DDT:DDE ratio suggested historic, not recent, use. Our data suggest a need to further research the effect of farming techniques on the degradation of DDT on farms that historically grew cotton.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 A
Presentation/Poster Number: 2
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Soil Nematode Extraction- An Educational Project for K-12 Students

Beckles, Delvonae; Vega, Nic

Presenter/s: Delvonae Beckles
Emory Faculty Mentor: Nic Vega

Soil nematodes are the most abundant animal on earth, and most people have no idea of the diversity and abundance of microscopic nematodes that literally surround them. This project was designed to create an educational science tool for K-12 students using the Ecological Society of America's T4EE framework for ecological education, to introduce children to the secret world of soil nematodes while providing an early introduction to ideas fundamental to modern biology. The primary learning objectives for this tool are focused on (1) diversity in the natural world, (2) ecosystem functions and how they are carried out by living things, and (3) the practice of science, how and why sampling is used. A secondary goal is that students who go through this activity will have a better understanding of soil nematodes and their importance to science and the world.

We developed a hands-on activity using a simplified version of the Baermann Funnel Method for soil nematode isolation, using materials that can be found at hardware stores and a modified protocol appropriate for children 5-16 (with age-appropriate variations). A mock trial was completed by a PhD student, a lab manager, and an undergraduate student, who were all able to easily understand and follow the protocol, and who provided feedback for revisions. We are in the process of writing an educational guide about nematodes to accompany the activity. Once the draft guide is completed, we will test the activity with middle school students to improve the material for this age group.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 A
Presentation/Poster Number: 1
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Quantification of Sympathetic Nervous System Receptors at the Nerve Muscle interphase.

Bell, Xavier; Ward, Jill

Presenter/s: Xavier Bell
Emory Faculty Mentor: Jill Ward

The sympathetic nervous system (SNS), a component of the autonomic nervous system, and its innervative processes modulate a wide array of bodily functions. Recently, as of 2016, it was revealed that sympathetic axons work in concert with, and directly contact neuromuscular junctions, highly specialized nerve muscle synapses. Within the neuromuscular junction, the SNS signals through β-2 adrenergic receptors (β2AR). This is of significance as the incoming sympathetic inputs from these β2ARs are vital in synapse maintenance, yet the extent of their function remains unknown. In this study, through the examination of medial/lateral gastrocnemius muscles of transgenic mice models, we visualized β2AR through immunohistochemical and confocal microscopy methods, and results characterized the density of these receptors at neuromuscular junctions. Further research aims to examine the role of β2AR in neural injury models and the effects of locomotor exercise on the density of these receptors at synaptic sites. Such findings and further implications would stimulate crucial ideas regarding the mechanisms activity-based therapies for promoting recovery for adult patients with spinal cord injuries or peripheral nerve transections.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 A
Presentation/Poster Number: 3
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

A Personal Reflection on the Connections Between Bipolar Disorder and Creativity

Bereaud, Sophia; Christle, Heather

Presenter/s: Sophia Bereaud
Emory Faculty Mentor: Heather Christle

I have used the SURE Affiliate program as an opportunity to conduct an inquiry into the relationship between creativity and mental illness, specifically bipolar disorder and the characteristic features of the manic phase of the illness. The possibility of a linkage between the two is highly contested among researchers, although statistical evidence points to far higher prevalence of the illness among artistic populations compared to general samples, and many of the symptoms of hypomania strikingly resemble the characteristics of creative states of mind. However, no study has managed to associate a particular neurological function with both creative faculty and bipolar disorder, in part because the concept of creativity is difficult to authoritatively define and quantify.

My work is one of creative nonfiction rather than psychiatric research. The purpose of the project is not to opine in one direction or another on this complex question, but to explore anecdotally the role of bipolar disorder in my own life and in the creative lives of a few prominent artists. The thrust of my writing lies in the retelling of a manic episode of my own, which was imbued with sudden creative aspirations. I supplement this writing with a laywoman's review of psychiatric literature and an archival exploration of the creative lives of playwright August Strindberg and novelist Virginia Woolf, artists known to have lived with bipolar disorder. I aim to convey the emotional scope of the illness, engrossing the reader in a retelling of a phenomenon with which many may be completely unfamiliar. Readers should emerge with a more nuanced understanding of the multifaceted - rather than unilaterally negative - experiences of those with bipolar disorder. This project is itself a work of art, one which I hope will be a credit to the writer and moving to the reader.

Research Discipline: Arts and Creative Expression
Presentation Type: Oral Presentation

Session: 3
Presentation/Poster Number: 2 of 6
Presentation Time: 10:30 AM to 12:00 PM
Presentation Link: https://emory.zoom.us/j/95598055387

Evaluating the Effectiveness of a Novel Paradigm for Investigating Social Decision-Making and Social Motivation Behavior in Mice

Bhatta, Manish; Murugan, Malavika; Schappaugh, Nick

Presenter/s: Manish Bhatta
Emory Faculty Mentor: Malavika Murugan

Social decision-making behavior makes up a large part of an individual's day-to-day choices. For instance, the decisions of when and how much to interact with others and choosing between social interaction and other behaviors such as eating, all play a role in social decision-making behavior. Therefore, it is useful to study social decision-making behavior in animals and determine the neural correlates associated with it. The goal of this project was to evaluate the effectiveness of a two-choice behavioral assay as a method of studying factors that affect social-decision making behavior and motivation in mice. This project was carried out with three stages of training to prepare for the two-choice assay in which mice learned to associate poking of two ports with a sucrose water reward (10 µL) and a social reward (20 seconds of social interaction through a gate with a same-sex novel conspecific mouse). The two-choice assay was tested in one-hour sessions in which the number of successful social and water pokes, choice latency, and reward latency were recorded. The behavior was studied under various factors including full water access, partial water (500 µL prior to session start), water deprivation, social isolation, and random reward. As expected, the primary results showed that under full water access, successful pokes and reward latency were similar for both the social and sucrose reward, while under water deprivation the number of sucrose pokes was significantly higher with lower reward latency. Results on partial water, social isolation, and random reward also indicated that the paradigm worked. These findings allow us to conclude that the two-choice behavioral assay is an effective paradigm for investigating social-decision making and social motivation behavior and identifying potential neural correlates. This research provides meaningful insight onto the development and intervention of social relations, cognition, and social psychological disorders.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 B
Presentation/Poster Number: 5
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Understanding How Unilateral Optogenetic Manipulation of Thalamus Inputs to the Motor Cortex Affect Directional Movement Initiation in Mice

Bian, Yuyang; Song, Joseph; Su, Li; Jaeger, Dieter

Presenter/s: Yuyang Bian
Emory Faculty Mentor: Dieter Jaeger

The cortico-basal ganglia-thalamo-cortical (CBGTC) loop is a neural circuit system in the brain with particular importance to action selection and movement. Previous studies have explored how the CBGTC loop regulates motor learning and habit formation in the cortex, striatum, and basal ganglia. This project examines how optogenetic stimulation of thalamic inputs impact the motor cortex's action selection. A hypothesis is that stimulating input in one hemisphere of the brain will cause the mouse to turn to the opposite side of the maze in a left/right decision-making task.

Following an Emory IACUC approved protocol, head-fixed 6 month-old Td Tom male mice (n=3) were trained to perform a cued locomotor task in a T- maze air-track setup. In each arm of the T-maze, a green LED serves as a visual cue for the mice to choose the lane that provides a water reward. The head-fixed mice are videotaped, and a machine-learning algorithm called DeepLabCut is used to analyse stride length, walking speed, reaction time latencies, and other indicators of motor trajectory.

As of 7/23/2021, the mice are capable of manipulating their environment and associating their performance with a reward. In addition, the DeepLabCut model has been trained. Tracked body parts include the nose, tail base, and four paws. These videos serve as a control state pre-intervention. Moving forward, the setup will be automated, with an Arduino microcontroller providing light cues and the reward. Programming is in progress. Once the mice are acclimated to the robotic setup, brain activity will be manipulated by activating ChannelRhodopsin-2 through optogenetic stimulation. This project will provide additional data about where this sensorimotor signal integration occurs, thus contributing to a better understanding of the communication pathway between the motor cortex and thalamus.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 A
Presentation/Poster Number: 3
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Comparing the Percent Yield of Medicinal Plant Extracts Obtained From Aqueous Decoction and Organic Maceration

Boraschi Umana, Sophia; Quave, Cassandra Leah; Caputo, Marco

Presenter/s: Sophia Boraschi Umana
Emory Faculty Mentor: Cassandra Leah Quave

Botanical remedies have often been used in medical practice and are known to contain healing properties that are highly sought after. Many plant compounds have been shown to make a great impact in anti-infective drug discovery shown through the process of extracting and analyzing these compounds to determine the efficacy of their medicinal potency. In order to extract the compounds from plants, various methods are used, including aqueous decoction and organic maceration. The objective of this experiment is to determine any difference in percent yield of the plant extracts obtained from the same plant and plant part using the decoction method versus maceration. The aqueous decoction method begins by creating a 1:10 ratio of plant material to water that is boiled, centrifuged, filtered, freeze-dried, evaporated, and collected. The organic maceration method utilizes a 1:10 ratio of plant material to 100% methanol that is left for 72 hours then filtered while retrieving the remaining solid plant material and using it to repeat the maceration process for another 72 hours. It is then freeze-dried, evaporated, and collected. The data of the extractions used in this experiment was obtained from 28 plants previously recorded in the Quave National Product Library Extract Database. A p-value of 0.004867 was produced from a paired t-test performed on the yields from decoction and maceration. The p-value demonstrates that there is a statistical significance in the difference in percent yields from the two different extraction methods since the value was less than the significance level of 0.05. The statistical difference between methods should be considered during experiments to prevent any error during the extract analysis of possible medicinal compounds. Further studies could be conducted on how different botanical parts are affected by decoction and maceration resulting in more optimized extraction methods.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 A
Presentation/Poster Number: 4
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Identification of the Critical Rvb1/2-mediated Molecular Interactions that Impact Cellular Function Using a Suppressor Genetic Screen

Bui, Johnny; Najmi, Saman M.; Ghalei, Homa

Presenter/s: Johnny Bui
Emory Faculty Mentor: Homa Ghalei

Ribosomes are essential macromolecules in all cells because they produce all cellular proteins. Ribosomes are composed of 4 ribosomal RNAs and 78 ribosomal proteins. For the ribosome to function correctly, the ribosomal RNAs must be correctly processed, folded, chemically modified, and assembled with the proteins. Ribosome assembly is a complicated process that requires the action of several assembly factors, including the essential AAA+ ATPase Rvb1/2, the heterohexameric complex of Rvb1 and Rvb2. While we know that the ATPase activity of Rvb1/2 is essential for ribosome assembly, the precise role of Rvb1/2 and its mechanism of function is unknown. To address this key knowledge gap, the Ghalei lab has introduced mutations that hamper the ATPase activity of Rvb1/2. The lab has identified a mutant yeast strain that expresses rvb2-R350A and has a cold-sensitive phenotype. My project aims to use this phenotype and perform a suppressor genetic screen to identify the critical Rvb2-mediated interactions that affect cellular function. So far, we have 13 potential candidate plasmids that need to be isolated and verified. Each plasmid encodes 5-6 genes. We, therefore, need to identify which gene in each isolated plasmid is responsible for the suppression of the cold-sensitivity phenotype of rvb2-R350A. Successful completion of this genetic screen will identify known and novel interactors of Rvb2 and aid in understanding the molecular interactions that regulate or are affected by the ATPase activity of Rvb1/2.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 A
Presentation/Poster Number: 4
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

A Structural Study of “CyClick” Peptides for Understanding Their Functionality as Inhibitors of Intracellular Protein-Protein Interactions

Buxton, Matthew; Bruce, Angele; Adebomi, Victor; Verma, Ashish; Shahin, Sophia; Raj, Monika

Presenter/s: Matthew Buxton
Emory Faculty Mentor: Monika Raj

Macrocyclic peptides are of increasing interest in the pharmaceutical industry due to their significantly greater stability, potency, and cell permeability compared to linear peptides. Macrocyclic peptides are also able to specifically disrupt protein-protein interactions (PPIs) that are inaccessible to small-molecule ligands, a property that is crucial for the development of novel therapeutics. However, these peptides can be very difficult to synthesize in the lab due to an unfavorable entropy change. Current methods of peptide cyclization often result in issues such as cyclo-oligomerization, C-terminal epimerization, and dimers and trimers forming. Our lab has recently reported the “CyClick” strategy for the macrocyclization of peptides which precedes via a solely intramolecular reaction between the peptide N-terminus and a C-terminal aldehyde. The cyclization facilitates the formation of a stable 4-imidazolidinone-fused cyclic peptide by internally directing the activation of the amide bond adjacent to the N-terminus. The conformational study on a seven amino acid-long “CyClick” peptide showed the formation of a turn structure. This is promising as a turn structure can mimic the interface of PPIs thus has a potential to act as an inhibitor of PPIs. Furthermore, preliminary data has shown that some of these “CyClick” macrocycles are highly cell permeable, a feature believed to be influenced by the intramolecular hydrogen bonding caused by secondary structures. Expanding upon former studies, this project is aimed at investigating if this turn-like structure is present in “CyClick” peptides of varying sequences and ring sizes–specifically peptides of 10 and 12 amino acid lengths. The data collected from 1H and ROESY NMR experiments will provide key information on dihedral angles and interproton distances that will be used to computationally model the overall structure.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 A
Presentation/Poster Number: 4
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Compatibility of Primary Amines in C-H Functionalization Catalyzed by Dirhodium Catalysts

Cai, Anna; Davies, Huw.

Presenter/s: Anna (Qinyan) Cai
Emory Faculty Mentor: Huw Davies

Functional groups play a crucial role in the modification and synthesis of chemical structures, while C-H bonds are conventionally known as stable and “unchangeable” groups. However, with rapid development in C-H functionalization by which a C-H bond is formed or broken, “unreactive” C-H bonds start to play a significant role in organic synthesis. The Davies group employs catalyst-controlled methods for the selective functionalization of C-H bonds. In other words, a particular C-H bond can be selected to react by using a matched catalyst. Rh2(2-Cl-5-BrTPCP)4 is a catalyst that selectively reacts with the unactivated site over the activated site stabilized by benzylic group. This key finding encourages further studies to determine the compatibility of the C-H functionalization to other functional groups, like carbonyls, amines, and alkenes. For this study, we focus on the compatibility of primary amines (NH2) which are often too reactive to allow C-H functionalization to occur elsewhere in the molecule. In the first phase, three effective protecting groups for these amines were found. They were tested and shown to perform C-H insertion with high selectivity. In the second phase, the three protecting groups were installed in more complex primary amines. These protected amines, in reactions catalyzed by the corresponding rhodium catalysts, were shown to be able to C-H insertions. Though more substrates need to be screened, these results demonstrate that reactions can be conducted at less reactive sites, like C-H bonds, and can be compatible with amines. It enriches the methods available to synthesize cores of pharmaceutical structures.

Research Discipline: Natural and Physical Sciences
Presentation Type: Oral Presentation

Session: 7
Presentation/Poster Number: 1 of 6
Presentation Time: 3:00 PM to 4:30 PM
Presentation Link: https://emory.zoom.us/j/97807604820

Characterizing DNA Supercoiling with Permanent and Electromagnetic Tweezers

Cartee, Allison; Doan, Jessie; Piccolo, Joseph; Dunlap, David; Finzi, Laura

Presenter/s: Allison Cartee
Emory Faculty Mentor: Laura Finzi

Deoxyribonucleic acids (DNAs) and their processes are the foundation for all cellular life. The replication of DNA followed by its transcription into RNA and translation into proteins, known as the central dogma of biology, is a heavily regulated, physical process. Much of this genetic regulation is related to DNA conformation, and more specifically the twist in the DNA molecule. Twist in DNA, defined as rotationally fixing one end of the molecule while applying torque along its longitudinal axis, influences looping behavior. DNA's physical properties lending to its rotational mechanics help regulate gene expression and epigenetics. Twisting DNA, also known as supercoiling, induces looping in the form of plectonemes. The formation of these plectonemes reduces the end-to-end DNA distance, a phenomenon measurable via magnetic tweezer (MT) microscopy. In these studies, one end of DNA is immobilized to glass while the other is attached to a micron-scale paramagnetic bead, forming a tether. When a spinning magnetic field is applied, the beads and thus the DNA are twisted via magnetic forces. We compared two different methods to generate this magnetic field. The first being a standard magnetic tweezer that uses a dynamic permanent magnet while the second uses solid-state electromagnets. This study seeks to characterize DNA's physical properties and compare the efficacy between the two methods using a custom DNA construct approximately 2,500 base pairs long. Twisting constructs under both methods produced similar hat curves, indicating both methods of generating magnetic forces successfully supercoiled DNA. Extensive characterization of these instruments will serve to standardize further studies of DNA mechanics using various transcription factors, polymerases, other nucleotides like diamino purine and or inosine. Potential applications include stabilizing DNA-based vaccines and understanding gene expression and epigenetics.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 B
Presentation/Poster Number: 5
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Comparing Yields of Different Methods of Chemical Compound Extraction from Plants

Cavagna, Isabella; Quave, Cassandra; Caputo, Marco;

Presenter/s: Isabella Cavagna
Emory Faculty Mentor: Cassandra Quave

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 B
Presentation/Poster Number: 6
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effectiveness of Parent Interventions on Parental Self Efficacy

Ceballos, Alex; McCarthy, Luke; Goodman, Dr. Sherryl

Presenter/s: Alex Ceballos
Emory Faculty Mentor: Sherryl Goodman

Abstract not available.

Research Discipline: Humanities
Presentation Type: Oral Presentation

Session: 4
Presentation/Poster Number: 1 of 5
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99643683271

Associated Demographic Categories: Implicit Links to Race, Gender, and Age

Chan, Cherice; Hall, Erika

Presenter/s: Cherice Chan
Emory Faculty Mentor: Erika Hall

Employees often encounter bias in the workplace due to their membership in certain stigmatizing demographic groups (e.g., Asian, gay). We argue that bias can arise even when an employee is not a member of a particular stigmatized group, because when one demographic group is noted (e.g., Black), another demographic group may be easily assumed (e.g., working class). In the current work, we investigate Associated Demographic Categories, defined as specific demographic categories that have an implicit cognitive link to one or more other demographic categories. To identify which categories are linked, we recruited 725 participants from Prolific and presented them with a fictional character's biographical information, manipulating either the character's race, gender, or age. Participants wrote a short story about the character and then completed a questionnaire about their character's demographics. We found that gender, socioeconomic status, and religion were significantly associated with race. Black characters were more likely assumed to be men and Asian characters were more likely assumed to be women. Race also influenced expectations about socioeconomic status. Asian characters were more likely to be categorized as upper-class and upper-middle class, whereas Black characters were more likely to be categorized as working class and lower class. Lastly, race influenced assigned religious affiliations: Asian characters were more likely to be Buddhist and Black characters were more likely to be Christian. Additionally, we found that sexual orientation and age was significantly related to gender. While both male and female characters were more likely to be straight overall, female characters were more likely to be non-heterosexual. On average, female characters were younger than male characters. These results provide evidence that demographic categories are intricately linked to one another: one category influences cognitions about another. Identifying these associated demographic categories can help predict the stereotypes that create biased interpersonal evaluations in the workplace.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 7 A
Presentation/Poster Number: 4
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Optimizing Tetracycline Systems through Directed Mutagenesis

Chen, Microl; Lee, Benjamin P.; Cooper, Garrett W.; Mittal, Karuna; Hong, Andrew L.

Presenter/s: Microl Chen
Emory Faculty Mentor: Andy Hong

A similar abstract was submitted as part of the NIDDK STEP-UP program.

Tetracycline inducible vectors are an integral tool in functional genomics. These lentiviral vectors are routinely used to regulate gene expression through the tetracycline response element (TRE) promoter and reverse tetracycline transactivator (rtTA). Although this system allows for target gene transcription, it has a tendency to initiate transcription in the absence of the intended catalyst (e.g. tetracycline). This leads to genes being expressed at inappropriate levels (e.g. leakiness); causing problems within experimental models that require precision such as the chromatin modifying gene and SWI/SNF complex member, SMARCB1.

Studies have shown that replacing glycine with different amino acids within rtTA at residue 72 could suppress this tendency for unintended transcription. We assessed a lentiviral Tet-ON vector harboring SMARCB1, and introduced G72V, G72A, and G72P mutations in its rtTA region using site directed mutagenesis and transduced the mutants carrying SMARCB1 into SMARCB1-deficient cells. Following this, we examined the expression of SMARCB1 at the transcriptional level using qRT-PCR and protein level with immunoblotting. We further examined aspects like viability and growth to determine how our mutations have affected the functional effects of SMARCB1 re-expression.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 A
Presentation/Poster Number: 3
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Uncovering the Visual Features Relevant for Human Visual Scene Recognition

Chen, Zirui; Cheng, Ruu Harn; Dilks, Daniel

Presenter/s: Zirui Chen
Emory Faculty Mentor: Daniel Dilks

Humans are incredibly good at recognizing “scenes” (e.g., recognizing an image as a kitchen, and not a beach). However, it remains unknown what are the precise stimulus features that humans use for scene recognition. Ongoing research in the lab has alluded to the global color of a scene image as a potential stimulus feature that humans use to differentiate different scenes; thus, in this study, I directly tested the role of global color for behavioral scene recognition. Specifically, I hypothesize that if global color is a stimulus feature that humans use for scene recognition, then participants will categorize scene images based on the similarity in the global color of the scene images.
To test my hypothesis, I collected a set of scene images that are highly variable in global color (e.g., a forest full of red versus green leaves, a house with white versus red walls). Participants (N=50) were shown these scene images two at a time and asked to determine the similarity between these images on a sliding scale from completely different to completely identical. We also included the grayscale versions of the same, exact scene images, as well as a separate set of object images (in both color and grayscale versions) as control comparisons. We found that participants show different similarity judgements for the color versus grayscale version of the same, exact scene images, but not for the color versus grayscale object images. Moreover, participants also rated scene images with similar global color to be more similar, but not for object images. Together, these results suggest that the global color of a scene image is a stimulus feature that human selectively use for scene recognition.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 B
Presentation/Poster Number: 6
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

YB-1 is a Potential Therapeutic Target for Mediating Treatment Resistance in Sonic Hedgehog Medulloblastoma

Chen, Victor; McSwain, Leon; Kenney, Anna

Presenter/s: Victor Chen
Emory Faculty Mentor: Anna Kenney

Medulloblastoma (MB) is a pediatric malignancy of the brain that accounts for about 20% of all childhood brain tumors. The Sonic hedgehog (SHH) subgroup of MB, which is characterized by tumor development via perturbations in the SHH signaling pathway, accounts for 30% of MB cases. Current treatment options for SHH-driven MB are limited to harsh irradiation and cytotoxic therapies that can cause long-term detriments to pediatric patients. Our research investigates therapeutic targets that can molecularly sensitize these tumor cells to irradiation treatments. The primary focus of our project is Y-box-binding-protein 1 (YB-1), a regulatory protein that is implicated in the DNA damage response. Recent data from our group has demonstrated elevated YB-1 in primary MB cells, denoting a role in driving irradiation resistance and tumor death evasion. In this study, we measure the effects of modulating YB-1 activity on DNA damage accumulation and epigenetic regulation. Our results suggest a potential mechanism by which YB-1 facilitates treatment resistance. Future studies will further elucidate this mechanism and test the viability of targeting YB-1 for clinical application.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 B
Presentation/Poster Number: 5
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Chromodomain-Helicase-DNA Binding 5 promotes DNA end resection to facilitate homologous recombination mediated repair of DNA double strand breaks

Chen, Linda; Rath, Sandip Kumar; Yu, David

Presenter/s: Linda Chen
Emory Faculty Mentor: David Yu

Cells are constantly exposed to endogenous and exogenous agents that induce DNA damage including DNA double strand break (DSB), which aids in progression of cancer by fostering genomic instability. Ongoing studies have highlighted chromatin remodelers as new guardians of genomic stability. The chromodomain-helicase-DNA binding (CHD) proteins belong to the largest family of chromatin remodelers. Most proteins of this family are well characterized for their involvement in DNA damage and repair (DDR) responses. However, CHD5 involvement in DDR remains unclear. Previous studies from our group demonstrate that loss of CHD5 results in spontaneous induction of DNA DSBs in cancer cells. While these findings suggest a potential involvement of CHD5 in DDR response, the role and mechanism of it are yet to be explored. Ongoing studies in the lab using DNA repair reporter constructs have shown that loss of CHD5 impairs homologous recombination (HR) mediated DNA repair efficacy. DNA end resection is a key step in HR repair responses. Therefore, we hypothesize that the impaired HR efficacy upon CHD5 knockdown is linked with decreased DNA end resection. To investigate this, we studied the recruitment of carboxy-terminal binding protein interacting protein (CtIP), a key DNA end resection factor and ATR-interacting protein (ATRIP), a downstream factor in HR at laser induced DNA DSBs in the presence or absence of CHD5. Our result demonstrates that in the absence of CHD5, recruitment of both CtIP and ATRIP at the break sites were significantly impaired. This suggests that CHD5 is involved in HR mediated DDR by facilitating recruitment of DNA end resection factors. This pathway can be therapeutically exploited for novel drug targeting in a subset of cancer cells.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 B
Presentation/Poster Number: 5
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Correlation of Gene Expression of Secreted Cellular Factors and Their Receptors with Immune Cell Markers in Head and Neck Cancer using TCGA Data

Chen, Jianze; Chen, Nelson; Chen, Georgia

Presenter/s: Jianze Chen
Emory Faculty Mentor: Georgia Chen

Head and neck cancer is diagnosed worldwide and is responsible for 430,000 deaths globally per year. Due to development of immune therapy, regulation of head and neck cancer progression by immune system has been a research focus in recent years. However, the interactions between immune regulatory cells and certain secrete cellular factors, such as chemokines/cytokines, are still poorly understood. Using the cancer genome atlas (TCGA) database, this project seeks to identify possible relationships between secreted cellular factors and immune cell markers such as CD3 (T cell), CD4 (T cell), CD8 (toxic T-cell), FOXP3 (Treg cell), and CD163 (tumor associate macrophage) in head and neck cancer. In order to do this, RNA seq data from the TCGA was gathered and a pearson test was used to find possible significant correlations between certain immune markers and the secreted cellular factors and their receptors. The significant correlations between these proteins and Treg marker to toxic T cell marker ratio was also obtained. Afterwards, survival data was gathered by Kaplan-Meier analysis to see how certain levels of secreted cellular proteins would affect patient's survival. For the correlation between immune markers and secreted cellular proteins many significant associations were found, suggesting that tumor immunity was heavily regulated by signals from these secreted proteins. In addition, a high Treg to CD8 positive T cell suggested immunosuppression, which may also be largely regulated by certain secreted proteins. Lastly, survival curves indicated that IGF2BP2, TNFRSF4, IFNG expression levels affected overall survival and progression free survival significantly. Low levels of IFNG resulted in worse survival; high levels of IGF2BP2 resulted in worse survival as did TNFRSF4. These immune markers are important as they give a clue to what proteins should have prognosis values and deserve to be studied in the future.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 B
Presentation/Poster Number: 6
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Observation of Brownian motion of dusty plasma suspended in a strong magnetic field

Cho, Jonathan; Burton, Justin; Yu, Wentao

Presenter/s: Jonathan Cho
Emory Faculty Mentor: Justin Burton

A whirlpool is a phenomenon in which a body of fluid is spinning in a circular fashion. The traits of whirlpool can be observed by dropping colored balls within the whirlpool and watch how the balls react over time. Similarly, the vortex produced by a magnetic field can be characterized by observing ionized dust particles suspended in air above a strong magnetic influence. We used this method of observation to be able to predict the Brownian motion of in both single particle and multi-particle systems using a machine learning model. We dropped equally sized spherical dust particles inside a vacuum chamber which contains a strong magnet and a charged plate. Using the weight of particles, we suspended the particles in midair by ionizing the particles such that their movements are confined within a two-dimensional plane and observed their behaviors using a camera and a laser. We produced an equation that describes the general behavior of the motion of the particles and can simulate dusty particle experiments. By observing and being able to predict particle motion influenced by electromagnetic factors, we envision relevant applications with observing dust cloud migrations on Earth and extraterrestrial gaseous bodies.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 4 B
Presentation/Poster Number: 5
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The effect of context versus sequence in the localization of transcription factors to similar cis elements throughout the genome.

Cho, Dabin; Hodkinson, Lauren; Rieder, Leila.

Presenter/s: Dabin Cho
Emory Faculty Mentor: Leila Rieder

Within the Drosophila melanogaster genome, transcription factors bind many similar cis elements throughout the genome but are able to perform unique functions at these different loci. Despite showing sequence similarity, the context around where cis elements are located can contribute to the difference in functionality of these transcription factors. At the Drosophila histone locus, an important cis element consisting of GA-repeats is found in the bidirectional promoter of histone genes 3 and 4. These GA-repeats are bound by a transcription factor called CLAMP which helps recruit the factors that make up the histone locus body (HLB) and to initiate histone gene transcription. On the X chromosome, CLAMP also binds to GA-rich sequences but, in this context, recruits the MSL complex to allow for dosage compensation. The extent to which cis element sequence versus the context around these cis elements informs CLMAP on where to bind and what factors to recruit at it's different binding sites is still unknown. We hypothesize that the context near where the cis element is located is propagating the recruitment of the specific factors related to the site. Therefore, we expect GA-rich cis elements within a histone locus recruit HLB factors whereas GA-rich cis elements within an X-Chromosome context to recruit MSL components. To test this hypothesis, seven transgenes are currently being constructed to contain GA-rich cis elements in either a histone locus context or an X chromosome context. Once these transgenes have been integrated into the fly genome, polytene chromosome immunostaining for MSL proteins and a HLB specific factor, Mxc, will be used to understand how the different contexts of each GA-rich cis element impacted transcription factor recruitment.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 B
Presentation/Poster Number: 7
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Immunostaining of TBX-18 gene-induced 3D cardiac pacemaker microtissue treated with TGF-Beta inhibitor shows less aSMA expression level.

Chung, Mingee; Kim, Tae Yun; Cho, Hee Cheol

Presenter/s: Mingee Chung
Emory Faculty Mentor: Hee Cheol Cho

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 6
Presentation/Poster Number: 3 of 6
Presentation Time: 1:30 PM to 3:00 PM
Presentation Link: https://emory.zoom.us/j/95175843929

Detecting Motif Biomarkers in Brain Networks

Dalamal, Dheep; Yang, Carl

Presenter/s: Dheep Dalamal
Emory Faculty Mentor: Carl Yang

Finding Motif-Based Biomarkers of Disease in Brain Networks

The goal of our project is to find certain patterns in brain networks that could indicate if a person is diseased. More specifically, we are looking for differences in substructures (called motifs) between the brains of diseased and non-diseased individuals. Successfully identifying markers of disease could help healthcare professionals investigate whether patients have this disease at an early stage, and offer more effective treatment.

We have datasets of brain networks represented as graphs (a data representation in computer science), and each graph is labelled as diseased or not diseased. We currently have datasets for Bipolar and HIV. For every possible motif of a given size, we obtain average counts for the diseased networks and non-diseased networks. If there is a statistically significant difference in average number of a specific motif between both groups, this motif's count could be a biomarker of disease.

We are still in the process of finding motif counts, but we will use statistical tests to find if motif differences are significant. If a significant difference is found, this could help indicate if a person has a disease at an earlier stage, which could benefit treatment. We also plan to sample only motifs that are present in brain networks to reduce our algorithm’s runtime and improve its accuracy. For further planned work, we aim to devise a motif-based method to classify brain networks into diseased and not diseased.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 B
Presentation/Poster Number: 7
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Measuring Cerebrovascular Reactivity in a Mouse Model of Alzheimer's Disease Via Diffuse Correlation Spectroscopy

Christy Daniel; Rowan Brothers; Erin Buckley

Presenter/s: Christy Daniel
Emory Faculty Mentor: Erin Buckley

Repetitive mild traumatic brain injury (mTBI) is associated with a higher risk of Alzheimer's Disease (AD) and other neurodegenerative diseases. Cerebrovascular reactivity (CVR), the ability of cerebral vessels to dilate or constrict in response to vasoactive stimuli, is a potential biomarker of AD pathology after rmTBI. Impaired CVR has been associated with worse outcome post-rmTBI and mild cases of AD. The goals of this pre-clinical project are to determine if CVR impairments after repetitive mTBI are associated with development of AD-like pathology in a mouse model of AD (3xTg). CVR will be measured with intraperitoneal administration of acetazolamide, a potent vasodilator. Diffuse correlation spectroscopy will be used to assess the cerebral blood flow response to acetazolamide. Measurements will be made in N=X male and female 3xTg mice by attaching a minimally invasive sensor to the skull to measure cerebrovascular reactivity. To date, we have constructed the DCS sensor that will be used for these measurements. Future work will quantify the repeatability of CVR measurements in 3xTg mice. Further, we will employ a well-established repetitive mTBI model to quantify longitudinal changes in CVR and we will correlate CVR with the development of amyloid beta and tau at 1 month post-injury. The findings from this study are expected to provide insight in the relationship between mild traumatic brain injuries, impaired cerebrovascular reactivity, and Alzheimer's Disease pathology in transgenic mice.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 A
Presentation/Poster Number: 4
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Shape-driven interlocking of triangular particles

Datta, Swagata; Weeks, Eric

Presenter/s: Swagata Datta
Emory Faculty Mentor: Eric Weeks

We look at how triangular hard particles with notches cut at their sides arrange themselves under shaking. Self-assembly of particles is of great interest because of the insight it provides on building nanoparticle or colloidal systems. Moore et al. used simulations to show that interlocking triangles can form large hexagonal structures due to entropy maximization. This requires the presence of rectangular guest particles which become trapped inside the hexagons. In our experiment, the triangles and rectangles, called the host and guest particles respectively, were obtained by laser-cutting acrylic plastic. The particles lie over a flat horizontal surface which is shaken by a DC motor, giving us a quasi-2D-experiment. The experiment involves taking video of the evolution of system over a period of ten minutes from different initial phases. The video analysis is automated where we look at how the triangles interlock and the various attributes of the structures it forms. We observe the system evolve into a stable configuration regardless of the initial phase, depending on the number and area of particles. This stable state mostly consists of a low convex area and a stable number of interlocked triangles rather than forming the aforementioned hexagonal structures. Moreover, when we start with an ideal hexagonal structure, we find that it quickly melts and reaches the same imperfect stable configuration that we find when we start from a disordered structure.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 A
Presentation/Poster Number: 2
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Synthesis of a Collagen-mimetic Peptide through the Design of a Dynamic Chemical Network

Davis, Griffin; Blake, Alexis; Young, Seth; Gordon, Christella; Lynn, David

Presenter/s: Griffin Davis
Emory Faculty Mentor: David Lynn

Collagen is the most abundant protein in the human body and its structure exhibits a great degree of versatility that plays a vital role in the survival of multicellular organisms. Strong intermolecular forces between collagen fibrils provide structural support, while the presence of interspaced flexible elements allows the overall structure to remain dynamic. Previous studies of collagen-mimetic peptides have achieved mimicry of mechanic strength but failed to capture its flexible and dynamic nature. Building on previous synthetic strategies, we aim to imitate both the structure and flexibility of natural collagen by preparing a C-terminal aldehyde tripeptide, NPG-CHO, which polymerizes via formation of metastable pyrimidinone linkages. The supramolecular assembly of NPG-CHO was found to decrease the rate of apoptosis and increase the rate of differentiation of neurons in brain organoids. Successful preparation of NPG-CHO will allow us to examine the reproducibility of previously observed supramolecular collagen assemblies and assess its adequacy as a collagen-mimetic peptide. The development of such chemistry will also provide a precedent by which other protein folding landscapes, such as that of alpha-synuclein and other intrinsically disordered proteins, may be studied.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 B
Presentation/Poster Number: 7
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The effect of Lipopolysaccharide-induced peripheral inflammation on locomotor and pain behavior of Spinal Cord Injured mice

Deng, Bowei; Parvin, Shangrila; Martin, Karmarcha; Garraway, Sandra M.

Presenter/s: Bowei Deng
Emory Faculty Mentor: Sandra M. Garraway

Neuropathic pain is common after spinal cord injury (SCI). Studies have focused on the central nervous system's effects on pain chronification, the process of transient pain advancing into persistent pain, and the expression of neuropathic pain after SCI. However, little is known about the contribution of peripheral mechanisms to pain after SCI. Low doses of lipopolysaccharide (LPS) is shown to induce a systemic inflammatory response. To explore the contribution systemic inflammation makes to pain after SCI, this study examines the effect of LPS on well-characterized pain responses after SCI.
Adult mice received a thoracic level SCI 4 hours after intraperitoneal administration of LPS (SCI-LPS, n=5) or saline (SCI-Veh, n=3). Hind-paw responses to von Frey stimulation (VF) and changes in respiratory rate (RR) were examined weekly, up to 4 weeks post-SCI. A two-chamber conditioned place aversion (CPA) paradigm was used to assess affective pain responses following mechanical stimulation of trunk skin at 4-5 weeks post-injury, and recovery of hind-paw locomotion was evaluated with the Basso Mouse Scale (BMS).
Our results showed that while both SCI-LPS and SCI-Veh mice had significantly decreased withdrawal threshold in response to VF over time (p <.0001, RM-ANOVA), there was no difference between the two groups. No significant difference in RR was found between groups, although SCI-LPS mice had decreased RR on day 1 (p <.05, t-test) and 14 (p <.01) compared to baseline. The SCI-LPS group had significantly reduced BMS at day 21 (p<0.05) and 28 (p=0.01) compared to SCI-Veh. CPA results revealed no group difference in time spent in the aversive chamber before and after stimulation; however, SCI-LPS mice had reduced number of transitions between chambers after stimulation compared to baseline (p <.05, t-test). These preliminary results suggest that whereas LPS treatment fails to exacerbate pain responses after SCI, it attenuates the recovery of locomotion.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 2
Presentation/Poster Number: 1 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/95175906316

Comparison and Visualization of Exosome Uptake in Irradiated and Non-irradiated Lung Cancer Cells (A549 Cells)

Dhabaan, Layla; Dynan, William

Presenter/s: Layla Dhabaan
Emory Faculty Mentor: William Dynan

Exosomes are extracellular vesicles secreted by cells. Their function is to deliver specific biological molecules, including DNA, lipids, and proteins. When comparing exosomes secreted by tumor cells that have and have not been exposed to therapeutic radiation, an “anti-tumor effect” is observed, through which the innate immune system is engaged. Therapy treatments require newer alternatives, so the “anti-tumor effect” can be applied to patients with non-small cell lung cancer. The goal of this study is to observe and visualize differences in exosome uptake in irradiated and non-irradiated A549 cells, which stem from a lung cancer cell line. We tested the hypothesis that exosomes are taken up more efficiently in irradiated cells. We used innovative click chemistry, which involves using molecular probes to locate and attach to targets on live cells: the dye “DBCO-Cy5” was applied to label exosomes, and thus track their uptake. We irradiated one chamber well of cells (at 10 Gy) and left another chamber well of cells non-irradiated for comparison. We fixed and observed exosome uptake 0, 2, 6, and 24 hours after radiation by fixing and extracting cells from chamber wells and inserting them onto microscope slides. To analyze exosome uptake in cells, we imaged samples on a DeltaVision microscope. We will quantify our data through “ImageJ,” a Java-based image processing program, to analyze the differences in exosome production between irradiated and non-irradiated cells. Part of my work in the lab is to learn valuable methods, including how to culture A549 cells in bulk. I successfully carried out exosome labelling and assisted another lab member by preparing a culture medium that was the source of the exosomes. By conducting experiments in an independent manner, I was geared to become self-reliant and potentially discover an alternative therapy treatment for patients with non-small cell lung cancer.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 B
Presentation/Poster Number: 8
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Social context influences vocal activity in prairie vole pups

Dharani, Ammar; Warren, Megan; Borie, Amelie; Ford, Charles; Campbell, Drayson; Young, Larry; Liu, Robert

Presenter/s: Ammar Dharani
Emory Faculty Mentor: Robert Liu

Deficits in vocal communication are hallmarks of neurodevelopmental disorders. To explore the underpinnings of these disorders, prairie voles (Microtus orchrogaster) provide a promising model, as they exhibit complex social behaviors such as biparental care for offspring and monogamous social bonds. Prairie voles also emit ultrasonic vocalizations (USVs), sounds above the range of human hearing, as a form of social communication. For instance, pups vocalize when outside the nest as a signal to elicit retrieval by their mother. Prior work in the lab indicated context-dependent changes in vocal rate when pups transitioned from isolation to a social context in which the mother was present in an adjacent but physically distinct chamber. However, the previous work could not determine whether USVs were emitted by the mother or the pup. Thus, we replicated the previous study with pups at P6, P8, P10, and P18 (n = 6-8 pups per age) using a two-microphone setup to determine which vole emitted individual vocalizations and specifically quantify pup-emitted USVs. Another potential explanation for the previous results could be the pups habituating to their environment instead of reacting to a change in social context. Therefore, we also recorded pups (n = 4-5 pups per age) that remained isolated in the arena for the entirety of the recording period without the mother being added. Our results indicate that in pups older than P6, habituation alone cannot account for the previously observed changes in vocal activity across social contexts. Additionally, when assessing vocalizations that were accurately attributed to the pup, we substantiated the previous finding that younger (P6, P8) pups vocalize more and older (P18) pups vocalize less in the presence of their mother. Our data verifies the finding that social context modifies the number of pup-emitted vocalizations, further developing the prairie vole as a model of social and vocal communication.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 A
Presentation/Poster Number: 4
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Dysregulated retinoic acid signaling in Fragile X syndrome

Dhinojwala, Maria; Raj, Nisha; Bassell, J. Gary

Presenter/s: Maria Dhinojwala
Emory Faculty Mentor: Gary Bassell

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 B
Presentation/Poster Number: 5
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Awake in-vivo Two Photon Calcium Imaging and Electrophysiological Recording of Cortical Spreading Depression in a Mouse Generalized Seizure Model

Diamond, Jake L.; Stern, Matthew A.; Berglund, Ken; Gross, Robert E.

Presenter/s: Jake Diamond
Emory Faculty Mentor: Robert Gross

Epilepsy, a disorder characterized by the occurrence of at least two unprovoked seizure events, affects roughly three million people across the United States. Despite current treatments being effective for the majority of patients, there remains a subset in whom seizures persist. Cortical spreading depression (CSD) provides an intriguing phenomenon in which researchers may gather a better understanding of factors contributing to seizure activity. Characterized by synchronous neuronal depolarization, CSD is hypothesized to be caused by disruptions in ion homeostasis and has been observed preceding, during, and following seizure events. However, a causal link between epilepsy and CSD remains unclear. It is our aim to uncover the currently ambiguous relationship of neuronal recruitment and CSD occurring amidst seizure activity. Implanted electrodes have been used to describe the summated and synchronous electrophysiology of CSD across large networks. However, these methods cannot accurately characterize the activity of individual neurons or specific neuronal subtypes. Two-photon calcium imaging (2PCI), coupled with targeted expression of genetically encoded calcium indicators (GECIs), enables in vivo recordings of such specificity and resolution. Leveraging transgenic mice with a Cre-driver localized to GABAergic neurons, we selectively expressed different color GECIs, delivered via adeno-associated viruses, in distinct neuron populations in mouse primary motor cortex. We then performed awake in-vivo 2PCI and simultaneous local field potential recordings in head-fixed mice during generalized seizures induced by the chemo-convulsant pentylenetetrazol. We collected subtype specific calcium activity of CSD in generalized seizure events. At seizure termination we observed CSD occurring in all neurons across our focal view, which suggests a possible role in seizure cessation. Through the continued study of specific neuronal subtype dynamics during CSD coincident with seizures, we hope to better characterize their relationship and in turn inform future developments of novel treatment approaches.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 A
Presentation/Poster Number: 3
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

A Structural and Mechanistic Evaluation of B12-Radical SAM Enzyme PoyC which Catalyzes Cβ-Methylation

Djafari Rouhani, Sina; Jones, Stacey; Davis, Katherine M.

Presenter/s: Sina Djafari Rouhani
Emory Faculty Mentor: Katherine Davis

B12-dependent radical S-adenosyl-methionine (rSAM) enzymes are an important class of metalloenzymes that perform unique modifications on ribosomally synthesized and post-translationally modified peptides (RiPPs). These enzymes have been implicated in the biological production of numerous health relevant compounds, such as potent antibiotics and antitumor agents, as well as bacteriochlorophyll and methane. PoyC is a B12-dependent rSAM methyltransferase that post-translationally modifies polytheonamide, a highly cytotoxic molecule that accrues approximately fifty post-translational modifications that are orchestrated by nine Poy enzymes, by catalyzing chemically challenging sequential Cβ-methyl transfer reactions. As such, a thorough understanding of the enzymatic chemistry of PoyC could make it an integral component for the enzymatic production of antimicrobials in an industrial complex. Although there is evidence for the chemical significance of PoyC, its structure and mechanism remain open questions due to the challenge of expressing copious amounts of soluble B12-rSAMs. Currently, it is believed that the inability of E. coli cells to uptake cobalamin efficiently inhibits the production of soluble protein. This study aims to use x-ray crystallography and absorption spectroscopy to obtain structural and mechanistic evidence for the role of cobalamin in the methyl transfer reaction observed by PoyC. We have been able to successfully co-express proteins responsible for cobalamin uptake in E. coli with PoyC. We are currently optimizing the purification of PoyC towards the goal of obtaining pure, native PoyC for x-ray crystallography. Collective results will be used to gain insight into the role of B12-dependent rSAM enzymes for sp3 carbon methylation, the process of methyl incorporation by the cobalamin domain, and the physiological oxidation states of the cobalamin domain.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 4 B
Presentation/Poster Number: 6
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effects of Galactose exposure on Cataract Formation in Rats across Genotypes

Druss, Jared; Wozniak, Aaron; Fridovich-Keil, Judith

Presenter/s: Jared Druss and Aaron Wozniak
Emory Faculty Mentor: Judith Fridovich-Keil

Classic galactosemia is a genetically inherited disease caused by mutations in the GALT gene, resulting in a buildup of the sugar galactose due to a deficiency of functional GALT enzymes. The inability to effectively metabolize galactose leads to numerous developmental complications in humans and rats, such as delayed growth and cataract formation. The purpose of this study was to explore the interplay between dietary galactose exposure and GALT genotype (wild type, GALT null, or heterozygous). Rats of each genotype were weaned at age 3 weeks to 5% galactose dissolved in their drinking water. At three months of age, the rats were euthanized and post-mortem images were taken of each individual rat eye. Eye photos were then scored on a scale of 0 (no cataract) to 3 (severe cataract). Data analyzed by linear mixed effects model in R produced a p-value less than 0.0001, indicating that formation of cataracts does indeed differ among genotypes. Additional analyses using estimated marginal means found no significant difference between the wild-type and heterozygous groups (p = 0.8394), highly statistically significant differences between the GALT null and heterozygous groups (p = value less than 0.0001) and between the GALT null and wild-type groups (p = value less than 0.0001). Specifically, GALT null rats displayed a higher prevalence and severity of cataracts than did either heterozygous or wild-type rats. This result is fully consistent with the autosomal recessive inheritance pattern characteristic of classic galactosemia. Of note, while no cataracts were observed in wild-type rats despite high galactose exposure, small white formations at the periphery of the iris were sometimes seen and may warrant further study.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 F
Presentation/Poster Number: 21
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Conversion of Glioblastoma Astrocytes to Neurons to Treat Neuronal Tumors

Dulam, Pranavi; Jiang, Michael; Yu, Shan Ping

Presenter/s: Pranavi Dulam
Emory Faculty Mentor: Shan Ping Yu

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 B
Presentation/Poster Number: 8
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Bioluminescent optogenetics to enhance recovery from peripheral nerve injury

Ecanow, Anna; Carrasco, Dario; Isaacson, Robin; Berglund, Ken; English, Arthur

Presenter/s: Anna Ecanow
Emory Faculty Mentor: Arthur English

Functional recovery from peripheral nerve injury (PNI) is poor. Experimental therapies increasing injured neuronal activity are effective in accelerating axon growth and improving functional recovery. Bioluminescent optogenetics (BL-OG) is a novel approach to increasing injured neuron activity. BL-OG uses luminopsins – light sensing ion channels (opsins) fused with light-emitting luciferase, which generate bioluminescence when exposed to a suitable substrate, such as coelenterazine (CTZ). Injured neurons expressing an excitatory luminopsin could be activated by BL-OG to promote axon regeneration. We hypothesized that induction of BL-OG after PNI would result in an increased number of neurons that have successfully regenerated, relative to controls. Sciatic nerves of mice were injected unilaterally with an adeno-associated viral vector encoding either an excitatory luminopsin or a mutated form that can generate bioluminescence but not activate neurons. After waiting two weeks for retrograde viral transport and transduction of spinal motoneurons, injected sciatic nerves were cut and repaired, and mice were then treated with a single dose of CTZ (10 mg/Kg, i.p.). Four weeks later, different retrograde fluorescent tracers were injected into the gastrocnemius and tibialis anterior muscles to mark motoneurons innervating the injected muscles. Counts of neurons were made from histological sections of spinal cords and included those that were only retrogradely labelled and those that were both retrogradely labelled and contained yellow fluorescent protein (YFP), indicating presence of the viral vector. The number of retrogradely labelled motoneurons in mice expressing an excitatory luminopsin was significantly greater than the number found in mice expressing the mutant luminopsin. However, only a small proportion of labelled cells also contained YFP, indicative of luminopsin expression. Treatments using CTZ to induce BL-OG enhanced motor axon regeneration but illuminating the exact mechanism will require further investigation.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 B
Presentation/Poster Number: 5
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Migration and Gene Expression of 4T1

Ferguson, Chavis; Williams Natecia; Haynes, Karmella

Presenter/s: Chavis Ferguson
Emory Faculty Mentor: Karmella Haynes

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 B
Presentation/Poster Number: 6
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Deep Learning Model for Predicting Mortality and Medical Conditions from Chest Radiographs

Francois, Julia; Gichoya, Judy

Presenter/s: Julia Francois
Emory Faculty Mentor: Judy Gichoya

Purpose: Patients' medical conditions are usually captured as problem lists and are coded in ICD-9 and ICD-10 codes. Problem lists help assist in patient care by providing an easily accessible account of patient problems in one place. Alongside these problem lists, healthcare physicians often use Hierarichal condition category (HCC) coding which relies on ICD-10 coding to assigns risk scores to patients. This risk-adjustment model is used to predict patient healthcare costs for patients. These problem lists are oftentimes incomplete and must be completed by a medical coder. This study aims to validate the generalizability and performance of deep learning (DL) models in predicting these medical conditions from frontal chest radiographs and then uses these results to compare the model's performance with HCC mortality outcomes.

Methods and Materials: A ResNet34 classification model was developed and tested on frontal chest radiographs from 2010 to 2019 at a single institution (Institution A). Select medical conditions were modeled using the value-based Medicare Advantage HCC Risk Adjustment Model. Sex, age, HCC codes, and risk adjustment factor (RAF) scores were used. At Institution A, this model (DL model) was tested on both an internal and external cohort. The internal cohort consisted of 413 patients with COVID-19 and the external cohort consisted of 487 COVID-19 hospitalized patients. At Emory, this model was trained on a cohort of 4098 frontal chest radiographs.

Conclusion: When predicting pulmonary diseases as well as congestive heart failure our model works well on both Emory's data as well as Institution A's data. However, when predicting arrhythmias and diabetes the model performs well at Institution A but does not perform as well on Emory's data. These results prove that the model is fairly generalizable but still needs improvement.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 B
Presentation/Poster Number: 7
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Screening botanical natural products for Cytochrome P450 Enzyme Inhibition

Fuentes, Janissa; Edwards, Emily; Risener, Caitlin J.; Caputo, Marco; Quave, Cassandra L.

Presenter/s: Janissa Fuentes
Emory Faculty Mentor: Cassandra Quave

The number of people consuming herbal dietary supplements for treatment or prevention against illnesses has changed in the last year during the pandemic. About 91% of people reported having increased their consumption of botanical supplements such as green tea, elderberry, garlic, and echinacea without direction from a healthcare provider. However, there are few studies showing the interaction between natural supplements and prescription pharmaceuticals. Our objective is to identify specific herbs with inhibitory effects on enzymes responsible for drug metabolism. We tested the Quave Natural Product Library (QNPL) for interactions against eight cytochrome P450 enzymes (CYPs), six of which are responsible for >90% of drug metabolism. The QNPL is composed of >2000 botanical and fungal extracts used in human medicine and food, including the top 40 most frequently sold medicinal herbs in the United States. These extracts are being screened for enzyme inhibitory effects in an in vitro assay at a concentration of 8 µg/mL. Once specific extracts with inhibitory effects are identified, we will pursue bioassay-guided fractionation to identify compounds responsible for these potentially harmful natural product-drug interactions. This project will increase knowledge of how natural products interact with drug-metabolizing enzymes to improve the safety and efficacy of natural product consumption.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 A
Presentation/Poster Number: 4
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Male Ratings of Infant and Female Stimuli Dependent Upon Chronological Presentation

Gallagher, Paige; Factor, Sophie; Kim, Joseph; Rilling, JK

Presenter/s: Paige Gallagher
Emory Faculty Mentor: James Rilling

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 B
Presentation/Poster Number: 7
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

How Practicing Engagement can Improve Facets of Healthcare

Gao, Antonio; Jimenez, Marta; Fullarton, Catherine

Presenter/s: Antonio Gao
Emory Faculty Mentor: Marta Jimenez

Empathy and compassion are increasing in popularity, prompting many institutions to also incorporate teaching methods of the attributes into their curriculum. Though medical students are tested on having these two attributes by the US Medical Licensing Examination, and a majority of programs include them as a competency (American Association of Medical Colleges), there is little clarity as to how they teach them. This project aims at shedding some light about how to teach and learn empathy and compassion by centering around two questions: How does practicing engagement help increase empathy and compassion? And what kind of practiced engagement is most effective to that aim?

Practicing engagement with patients is often done directly, with the participation of simulated or real patients. Using both kinds of patients for medical training, i.e. a "combined method," is preferred for many current programs (such as Emory and UVA) because each can easily be assessed for knowledge and conduct of the student. These methods provide the most accurate educational and operational, but not emotional, pathway for students to garner more experience from real patients and build their accuracy with simulated.

An alternative to utilizing patients is having students participate in, or view, a medical drama. Since it is a newer method, this has been scarcely used, but when it has, it has seemingly proved effective (Deloney, Walsh). By immersing themselves in a character, students can attempt to determine how to convey sincere, or seemingly sincere, empathy or compassion. With repetition, there are hopes that students can have a firmer grasp on the subject.

Overall, because they contribute different components of empathy and compassion to the students, a curriculum incorporating all of these methods seems the most effective when creating an all-encompassing experience for medical students, preparing them for different facets of the medical field.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 3 B
Presentation/Poster Number: 8
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

An Investigation of Lumazine Peptides as a Potential Antimicrobial

Garrison, Michelle; Mahoney, Andrew; Wuest, William

Presenter/s: Michelle Garrison
Emory Faculty Mentor: William Wuest

The overuse and misuse of antibiotics has led to the rapid evolution of antibiotic resistant bacteria, creating the need for novel antimicrobial compounds to combat this loss of efficacy. Compounds isolated from nature often have potent biological properties that make them suitable as antibiotic agents. Lumazine peptides, isolated from a Hawaiian marine fungus, Aspergillus flavipes, show the potential for antimicrobial activity. These molecules are of particular interest because of the presence of a naturally occurring isonitrile group on select peptides. Isonitriles are known chelators of copper, which may serve as a means to attenuate the virulence of clinically relevant strains of bacteria. The basic structure of these peptides consists of a dimethyllumazine fragment coupled to an amino acid (such as alanine and glutamine) and anthranilic acid. To access novel isonitrile analogs, the carboxylic acid of anthranilic acid will be replaced with an isonitrile group. Currently, we are working towards the completion and optimization of the synthetic route used to access these peptides. We will then investigate the role that isonitrile functionality plays in the antimicrobial properties of these peptides by testing their biological activity against a panel of clinically-relevant gram-positive and gram-negative bacteria. Finally, a fluorophore titration will be performed in order to investigate the metal binding ratio of the isonitrile analogs.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 4 B
Presentation/Poster Number: 8
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Associations between Childhood Trauma and Psychological Distress in Response to the COVID-19 Pandemic: Does Perceived Social Support Matter?

Gibbons, Rebecca; Fani, Negar; Eghbalzad, Leyla

Presenter/s: Rebecca Gibbons
Emory Faculty Mentor: Negar Fani

The COVID-19 pandemic has created unprecedented challenges for mental health and wellbeing, with emerging research suggesting that individuals with pre-existing mental health conditions may be particularly vulnerable to negative psychological outcomes in response to the pandemic. Childhood trauma, specifically abuse, is a significant risk factor for development of psychiatric disorders into adulthood; therefore, individuals exposed to childhood abuse may be particularly vulnerable to experiencing psychological distress during the pandemic. Meanwhile, perceived social support has long been studied as a resilience factor protecting individuals against potential psychological impacts of stressful experiences, and thus, may play a role in protecting trauma-exposed individuals against distress during the pandemic. Using interview data collected as part of an ongoing study of posttraumatic stress disorder (PTSD), we investigated the association between experiences of childhood abuse and indicators of psychological distress (levels of general worry, happiness vs sadness, enjoyment of activities, and relaxation vs anxiousness) in adults in response to the COVID-19 pandemic. In addition, we explored the potential mediating role of perceived social support in this association. Overall, participants reported higher levels of distress during the pandemic compared to 3 months prior to the outbreak. More frequent childhood abuse was associated with higher distress in domains of sadness, anxiousness, and decreased enjoyment of activities during the pandemic, as well as with lower perceived social support. However, level of perceived social support did not significantly mediate associations between childhood abuse and experience of psychological distress during the pandemic. These findings support emerging research to suggest that a history of childhood abuse is a strong risk factor for developing higher levels of psychological distress during the COVID-19 pandemic. We hope that further investigation of mediating variables will allow us to better understand mechanisms underlying this association, and explore implications for clinical interventions.

Research Discipline: Public Health
Presentation Type: Poster Presentation

Session: 1 B
Presentation/Poster Number: 6
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining Artistic Impacts of the COVID-19 Pandemic: Transitions of Live Music Performers In Response to Pandemic-Induced Restrictions on In-Person Events

Dowd, Timothy J.; Tai, Yun; Zaras, Dmitri; Gibbons, Ryan

Presenter/s: Ryan Gibbons
Emory Faculty Mentor: Timothy Dowd

Abstract not available.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 3 C
Presentation/Poster Number: 9
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Localizing Motion Processing Regions in Dogs' Brains Using Awake-fMRI

Gillette, Kirsten; Paczuski, Anna; Berns, Gregory

Presenter/s: Kirsten Gillette
Emory Faculty Mentor: Gregory Berns

Previous research has shown that humans and non-human primates have regions of the visual cortex dedicated to processing motion-related stimuli. Furthermore, these species are able to identify, track, and interpret features from the motion of living creatures, known as biological motion. Humans process biological motion separately from other forms of motion. In order to study biological motion, we use impoverished stimuli, such as a point-light walker, in which dots that are placed on joints to track movement are shown without any additional confounding features, such as color, facial features, and body shape. However, our understanding of how other species perceive biological motion is limited. In this study, we aim to localize the motion and biological motion regions of the canine brain. We will present clips of both human and canine point-light walkers to awake canine participants undergoing functional magnetic resonance imaging (fMRI), as well as randomized moving and non-moving dot arrays. Based on current understandings of canine social behavior and their ability to engage in human and canine social settings, we expect to find analogs of regions in the human brain that process motion, namely the medial temporal area for motion and the medial superior temporal area for biological motion. This research will serve as an important foundation for further research on canine perception and the organization of the canine visual cortex.

Research Discipline: Social Sciences
Presentation Type: Oral Presentation

Session: 3
Presentation/Poster Number: 3 of 6
Presentation Time: 10:30 AM to 12:00 PM
Presentation Link: https://emory.zoom.us/j/95598055387

A budding yeast model to explore how oncohistones alter cellular pathways

Gomez, Valeria; Tumminikati, Rhea; Corbett, Anita; Lemon, Laramie; Sterret, Maria; Saha, Agniva

Presenter/s: Valeria Gomez
Emory Faculty Mentor: Anita Corbett

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 B
Presentation/Poster Number: 5
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Exploring sex based differences in downstream factors of EGFR in Drosophila GBM models

Gonzalez Varela Saborio, Julia; Read, Renee

Presenter/s: Julia Gonzalez
Emory Faculty Mentor: Renee Read

Glioblastoma multiforme (GBM) is the most common primary brain tumor in adults, and is highly aggressive, malignant, and invasive. Currently, treatment involves resection and chemo therapies, but GBM tumors recur and remain resistant to treatment. Therefore, it is important to explore the mutated genes and their associated pathways in GBM tumors in order to identify therapeutic targets and develop therapies to successfully eliminate tumor cells. In Drosophila melanogaster, activation of receptor tyrosine kinases (RTKs) and downstream Phosphoinositide 3-kinase (PI3K) signaling leads to development of glial tumors with key features of human gliomas in Drosophila, as these pathways are involved in regulation of cell cycle progression. Furthermore, many genes of interest in mammalian GBMs have functional homology to their Drosophila orthologs. Read et al. developed a model using a UAS-GAL4 system to allow for cell-type specific tissue manipulation, expressing the constitutively active forms of epidermal growth factor receptor (EGFR) and dp110, a subunit of PI3K, both of which are frequently mutant in human GBM tumors, in order to drive tumorigenesis. Although previous studies have demonstrated EGFR signaling's association with cancer, we aim to explore downstream players in order to better develop an understanding of tumorigenesis. Therefore, Read et al. created a GBM model in Drosophila, which will be used to explore the sex-based differences in glial-based innate immunity in order to learn about new aspects of tumor cell biology. The genes explored function downstream of EGFR, which controls growth, survival, proliferation, and differentiation of glial cells. The single functional orthologs that will be studied include PTEN, Raf, Ras, Akt, and Spz, all of which function downstream of EGFR. The effect of over or under expression of these will be tested against wildtype or tumor controls. Age and sex matched larvae brains will be imaged and compared to analyze sex based differences.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 C
Presentation/Poster Number: 9
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Developmental Effects of Social Stress and Obesogenic Diets on the growth of Brain Sensory Cortical Regions in Female Macaques

Gopakumar, Adway; Kovacs-Balint, Zsofia; Kyle, Margaret; Siebert, Erin; Pincus, Melanie; Godfrey, Jodi; Styner, Martin; Wilson, Mark; Sanchez, Mar

Presenter/s: Adway Gopakumar
Emory Faculty Mentor: Mar Sanchez

Low socioeconomic status (SES) is associated with lack of resources, chronic stress, and higher consumption of highly caloric -obesogenic- diets. All these factors have potential synergistic effects on both physical and mental health. Our lab has been studying a nonhuman primate model of translational value for low SES (low social rank or social subordination) that causes chronic stress and increased intake of highly caloric diets (HCD). While these studies focused on the effects of diet and social subordination stress on the prefrontal cortex and amygdala, it is not understood whether primary sensory cortices (visual, olfactory, gustatory) are affected. The goal of this study was to understand the effects of social subordination stress and obesogenic diets on the development of primary sensory cortices. Forty-four female rhesus macaques were cross-fostered at birth and randomly assigned to either dominant or subordinate foster mothers and assigned to either a low calorie diet (LCD) or to a “Choice” diet condition (LCD and HCD). MRI scans were acquired at 6 (infancy) and 16 months (juvenile period) and data was processed using the AutoSeg pipeline. We found a strong developmental effect of the obesogenic Choice diet on brain structure, resulting in bigger visual, gustatory and piriform cortices volumes, and overall brain size (ICV) compared to animals eating the LCD diet. A rank by laterality interaction effect was also found where subordinate animals had bigger volumes of the left gustatory cortex than Dominants. When ICV was added as a covariate, all significant results were lost, suggesting that the effects of rank and diet on sensory cortices were not region-specific but driven by general effects on whole brain size. These findings suggest that exposure to social subordination and obesogenic diets during development affects brain structural development driven by potential mechanisms such as increased cortisol, inflammation and Kcal consumption.

Research Discipline: Natural and Physical Sciences
Presentation Type: Oral Presentation

Session: 5
Presentation/Poster Number: 2 of 6
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99538389212

Bee gut Microbiome changes and pathogen prevalence after exposure to Agricultural Antibiotics

Gray, Ashlynn*; McGrath, Alexa*; Avila, Dr. Laura
*first authors

Presenter/s: Ashlynn Gray and Alexa McGrath
Emory Faculty Mentor: Laura Avila

The application of agricultural antibiotics has exponentially increased in the last decade, but the impact of these applications on beneficial insects such as bees, is not well understood. Yet, antibiotic exposure in the lab can deplete the core bee gut symbionts and lead to pathogen invasion. The microbiome of the North American honey bee (Apis mellifera) are developing antimicrobial resistance, presumably through exposure to antibiotics used to prevent bacterial disease in crops. Such antibiotic resistance, while negative from a human and animal health standpoint, could allow bee symbionts to survive field antibiotic applications. However, to date, no study has tracked the impact of antibiotic applications on the microbiome composition, pathogen presence and antibiotic-resistance development. The objectives of this research are to evaluate bee microbiome composition changes, in particular the prevalence of antibiotic resistant genes, and to screen for the presence of Serratia marcescens, a common bee gut pathogen, in honeybee workers. In Spring 2021, we sampled 15 to 25 honey bee workers per site, at three apple orchards and three strawberry sites in Northern Georgia. Apple orchards were sprayed with antibiotics (streptomycin and oxytetracycline) to control a bacterial plant pathogen (Erwinia amylovora). The bee's gut microbiome is extracted using a commercial DNA extraction kit. We will sequence the V4 region of the 16s rDNA gene. We will screen for the prevalence of antibiotic resistance and the pathogen Serratia marcesens via PCR using published primers. We expect to find greater prevalence of antibiotic resistant genes in bees collected at apple orchards. However, lack of antibiotic resistance genes across sites could indicate that the resistance takes time to develop. A microbiome that is susceptible to antibiotic applications could exhibit high prevalence of pathogenic and opportunistic bacteria.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 B
Presentation/Poster Number: 7
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Self-examination through genre and character: Writing and producing a 20-minute album on toxic masculinity

Gray, Sawyer; Young, Katherine

Presenter/s: Sawyer Gray
Emory Faculty Mentor: Katherine Young

Consider your self as the reflection of your environment, processed and incorporated into individuality. This 5-song collection, written and produced over the course of the SURE program, was both an exercise in self-definition, through its compositional and performance elements, as well as an exercise in social critique with its subject matter. By choosing sonic elements of synthpop, trap, and indie rock, the piece's foundation is contemporary, commercial, and familiar. These materials are somewhat subverted throughout the work, in part by virtue of their own incompatibility, but also through abrupt transitions, time signature change, or in one case a long period of sparse, reflective solo piano chords. In the text, I play the role of a disillusioned and angry character, someone who feels left behind by the quick evolution of social life brought about by the internet. Through a feminist lens, this character both perpetuates toxic masculinity and is a casualty of it. By the end of the piece, my hope is that the audience leaves grappling between empathy and disgust. The full 20 minute piece will premier as part of my honors recital in May of 2022.

Research Discipline: Arts and Creative Expression
Presentation Type: Oral Presentation

Session: 4
Presentation/Poster Number: 2 of 5
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99643683271

Reproductive consequences of hybridization between squash bug species

Grenci, Eliza C.; Li, Ziyu; Dodd-Shojgreen, Jade; Villa, Scott M.; Gerardo, Nicole M.

Presenter/s: Eliza Grenci
Emory Faculty Mentor: Nicole Gerardo

Anasa tristis and Anasa andresii are common agricultural pests that are known to mate with each other. However, the reproductive and ecological consequences of this heterospecific mating remain unknown. Mating between species often results in hybrid vigor, where hybrid offspring are more fit than either parental species. The goals of this study were: 1) to observe mating behavior between A. andresii and A. tristis, 2) to quantify hybrid morphology, and 3) to measure plant damage caused by hybrids. We video recorded a total of 36 pairs of squash bugs (17 conspecific, 19 heterospecific) over the course of five days. From each video, we quantified mating behavior. Following the mating trials, we took pictures of each pair and their offspring to digitally analyzed their morphology. Finally, we placed bugs on squash plants for five days and measured the number of leaf lesions caused by each species and their hybrids. We found that A. tristis and A. andresii readily mate and produce viable hybrid offspring. We also found that hybrids retain morphological aspects of both parental species. However, they were significantly larger than both A. tristis and A. andresii. Subsequent tests revealed that these larger hybrid bugs cause significantly more damage to squash plants than either parental species alone. Our study is the first to show that A. tristis and A. andresii hybridize and that their hybrids are especially bad pests. These results highlight the potential problems hybrids have for agriculture.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 B
Presentation/Poster Number: 8
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Bean Beetle Fitness Impacted by the Manipulation of their Microbiome Through Antibiotics

Hancock, Sarah; Zelaya, Anna; Nicole, Gerardo

Presenter/s: Sarah Hancock
Emory Faculty Mentor: Anna Zelaya

Microorganisms can have a symbiotic relationship with their hosts in which both parties are necessary for survival. Callosobruchus maculatus, commonly known as the Bean Beetle, lacks the gene to produce the enzyme cellulase, even though they develop within the cellulose-rich legumes. Symbiotic microbes that survive in the gut of C. maculatus, specifically gram-positive Staphylococcus sp., are largely responsible for the digestion of cellulose. However, the whole bacterial community makeup, their functional roles, and their greater effects on host beetles are unknown. Previous research found that attempting to eliminate symbionts by treating beetles with gram-positive targeting antibiotics resulted in minimal larval development and no adult survival. These results suggest the significant role of symbionts in bean beetle survival. In this study, we tested the significance of gram-positive microbes on C. maculatus fitness by both treating beetles with antibiotics and supplementing their diet with compounds believed to be bacterially derived. Artificial beans were created to contain antibiotics and combinations of cellulase and vitamin B12, compounds known to be produced by bacterial symbionts. It is anticipated that a low larval development and emergence rate will be observed for beetles treated with antibiotics, but that development and emergence will be restored when supplemental compounds are present. This would mean that microbes such as Staphylococcus sp. perform necessary functions and provide nutrients that are fundamental for beetle fitness. Future manipulations could include targeting gram-negative bacteria or changing the beetles' diet to further understand the role and community of microbes.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 B
Presentation/Poster Number: 6
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Binding Behaviors of the tRNA Methyltransferase Trm10

Hancock, Clio; Strassler, Sarah; Conn, Graeme

Presenter/s: Clio Hancock
Emory Faculty Mentor: Graeme Conn

tRNA is essential in the process of protein synthesis, translating the information from mRNA into a growing polypeptide chain. Before tRNAs are functional, they typically undergo a series of chemical modifications including a number in the core region that may impact tRNA folding and stability. Trm10 is a tRNA methyltransferase that methylates tRNAs at their 9th nucleotide in the core region. However, Trm10 only modifies 14 of the 26 yeast tRNA candidates (i.e. tRNAs with a guanosine at position 9) and there are no clear tRNA sequence or structural features that would explain such selectivity. The current hypothesis maintains that Trm10 uses a stepwise catalytic mechanism in which the enzyme binds to tRNA, then only methylates if Trm10 is able to induce the correct conformational change in tRNA to access the target nucleotide. Previous experiments have elucidated potentially important conformational changes and methylation status of various tRNAs, but they did not give any information about the binding step. The goal of this project is to investigate the binding of Trm10 to both substrate and nonsubstrate tRNAs using a wild-type and a catalytically inactive Trm10. Electrophoretic mobility shift assays (EMSAs) were used to test binding of Trm10 to tRNAs and showed, as expected, that wild-type Trm10 binds to substrate tRNAs (tRNA Gly and Trp). However, wild-type Trm10 also binds to nonsubstrate tRNAs (tRNA Leu and tRNA Val). The inactive Trm10 variant shows similar behavior with the ability to efficiently bind the same substrate and nonsubstrate tR1N1A1s1.1 1T1h1e1s1e1 1r1e1s1u1l1t1s1 1p1r1o1v1i1d1e1 1f1u1r1t1h1e1r1 1e1v1i1d1e1n1c1e1 1t1h1a1t1 1p1r1o1t1e1i1n1 1b1i1n1d1i1n1g1 1a1n1d1 1m1e1t1h1y1l1a1t1i1o1n1 1a1r1e1 1t1w1o1 1d1i1s1t1i1n1c1t1 1e1v1e1n1t1s1 1t1h1a1t1 1h1a1p1p1e1n1 1s1e1q1u1e1n1t1i1a1l1l1y1 1a1n1d1 1t1h1a1t1 1d1i1s1c1r1i1m1i1n1a1t1i1o1n1 1b1e1t1w1e1e1n1 1s1u1b1s1t1r1a1t1e1 1a1n1d1 1n1o1n1s1u1b1s1t1r1a1t1e1 1t1R1N1A1s1 1h1a1p1p1e1n1s1 1o1n1l1y1 1a1t1 1t1h1e1 1m1e1t1h1y1l1a1t1

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 2
Presentation/Poster Number: 2 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/95175906316

Synthetic and Biological Investigations into the Natural Product, SF2768

Haney, Brittney; Schrank, Cassandra; Wuest, William

Presenter/s: Brittney Haney
Emory Faculty Mentor: William Wuest

SF2768 is a small molecule that was first isolated in a 1995 study from the bacteria Streptomyces sp. SF2768. After its isolation, it was found to have antibacterial activity and characterized as a bacterial chalkophore, meaning that it is able to bind to copper and shuttle it into a bacterial cell for sustaining life processes. Because of this, SF2768 is a potential molecule of interest for use as an antibiotic. A recent publication by Tan and co-workers outlined a total synthesis of SF27681 as well as two linear derivatives. Using this as a base, our group hypothesized that we could employ small structural changes to the molecule which we could use to analyze their antibacterial activity in hopes of understanding its mechanism of action. We were successfully able to synthesize two of the linear molecules of SF2768 and made significant progress towards the synthesis of SF2768 as well as our planned analogs. After completing the synthesis of all the planned molecules, we will test the antibacterial capability of each of the molecules in hopes of determining new strategies in which to combat harmful bacteria.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 3 C
Presentation/Poster Number: 10
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

A Multiregional Object-Oriented Solver of SIR-like Models for the COVID-19 Outbreak

Hao, Yujia; Hou, Yuting; Xu, Siwei; Chang, Kai; Wu, Zhen; Veneziani, Alessandro

Presenter/s: Yujia Hao
Emory Faculty Mentor: Alessandro Veneziani

With the COVID-19 disease still evolving and spreading over a year following its identification, the development of reliable mathematical models to accurately monitor and predict the long-term dynamics of the pandemic becomes crucial to saving lives and preventing further financial sacrifices. Expanding upon the classical mono-regional Susceptible-Infected-Recovered (SIR) compartmental models, this project focuses on the design and implementation of a multiregional SIR-like model to reflect cross-regional interactions within a global context. In our design, a network of regions is connected by movement matrices that describe inter-regional traveling among regions of interest.

The solver of this problem can be efficiently constructed in an object-oriented framework. In this way, different regional features, such as local infection and recovery rates, are promptly incorporated. Also, the individual regional dynamics can be easily adapted to more sophisticated models or scenarios such as SEIR models (or models with more than 3 compartments) or the impact of vaccinations and lockdowns. In this project, we have successfully implemented this model with pseudo-datasets in two different programming languages (MATLAB and Python) and found consistent results. When we disregard the cross-regional interactions, the computational results of each individual region's dynamics are congruent with the theoretical values from the classical mono-regional SIR model. Hence, we expect the solver to produce reliable simulations of the actual progression of the pandemic once real data is applied. The object-oriented framework makes the solver easily adapted to different space-scales, ranging from a few numbers of connected regions to hundreds.

Research Discipline: Natural and Physical Sciences
Presentation Type: Oral Presentation

Session: 3
Presentation/Poster Number: 4 of 6
Presentation Time: 10:30 AM to 12:00 PM
Presentation Link: https://emory.zoom.us/j/95598055387

Influence of cell contractility and clot mechanics on contraction and fibrosis of the microfracture environment

Hasson, Maddie; Fernandes, Lorenzo; Kowalski, Mike; Patel, Jay

Presenter/s: Maddie Hasson
Emory Faculty Mentor: Jay Patel

Cartilage injuries are one of the most common musculoskeletal injuries, and due to the tissue's inherent lack of regenerative capacity, it is unable to self-heal. One of the most common methods of treating cartilage damage is microfracture, which consists of puncturing the subchondral bone to recruit marrow elements into the defect. While this treatment provides short-term relief, inferior fibrous tissue often forms and is susceptible to wear. The negative impacts of fibrosis on the mechanical properties of regenerated cartilage are recognized, but the connection between clot contraction and fibrosis remains unexplored. Here, we use fibrin gels seeded with juvenile bovine MSCs as a model for microfracture clots. We explore the role of cell contraction and clot mechanics on fibrosis by introducing pharmacologic agents including Fasudil, a ROCK inhibitor, and lysophosphatidic acid (LPA), an upstream activator of the Rho-ROCK pathway. Clot mechanics were varied via thrombin concentration to better assess the impacts of initial mechanics. Clots were evaluated using mechanical testing, macroscopic imaging, histology, and gene expression analysis. We show that increasing cell contraction (LPA) exacerbates fibrosis and the prevention of contraction (Fasudil) impedes fibrosis. Furthermore, stiffer clots exhibited less contraction, and fibrosis, over time. These findings suggest that microfracture clot contraction is detrimental to healthy cartilage regrowth because it plays a critical role in the formation of fibrous tissue, which is known to exhibit limited functional properties in comparison to native hyaline cartilage and can hinder functional cartilage restoration. Drug strategies that prevent early fibrosis of these clots can enable chondrogenesis and superior cartilage formation. This association between cell contraction and fibrosis encourages further research into drug-related methods of influencing healthy cartilage regrowth by exploring the capabilities of drugs that prevent contraction, and the resulting fibrosis, in microfracture clot applications.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 C
Presentation/Poster Number: 10
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Ovarian Insufficiency in a Sprague Dawley GALT-null Rat Model of Classic Galactosemia

Hendrickson, Emma; Fridovich-Keil, Judith

Presenter/s: Emma Hendrickson
Emory Faculty Mentor: Judith Fridovich-Keil

Galactosemia, an umbrella term used for a group of inherited autosomal recessive disorders in which the body cannot metabolize galactose, results from dysfunction of the Leloir pathway. Classic galactosemia, also known as Type I, is caused by a deficiency of the second enzyme in this pathway: galactose-1-phosphate uridylyltransferase. Though a galactose restricted diet from infancy can lessen acute effects from the disorder, affected individuals still encounter a variety of symptoms throughout life, with ovarian insufficiency in female patients being an especially pertinent issue. This research project aims to build upon previous findings that demonstrated at least 80% of women with classic galactosemia suffer from premature ovarian insufficiency (POI)[1], using a Sprague Dawley GALT-null rat model. To further study the hypothesis that galactosemia causes ovarian insufficiency, female rat pups were exposed to elevated galactose both before and after birth, with exposure continuing throughout life, then euthanized at 3 months old when in proestrus phase of their estrus cycle. Ovarian tissue was collected following PBS perfusion, fixed in paraformaldehyde, dehydrated in ethanol, and embedded in paraffin wax. The paraffin embedded tissue was then sectioned and stained with hematoxylin and eosin (H&E) to reveal cells and structures. Stained slides were scanned to produce high resolution images for counting of ovarian follicles. Methodology for counting follicles included examining each scan for primordial, primary, secondary, and tertiary follicles, based on anatomy of granulosa cells, oocyte visibility, and follicle size. Preliminary findings indicate that GALT-null rats show fewer primary, primordial, and secondary follicles per single ovary section than GALT+ rats, but more tertiary follicles per single ovary section. These differences could be indicative of premature ovarian insufficiency. Future studies will be needed to explore the timing, progression, and mechanism underlying the apparent differences.

[1] Fridovich-Keil JL, Gubbels CS, Spencer JB, Sanders RD, Land JA, Rubio-Gozalbo E. Ovarian function in girls and women with GALT-deficiency galactosemia. J Inherit Metab Dis. 2011;34(2):357–66l.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 2
Presentation/Poster Number: 3 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/95175906316

Characterizing epitopes within human immunodeficiency virus-1 transmitted founder envelope glycoproteins targeted by autologous neutralizing antibodies

Hendrix, Michael A.; Salazar-Quiroz, Natalia; Smith, S. Abigail; Burton, Samantha; Allen, Susan; Derdeyn, Cynthia A.

Presenter/s: Michael Hendrix
Emory Faculty Mentor: Natalia Salazar-Quiroz

Human immunodeficiency virus-1 (HIV-1) is a retrovirus that weakens the immune system by targeting CD4+ T cells, using its envelope (Env) glycoproteins to bind the CD4 receptor. Initially, Transmitter/Founder (T/F) viruses establish infection and elicit neutralizing antibodies. Overtime, these antibodies could serve as precursors to broadly neutralizing antibodies (bnAbs) and target global neutralizing epitopes within HIV-1 Env, such as the CD4 binding site (CD4bs), the V3 loop, and the V1/V2 apex.

A previous study isolated eight monoclonal antibodies (mAbs) from two HIV-1 individuals 7.5 months after infection: Z1047M (1C9, 3A5, 3F8, 3C1, and 1B5) and Z1800M (1A8, 1E12 and 2H10). These mAbs exhibit neutralizing activity against their autologous HIV-1 T/F Env but have unknown binding sites. Hence, our aim is determining which Env epitopes are targeted by these mAbs. Through Enzyme-Linked Immunosorbent Assays (ELISAs), we characterized binding of these mAbs to their autologous HIV-1 T/F Env gp120, measuring competition against well-known bnAbs and non-neutralizing mAbs: VRC01, B6, F105 (CD4bs), PGT121 and 447-52D (V3-glycan), and A32 (CD4 induced). We hypothesized that mAbs from both individuals will target at least one known HIV-1 Env neutralizing epitope.

For both Z1047M and Z1800M Env gp120 proteins, binding of B6, PGT121, 447-52D, and A32 reached an optical density of 1. F105 and VRC01 also reached the threshold of 1 against Z1047M gp120. Results showed 1A8 and 1E12 competing with B6 binding to the Z1800M gp120 Env. All Z1047M mAbs competed with VRC01, with slight competition against PGT121 and 447-52D, and no competition observed against B6.

The current results indicate that most of the neutralizing mAbs from early HIV-1 infection recognize epitopes in or near the CD4bs. Future directions of the study will confirm the epitopes targeted, and also compare binding affinity and neutralization potency between the autologous mAbs and well-known bnAbs.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 C
Presentation/Poster Number: 9
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Biologic Mechanisms Linking Structural Racism to Cancer Disparities: A Critical Gap in Cancer Epidemiology

Henry, Kashari; Miller-Kleinhenz, Jasmine; McCullough, Lauren

Presenter/s: Kashari Henry
Emory Faculty Mentor: Lauren McCullough

Abstract not available.

Research Discipline: Public Health
Presentation Type: Poster Presentation

Session: 2 B
Presentation/Poster Number: 7
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

An Evaluation of NICE! Nice Incentives for Care Engagement, Patient Technology Access, and Patient Appointment Preference in Outpatient Behavioral Health Engagement

Hewitt, Paige; Broussard, Beth; Cotes, Robert

Presenter/s: Paige Hewitt
Emory Faculty Mentor: Robert Cotes

The transition from a psychiatric hospital to outpatient mental health treatment is critical for those diagnosed with serious and persistent mental illness (SPMI). However, follow-up rates at scheduled outpatient appointments post-discharge are low. Between January 2018 and October 2019, 47% of the patients discharged from the inpatient unit at Grady Memorial Hospital (GMH) who were referred to Grady Behavioral Health for outpatient care did not attend their first appointment. Additionally, COVID-19 has interrupted traditional in-person interaction and transformed mental healthcare facilities into virtual practices. Currently, at Grady Memorial Hospital in Atlanta, Georgia, the longitudinal survey study of NICE! Nice Incentives for Care Engagement Initiative is being conducted to evaluate the feasibility and outcomes of providing financial incentives for outpatient behavioral health engagement and assess the digital readiness of individuals with SPMI. NICE! consists of individuals with SPMI diagnosis who have recently been discharged from the GMH inpatient psychiatric unit. This ongoing study aims to identify access to technology and determinants in this population while also evaluating patient preferences toward virtual appointments amid COVID-19 using descriptive statistics. A shift towards virtual or phone appointment preference during COVID-19 is predicted. In this preliminary sample, (n=8), results indicate that 75% of participants own a cell phone, 25% have a land line, 62.5% have computer access, and 75% have Wi-fi access. 12.5% of participants prefer in-person appointments over virtual appointments or a combination of both. We aim to increase the number of enrollees in the program who participate in the research in order to obtain conclusive results. The study will continue in the attempt to identify additional barriers patients may face in outpatient behavioral health engagement. Further research regarding patient technology access and appointment preferences can be done to determine whether or not continuing to offer virtual appointments could potentially increase follow-up rates.

Research Discipline: Public Health
Presentation Type: Poster Presentation

Session: 6 B
Presentation/Poster Number: 6
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Evaluating the potential usage for multi-generation ancient DNA datasets in simulations to identify patterns of selection on genetic circadian-clock/immune-system crosstalk

Hirst, Cora; Lindo, John

Presenter/s: Cora Hirst
Emory Faculty Mentor: John Lindo

Evolutionary studies regarding human immunity provide a framework for targeted immunotherapies. These studies have largely been restricted to asexually reproducing model organisms with short generation times. These “evolve and resequence” studies often mask selective sweeps, inflate the count of rare alleles, and fail to capture naturally occurring diversity due to lack of recombination. The emerging field of ancient DNA (aDNA) allows for the identification of historical selection events in human populations, but the current availability of genome-wide SNP datasets is limited both temporally and in sample size. This project aims to identify potential datasets for a selection study on genes involved in circadian clock/immune system crosstalk. First, four circadian clock genes and eight of their regulatory targets in macrophages were selected according to their variation in modern populations and knowledge of their molecular interactions. Six datasets collected by the David Reich Laboratory and one dataset collected by the Max Planck Institute for the Science of Human History were then evaluated according to the following criteria: 1) sample size, 2) population history, 3) temporal scope, and 4) coverage at loci of interest. Two datasets - the first a collection of 36 individuals from medieval Europe from the Max Planck Institute, and the second a Reich dataset of 225 individuals spanning the late Neolithic to early Bronze Age Mediterranean - demonstrated the greatest coverage at select circadian clock genes and their regulatory targets on immune genes, as well as sufficient variation between temporally segregated populations. This pilot study suggests that multi-generational aDNA SNP datasets can be clustered by age and identifies two datasets with sufficient coverage at clock- and immune-gene loci to run a selection simulation. Before a dataset can be selected, research into the pathogenic pressures and allelic variation spanning the temporal and geographic range of both sets is necessary to identify the stronger case for selective pressure.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 C
Presentation/Poster Number: 11
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Enhancing axonal growth after Peripheral Nerve Injury after treatment with R-13, a small trkB agonist

Hoffman, Dustin; Isaacson, Robin; English, Arthur

Presenter/s: Dustin Hoffman
Emory Faculty Mentor: Arthur English

In the United states, 20 million Americans suffer from peripheral nerve injuries and approximately 150 billion dollars is spent in treatment for these individuals.Many of these individuals never recover full function and the slowness and inefficiency of axon regeneration is often linked to this poor recovery. Activity-dependent experimental therapies that increase neuronal expression of the protein Brain Derived Neurotrophic Factor (BDNF) and its cognate receptor TrkB have been shown to enhance regeneration of peripheral nerves. Treatments with BDNF are hampered by its poor oral bioavailability and short half-life. 7,8-dihydroxyflavone (7,8-DHF), a small molecule selective TrkB agonist that mimics the activity of BDNF has shown promise but despite its improved pharmacokinetic profile,therapeutic use F is still limited. R13 is a prodrug of 7,8-DHF which upon oral administration is converted into 7,8-DHF by the liver. We hypothesize that oral treatment with R13 following peripheral nerve injury will enhance subsequent axon regeneration. In our experiments with YFP-16 mice, in which a subset of sensory and motor axons are marked completely by yellow fluorescent protein (YFP), we transected and repaired the sciatic nerve and treated daily with an oral dose of R13 (43.6 mg/kg) or vehicle for two weeks. The axons of R13-treated mice regrew more than 3x longer than vehicle-treated controls. More than 40% of these axons were longer than the longest regenerating axon found in either the vehicle-or 7,8-DHF-treated mice. Direct muscle EMG responses (M waves) were 2-3 times larger in R13-treated animals than in controls. Oral treatments with R13 significantly enhanced axon regeneration, suggesting that this prodrug could be a powerful, noninvasive treatment for peripheral nerve injury.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 C
Presentation/Poster Number: 11
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Sociological Research Methods

Scott, Tracy; Horse, Matowacipi

Presenter/s: Matowacipi Horse
Emory Faculty Mentor: Tracy Scott

The purpose of this research is an exploration of student culture (values, beliefs, discourse) around college-to-career issues at a selective liberal arts university. Using ethnographic methods, we will explore students' own experiences related to academic majors, desirable work outcomes and career paths. We will also investigate how students talk about these issues among themselves and what they hear about these issues from faculty and administrators on campus. While we have statistics and research about the fields students choose after University this research serves to give further insight to the factors that influence and shape students choices while in University.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 7 B
Presentation/Poster Number: 8
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Impacts of Antibiotic Exposure on Bumble Bee Foraging Behavior and Gut Microbiome Composition

Hossain, Afsha; Molumo, Zainab; Avila, Laura

Presenter/s: Afsha Hossain and Zainab Molumo
Emory Faculty Mentor: Laura Avila

Rampant bacterial crop pathogens have compelled the rising agricultural use of broadcast-spray antibiotics in the United States in the past decade. Our research is interested in how antibiotic exposure affects pollinator behavior and learning. Bee gut bacteria produce neuromodulators like dopamine that have been shown to modulate bee learning, and if symbionts are distributed by the field-level antibiotics, this dietary exposure to antibiotics could negatively impact bee learning. We are investigating the impacts of the lowest field-relevant concentration applied to crops, 50 ppm of streptomycin, on bumble bee (Bombus impatiens) behavior via the “free movement proboscis extension assay” standard method and thee-flying foraging assays”. Behavioral assays were used to compare the learning and reward-seeking behaviors of bees treated with and without 50 ppm streptomycin when presented with a color stimulus (blue or yellow). We have performed 62 free proboscis extension behavioral assays on wild-type, control, and antibiotic-treated bees from three colonies and have observed no statistically significant difference in appetitive motivation or learning behavior thus far. We are currently analyzing the data collected from 70 bees across two colonies that were tested in the free-flying video foraging assays. We expect that the wild-type bees will display better performance in the foraging assay than the antibiotic-treated bees. We are also analyzing morphotype and antibiotic susceptibility data for bee gut symbionts from two colonies which will be identified through Sanger sequencing. We have found symbionts resistant to 50 ppm streptomycin which may explain the behavioral resiliency of the bees at this concentration. Our research serves to inform preventive management practices and promote sustainable use of antibiotics at the field level to address health and ecological issues created by the overuse of antibiotics on U.S. crops.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 C
Presentation/Poster Number: 10
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Identification of 14-3-3 Isoform-Selective Binding Partners

Hu, Maylynn; Fan, Dacheng; Fu, Haian

Presenter/s: Maylynn Hu
Emory Faculty Mentor: Haian Fu

The 14-3-3 family of phosphoserine/threonine-recognition proteins control diverse physiological and pathophysiological functions. They are promising therapeutic targets for such diseases as cancer and neurodegenerative disorders. 14-3-3 mainly acts as an adaptor protein that controls the function of its target proteins through highly regulated protein-protein interactions (PPI). This stresses the importance of targeting these 14-3-3-moderated processes during the development of cancer therapies. Seven isoforms of human 14-3-3 protein, and their isoform-specific functions have been identified. They have shared and distinct binding partners and have shown key roles in various cancers, including mitogenic signal transduction, apoptosis and regulation of the cell cycle, making them prime prognostic markers in various cancers. The 14-3-3σ isoform has been notably established to function in tumor suppression, while the 14-3-3ζ isoform has shown to be oncogenic, correlating with a low prognosis rate; the mechanisms for the differential effects on tumors are unknown. Differential binding to protein partners may be one possibility. Previously, we showed the results from a primary high-throughput screening study which identified Interferon Gamma Receptor 1 (IFNGR1) as having differential PPIs with the 14-3-3σ and 14-3-3ζ isoforms. IFNGR1, the larger of two subunits of the IFN-γ receptor, is known for its involvement in tumor progression, regression, and immunogenicity. Studying these differential PPIs may provide some insight into the opposing nature of these two isoform-specific mechanisms. Thus, in the current study, we sought to confirm the difference and selectivity in the interactions between the tumor-suppressive 14-3-3σ and oncogenic 14-3-3ζ isoforms and IFNGR1 using various PPI approaches, including GST-pull down and TR-FRET. The results of this study may reveal isoform-specific 14-3-3 protein-protein interactions as potential targets for future therapeutic discovery.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 C
Presentation/Poster Number: 9
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Utilizing the Target Specific A20FMDV2 Peptide Sequence to Engineer an αvβ6 Integrin on Carcinomas Targeting Chimeric Antigen Receptor (CAR) Binding Domain

Humphrey, Kennedy; Evans, Alysa; Hossian, A K M Nawshad; Rafiq, Sarwish

Presenter/s: Kennedy Humphrey
Emory Faculty Mentor: Sarwish Rafiq

Chimeric antigen receptors (CAR) T cells have been proven to be an effective therapy for treatment of hematological cancers but not solid cancers. Research is being done to discover more effective solutions to targeting solid cancers. A20 amino acid sequence known as A20FMDV2, derived from Foot-Mouth-Disease-Virus2 VPI coat protein has been found to bind specifically to integrin αvβ6, which is overexpressed in carcinomas such as PDAC, ovarian cancer, breast cancer, and head and neck cancers but not on normal cells thus decreasing the likelihood of on target off tumor effects. My project centers on engineering a CAR containing the A20FMDV2 peptide as a binding domain. If the binding domain on CAR T cells can be genetically engineered to the A20FMDV2 peptide then CAR T cells could target integrin αvβ6 on solid cancer tumors. We constructed a CAR T cell that encodes the A20FMDV2 peptide. The next step would be making T cell cultures with the newly constructed CAR. Further testing needs to be done in order to find if the A20FMDV2 does target integrin αvβ6 on solid cancers.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 C
Presentation/Poster Number: 12
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Assessing Lactam Ring-Size in N-Acyl Serotonin Derivatives for Treating Trauma-Induced Vision Loss

Hung, Tiffany G.; McDonald, Frank E.

Presenter/s: Tiffany Hung
Emory Faculty Mentor: Frank McDonald

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 4 C
Presentation/Poster Number: 12
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

A qualitative study of the pain experience with hematopoietic cell transplantation for sickle cell disease

Hurreh, Asha; Bakshi, Nitya

Presenter/s: Asha Hurreh
Emory Faculty Mentor: Nitya Bakshi

Background: Pain is the hallmark of Sickle cell disease (SCD) is a multi-system chronic illness that affects about 100,000 patients in the United States. Hematopoietic Cell Transplant (HCT) is a curative therapy that when successful, can lead to improvement and resolution of pain.

Objectives: We sought to understand the experience of pain and quality of life in patients with SCD before and following HCT, and the role of SCD pain in patient decision-making regarding HCT.

Methods: In this study, we used qualitative interview data collected from pediatric patients with SCD enrolled on a study of pain before and after HCT. These interviews were conducted before, and at 3, 6 12, and 24-months following transplantation. We used a content analysis approach to organize participant narratives. We developed categories based on a priori study goals as well as categories derived from the data, and then organized into overarching themes.

Results: We analyzed interviews from 6 participants, with a median age of 13.5 years, and 4 of 6 were male. We found that most participants had a significant pain experience prior to HCT, with impact on daily activities, school, play or social activities, and other aspects of their life. Following HCT, they reported reduction or resolution of pain, improved quality of life, and some described improved energy. Participants described many activities that they couldn't do before HCT due to pain, but could do post-HCT, particularly activities that other children their age did. We also found that the experience of pain was a significant factor in their decision to pursue HCT as a curative option.

Conclusions and significance: We found improvement in pain and quality of life after successful HCT in SCD, and pain was a significant consideration in the decision for HCT in SCD.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 C
Presentation/Poster Number: 11
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Evaluation of Small Molecule Inhibitors of Pseudomonas Virulence factor LasB as Non-Traditional Immunotherapeutics

Hwang, Sophia; LaRock, Christopher

Presenter/s: Sophia Hwang
Emory Faculty Mentor: Christopher LaRock

Pseudomonas aeruginosa can cause severe opportunistic pulmonary infections associated with mechanical ventilation and the genetic disease cystic fibrosis. Due to its multidrug resistance, it is a priority pathogen for therapeutic development. Inflammation during such infections, which causes destruction of lung architecture and function, is activated in part through the maturation of IL-1β by the virulence factor LasB. Previous results in mouse models suggest that matrix metalloprotease inhibitor drugs also inhibit LasB, preventing cell death and inflammation caused by caused by P. aeruginosa. We hypothesized that other inhibitors of matrix metalloproteases, including tetracycline-family antibiotics, could be used to target Lab. We evaluated small molecule inhibitors against LasB activation during infections of macrophages, neutrophils, and monocytes and the synergy of these inhibitors with conventional antibiotics and anti-inflammatories. We first optimized the drug concentration by testing the ability of the various drugs to inhibit LasB at various dilutions. Using an effective concentration, we then infected the various cell types with P. aeruginosa and analyzed the impact of the inhibitors on cell death and maturation of IL-1β in infected cells. The results indicate that several tetracycline-family compounds inhibit LasB during P. aeruginosa infections and decrease cell death. This was true for compounds that had no antimicrobial activity yet still inhibited LasB. In addition, the results suggest that the drugs target different cell types. Together, we find that tetracyclines may have therapeutic benefits, even against resistant bacteria, due to their ability to decrease inflammation. This may serve as an effective adjunctive therapy during infection to limit tissue damage and give the immune system and antibiotics more time to respond.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 B
Presentation/Poster Number: 7
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effects of Thapsigargin-induced Endoplasmic Reticulum Stress on Autonomous Gene Regulation of ATF4

Iqbal, Sabina; Berglund, Ken; Gross, Robert E

Presenter/s: Sabina Iqbal
Emory Faculty Mentor: Ken Berglund

Improper protein processing and folding in neuronal cells is a common characteristic of many neurodegenerative diseases. While proteins perform countless functions in the cell, one protein interaction of note is the binding of protein ligands to DNA or mRNA sequences that regulate downstream transcription and translation, respectively. One such regulatory mRNA sequence is ATF4, which functions via translational repression when bound to the correct ligand. In theory, disruption of proteostasis would prevent ATF4 from binding to its protein ligand, thus allowing unregulated translation of any downstream sequences. The purpose of this investigation was to determine if proteostasis dysfunction could be used favorably as a trigger for translation of a desired gene. To mimic the cellular conditions of proteostasis dysfunction, Thapsigargin (Tg), an inhibitor of the Ca2+ ATPases in the endoplasmic reticulum (ER)), was applied to cells. Genetic regulation carried out by the ATF4 sequence under these conditions of ER stress can be monitored with a downstream sequence that codes for a reporter protein. In this experiment, the reporter protein of choice was a luciferase called AkaLuc, which creates bioluminescence when it binds to its appropriate luciferin substrate, AkaLumine. When the entire sequence goes unregulated by ATF4, translation of AkaLuc can be detected by measuring luminescence in the presence of AkaLumine. HEK293FT cells (which have generally high transferability of results to neuronal cells) were transfected with the appropriate DNA sequence, treated with Tg, and subjected to hourly luminescent measurements for 24 hours. Results demonstrated that increased stress of the ER induced by Tg caused an increase in the expressed luminescence of the cells. Ultimately, these results could serve as a basis for neurodegenerative treatments, as the reporter protein sequence could be replaced with a therapeutic gene.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 C
Presentation/Poster Number: 10
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

LSD1 co-localizes with tau aggregates in rare tauopathy cases

Kang, Semin; Bai, Yu; Engstrom, Amanda K.; Walker, Alicia C.; Moudgal, Rohita A.; Myrick, Dexter A.; Kyle, Stephanie M.; Christopher, Michael; Katz, David J.

Presenter/s: Semin Kang
Emory Faculty Mentor: David Katz

Alzheimer's disease (AD), which affects more than 10 million people across the world per year, is a secondary tauopathy characterized by abnormal aggregation of β-amyloid plaques and neurofibrillary tangles of hyperphosphorylated tau (NFTs). Previously, our lab has shown that the inhibition of the lysine-specific histone demethylase, LSD1 in adult mice induces cortical and hippocampal neurodegeneration, learning and memory deficits, and transcription alternations that match human AD cases. Additionally, we have found that reduction of LSD1 in P301S tau mice, a transgenic line that overexpresses an aggregation prone version of tau throughout the nervous system, exacerbates neurodegeneration while overexpression of LSD1 rescues hippocampal neurodegeneration. Most importantly, LSD1 colocalizes with cytoplasmic pathological tau in P301S tau mice and AD cases. Based on this, we hypothesize that after translation, LSD1 interacts with pathological tau in the cytoplasm. This process will prevent LSD1 from entering the nucleus and cause neurodegeneration. AD and other types of rare tauopathy cases, such as Corticobasal Degeneration (CBD), Progressive supranuclear palsy, Pick's disease, and Frontotemporal dementia with parkinsonism-17 cases have varying tau pathology. This provides an unique opportunity to interrogate the specificity of LSD1's interaction with pathological tau. To examine this specificity, we perform LSD1 immunohistochemistry and LSD1-pathological tau dual immunofluorescence in tauopathy and age matched non-demented cases. Upon observation, we report that LSD1 co-localizes with all forms of pathological tau in these rare tauopathy cases, which suggests that the cell type, aggregated structure and particular isoform are not required for co-localization. As a result, we will follow up with fractionation to look at the co-localization in further detail. Importantly, since LSD1 co-localizes with pathological tau in all of these rare tauopathies, we can support that any successful therapeutic intervention targeted to the LSD1 pathway in the future could also potentially be effective in these diseases.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 D
Presentation/Poster Number: 13
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining the anatomical substrates of circuitry in the lateral septum

Isaac, Jennifer; Karkare, Sonia; Murugan, Malavika

Presenter/s: Sonia Karkare
Emory Faculty Mentor: Malavika Murugan

The lateral septum (LS) has been implicated in a wide range of social behaviors, but much is still unknown about how the LS contributes to these behaviors. In order to elucidate the role of the LS, we must understand how the LS interacts with other brain regions. For this study, we targeted the LS to nucleus accumbens (NAc), LS to bed nucleus of the stria terminalis (BNST), and the LS to ventromedial hypothalamus (vmH) projection populations. We expected that the LS neurons that project to each of these target regions would have different presynaptic inputs due to the varied nature of the social behaviors associated with these target regions. We used monosynaptic rabies tracing to examine these projections. Our results show distinct presynaptic populations projecting to each LS projection population. Using whole brain mapping techniques, we found that the LS-BNST and LS-vmH received inputs from the same compartments of the hippocampus. The LS-BNST projection appears to receive more inputs from the dorsal CA1 and the ventral subiculum. In contrast, the LS-vmH projection receives from inputs from the ventral CA1 and also receives dense thalamic input. This indicates that different LS projections receive distinct inputs, which may shape their behavioral outputs. To further investigate these findings, we will use projection specific calcium imaging to determine how they are involved in social behaviors.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 C
Presentation/Poster Number: 12
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Synthesis of Extracellular Vesicle-Like Vehicles for Cardiac Repair

Kassouf, Brandon; Bheri, Sruti; Davis, Michael

Presenter/s: Brandon Kassouf
Emory Faculty Mentor: Michael Davis

Myocardial infarction (MI) is one of the leading causes of morbidity and mortality worldwide.1 MI leads to local ischemia, tissue damage and eventually cardiac failure.2,3 Small extracellular vesicles (sEVs) are nanoscale vesicles released by cells which carry pro-reparative microRNAs (miRs).4 Given their native origin, they contain favorable membrane proteins which enhance their local uptake and minimize immune responses during delivery. However, the type and concentration of cargo encapsulated in sEVs are difficult to control, and their potency is limited by their low yield, dependency on parent cells, and low miR cargo copy number.5 To address this problem, this research aims to design extracellular vesicle-like vehicles (ELVs) with customizable cargo and sEVs' proteins embedded in the membranes. The primary objectives are to (1) synthesize ELVs with sEV-like membrane protein composition and (2) encapsulate reparative miRs in the ELVs. sEVs were isolated from the conditioned media of c-kit+ progenitor cells through differential ultracentrifugation. A modified detergent-based approach was developed to reconstitute sEV membrane proteins in ELVs. Specifically, sEVs were solubilized with detergent (n-Octyl-β-D-thioglucoside) and reconstituted as vesicles through BioBead-mediated detergent removal. Spectrophotometry was used to track detergent solubilization and the degree of detergent removal. The sizes and concentrations of sEVs and ELVs were measured with nanoparticle tracking analysis and membrane protein content was analyzed with BCA. Through electroporation, miR-126, a pro-angiogeneic cargo, was encapsulated in ELVs. Encapsulation efficiency and ELV reparative capacity were assessed through a tube formation assay. sEVs and ELVs were found to contain 10.0±5.67 fg and 13.7±7.41 fg of RNA per particle respectively. Following BCA analysis, sEVs and ELVs contained 7.44±2.02 fg and 55.5±42.6 fg of protein per particle respectively. These findings suggest that this methodology can form ELVs with proteins incorporated. Combined with electroporation, this detergent-based approach could synthesize vesicles with favorable uptake to deliver cardioprotective cargo post-MI.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 D
Presentation/Poster Number: 13
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Production of Lamprey VLRB Antibodies Against Ovarian Cancer Cells

Kazzi, Bahaa; Cooper, Max, Valadez Sanchez, Gerardo, Hirano, Masa

Presenter/s: Bahaa Kazzi
Emory Faculty Mentor: Max Dale Cooper

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 C
Presentation/Poster Number: 9
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Sensory-evoked calcium responses in spinal motor neurons and their modulation by descending motor systems

Khan, Uswa; Giorgi, Andrea; Perreault, Marie-Claude

Presenter/s: Uswa Khan
Emory Faculty Mentor: Marie-Claude Perreault

In the nervous system, it is not fully understood how descending systems from the brainstem interact with spinal sensorimotor systems to produce adaptive motor movement. Most past research has studied modulation by descending systems of spinal sensory circuits and motor circuits separately, but it is unclear how descending systems modulate the integration of sensory inputs by motor circuits. In this project, we test the influence of a descending serotonergic raphespinal pathway on the recruitment of motoneurons by sensory inputs. Experiments were performed on newborn TpH2-ChR2-eYFP mice from postnatal days 0 to 4. Mice were dissected for brainstem/spinal cord preparations, which were retrogradely labelled using Calcium Green-1 Dextran Amine crystals in the ventral root of the second lumbar segment (L2) of the spinal cord. To activate sensory afferents, the L2 dorsal root was activated using a single, 0.2 ms electrical pulse. Channelrhodopsin-expressing serotonergic neurons in the raphe pallidus (RPa) were optically activated with blue light (473 nm), via 10s trains of 30 ms pulses at 10 Hz. DR-evoked calcium responses were analyzed in 132 MNs (n=7 animals) in the absence and presence of RPa stimulation. We found that RPa stimulation decreased DR-evoked calcium responses in MNs by 41 ± 4%. These data suggest an inhibitory effect of the serotonergic neurons descending from the RPa on the recruitment of lumbar MNs by sensory afferents. In future experiments, we will examine how RPa serotonergic neurons affect sensory recruitment of different populations of spinal interneurons that connect to MNs.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 D
Presentation/Poster Number: 14
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The effect of the trkB ligand prodrug R13 on sensory axon regeneration after peripheral nerve injury

Khan, Samia; Carrasco, Dario; Isaacson, Robin; English, Arthur

Presenter/s: Samia Khan
Emory Faculty Mentor: Arthur English

Poor recovery from peripheral nerve injuries (PNIs) is a significant public health issue due to the slow and inefficient process of axon regeneration. Experimental therapies that increase expression of neuronal brain derived neurotrophic factor (BDNF) or its trkB receptor are known to promote axon regeneration. Treatments using recombinant human BDNF or even the small molecule BDNF mimetic, 7,8-dihydroxyflavone (7,8-DHF), are not feasible because of their short biological half-life. A prodrug R13 is metabolized in the liver and forms 7,8-DHF, which prolongs trkB signaling. The effectiveness of R13 treatments on motor axon regeneration has been studied. The goal of this project was to evaluate the effect of R13 treatments on the regeneration of sensory axons following PNI. We hypothesized that R13 treatments following PNI would result in enhanced regeneration of sensory axons. Using a mouse model of PNI, the sciatic nerve was cut and repaired using fibrin glue. Mice were then treated with two weeks of daily oral administration of either R13 (43.6 mg/Kg) or a vehicle treated control. Four weeks after surgery, different fluorescent retrograde tracers were injected into the lateral gastrocnemius (GAST) and tibialis anterior (TA) muscles to mark sensory (dorsal root ganglion, DRG) neurons that had reinnervated these muscles. Preliminary counts and sizes of labeled DRG neurons were compared between R13 treated and control mice. In mice treated with R13, the number of retrogradely labelled neurons was not significantly larger than that of the control mice, including large, intermediate, and small neurons. Unlike motoneurons, the success of R13 as an oral treatment to promote sensory axon regeneration is questionable. Further study is warranted to investigate a more accessible and efficient therapy for PNIs.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 C
Presentation/Poster Number: 10
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The expression of CD62LhiCD44lo in LCMT-1 KO mice

Kim, Emily; Tam, Duncan; Pallas, David

Presenter/s: Emily Kim
Emory Faculty Mentor: David C. Pallas

One of the key regulators of PP2A through methylation is LCMT-1 (leucine carboxyl methyltransferase). This enzyme is a highly specific protein methyltransferase that regulates the formation of certain PP2A heterotrimeric forms in combination with PME-1 (Protein Phosphatase Methylesterase-1). Both PME-1 and LCMT-1 are essential in regulating the cell cycle, apoptosis, Tau phosphorylation, and further evidence showed that LCMT-1 and PME-1 play a major role in therapeutic benefits for cancer and Alzheimer's disease. In order to investigate the possibility of autoimmunity of mice without LCMT-1 to methylate PP2A, we will be studying mice with conditional LCMT-1 knockout (cKO) cells in blood cells, specifically whether the loss of LCMT-1 causes premature and excessive activation of T cells compared to control mice that have functioning LCMT-1 proteins. Studies have led to investigations of surface adhesion molecules, CD62L and CD44, as useful markers for differentiating naïve and memory T cells. We plan to use these markers to test for premature activation of T cells in our LCMT-1 knockout mice. We will also determine whether premature activation is of CD4+ helper cells, CH8+ effector cells, or both. Flow cytometry analysis will determine whether memory T cell phenotypes (CD62LloCD44hi) or naïve T cell phenotypes (CD62L hi CD44lo) would appear in CD4 and/or CD8 T spleenocytes. Following an intital wash to a 20 minute external staining to a final wash treatment on cells, an analysis through flow cytometry resulted in the LCMT-1 KO mice to have an increase in CD8+ cells that expressed CD62LloCD44hi memory T cell phenotypes, whereas CD4+ cells had no selective increase in expression of CD62LloCD44hi memory T cell phenotype. These experiments will help determine the role of LCMT-1 in the functioning and regulation of our immune system and may aid in identifying a novel drug target to treat autoimmune diseases.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 C
Presentation/Poster Number: 9
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effects of Adapted Tango and Walk Interventions on Heart Rate and Rate of Perceived Exertion in patients with Prodromal Alzheimer's Disease or Parkinson's Disease

Kim, Shiyeon; Hackney, Madeleine E.

Presenter/s: Shiyeon Kim
Emory Faculty Mentor: Madeleine Hackney

Prodromal Alzheimer's disease (pAD) is a stage of mild cognitive impairment that affects complex cognitive and motor abilities such as episodes of memory loss, delayed recall, or altered executive abilities (Scharre, 2019). Parkinson's disease (PD) is a progressive neurodegenerative movement disorder that results in impaired balance, walking, and reduced quality of life (Hackney & Earhart, 2009). Studies show that physical activity can improve health and cognitive/motor functioning in individuals with pAD or PD, such as walking or dancing which presents health benefits like improved static and dynamic balance or knee extensor muscle strength (Bennett, 2018). Participants with pAD and PD were randomly assigned to WALK (at least 60 minutes of walking with breaks and ½ hour of balance/stretching) or Adapted Tango interventions (interpreting motor goals through touch, developing understanding of temporal relationship of movement to music, and connecting previously learned with novel step elements), both equivalent in dose, volume, frequency, intensity, and duration of exercise (Hackney & Earhart, 2010). During both interventions, rate of perceived exertion (RPE), a means of measuring intensity levels experienced during exercise, and heart rate (HR) will be measured as studies show strong associations between higher RPE and increased HR (Bevan, 2020). The aims of this study are to determine 1) how the average HR and RPE values vary between the first and tenth classes for Adapted Tango and WALK interventions at each time point (pre-class, after warmup, 15 minutes, 30 minutes, and 45 minutes); 2) differences in HR and RPE between patients with pAD and PD for their first and tenth classes; 3) correlations between HR and RPE for the pAD and PD participant groups. This study is significant because the efficacy of WALK or Adapted Tango interventions on physically challenging participants with pAD or PD could be determined. The preliminary findings are currently inconclusive.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 B
Presentation/Poster Number: 8
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining predictors of constructive parenting behaviors in a sample of Black American mothers

Kim, Sarah; Cohen, Madeleine; Brennan, Patricia

Presenter/s: Sarah Kim
Emory Faculty Mentor: Patricia Brennan

Warm and responsive (constructive) parenting received during childhood is associated with greater constructive parenting displayed as a parent. Environmental factors such as lower stress and secondary caregiver support are also associated with greater constructive parenting. The current study examined predictors of constructive parenting behaviors in n = 155 African American mothers. We hypothesized that mothers who received more constructive parenting as children would display more constructive parenting, and that lower self-reported stress and the presence of a secondary caregiver would predict greater constructive parenting behaviors above and beyond mothers' received parenting.

Inclusion criteria were completion of the Parental Bonding Inventory (PBI) when infants were 6-months-old or participation in a 5-minute free play to assess constructive parenting when infants were 6-, 12-, or 18-months-old. Missing data were multiply imputed. We performed three multiple linear regressions; mothers' constructive parenting at 6-, 12-, or 18-months was the dependent variable. We entered covariates – maternal age, parity, socioeconomic status (SES), child sex, child age – as predictors in the first block. Mothers' scores on the PBI were entered in the second block. Scores on the PSS and secondary caregiver presence were entered in the third block. Sociodemographic variables explained a significant percentage of the variance (all R2's ≥ 0.13, p's < 0.001) in constructive parenting at all timepoints. Received parenting, stress, and caregiver presence did not explain additional variance.

While we did not find support for intergenerational transmission of constructive parenting, our null findings suggest resilience: receiving less constructive parenting and/or experiencing greater stress did not prevent mothers from exhibiting constructive parenting behaviors. Our assessment of secondary caregiver support focused on the presence/absence of a caregiver. Further study is needed regarding quality of caregiver support. Mothers' SES, age, and parity predicted constructive parenting. Understanding how these contextual factors influence parenting might inform early parenting interventions.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 3 D
Presentation/Poster Number: 13
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The Myth of Progress: Industrial Religion and the Legacy of Atticus G. Haygood

Kim, Gabriele; Gordon, Michelle

Presenter/s: Gabriele Kim
Emory Faculty Mentor: Michelle Gordon

History is often defined as change over time, but a common assumption that comes along with this change is that society is progressing towards a better future-- progress being urbanization, comfort, technology, innovation, justice, equality, etc. The Industrial Religion as discussed by theologian Richard Callahan examines progress through coal which fueled industries, the gospel of conversion, and cleanliness. Using this framework, I seek to contribute a more complete biography to the existing narrative of Bishop Atticus G. Haygood, a former president of Emory who is most popularly praised as a great educator for his work with the Slater Fund which was philanthropy dedicated to educating the 'negro race.' Haygood as aforementioned was a proponent of educating the formerly enslaved and especially their descendants, but it is often not noted that he was a pro-segregationist and desired only for industrial education of Black people; he opposed liberal arts education for all people. He also emphasized God's timing and urged patience towards educating Black people, but this often implies a white benevolent but hegemonic reign over what people are allowed to study based on arbitrary assumptions of inherent intelligence associated with the color of one's skin. Perhaps the more nefarious phenomena regarding racial tensions in America is not the openly condemning of those who are not part of the dominant culture, but rather those who were heralded for being progressive but in actuality delivered the same messages of white supremacy in a more palatable fashion-- even if it was well-meaning.

Research Discipline: Humanities
Presentation Type: Oral Presentation

Session: 1
Presentation/Poster Number: 2 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/92988928818

Alterations of Intestinal Microbiota in Male vs. Female in Cholestatic Liver Disease

Koduri, Nitya; Thapa, Manoj

Presenter/s: Nitya Koduri
Emory Faculty Mentor: Arash Grakoui

The interaction between the gut microbiome and the immune cells has not been fully understood. It was shown that alterations in gut microbiota drove the progression of cholestatic liver disease. However, it is not clear how the gut bacteria directly influence the subset of T cells to produce IL-17 during cholestatic liver disease progression. Moreover, it is unknown whether alteration of gut microbiota is sex specific. Through investigating the differences in the gut microbiome of male and female, this project aims to identify specific biomarkers that directly influence immune cells and provide background for future therapeutic interventions against cholestatic liver disease. The mouse model multidrug resistance gene 2 knock-out (Mdr2-/-) was used to investigate cholestatic liver disease. To carry out this experiment, 12-weeks old male and female Mdr2-/- and FVB/N (WT control) mice were used. The mice were treated with a high fat diet (HFD) with 5% sodium cholate to investigate how HFD would modulate disease progression. Interestingly, we found a prolonged survival in female Mdr2-/- mice compared to male mice in response to HFD. Both males and females had enriched gut pathogenic bacteria Klebsiella in tissues such as ileum, liver, and brain on HFD treatment; however, males enriched the bacteria at earlier timepoints compared to females. We plan to analyze microbiome genomic sequencing for bacterial populations in the gut microbiome following HFD treatment. Further analysis can be performed on the mouse serum for liver injury markers and cytokine levels, and histopathological analysis of tissues such as ileum, liver, and heart specimens for HFD-induced pathology. Additionally, future studies aim to investigate organs at the peak of hepatic fibrosis in Mdr2-/- mice at 25 weeks of age. The analysis of liver tissues will be performed in both male and females to determine differences in liver microbiota during cholestatic liver disease progression.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 D
Presentation/Poster Number: 15
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Mapping Genetic Diversity Within Ecuador And Broader South America Through The Sequencing of Ancient Ecuadorian Genomes

Korder, Ruth; Joseph, Sophie; Pryor, Yemko; Lindo, John

Presenter/s: Ruth Korder
Emory Faculty Mentor: John Lindo

Abstract not available.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 8 C
Presentation/Poster Number: 11
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Validating an Exercise Model for Neuroprotection in the 6ODHA Mouse Model of Parkinson's Disease

Kotlure, Amrutha; Skelton, Henry; Grogan, Dayton; Berglund, Ken; Gutekunst, Claire-Anne; Gross, Robert

Presenter/s: Amrutha Kotlure
Emory Faculty Mentor: Claire-Anne Gutekunst

Parkinson's disease (PD) is a neurodegenerative disorder that causes dopaminergic cell death in the substantia nigra. The loss of these cells results in motor deficits including tremor, bradykinesia, and rigidity. Studies have shown that exercise is neuroprotective in animal models of PD, but the mechanism is not fully understood. We hypothesize that exercise protects dopaminergic cells by increasing their activity. In order to test this, we developed a forced exercise wheel compatible with electrophysiology and did a pilot treatment study using an eight week forced exercise regimen on mice unilaterally lesioned with 6-OHDA. We quantified exercise using markerless pose estimates with DeepLabCut and measured speed and position of the hind leg. DAB-TH immunohistochemistry was used to stain dopaminergic cells in the substantia nigra and striatum. The deficit in dopaminergic cells in the injected vs non injected site was measured using stereology. The amphetamine induced rotation test was done to assess the behavioral impact of the 6-OHDA lesion. This measured ipsilateral rotations relative to the site of injection of the 6-OHDA. Pose tracking data showed the mice in the cohort exercised at a similar, high level on the new wheel even after lesioning. Steriology showed significant differences in neuroprotection between the exercise group of 6-OHDA mice compared to the sedentary group. The sedentary mice had a mean 74% cell loss while the exercise mice had a mean 41% cell loss. An independent sample t-test showed statistical difference between the mean groups ($p = 0.0021$). The next steps include analyzing the behavioral data, measuring nigral electrophysiology during exercise, and measuring the impact of inhibitory neuromodulation using luminopsins on the neuroprotective effects of exercise.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 B
Presentation/Poster Number: 8
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Ultrastructural analysis of GluD1-Cbln1 signaling in the spino-parabrachio-amygdaloid pain pathway

Kozuch, Christopher; Choi, Diane; Pare, Jean-Francois; Smith, Yoland

Presenter/s: Christopher Kozuch
Emory Faculty Mentor: Yoland Smith

The spino-parabrachial-amygdaloid pathway is involved in the modulation of nociceptive and emotional-affective processes in chronic pain. Chronic pain affects over 50 millions of American adults, oftentimes leading to long-term disabilities, increased drug use and psychiatric disorders. Preliminary data has implicated the glutamate- delta 1 receptor (GluD1) – cerebellin1 (Cbln1) signaling pathway in the central amygdala (CeLC) to be a key modulator of chronic pain. GluD receptors are different from typical ionotropic glutamate receptors (AMPA/kainate, NMDA) as they function more as synaptogenic molecules. By interacting with presynaptic elements Neurexin1 and Cbln1, GluD1 forms a trans-synaptic complex that regulates the formation and maintenance of synapses. Neurons in the parabrachial (PB) nucleus, which highly express Cbln1, project to the lateral and capsular regions in the CeLC. At the synaptic level, GluD1 neurons in CeLC receive synaptic inputs from calcitonin gene-related peptide (CGRP) terminals, which arise exclusively from the PB nucleus. Electrophysiological evidence suggests that the GluD1-Cbln1-Neurexin1 trans-synaptic complex plays a significant role in the PB-driven excitation-inhibition balance in the CeLC. Based on these findings, we hypothesize that chronic pain is associated with changes in the expression of GluD1 at synapses formed by CGRP+ terminals in the CeLC. To address this issue, we used a double-immunolabeling approach at the electron microscopic level to quantify changes in the prevalence of CGPR+ terminals associated with post-synaptic GluD1 in the CeLC of control mice and a mouse model of chronic pain. Preliminary data obtained so far confirms a strong expression of GluD1 at synapses formed by CGRP+ terminals in control mice. Overall, this project aims to obtain a better understanding of the structural and molecular mechanisms related to chronic pain and to reveal novel targets for minimizing the effects of chronic pain.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 D
Presentation/Poster Number: 14
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

In-Vitro Contact Independent Inhibition of Microbial Insect Mutualists

Kwong, Zee; Chen, Jason; Gerardo, Nicole; Vega Nic

Presenter/s: Zee Kwong
Emory Faculty Mentor: Nicole Gerardo

Microbial symbionts fundamentally transform how their hosts utilize nutritional resources and respond to environmental stresses, emphasizing the importance of understanding the formation of these mutualisms. We explored this assembly through horizontally transmitted Burkholderia which forms a symbiosis with Anasa tristis. Although A. trisis likely implements techniques such as an intestinal constricted region and antimicrobial protein secretion that filter out undesired microbes, we hypothesized that Burkholderia employs mechanisms to outcompete similar microbial strains not eliminated by the host. We explored this competition through high throughput in vitro conditioned media assays that measured the growth of Burkholderia in the filtered media of another Burkholderia strain. Based on the results, there was strong evidence of contact-independent interactions between Burkholderia strains due to deviated growth in various condition media. Additionally, utilizing 16S sequencing data, we have identified clade-dependent patterns that explain condition media growth. Finally, there were variations in growth depending on whether Luria Broth, Minimal Media, or Squash Juice was used as the nutritional media, illustrating how the environment dictates microbial interactions. This experiment demonstrated that Burkholderia exhibits genetically related inhibition that may provide them a competitive advantage in colonizing the midgut crypt of A. tristis. These results open the path to in vivo competition assays within the crypts of A. tristis and the eventual identification of the competition mechanisms.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 7 C
Presentation/Poster Number: 11
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Behavioral Mechanisms of Socially-Guided Vocal Learning in Juvenile Male Bengalese Finches

Lagerquist, Megan; Baran, Nicole M.; Maney, Donna L.

Presenter/s: Megan Lagerquist
Emory Faculty Mentor: Donna Maney

Socially-guided vocal learning, or the ability to modify vocal output based on experience, is critical to the development of complex social behaviors. Song learning in birds and vocal learning in humans both occur in critical periods of development during which the organism learns song or speech from adult caregivers. Juvenile male songbirds learn a caregiver's song best from live tutoring, but the neural and behavioral mechanisms that promote socially-guided song learning have not been established. This study aims to identify socially-relevant behaviors exhibited by both the juvenile and the father during a live tutoring session. At 45 days post-hatch, at the peak of sensory song learning, juvenile male Bengalese finches were placed in a cage adjacent to either their father (tutor condition, n = 4) or a familiar female (control condition, n = 4). We recorded the behavior of both the juvenile and stimulus bird for 45 minutes and scored typical behaviors, such as proximity, beak wipes, and general activity, which we suspected to be associated with attention and arousal. We found that juveniles in the tutor condition and tutors themselves spent significantly more time with two feet on the shared wall and performed more beak wipes, suggesting these behaviors are relevant to communication during tutoring. Additionally, there were trends approaching significance that suggest that juveniles in the tutor condition were more active and pecked more frequently while in the proximal zone, although more samples are needed to confirm these findings. These preliminary results lay the groundwork for future analysis of the association between behavior exhibited during social interactions with the father and neural markers of social learning. Ultimately, understanding socially-guided vocal learning in other species can promote our understanding of the behavioral contingencies and neural mechanisms important to human language acquisition and related neurodevelopmental deficits.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 C
Presentation/Poster Number: 10
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Isoform of Transcription Factor Induces Pro-Atherogenic Pathways

Lam, Shivani; Andueza Lizarraga, Aitor; Jo, Hanjoong

Presenter/s: Shivani Lam
Emory Faculty Mentor: Hanjoong Jo

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 C
Presentation/Poster Number: 11
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining if Endometriosis Pain Symptoms Can be Lessened by Alda-1 in Rats

Lang, Lindsey; Arthurs, Erin; McAllister, Stacy

Presenter/s: Lindsey Lang
Emory Faculty Mentor: Stacy McAllister

Endometriosis is an estrogen-dependent condition where ectopic endometrial tissue grows on multiple organs outside the uterus. The main symptom of the disease is pain which can be lifelong and debilitating. Previous work shows that the enzyme ALDH-2, responsible for metabolizing reactive aldehydes, has decreased activity in women with endometriosis. Alda-1 is an activator of ALDH-2, which can increase the metabolism of reactive aldehydes. This study analyzes the effectiveness of Alda-1 in reducing endometriosis pain symptoms in rats. Rats were trained through behavioral conditioning to respond to vaginal distention, emulating vaginal canal pain associated with endometriosis. Rats then undergo a procedure to induce endometriosis-like symptoms. Rats will receive either Alda-1 or Disulfiram to see how rats' pain symptoms change when reactive aldehydes metabolism increases or decreases. Rats will go through behavioral testing to see if pain responses have changed post-treatment. This research seeks to find new therapeutic options to decrease endometriosis pain symptoms, which will help to improve the quality of life of women who suffer from these symptoms.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 C
Presentation/Poster Number: 9
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Reduced Push-off During Lateral Jumps after Anterior Cruciate Ligament Surgery

Lee, Frances; Lyle, Mark

Presenter/s: Frances Lee
Emory Faculty Mentor: Mark Lyle

Following anterior cruciate ligament reconstruction (ACLR), ~25% experience a second ACL injury within the first year back to normal athletics and ~50% do not return to play at the same level of competition. Asymmetries in sagittal plane knee kinetics are likely a predominant factor in ACL re-injury, which could result in poorer sports performance. Most research has focused on sagittal plane tasks (vertical or forward jump), but athletes must also rapidly change direction requiring lateral pushing which if impaired, could reduce sports performance. The purpose of this study was to compare impact jump performance between the ACLR and non-surgical leg during lateral jumps. Twenty participants (17.2 ± 3.2 years) completed 3 maximal effort lateral jumps off of one limb for the ACLR and non-surgical limbs. The jumps were completed with the jumping leg on a force plate (AMTI Waterton, MA) to record ground reaction forces (GRFs), focusing on peak Fy and Fz. In support of vertically tasked vertical GRF (VGRF) results, participants were expected to have a similar trend of lateral vertical GRF (LGRF) in the surgical limb versus the non-surgical limb due to using the same knee and hip biomechanics. Results showed that peak Fy for the ACLR limb was significantly smaller than the non-surgical limb (515.94 ± 171.03 N vs. 540.83 ± 160.94 N, p=0.0053). The peak Fz for the ACLR limb was significantly smaller than the non-surgical limb (1281.87 ± 350.31 N vs. 1355.34 ± 351.31 N, p=0.0023). This data suggests that those who have had ACLR will have an overall lower LGRF and VGRF on the surgical limb. Through these results, the higher lateral GRF on the non-surgical limb shows the flaws in ACLR rehabilitation evaluations and protocols preventing further ACL re-injuries.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 D
Presentation/Poster Number: 15
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Reduction of Carbon Dioxide via Carbon Monoxide Dehydrogenase II in a Photochemically Activated Catalytic System

Lee, Sam; White, David; Dyer, R. Brian

Presenter/s: Sam Lee
Emory Faculty Mentor: R. Brian Dyer

With the alarmingly sudden increase of atmospheric CO2 levels, it would be ideal to find use in the ubiquitous greenhouse gas. An elegant solution would be to convert it into a useful product, but available catalysts for the reduction of CO2 suffer from efficiency and selectivity issues due to the requirement of large overpotentials. However, carbon monoxide dehydrogenases (CODHs) can catalyze the reversible reduction of CO2 to CO quite efficiently. Recent efforts have focused on activating these enzymes with light to sustainably convert CO2 to CO. In this research, a photosensitizer was employed in conjunction with an electron mediator to drive the reduction of CO2 to CO via CODH II from Carboxydothermus hydrogenoformans. For the photosensitizer, nanocrystalline CdSe/CdS dot-in-rod structures were selected and synthesized. In addition, reaction conditions such as CO2 concentration were investigated to improve the efficiency of the photocatalytic system. In the optimized photocatalytic system, a quantum yield of >1% was achieved. These results demonstrate that CODH II can be activated by light, a finding that opens up new avenues of research to tackle the looming problem of greenhouse-gas-induced climate change.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 C
Presentation/Poster Number: 12
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Growth Differentiation Factor 15 Causes Cardiac Cachexia In Heart Failure

Lee, Da Young; Jiao, Zhe; Antolic, Andrew; Weiss, Daiana; Weitzmann, M. Neale; Burke, Michael A.

Presenter/s: Da Young Lee
Emory Faculty Mentor: Michael A. Burke

Cachexia, the wasting of normal body tissue, is a common complication of heart failure (HF) that is associated with high mortality. Growth differentiation factor 15 (GDF15) regulates food intake and causes cachexia in cancer. GDF15 is a sensitive biomarker in humans, though its biologic function in HF is unknown. We investigated the role of GDF15 in HF by utilizing a genetic mouse model of HF caused by a mutation in the phospholamban gene (PLNR9C). Q-PCR and ELISA were performed to assess expression, tissue distribution and circulating levels of GDF15 in PLNR9C and age-matched wild type (WT) mice. A double transgenic mouse was created by crossing PLNR9C with a constitutive Gdf15 knock-out (KO). Using this novel model, we quantified food intake, and assessed fat and lean tissue mass by tissue weight at necropsy and by dual-energy X-ray absorptiometry (DXA). Cardiac function was assessed using echocardiography, and histochemistry performed to quantify cardiac fibrosis. Survival was assessed by Kaplan-Meier. GDF15 was increased in heart tissue (mRNA, 43-fold; protein, 54-fold, p<0.01 for both) and serum (8.3-fold; p=0.03) from PLNR9C mice. Gdf15 was expressed at low levels and was not increased in other organs in PLNR9C mice. PLNR9C mice developed cachexia (reduced fat and lean mass by tissue weight, reduced fat mass by DXA vs. WT; p<0.01 for all) and consumed less food (p<0.01 vs. WT). Gdf15 KO in PLNR9C preserved fat and lean tissue mass (p≤0.01 for all). Surprisingly, Gdf15 KO had no effect on cardiac structure or function by echocardiography and only reduced cardiac fibrosis slightly (PLNR9C 21% vs. PLNR9C/Gdf15 18%, p<0.01; vs. WT ~1%), suggesting a systemic mechanism of action. Despite this, Gdf15 KO prolonged survival by 15% in PLNR9C (p<0.01). In summary, GDF15 is a novel cardiac hormone produced in HF that triggers cachexia by an extra-cardiac mechanism.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 2
Presentation/Poster Number: 4 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/95175906316

Effect of BIM and NOXA Proteins on MCL1 Protein Stability

Author 1 Lett, Jason; Author 2 Owens, Rebecca; Author 3 Boise, Lawrence
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Presenter/s: Jason Lett
Emory Faculty Mentor: Lawrence Boise

Multiple Myeloma is the second most common hematological malignancy. Myeloid cell leukemia-1 (MCL1) is an anti-apoptotic protein that is induced during plasma cell differentiation and essential for plasma cell and myeloma cell survival. MCL1 is the target of many drugs that are currently being developed. When B-cell lymphoma-like protein 11 (BIM) binds to MCL1 it stabilizes the protein and allows the concentration of MCL1 to increase because it is not being degraded as it should. This research aims to analyze the effect the presence BIM and NOXA have on the stability of the MCL1 protein and evaluate the effectiveness of multiple MCL1 inhibitors. MCL1 inhibitors are likely to be effective in a broader range of patients and are currently in early clinical trials. Samples have been collected from a specific cell line (KMS 34) and undergone CRISPR editing to generate knockouts for the genes responsible for producing both BIM and NOXA. The cells are split to be treated with each drug at multiple concentrations. These cells are treated by either AZD4573, a Cyclin Dependent Kinase 9 (CDK9) inhibitor that interrupts RNA transcription and therefore production of proteins like MCL1, AZD5991, a MCL1 inhibitor to disrupt MCL1 itself, or Bortezomib, a proteasome inhibitor that prevents the breakdown. Of proteins. After drug exposure the cells are fluorescently labelled and taken for flow cytometry where they are then excited by a laser to emit light at varying wavelengths. Cells that are dead because of the drug treatment are exposed to more of the fluorescent markers, dying cells are exposed to slightly less and living cells next to none. This dead-alive assay allows for researchers to determine how effective each treatment is on the myeloma cell.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 C
Presentation/Poster Number: 12
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating the Effect of Tethered Chain Length on Local Glass Transition Temperature of Polystyrene by Grafted-chain-covered Silica Substrates

Li, Carl; Merrill, James; Roth, Connie

Presenter/s: Carl Li
Emory Faculty Mentor: Connie Roth

Recently, Huang and Roth demonstrated a 50°C increase in local glass transition temperature (Tg) within a bulk polystyrene (PS, Mw ≈ 1900 kg/mol) film next to a layer of end-grafted polystyrene (Mw ≈ 100 kg/mol) chains, indicating a dramatic slowing down of dynamics near the substrate. This study follows up on how end-grafted polymer chains on silica substrates change the glass transition temperature of a film of polystyrene on top of the grafted layer by varying the chain length (molecular weight) of the grafted chains. The local glass transition temperature next to the substrate within the polystyrene film has been determined using a multilayer sample geometry consisting of a layer of grafted chains, a 12 nm fluorescently-labelled polystyrene probe layer above, and a 590 nm bulk polystyrene layer on top, while measuring fluorescence intensity on cooling. Temperature dependence of the pyrene fluorescence intensity, due to its sensitivity to the local density and polarity of the polymer matrix surrounding the fluorophore, has been associated with the glass transition, enabling the use of pyrene as a molecular probe for the glass transition temperature in polymer films. Here we present measurements of Tg next to the substrate as a function of grafting density using the original molecular weight (100 kg/mol) showing reasonable agreement with the existing results in the literature. We then study the influence of the chain length of the tethered chains by reducing the molecular weight from 100 kg/mol to 50 kg/mol, which in turn changes the dynamical perturbation caused by the tethered chains interpenetrating with the bulk layer. Such a comparison between the different tethered chain lengths would be informative of the mechanism by which grafted chains slow down dynamics in adjacent polymer films.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 D
Presentation/Poster Number: 13
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

From San Francisco Chinatown to the American South: Chinese American Christians in the Civil Rights Movement

Li, Annie; Suh, Chris

Presenter/s: Annie Li
Emory Faculty Mentor: Chris Suh

The Civil Rights Movement, loosely bound by the Montgomery Bus Boycott of 1955 to the Civil Rights Act of 1968, witnessed the mass organization of ordinary people in pursuit of freedom and justice. Given the direct links between the Black church's theology and activism, this project seeks to uncover the less apparent relationship between the Chinese American church and its activism. Using Chinese American Christians in the Civil Rights Movement as a case study, this project confronts the following questions: How did a distinctly Asian American theology resonate with and motivate people to get involved in the Black freedom struggle? Broadly, what theological or ethical notions compel people to align themselves with the communal struggle for justice? Leveraging materials from the San Francisco Chronicle, API Women Faith, & Action oral history project, and Civil Rights Movement online archive, this paper argues that the theological principles of the Presbyterian Church in Chinatown motivated its members to travel to the American South and invest in the Black civil rights struggle. Franklin Fung Chow, Rev. Larry Jack Wong, Doreen Der-McLeod, Marion Kwan, and Adrienne Fung belonged to the circle within the church and Cameron House, a social service agency. Their experiences in these two communities served as a cornerstone of their spiritual and political consciousness. In the existing scholarship, the Black-Asian American civil rights narrative typically centers on figures in the Black Power Movement, such as Malcolm X and Yuri Kochiyama, Huey Newton and Richard Aoki. This project complicates and expands the historiography of Black-Asian alliances in the United States, as well as forges new connections between Asian American theology and activism. The preliminary findings invite further research using documents housed at UC Berkeley and San Francisco Public Library, for more nuanced analysis on the lives of these individuals, the church, and Cameron House.

Research Discipline: Humanities
Presentation Type: Oral Presentation

Session: 3
Presentation/Poster Number: 5 of 6
Presentation Time: 10:30 AM to 12:00 PM
Presentation Link: https://emory.zoom.us/j/95598055387

Effects of Catecholamine Lesions in the Robust Nucleus of the Arcopallium in Adult Bengalese Finches

Li, Joyce; Sober, Samuel; Wood, Alynda

Presenter/s: Joyce Li
Emory Faculty Mentor: Samuel Sober

Complex motor tasks, such as vocal behavior, require sensory input from the environment to aid in the acquisition and maintenance of the skill. The songbird system is an excellent model for studying such complex motor behaviors due to its similarities to human vocalization. The area of interest, the robust nucleus of the arcopallium (RA), is a key motor structure in the songbird brain that has been shown to be involved in the control of song. RA receives dopaminergic and noradrenergic inputs, though the function of these catecholamine inputs in RA on a bird's song have yet to be understood. This study proposes that catecholamine lesions within the RA of Bengalese finches disrupts the bird's ability to maintain its song via sensorimotor learning. The loss of dopamine and norepinephrine is hypothesized to increase pitch variability and increase spectral entropy. The RA of adult Bengalese finches were bilaterally lesioned using 6-hydroxydopamine and their song was recorded for up to twelve weeks post-lesion. Initial results reveal that catecholamine lesions in RA result in a pitch decrease in several syllables. This effect has not been observed in control lesion birds. Overall, these results suggest that catecholamine inputs in RA contribute to the maintenance of song in reference to pitch. Investigation into the function of catecholamine, and specifically dopaminergic, inputs in RA may improve our understanding of dopamine's role in motor behavior and sensorimotor adaptation.

Research Discipline: Natural and Physical Sciences
Presentation Type: Oral Presentation

Session: 7
Presentation/Poster Number: 2 of 6
Presentation Time: 3:00 PM to 4:30 PM
Presentation Link: https://emory.zoom.us/j/97807604820

Pharyngeal muscle satellite cell activation through HGF release from fibroadipogenic progenitor cells

Lim, Danbi; Choo, Hyojung

Presenter/s: Danbi Lim
Emory Faculty Mentor: Hyojung Choo

Satellite cells (SCs), skeletal muscle stem cells, reside within the basal lamina of muscle fibers. SCs in limb muscles are quiescent under normal conditions, but quickly proliferate, differentiate, and fuse in times of muscle regeneration. However, in pharyngeal muscles, SCs differentiate and fuse in an absence of muscle injury. Still, what factor increases pharyngeal SC activity more than limb SC is unknown. In this study, we compare SCs from limb and pharyngeal muscles to determine if cell-intrinsic and extracellular components, such as growth factors released by neighboring cells, of pharyngeal muscles induce SC activity. To investigate cell autonomous effects, we culture pharyngeal and gastrocnemius SCs in vitro. The result shows that pharyngeal SCs proliferate and differentiate more than limb SCs. As an extrinsic factor to stimulate pharyngeal SCs, we study the role of hepatocyte growth factor (HGF), a known SC activator. Fibroadipogenic progenitor cells in the pharyngeal muscle niche release HGF, which may activate pharyngeal SCs without injury. This study shines a light on differential SC activity in pharyngeal muscles, which gives new insights into their distinct susceptibility to muscular dystrophies, such as oculopharyngeal muscular dystrophy.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 C
Presentation/Poster Number: 9
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Sub-cellular Localization of Tight-junction Proteins with Striatin during Remodeling

Lin, Priscilla; Cai, Benjamin; Pallas, David

Presenter/s: Priscilla Lin
Emory Faculty Mentor: David Pallas

Epithelial layers are essential for a plethora of physiological processes, regulated by intracellular adhesive structures: adherens junctions (AJs), tight junctions (TJs), and desmosomes. In particular, tight junctions are essential for epithelial barrier integrity and solute flux, and its loss has been linked to the pathogenesis of many diseases. Recent studies have shown that one or more members of the striatin family of proteins are present in cellular tight junctions. However, the specific members and domains important for colocalization of striatin proteins and endosome markers during the recycling process remain unknown; insight into such information will be useful in understanding the role striatin plays in tight junction formation and regulation. Therefore, the objective of the present study seeks to identify areas of subcellular localization of tight-junction proteins and striatin during remodeling in the well-studied human epithelial colon cell line, Caco-2. A series of experiments were conducted to compare subcellular distributions and colocalizations of known tight-junction proteins during junction remodeling induced by EGTA, as visualized by immunofluorescence. Although research is still ongoing, initial studies have identified tight-junction proteins that are of particular interest, which will then be used to determine striatin's role in tight junctions. Understanding the roles striatin and its family members play in tight junctions will shed light on tight junction formation, remodeling, and diseases related to its dysfunction.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 C
Presentation/Poster Number: 10
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Diversity of Fungal Parasite Interactions in Coinfective Environments

Lin, Sandy; Singh, Rohan; Gerardo, Nicole

Presenter/s: Sandy Su-Ting Lin and Rohan Singh
Emory Faculty Mentor: Nicole Gerardo

Coinfection occurs when multiple parasites infect the same host. This can alter host-parasite ecology as parasites have previously demonstrated the ability to inhibit or facilitate the colonization of the host for one another. Fungus-growing ants, their cultivated fungi (cultivar), and their parasites (Escovopsis sp.) are an ideal model system for studying how these different interactions can occur because they exhibit frequent instances of coinfection as well as considerable phylogenetic diversity. We studied how different strains of Escovopsis interact with each other across the phylogeny to better understand their patterns of interaction. We plated combinations of two strains of Escovopsis on petri dishes and assessed their growth over multiple weeks. By assaying multiple pairings of Escovopsis, we were able to categorically identify the ways in which the parasite interacts with other strains of Escovopsis including, but not limited to, attraction and inhibition. A deeper understanding of coinfection patterns could be helpful in mapping the coevolutionary history of hosts and parasites as well as in applications of managing virulent parasitic organisms. Further research could establish how these fungi are changing at the molecular level in reaction to one another as well as investigate a broader range of Escovopsis strains.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 D
Presentation/Poster Number: 14
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Split TurboID Proximity Labeling to Identify Kv1.3 Channel Interactors in Mammalian Cells

Lin, Young; Bowen, Christine; Xiao, Hailian; Ramelow, Christina; Rangaraju, Srikant

Presenter/s: Young Lin
Emory Faculty Mentor: Srikant Rangaraju

Kv1.3 potassium channels expressed by immune cells, such as microglia and lymphocytes, have emerged as promising therapeutic targets for several neurological diseases. These channels regulate membrane potential and calcium signaling in immune cells. Kv1.3 is a tetramer of four alpha subunits (Kcna3) which co-assemble with auxiliary beta subunits (Kvβ2). Based on the domain topology of Kv1.3, we suspect that Kv1.3 channels interact with key signaling pathways which impact cellular function and gene regulation. However, the exact role Kv1.3 plays in such signaling pathways is unclear. In order to identify proteins that interact with functional Kv1.3 channels assembled in the cell membrane, we employed conditional proximity labeling using the split-TurboID approach. TurboID is a biotin ligase that biotinylates proteins within a 10nm radius, allowing us to map interacting proteins when TurboID is fused with the protein of interest. Split-TurboID consists of two inactive fragments that can each fuse to different proteins of interest. TurboID only becomes functionally active when the fused proteins interact in close proximity. We fused split-TurboID components to the C- and N- terminuses of Kcna3 and Kvβ2 with a flexible linker. We then performed a series of transfection experiments in HEK 293 cells and ran a western blot for streptavidin to detect biotinylated proteins. We found that transfection only with one component of the split TurboID resulted in no biotinylation, while co-transfection of Kcna3/Kcna3 and Kcna3/Kvβ2 combinations resulted in robust biotinylation of proteins. Specifically, we observed the highest biotinylation in the Kcna3/Kvβ2 combinations, suggesting that functional channels recruit several proteins that co-assemble or interact with the Kv1.3 channel complex. Based on these promising results, we will now enrich biotinylated proteins from various conditions and use mass spectrometry to identify proteins that interact with specific domains of the Kv1.3 channel complex.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 6
Presentation/Poster Number: 4 of 6
Presentation Time: 1:30 PM to 3:00 PM
Presentation Link: https://emory.zoom.us/j/95175843929

“First Contact”: What demographics and the first serum creatinine determination reveals about the risks of Acute Kidney Injury and Sepsis

Ling, Jeffrey; Buchman, Timothy

Presenter/s: Jeffrey Ling
Emory Faculty Mentor: Timothy Buchman

Acute Kidney Injury (AKI) and Sepsis are two life-threatening organ dysfunctions that often occur together. This study aims to find out how these two conditions overlap and interact. Moreover, we wish to find whether hints of these conditions exist at first points of contact.

We obtained the Electronic Medical Records of 5050 patients admitted in CY2019 to Emory University Hospital. Exclusion criteria were hospital stay <5 days or pre-existing chronic renal failure. Demographic and laboratory data were extracted to examine whether AKI and Sepsis populations were distinct. Chi-Square and Mann-Whitney tests were conducted to check statistical significance and R studio was used to process and visualize data.

Key Findings

- Among 7448 admissions (5050 patients), 710 (11%) had AKI, 533 (7%) had Sepsis. Among 710 AKI admissions, 119 (11%) had Sepsis. Among Sepsis admissions, 22% had AKI.
- AKI occurs in 12.3% of men (vs 9.1% of women), 11.1% of those older than 45 (vs. 8.6% < 45). Sepsis occurs in 8.4% of men (vs 6.0% of women).
- While no initial creatinine could predict sepsis or AKI class membership, the populations with and without AKI differed with respect to the distributions of initial creatinine with average creatinine for AKI patients higher at 1.35 mg / dl (vs. 1.07 mg/dl for non-AKI).

In conclusion, AKI and to some extent Sepsis do not appear randomly and sometimes they overlap. While demographics and initial serum Creatinine are insufficient by themselves to predict classifications of individual patients, the fact that the populations are statistically distinguishable points to their potential inclusion as features in predictive models.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 D
Presentation/Poster Number: 14
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Pharmacological and Neuroanatomical Investigation of Aberrant Innate Behavioral Responses to Predator Odor in Mice Deficient for Dopamine Beta-hydroxylase

Liu, Joyce; Lustberg, Daniel; McCann, Kate; Weinshenker, David

Presenter/s: Joyce Liu
Emory Faculty Mentor: David Weinshenker

Fear is an innate emotional response critical for survival, and dysregulation of fear responses is implicated in psychiatric disease, including anxiety and post-traumatic stress disorders. Although norepinephrine (NE) has long been implicated in stress responses, pharmacotherapies targeting this system are limited. Toxoplasma gondii infection in mice reverses innate fear of predator odor, and may provide insight into the role of NE in fear responses because Toxoplasma infection suppresses the expression of dopamine beta-hydroxylase (DBH), the enzyme that converts dopamine (DA) to NE. However, the contribution of NE and DA to innate fear responses are not fully understood. In this study, we aimed to determine the effects of genetic and pharmacological disruption of DBH on behavioral responses and neuronal activity following exposure to predator odor. We first compared behavior between DBH knockout (DBH KO) mice that lack NE and have increased DA with their NE-competent littermate controls when exposed to predator odor. We then examined the behaviors of control mice treated with the selective DBH inhibitor nepicastat or saline vehicle when exposed to predator odor. Finally, we euthanized DBH KO and control mice after predator odor exposure and analyzed induction of Fos as a proxy of neuronal activity in brain regions implicated in stress responses to predator threat. Our results show that DBH KO mice exhibit abnormal behavioral responses to predator odor, including decreased digging and increased grooming, along with differences in neuronal activity in the locus coeruleus and target structures implicated in arousal, defensive behavior, and anxiety. The aberrant grooming and digging phenotypes could be recapitulated in control mice following acute DBH inhibition with nepicastat. These findings support a role for DBH function in innate fear and suggest that disruptions of NE and/or DA transmission may alter the recruitment of neural circuits that organize behavioral responses to predator threat.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 D
Presentation/Poster Number: 13
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effect of intraspecies interaction on growth dynamic and rate of antibiotic resistance evolution in Staphylococcus aureus isolated from sputum samples of cystic fibrosis patients

Hui Qi, Loo; Alexander, Ashley; Goldberg, Joanna

Presenter/s: Hui Qi Loo
Emory Faculty Mentor: Joanna Goldberg

Staphylococcus aureus was recently recognized as the most common bacterial pathogen found in the airway of patients with cystic fibrosis (CF). Current medical microbiology tests in CF are somewhat limited in their ability to predict antimicrobial treatment responses in patients as the roles of intrahost genotypic diversity and microbial interactions are yet to be elucidated. Studies have shown that S. aureus isolated from CF lungs are diverse phylogenetically and vary in their virulence and interactions with other bacterial species, which may result from multiple inoculation events or within-host evolution. My previous work also presented evidence for within-host heterogeneity in the antibiotic resistance gene profile of S. aureus isolated from CF patients. Here, we investigated the effect of interactions between different S. aureus strains isolated from a single CF patient on their growth dynamics and the evolution of antibiotic resistance phenotypes. Specifically, we studied intraspecies interactions between methicillin-resistant S. aureus (MRSA) and methicillin-sensitive S. aureus (MSSA) strains. By fluorescently labelling S. aureus strains, we assessed bacterial growth in monocultures and cocultures. In preliminary results, we compared the growth of these S. aureus strains by using area under curve (AUC) of growth curves as a proxy for growth potential and evaluate the relative fitness of these strains when in coculture, which provided insight into whether intraspecies coexistence may be an adapted trait for S. aureus. We also experimentally evolved cocultures of the MRSA and MSSA strains with monoculture controls along a concentration gradient of oxacillin to assess the rate of resistance evolution. Preliminary results showed that both MRSA and MSSA strains evolve oxacillin resistance more quickly in monoculture than when evolved in cocultures, suggesting a trade-off between resistance evolution and coexistence. Our results have implications on efforts to improve the clinical outcome of treatments towards infection in CF patients.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 1
Presentation/Poster Number: 1 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/92988928818

High-throughput screening of compounds against SARS-CoV-2 tool

Lorson, Zach; Shuiyun, Lan; Kirby, Karen; Sarafianos, Stefan

Presenter/s: Zachary Lorson
Emory Faculty Mentor: Stefan Sarafianos

SARS-CoV-2 rapidly began to spread across the globe in late 2019. The disease caused by SARS-CoV-2, COVID-19, has devasted communities with its highly contagious nature. Despite vaccines now being widely available to the public, there is still a need for effective therapeutics that can treat severe cases of COVID-19 caused by new variants like the highly infectious Delta variant, B.1 .617. 2.

In this study, we evaluated the effectiveness of a series of compounds that target the SARS-CoV-2 main protease (Mpro). We used two different methods to determine inhibition and binding of the compounds to the Nsp5 protein, Sars-CoV-2 tool in throughput screenings and thermal shift assays (TSA). The inhibition screening was compared the compounds against Gilead Sciences' Remdesivir (RDV) in 96 well plates. The compounds were further tested in thermal shift assays to determine the ability to bind to the Nsp5 protein.

In the initial screening using a stable cell line, there were 16 compounds that had promising results in comparison to RDV. We then tested these hit compounds in thermal shift assays to confirm our results and determine their affinity for Mpro. However, the TSAs showed no binding as there was not a significant shift in comparison to the negative control, Dimethyl Sulfoxide.

As there were mixed results from these two assays, these compounds will undergo further testing in the form of enzymatic assays. Additionally, learning the proper conditions for each of the assays is a crucial take away from this experiment and will be used to screen a larger library of compounds.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 D
Presentation/Poster Number: 15
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The ORF1ab and N Mutations in B.1.1.7 and B.1.351 SARS-CoV-2 Variants Do Not Enhance Replicon Replication

Lulkin, Nicole; Lan, Shuiyun; Cilento, Maria; Tedbury Philip; Sarafianos, Stefan

Presenter/s: Nicole Lulkin
Emory Faculty Mentor: Stefan Sarafianos

The COVID-19 pandemic has resulted in the deaths of 4 million people globally and has had negative impacts across all sectors of society. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the causative agent of the pandemic. It is (+) strand RNA virus that has been accumulating several mutations in structural and non-structural genes leading to variants with different infection and therapeutic neutralization rates. The B.1.1.7 (UK) and B.1.351 (South Africa) SARS-CoV-2 variants are two coronavirus lineages with particularly high propagation rates worldwide. The purpose of this study is to determine the significance of the various B.1.1.7 mutations (ORF1ab: T1001I, A1708D, I2230T, del3675-3677 SGF; N: D3L, S23SF) and B.1.351 mutations (ORF1ab: K1655N; N: T205I) on replication capacity and inhibition by a series of compounds through the creation of noninfectious SARS-CoV-2 replicons. The B.1.1.7 and B.1.351 replicons were constructed through the digestion, ligation, and assembly of gene fragments that allowed for the replacement of the spike protein (S), envelope protein (E), membrane protein (M) along with other open reading frames (ORFs) with a green fluorescent protein and neomycin resistance gene (eGFP-NeoR) along with NanoLuc luciferase gene (Nluc). All the mutations were confirmed with DNA sequencing. Compound susceptibility testing with a variety of antiviral inhibitors including remdesivir (RDV), ß-d-*N*4- Hydroxycytidine (NHC), Molnupiravir (EIDD_2801), and protease inhibitor (GC-376) was performed through Nano luciferase measurement following transfection in 293T/17 cells. Neither B.1.1.7 nor B.1.351 variants showed statistically significant differences in compound resistance and replication capacity compared to wild-type SARS-CoV-2. These results indicate that ORF1ab and N mutations in B.1.1.7 and B.1.351 are not primarily responsible for the worldwide prevalence of these SARS-CoV-2 variants. Further experiments need to be conducted to discover if a combination of mutations, including mutations in the S and ORF8 sequences, causes significant changes in the infectivity of the variants.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 C
Presentation/Poster Number: 10
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Synthesis of 2,6-chloro diaryl cyclopropane for enantioselective dirhodium DPCP catalyst

Ma, Carolyn; Tracy, William; Davies, Huw

Presenter/s: Carolyn Ma
Emory Faculty Mentor: Will Tracy

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 3 D
Presentation/Poster Number: 16
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Dopaminergic and Noradrenergic Impacts on Cognition in Progressive Supranuclear Palsy

Maan, Saad; Tucker, Kelsey; Langley, Jason; Huddleston, Daniel E

Presenter/s: Saad Maan
Emory Faculty Mentor: Daniel E. Huddleston

Progressive supranuclear palsy (PSP) is a devastating neurodegenerative disease manifesting with a complex array of motor and cognitive deficits. The neuromelanin-containing catecholamine nuclei, substantia nigra pars compacta (SNc) and locus coeruleus (LC), undergo profound neurodegeneration and depigmentation in PSP, but the relationship between this neuropathology and the clinical features of PSP is not well understood. In vivo quantitative analysis of these brain regions and investigation of their potential involvement in PSP symptoms are important unmet needs. In this study, we assessed for relationships between cognition and both SNc volume and LC volume. PSP cognitive impairment was also characterized across domains using the Montreal Cognitive Assessment (MoCA) and its subscores. Neuromelanin-sensitive MRI, an imaging modality that generates contrast in neuromelanin-containing nuclei, was used to measure SNc and LC volumes in 8 PSP patients. PSP patients have statistically significant decreases in global cognition, visuospatial and executive function, language function, and orientation as compared to age-matched controls. There is a significant positive correlation between LC volume and visuospatial/executive function. Interestingly, we observed a significant negative correlation between SNc volume and the trails test, which specifically measures executive function. This inverse relationship between SNc volume and executive function is especially intriguing and unexpected because decreased brain volumes (atrophy) are typically associated with worsened function. This study cannot elucidate the mechanism underlying this finding, but multiple lines of evidence suggest that neuromelanin increases during the initial phases of neurodegeneration prior to its clearance by microglia. We hypothesize that these PSP patients may have been imaged during a period of pathologic neuromelanin accumulation. These findings highlight the need for a large longitudinal study of these phenomena in PSP.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 D
Presentation/Poster Number: 16
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Language Evolution May Be Shaped by the Same Pressures in Both Transmission Between Generations of New Learners and Transmission by A Single Individual Taught Using Their Own Feedback

MacDonald, Calen; Wilson, Ben

Presenter/s: Calen MacDonald
Emory Faculty Mentor: Ben Wilson

Language is shaped by those who use it and is sensitive to competing pressures to make it both simple enough to learn as well as sufficiently expressive to be useful for communication. These pressures can be seen in iterated learning experiments using artificial languages, where these languages are transmitted across generations to new learners. Previous research has demonstrated that generational transmission alone can result in a structured language, creating the appearance of design without a designer (Kirby et al. 2008). Cumulative cultural evolution results in compositional languages, wherein easy-to-remember components can be recombined to produce new meanings. This lessens constraints on a speaker's memory, while still allowing for expressive communication. We have created a novel iterated learning task in which participants must generate symbols (rather than spoken or typed words based on an existing script) as labels for abstract stimuli. The goal of the experiment is to observe how this symbolic language changes with repeated use within individual participants. This methodology diverges from the common practice of iterated learning studies, where languages are transmitted across chains of participants. Although data collection has been limited by the COVID-19 pandemic, early results from online experiments suggest that the pressures influencing language development in intergenerational language transmission hold true in self-supplied transmission. If further data collection supports this claim, it could indicate that language is shaped by its use in all forms, rather than exclusively its role in social communication.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 4 E
Presentation/Poster Number: 17
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Understanding Pair Bonding Behaviors in Prairie Voles Through Fiber Photometry

Mahmood, Rahil; Zhu, Hong; Liu, Robert; Young, Larry

Presenter/s: Rahil Mahmood
Emory Faculty Mentor: Robert Liu

The formation of a long-lasting pair-bond is one of the defining features of a monogamous relationship. While most humans inhabit a society that is primarily governed by monogamy, interestingly, the vast majority of mammals that we know of are polygamous. Prairie voles, Microtus ochrogaster, however, unlike most other species of voles, are mammals that in fact display monogamy. Previous research has shown that as a result of various evolutionary forces, such as climatic conditions and natural habitat, certain neuropeptides, primarily oxytocin and vasopressin, have gained the ability to influence and regulate this monogamous behavior in order to promote the species' survival. Past research has shown that, when compared to other vole species with close evolutionary distance, prairie voles are known to have a significantly greater expression of oxytocin receptors in the nucleus accumbens (NAcc) and its input regions, including the medial prefrontal cortex and amygdala. In an attempt to get a better understanding of when and how the NAcc neurons are activated during social interactions, and also the extent to which the firing of these neurons contributes to the formation of a pair-bond, this study used fiber photometry to track calcium activity in free-moving prairie voles. Through a series of cohabitations and partner-preference tests, mature male voles were observed for typical pair-bonding behaviors, such as social investigations, huddling, and mating when kept in chambers consisting of known partners as well as novel stimuli animals. The preliminary results of these investigations showed that the NAcc is activated during initial social encounters in cohabitation with female voles and underlies pair-bonding formation. These findings are vital in giving rise to a better understanding of the complex neural circuitry between the nucleus accumbens and its input regions.

Keywords: Pair-bond, nucleus accumbens (NAcc), amygdala, fiber photometry, partner-preference test.

Research Discipline: Natural and Physical Sciences
Presentation Type: Oral Presentation

Session: 4
Presentation/Poster Number: 3 of 5
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99643683271

Visualizing Indoleamine 2,3-Dioxygenase with L-Tryptophan and N-formylkynurenine Through X-ray Crystallography.

Mancia, Andrea; Ireland, Kendra; Davis, Katherine

Presenter/s: Andrea Mancia
Emory Faculty Mentor: Katherine Davis

Indoleamine 2,3-dioxygenase (IDO) is a heme-containing enzyme that partakes in L-tryptophan (L-Trp) metabolism and produces N-formylkynurenine (NFK). It suppresses the immune response of the human body, and is therefore a health-relevant enzyme whose inhibition could be beneficial in the treatment of a variety of diseases such as cancer. Research has focused on formulating IDO inhibitors as a method to increase immune response, yet many have failed, perhaps due to IDO's reaction mechanism not being fully understood. A lack of structural insights regarding IDO'S catalytically relevant states additionally contribute. However, using novel approaches, X-ray crystallography can be used to determine these structures. The main focus of this project is to visualize IDO bound to its product NKF. From previous work, crystallization occurs most reproducibly with truncated and mutated IDO dubbed as "T. IDO K116A/K117A," in which residues 1 through 14 are removed and lysines at residues 116 and 117 are changed to alanines. We expressed the variant IDO using E.coli Rosetta cells transformed with a pET28a plasmid and purified with Co-NTA, cation exchange, and size-exclusion columns. UV-vis spectra indicate that NFK only binds to ferrous IDO, indicating anaerobic conditions, perhaps explaining why no product-bound structures have currently been solved. Optimizing the anoxic crystallization and harvesting processes were the primary activities of this summer research. Screening methods began with sparse-matrix screens to discover initial conditions. Finer hanging drop, sitting drop, and additive screens were used to optimize these conditions through a series of small increments surrounding the initial condition to produce ideal IDO crystals. Majority of trials co-crystallized IDO with its substrate L-Trp in the presence of small amounts of molecular oxygen to enzymatically generate NFK, while others were co-crystallized with commercial NFK. Crystals were then looped, frozen with liquid nitrogen, and shipped to a synchrotron for data collection.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 D
Presentation/Poster Number: 16
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The impact of size-dependent competition on parasite transmission

Mangabat, Danielle; Civitello, David; Shaw, Kelsey

Presenter/s: Danielle Mangabat
Emory Faculty Mentor: David Civitello

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 E
Presentation/Poster Number: 17
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Chemical foundation of the interactions between cultivars and Escovopsis

Gerardo, Nicole; Marko, Annabelle; Patterson, Rachel; Rajani, Mira
(All authors contributed equally and are presented in alphabetical order)

Presenter/s: Annabelle Marko, Rachel Patterson, and Mira Rajani
Emory Faculty Mentor: Nicole Gerardo

Escovopsis is a genus of fungus that parasitizes ant cultivars to form a coevolutionary fungal system. The mechanisms through which these two interact are still largely unknown. There has been previous literature that suggests that Escovopsis releases different volatile organic compounds (VOCs) in the presence of a cultivar. In this study, we are investigating whether VOCs mediate cultivar-parasite interactions. We hypothesized that the difference in the growth rate between the experimental and control conditions would be significant. To test this hypothesis, we grew Escovopsis (A.dentigerum) and cultivars (A.Auriculatum, A. dentigerum, and C. costatus) in an enclosed space, where they could not physically interact, but could respond to volatiles released by one another. We monitored and measured growth form and growth rate every week over the course of 3 weeks.
Our findings showed that there was no statistically significant difference in growth rate amongst the control and experimental groups. More interestingly, there were some differences in growth form, including variation in coloration of the Escovopsis in the presence vs. the absence of the cultivar and increased sporing behavior in the presence of the cultivar. This could potentially indicate that the Escovopsis is reproducing more in the presence of the cultivar suggesting that there is a volatile chemical indicator present. This study could lead to a greater understanding of the mechanisms behind inhibition and attraction in these systems.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 7 C
Presentation/Poster Number: 12
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Transgenerational Epigenetic Heritability of Germline Defects in Caenorhabditis Elegans

Martin, Amaya; Kelly, William; Kent, Tori

Presenter/s: Amaya Martin
Emory Faculty Mentor: William Kelly

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 C
Presentation/Poster Number: 11
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Synthesis of Novel Quaternary Ammonium Compounds Derived From Bioactive Natural Products

McCormack, Caroline; Allen, Ryan; Wuest, William.

Presenter/s: Caroline McCormack
Emory Faculty Mentor: William Wuest

Quaternary ammonium compounds (QACs) are a class of common hospital and household disinfectants that have been used for almost a century. These compounds typically contain a positively charged nitrogen with four carbon-containing groups, one of which is a long alkyl tail. The prevalence of resistance to commercially available QACs is on the rise as a result of their increased use over the years and especially during the COVID-19 pandemic. This is a pressing problem because it can lead to hospital-acquired infections with an increased risk of death from multi-drug-resistant bacteria. Therefore, it is imperative to develop next-generation QACs with better activity against resistant pathogens. We envisioned utilizing the structures of natural products with antibacterial activity to develop novel QAC scaffolds. Ianthelliformisamines A and C, two natural products originally isolated from the marine sponge Suberea ianthelliformis, will be synthesized with the goal of converting them into QACs and investigating their activity against clinically relevant bacteria. These natural products will be produced in five steps starting from 4-hydroxybenzaldehyde. The first four steps were completed with an overall yield of 26%, producing (E)-3-(3,5-dibromo-4-methoxyphenyl) acrylic acid. This will undergo peptide coupling with spermine to produce both Ianthelliformisamines A and C in one step, which will then be quaternized by adding long alkyl tails to produce the final QAC products.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 C
Presentation/Poster Number: 11
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Total synthesis and biological evaluation of bisabolene sesquiterpenoids against Vibrio strains

Author 1 Wuest, William; Author 2 Demeritte, Adrian; Author 3 Mcdonald, Alejandro

Presenter/s: Alejandro McDonald
Emory Faculty Mentor: William Wuest

The biological evaluation of secondary metabolites from marine-derived organisms has brought about many bioactive molecules, some of which are currently FDA approved treatments. V. harveyi is a gram-negative bacteria that causes gastroenteritis, severe necrotizing soft-tissue infections, and primary septicemia. Recently, a culture of Penicillum aculeatum yielded the natural product 1-hydroxy-boivinianin A which showed selective activity against both V. harveyi (MIC = 4.0 µg/mL) and E. tarda (MIC = 8.0 µg/mL). In a separate research paper, another bisabolene sesquiterpenoid with similar structural moieties to 1-hydroxy-boivinianin A was tested for alpha-glucosidase inhibitory activity. Though this molecule lacked activity towards this particular enzyme, it is predicted to have antibacterial activity akin to that of the 1-hydroxy-boivinianin A due to its structural similarity. This work covers the progress towards the first diverted total synthesis of this furan from readily available starting materials through a lithium halogen exchange, Wittig, Grubbs Cross Metathesis, and CAN (Cerium Ammonium Nitrate) cyclization sequence. This work also provides the synthetic framework for other biologically active phenolic bisabolene sesquiterpenoids which have yet to be synthesized.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 E
Presentation/Poster Number: 17
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Analyzing the Effects of Environmental Antibiotic Agrochemicals on Honeybee Gut Microbiomes and Prevalence of Antimicrobial-resistant Genes

Gray, Ashlyn*; McGrath*, Alexa; Avila, Laura
*first authors

Presenter/s: Alexa McGrath and Ashlyn Gray
Emory Faculty Mentor: Laura Avila-segura

Though small in size, honeybees (Apis mellifera) have a profound impact on the environment and agricultural economy. These extraordinary creatures are vital to the pollination of some of the world's most essential plant products (Klein et al. 2007). Yet, while pollinating crops, they are exposed to many agricultural pesticides harmful to their health (Williamson & Wright, 2013). To our knowledge, no study to date has directly examined the extent to which honeybees are exposed to antibiotic residues while pollinating trees in orchards sprayed with antibiotics, let alone whether there are immediate impacts on the bee microbiome community composition and on the evolution of antibiotic-resistance. This study aims to address this knowledge gap by evaluating the impacts of agricultural antibiotics sprayed to orchards, on the composition of honeybee gut microbiomes and the prevalence of antimicrobial-resistant genes.
In Spring, 2021, 15 to 30 worker bees per site were collected at three apple orchards which received streptomycin and oxytetracycline applications to control a bacterial plant pathogen (Erwinia amylovora). Additionally, honeybees were collected from three strawberry farms (control sites), which did not receive antibiotic applications. The samples were kept frozen until laboratory analysis. The gut tract of 115 honeybees were dissected and their DNA extracted using a commercial microbiome extraction kit. Template DNA from these samples will be screened for the prevalence of twelve antibiotic resistant genes via PCR, and for changes in the microbiome composition by sequencing the V4 region of the 16S rDNA gene. We expect that antibiotic resistant genes will be more prevalent in bees from apple orchards than strawberry farms. On the one hand this is concerning because it generates the possibility for bee pathogens that are resistant to treatment. On the other hand, the development of antibiotic resistance may allow bee gut symbionts to survive field antibiotic applications.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 B
Presentation/Poster Number: 7
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Coevolving parasitic bacteria select for outcrossing in Caenorhabditis elegans

Measimer, Kylie; Gresham, Jennifer; Morran, Levi

Presenter/s: Kylie Measimer
Emory Faculty Mentor: Levi Morran

Despite the significant cost of outcrossing when compared to self-fertilization or asexual reproduction, outcrossing is the primary reproduction strategy for many eukaryotes. Determining the impact of parasitic bacteria on the evolution of outcrossing in hosts may elucidate why eukaryotes practice outcrossing despite associated reproductive costs. One idea, the Red Queen hypothesis, postulates that bacteria coevolve with the host to impose negative frequency-dependent selection on the most common host genotypes, thus selecting for the host reproductive strategy that produces the greatest genetic diversity. Another hypothesis, named Hill-Robertson effects, suggests that bacteria create a rapidly changing environment that selects against genomes with many deleterious alleles while maintaining a common genome with several beneficial alleles, hence favoring recombination through outcrossing. An experimental evolution study was performed to determine which of these hypotheses more strongly selects for outcrossing in Caenorhabditis elegans hosts. C. elegans hosts were either subjected to heat-killed, coevolved, ancestor, or rotating Serratia marcescens strains, then assayed for relative fitness against each bacteria treatment. Outcrossing was favored and maintained in populations coevolving with parasites. However, rapid shifts in parasite genotypes favored self-fertilization after less than ten generations. Further, host populations that evolved with different parasite genotypes did not maintain resistance over time. Therefore, there is evidence that coevolving parasites select for outcrossing, thus supporting the Red Queen hypothesis. In addition, Hill-Robertson effects were not supported since outcrossing was not favored when hosts were exposed to rotating bacterial strains. These results imply that the coevolution of parasites and hosts may influence the maintenance of outcrossing as a primary reproductive strategy by resulting in a selection against genetic uniformity.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 3 E
Presentation/Poster Number: 18
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining the Mechanisms of Radioresistance in Glioblastoma Multiforme through DNA Damage Response and Stem Cell Character

Minocha, Trisha; Parwani, Kiran; Spangle, Jennifer

Presenter/s: Trisha Minocha
Emory Faculty Mentor: Jennifer Spangle

Glioblastoma multiforme (GBM) is the most common and lethal adult malignant brain tumor, with a prognosis of about 15 months after diagnosis. The dismal prognosis of GBM can be attributed to its aggressive nature and resistance to standard therapy. While radiotherapy has played a crucial role in the treatment of GBM, most GBMs have shown to be resistant to radiation therapy. Thus, in order to improve the effectiveness of GBM treatment, it is critical to further understand the mechanisms that drive radioresistance. An increase in DNA damage response (DDR) mechanisms and a greater population of glioblastoma stem-like cells are factors that have been shown to have significant roles in radioresistance. Hyperactivity of the PI3K/AKT pathway is greatly prominent in GBM, and has been associated with tumor progression, recurrence, and radioresistance. Here, we further examine the mechanisms of radioresistance through investigating the role of AKT-mediated phosphorylation of histone H3T45 (pH3T45) in relation to DDR and stem cell character. The role of pH3T45 in DDR was examined through studying the association of pH3T45 with γH2AX, a significant molecular marker for DNA double strand break repair. Through western analysis and immunofluorescence imaging it was determined that pH3T45 has a potential association and co-localization with γH2AX, indicating its potential role in DNA damage repair. PI3K/AKT induced histone H3 post translational modifications (PTM) were examined in fetal, adult, and GBM brain tissue samples. It was found that, when compared to non-cancerous adult cortex tissue, the H3 PTM profile of GBM patients was most similar to that of fetal brains, demonstrating the prospective role that H3 PTMs play in stem cell character. Overall, greater knowledge regarding the mechanisms of GBM radioresistance enables prospective improvements to be made in the efficacy of radiation therapy, allowing for an increase in the effectiveness of the overall GBM treatment model.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 D
Presentation/Poster Number: 14
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

“Understanding the Roles of RNA-Binding Proteins in C9orf72-linked ALS/FTD”

Mishkovsky, Elena; McEachin, Zachary; Bassell, Gary

Presenter/s: Elena Mishkovsky
Emory Faculty Mentor: Gary Bassell

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 D
Presentation/Poster Number: 13
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Impacts of Antibiotic Exposure on Bumble Bee Foraging Behavior and Gut Microbiome Composition

Hossain, Afsha; Molumo, Zainab; Avila, Laura

Presenter/s: Zainab Molumo and Afsha Hoosain
Emory Faculty Mentor: Laura Avila

Rampant bacterial crop pathogens have compelled the rising agricultural use of broadcast-spray antibiotics in the United States in the past decade. Our research is interested in how antibiotic exposure affects pollinator behavior and learning. Bee gut bacteria produce neuromodulators like dopamine that have been shown to modulate bee learning, and if symbionts are distributed by the field-level antibiotics, this dietary exposure to antibiotics could negatively impact bee learning. We are investigating the impacts of the lowest field-relevant concentration applied to crops, 50 ppm of streptomycin, on bumble bee (Bombus impatiens) behavior via the “free movement proboscis extension assay” standard method and thee-flying foraging assays”. Behavioral assays were used to compare the learning and reward-seeking behaviors of bees treated with and without 50 ppm streptomycin when presented with a color stimulus (blue or yellow). We have performed 62 free proboscis extension behavioral assays on wild-type, control, and antibiotic-treated bees from three colonies and have observed no statistically significant difference in appetitive motivation or learning behavior thus far. We are currently analyzing the data collected from 70 bees across two colonies that were tested in the free-flying video foraging assays. We expect that the wild-type bees will display better performance in the foraging assay than the antibiotic-treated bees. We are also analyzing morphotype and antibiotic susceptibility data for bee gut symbionts from two colonies which will be identified through Sanger sequencing. We have found symbionts resistant to 50 ppm streptomycin which may explain the behavioral resiliency of the bees at this concentration. Our research serves to inform preventive management practices and promote sustainable use of antibiotics at the field level to address health and ecological issues created by the overuse of antibiotics on U.S. crops.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 C
Presentation/Poster Number: 10
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The Effect of the Presence of Iron on the Phytoremediation of Copper by Water Hyacinth (Eichhornia crassipes) and American Water Willow (Justicia americana)

Moore, Rhiannon; Hage, Melissa; Nkomo, Simbarashe

Presenter/s: Rhiannon Moore
Emory Faculty Mentor: Melissa Hage

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 D
Presentation/Poster Number: 15
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Design of Metalloamyloid Nanomaterial Templates for Constructing Ecocircular Polyamides

Kim, Youngsun; Mudigonda, Abhijay; Lynn, David

Presenter/s: Abhijay Mudigonda
Emory Faculty Mentor: David Lynn

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 C
Presentation/Poster Number: 12
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Barriers and facilitators to continued breastfeeding of infants less than 6 months of age with acute illness requiring emergency department visits and inpatient hospital stays

Badio, Laetitia Arvel; Murray, Brittany; Mukherjee, Ishika

Presenter/s: Ishika Mukherjee
Emory Faculty Mentor: Brittany Murray

Introduction: Breastmilk is an optimal source of nutrition for the majority of infants less than 6 months of age. There has been little research into the effect of acute illness or hospitalization on the continuation of breastfeeding within this age group. In this study, we hope to identify barriers and facilitators to continued breastfeeding of infants with acute illness requiring emergency department visits. Awareness of these factors will aid pediatric hospitals in encouraging continued breastfeeding post-hospitalization.

Methods: This is a cross sectional, prospective study consisting of qualitative interviews of breastfeeding Mothers to assess facilitators and barriers to their continued breastfeeding during emergency department visits and hospitalizations for their infants. The study population of investigation includes breastfeeding mothers of infants with a gestational age of 32 weeks or greater who are less than 6 months old who present with acute illness to the Emergency Department at Egleston Children's Hospital. We estimate that we will recruit 20-30 participants to obtain thematic saturation. A Semi-structured interview will be performed to gather qualitative data and audio recorded. To facilitate in-depth answers, interview guide prompts will be asked with followup questions when necessary. After recording, the interviews will be transcribed and anonymized during transcription. Transcriptions will be analyzed through thematic analysis. The researchers will code data using an inductive, iterative approach. Coding will be performed through Dedoose (Version 7.0. 23, web application for managing, analyzing, and presenting qualitative and mixed method research data, 2016). This process will use open coding, axial coding, and selective coding to generate themes. Themes will then be identified and refined through reflection and the iterative process.

Significance: This research is ongoing. The results will be shared with key stakeholders at Egleston Children's Hospital, as well as submitted for journal publication.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 2 D
Presentation/Poster Number: 13
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Understanding the role of SLC25A1 in congenital heart defects caused by 22q11.2 Deletion Syndrome

Murthy, Sejal; Peoples, Jessica N.; Ghazal, Nasab; Kwong, Jennifer Q.

Presenter/s: Sejal Murthy
Emory Faculty Mentor: Jennifer Kwong

22q11.2 Deletion Syndrome (DS), or DiGeorge Syndrome, is a multifaceted disease affecting craniofacial, nervous, immune, and cardiovascular systems during development. This disorder, in which 3 Mbp are deleted from chromosome 22, also increases risks of congenital heart defects (CHD) arising from abnormal development of the heart and surrounding vasculature. Classical 22q11.2DS mouse studies focus on how the development gene, Tbx1, contributes to the CHD phenotype. However, single gene loss of Tbx1 does not fully replicate the deficiencies present in the human disease, suggesting other genes within the microdeletion domain could be responsible for cardiac defects. Our recent study identified the mitochondrial citrate carrier, SLC25A1, as a potential candidate for contributing to the neuropathology associated with 22q11.2DS. Additionally, other studies have demonstrated that the loss of Slc25a1 reduced heart size in developing zebrafish. As a result, we hypothesized that the Slc25a1 gene can cause mitochondrial dysfunction leading to cardiac defects during development. To study SLC25A1 in the developing heart, we generated a novel knockout mouse model of systemic Slc25a1 deletion. We found that loss of the Slc25a1 gene caused lethality by embryonic day 18.5 (E18.5) and that reduction in Slc25a1 gene dosage caused a spectrum of cardiac defects including ventricular septal defects and right ventricular hypoplasia. In addition, histological analysis surprisingly revealed ventricular non-compaction with increased trabeculated-to-compacted myocardium ratios in E18.5 Slc25a1+/- and Slc25a1-/- hearts. Our preliminary data also showed that Slc25a1 expression increased significantly over the course of cardiac development, while cardiomyocyte cross-sectional areas at E18.5 between Slc25a1+/+ and Slc25a1-/- hearts were unchanged. Collectively, this data suggests that SLC25A1 is a critical factor in embryonic cardiac morphology and potentially plays a mechanistic role in CHD phenotypes of 22q11.2DS.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 E
Presentation/Poster Number: 18
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating the Role of Leucine Carboxyl Methyltransferase-1 in T and B Cell Function

Nalluri, Rahul; Tam, Duncan; Pallas, David.

Presenter/s: Rahul Nalluri
Emory Faculty Mentor: David Pallas

Leucine carboxyl methyltransferase-1 (LCMT-1) is an enzyme that functions to regulate the formation of a group of heterotrimeric (three different subunits) complexes—protein phosphatase 2A (PP2A) subfamily—through the methylation of their catalytic subunits. PP2A enzymes are responsible for dephosphorylating different proteins within important signaling pathways—Raf-Mek-Erk and mTOR—in cells. Previous research has shown that a global knockout of LCMT-1 in mice caused anemia, a lower stem cell count, and leukopenia (reduced white blood cells). The focus of this research is leukopenia, and in particular understanding the loss of function in a class of leukocytes called lymphoid cells (T and B Cells). This research will attempt to showcase how a conditional, rather than a global, knockout of LCMT-1 in blood can affect lymphoid cell growth, survival, differentiation, and function. I hypothesize that since PP2A is important for the regulation of cell signaling pathways, a knockout of LCMT-1 in blood would lead to differences in phosphorylation of proteins. This will be done by using mice that are conditionally knocked out for LCMT-1 and comparing their lymphoid cells from the spleen with those present in control mice. The lymphoid cells will be identified from the spleen cultures via immunophenotyping with external antibodies (CD3 and B220) using flow cytometry. Once identified, phosphoflow cytometry and internal antibodies (MEK, two pMEKs, S6, pS6, ERK, pERK) will be used to study the phosphorylation in knockout and control mice. There was no significant difference between knockout and control in T and B cells, but non-T, non-B cells showed a significantly higher pS6 and pERK staining for knockout mice ($p=0.03$, $p=0.004$). The research suggests that myeloid (monocytes and granulocytes), rather than lymphoid leukocytes, might be of more interest for future research projects in studying the role of LCMT-1 in mice.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 C
Presentation/Poster Number: 12
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Measuring forces generated by nanoscale-sized synthetic DNA motors

Namazi, Arshiya; Piranej, Selma; Blanchard, Aaron; Holt, Brandon; Salaita, Khalid

Presenter/s: Arshiya Namazi
Emory Faculty Mentor: Khalid Salaita

Movement in biological systems is powered by molecular motor proteins such as dynein, kinesin, and myosin which use microtubules and actin filaments as tracks. Recapitulating the properties of molecular motor proteins has been a longstanding goal of synthetic biology. DNA-based materials have shown great promise in creating synthetic nanoscale machinery due to the specificity and programmability of Watson-Crick base pairing which allows for the rational design in nanoscale motors and machinery. DNA-based motors can be used to transport and assemble nanoscale cargo however, not many have been shown to generate sustained forces akin to those of biological motor proteins. Molecular force probes such as tension gauge tethers (TGTs) were recently applied towards measuring forces generated by highly polyvalent DNA-based motors. As a result, DNA-based motors, which act as cooperative teams of thousands of DNA walkers attached to a 5 μm microsphere, have been shown to generate forces in the 100+ pN regime. Since then, nanoscale synthetic motors with higher speed and processivity have been developed. Unlike the micron-sized motors, we are uncertain of the force generating capabilities of the nanoscale motors. Preliminary results using TGTs as force sensors suggest that the forces generated by synthetic motors scale linearly with motor size, and the 500 nanometer and 50 nanometer particles generate ~15 and 1.5 pN forces, respectively. Our findings demonstrate that nanoscale DNA-motors can be used for engineering application that require low pN-scale force generation.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 D
Presentation/Poster Number: 14
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Comparing Extraction Efficiency of Organic Ultrasonication and Aqueous Decoction for Plants with Potentially Potent Medicinal Properties

Narula, Jasleen; Caputo, Marco; Quave, Cassandra

Presenter/s: Jasleen Narula
Emory Faculty Mentor: Cassandra Quave

Various aqueous and organic extraction methods have been conducted on plants to isolate and obtain chemicals with potentially potent medicinal properties. An experiment was conducted to study the efficacy of organic ultrasonication and aqueous decoction extraction methods by comparing the percent yield of extracts using the same plant and plant part. Sample preparation using the ultrasonication method with organic solvent is performed by preparing a 1:10 plant to 80% ethanol solvent ratio that is sonicated, filtered, evaporated, and freeze dried to obtain the pure extract. The procedure for aqueous decoction includes preparing a 1:10 ratio of plant to water that is boiled for 20 minutes, filtered, evaporated, and freeze dried to obtain the pure extract. The percent yield data was gathered from the Quave National Product Library Extract Database where all previous extractions are recorded. Thirty plants were chosen based on their proximity in extraction dates and their collection dates. All plants were collected on the same day and extracted within three weeks of each other. The results were analyzed statistically using a two-tailed, paired t-test with a 0.05 significance level. The test revealed a p value of 0.8400 which is greater than the significance level of 0.05, indicating that the difference between the percent yield of the two extraction methods is not statistically significant. The data conveys that there is no difference in the overall yield between organic ultrasonication and aqueous decoction. However, the extraction methods result in different groups of compounds based on polarity, so the resulting chemical profiles of the extract can be different. The conclusion of this study is that researchers can use either method of extraction, depending on which chemical profile works best with the purpose of the experiment, to obtain the pure extract without taking into consideration the efficiency of extraction.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 E
Presentation/Poster Number: 18
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Validation of in vivo cell type-specific biotinylation technique using immunofluorescence staining.

Rayaprolu, Sruti; Rangaraju, Srikant; Nelson, Ruth

Presenter/s: Ruth Nelson
Emory Faculty Mentor: Srikant Rangaraju

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 D
Presentation/Poster Number: 16
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Digital Activism and Offline Activism in the 2014 Black Lives Matter Movement

Ng, Jasmine; Gade, Emily

Presenter/s: Jasmine Ng
Emory Faculty Mentor: Emily Gade

Existing research has found that there is an increasing number of people using social media for what is known as “digital activism”, aiding in social movements through online actions. Does online activism translate to offline activism? In the 2014 Black Lives Matter movement, digital activism was particularly pivotal for spreading information about protests and movement goals. This study aims to understand to what extent digital activism on Twitter through the use of hashtags about the Black Lives Matter movement was effective in organizing turnout for offline protests. I evaluate whether this online activism translated into offline protest presence through a statistical analysis of BLM protest attendance nationally in 2014. I hypothesize that social media aided in spreading awareness and educating many on issues of police brutality in 2014 through increased usage of hashtags, but it was less impactful in aiding turnout for protests offline. I consider a range of alternative explanations, including the demographics of a given city, xxx, and xxx. Although this study is currently still in process, the findings will be important for understanding how to sustain social movements and how digital activism will play a role in mass mobilization toward political activism in the future.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 4 E
Presentation/Poster Number: 19
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

An Investigation of the domain-domain interactions of A Disintegrin Metalloproteinase domain-containing protein 10 (ADAM10)

Nwakamma, Richard; Qian, Kun; Fu, Haian; Johnson, Erik; Betarbet, Ranjita

Presenter/s: Richard Nwakamma
Emory Faculty Mentor: Haian Fu

Alzheimer's disease (AD) is the most common form of dementia and is characterized as a chronic neurodegenerative illness leading to memory loss and loss of cognitive function. A Disintegrin and Metalloproteinase domain-containing protein 10 (ADAM10) is a key protein involved in many biological processes including neuropathology, inflammatory response, and tumor progression. In neurons, ADAM10 acts as an α-secretase to mediate proteolytic processing of the amyloid precursor protein (APP). It plays a critical role in reducing the generation of amyloid-β (Aβ) peptides which helps reduce the pathogenesis of AD. ADAM10 is a membrane protein, and its extracellular component consists of four functional domains, including a pro domain (P), metalloprotease domain (M), a disintegrin domain (D) and a cysteine rich domain (C). The crystal structure of a truncated ADAM10 containing M, D, and C domains revealed the molecular details of how D and C domain regulates M domain activity. However, studies have shown that ADAM10 is active only when the P domain is cleaved and how the P domain interacts with other domains remains unknown. To further explore the regulatory roles of the four functional domains on ADAM10 activity, we designed protein domain truncations of ADAM10 fused with various molecular tags and performed protein-protein interaction assays. The techniques include Gateway cloning, mammalian cell culture and overexpression of recombinant protein domains, GST pulldown, SDS-PAGE, and Western blotting. The data showed that the P domain interacts with both the M and D domains. This study helps to provide a better understanding on the regulation of ADAM10 activity by its functional domains. Due to the neuroprotective role of ADAM10, restoring its enzyme activity could be beneficial. Information gained from this investigation could assist in discovery of a novel therapeutic strategy for treating AD.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 6
Presentation/Poster Number: 5 of 6
Presentation Time: 1:30 PM to 3:00 PM
Presentation Link: https://emory.zoom.us/j/95175843929

Mechanism of Endogenous Bacterial Toxin Activation and Impact on Antibiotic Resistance

Obialor, Michella; Tanquary, Julia; Dunham, Christine Ph.D.

Presenter/s: Michella Obialor
Emory Faculty Mentor: Christine Dunham

In recent years, cases of antibiotic resistance have steadily increased, which poses a problem as modern medicine cannot exist without antibiotics. However, persister bacteria, which are recalcitrant to antibiotics, may have contributed to this phenomenon of antibiotic resistance. We've noticed a promising connection between toxin-antitoxin systems, which are a set of closely linked genes that together encode both a "toxin" protein and a corresponding "antitoxin" protein, and persistence. To study this relationship, we've utilized the Keio collection, which is composed of deleted non-essential genes, including antitoxins. We hypothesize that antitoxins are likely essential genes and compensatory mutations are present allowing for survival. To test this, we've been utilizing colony PCR to conduct an initial screening, followed by whole genome sequencing to finalize our findings. Our gel electrophoresis has shown that the majority of our antitoxin deletions with kanamycin resistance were successful, however, our ΔPasI strains were much shorter than the expected length of the strain if the antitoxin was deleted and our kanamycin cassettes were successfully inserted. In the future, we could continue to run extensive experiments on the rest of the Keio collection, mainly the correct strains, in which we will perform whole genome sequencing to identify if compensatory mutations are present. Ultimately, TA systems have immense potential to solve this occurrence of antibiotic resistance and we believe that our solution lies within toxin and antitoxin research.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 E
Presentation/Poster Number: 19
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating reproductive outcomes in a galactose-1-phosphate uridylyltransferase-null rat model of classic galactosemia

Anshen, Lauren; Orloff, Danielle; Rasmussen, Shauna; Fridovich-Keil, Judith

Presenter/s: Danielle Orloff and Lauren Anshen
Emory Faculty Mentor: Judith Fridovich-Keil

Classic galactosemia (CG) is a genetic disorder that results from a lack of galactose-1-phosphate uridylyltransferase (GALT), an enzyme essential for the efficient metabolism of galactose via the Leloir pathway. Detection of the disease in newborns and immediate restriction of galactose consumption can avert the acute and often-times lethal symptoms characteristic of CG. However, a majority of patients still encounter galactosemia-associated complications long-term. Premature ovarian insufficiency (POI), for instance, affects 80-90% of girls and women with CG. Our objective in this study was to assess the ovarian function of the females in our GALT-null rat model by examining reproductive outcomes. To evaluate this, daily vaginal smears were obtained following a vaginal flush with 200 µL of saline from wild type and GALT-null female rats for a minimum of four days. 25µL of concentrated samples were placed on glass slides, air dried, stained with crystal violet, and observed under a light microscope to establish the estrous cycle stage. If in the proestrus phase, the female was paired with a male overnight for breeding. Copulation was confirmed the next morning by obtaining a vaginal smear and repeating the above steps while staining with Giemsa stain and recognizing sperm under a light microscope. We observed no difference in the length of the estrous cycle between wild-type and GALT-null female rats. Moreover, the differences in length of gestation and number of pups delivered across genotypes did not differ significantly ($p=0.08$ and $p=0.55$). This suggests that if GALT-null female rats experience POI, it is subtle and does not impact reproductive ability, at least during the age range included in our study (2-7 months). Future studies could further determine the presence of POI in this model by analyzing age and follicle cell development in GALT-null female rats as well as the percent of successful crosses by genotype.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 A
Presentation/Poster Number: 1
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Role of DNA sequences in centromere identity in mammals using an evolutionary guided approach

Packiaraj, Jenika; Thakur, Jitendra

Presenter/s: Jenika Packiaraj
Emory Faculty Mentor: Jitendra Thakur

Centromeres are the sites on chromosomes where spindle fibers attach to allow chromatid separation during cell division. Mammalian centromeres are marked by histone H3 variant Cenp-A which assembles on centromeric DNA composed of long tandem arrays of repeats called satellites. Little is currently known about the role of centromeric DNA in determining centromere identity and function due to the rapid evolution of centromeric satellites. Our study investigates the role of DNA in centromere specification by identifying and characterizing centromeric minor satellite variants in early diverging wild house mouse lineages, the Eastern European M.m. musculus (Mmm) and the Western European M.m. domesticus (Mmd). My analyses of whole genome datasets have revealed that both lineages carry some new minor satellite variants that carry unique mutations. Using high throughput chromatin profiling genomics method called Cleavage Under Targets & Release Using Nuclease (CUT&RUN), I am further investigating if minor satellite variants in Mmm and Mmd have different Cenp-A binding affinity. Toward this, I have successfully established CUT&RUN protocol in a cell line. Currently, I am applying the method on Mmm and Mmd liver tissues using anti-Cenp-A antibodies. The findings from Cenp-A CUT&RUN in Mmm and Mmd will determine if the minor satellite variants in both strains bind different amounts of Cenp-A, which will reveal centromeric DNA sequence features that affect Cenp-A binding and centromere specification. Understanding consequences of centromeric satellite variations in a mammalian model system has direct implications for human health as expansions and sequence variations in centromeric DNA are associated with certain cancers and diseases.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 D
Presentation/Poster Number: 14
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Milkweed toxins reduce parasite infection in monarch butterflies

Pahnke, Andrew; Chavez, Joselyne; Duckett, Marissa; de Roode, Jacobus

Presenter/s: Andrew Pahnke
Emory Faculty Mentor: Jacobus de Roode

Herbivores and plants have coevolved over millions of years, with plants evolving defenses against herbivores, and herbivores evolving tolerance to these defenses. Monarch butterflies and milkweed plants are a prime example of this relationship with the addition of a parasite (O. elektroscirrha) hosted by the butterflies. Milkweeds have evolved cardenolide compounds which act as a toxin to most insects. However, monarchs have evolved a tolerance to these compounds and may even use them in defense against their own parasites. Tolerance is described as the ability to host a toxic compound or parasite without the host being adversely affected strongly. The nature of the relationship between the milkweed cardenolides and the parasites is unknown. In our lab, we used varying concentrations cardenolide extracts from the tropical milkweed Asclepias curassavica onto leaves of the low-cardenolide swamp milkweed, A. incarnata. Previous studies have shown that A. curassavica reduces the parasite infection in monarchs. Afterwards, these modified leaves were fed to monarch, along with infectious doses of the parasite. We predicted that the modified leaf discs would provide monarchs a similar resistance to the parasites compared to monarchs solely fed the A. curassavica plants. Once grown, we measured parasite spore load and the monarch lifespan. We found that monarchs fed with an intermediate concentration of cardenolide extracts experienced similar reductions in parasite load as the monarchs fed A. curassavica. Our results suggest that cardenolides are an active component in the resistance against the parasites that infest monarch butterflies.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 D
Presentation/Poster Number: 13
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Longitudinal Analysis of Antibody Responses Following COVID-19 Vaccination Stratified by Prior Infection Status

Panjwani, Anusha; Edupuganti, Neena; Espinoza, Daniel O; Collins, Matthew H

Presenter/s: Anusha Panjwani
Emory Faculty Mentor: Matthew Collins

The development and safe implementation of COVID-19 vaccines has been of extreme importance amid the COVID-19 pandemic. While COVID-19 vaccines have been authorized in remarkable time, questions remain about the durability of immunity. The mRNA COVID-19 vaccines use synthetic mRNA encoding the spike protein (S) of SARS-CoV-2, a major target of the humoral immune response to this virus. Antibodies targeting the receptor-binding domain (RBD) of the spike protein have been shown to be associated with neutralizing antibodies, a correlate of immune protection. We asked whether prior SARS-CoV-2 infection affects the magnitude and duration of antibody responses to the RBD elicited by mRNA COVID-19 vaccines. We hypothesized that antibodies will be maintained at higher levels and longer in individuals with prior infection compared to SARS-CoV-2-naïve individuals. This study is a preliminary analysis of AID-CoVax (Adaptive Immune Determinants of protection in COVID-19 Va(x)ccination), a cohort study comprising individuals (n=60) with known SARS-CoV-2 infection status for the 6-9 months prior to receiving COVID-19 vaccination. An enzyme-linked immunosorbent assay (ELISA) was used to measure end point dilution titers of IgG to RBD in subjects' sera. Subjects were grouped according to previous SARS-CoV-2 infection status, and titers were compared between the two groups at the pre-vaccine visit and 60 days post second vaccine dose. As expected, the mean IgG titer against RBD was greater in those with previous SARS-CoV-2 infection; however, no significant difference (p>0.05) was observed at 60 days post-vaccination. Future studies will examine the kinetics of IgG titers in detail, and we expect the greatest difference between the groups 7-14 days after the first vaccine dose. We will also assess neutralizing antibody responses up to one year post-vaccination. These findings are critical as vaccine availability could be increased if a single dose is highly effective in those with prior SARS-CoV-2 infection.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 D
Presentation/Poster Number: 15
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Encapsulation of Pediatric c-kit+ Cells in Myocardial Extracellular Matrix Hydrogels for Enhanced Progenitor Functions

Park, Se Hyeon; Shakya, Preety; Brown, Milton; Davis, Michael

Presenter/s: Se Hyeon Park
Emory Faculty Mentor: Michael Davis

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 D
Presentation/Poster Number: 16
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The Protective Effects of Indole derived from commensal microbiota on Reproduction in C. elegans: Understanding and Exploring Possible Transgenerational Implications

Parulekar, Noyonika; Sonowal, Robert; Kalman, Daniel

Presenter/s: Noyonika Parulekar
Emory Faculty Mentor: Daniel Kalman

Indole, a metabolite produced by gut bacteria via enzyme tryptophanase (TnaA), is known to limit aging associated infirmities, extending healthspan and reproductive span. It's unclear whether this protective effect extends to next generations without continuous intake of indole, via modulation of an epigenetic factor. It's been observed that some indole derivatives are inhibitors of HDAC (histone deacetylase), an enzyme associated with epigenetic modulation of gene expression. Wild-type C. elegans strain, N2, was grown on NGM (nematode growth media) plates containing either indole (K12 bacteria as food) and methanol as control (K12ΔTnaA bacteria as food). Adults from the indole plates were transferred and bleached onto 2 types of plates--indole (indole-indole) and methanol control (indole-control). Adults from methanol plates were transferred and bleached onto another control plate (control-control). The bleaching killed and lysed the adults, releasing their eggs (embryos) (F1 eggs (first generation)). The plates were allowed to grow at 16 degrees celsius for 2-3 days till the eggs became adults and laid eggs (F2). Adults developed from F2 eggs were isolated onto ~18 single plates, each plate with 1 worm, and heat-stressed at 30 degrees celsius for 6 hours. Stressed adults were transferred to 16 degrees celsius and the quality of their progeny was monitored by counting the frequency of unhatched eggs. F2 adults from control-control had 36.65%, indole-indole had 29.29%, and indole-control had 31.68% dead eggs. An ANOVA test's p-value was 0.53 (>p=0.05). The results are statistically insignificant. Worms that stopped consuming indole in the F1 generation had a similar protective effect to those that consistently consumed indole even in F2 generation, allowing reason for further investigation with more trials. Possible transgenerational protective effects of indole can be tested with radiation and starvation C. elegans treatment groups and extended to treatment of epigenetic diseases.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 3 E
Presentation/Poster Number: 19
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Does Napping Affect Working and Prospective Memory in People with Disorders of Excessive Sleepiness?

Patel, Aneri; Trotti, Lynn Marie

Presenter/s: Aneri Patel
Emory Faculty Mentor: Lynn Marie Trotti

Background: Sleep inertia is a physiologic state of impaired cognitive performance, drowsiness, and disorientation, immediately after awakening. Typically, this period is brief for healthy people, but can be prolonged for patients with sleep disorders. The purpose of this study was to measure sleep inertia in sleepy patients via two cognitive performance tests before and after a nap.
Methods: Patients undergoing sleep testing for hypersomnia disorders completed two computerized cognitive tasks, the n-back (a test of working memory, including 0-back and 3-back trials) and a prospective memory (PM) task. They performed each task twice, once before and once after a nap of up to 15 minutes duration. Paired t-test was used to compare performance pre- and post-nap. For measures that worsened with napping, relationship between sleep duration and performance worsening was assessed via Pearson correlation. ANOVA was used to compare post-nap worsening by final diagnosis.
Results: Our sample consisted of 31 patients (71.0% female and 29.0% male), with diagnoses of narcolepsy (n =7), idiopathic hypersomnia (n =14), and undetermined (n =10). On the n-back, there were no significant performance changes before and after napping, for either 0-back or 3-back, for either accuracy or reaction time for target stimuli. On the PM task, there was a significant worsening of reaction time for target stimuli post-nap (worsening by 269.4 ms +/- 525.1 ms, p = 0.02), but there was no change in accuracy in responding to the target. There was no correlation between nap sleep duration and worsening reaction time on the PM task. There was no significant difference in post-nap reaction time worsening on the PM task across the three diagnostic groups.
Conclusion: This suggests that a short nap has a negative impact on prospective memory but not on working memory, in hypersomnolent patients, but this effect is not diagnosis-specific.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 E
Presentation/Poster Number: 20
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Vestibulosympathetic Input to Thoracic Interneurons Provide Novel Insights into an Unmapped Pathway

Patel, Niki; Giorgi, Andrea; Perreault, Marie-Claude

Presenter/s: Niki Patel
Emory Faculty Mentor: Marie-Claude Perreault

Vestibular nuclei have pertinent functions in essential autonomic processes such as the regulation of blood pressure, body balance, and head movement (McCall et al., 2017). Three pathways are known to descend from these nuclei: the lateral vestibulospinal, the medial vestibulospinal, and the vestibulosympathetic pathways. This investigation focuses on mapping the regions of the spinal cord involved in the lesser-known vestibulosympathetic pathway by studying the recruitment of excitatory sympathetic interneurons (SINs) in response to vestibular stimulation (Kasumacic et al 2012). Vestibular nuclei were electrically stimulated in postnatal mice (P0-P4) and two cervical lesions, 1) to the ipsilateral ventral funiculus and ventrolateral funiculus and 2) a contralateral hemisection, were made to sever the vestibulospinal pathways and thus leave the vestibulosympathetic pathway intact. Recordings of calcium signals in glutamatergic SINs in T10 were taken along the ventral and dorsal horn before and after making these lesions to determine which regions of the spinal cord remained responsive and thus recruited SINs. These findings indicate that the spinal component of the vestibulosympathetic pathway is likely localized to the intermediate region and ventral horn of the spinal cord (lamina V, VII, & X) as these areas remained responsive to vestibular stimulation once the vestibulospinal pathways were eliminated.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 E
Presentation/Poster Number: 17
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining the transduction efficiency of scAAV9 in galactose-1-phosphate uridylyltransferase -null rat model of classic galactosemia

Patel, Sneh; Rasmussen, Shauna; Fridovich-Keil, Sara; Fridovich-Keil, Judith

Presenter/s: Sneh Patel
Emory Faculty Mentor: Judith Fridovich-Keil

Classic Galactosemia (CG) is a potentially lethal autosomal recessive disorder caused by a severe deficiency of galactose-1-phosphate uridylyltransferase (GALT). We used immunohistochemistry (IHC) in sections of fixed liver tissue to quantify the transduction efficiency of scAAV9.CBh.HA.hGALT administered intravenously to neonatal GALT-null rats. Due to the predominantly non-integrating nature of scAAV9 virus, a decrease in transgene expression over time was anticipated. We also aimed to assess the effectiveness of the gene therapy approach through analyzing GALT activity restoration in conjunction with IHC. Animals were treated on day 2 and harvested on days 14, 30, or 60. The fixed, dehydrated livers were embedded in paraffin wax and cut into 5 serial sections. The presence of GALT transgene product was detected using a primary antibody that bound to the HA tag, which was then conjugated with an HRP based secondary antibody. The secondary antibody was then visualized using diaminobenzidine which stained the positive cells by producing a brown precipitate while hematoxylin was applied for counterstain. The percentage of cells stained was quantified using custom software that calculated the normalized red minus blue color of each pixel. As expected, we observed a strong positive correlation between the percentage of cells stained and the level of liver GALT activity. The distribution of the normalized red minus blue pixel color indicated a greater variation in the intensity of the staining among cells in livers harvested at day 14 which can be attributed to the rapid growth and mitosis early in life. We also observed a significant decrease in the level of transgene expression over time, paralleling the decrease in GALT activity detected over time. Combined, these results demonstrated that even moderate levels of scAAV9-virus can achieve efficient GALT replacement in rat liver, suggesting that gene therapy may offer a viable option for intervention in classic galactosemia.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 2
Presentation/Poster Number: 5 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/95175906316

Chemical foundation of the interactions between cultivars and Escovopsis.

Gerardo, Nicole; Marko, Annabelle; Patterson, Rachel; Rajani, Mira

(All authors contributed equally and are presented in alphabetical order.)

Presenter/s: Rachel Patterson, Mira Rajani, and Annabelle Marko
Emory Faculty Mentor: Nicole Gerardo

Escovopsis is a genus of fungus that parasitizes ant cultivars to form a coevolutionary fungal system. The mechanisms through which these two interact are still largely unknown. There has been previous literature that suggests that Escovopsis releases different volatile organic compounds (VOCs) in the presence of a cultivar. In this study, we are investigating whether VOCs mediate cultivar-parasite interactions. We hypothesized that the difference in the growth rate between the experimental and control conditions would be significant. To test this hypothesis, we grew Escovopsis (A.dentigerum) and cultivars (A.Auriculatum, A. dentigerum, and C. costatus) in an enclosed space, where they could not physically interact, but could respond to volatiles released by one another. We monitored and measured growth form and growth rate every week over the course of 3 weeks.

Our findings showed that there was no statistically significant difference in growth rate amongst the control and experimental groups. More interestingly, there were some differences in growth form, including variation in coloration of the Escovopsis in the presence vs. the absence of the cultivar and increased sporing behavior in the presence of the cultivar. This could potentially indicate that the Escovopsis is reproducing more in the presence of the cultivar suggesting that there is some sort of volatile chemical indicator present. This study could lead to a greater understanding of the mechanisms behind inhibition and attraction in these systems.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 7 C
Presentation/Poster Number: 12
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

BRaf Mutations Alter Host Immunity and T-Helper Cell Phenotypes Within the Melanoma Tumor Microenvironment

Pavuluri, Bhavana; Ware, Michael Brandon; Paulos, Chrystal

Presenter/s: Bhavana Pavuluri
Emory Faculty Mentor: Chrystal Paulos

BRAF mutations are highly common within melanomas (~50%) (Pavlick et al., 2019) and can influence immunological phenotypes of tumors by promoting the infiltration and activity of suppressive myeloid cells and Tregs. Further, the production of inflammatory cytokines such as IL-6, TGFβ, IL-4, and IL-10 are driven by mutant BRAF in melanoma (Tsai et al., 2017). We hypothesize that this BRAF-associated cytokine milieu drives differences in CD4+ T cell phenotypes between BRAF mutant and wild-type tumors, and data presented here are initial investigations detailing such differences. Specifically, we predict that BRAF mutations promote Th17 cell expansion within the tumor microenvironment. We assessed the impact of BRaf mutations on host immunity utilizing BRaf mutant (YUMM1.7) and wild-type (YUMM4.1) congenic models of murine melanoma. These Yale University Mouse Melanoma cell lines contain clinically relevant mutations in BRaf, Pten, and Cdkn2a. The BRaf-WT B16F10 cell line, which lacks a clinically relevant mutational landscape, was also assessed. The production of over 55 different cytokines, chemokines, and growth factors was analyzed between these cell lines using chemokine/cytokine arrays. Tumor-infiltrating lymphocytes were assessed by flow cytometry, and transgenic murine models and western blots determined the expression of the melanoma antigen Trp1 between these cell lines. B16F10 tumors consistently promoted Th1 phenotypes, while YUMM1.7 tumors elicited a strong Th17 response in vivo and in vitro. Additionally, stark differences in myeloid infiltration and phenotype were observed. We noted unique cytokine and chemokine profiles between B16F10 and YUMM1.7 tumors, which provide insight into potential tumor immunity mechanisms. Finally, in vitro data with primary human CD4+ T cells parallelled these findings. Together, these data establish that BRAF mutations in melanoma lead to significant changes in T-helper phenotypes. This provides a foundation to understand how immunotherapy can best be tailored to melanoma patients with distinct mutational profiles.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 F
Presentation/Poster Number: 21
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating how Imatinib Induces Myelopoiesis and Augments Immune Responses Against Mycobacterium tuberculosis

Peddineni, Siri; Cleverly, Tesia; Kalman, Dan

Presenter/s: Siri Peddineni
Emory Faculty Mentor: Dan Kalman

Tuberculosis (TB) is an infectious disease caused by the bacteria Mycobacterium tuberculosis (Mtb). Though TB is treated with antibiotics, the rise of antibiotic resistant strains has created a public health emergency as many strains are now resistant to some or all available antibiotics. Research from our lab has shown that the cancer drug Imatinib mesylate (Gleevec), which is used to treat chronic myelogenous leukemia, could be repurposed for TB. Research with Imatinib in mice and primates has shown that Imatinib induces fusion of the phagosome with the lysosome to kill that bacteria, a host defense mechanism that the Mtb bacillus is usually able to subvert. Imatinib has also been shown to increase the number of myeloid cells and enhance the host's capacity to destroy the bacteria. Current research is focused on studying these effects in a human clinical trial. Here we will determine the optimal dosage of Imatinib required to induce phagolysosomal fusion and increase in myeloid cell numbers. Current experiments are focused on developing a model of how Imatinib affects the immune response. We have used RNA-seq to characterize the effects of Imatinib in a mouse model of tuberculosis. Our hypothesis is that Imatinib augments the development of immune response by increasing numbers of myeloid cells, thereby overcoming the delay often seen in this model and in TB patients. Currently, qPCR is being done to confirm the RNA-seq data from previous murine trials to better direct the clinical trial. Time course assays are also being run to investigate the rate of macrophage activation which we hypothesize will be increased with Imatinib because of the increase in phagolysosomal fusion. If successful, Imatinib may revolutionize how we treat TB, particularly disease caused by antibiotic-resistant strains. Moreover, because Imatinib is host-directed, it is less likely to engender resistance compared to conventional antibiotics.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 E
Presentation/Poster Number: 18
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effects of Low-Dose Radiation Therapy for the Treatment of Lung Inflammatory Syndrome in Mice

Perez Daisson, Alvaro; Kebler, Troy; Hess, Clay; Taverna, Luisa; Khan, Mohammad

Presenter/s: Alvaro Perez
Emory Faculty Mentor: Mohammad Khan

COVID-19 is the worst pandemic we have seen in our lifetime. The disease, caused by the SARS-CoV-2 virus, has pulmonary, coagulation disorders, and organ damage amongst its most lethal features. It is hypothesized that an unregulated storm of cytokines is associated with the mechanisms underlying these pathologies. Because the lymphocytes that produce cytokines are sensitive to radiation, low-dose radiation therapy (LD-RT) has been proposed as a possible treatment method. Previous studies have shown that low dose radiation therapy is a worthy candidate for more in-depth research and randomized trials to assess its efficacy. The purpose of our investigation is to realise said assessments. We will inject mice with 20 mg/kg of lipopolysaccharide (LPS), a potently immunostimulatory molecule produced by E. Coli that plays an important role in murine models that mimic lung inflammatory syndrome, and then expose them to different levels of low dose radiation therapy to test

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 E
Presentation/Poster Number: 19
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Delineating the Impact of Bone Marrow Stromal Cell Conditioned Media on CAR T-cell Manufacturing

Petit, Nicole; Sullivan, Emily; Henry, Curtis; Raikar, Sunil

Presenter/s: Nicole Petit
Emory Faculty Mentor: Sunil Raikar

B-cell acute lymphoblastic leukemia (B-ALL) comprises a significant subset of pediatric cancer diagnoses. Chimeric antigen receptor (CAR) T therapy, a treatment which enhances the body's anticancer properties through genetic modification of T-cells, has emerged as a last line of defense in cases of relapsed/refractory B-ALL; however, approximately half of patients receiving CAR T therapy will relapse. Improving upon T-cell function by increasing cellular longevity and/or cytotoxicity could be achieved by optimizing manufacturing techniques. Thus, we hypothesized that using physiologically relevant stromal cell conditioned media (SCM) may improve CAR T-cell efficacy.

Experimental Procedure: T-cells purified from human peripheral blood mononuclear cells were activated in vitro using anti-CD3 and anti-CD28 beads. T-cells were expanded for two weeks using unconditioned media or media supplemented with IL-2 alone, IL-2/IL-7, IL-7/IL-15, and SCM. T-cells were enumerated every three days using trypan exclusion assays. T-cell characterization was determined via immunophenotyping of surface markers via flow cytometric analysis.

Results: Human T-cells cultured in SCM exhibited compromised expansion after 2 weeks of growth relative to the other groups tested. Flow cytometric analysis revealed differences in the size and granularity of human T-cells grown in each condition, with human T-cells grown in SCM exhibiting a less blasted phenotype. Interestingly, T-cells grown in SCM exhibited outgrowth of two CD8+ T-cell populations. These results demonstrate that human T-cell expansion is suppressed when expanded in SCM; however, of the cells that remain; their phenotype is distinct from every condition tested.

Future Directions: We will next define the cytolytic capacity of our expanded T-cells in co-culture assays with human B-ALL cells (killing will be initiated by the FDA-approved immunotherapy Blinatumomab). Furthermore, based on Luminex and mass spectrometry profiling of our conditioned media, we will determine the impact of stromal cell-derived cytokines and metabolites on human T-cell expansion, stemness, and cytolytic potential.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 E
Presentation/Poster Number: 20
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Role of Satellite Cells in Myonuclear Homeostasis of Muscle Fibers

Pincate Esther; Hyojung Choo

Presenter/s: Esther Pincate
Emory Faculty Mentor: Hyojung Choo

Muscle fibers are contractile units of skeletal muscles that facilitate the organized movement of limbs and tissues. In adults, the skeletal muscle fibers maintain a certain number of nuclei (myonuclear homeostasis) to support large areas of the cell. Muscle tissues have muscle-specific stem cells, also known as satellite cells, which play a crucial role in the repair and regeneration of muscular tissue in case of muscle damage. Although various research has established the function of satellite cells, their role in myonuclei homeostasis maintenance is yet to be explored. Satellite cells remain fused in muscles even without injury, and their fusions vary between different muscles, (hind limb, diaphragm, etc..). Thus, it is still unclear how myofibers maintain a certain number of nuclei given the continuous fusion of satellite cells. To determine the role of satellite cells in homeostasis maintenance, we employed genetic mouse model (Pax7CreERT-DTA) expressing Diphtheria Toxin Subunit A (DTA) under Pax7 promotor conjugated tamoxifen-inducible Cre recombinase. Muscle fibers were isolated from these genetic mouse model with depleted satellite cells and were used to analyze myonuclear densities per fiber lengths between normal and satellite cell-depleted muscle fibers. Preliminary results show that myofibers without satellite cells have a higher myonuclei population in comparison to those with fused satellite cells. This infers that despite the important role of satellite cells in the repair and regeneration of muscle tissue, satellite cells may not be the primary factor responsible for maintaining homeostasis in myofibers. Ultimately, we will further study and explore the mechanistic factor that could be responsible for myonuclear homeostasis and their role as an underlying pathogenic mechanism of muscular dystrophies, such as oculopharyngeal muscular dystrophy.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 E
Presentation/Poster Number: 17
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effects of early hippocampal damage on regional thickness of the prefrontal cortex in a monkey model of neurodevelopmental disorders: a pilot study

Pineda, Diana Laura; Rodman, Hillary; Moon, Paul Eugene

Presenter/s: Diana Pineda
Emory Faculty Mentor: Hillary Rodman

Neurodevelopmental disorders like schizophrenia (SCZ) and autism are characterized by alterations in the hippocampus, amygdala and prefrontal cortex (PFC) circuitry. These alterations are thought to cause deficits in working memory and emotion, symptoms found in individuals with schizophrenia and related disorders. Previous research investigating adult human SCZ patients have found decreased cortical thickness in the dorsolateral PFC (dlPFC), ventromedial PFC (vmPFC), and anterior cingulate cortex (ACC). Further, the hippocampus matures faster than the prefrontal cortex and interference with their interconnected circuitry may be a cause for reduced cortical thickness in specific PFC brain regions. Therefore, the hypothesis for our study investigating the effect of cortical thickness in monkeys with neonatal hippocampal lesions is that our experimental group (Neo-H) will display reduced cortical thickness in the dlPFC, vmPFC, and the ACC compared to our control group (Neo-C). Additionally, our control brain region across all subjects is the dorsal premotor area. Our subjects included 11 macaque monkey brains: 5 subjects with neonatal hippocampal lesions (Neo-H) and 6 control subjects (Neo-C). A previous study processed the brains with immunochemistry and a Giemsa counterstain. Each brain had four coronal slices of the PFC all of which were placed under a microprojector with 12X magnification for tracing. The regions of interest were labeled accordingly, and cortical thickness was measured in millimeters using a standard 12-inch ruler while also remaining blind to their respective groups (Neo-H and Neo-C). Averages for each region of interest were calculated for each hemisphere. We ran independent samples t-tests, and our findings did not support our hypothesis demonstrating a significant difference only in the dorsal premotor area. In future studies, it is suggested to further investigate the dorsal premotor area and its possible relation to neurodevelopmental disorders with deficits in working memory and emotion.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 D
Presentation/Poster Number: 14
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

DNA Conformation in Peptide Nanostructures

Poppitz, George; Gordon, Christella; Roberson, Alexis; Lynn, David.

Presenter/s: George Poppitz
Emory Faculty Mentor: David Lynn

DNA can template peptide nanostructure formation through electrostatic interactions between negatively-charged phosphate groups along the DNA backbone and positively-charged amino acids. This templating phenomenon is possible with both single- and double-stranded DNA, but we do not know the conformation of the DNA when incorporated within the peptide structure. To answer this question, we used 2-aminopurine (2AP), an adenine analog, as a fluorescent probe, which should induce minimal perturbation. As well as 2AP-tagged PolyA ssDNA and 2AP-tagged dsDNA, we used the peptide Ac-KLVIIAG-NH2 because the positive lysine sidechain interacts with the negative DNA backbone. Ac-KLVIIAG-NH2 was co-assembled with either single-stranded or double-stranded DNA in 40% acetonitrile solutions with high (150 mM) or low (10 mM) concentrations of NaCl or LiCl to probe for competing electrostatic interactions. We used a plate reader to measure 2AP and ThT fluorescence, circular dichroism (CD) spectroscopy to measure β-sheet character in each assembly, and transmission electron microscopy (TEM) to visualize nanostructure morphology. CD, ThT fluorescence, and TEM all show that single-stranded and double-stranded DNA drive nanoribbon and nanotube formation. Crucially, 2AP fluorescence data show that single-stranded DNA fluorescence is quenched, indicating that DNA within the peptide nanostructure is duplexing. This quenching is greatest with no salt and decreases with added NaCl or LiCl salts, possibly suggesting competing electrostatic interactions with salt ions. Single-stranded PolyA duplexes at low pH, so as well as the DNA structure this result sheds light on the local pH of the peptide and DNA interactions and opens the door for using pH-controlled DNA template sequences to create different peptide morphologies.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 E
Presentation/Poster Number: 20
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The effects of color manipulation on the mating behavior of monarch butterflies (Danaus plexippus)

Williams, Ashley; Portil III, Karl; Zhao, Ella; Villa, Scott; de Roode, Jacaobus

Presenter/s: Karl Portil and Ashley Williams
Emory Faculty Mentor: Scott Villa

Monarch butterflies are famous for their 4000km journey from Southern Canada to Central Mexico. However, very little is known about the traits that are important for successful mating. Previous work shows that size and color are essential for mating in butterflies. Here we investigate their potential roles in monarchs. We hypothesize that body size influences mating success, where males and females of the same size prefer to mate with each other. In addition, wing color may also influence monarch mate choice, where more melanized individuals are favored. To test these hypotheses, we experimentally manipulated both size and color of captive-reared butterflies. These monarchs were placed in mating cages and filmed for five days. We quantified the number of times monarchs mated and assessed their preference for different sizes and color mates from each film. Preliminary results suggest that size and color interact to influence mating decisions. Our study was the first to identify the particular traits that govern mate choice in monarch butterflies.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 G
Presentation/Poster Number: 25
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Computational Studies of Properties and Synthesis of 10,11-diphenylcyclobuta[5,6]pyrazino[2,3-f][1,10]phenanthroline

Powell, Justin; Saadein, M. Reza; Nkomo, Simbarashe

Presenter/s: Justin Powell
Emory Faculty Mentor: Simbarashe Nkomo

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 E
Presentation/Poster Number: 18
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Data Comparison, Evaluation, and Correction for Low-cost Air Quality Sensors and Potential Site Identification in Georgia

Pu, Siyan; Saikawa, Eri

Presenter/s: Siyan Pu
Emory Faculty Mentor: Eri Saikawa

Air pollution comprises the largest environmental risk factor for morbidity and mortality worldwide. Environmental Injustice is a persistent issue in Georgia with low-socioeconomic status counties suffering from air pollution the most. Building an air quality monitoring network that can represent different parts of Georgia at finer spatial scales is helpful to identify heavily polluted places and analyze potential health effects. To fill the air quality data gaps due to sparsely placed regulatory monitors in Georgia, we initiated a project to place low-cost air quality sensors at 30 schools in Georgia. The network comprised of the validated low-cost sensors and existing regulatory sensors could provide a more refined indicator of air quality in Georgia. As a preparatory project for this objective, multiple work has been done. (i) Data comparison and evaluation for air quality data, including PM2.5, PM10, O3, and NO2 from two different low-cost sensors at Emory along with the county-level regulatory data was conducted. Results showed that Airly sensor has a greater accuracy compared to Dylos. (ii) A function to automatically compare data from various sites was developed for evaluating sensor data. (iii) Interactive maps were created to help identify appropriate locations for 30 sensors to be placed in Georgia. Existing regulatory sensors were found to be unevenly spread out, with most in the metro-Atlanta area and very few in other parts of Georgia. (iv) Finalized a plan to validate low-cost sensors by collocating them with existing regulatory sensors. These have provided a good ground for us to implement the project, automate the data validation process, and visually identify potential sites in the future.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 D
Presentation/Poster Number: 15
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigation of Cavity-Mediated Intermolecular Energy Transfer

Qi, Charles; Ribeiro, Raphael

Presenter/s: Charles Qi
Emory Faculty Mentor: Raphael Ribeiro

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 D
Presentation/Poster Number: 15
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Creating a Bounded Body of Knowledge for Republican Women

Qian, Virginia; Fu, Jia-Chen

Presenter/s: Qian Qian
Emory Faculty Mentor: Jia-Chen Fu

In this study, I explore the connections between women and science in the Republican period China (1912-1949) by examining Linglong, a women's periodical published in Shanghai between 1931 and 1937. The magazine was intended to capture and foster urban educated female readers while its editorial board consisted of mostly men. The magazine was designed to be read bi-directionally such that the printed orientation of the text naturally partitioned the magazine in two and guided the readers to read the magazine from both the front and back covers. The articles read from the back cover were formatted with horizontally-oriented text, incorporated more progressive content, and provided readers exposure to new or exotic information, such as Hollywood movie stars, western entertainment, and scientific practices. In contrast, vertically-oriented text tended to cover topics that pertained to the interests of women derived from their traditional roles. Throughout the seven years of its publication, the magazine did not maintain a consistent format, presentation, and content.

Linglong offered a space for Republican women to confront the disorienting atmosphere where public and intellectual debate on women's role in saving the nation and the influx of western information contributed to changing norms and expectations for women. Republican period intellectuals claimed that women's weakness and subordination were linked to the nation's weakness, and women's emancipation linked to modernity. Reading Linglong, women asserted some control over how they understood the roles and responsibilities of the New Women and were no passive recipient of modern transformation as cast by intellectuals. At the same time, there was no clear path to this transformation. Linglong displayed diverse presentations of western information and contradictions among its articles. The cacophony of voices in Linglong was the editors and writers' experimentation with the figure of New Woman. They assembled a body of scientific knowledge to establish the expected specific abilities and responsibilities for a modern woman and redress the nation's ills. Science in Linglong offered solutions to basic household management problems and knowledge on trendy items and provided roots of rational and scientific thinking to women.

Research Discipline: Humanities
Presentation Type: Poster Presentation

Session: 5 E
Presentation/Poster Number: 20
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Streptococcal protease SpeB processing of cathelcidin regulates wound healing.

Qu, Claire; LaRock, Christopher

Presenter/s: Claire Qu
Emory Faculty Mentor: Christopher LaRock

Streptococcus pyogenes (group A Streptococcus, GAS) is a nearly ubiquitous, highly transmittable, human pathogen that infects over 700 million and kills 600,000 people per year. GAS deeply manipulate host immune responses, in part through the protease SpeB, which cleaves numerous human proteins including the active form of the innate immune antimicrobial, LL-37 (Walker 2014). LL-37 cathelicidin promotes wound healing, however, the wound healing abilities of SpeB-cleaved LL-37 peptides are unknown. Since this could impact recovery from infection, we examined whether these LL-37 cleavage products impede wound healing. We hypothesized that SpeB inhibits healing by cleaving LL-37 into inert products. We first examined cleavage of LL-37-derived peptides tessellated along the sequence that had fluorescent labels incorporated to report cleavage. We found that the high affinity cleavage sites were concentrated on the ends of the alpha-helix protein. Previous results suggested that the N-terminus side of LL-37 associated with wound healing was removed, suggesting that SpeB disrupts LL-37-mediated wound healing. We next performed an in vitro model of wound closure, aka 'scratch assay'. Preliminary analyses identify several novel natural truncated forms of LL-37 generated by SpeB cleavage. These peptides, diluted at concentrations within the physiological range found in health and disease, were added to cultured HaCat human keratinocytes. Cells treated with LL-37 products generated by SpeB cleavage, surprisingly, still promoted wound closure relative the negative control cells. LL-37 treated cells still had the greatest recovery, suggesting GAS does moderately impair keratinocyte-mediated healing of wounds by disrupting LL-37 signaling. Future studies will use mass spectrometry to map the cleavage sites in finer detail. This will allow the development of LL-37 forms that retain antimicrobial activity toward GAS and have greater regenerative potential that can be used adjunctively as an effective therapeutic and prophylactic countermeasure to GAS skin infections.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 D
Presentation/Poster Number: 16
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Chemical foundation of the interactions between cultivars and Escovopsis.

Gerardo, Nicole; Marko, Annabelle; Patterson, Rachel; Rajani, Mira
(All authors contributed equally and are presented in alphabetical order)

Presenter/s: Mira Rajani, Annabelle Marko, and Rachel Patterson
Emory Faculty Mentor: Nicole Gerardo

Escovopsis is a genus of fungus that parasitizes ant cultivars to form a coevolutionary fungal system. The mechanisms through which these two interact are still largely unknown. There has been previous literature that suggests that Escovopsis releases different volatile organic compounds (VOCs) in the presence of a cultivar. In this study, we are investigating whether VOCs mediate cultivar-parasite interactions. We hypothesized that the difference in the growth rate between the experimental and control conditions would be significant. To test this hypothesis, we grew Escovopsis (A. dentigerum) and cultivars (A. Auriculatum, A. dentigerum, and C. costatus) in an enclosed space, where they could not physically interact but could respond to volatiles released by one another. We monitored and measured growth form and growth rate every week over the course of 3 weeks.

Our findings showed that there was no statistically significant difference in growth rate amongst the control and experimental groups. More interestingly, there were some differences in growth form, including variation in coloration of the Escovopsis in the presence vs. the absence of the cultivar and increased sporing behavior in the presence of the cultivar. This could potentially indicate that the Escovopsis is reproducing more in the presence of the cultivar, suggesting that there is a volatile chemical indicator present. This study could lead to a greater understanding of the mechanisms behind inhibition and attraction in these systems.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 7 C
Presentation/Poster Number: 12
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The Psychosocial Effects of COVID-19 on Undocumented Latinx People Living in the U.S.

Ramos Correa, Idalis; Woods-Jaeger, Briana

Presenter/s: Idalis Ramos Correa
Emory Faculty Mentor: Briana Woods-Jaeger

Abstract not available.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 7 D
Presentation/Poster Number: 15
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Optimized Conditions for the Production of Gold Nanoparticles Functionalized with I-Motif DNA.

Ramrattan, Tsian; Narum, Steven; Salaita, Khalid.

Presenter/s: Tsian Ramrattan
Emory Faculty Mentor: Steven Narum

Gene therapy has seen recent advancements toward becoming a highly specific form of treatment for a variety of chronic diseases such as cancer, multiple sclerosis, and cystic fibrosis. Gene therapeutics such as antisense oligonucleotides necessitate a very precise delivery method as they are limited by cellular barriers, namely endosomes. Spherical nucleic acids (SNAs) have the unique ability to overcome a variety of biological barriers while invoking minimized immune responses in patients.1 These ideal characteristics can be attributed to their high-affinity constants and the ability to bind to scavenger receptors of cells, affording the capacity to effectively deliver gene therapeutics. Intercalated motif (i-Motif) DNA is a newly discovered form of DNA to be naturally occurring within humans. The i-Motif is characterized by intercalating cystines (C+:C) that are prompted to self fold under acidic conditions.2 This response sustains the potential shrouding the i-Motif sequence in gene therapy. Uncovering optimized conditions for the prod1u1c1t1i1o1n1 1o1f1 1n1a1n1o1p1a1r1t1i1c1l1e1s1 1f1u1n1c1t1i1o1n1a1l1i1z1e1d1 1w1i1t1h1 1i1-1M1o1t1i1f1 1D1N1A1 1c1a1n1 1c1o1n1t1r1i1b1u1t1e1 1t1o1 1t1h1e1 1c1r1e1a1t1i1o1n1 1o1f1 1v1a1l1u1e1d1 1p1r1o1d1u1c1t1s1.131 1 1M1a1x1i1m1i1z1i1n1g1 1t1h1e1 1D1N1A1 1d1e1n1s1i1t1y1 1p1e1r1 1p1a1r1t1i1c1l1e1 1w1a1s1 1a1s1s1e1s1s1e1d1 1b1y1 1a1s1s1a1y1i1n1g1 1t1h1e1 1e1f1f1e1c1t1 1t1h1e1 1r1a1t1i1o1 1o1f1 1o1l1i1g1o1n1u1c1l1e1o1t1i1d1e1s1 1t1o1 1g1o1l1d1 1n1a1n1o1p1a1r1t1i1c1l1e1s1 1(1A1u1N1P1s1)1 1h1a1s1 1o1n1 1t1h1e1 1f1u1n1c1t1i1o1n1a1l1i1z1a1t1i1o1n1 1o1f1 1t1h1e1 1p1a1r1t1i1c1l1e1s1.1 1G1r1o1u1p1s1 1o1f1 1510101,1 1410101,1 1310101-1 1a1n1d1 1210101-1t1i1m1e1s1 1e1x1c1e1s1s1 1o1f1 1D1N1A1 1t1o1 1A1u1N1P1s1 1w1e1r1e1 1c1r1e1a1t1e1d1 1a1n1d1 1t1h1e1 1D1N1A1 1d1e1n1s1i1t1i1e1s1 1o1f1 1t1h1e1 1n1a1n1o1p1a1r1t1i1c1l1e1s1 1i1n1 1e1a1c1h1 1s1o1l1u1t1i1o1n1 1w1e1r1e1 1q1u1a1n1t1i1f1i1e1d1.1 1A1 1s1t1a1t1i1s1t1i1c1a1l1l1y1 1s1i1g1n1i1f1i1c1a1n1t1 1d1i1f1f1e1r1e1n1c1e1 1w1a1s1 1n1o1t1e1d1 1b1e1t1w1e1e1n1 1t1h1e1 1210101 1a1n1d1 1t1h1e1 1510101 1g1r1o1u1p1s1 1a1n1d1 1t1h1e1 1310101 1a1n1d1 1t1h1e1 1510101 1g1r1o1u1p1s1 1b1u1t1 1n1o1 1s1t1a1t1i1s1t1i1c1a1l1 1s1i1g1n1i1f1i1c1a1n1c1e1 1w1a1s1 1o1b1s1e1r1v1e1d1 1b1e1t1w1e1e1n1 1t1h1e1 1310101 1a1n1d1 1410101 1g1r1o1u1p1s1 1a1n1d1 1t1h1e1 1410101 1a1n1d1 1510101 1g1r1o1u1p1s1.1 1l1t1 1c1a1n1 1t1h1e1r1e1f1o1r1e1 1b1e1 1i1n1f1e1

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 F
Presentation/Poster Number: 21

Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The Effects of Early Life Stress on the Development of Language in Macaques

Reddy, Shreya; Kovacs-Balint, Zsofia; Flamenbaum, Lauren; Siebert, Erin; Kochoian, Brik; McCormack, Kai; Howell, Brittany; Styner, Martin; Sanchez, Mar

Presenter/s: Shreya Reddy
Emory Faculty Mentor: Mar Sanchez

Humans have specialized brain language regions, called Broca's and Wernicke's areas, responsible for speech production and language processing, respectively. Although still a point of controversy, cortical areas 44 and 45 of the macaque frontal cortex have been proposed as homologs of Broca's area, and vocalizations stimulate the macaque temporoparietal cortex (Tpt area), considered the Wernicke's homolog area. This study examined these language regions in 41 macaques during adolescence and long-term structural effects of early life stress (ELS: poor maternal care) using structural MRI. We also compared the development of vocalizations and anxiety behaviors in both ELS and Control groups through focal observations of the subjects from 1-18 months. ELS is linked to negative developmental outcomes, such as anxiety/depression and social deficits. Cortical volumes were analyzed using a Two-Way ANCOVA with ICV as a covariate because of sex differences in brain size; vocalization data was analyzed using Repeated Measures ANOVA. We found that infants that experienced ELS vocalized more than control infants during the first 3 postnatal months. The increased vocalizations in ELS infants were driven by increased rates of screams in the first 3 postnatal months, which is when they receive the highest rates of maternal abuse and rejection. Although no significant effect of ELS was found on anxiety, the rates in both groups increased with age, due to weaning and increased social interactions. Despite higher rates of distress vocalizations in infant ELS macaques, ELS had no effect on volumes of cortical areas 44, 45, and Tpt in adolescence, suggesting that ELS did not affect the structural development of language brain regions. However, these findings do not rule out potential connectivity or functional differences in language areas. Understanding the impact of ELS on language development in translational nonhuman primate models will inform the diagnosis and treatments of human language deficits.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 5
Presentation/Poster Number: 3 of 6
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99538389212

Interventions for African Americans with Anxiety and Stress-Related Disorders

Carmola, Ludy; Renard, Destini

Presenter/s: Destini Renard
Emory Faculty Mentor: Joya Hampton-Anderson

Abstract not available.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 3 F
Presentation/Poster Number: 22
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Functional Characterization of TRIP13 in Wilms Tumor

Riembauer, Joshua; Mittal, Karuna; Lee, Benjamin; Cooper, Garrett; Hong, Andrew

Presenter/s: Josh Riembauer
Emory Faculty Mentor: Andrew Hong

Survival rates of patients with Wilms tumor, the most common pediatric kidney cancer, have improved over the past 7 decades. Despite this, almost 20% of patients' cancer will recur and outcomes remain poor despite aggressive therapy. Furthermore, new therapies are lacking due in part to the lack of well established cell culture models. Our lab has developed these models and preliminarily found that Favorable Histology Wilms Tumor requires TRIP13 for survival. Here, we aim to determine if Anaplastic Wilms Tumor cell lines also require TRIP13 for survival. We used functional genomics to study the function of TRIP13 in PEDS204T, an anaplastic Wilms Tumor cell line with a 469G>T mutation in TP53, through overexpression, suppression, and mutation of TRIP13. We generated the TRIP13 1060C>T construct, a mutation which prior studies have shown may be important in a subset of patients with Wilms tumor, and validated our tools to either overexpress or suppress TRIP13. We transduced our TRIP13 constructs into PEDS204T cells and are currently determining the functional consequences in this cell line. This study contributes to our understanding of Wilms tumor biology. Further work will be required to validate our findings in other anaplastic Wilms tumor cell lines and delve further into the mechanism by which TRIP13 acts in anaplastic Wilms.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 F
Presentation/Poster Number: 21
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Lateralization of Noxious Stimuli

Rivera, Adrian; Hentschel, Matthew; Harper, Daniel, Ph.D.; Alsouhibani, Ali, Ph.D.; Gregory, Mia

Presenter/s: Adrian Rivera
Emory Faculty Mentor: Daniel Harper

Current research on pain processing mechanisms suggests that there are differences in how the brain processes noxious stimuli based on the side of the body where the noxious stimulus is applied. Specifically, the literature seems to suggest that some regions of the cortex may be exhibit bias in the processing of pain toward the right hemisphere. It is not known, however, whether these differences in processing are due to differences in modality (e.g. mechanical pain or thermal pain). Therefore, the main aim of this study is to analyze differences in pain processing using moderately painful stimuli (i.e. rated 40 out of 100) presented to both the left and right side of the body, with multiple modalities of noxious stimuli. One thermal and two mechanical noxious stimuli will be applied on 30 healthy individuals on the left and right leg in separate runs. The intensity of the stimuli will be presented in an ascending and descending manner and subjects will be asked to rate pain intensity using a visual analog scale. Using these ratings, a stimulus intensity that results in a pain rating of 40 on a scale of 0 to 100 will be calculated—0 being no pain at all and 100 being the worst painful sensation imaginable from the stimulus. This stimulus, considered to be moderately painful, will then be presented for longer periods of time to observe how subjective ratings vary between the two sides (i.e. right and left). The experiment will be conducted inside a Siemens 3T Magnetic Resonance Imaging (MRI) scanner to investigate any differences in activation and/or connectivity in processing brain regions—using a neuroimaging technique known as functional MRI (fMRI) which allows to observe brain activation as subjects experience the stimuli. Though at the time of writing of this abstract no results were available, the study team hypothesizes that results of the study will be in line with previous experiments—which find activation in cortical regions during acute pain to be either “exclusively in the right hemisphere” or “strongly lateralized to the right” (Symonds, Gordon, Bixby & Mande, 2006).

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 F
Presentation/Poster Number: 21
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Probing the Dynamic Network of Nucleic Acid and Protein Co-assembly

Roberson, Alexis; Gordon, Christella; Poppitz, George; Lynn, David

Presenter/s: Alexis Roberson
Emory Faculty Mentor: David Lynn

Biomolecular condensates enable spatial and temporal organization of biochemical reactions that control key cellular information processes from transcriptional regulation to translation and replication (1,2). Understanding the two-step nucleation pathway of peptide assembly and the ability of nucleic acids to template protein structural arrangement is a critical first step with protein mutations underlying diseases ranging from cancer to neurodegeneration. While the obvious electrostatic interactions are primarily driven by complementarity between positively charged residues and the negative phosphate backbone of DNA, current research aims to explore the extent to which other non-covalent interactions contribute to the formation and stability of templated co-assemblies. Here we specifically explore cation-pi interactions with the design of three peptides, Ac-KLVIIAG-NH2 (N-capped), Ac-HLVIIAG-NH2 (N-capped), H-HLVIIAGNH2 (uncapped), templated with PolyA9(2AP). Templated assembly is observed with Thioflavin T (ThT) fluorescence, 2-Aminopurine (2AP) fluorescence, and circular dichroism spectroscopy. Data from 2AP fluorescence suggest a role for cation-pi interaction with the positively charged lysine, as shown by the time-dependent growth of ThT fluorescence with significant 2AP fluorescence quenching. In comparing the capped and uncapped HLVIIAG peptides, data suggest that acetylation of the N – terminal histidine, reducing the positive charge on the histidine residue, prevents significant electrostatic interactions or cation – pi interactions between the peptide and PolyA9(2AP) as demonstrated by almost zero 2AP and ThT fluorescence. Further, some 2AP fluorescence for uncapped HLVIIAG and very little ThT fluorescence suggest the presence of a repulsive cation-pi or pi-pi interaction destabilizing the peptide's co-assembly with PolyA9(2AP). CD spectra are consistent with the formation of beta sheet secondary structures as indicated by minimum peaks for each sample near 218 nm.

1. Brangwynne et al., Science 2009, 324:1729-1732
2. Li et al., Nature, 2012, 483: 336-340.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 E
Presentation/Poster Number: 19
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Development of an Extracellular Vesicle-based mRNA delivery system

Rojas, Alexander; Dobosh, Brian; Tirouvanziam, Rabindra

Presenter/s: Alex Rojas
Emory Faculty Mentor: Rabindra Tirouvanziam

The progression of cystic fibrosis (CF) is characterized by the chronic recruitment of polymorphonuclear neutrophils (PMNs) into the lung resulting in inflammation. However, PMNs fail to kill the bacteria resulting in respiratory infections. PMNs are also highly pinocytic, which makes them a good target for extracellular vesicle (EV)-based therapies. EVs are lipid particles which form a ubiquitous mechanism of cell-to-cell communication. An in-depth profile of the RNA composition of EVs from healthy endothelial cells was determined [1]. It was discovered that there are genetic motifs, which we have termed Pérez-Boza sequences, that promote packaging of RNA into EVs [1]. We hypothesized that we could include the identified motifs in the 3'UTR of mRNA to package the transcript into EVs. Cloning was used to create seven plasmids (pAR007-13) containing potential Pérez-Boza-EV localization motifs in the 3'UTR of EGFP, which were then transfected into H441 epithelial cells with Lipofectamine 3000. Total RNA was extracted from the EVs in the conditioned media and transfected H441 epithelial cells. The RNA was reverse transcribe with an anchored oligo(dT) primer and Superscript IV followed by qRT-PCR to quantify the EGFP mRNA content in the EV- and cell-fractions. The ΔΔCt method relative to GAPDH was used to analyze the qRT-PCR results. Plasmids pAR008, pAR009, and pAR011 showed an increased ration of cellular:EV EGFP mRNA compared to pAR014 (no Pérez-Boza motif) via the ΔΔCt method. Taking the total amount of EGFP in EVs compared to the total cellular RNA content we also found that pAR007, pAR008, pAR009, and pAR011 showed increased packaging efficiency compared to pAR014. These motifs may promote the packaging of mRNA into EVs, which can be utilized for therapeutic development. More replicates need to be done to confirm any conclusions.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 E
Presentation/Poster Number: 20
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Mapping Rebel Groups & Alliances in the Syrian Civil War: An Exploration into the Driving Forces of Rebel Group Collaboration and Fragmentation

Gade, Emily; Leung, Brian; Jensen, Bree; Sharifi, Ava; Salehian, Kayla; Thomas, Emily; Clerkin, Connor

Presenter/s: Kayla Salehian
Emory Faculty Mentor: Emily Gade

Given the multitude of rebel groups active in the Syrian Civil War and the complexity of this conflict, a comprehensive dataset of information about each main rebel actor does not yet exist in the literature. However, the collaboration patterns of these rebel groups are unique in that groups collaborate in numerous ways: operations rooms, joint collaboration in battles, formalized alliances, and fronts. Operations rooms are formal, cooperative tactical units that collaborate frequently in battles but differ significantly from formalized alliances. This study, in part, aims to discover the motivations rebel groups have to join operations rooms instead of alliances or fronts. Despite the myriad of ways groups collaborate with each other, there are many problems related to alliance and group stability: splintering, merging, and “frenemies” relationships between groups. Previous literature has cited ideological incompatibility, factional leadership, internal decision-making structures, and the amount of violence present as variables that contribute to the fragmentation of rebel groups and alliances. Because the Syrian Civil War is a dynamic conflict, we* coded key variables for groups at both a general and year-group level in order to capture changes in alliance and splintering patterns over time. We chose key variables based upon relevant previous literature and significant discoveries made during our data collection process. This covariate dataset will provide insight into the most significant factors driving rebel group alliance formation, merging, group durability/fragmentation, and overall collaboration. Understanding these factors has the potential to provide insight into future non-state actor collaboration patterns and may help scholars better understand why the Syrian conflict has lasted for over a decade.

Research Discipline: Social Sciences
Presentation Type: Oral Presentation

Session: 4
Presentation/Poster Number: 4 of 5
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99643683271

The National LGBTQ+ Women's Community Survey

Ali Sewell, Alyasah; Brinson, Clark; Sarette, Nicole

Presenter/s: Nicole Sarette
Emory Faculty Mentor: Alyasah A Sewell

This survey aims to create a sampling field for LGBTQ+ women, as there is a lack of data available for this population. The survey targets people who currently identify or have ever identified as women at any point in their lives and want to share their experiences of centering women in their sexual, emotional, familial and social lives. The survey and resulting research that comes from the data it provides, aims to enhance knowledge, policy analysis, organizing, and advocacy around the life experiences, priorities, needs, and challenges of women in the LGBTQ+ community. The real-world applications of the survey data are to provide policymakers and the general public with valuable information on the lives and experiences of LGBTQ+ women. The survey is conducted through Qualtrics software, with a sampling goal of 20,000 respondents. The minimum sample desired by the research team is 15,000, and the ideal sample would reach 24,000 respondents. The demographics listed for the survey are not cross-cutting strata. Select quota samples are set in order to capture hyper-invisible, hard-to-reach (formerly or current) women-identifying people. The quota sampling's function for the survey is to continuously run until researchers reach the minimum number of observations set for each of the targeted categories

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 4 F
Presentation/Poster Number: 22
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating EP2 antagonism in a two-hit mouse model of Alzheimer's disease

Sau, Michael; Banik, Avijit; Rojas, Asheebo; Ganesh, Thota

Presenter/s: Michael Sau
Emory Faculty Mentor: Thota Ganesh

Alzheimer's disease (AD) is a neurodegenerative disorder, characterized by loss of neurons, the formation of pathological proteins like amyloid-beta (Aβ), and activation of glial cells in the brain all leading to progressive cognitive decline and dementia. So far, there is no effective therapy available to reverse the underlying pathology of AD. We have recently demonstrated that the prostaglandin E2 receptor (EP2) has a role in neuroinflammation in mouse models of neurodegeneration as small molecule EP2 inhibitors attenuates the robust inflammatory bursts caused by seizures. Here, we aim to use a two-hit model of Alzheimer's disease where transgenic 5xFAD mice will be administered lipopolysaccharide (LPS) to induce an additional level of inflammation in the AD brain. Subsequently, the mice will be treated with a potent EP2 antagonist dissolved in the drinking water and their brains will be investigated for amyloid pathology and associated neuroinflammation. This project aims to quantify the brain levels of amyloid plaques by Congo red staining in LPS insulted 5xFAD mice either treated with EP2 antagonist or vehicle (drinking water at 2.8 pH) and quantify the levels of inflammatory mediators and glial markers in these mice by qRT-PCR and immunohistochemistry of inflammation-associated proteins. The hypothesis is that oral dosing of a selective and potent EP2 antagonist significantly reduces the amyloid burden and associated neuroinflammation in 5xFAD brains. The overall goal of this study is to investigate the therapeutic efficacy of EP2 antagonists in ameliorating AD pathology and inflammation. Successful completion of this project will strengthen the candidacy of a small molecule EP2 antagonist as a potential adjunct therapeutic for AD.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 E
Presentation/Poster Number: 17
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining Vascular Measures for Arterial Stiffness and their Relationship with Demographic, Motor, and Cognitive Variables in Parkinson's Disease Patients

Saxena, Varun; Hackney, Madeleine; Lewis, Eliza

Presenter/s: Varun Saxena
Emory Faculty Mentor: Madeleine Hackney

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 F
Presentation/Poster Number: 23
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Not Waiting for an Invitation: Gender and Diplomacy in American Ambassadorial Appointments to Asia in the Post-Cold War Era

Scheel, Bethany; Suh, Chris

Presenter/s: Bethany Scheel
Emory Faculty Mentor: Chris Suh

Historically, the American Foreign Service has been “white, male, and Ivy League” as described by former Undersecretary of State Benjamin Reid during the 1989 Alison Palmer proceedings exposed the long-standing gender inequality within the State Department. Though modern research is slowly expanding to investigate how women have shaped international relations in the 20th century, especially in the field of global human rights, there is still a lack of scholarship that examines women ambassadors and their role as representatives of the United States abroad. Therefore, it is necessary to focus on two women ambassadors, Julia Chang Bloch, Ambassador to Nepal 1989-1992, and D. Kathleen Stephens, Ambassador to the Republic of Korea 2008-2011, whose work has not been taken seriously by historians, asking questions such as “Why is their history excluded?” and “What can these women’s contributions to American foreign policy teach us about our inter and intranational dynamics?” to help fill a vital gap in women’s history. This research hinges on primary sources such as interviews and secondary sources like journal articles to illuminate the entirety of these women’s lives and careers. This work argues that Ambassadors Julia Chang Bloch and D. Kathleen Stephens’s appointments are historically significant, both due to their novelty and to their adherence to pre-established themes found in women’s role in American foreign policy. Their lives and careers exemplify the diversity of women's ambassadorial appointments to Asia, further informing historians about the significant place these women hold in our collective diplomatic history.

Research Discipline: Humanities
Presentation Type: Poster Presentation

Session: 5 F
Presentation/Poster Number: 22
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

A Conformational Study of “CyClick” Peptides for Targeting Intracellular Protein-Protein Interactions

Shahin, Sophia; Bruce, Angele; Adebomi, Victor; Verma, Ashish; Buxton, Matthew; Raj, Monika

Presenter/s: Sophia Shahin
Emory Faculty Mentor: Monika Raj

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 D
Presentation/Poster Number: 16
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The Effect of Chronic Chemogenetic Locus Coeruleus Activation on Alzheimer's Disease-like Pathology in a Transgenic Rat Model

Shanmugam, Akash; Kelberman, Michael; Chawla, Shivaang; Rorabaugh, Jacki; Weinshenker, David

Presenter/s: Akash Shanmugam
Emory Faculty Mentor: David Weinshenker

The locus coeruleus (LC), the major noradrenergic nucleus in the brain, plays a critical role in attention, arousal, stress responses, learning, and memory. The LC is the first site of hyperphosphorylated tau development in early Alzheimer's disease (AD), and these neurons die as the disease progresses. Norepinephrine (NE) possesses potent anti-inflammatory properties, slows neurodegeneration in animal AD models, and inhibits the accumulation of AD-like neuropathology. We have previously shown that TgF344-AD rats that overexpress mutant human amyloid precursor protein and presenilin-1 display early hyperphosphorylated tau in the LC, which is associated with loss of noradrenergic fibers in the hippocampus (HC), and chemogenetic stimulation of the LC rescues impairments in reversal learning in this rat model of AD. Here, we sought to understand the effects of chronic LC activation on AD-like neuroinflammation and pathology in the LC and HC. 15-month-old TgF344-AD rats (N=12) received bilateral intra-LC injections of a noradrenergic-specific virus to express excitatory (hD3Mq) designer receptors exclusively activated by designer drugs (DREADDs). Half the rats were administered the DREADD agonist clozapine N-oxide (1 mg/kg) 5 days per week for 6 weeks, while the other half were administered saline through intraperitoneal injections. HC subregions were analyzed for neuroinflammatory markers (GFAP and IBA1), AD-like neuropathology pathology (Aβ and P-tau), and LC innervation to the HC (norepinephrine transporter). We observed strong trends towards decreased pathology and inflammation in TgF344-AD rats that received CNO compared to the rats that received saline. These differences were especially pronounced in the dentate gyrus, the hippocampal region that receives the densest noradrenergic innervation from the LC. These preliminary results support a neuroprotective role for the LC in AD animal models.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 F
Presentation/Poster Number: 24
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Saponin Tolerance and Degradation of Enterobacter and Staphylococcus in Bean Beetle Microbiome

Shao, Wenyi; Beck, Christopher; Zelaya, Anna

Presenter/s: Wenyi Shao
Emory Faculty Mentor: Christopher Beck

Callosobruchus maculatus, commonly known as bean beetles, is a pest that feed on legumes. Some of the beans contain plant secondary compounds, which can be potentially toxic to the beetles. Adzuki beans have several types of such compounds, including flavonoids and saponins. Two genera of bacteria from the beetle's gut microbiome, Enterobacter and Staphylococcus, show particularly high tolerance to a saponin similar to the ones found in adzuki beans. It is not yet known if the two genera of bacteria are naturally tolerant to saponin, or if the species present in the bean beetles have evolved to be tolerant, and even use it as a carbon source. In this research, lab strains and beetle gut microbiome isolates of Enterobacter and Staphylococcus genera are grown in liquid media culture, with saponin and either nutrient broth or minimal media, to determine their tolerance and ability to digest saponin. The results from lab strain cultures show a natural tolerance of both genera, with Enterobacter exhibiting relatively higher tolerance and the ability to use saponin as a carbon source. The results from beetle gut microbiome isolates are yet to be determined.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 E
Presentation/Poster Number: 18
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Examining the effects of CRISPR-Cas9-mediated KLF17 upregulation on the aggressive behaviors of metastatic triple-negative breast cancer cells

Shen, Yishen; King, Katelyn; Taliaferro-Smith, LaTonia

Presenter/s: Yishen (Angela) Shen
Emory Faculty Mentor: LaTonia Taliaferro-Smith

Triple-negative breast cancer (TNBC) is a highly aggressive breast cancer subtype. Due to the lack of estrogen and progesterone receptors and HER2 receptor overexpression, treatment options are limited to surgery and conventional chemotherapy. However, chemoresistance and relapse render these treatments for metastatic TNBC largely ineffective. Therefore, great potential lies in identifying specific molecular targets for metastatic TNBC. Previous studies show that KLF17, a zinc-finger transcriptional regulator, suppresses breast cancer cell invasion and epithelial-mesenchymal transition (EMT) by binding directly to the promoter region of and decreasing ID-1 expression. However, less is known about KLF17's role in TNBCs specifically. This study sought to determine the effect(s) of KLF17 upregulation on the aggressive behaviors of TNBC cells. CRISPR-Cas9 lentiviral particles were used to transiently overexpress KLF17 in human mesenchymal MDA-MB-231. Western blots, colony formation assays, Transwell migration and wound-healing assays, and Transwell invasion assays were used to assess KLF17's effects on EMT, clonogenicity, migration, and invasive potential, respectively, in these highly metastatic cells. Although a minimal increase in KLF17 protein expression levels was detected, the epithelial marker, E-cadherin, and the tumor suppressor protein, p53, were both increased. Conversely, protein levels decreased for mesenchymal markers vimentin and ZEB1. More importantly, the potential for MDA-MB-231 cells to migrate, invade, and colonize were all significantly reduced in cells overexpressing KLF17 compared to untreated/negative control cells. Although very preliminary, collectively these results suggest that KLF17 may play a prominent role in reducing the metastatic potential of TNBC cells and warrants additional studies to determine whether it could be a prospective therapeutic strategy to combat metastatic TNBC.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 G
Presentation/Poster Number: 25
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Comparing Conditional Antisense Oligonucleotide Scaffold Efficiency for Gene Regulation

Shen, Patrick; Zhang, Jiahui; Sharma, Radhika; Narum, Steven; Salaita, Khalid

Presenter/s: Patrick Shen
Emory Faculty Mentor: Radhika Sharma

HIF1a is a master transcription factor that plays a large role in mediating cellular responses to hypoxia and regulating the activation of glycolytic genes. Hypoxic regions are a common characteristic in most solid tumors, making HIF1a an important cancer drug target. However, continuously inhibiting the HIF1a gene can also impair the growth and survival of normal hypoxic liver cells. Antisense oligonucleotides (ASO) provide a unique alternative in clinical applications for drug delivery to help regulate gene expression. Therefore, we designed a conditional ASO that can be activated by a synthetic tissue-specific transcript via a toehold displacement reaction to control the on/off switch for the HIF1a gene. In our reaction, the miR-122-inducible HIF1a ASO conditionally inhibits HIF1a in the presence of a hepatocyte-specific miRNA called miR-122. miR-122 makes up 70% and 52% of the total hepatic miRNA pool in adult mouse and humans, respectively, making them an ideal miRNA trigger. To further investigate the efficiency of this reaction, we were also interested in conjugating liposomal spherical nucleic acids (SNA) and gold nanoparticles to the conditional ASO and comparing the first order displacement reaction rates. Liposomal SNAs were predicted to have better efficiency due to the endogenous nature of high-density lipoproteins (HDL) and greater stability. The liposomal SNA was covalently attached with maleimide thiol and AuNP via freezing method. The antisense strand was tagged with a fluorescent dye to quantify displacement. We showed that the conditional ASO can be modified to be more thermodynamically stable and proceeds with the displacement reaction as expected. The design mechanism of using miRNA inducible ASO has potential as an alternative for drug delivery by enhancing specificity and conducting conditional regulation of HIF1a.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 5 F
Presentation/Poster Number: 23
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Co-localization of MBNL1 Protein with Endosomes in Murine Neuroblastoma Cell Line

Shen, Annie; Janusz-Kaminska, Aleksandra; Bassell, Gary

Presenter/s: Annie Shen
Emory Faculty Mentor: Gary Bassell

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 F
Presentation/Poster Number: 22
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Functional Evaluation of a Loss-of-Function GRIN2B Variant Associated with Neurodevelopmental Disorders

Shi, Ethan; Yuan, Dr. Hongjie; Song, Rui; Traynelis, Dr. Stephen

Presenter/s: Ethan Shi
Emory Faculty Mentor: Hongjie Yuan

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 F
Presentation/Poster Number: 24
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Characterization of human antibody responses after SARS-CoV-2 vaccination of COVID-19 naïve and convalescent donors

Shih, Samuel; Gupta, Sneh Lata; Mantus, Grace; Nyhoff, Lindsay; Wrammert, Jens

Presenter/s: Samuel Shih
Emory Faculty Mentor: Jens Wrammert

SARS-CoV-2, the virus causing Covid-19, continues to threaten public health worldwide, despite the rapid deployment of safe and effective vaccines. SARS-CoV-2 enters cells in the lungs through the interaction of the receptor-binding domain (RBD) of the spike-protein with the hACE-2 receptor, leading to a variety of symptoms, from mild to severe, lethal outcomes. The Pfizer and Moderna mRNA vaccines were developed and approved in record time with continued availability in the US. While vaccination has proven to be highly effective at preventing hospitalization and death, much remains to be understood in terms of the impact of a previous infection on the magnitude, dynamics, and breadth (against emerging viral variants) of vaccine responses. To address these questions, we conducted a longitudinal study of the magnitude and dynamics of antibody responses in COVID-19 naïve or convalescent donors. We hypothesized that antibody titers would rise more rapidly after vaccination in COVID-19 convalescent donors, with greater viral neutralizing potency and increased breadth against emerging viral variants. We used the Meso-Scale Discovery's (MSD) multiplex electro-chemiluminescence immunoassay platform which allows simultaneous detection of titers against 9 different antigens or emerging viral variants. Our studies showed that naïve donors displayed peak immune response only after the booster shot, while COVID-19 convalescent donors responded much more vigorously and reached peak robust antibody responses already after the first vaccination. We also found that the COVID-19 convalescent vaccinees reached higher neutralizing antibody titers as compared to the naïve vaccinees. Taken together, our results demonstrate that the dynamics of the vaccine response are very different in previously COVID-19-immune vaccinees and that the functional quality of induced antibody response is also improved. Our results further our understanding of humoral antibody responses against the COVID-19 vaccine, suggesting potential dose-sparing strategies, and provide a foundation for future vaccine studies of emerging viral variants.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 F
Presentation/Poster Number: 23
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Glutamine Dependence of HCT116 Colorectal Cancer Cells

Shin, Seung Won (Jenna); AbuSalim, Jenna; Zhou, Grace; Kesarwala, Aparna

Presenter/s: Seung Won (Jenna) Shin
Emory Faculty Mentor: Aparna Kesarwala

Cancer cells convert glucose to lactate via aerobic glycolysis and glutamine to alpha-ketoglutarate (aKG) via glutaminolysis in order to sustain the tricarboxylic acid (TCA) cycle. Radiation therapy decreases flux through the TCA cycle as it induces an increase in aerobic glycolysis. In our research, we used HCT116 colorectal cancer cells and analyzed clonogenic assays to compare cell survival with combinations of varying glutamine concentrations and varying doses of radiation. Since Lactate Dehydrogenase (LDH) enzyme activity is the final step of aerobic glycolysis, we also used western blotting to compare LDH expression at specific time points after cells were either irradiated, grown with low concentrations of glutamine, both, or neither. We hypothesized that colorectal cancer cells depend on glutaminolysis to supply the TCA cycle and that radiation causes increased dependence on glutaminolysis. Full glutamine deprivation immediately after radiation as well as 90% glutamine deprivation 24 hours prior to radiation resulted in lower cell survival, which strongly supports our hypothesis and allows us to conclude that glutamine deprivation sensitizes the cells to radiation. The conclusions of our research allows us to consider the glutaminolysis pathway as a potential target for increasing responses to radiation therapies in colorectal cancer patients.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 6
Presentation/Poster Number: 6 of 6
Presentation Time: 1:30 PM to 3:00 PM
Presentation Link: https://emory.zoom.us/j/95175843929

Mating Preferences of Hybrid Female Squash Bugs

Simmons, Camille; Dodd-Shojgreen, Jade; Villa, Scott; Gerardo, Nicole

Presenter/s: Camille Simmons
Emory Faculty Mentor: Scott Villa

Anasa tristis and Anasa andresii are widespread agricultural pests of Cucurbits that are known to hybridize. These hybrids are especially large and kill host plants at higher rates than either parental species alone. However, the mating success and preference of these hybrids remain unknown. Previous studies in other systems have shown that hybrids often prefer to mate with other hybrids, leading to the formation of a new species. Here we test this possibility by conducting mating experiments with Anasa andresii, Anasa tristis, and their hybrids. Using small plastic boxes and video cameras, we quantify the mating behavior of squash bugs. We conducted choice mating trials where hybrid females were placed in arenas with either: 1) one hybrid male and one A. tristis male, 2) one hybrid male and one A. andresii male, or 3) one A. tristis male and one A. andresii male. Additionally, we conducted no-choice mating trials where hybrid females were placed in arenas with either a single A. tristis, A. andresii, or hybrid male. All trials were continuously videotaped for five days. From each video, we collected data on how many successful and unsuccessful mating attempts were made. In the case where two males were in a box, data were also collected on male-male mating attempts. Preliminary results suggest that hybrid females readily mate with hybrid and A. tristis males, but appear less willing to mate with A. andresii males. Our results are the first to test the preference of squash bug hybrids and provide evidence that these hybrids may form their own species in the future.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 E
Presentation/Poster Number: 17
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Diversity of fungal parasite interactions in coinfective environments

Gerardo, Nicole; Lin, Sandy; Singh, Rohan

Presenter/s: Rohan Singh and Sandy Lin
Emory Faculty Mentor: Nicole Gerardo

Coinfection occurs when multiple parasites infect the same host. This can alter host-parasite ecology as parasites have previously demonstrated the ability to inhibit or facilitate the colonization of the host for one another. Fungus-growing ants, their cultivated fungi (cultivar), and their parasites (Escovopsis sp.) are an ideal model system for studying how these different interactions can occur because they exhibit frequent instances of coinfection as well as considerable phylogenetic diversity. We studied how different strains of Escovopsis interact with each other across the phylogeny to better understand their patterns of interaction. We plated combinations of two strains of Escovopsis on petri dishes and assessed their growth over multiple weeks. By assaying multiple pairings of Escovopsis, we were able to categorically identify the ways in which the parasite interacts with other strains of Escovopsis including, but not limited to, attraction and inhibition. A deeper understanding of coinfection patterns could be helpful in mapping the coevolutionary history of hosts and parasites as well as in applications of managing virulent parasitic organisms. Further research could establish how these fungi are changing at the molecular level in reaction to one another as well as investigate a broader range of Escovopsis strains.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 D
Presentation/Poster Number: 14
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Endogenous household reorganization and social welfare program manipulation

O'Connell, Stephen; Skelley, Nicholas

Presenter/s: Nicholas Skelley
Emory Faculty Mentor: Stephen O'Connell

We study the effects of unconditional cash transfers to Syrian refugees in Lebanon on household composition and child migration between households. Using a regression discontinuity design, we do not find evidence that children regularly move from non-beneficiary households to those receiving benefits. While a survey of households appears to support the hypothesis that they reorganize based on whether they receive assistance, other data sources concerning the same households suggest otherwise. Instead, we find evidence that non-beneficiary households likely overreport the number of household members in an effort to increase the assistance they receive. In addition, we find that misreporting is predominantly driven by overreporting from households that have recently stopped receiving program assistance. Furthermore, more than 85% of the effect of treatment on reported household size is explained by non-beneficiary households overreporting the number of girls aged five and below. There is strong evidence that these reports are not representative of fostering out of family and are instead claims of additional biological children. These results underscore the importance of considering the incentives for endogenous household reorganization and misreporting in the context of aid policies. Differing characteristics across policies can produce a variety of effects on household reorganization and program manipulation through deception, changing the implications for policymakers and analysts.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 7 D
Presentation/Poster Number: 16
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Development of the in scanner Functional Magnetic Resonance Imaging Block Span Task for assessment of visuospatial mechanisms

Slusarenko, Alexandra; Hackney, Madeleine E.

Presenter/s: Alexandra Slusarenko
Emory Faculty Mentor: Madeleine E. Hackney

Parkinson's disease (PD) is the second most common neurodegenerative brain disorder that often leads to motor and cognitive impairment. The causes are still not well understood, and three-fourths of people with PD experience medication-related motor fluctuations, known as "OFF-time". A two arm, randomized controlled trial in individuals with diagnosed mild-moderate PD is ongoing to determine the relationship between partnered dance aerobic exercise versus walking for impacting OFF-time and visuospatial cognition among individuals with PD. Cognitive variables include measures of executive function, attention, and additional visuospatial function measures. The Corsi Blocks product score is a primary outcome variable used to determine the visuospatial function of patients with PD. The Block Span task was adapted from Corsi Blocks for assessment during functional magnetic resonance imaging (fMRI) in a scanner to investigate neural mechanisms of visuospatial function and any changes that will occur after treatment. The participant is visually presented 5 squares. Each square corresponds to 1 of 5 keys (one for each finger on the right hand) on a Celeritas response pad. Participants are exposed to three active conditions and two rest periods: pre-baseline rest, visual sequence, motor response, motor random (control), and post-baseline rest. The experiment contains 24 visual sequence periods and 24 motor sequence periods over the course of 3 runs programmed in E-Prime. The sequence length of four stimuli was determined by calculating the mean span on the Corsi block task of a previous study with 434 participants with PD. After the scan, 9 out of 12 participants reported numbering and assigning fingers to each box to remember the pattern. On average, 12 participants got 47.7± 33% [0,93.3] of the patterns correct of the Block Span task before attending interventions. Results from the scans will be used to improve non-pharmaceutical options for PD patients with OFF-time.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 F
Presentation/Poster Number: 21
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Analysis of simultaneous single-cell ATAC- and RNA-sequencing in SMARCB1-deficient cancer cell lines

Smyth, Nate A; Lee, Benjamin P; Cooper, Garrett W; Gorkin, David U; Hong, Andrew L

Presenter/s: Nate Smyth
Emory Faculty Mentor: Andrew Hong

Simultaneous single-cell ATAC- and RNA-seq (scMultiome) enables enhanced mapping between the epigenome and transcriptome. We performed scMultiome on a mixed sample of the atypical teratoid/rhabdoid tumor cell-line, BT16, and malignant rhabdoid tumor of the kidney cell-line, G401, to understand the feasibility of mixing samples using scMultiome technologies without hashing and compare the epigenomes and transcriptomes between these models. We first confirmed loss of SMARCB1, a tumor suppressor part of the BAF chromatin remodeling complex. There is a large scale bi-allelic deletion in G401 while there is a small indel in BT16. We performed the scMultiome on a combined sample of these cell lines (5,000 nuclei per cell line). We sequenced this sample on a Novoseq 6000 at approximately 25k reads per cell. We subsequently used CellRanger ARC to map and align these sequences to reference libraries. We then used the Seurat 4.0.3 R package to analyze these results. Indeed, we identified two overarching clusters that likely represent these two cell lines which correlated with chromatin accessibility at the promoter region of SMARCB1. We then took bulk RNA-sequencing data and quantified this with salmon to serve as a method to disaggregate this mixed sample using Clustify. We confirmed that these two clusters identified by scATAC-seq indeed correlated with Clustify for the respective cell lines. Further analysis of chromatin and transcriptome features and heterogeneity within cell lines is still ongoing.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 E
Presentation/Poster Number: 18
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Monarch Butterfly Diet Microbial Diversity; an Analysis of the Microbial Communities on Milkweed Plants

Soloff, Hannah; Chavez, Joselyne; de Roode, Jaap; Gerardo, Nicole

Presenter/s: Hannah Soloff
Emory Faculty Mentor: Nicole Gerardo

Monarch caterpillars (Danaus plexippus) feed on multiple species of Asclepias spp. host plants. Leaves of plants contain microbial communities (microbiomes) consisting of bacterial, fungal, and viral organisms. Within leaves, these microbes are known as foliar endophytes. Previous research indicates that a certain species of Asclepias, A. curassavica, provides parasite resistance effects on the caterpillars that feed on them (Harris et al. 2020). My research intends to answer whether the foliar endophyte community is responsible for this antiparasitic effect. This experiment serves as the first step to answering this question by isolating the fungi and bacteria present in both A. curassavica and A. incarnata to create a catalog of the morphotypes for future analysis while comparing the morphotypes between the two species.

The methods used to isolate the microbes include sampling of leaves from A. incarnata and A. curassavica plants in which each had multiple leaves sampled at different locations on the plants. These leaves were sampled via hole punch and plated onto multiple media plates in order to isolate a representative array of bacterial and fungal species. Plates were allowed to grow in an incubator at 27˚C for about a week before storage and morphotyping. Bacterial samples were streaked and stored using stabs before being sent for Sanger sequencing, while fungal samples were subcultured and stored via water stocks. Both bacteria and fungi were categorized via morphotype.

Thus far, we have completed comparisons of the fungi isolated, which indicates A. incarnata and A. curissavica had mostly differing predominant fungal morphotypes with one shared morphotype.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 E
Presentation/Poster Number: 19
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Comparing Mass-Univariate Versus Multivariate Analysis of Whole-Brain Task-fMRI in Persons with Aphasia

Song, Serena; Rodriguez, Amy; Krishnamurthy, Venkatagiri

Presenter/s: Serena Song
Emory Faculty Mentor: Venkatagiri Krishnamurthy

The reliability of conventional methods of brain-behavior analysis involving mass-univariate methods has been challenged due to the underlying assumption of voxel independence, giving rise to the development of multivariate approaches. Multivariate analysis has not yet been used on whole-brain task-fMRI and may offer comprehensive insight to the network-like nature of neurocognitive mechanisms. Our study aims to compare mass-univariate and multivariate analysis of whole-brain task-fMRI in persons with aphasia (PWA). Functional task-fMRI data was collected from 14 PWA who participated in category exemplar generation (CEG) during the scan. Whole-brain task-activity was measured as the z-transformed area-under-the-curve (ZAUC) for each voxel. Behavioral data of CEG z-scores were used as the behavioral input. ZAUC and CEG values were loaded into mass-univariate and multivariate methods to compare for meaningful network-level analysis. The multivariate method utilized was sparse canonical correlation conducted through LESYMAP. An overlap whole-brain mask including voxels that were representative of at least four subjects was used. All ROI clusters were corrected for multiple comparisons (p<0.05, cluster size=50). Results reveal that both methods statistically located significant ROIs with consistent spatial overlap; however, multivariate analysis offered more stable parameters in ROI discovery given a small cohort of subjects. Multivariate analysis demonstrated more sensitivity by identification of a greater number of significant task clusters above the significance threshold (p<0.05). Our proof of principle study in this small sample, shows the viability of using multivariate analysis on whole-brain task-fMRI and demonstrates that it may be more attuned to finding meaningful brain-behavior relationships than mass-univariate analysis. Further development and evaluation of this methodology in larger samples will set the platform for understanding neurocognitive models of language and identifying predictors of treatment outcome in PWA.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 F
Presentation/Poster Number: 22
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Regulating Movement by Stimulating the Thalamus Output mediated by the Substantia Nigra Reticulata

Song, Joseph; Bian, Yuyang; Li, Su; Jaeger, Dieter

Presenter/s: Joseph Song
Emory Faculty Mentor: Dieter Jaeger

A major output nucleus of the basal ganglia is the substantia nigra reticulata (SNr), containing GABAergic neurons that project out to the thalamus. The firing rates of GABAergic neurons inhibit the thalamic neurons from communicating with the motor cortex, thus suppressing movement. This project observes if optogenetically inhibiting the SNr will prolong locomotion and forelimb activity in mice that are trained to stop for a reward after an auditory cue. In addition, it will test if implementing a closed-loop deep brain stimulation on the motor thalamus can sustain movement in Parkinsonian mice. It is hypothesized that photoinhibition of the SNr would result in the continuation of locomotion and forelimb activity in mice. Thus, we speculate closed-loop DBS on the motor thalamus will improve motor ability in Parkinsonian mice. This project initially entailed training male mice (n=3), aged approximately 6 months, to master a locomotion and forelimb task on a circular and on an open-field air-track while being head-fixed. The mice were placed on a water restriction diet and given 1.5-2 mL of water every day as a reward for when they got acclimated to head-fixation and learning the task. As of this summer, the mice have become accustomed to being head-fixed in the air-track environment. While being head-fixed, the mice have also learned to run forward on a circular air-track to obtain a liquid reward and pick up food pellets with their forelimbs. All training and procedures followed an approved Emory IACUC protocol. Currently, a machine learning algorithm, called DeepLabCut, is being refined to track the mice's paws, head, and tail. This analysis provides information about the mice's speed, stride length, and baseline behaviors. The future results could provide further insight into how the thalamus registers and transmits the outflow of the SNr, a relationship that is not thoroughly explored.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 F
Presentation/Poster Number: 23
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Analysis of THP-1 NF-κβ-Luc2 Optimal Seeding Density, Growth Rate, and Function in a High-throughput Anti-inflammatory Drug Screening Platform

Song, Colin; Gavegnano, Christina; Reece, Monica

Presenter/s: Colin Song
Emory Faculty Mentor: Christina Gavegnano

THP-1 NF-κβ-Luc2 cells are a monocytic cell line derived from a one-year-old patient with acute monocytic leukemia. The cells used in this project are THP-1 NF-κβ-Luc2 cells, which have been transfected with the luciferase reporter gene. THP-1 NF-κβ-Luc2 cells have the capacity to differentiate into macrophages with stimulation by mitogens and are often used in in vitro studies as a first line screening model to mimic dynamics of primary human macrophages. In THP-1 NF-κβ-Luc2 cells, luciferase is produced due to the transcription of the reporter gene, and bioluminescence is observed. The intensity of emitted light is an indicator of NF-kB activity. A reporter gene assay can show if a particular agent, extract, or compound is effectively preventing NF-kB from initiating transcription. The goal of this project was to identify the optimal seeding density and define the growth rate for THP-1 NF-κβ-Luc2 cells, with a long-term goal of using these conditions in our high-throughput anti-inflammatory screening platform to identify agents that can block inflammation and immune dysregulation in myeloid cells. Three different seeding densities were chosen: 2.5 x 105 cells/mL, 5.0 x 105 cells/mL, and 7.5 x 105 cells/mL. Using proper sterile technique in a biosafety cabinet, the cell suspensions were made, transferred into T-25 flasks, and stored in an incubator (37□ C, 5% CO2). Cell counts were conducted at 0, 24, 48, 72, 96, and 144 hours after initial seeding. Growth curves revealed that a seeding density of 2.5 x 105 cells/mL produced the highest growth rate. This project focused on optimizing culture technique for THP-1 NF-κβ-Luc2 cells and their use in a primary screen assessing the efficacy of novel drugs that can potentially treat a wide variety of inflammatory diseases.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 F
Presentation/Poster Number: 23
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Understanding the Link Between Loss of Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) and Dysregulation of Glucose Trafficking

Song, Christy; Vazquez Cegla, Analia; McCarty, Nael

Presenter/s: Christy Song
Emory Faculty Mentor: Nael McCarty

Cystic Fibrosis (CF) is a lethal genetic disorder that affects over 30,000 people in the United States and over 70,000 people worldwide. Different mutations in Cystic Fibrosis Transmembrane conductance Regulator (CFTR) such as being absent, dysfunctional, and in the wrong location, can cause CF. Having insufficient quantities of CFTR can lead to airway dehydration, leaving thick mucus in the CF patients' lungs, which makes it harder to clear accumulates in the lungs. This creates an optimal environment for bacteria to proliferate, and bacterial infections lead to a gradual decline in lungs. Cystic Fibrosis Related Diabetes (CFRD) is the most common comorbidity of CF. CFRD patients have higher rates of airway bacterial infections, which leads to rapid lung function decline. The causes that lead to glucose dysregulation in CF patients remains to be determined. This is important in CF research because the study can provide targets for controlling the effects and prevent rapid lung function decline. We hypothesize that CFRD leads to dysregulation of glucose barrier components, which leads to higher glucose levels in the airways. Having more nutrients in the airway contributes to faster bacterial growth. To test this hypothesis, mammalian cells were cultures with either normal glucose or high glucose levels (5.5 and 14.0 mM). The model cell line used was 16HBE (Human Bronchial Epithelial cell) wild type cells. These cells were grown on Transwells to simulate airway conditions. Monolayers of cells were challenged with a Staphylococcus aureus mutant without alpha-toxin to test for bacterial growth differences between glucose conditions. Preliminary data shows that higher glucose concentration leads to higher levels of bacterial growth. In conclusion, bacteria can grow better in a higher glucose level environment, causing CF patients with diabetes to be more prone to bacterial infections. This puts us one step closer to finding better treatments for CFRD.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 F
Presentation/Poster Number: 24
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Developmental lead toxicity in human induced pluripotent stem cell (hiPSC) derived cortical organoids and primary fetal brain cells

Sonsurkar, Sayli; Sampson, Maureen; Sloan, Steven

Presenter/s: Sayli Sonsurkar
Emory Faculty Mentor: Steven Sloan

Lead (Pb) neurotoxicity is well established however the complex mechanisms behind neurotoxicity and the roles of different cell types are not well understood. We examined developmental Pb exposures in human induced pluripotent stem cell-derived (hiPSC) 3D cortical organoids and primary fetal brain samples. The novel hiPSC-derived organoid system uniquely allows human neural cells to be studied at critical points of neurodevelopment that could otherwise not easily be observed. This model better recapitulates human toxicity than animal models due to human-specific gene-environment interactions. Pb dose-dependent cell death was quantified in organoids using TUNEL assays with immunohistochemistry and fluorescence microscopy. Pb uptake over time was also measured through live imaging of primary fetal astrocytes and neurons using a fluorescent Pb sensor. We used organelle-targeted fluorescent sensors to examine subcellular localization of Pb in living cells, but did not observe significant Pb sequestration in the ER or mitochondria during acute exposures (<3 hrs). The recent, high-profile water contamination in Flint, Michigan highlights the relevance of this ongoing public health concern. Our research can help better understand Pb toxicity and adequately inform public health policy for regulating neurotoxicant exposure.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 E
Presentation/Poster Number: 20
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The influence of Hip1 protein in Dendritic Cells Inflammatory Pathway Responses

Stallings, Kris; Enriquez Ana; Dkhar, Hedwin; Woods Nicole, Rengarajan Jyothi.

Presenter/s: Kris Stallings
Emory Faculty Mentor: Jyothi Rengarajan

Abstract not available.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 1 F
Presentation/Poster Number: 24
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Sound Symbolism and the Underlying Effects Involving Sensory Imagery

Nygaard, Lynne; Michelini, Leonardo; Stamper, Abigal

Presenter/s: Abigal Stamper
Emory Faculty Mentor: Lynne Nygaard

Sound symbolism is the non-arbitrary connection between speech sounds and meaning. For example, specific sounds of a word such as the vowels in mal and mil invoke a connection to abstract concepts such as big and small, respectively. Scientists have hypothesized that sound symbolism is a particular case of high-level cross-modal correspondences that occurs on base level processing outside of language. Cross modal correspondences are the mapping of features from one sensory modality onto another. With regards to sound symbolism, features of sound may be associated with modalities such as size, shape, or other properties. For example, high and low pitch sounds are mapped to small and big shapes, respectively. Thus, sound symbolic correspondences are thought to rely on pre-linguistic connections between auditory properties and meaning. However, if, instead, sound symbolism is supported by linguistic processes, then sensory representations would not influence sound symbolic mappings. Our study will examine whether individual differences in basic sensory imagery ability are associated with the strength of the cross-modal correspondences underlying sound symbolism. We will assess auditory and visual imagery vividness using four different tasks. Participants will be asked to think of auditory and visual concepts and rate the level of vividness and clarity of the mental representations. To measure sensitivity to sound symbolism, we will ask participants to match pseudowords that sound big or small to images containing animal silhouettes of different sizes. We hypothesize that sensory imagery vividness will predict sensitivity to sound symbolic mappings. This study will elucidate whether sound symbolism is undergirded by basic sensory perceptual abilities. Expected findings will contribute to the underlying processes of sound symbolism and which context it occurs in.

Research Discipline: Social Sciences
Presentation Type: Oral Presentation

Session: 1
Presentation/Poster Number: 3 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/92988928818

Diversity in Ethnicity, Race, and Sex Across Neuroimaging Studies: A Systematic Review

Sterling, Elijah; Pearl, Hannah; Fleischer, Candace

Presenter/s: Elijah Sterling
Emory Faculty Mentor: Candace Fleischer

Previous studies have suffered from a lack of diversity in sex and race. In response, the NIH Revitalization Act of 1993 was created to encourage researchers receiving federal funding to include a diverse selection of subjects. Follow up studies after 1993 have revealed a continuous lack of diversity according to sex. The goal of the current research is to conduct a systematic review of the reported demographics in neuroimaging studies according to sex, race, and ethnicity. We hypothesize a lack of diversity among human subjects in neuroimaging studies when compared to the 2019 U.S. census survey data.

The Web of Science database was used to perform searches. Inclusion criteria were papers written in English, document type being article, article topic “human brain magnetic resonance (MR)”, and the dates indexed from 2000-2020. Articles were excluded if they were not accessible, were literature reviews, did not include human subjects, included less than 10 human participants, did not acquire in vivo brain MR data, or data was acquired at a site outside the United States.

To date, 1,550 articles have been reviewed, with 185 included from the years 2016-2020. The most frequent reasons for exclusion were imaging data collected outside the United States, the study included less than 10 human participants, or the study did not include human subjects. Preliminary results indicate most studies do not report race and ethnicity. For studies where race and ethnicity are reported, they are not reflective of the U.S. population.

Our findings to date support the initial hypothesis. In addition, for studies with reported demographics, they are often inconsistent with the diversity of the U.S. population. Future work will complete this systematic review and conduct a meta-analysis to characterize reported diversity in neuroimaging research studies.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 F
Presentation/Poster Number: 21
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Establishment of a Stable Chinese Hamster Ovarian Cell Line Expressing Glycoprotein Ibα (W230L) to Mimic Rare Platelet-Type von Willebrand Disease

Su, Ally; Arce, Nicholas; Li, Renhao

Presenter/s: Ally Su
Emory Faculty Mentor: Renhao Li

Von Willebrand disease (VWD) results from a quantitative or qualitative defect in von Willebrand factor (VWF). VWF binds to glycoprotein(GP)Ibα on platelets, capturing platelets and priming them for activation to initiate coagulation. VWD is categorized into different subtypes depending on the nature of the defect. Two subtypes of VWD—type 2B and platelet type (PT)—are both gain-of-function diseases with enhanced VWF binding to platelets. However, the source of enhancement is different. In type 2B, this occurs on VWF; in PT-VWD, on GPIbα. PT-VWD is rare and only identified through gene sequencing, a lengthy and inaccessible process for most hospitals. Yet, blood samples of the rare disease are required to develop a more accessible diagnostic tool. Expressing GPIbα on Chinese hamster ovarian (CHO) cells can circumvent this problem. GPIbα in CHO cells is hypothesized to mimic PT-VWD W230L—the disease's most detrimental mutation. A W230L GPIbα expressing stable cell line can be used to establish better diagnostic tools for PT-VWD, as it mimics the rare mutated platelets in platelet-rich plasma and is a replenishable resource. A plasmid containing the mutant was transiently transfected into CHO cells stably expressing GPIbβ and GPIX. The expression of GPIbα, GPIbβ, and GPIX in CHO cells was confirmed with western blotting. The transfected cells underwent selection with hygromycin to select for those expressing GPIbα. Next, the CHO cells were sorted for high expression of GPIbα and GPIX using fluorescent antibodies targeting these subunits. Subsequent flow cytometry experiments after several rounds of cell amplification confirmed a homogeneous population expressing high levels of GPIbα. In conclusion, the data have shown the existence of a stable CHO cell line with high GPIbα expression. Future flow cytometry assays can investigate the relationship of wild-type GPIbα and W230L GPIbα against VWF and establish a more accessible diagnostic tool for PT-VWD.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 E
Presentation/Poster Number: 20
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

SARS-CoV-2 variant analysis by real-time RT-PCR, Asunción, Paraguay

Su, Maxwell; Waggoner, Jesse

Presenter/s: Maxwell Su
Emory Faculty Mentor: Jesse Waggoner

Detection and surveillance of SARS-CoV-2 variants, including variants of concern (VOCs) and variants of interest (VOIs), is essential to the public health response to the pandemic. VOCs/VOIs carry specific mutations that may increase infectivity and evade immune responses from prior infection or vaccination. However, VOC/VOI detection by whole-genome sequencing is not feasible in many locations, such as Paraguay, where access to sequencing technology is limited. We hypothesized that real-time RT-PCR (rRT-PCR) could sensitively detect mutations associated with VOCs/VOIs in samples from Asunción, without the need for sequencing and that the gamma (P.1) variant would be common in this population. We tested 201 acute-phase, SARS-CoV-2 RNA-positive nasopharyngeal samples from patients in metropolitan Asunción and the Central Department of Paraguay, collected between 11/22/20 and 4/11/21. Samples were tested in a protocol including the N2RP assay (a duplex rRT-PCR for the SARS-CoV-2 N2 target and RNase P), a triplex assay to detect specific deletions, and the Spike SNP assay, which utilizes a single primer set and tiled probes to detect mutations in the receptor binding domain of spike. All 201 samples were positive for SARS-CoV-2 in the N2RP assay (mean CT, 20.80; SD 5.57); 198/201 (98.5%) tested positive in the Spike SNP assay. 104/198 samples (52.5%) showed results corresponding to the gamma variant (E484K, N501Y, and absence of 417K); 23 samples (11.6%) were consistent with the P.2 variant (E484K, 417K). One alpha variant (B.1.1.7) was confirmed (N501Y; 417K). Seven samples (3.5%) of unknown lineage tested positive for L452R, and one additional sample tested positive for 490S. Results were confirmed by amplicon sequencing. Our analysis provides the first systematic evaluation of SARS-CoV-2 variant distribution in Paraguay. The Spike SNP assay may allow other areas that lack widespread sequencing infrastructure to monitor the emergence of significant spike mutations and improve capacity for SARS-CoV-2 VOC/VOI detection.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 F
Presentation/Poster Number: 24
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Establishing a Time-Course of Recovery of DNA Damage Following X-Ray and Neutron Irradiation of Human Bronchial Epithelial Cells

Su, Zitong; Dynan, William

Presenter/s: Zitong Su
Emory Faculty Mentor: William Dynan

A critical hazard of space exploration is the extraplanetary radiation (i.e., highly energetic protons and other atomic nuclei) encountered by those living for extended periods in space, beyond Earth's protective atmosphere. To better understand the effects of this radiation on the human body, specifically the DNA damage it causes, radiation sources that suitably mimic the linear energy transfer (LET) spectrum of extraplanetary radiation must be available. The efficacy of one such potential mimic to produce recoil particles with the desired energy spectrum, a deuterium-deuterium neutron generator, will be evaluated against a reference X-ray source. Human bronchial epithelial cells (HBEC-3KT) were irradiated by X-ray and neutron sources and fixed following varying lengths of recovery. DNA damage was evaluated by γH2AX and 53BP1 repair foci and visualized with immunofluorescence. Both X-ray and neutron irradiation displayed evidence of DNA damage, with shorter recoveries exhibiting more abundant foci. These findings validate the neutron generator's ability to deliver radiation capable of creating double-stranded breaks in DNA. However, X-ray radiation appeared to cause more repair foci than neutron radiation, signaling perhaps a difference in the number of tracks formed. Further investigation and optimization of the neutron generator's dosimetry is required.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 3
Presentation/Poster Number: 6 of 6
Presentation Time: 10:30 AM to 12:00 PM
Presentation Link: https://emory.zoom.us/j/95598055387

Is there a Thucydides's Trap between the U.S. and China? Evidence from a Survey Experiment

Tang, Jiarui; McAlister, Kevin

Presenter/s: Jiarui Tang
Emory Faculty Mentor: Kevin McAlister

Throughout history, rivalry often occurs between a ruling power and a rising challenger. According to the Thucydides's Trap project, 12 of the 16 historical cases that involve this power dynamics have resulted in war. In the present day, the central international tension belongs to that of the U.S. and China. While Thucydides's Trap predicts an inevitable conflict between these two nations, it does not specify how citizens of one country would regard the other. In this project, I seek to investigate whether citizens of the more powerful state hold consistent views as predicted by Thucydides's Trap.

I hypothesize that U.S. citizens will increase their support on foreign policies targeted towards China after receiving information that the relative power gap between them is closing. To test this theory, I leverage an original survey experiment where subjects view either converging trends of U.S. and Chinese military spending or non-converging trends. I then access their perception of the U.S.'s international status, defense spending, and military use through a series of questions and collect information about mediating covariates, such as political ideology. While much study has been done on defense policy attitude, few have utilized an experimental survey design. Unlike observational survey approaches, this approach can causally identify the effect of perceived increases in Chinese military strength on changes in U.S. public opinion on foreign policy.

The larger purpose of this research is to test a piece of the puzzle between minority-majority group dynamics. Inspired by seminal works in sociology and political science, I postulate that a dominant group always views subordinate groups more negatively if it perceives a threat of status change from the latter. These groups can be nations, ethnicities, industries, and firms. This research regards the nation as a group and the threat being a rise in military power.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 2 F
Presentation/Poster Number: 22
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Assessing distinct in vivo consequences of RNA Exosome disease linked mutations in Saccharomyces cerevisiae

Tendoh, Foje; Sterrett, Maria; Corbett, Anita

Presenter/s: Foje Tendoh
Emory Faculty Mentor: Anita Corbett

The RNA exosome is an evolutionarily conserved, 10 - subunit protein complex involved in the processing and degradation of RNA in the cell. The complex is composed of 9 structural subunits and one catalytic exo/endoribonuclease. Recently, a class of diseases in humans known as “RNA Exosomopathies” have been linked to missense mutations in genes that encode the structural subunits of the RNA exosome. Although the RNA exosome is ubiquitously expressed, these mutations result in tissue specific diseases, suggesting that there are distinct molecular consequences in RNA exosome function that underly each RNA exosomopathy. To assess the molecular consequences of each RNA exosomopathy mutation, we modeled patient missense mutations in Saccharomyces cerevisiae genes that encode for the yeast RNA exosome. Previous studies using these yeast RNA exosomopathy mutant models have shown distinct consequences in the function of the RNA exosome; however, these defects have not been assessed comparatively nor have downstream cellular processes been analyzed in these mutant cells. We performed a drug screen on the mutant cells rrp4 G226D, rrp40 W195R, and rrp46 L191H to assess the cellular defects resulting from the different modeled RNA exosomopathy mutations. We found that the exosome mutants showed differential sensitivity to drugs that induced damage in RNA processing pathways and DNA repair pathways, with rrp4 G226D and rrp46 L191H having severe defects in repairing double stranded DNA breaks (DSB). These data suggest that the RNA exosome function in RNA turnover and processing may be differentially affected by different RNA exosomopathy mutations. Furthermore, these data show deficiency in DNA damage response (DDR) pathway in our rrp4 G226D and rrp46 L191H cells, suggesting that consequences in DNA repair could affect disease pathology of some specific RNA exosomopathies. This comparative screening of our RNA exosomopathy mutant models provides insight into the molecular consequences of these missense mutants found in patients and can expand our knowledge of the functions of the RNA exosome.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 F
Presentation/Poster Number: 23
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Precursors to Privilege: The Availability Heuristic in Adults and Children

Terrell, Timethius; Kinzler, Katherine; Santhanagopalan, Radhika

Presenter/s: Timethius Terrell
Faculty Mentor: Katherine Kinzler

Prior studies have documented that adults' reliance on heuristics can often lead to judgment errors. Despite the prevalence of these errors, little is known about when these errors in judgement emerge and how they change across development. We will conduct four studies to examine the ontogeny and development of the availability bias (a heuristic used to make probability estimates about the state of the world) in children. In Study 1 (adults) and Study 2 (children), we ask participants to (1) estimate the proportion of people who have access to different items, (2) estimate the proportion of people who have access to specific public goods and services, and (3) determine the degree to which individuals from different socioeconomic statuses want or care about items associated with each level of Maslow's Hierarchy of Needs. We hypothesize that participants from more privileged groups (i.e. higher socioeconomic status) will make less accurate judgements than those from less privileged groups, and the gap in judgements will be higher for older children and adults. In Studies 3 (adults) and 4 (children), we extend our examination of the availability bias to the domain of racial privilege. We expect to find that participants from certain demographics are less accurate in their judgements of the privileges held by participants of other racial groups. Beyond documenting the trajectory by which the availability bias develops with age, these findings also offer insight into the development of children and adults' thinking about privilege.

Research Discipline: Social Sciences
Presentation Type: Oral Presentation

Session: 7
Presentation/Poster Number: 3 of 6
Presentation Time: 3:00 PM to 4:30 PM
Presentation Link: https://emory.zoom.us/j/97807604820

Role of the Ventral Hippocampus-Lateral Septum Pathway in Mediating Social Recognition.

Thomas, Sarah; Rashid, Maha; Murugan, Malavika

Presenter/s: Sarah Thomas
Emory Faculty Mentor: Malavika Murugan

Social recognition, the ability to recognize each other, is essential for the survival of many mammalian species. Core symptoms of several neurodegenerative diseases, such as Alzheimer's disease, include deficits in social recognition. Despite the importance of social recognition, the neural circuits underlying social recognition remain poorly understood. One area of interest is the ventral hippocampus since lesion studies in humans have found deficits in social recognition. However, the ventral hippocampus is a multifaceted brain area with projections to multiple downstream regions. One of the main outputs from the ventral hippocampus is to the lateral septum, a region known to be involved in kinship behavior. In this study, we used excitatory and inhibitory optogenetics in mice to investigate the role of the ventral hippocampus to lateral septum pathway in mediating social recognition. Surprisingly, both activation and inhibition of the ventral hippocampus-lateral septum pathway led to an increase in time spent near the stimulated mouse. Activation and inhibition, however, did not influence place preference, anxiety, or speed of the animal, suggesting that the pathway is specific to social interaction. One possible reason for these findings may be that both inhibition and activation disrupt the pathway which may lead to disinhibition of downstream regions such as the nucleus accumbens. Further investigation will be required to fully understand the function of the ventral hippocampus-lateral septum pathway in mediating social recognition.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 F
Presentation/Poster Number: 24
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Building Soil Organic Matter Through Biochar Amendment: A Climate-Smart Approach to Ensure Food Security

Sihi, Debjani; Trifonova, Kristina

Presenter/s: Kristina Trifonova
Emory Faculty Mentor: Debjani Sihi

One of the biggest threats to global food security are intensive land-management practices that degrade soil and cause it to lose essential nutrients and release higher amounts of CO2 into the atmosphere. Biochar, a soil amendment created by exposing biomass to very high temperatures under oxygen-limited conditions, has been identified as a potential solution to this issue, as it has been shown to mitigate soil CO2 release and increase soil nutrient retention and organic matter. This study aims to evaluate the effect of biochar on the component fractions of soil organic matter (SOM) and CO2 release, as well as its effects on plant growth and yield. This summer, the initial phase of this project was completed. Soil sampling, microbial CO2 analysis, and moisture content analysis were done on soil collected from the Oxford College Organic Farm and Emory's Briarcliff Campus, and the soils were prepared for future elemental analysis. Soil from the Briarcliff campus was, on average, 33.5% water (w/w) and produced 126-195 mg of microbial CO2/kg of soil per day, indicating abundant microbial activity. Soil from the Oxford College Organic Farm had a much lower moisture content and was, on average, 15.01% water (w/w). An airtight chamber, equipped with irrigation and gas dispersal systems, was constructed; soil and biochar mixtures (2%, 5%, and 10%, w/w ratio) were created; and maize and cover crops (white clover, cereal rye, and crimson clover) were germinated and potted. The baseline soil data obtained as a result of this work will be vital to accurately assessing biochar's soil effects and the planning and construction work will enable 13C-CO2 labeling of plants and evaluation of the effect of biochar amendment on SOM dynamics by stable isotope analysis of soil and gas samples.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 G
Presentation/Poster Number: 25
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Recognizing places and navigating through them are supported by two distinct cortical systems?

Trinkl, Nathan; Byland, Josh; Dilks, Daniel D.

Presenter/s: Nathan Trinkl
Emory Faculty Mentor: Daniel Dilks

It has recently been hypothesized that our ability to recognize the kind of place we are in (e.g., a kitchen versus a beach), and how we navigate through that place are supported by two distinct cortical systems. More specifically, the parahippocampal place area (PPA) has been implicated in “scene categorization”, while the occipital place area (OPA) and the retrosplenial complex (RSC) have been implicated in navigation. Here we directly test this hypothesis. If OPA and RSC are indeed involved in navigation, then they will respond significantly more to images of scenes that are upright (and hence navigable) versus those same images rotated 90 degrees (and hence not navigable). By contrast, if PPA is involved in scene categorization, then it will respond similarly to both the upright and rotated images, since it has been shown that one can recognize/categorize a place from any orientation. To test our predictions, we used functional magnetic resonance imaging (fMRI). While in the scanner, participants were shown images of scenes from two orientations: upright and rotated. The response to each of these conditions was then measured in each of the three scene regions, as well as two control regions. Contrary to our predictions, we found that all three scene regions—and even the control regions—displayed the same pattern, with all responding more to the rotated than upright condition. This unexpected response to the rotated condition over the upright condition across all cortical regions tested is likely due to the fact that the rotated scenes were simply more surprising than the upright ones; in other words, more attention grabbing. Given this attentional confound then, we were unable to “see” whether OPA and RSC, but not PPA, are indeed involved in navigation. Hence, future work matching attention across these two conditions is needed.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 4 G
Presentation/Poster Number: 25
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Functional and anatomical changes in the lateral septal connectivity in facilitating social recognition and discrimination between conspecifics

Trisal, Jhillika; Isaac, Jennifer; Murugan, Malavika

Presenter/s: Jhillika Trisal
Emory Faculty Mentor: Malavika Murugan

As a species in a generally socially structured world, we are involved and influenced by a myriad of complex behaviors. Rodents like human beings spend a substantial amount of time engaging in social interactions. Social behaviors among conspecifics are the hallmark of survival, health, and reproduction in all sexually reproducing organisms. This research examines the functional and anatomical changes in the lateral septum connectivity in social recognition and discrimination between male vs. female vs. object conspecifics. The lateral septum is interconnected with regions like the hippocampus, hypothalamus, medial amygdala, and periaqueductal gray. There is adequate literature substantiating the pivotal role of the lateral septum (LS) in regulating processes related to motivation and emotion. It is recognized to play an essential role in social behavior, social recognition, and aggression. The lateral septum (LS) is said to convey context during social interaction and investigation. However, its function is very poorly elucidated. Social behavior is highly complex and variable involves an extraordinarily intricate network of neural circuits, and in this research, we have primarily reviewed anatomical literature highlighting the function, connectivity, and chemoarchitecture of the lateral septal nuclei in rats. To validate our studies, we have used rabies viral neuronal tracing techniques. Powerful and sophisticated transneuronal tracing technologies harness the ability of certain neurotropic viruses to travel through neural pathways and act as self-amplifying markers. Rabies virus is the only viral tracer that is entirely specific as it is transmitted exclusively between neurons connected by monosynaptic transneuronal transmission (upstream), allowing step-by-step identification of higher-order neural connections. Specifically, it receives distinct inputs from compartments of the hippocampus which indicates that different LS neurons participate in different social behaviors.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 1
Presentation/Poster Number: 4 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/92988928818

Analyzing suppression of growth defects caused by histone mutations implicated in cancers

Tumminkatti, Rhea; Corbett, Anita; Lemon, Laramie

Presenter/s: Rhea Tumminkatti
Emory Faculty Mentor: Anita Corbett

Many cancer-driving mutations have been identified, but how many mutations influence cancer is unknown. Recent work has identified missense mutations in histone genes that cause cancer, which are referred to as oncohistones. Histone proteins play critical roles in packaging DNA within the nuclei of all cells to form chromatin. This packaging is key for dynamic processes such as DNA replication and transcription. Interestingly, different oncohistones in the same gene cause distinct forms of cancer, including brain cancers known as gliomas and bone cancers called chondroblastomas. The mechanisms by which these missense mutations alter histone protein function and affect biological pathways remain a mystery. To examine the molecular consequences of individual amino acid changes in histone proteins in vivo, the Corbett Lab has used Saccharomyces cerevisiae to model oncohistone mutations in conserved histone genes. Studies have focused on introducing missense mutations in the yeast gene encoding histone H3, H3K36M and H3K36R. Budding yeast that express these histone H3 variants show growth defects that are exacerbated by various drugs that disrupt RNA metabolism and cellular processes, suggesting defects in specific biological pathways. Through a high copy suppressor screen, the Corbett lab identified several suppressors including ESA1, which encodes a histone H4 acetyl transferase enzyme. The goal of my summer project was to validate the high copy suppressor screen. I performed serial dilution growth assays with the yeast H3K36M and H3K36R variants overexpressing ESA1 in the presence of formamide, a drug that affects RNA metabolism, and caffeine, which affects the cellular stress response. These assays suggest that overexpression of ESA1 suppresses growth defects on plates containing caffeine; however, ESA1 does not suppress the growth defects of H3K36M and H3K36R on formamide-containing plates. The results suggest that Esa1 and likely acetylation of histone H4 may be linked to the cellular stress response, but may not be implicated in an RNA processing pathway. However, further experiments are necessary to confirm these conclusions.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 G
Presentation/Poster Number: 25
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

An Analysis of Speech Deterioration and Volume of Tissue Activated in Parkinson's Patients Receiving Deep Brain Stimulation

Ujre, Ashwin; Miocinovic, Svjetlana; Opri, Enrico

Presenter/s: Ashwin Ujre
Emory Faculty Mentor: Svjetlana Miocinovic

Deep brain stimulation (DBS) at the subthalamic nuclei (STN) and the globus pallidus internus (GPi) has proven to be an effective treatment for Parkinson's Disease (PD), with studies reporting marked improvement in cardinal motor symptoms. However, despite improvement in cardinal symptoms, long-term STN-DBS can trigger the deterioration of axial motor symptoms, most notably dysarthria. The variability in speech changes between patients receiving DBS for PD has led researchers to hypothesize that other variables may play a large role, namely lead location and volume of tissue activated (VTA). This project therefore aimed to find a correlation between VTA, both inside and outside the stimulation target, and speech impairment in patients receiving DBS for PD, with the hypothesis that higher out-of-target VTAs will exhibit higher deterioration of speech. Further, correlations between speech impairment and the VTA of different regions of the stimulation target were also assessed. In order to gauge changes to patients' speaking ability, changes from on-medication and off-medication baselines in the Part III (Motor Examination) speech scores of the MDS-Sponsored Revision of the Unified Parkinson's Disease Rating Scale (MDS-UPDRS) were calculated for each follow-up visit (6 months and 12 months). Using the Lead-DBS toolbox, patients' pre-operative T2 MRIs and post-operative CTs were co-registered to their pre-operative T1 MRIs, and the co-registered scans were normalized to the MNI space. Finally, the leads were reconstructed, 3D models of the normalized brains were generated and the VTAs were visualized after inputting the patients' active contacts and stimulation amplitude. The calculated in-target and out-of-target VTAs were compared to the change in speech scores both on and off medication as well as with and without stimulation. Of a population of 18 PD patients that underwent DBS surgery, 16 had on-medication scores and 17 had off-medication scores at a pre-op baseline, a 6-month follow-up and a 12-month follow-up. Changes in speech scores from baseline at both follow-ups were modelled as linear regressions against the total out-of-target VTA as well as the VTAs of specific non-target structures. The mean out-of-target VTA was 9.4 mm3 and the most commonly stimulated non-targets were the GPe (28.4 mm3), internal capsule (3.1 mm3) and zona incerta (3.5 mm3). While the linear regressions did not reveal a significant correlation between these VTAs and the change in speech scores, it is interesting to note that two patients that suffered worsening of speech scores under all three evaluation conditions had out-of-target VTAs limited to the internal capsule, with one possible explanation being that VTAs included the corticobulbar tract. Since this project is still ongoing, future work will involve analyzing more patients. Further, in order to verify the hypothesis involving the corticobulbar tract, patients' DTI images can be used in Lead-DBS to visualize stimulated fibers. Given that the co-registration and normalization processes have a significant margin of error, it is possible that the lead reconstructions and the modelled VTAs were not fully accurate, making it a limitation of this study.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 G
Presentation/Poster Number: 26
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Living ACTS: Reducing Disparities in Access to Living Donor Kidney Transplantation among African American End-Stage Renal Disease Patients through a Web-Based, Culturally-Sensitive Educational Intervention

Patzer, Elizabeth; Jacob Arriola, Kimberly; Retzloff, Samantha; Useche De Abreu, Sara

Presenter/s: Sara Useche De Abreu
Emory Faculty Mentor: Rachel Patzer

The optimal treatment for patients with ESRD is living donor kidney transplantation; however, there are prevalent racial disparities in access to transplantation, including living donor transplantation (LDKT). By adapting a theory-driven, culturally sensitive intervention for African American patients with kidney disease called Living ACTS (About Choices in Transplantation and Sharing), and implementing a web-based version, we hope to increase access to living donor transplantation among African American patients. To contribute to the overall goals of this study, I aimed to implement an IRB-approved, NIH-funded study protocol by recruiting patients and obtaining consent, collecting qualitative and quantitative data, and following study procedures. To recruit and enroll patients in the web-based Living ACTS study, which aims to enroll 850 patients total across four transplant centers, I assisted study staff at one of the four transplant centers, called over 40 patients, and enrolled 8 participants thus far. Each interview takes around 45 minutes to 1 hour in-person and up to 1 hour and a half virtually. Though there have been some challenges with recruiting the targeted sample size for this study, especially due to COVID-19, we believe the addition of culturally-sensitive, web-based education on LDKT to African American ESRD patients will increase interest in and access to LDKT among these patients. In order to mitigate the racial disparities that exist in kidney transplantation, it is essential that interventions are targeted to increase access to transplants among ESRD patients who historically have been disadvantaged and underserved compared to their white counterparts.

Key Words: End-Stage-Renal-Disease, Living Donor Kidney Transplant, Living ACTS

Research Discipline: Public Health
Presentation Type: Poster Presentation

Session: 3 G
Presentation/Poster Number: 26
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Characterization of clonally expanded antibodies from a rhesus macaque immunized with the HIV-1 BG505 SOSIP envelope trimer

Vazquez Narvaez, Kiara; Charles, Tysheena; Burton, Samantha; Arunachalam, Prabhu; Legere, Traci; Hunter, Eric; Amara, Rama; Pulendran, Bali; Derdeyn, Cynthia

Presenter/s: Kiara Vazquez Narvaez
Emory Faculty Mentor: Cynthia Derdeyn

Neutralizing antibodies (nAbs) have demonstrated robust protection against many viruses. However, protection against HIV-1 remains elusive due to its high mutation rates and escape mechanisms. To model vaccine elicited protection against HIV-1, we immunized rhesus macaques (RM) and challenged them with an autologous SIV/HIV (SHIV) virus in a previous study. The vaccine consisted of four immunizations with the HIV-1 envelope (Env) BG505 SOSIP stabilized trimer protein at weeks 16, 24, 40, and 80, with or without heterologous viral vectors to induce cellular immunity. At week 84, RM received ten low-dose intravaginal challenges with SHIV-BG505 virus. A clonal family of monoclonal antibodies (mAbs) was isolated from one immunized RM that developed high serum nAb and was protected against challenge. Those mAbs had potent neutralizing activity against the challenge virus. The goal of current project was to identify additional antibody clonal families from this RM, produce the corresponding mAbs, and test them for neutralization.

DNA sequences corresponding to immunoglobulin variable domain heavy (VH) and light (VL) genes obtained previously from antigen specific B cells using PCR were inspected for clonality. Selected VH and VL amplicons were cloned into DNA expression plasmids, which were co-transfected into 293F cells to produce the mAbs. Each mAb was tested in an enzyme-linked immunosorbent assay (ELISA) to confirm binding to the HIV-1 BG505 Env protein.

Ten mAbs representing three clonal families were successfully cloned, expressed, and purified. All mAbs bound to the BG505 Env gp120 protein in ELISA. The mAbs will be tested for neutralization against the challenge virus, as only a subset of vaccine elicited antibodies have this property. We will also determine whether the mAbs can neutralize other HIV-1 variants.

By characterizing individual vaccine-induced antibodies, we will gain insight into how nAb developed during HIV-1 Env immunization and why they protected against the SHIV challenge.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 E
Presentation/Poster Number: 17
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Studying the evolution of centromeric proteins in geographically separated house mouse lineages.

Vellore, Aditi; Morrison, Olivia; Thakur, Jitendra

Presenter/s: Aditi Vellore
Emory Faculty Mentor: Jitendra Thakur

Chromosome segregation ensures faithful segregation of sister chromatids or paired homologous chromosomes by spindle microtubules that bind to chromosomal loci called centromeres via a protein complex called the kinetochore. Centromeres are marked by a histone H3 variant, Cenp-A. Cenp-A is recruited to centromeres by a histone chaperone Hjurp. It remains poorly understood how Hjurp, carrying newly synthesized Cenp-A, is recruited specifically to centromeric DNA. My goal is to understand the functioning of Hjurp in targeting Cenp-A to centromeres by studying its evolution in closely related house mouse subspecies, Mus musculus musculus (Mmm) and M.m.domesticus (Mmd). Mmm and Mmd are undergoing rapid evolution due to their geographical separation in Eastern and Western Europe. Interestingly, Mmm centromeres assemble higher Cenp-A than those of Mmd. Higher Cenp-A levels lead to the formation of a larger kinetochore complex and stronger spindle binding. Preliminary findings in our lab have suggested that Hjurp is evolving rapidly under selective pressure in Mmm and Mmd. My goal is to investigate if changes in Hjurp alone or in combination with other centromeric proteins contribute to differences in Cenp-A recruitment observed in Mmd and Mmm. Using Sanger sequencing of multiple HJURP exons, I am characterizing Hjurp sequence changes in the liver tissues of Mmm and Mmd. Additionally, I have also performed comparative sequence analysis in the Mus genus to identify other rapidly evolving centromeric proteins that can potentially contribute to Cenp-A targetting. In the future, I will study the cytological localization of Hjurp variants and Cenp-A on Mmm and Mmd centromeres to understand the involvement of Hjurp in Cenp-A targeting. Findings from my research will also help understand involvement of Hjurp in multiple cancer types, such as bladder cancer, liver cancer, and lung cancer, where Hjurp is found to be overexpressed.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 5 G
Presentation/Poster Number: 27
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Gene Manipulation of MADR HEK293T Cells via Lipid-Based Transfection

Vera Pimentel, Natali; Lanjewar, Samantha; Sloan, Steven

Presenter/s: Natali Vera Pimentel
Emory Faculty Mentor: Samantha Lanjewar

A transfection is a process that allows a plasmid or circular DNA to enter a cell using either physical or chemical methods. Transfections allow scientists to create new cell lines by integrating specific plasmids into the genome, manipulate gene expression, and test other cellular applications. However, transfections put a large amount of stress on cells, making it difficult for plasmids to successfully integrate into the genome. To help mitigate this problem, mosaic analysis with dual recombinase-mediated cassette exchange (MADR) was created to provide an efficient method that utilizes transfections to generate new cell lines. Using human embryonic kidney (HEK293T) MADR recipient cells (Kim et al., 2019), we can integrate large plasmids, such as dCas-9 effectors, into the genome with relatively high efficiency. dCas9-effectors allow for the manipulation of gene expression by using a deactivated CRISPR/Cas9 protein (dCas9) tethered to an activator (SAM) or repressor (KRAB or ZIM3) protein. This experiment attempts to answer the question: Can we transfect MADR HEK293T cells with dCas9-effectors while also integrating them into the genome? We created MADR SAM, MADR KRAB, and MADR ZIM3 plasmids and used a FlpO/Cre plasmid to integrate these MADR plasmids into the genome. I transfected 6 T-25 flasks of MADR HEK293T cells; 3 of the flasksw contained only a MADR plasmid (either SAM, KRAB, or ZIM3) (controls); the other 3 contained a MADR plasmid and the FlpO/Cre plasmid (experimental). If the experimental plasmids (MADR + FlpO/Cre) successfully integrate into the genome, the cells will no longer fluoresce blue and instead fluoresce red due to having a red fluorescent protein marker attached to the dCas9-effectors. Results suggest that the flask containing MADR ZIM3 and FlpO/Cre plasmid successfully integrated into the genome of the MADR HEK293T cells and had some cells that only had red fluorescence.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 4 G
Presentation/Poster Number: 26
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Human Immunodeficiency Virus (HIV) Prevention in the Rural U.S.

Villarino, Xaviera; Jones, Dr. Jeb

Presenter/s: Xaviera Villarino
Emory Faculty Mentor: Jeb Jones

The HIV epidemic in the United States is concentrated among men who have sex with men (MSM), who accounted for 69% of new diagnoses in 2018. The U.S. government's investment in response to this disease has surpassed $28 billion a year. However, HIV research among MSM has primarily been conducted in urban settings, leaving a gap in our understanding of how HIV prevention options can be made accessible, culturally competent, and cost-effective for rural Americans. We conducted a thorough examination of existing scientific literature on sexual behavior and healthcare access by urbanity through the use of PubMed, JSTOR, Google Scholar, and CoCites, which identifies articles that are frequently cited together. Key search terms included: MSM, PrEP, HIV, rural, and rural health. Articles were then excluded on the basis of location, study population, publication date, and type of paper. With this information, we conducted a literature review that summarizes what is currently known about HIV prevention in the rural U.S. Rural MSM face additional barriers to accessing HIV prevention services compared to MSM in urban settings. Rural MSM are at increased risk of experiencing negative stigma and discrimination from healthcare providers and a fear of being "outed." Results from several national surveys have shown that there is no significant difference in sexual risk behaviors among rural Americans (number of sexual partners, condom usage during receptive anal intercourse, etc.), but there is lower uptake of preventive services like HIV/STI testing and treatment. There is a pressing need to increase HIV research in these vulnerable communities to identify and implement effective methods to increase uptake of HIV/STI prevention.

Research Discipline: Public Health
Presentation Type: Poster Presentation

Session: 5 G
Presentation/Poster Number: 28
Presentation Time: 1:00 PM to 1:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Orientalism in De-Nile

Vo, Sophie; Campbell, Celia

Presenter/s: Sophie Vo
Emory Faculty Mentor: Celia Campbell

This investigation seeks to divorce Roman partiality and Egyptomania from Roman sources. It builds upon Philip Stockhammer's anthropological framework of 'cultural entanglement' to evaluate the cross-cultural transmission of Roman literature and artifacts classified as appropriative or adaptative of Egyptian ideology and imagery. Among the epics, elegies, hymns, prose, and gemstones examined were: Callimachus' hymns, Tibullus and Propertius' elegies, Cicero's Dream of Scipio, Vergil's Aeneid, Apollonius' Argonautica, and gemstones with Egyptianizing motifs of Isis, Bes, Osiris. The exploration elucidates the nuances of Egyptian influence on Roman cultural products within a two-tiered framework of Cultural Entanglement divided into relational and material entanglement, with the additional influence of Edward Said's postcolonial perspective in Orientalism. Initial assessments of the artifacts, mainly Roman gemstones, indicate that the corpus of "Egyptianizing" ideas could not be divorced into entirely separate categories of appropriation and adaptation without overlooking its social context and mode of transmission. After conducting a content analysis of Roman and Egyptian texts along with examining Roman artistic commodities, we found that Roman artifacts represented both a fascination with Egyptian culture as well as a legitimate absorption of Egyptian religious practices and beliefs. Additionally, we discovered that Egyptomania operated on two distinct levels: (1) on the imperial level which exoticizes and dilutes Egyptian influences and (2) on the household level which legitimately practices Egyptian rites and absorbs cultural beliefs. The direct and indirect process by which Roman society appropriated Egyptian culture and values is paramount to understand the power dynamics and modes of geocultural transmission across imperial boundaries. These processes can also serve as early models for the commercialization of culture and instances of cultural appropriation in modernity.

Research Discipline: Humanities
Presentation Type: Oral Presentation

Session: 4
Presentation/Poster Number: 5 of 5
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99643683271

Flow and Failure of Ice Mélange: A Floating Granular Material

Burton C, Justin; Nissanka, Kavinda; Vora, Nandish; Guasch, Marc; Mendez, Josh

Presenter/s: Nandish Vora
Emory Faculty Mentor: Justin Burton

A buoyant agglomeration of granular particles is often encountered in various geophysical contexts, such as log jams and debris flows. Ice mélange is a granular material that sits in front of the world's largest tidewater glaciers; an agglomeration of broken icebergs that can resist the calving of kilometer-scale icebergs associated with glacial earthquakes. Geophysical data reveals that calving events are preceded by random rearrangements and flow decoherence of large icebergs in the mélange. To further investigate these flow characteristics, we created a scaled-down model of a tidewater glacier system. Our system consists of a moving terminus and polypropylene particles cut in random shapes to mimic icebergs in ice mélange. As the floating particles are pushed through a channel with rough walls, they jam and buckle due to friction. This forms a thick wedge near the terminus, exerting a force on the terminus. The experimental set up allows us to image the movement of the particles while also measuring the force on the terminus. Using Particle Image Velocimetry, we can analyze the movement of particles and corelate that with the force experienced by the terminus. We are especially interested in large unjamming events that are associated with a force drop on the terminus. We think that these unjamming events are caused by large rearrangements and buckling of particles releasing strain on the terminus which corresponds to calving events at the glacier level. The objective is to look for indicators of a large unjamming event; one such indicator seen in the terrestrial data is a sudden increase in the gradient of the velocities of the particles in the mélange. An understanding of how the mélange flow affects the force on the terminus, which is directly implicated in calving events, could allow detection of failure in glacial and other geophysical systems.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 G
Presentation/Poster Number: 25
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Developing a Live Cell Imaging Technique Using CRISPR/dCas13 to Label HIV-1 RNA and Investigate HIV-1 Latency

Wahoski, Claudia; Shah, Raven; Mahboubi, Darius; Sarafianos, Stefan; Tedbury, Philip

Presenter/s: Claudia Wahoski
Emory Faculty Mentor: Philip Tedbury

Human Immunodeficiency Virus type 1 (HIV-1) is a retrovirus that infects human CD4+ cells and is the cause of acquired immunodeficiency syndrome (AIDS). A major barrier to curing HIV-1 is latent or dormant infections, which occurs in long-lasting CD4+ immune cells that are not transcriptionally active, thus do not produce virus. Current approved HIV-1 treatments cannot target latent cells. Since latent cells can persist for long periods of time, these cells can reactivate and become transcriptionally active, leading to spreading of the infection. The mechanisms of HIV-1 latency induction and maintenance are poorly understood, however it is necessary that the viral genome integrates into the host genome. Previous data from the Sarafianos lab suggest that interfering with host factors involved in integration lead to increased antisense RNA. These host factors are also associated with latency; therefore, we hypothesize that the accumulation of antisense RNA is involved in establishing and/or maintaining latency. To study the relationships between HIV-1 RNA and latency, we are developing a live-cell imaging technique using clustered regularly interspaced short palindromic repeats (CRISPR) and dead CRISPR associated (dCas) 13 protein technology. We aim to optimize the CRISPR/dCas13 system to label viral RNA and track sense and antisense viral RNA following infection. To validate the efficacy of the CRISPR/dCas13 RNA labeling system, we used fluorescent in situ hybridization (FISH) to image HIV-1 RNA in cells. The RNA FISH experiments suggest that the CRISPR/dCas13 system is not effectively labeling HIV-1 RNA, therefore we are optimizing the guide RNA designs. This work will result in the development of novel technology to image HIV-1 RNA in live cells, which will allow us to track cell fates over time and better understand the relationship between HIV-1 antisense RNA and latency.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 F
Presentation/Poster Number: 21
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Chronic and Acute Stress Induces Behavioral Changes in Mice

Walia, Nevin; Kuehner, Janise; Martinez-Feduchi, Paula; Westover, Katherine; Yao, Bing

Presenter/s: Nevin Walia
Emory Faculty Mentor: Bing Yao

Stress is the biological response of an organism to an aversive stimulus that can be experienced chronically or acutely. Acute stress is associated with survival-based responses, whereas chronic stress has multisystemic consequences on body, particularly on the brain. Evidence suggests that epigenetics mechanisms, such as chemical modifications on DNA, have critical roles in brain development and function. However, much remains to be understood about the mechanism through which stress-induced alterations to the DNA modifications landscape may contribute to stress susceptibility or resilience at the behavioral and molecular level. This study investigates how exposure to chronic or acute stress alters DNA modifications in mouse brain tissue. Three-month-old male mice were exposed to either 10 or 2 days of physical and sensory stress to induce either chronic or acute stress, respectively. Initial findings utilizing the social interaction behavior paradigm suggest that mice exposed to either chronic or acute stress are significantly more stress susceptible compared to control animals, indicating that the stress paradigms are successfully inducing depression-like phenotype as expected. Blood plasma corticosterone levels, a biological indicator of stress, was more significantly elevated in the chronic stress group. Finally, results from the sucrose preference test suggest that chronically stressed animals were not anhedonic, a loss of pleasure that can result from stress exposure, whereas the acutely stressed animals showed anhedonic-like behavior. In the coming months, future work will focus on repeating the acute stress experiments with new cohorts of mice to gather more behavioral data. Then, harvested brain tissue from all cohorts will be used to compare important DNA modifications in different parts of the brain, such as the cortex and hippocampus. The DNA modifications 5-hydroxymethylcytosine, 5-methylcytosine, and N6-methyldeoxyadenosine will be analyzed in order to examine the differences between the epigenetic landscape of stress susceptible and stress resilient mice.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 E
Presentation/Poster Number: 18
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Novel Role for a Helicase with Zinc Finger in Homologous Recombination

Wang, Crystal; Haji Seyed Javadi, Ramona; Yu, David

Presenter/s: Crystal Wang
Emory Faculty Mentor: Ramona Haji Seyed Javadi

Lung cancer is one of the leading causes of death and a large part of unsuccessful cancer therapy is due to resistance by cancer cell's repair mechanisms through DNA damage response. To identify genes that mediate etoposide resistance in small cell lung cancer (SCLC), our laboratory performed a screen in an etoposide-resistant SCLC cell line, H128. HELZ (Helicase with Zinc finger) was one of the most significant etoposide sensitization hits. Further investigation demonstrated that HELZ's depletion in other cell lines causes hypersensitivity to etoposide and ionizing radiation (IR) resulting in impaired homologous recombination (HR). HELZ is an RNA helicase that may potentially mediate ATP-dependent unwinding and promoting structural rearrangement of RNA protein complex. However, the function of HELZ in DNA double strand break (DSB) repair have not yet been shown. Based on preliminary data collected by previous lab members, we hypothesize that HELZ has a potential role in HR to promote DNA DSB repair. To test this hypothesis, I performed knockdown (KD) of HELZ, using siRNA, and knockout (KO) of HELZ by CRISPR cas9 system followed by flow cytometry sorting of cells to look at DNA damage markers. I successfully confirmed the KD and KO of HELZ by western blot. My current ongoing experiments include KD of HELZ with more than one siRNA to assess whether depletion of HELZ would result in induction of γH2AX, an indicator of DNA damage. Upon completion of these steps, I will perform a rescue assay using wild type and mutant GFP-HELZ with impaired ATPase activity, to validate the results. If HELZ's overexpression rescues DNA damage, this would suggest that HELZ plays a role in promoting genome stability. The long-term goal of this research is to understand how HELZ may be exploited as a novel therapeutic target for patients with resistant SCLC to cancer therapies.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 G
Presentation/Poster Number: 25
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Molecular characterization of V1-Foxp2 interneurons reveals discrete subpopulations

Wang, Anthony; Worthy, Andrew E.; Alvarez, Francisco J.

Presenter/s: Anthony Wang
Emory Faculty Mentor: Francisco Alvarez

Terrestrial vertebrates interact with their environment through locomotion. For movement at limb joints, antagonist pairs of flexors and extensors contract in alternating patterns so that coordinated flexion-extension movements are generated. Dysregulation of flexor-extensor alternation is a common feature in motor pathologies such as amyotrophic lateral sclerosis (ALS). The circuit architecture that controls motoneuron firing involves the ventral V1 interneurons (V1s). This group is largely heterogeneous and organized into four major clades, each named after a transcription factor that genetically distinguishes them. The largest clade of V1s is defined by expression of the forkhead box transcription factor Foxp2 (V1-Foxp2s), and previous work indicates that they provide the principal inhibitory input to the cell bodies of motoneurons. In addition, some V1-Foxp2s form connections that suggest their involvement in reciprocal inhibitory circuits between flexors and extensors. The molecular diversity within the V1-Foxp2 group, however, impedes a detailed understanding of its role(s) in motor control. Thus, we used an intersectional genetics approach to investigate whether they can be differentiated by combinatorial transcription factor expression. Immunohistochemical staining of lumbar segments from neonatal mice (P5) revealed that approximately half of V1-Foxp2s express OTP and a fifth express Foxp4. We found that the OTP+ and Foxp4+ cells belong exclusively to the V1-Foxp2 clade. In addition, expression of Foxp4 invariably coincides with expression of OTP, suggesting that the OTP subpopulation of V1-Foxp2s contains two distinct groups: OTP+ Foxp4+ and OTP+ Foxp4– neurons. Given the relevance of these cell types to motor control, we also characterized their spatial distributions in the ventral horn: OTP+ Foxp4+ V1-Foxp2s are positioned more ventrolaterally and closer to the motoneurons in comparison to OTP+ Foxp4– V1-Foxp2s. In light of these findings, it is likely that V1-Foxp2 subpopulations with different genetic identities and discrete settling locations each fulfill different roles in spinal locomotor circuitry.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 F
Presentation/Poster Number: 22
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Exploring the Potential of Natural Products to Combat COVID-19 infections

Waters, Alaina; Risener, Caitlin; Caputo, Marco; Porras, Gina; Woo, Sunmin; Quave, Cassandra

Presenter/s: Alaina Waters
Emory Faculty Mentor: Cassandra Quave

The examination of biodiversity across the world has historically been a critical part of drug development and has led to the discovery of common medications for many medical issues including pain management, cancer, heart disease, and infection. During the SARS-CoV-2 pandemic, the use of natural supplements in the United States has increased. The efficacy of these natural products to prevent SARS-CoV-2 infection and the safety of their use remains unexplored; therefore more research must be done to determine which supplements have inhibitory properties.
The Quave Natural Product Library (QNPL) is a collection of over 2,000 botanical and fungal extracts and includes the 40 most used natural supplements in the United States. Collection of the biological samples for the library requires field expeditions to areas throughout the world with high levels of biodiversity. Each of these extracts were recently tested in a SARS-CoV-2 psudotyped virus system to test which, if any, have inhibitory properties against the virus entry, specifically the virus Spike protein binding to host cells ACE2 receptors. Cytotoxicity assays were run in parallel.
The QNPL screening against SARS-CoV-2 entry so far identified 17 extracts which both show inhibitory properties and low cytotoxicity levels. These extracts were further tested in a concentration-response assay. Future studies will include bioassay guided fraction to determine the specific single bioactive compounds with the inhibitory properties. This research will contribute to the understanding of the impact botanicals and medicinal herbs have on SARS-CoV-2 spike protein-ACE2 interactions. This will enable future studies in collaboration with virologists with intensive expertise in coronavirus biology to pursue testing in viral animal models (under BSL3 conditions) and to undertake an even more detailed query of mechanism of action.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 F
Presentation/Poster Number: 23
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Counterfactual Decision-Making in Anxiety

Wei, Andrew; Cooper, Jessica; Hahn, Emma; DeVries, Brittany; Treadway, Michael

Presenter/s: Andrew Wei
Emory Faculty Mentor: Michael Treadway

The current study focuses on understanding how anxiety influences counterfactual decision-making, receptiveness to counterfactual outcomes, and affective responses. Anxiety has been associated with aberrant decision-making and risk-aversion. During economic decision-making, individuals with anxiety exhibit persistent biases towards low-risk, low-reward options. There is evidence that suboptimal decision-making in people with anxiety may be mediated by both intolerance of uncertainty and regret sensitivity. These two manifestations of anxiety are potentially in competition to determine whether to receive or avoid information regarding the outcome of an unchosen option (i.e., counterfactual information). However, little is known about how intolerance of uncertainty and regret sensitivity influence decisions, affective responses, and receptiveness to counterfactual information. Here, we will recruit 100 undergraduates to complete a Counterfactual Gambling Task (CGT) and self-report assessments of anxiety, intolerance of uncertainty, and regret sensitivity. One component of the CGT assesses gambling decisions and affective responses to received outcomes. A second component of the CGT assesses preferences to receive or avoid counterfactual outcomes and measures subsequent affective responses to counterfactual information. We hypothesize that individual differences in anxiety will predict increased behavioral risk aversion and increased affective responses to counterfactual information. Additionally, we hypothesize that increased intolerance of uncertainty will be associated with increased willingness to seek counterfactual information, whereas increased regret sensitivity will be associated with greater avoidance of counterfactual information. These findings will help clarify how anxiety manifests in counterfactual decision-making, offering new insights into the processes underlying aberrant decision-making observed in individuals with anxiety.

Research Discipline: Social Sciences
Presentation Type: Poster Presentation

Session: 7 E
Presentation/Poster Number: 19
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Transcriptome analyses of patients with Renal Medullary Carcinoma

Wesley, Alexander; Lee, Benjamin; Cooper, Garrett; Mittal, Karuna; Hong, Andrew

Presenter/s: Alexander Wesley
Emory Faculty Mentor: Andrew Hong

Renal Medullary Carcinoma (RMC) is a rare and aggressive form of kidney cancer seen primarily in African American men between the ages of 11 and 39 who carry sickle cell trait. At the time of diagnosis, most patients have metastatic disease with a median survival rate of roughly 4 months post-diagnosis. Despite research advances, the standard of care has been treatment with cytotoxic, platinum-based chemotherapy and new therapeutic advances are limited. Recently, two efforts, including in our lab have performed RNA-sequencing on patients with RMC. We have combined these datasets to better characterize the difference between normal and tumor kidney samples at the transcriptome level. We first remapped and realigned the sequencing data and then quantified the transcripts with salmon. We then normalized the batch effects with Combat-seq and performed differential expression analyses with DEseq2. We compared the cohorts at the normal and tumor tissue level. We then combined these data sets and compared normal versus tumor. When we performed UMAP clustering and Gene Set Enrichment Analysis (GSEA), we found that when comparing the tumor samples from each cohort, SMARCB1 was downregulated, as is hallmark of RMC biology. Further, in our GSEA and UMAP analysis of tumor cohorts compared to normal kidney tissue cohorts, we found that genes relating to the MYC Proto-Oncogene pathway were enriched significantly when compared to the hallmark gene pathways found in GSEA(NES=3.4) Finally when comparing normal kidney tissue from the M.D. Anderson cohort to normal kidney tissue samples from our group we found that genes encoding proteins involved in oxidative phosphorylation were highly enriched in comparison to the hallmark gene sets found on GSEA (NES=3.29). Further research and in-vitro experimentation is needed to determine if these results are robust and reproducible in culture and may provide insights into new therapeutic targets.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 5
Presentation/Poster Number: 4 of 6
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99538389212

The use of a deep convolutional neural network artificial intelligence for coronary artery segmentation in Coronary CT angiography (CCTA)

Wessell, Jack; De Cecco, Carlo; van Assen, Marly

Presenter/s: Jack Wessell
Emory Faculty Mentor: Carlo De Cecco

Purpose: Cardiovascular diseases are the leading causes of death globally, with coronary artery disease (CAD) being the most common among them. To evaluate the severity of CAD, the Coronary Artery Disease Reporting and Data System (CAD-RADS) is used. CAD-RADS is a reporting system which is standardized for CCTA reports. This reporting system allows for clinical management recommendations for patients given their CAD-RADS score. Creating an Artificial Intelligence (AI) model that can accurately predict a patient's CAD-RADS score from a CCTA report would drastically improve interpretation efficiency and both inter-rater and intra-rater variability.

Method: Such an AI model consists of two parts: first a convolutional neural network (CNN) would view individual 2D slices of the 3D CCTA report and segment out the coronary arteries from the image. Then, those segmented images would be fed into a second network which would interpret the CAD-RADS score. My research focused on the first model. To develop this model, we used a dataset of 2380 CCTA slices containing the coronary arteries which had been segmented manually by radiologists. Of the 2380, the model was trained on 1904 of the images, with 48 being used for cross-validation. The remaining 428 were used for testing, so the model never learned from those images. We then tuned the structure, hyperparameters, and the loss function to create a model that produced an optimal dice score and recall on the test set.

Results: We found that a Unet++ model which was trained on a Tversky Loss function met our needs best, achieving a dice score of .783 with a recall of .906.

Conclusion: We feel that the model will produce segments that are accurate enough to minimize downstream errors in the second model, hopefully allowing for accurate and efficient CAD-RADS prediction.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 F
Presentation/Poster Number: 24
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The effects of color manipulation on the mating behavior of monarch butterflies (Danaus plexippus)

Williams, Ashley; Portil III, Karl; Zhao, Ella; Villa, Scott; de Roode, Jacaobus

Presenter/s: Ashley Williams and Karl Portil III
Emory Faculty Mentor: Scott Villa

Monarch butterflies are famous for their 4000km journey from Southern Canada to Central Mexico. However, very little is known about the traits that are important for successful mating. Previous work shows that size and color are essential for mating in butterflies. Here we investigate their potential roles in monarchs. We hypothesize that body size influences mating success, where males and females of the same size prefer to mate with each other. In addition, wing color may also influence monarch mate choice, where more melanized individuals are favored. To test these hypotheses, we experimentally manipulated both size and color of captive-reared butterflies. These monarchs were placed in mating cages and filmed for five days. We quantified the number of times monarchs mated and assessed their preference for different sizes and color mates from each film. Preliminary results suggest that size and color interact to influence mating decisions. Our study was the first to identify the particular traits that govern mate choice in monarch butterflies.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 G
Presentation/Poster Number: 25
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effect of Infection Status and Habitat Temperature on Littorina obtusata Grazing Patterns

Wolf, Amanda; Keogh, Carolyn

Presenter/s: Amanda Wolf
Emory Faculty Mentor: Carolyn Keogh

Because mesograzers influence algal communities in intertidal ecosystems, it is important to understand whether their grazing is influenced by climate change. The purposes of the study are to explore how temperature influences snail feeding patterns on macroalgae and whether grazing differs based on snail infection by trematode parasites. In the intertidal zone of Appledore Island, Maine, I collected 120 L. obtusata snails, 500g Ascophyllum, and 500g Fucus macroalgae. I transported the specimens to Emory and into aquarium tanks separated into three temperature treatments. To perform the grazing trials, I placed a focal snail on a frond of algae in a tray for 100 minutes in the first trial and 200 minutes in the second trial, keeping tank temperature consistent and marking the snail's position (on or off the algae) ten times per trial. Grazing patterns were quantified by tallying the number of new grazing scars observed under a microscope and measuring each scar to the nearest .25 mm. I also compared algal weight (g) before and after the trials and tested snail infection status by dissecting the specimens. The results revealed a significant association between algal species and the number of new scars present after grazing, and snail size was positively correlated with algae weight loss. In addition, all grazing quantification methods were associated, meaning that scar number, length, and algae weight loss are significant indicators of snail grazing patterns in the field. Most importantly, there was a significant positive relationship between temperature and grazing rates, demonstrated by a positive correlation between the number of new scars, new scar length, and temperature. Almost all specimens were uninfected, so further study is in progress for infection status effects. The effect of habitat temperature on snail grazing patterns holds important consequences for the future structure of algal communities under sea warming conditions.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 G
Presentation/Poster Number: 26
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

“A Fitting Scene for Unusual Capabilities”: Adrienne Herndon’s Trailblazing Black Theatrical Mobilization Across the Jim Crow South

Wolfram, Jack; Cahill, Patricia.

Presenter/s: Jack Wolfram
Emory Faculty Mentor: Patricia Cahill

The #BlackLivesMatter Movement’s unprecedented surge in 2020 spurred the United States to acknowledge and address its deep-rooted racism; in 2021, long-overdue investigations into suppressed Black history have gained increasing attention within scholarly spheres and popular culture accordingly. The Atlanta theatermaker Adrienne McNeil Herndon’s groundbreaking but tragically-short life in the early twentieth century is one such marginalized story. In the late 1800s, the thespian cultivated a promising performance reputation in the north while earning multiple academic degrees; when racism prematurely ended these exploits, Herndon returned south to helm the drama department at Atlanta (now Clark Atlanta) University. The faculty’s lone African-American woman established unprecedented access to serious drama for Georgia’s Black communities before her untimely death, radically reclaiming Shakespearian performance as the “birthright […] of the American Negro” and using theater as a means to bring together diverse populations of Black theatermakers in resistance to White supremacy.

Building upon recent work on Herndon (Cahill 2020), I set out to explore a shared suspicion that the scholar-creative mobilized Black thespians in the Jim Crow south beyond her home state’s borders. This entailed researching contemporary Black periodicals, university bulletins, event fliers, similar records, and secondary sources in the online and physical archives of Emory University, Clark Atlanta University, the HBCU Library Alliance, and Auburn Avenue Research Library. Uncovered findings thus far indicate that Herndon undertook a reading/performance tour throughout the south, going as far north as Chattanooga, TN. While these findings invite further exploration, this research may help expand perspectives about Black protest – specifically, that resistance to White supremacy was carried out not only by political organizations, but through cultural productions and pedagogy as well. It furthermore enables us to realize the complex politics of Shakespeare performance, given Shakespeare’s appropriation as a longtime White status symbol as well as a medium of Black resistance.

Research Discipline: Humanities
Presentation Type: Poster Presentation

Session: 7 E
Presentation/Poster Number: 20
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Effects of Galactose exposure on Cataract Formation in Rats across Genotypes

Wozniak, Aaron; Druss Jared; Judith, Fridovich-Keil; Rasmussen, Shauna

Presenter/s: Aaron Wozniak and Jared Druss
Emory Faculty Mentor: Judith Fridovich-Keil

Classic galactosemia is a genetically inherited disease caused by mutations in the GALT gene, resulting in a buildup of the sugar galactose due to a deficiency of functional GALT enzymes. The inability to effectively metabolize galactose leads to numerous developmental complications in humans and rats, such as delayed growth and cataract formation. The purpose of this study was to explore the interplay between dietary galactose exposure and GALT genotype (wild type, GALT null, or heterozygous). Rats of each genotype were weaned at three weeks of age and exposed to 5% galactose dissolved in their drinking water. At three months of age, the rats were euthanized and post-mortem images were taken of each individual rat eye. Eye photos were then scored on a scale of 0 (no cataract) to 3 (severe cataract). Data analyzed by linear mixed effects model in R produced a p-value < 0.0001, indicating that formation of cataracts does indeed differ among genotypes. Additional analyses using estimated marginal means found no significant difference between the wild-type and heterozygous groups (p = 0.8394), but highly statistically significant differences between the GALT null and heterozygous groups (p < 0.0001) and between the GALT null and wild-type groups (p < 0.0001). Specifically, GALT null rats displayed a higher prevalence and severity of cataracts than did either heterozygous or wild-type rats. This result is fully consistent with the autosomal recessive inheritance pattern characteristic of classic galactosemia. Of note, while no cataracts were observed in wild-type rats despite high galactose exposure, small white formations at the periphery of the iris were sometimes seen and may warrant further study.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 F
Presentation/Poster Number: 21
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Methods to identify new proteins that regulate Drosophila histone genes.

Xie, Mellisa; Comstra, H. Skye; Rieder, Leila

Presenter/s: Mellisa Xie
Emory Faculty Mentor: Leila Rieder

Nuclear bodies are membraneless structures containing concentrated regulatory factors that coordinate nuclear processes such as gene expression. The histone locus body (HLB) is a conserved nuclear body that is the main site of histone mRNA production in animals. The histone locus of the model organism Drosophila melanogaster contains ~100 tandem arrays of the five histone genes. While some HLB components of D. melanogaster are known, there are many uncharacterized factors that might target the histone locus and play a role in the HLB. One method to discover these proteins is to search for interaction partners for known HLB proteins. For example, the protein Myc contributes to cell growth and proliferation. Based on the established protein-protein interaction between known HLB component Myc and transcription factor Max, I predicted that Max is a novel HLB member. After mapping existing high-throughput sequencing datasets of Max, I determined that there is Max ChIP-seq and ChIP-nexus signal at the histone locus. To validate my bioinformatics results, I immunostained polytene chromosomes for Max and Mxc, an HLB-specific protein. The ChIP-seq and ChIP-nexus data suggested that Max was present at the histone locus, but polytene chromosome immunostaining revealed that Max binds broadly across chromosomes and does not colocalize with Mxc at the HLB. Although a bioinformatics approach can identify novel protein candidates, further wet-lab experiments are necessary to confirm the localization of these components to the HLB. Mining existing datasets is a useful method for identifying and screening potential HLB component proteins.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 3 G
Presentation/Poster Number: 27
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Response of Bean Beetle Gut Microbiome to Saponin

Xu, Tianyi; Zelaya, Anna

Presenter/s: Tianyi Xu
Emory Faculty Mentor: Anna Zelaya

Callosobruchus maculatus (bean beetle) is a stored-grain insect pest that exclusively feeds on legumes and can lead to globally economic loss and deterioration of food quality (Tuda et al., 2006). Saponin, a common secondary compound found in legumes has known insecticidal activity (De Geyter et al., 2007). Some herbivorous insects have evolved resistance towards plant-derived toxins through their gut microbiome (Hammer & Bowers, 2015). However, studies of such insect-microbiome interactions are limited to a few model species, and the mechanisms of insects' microbially-mediated defense to plant toxins remain unclear. In our experiments, we aimed to discover associations between C. maculatus, its gut microbiome and saponin, and we were specifically interested in the cultivability of the microbiome on saponin-rich media. We extracted the gut microbiome of beetles raised on black-eyed peas and plated it on solid media of nutrient broth, black-eyed pea and adzuki bean powders with a range of saponin concentrations (0%, 0.25%, 0.5%, 1.25%, 2.5%, 5%). Black- eyed pea has relatively low saponin compared to other legume species (Liu, 2015), therefore we hypothesized that as saponin concentration increased, there would be less bacterial growth since the microbiome could become susceptible under high saponin concentrations without previous exposures. Two lab strains of Staphylococcus (Gram-positive) and Enterobacter (Gram-negative) were selected for positive controls to determine if they exhibited different growth behaviors from closely related species found in bean beetle gut microbiomes. Preliminary results showed that neither the gut microbiome nor lab strains had significant growth inhibition from saponin treatments. Surprisingly, a saponin amount as low as 0.25% resulted in larger bacterial colonies, suggesting that certain bacteria may not only tolerate saponin, but also consume it as a carbon source. Improving our knowledge of insect-plant-microbe interactions is important for enhancing agricultural management strategies aimed at mitigating negative impacts of insect pests.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 4 G
Presentation/Poster Number: 27
Presentation Time: 12:00 PM to 12:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Malaria infection alters arachidonic acid metabolism in mice

Xu, Lennox; Singer, Grant; Liu, Ken; Morgan, Edward T; Lee, Choon-Myung

Presenter/s: Lennox Xu
Emory Faculty Mentor: Edward Morgan

Malaria is a parasite-driven infection that has had a global impact, with an estimated 3.4 billion people in 92 countries being at risk of infection and also the cause of 435,000 deaths in 2017 alone[1]. Previous studies have shown that, following infection, inflammation is a consequence of Malaria Plasmodium infection[2]. More specifically, this inflammation impairs drug clearance that is linked to downregulation of drug-metabolizing enzymes[2]. In this research investigation, we expanded on these previous studies and examined whether inflammation-related metabolites were altered in a mouse model of Malaria Plasmodium infection. We analyzed uninfected and infected mouse samples with high resolution metabolomics in order to identify metabolic pathways associated with this infection. Our data has shown that arachidonic metabolism pathways were altered by Plasmodium infection. This provides evidence that a certain set of metabolites are biologically validated as a metabolic response to infection, which could potentially serve as a template for inflammation-related pathways in mice. This template could lead to a better monitoring of inflammation in people infected with malaria and help facilitate the creation of more targeted anti-malarial drugs.

References
1. World Health Organization. Malaria. 2021 [cited 2021 7/22/2021]; Available from: https://www.who.int/data/gho/data/themes/malaria.
2. Mimche, S.M., et al., A non-lethal malarial infection results in reduced drug metabolizing enzyme expression and drug clearance in mice. Malaria journal, 2019. 18(1): p. 234-234.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 8 G
Presentation/Poster Number: 26
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Synthetic Method for Peptide Macrocyclization through C-H Amidation

Xu, Sophia; Poff, Christopher D.; Blakey, Simon B.

Presenter/s: Sophia Xu
Emory Faculty Mentor: Simon Blakey

Cyclic peptides, compared to the acyclic counterparts, are recognized with advantages for therapeutics such as high binding affinity, metabolic stability and target selectivity. Peptide-based macrocycles (with 12-or-more membered ring structure), particularly, can mimic the structure of protein-protein interactions and has a potential of improving the lead peptides in drug discovery1. Therefore, it is desirable to develop chemical methods for the synthesis of these macrocycles. Recently, transitional metal-catalyzed cross-coupling reactions have shown to aid in functionalization and macrocyclization of peptides, especially those that are not accessible to traditional methods including enzymatic resolution2.

Herein, we propose a cobalt-catalyzed aryl amidation process to couple the side chain of tyrosine (Tyr) with an acrylamide end on a linear peptide to achieve an intramolecular macrocyclization3. Current success in coupling tyrosine derivatives and phenylalanine (Phe) is promising to continue the test on linear peptides. An initial peptide for coupling will be Tyr-Pro-Gly-Phe, with a tripeptide being prepared through solid phase peptide synthesis and tyrosine being manually coupled after cleavage from the resin. Once the initial macrocyclization is successful, reaction scope can be expanded to longer peptides with various amino acids, which can ultimately be generalized to a procedure to prepare cyclic peptides.

(1) Tan, J.; Wu, J.; Liu, S.; Yao, H.; Wang, H. Macrocyclization of Peptidoarylacetamides with Self-Assembly Properties through Late-Stage Palladium-Catalyzed C(Sp2)—H Olefination. Sci Adv 2019, 5 (3), eaaw0323.
(2) Wang, W.; Lorion, M. M.; Shah, J.; Kapdi, A. R.; Ackermann, L. Late-Stage Peptide Diversification by Position-Selective C−H Activation. Angewandte Chemie International Edition 2018, 57 (45), 14700–14717.
(3) Lerchen, A.; Knecht, T.; Daniliuc, C. G.; Glorius, F. Unnatural Amino Acid Synthesis Enabled by the Regioselective Cobalt(III)-Catalyzed Intermolecular Carboamination of Alkenes. Angewandte Chemie International Edition 2016, 55 (48), 15166–15170.

Research Discipline: Natural and Physical Sciences
Presentation Type: Oral Presentation

Session: 5
Presentation/Poster Number: 5 of 6
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99538389212

Analysis of Striatin's Interactions with Tight Junction Proteins

Yang, Chloe; Cai, Benjamin; Pallas, David

Presenter/s: Chloe Yang
Emory Faculty Mentor: David Pallas

Tight junctions (TJ) maintain the integrity of epithelial cells that protect organisms from their external environment by regulating the passage of ions, water, and macromolecules; dysfunctional tight junctions cause a wide variety of diseases and cancers. Previous research has suggested that striatin, the regulatory subunit of protein phosphatase 2A (PP2A) colocalizes with known TJ protein ZO-1. Furthermore, preliminary co-immunoprecipitation data showed that striatin interacts with cingulin and occludin, known TJ proteins, in mouse keratinocytes. However, striatin's function at tight junctions and the exact mechanisms of tight junction formation are still unknown. This study tests the hypothesis that striatin plays a role in regulating the formation of tight junctions by interacting with TJ proteins. Co-immunoprecipitation assays in 293 cells were conducted to examine protein-protein interactions between striatin and known tight junction proteins such as claudin, occludin, and ZO-1. The resultant isolated proteins were then analyzed by 1D SDS-PAGE and Western blot. A series of preliminary experiments were conducted to consolidate the reagents and conditions necessary to execute future co-IP experiments. Furthermore, a novel method for immunofluorescence, boiling cells in a SDS/DTT solution, was developed to expose epitopes for better staining; this method has yielded positive results and will help us better identify colocalization of TJ proteins and striatin in the future. Though this research is still ongoing, the ultimate goal is to identify striatin domains and associated proteins essential for the localization of striatin in tight junctions. This will allow for a better understanding of the mechanisms of tight junction formation, thereby allowing for the development of targeted therapeutics that can address disorders related to their dysfunction.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 6 G
Presentation/Poster Number: 26
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Risk stratification for invasive imaging in perimesencephalic and aneurysmal angio-negative patterns

Yang, Chris; Akbik, Feras

Presenter/s: Chris Yang
Emory Faculty Mentor: Feras Akbik

Subarachnoid-hemorrhage (SAH) occurs when blood escapes into the space between the arachnoid layer and pia, a potential space that spans the superficial surface of the entire brain. SAH is caused by a rupture in the vasculature, often due to pathologic vascular anatomy. The most common form of non-traumatic SAH is aneurysmal-SAH, when a weak point (aneurysm) in a cerebral artery ruptures and leaks blood into subarachnoid space. When diffuse, subarachnoid-blood is noted in CT, the first step is to assess whether an aneurysm can be found. Patients undergo an initial CT angiography (CTA) and/or conventional cerebral-angiogram to image intracranial-blood vessels and assess for vascular-pathology. Patients fall into two categories: they either do or do not have an identifiable vascular lesion (usually cerebral aneurysm). This is known as aneurysmal or angio-negative SAH (negative CTA, negative cerebral-angiogram). If a vascular source of SAH is found, urgent surgical intervention and treatment ensue thereafter. Angio-negative SAH, however, represents a heterogenous set of pathologies with different natural histories that can be broken down into two subcategories depending on bleed pattern and location: perimesencephalic and aneurysmal angio-negative pattern (diffuse SAH in literature). Patients with perimesencephalic subarachnoid-hemorrhage (PMH) have subarachnoid-blood restricted to the basal cisterns near brainstem, whereas aneurysmal angio-negative SAH is characterized by subarachnoid-blood diffusely enveloping both brainstem and cortical surfaces. Both initially display similar symptoms yet have very different prognoses. PMH has low morbidity and exceedingly rare mortality while aneurysmal angio-negative SAH is worse than PMH but not as morbid as (angio-positive) aneurysmal-SAH. Nevertheless, aneurysmal angio-negative SAH patients are more likely to have an undiagnosed aneurysm identified during a follow-up CTA/angiogram workup, or even recurrent SAH. Here we aim to evaluate the utility of imaging in both high and low-risk patient populations and identify a risk stratification strategy to better select patients for invasive imaging.

Research Discipline: Public Health
Presentation Type: Poster Presentation

Session: 6 G
Presentation/Poster Number: 27
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Reduction of sleep spindles in non-human primate model of acute prefrontal seizures

York, Alizabeth; Vuong, Jocelyn; Connolly, Mark; Devergnas, Annaelle

Presenter/s: Alizabeth York
Emory Faculty Mentor: Annaelle Devergnas

Many epileptic patients experience comorbid sleep disorders characterized by increased sleep disturbances and reduced rapid eye movement. It has been suggested that seizures may disrupt the memory consolidation mechanism through the replay of neuronal diurnal seizure activity during NREM sleep stages, potentially contributing to sleep disturbance seen in epileptic patients and animal models. Further, a decrease in sleep spindles, a hallmark of stage 2 sleep associated with memory consolidation, has been noted in epileptic patients (Lanigar, 2017). In this study, we aim to explore how the frequency and timing of sleep spindles changes post seizure induction. In two adult rhesus macaques, ECoG activity and video recording were conducted prior to seizure induction, night of seizure induction, as well as several nights after. Data were manually sleep scored in thirty second epochs. Seizures were induced in the morning via penicillin injection in the frontal cortex and lasted 4-6 hours before stopping on their own. Sleep spindles were identified using a custom written Matlab code that identified spindles of frequencies between 9-16 Hz occurring for 0.4-2 seconds. Preliminary data shows a reduction in sleep spindles post seizure induction similar what is seen in epileptic patients, suggesting that cortical seizure activity may trigger a change in the thalamocortical pathway that inhibits the generation of spindles. In Monkey 1, there was significant decrease in overall spindles, as well as spindles occurring during stage 1 sleep and REM sleep. In Monkey 2, the decrease in spindles only reached significance in REM sleep. However, the underlying mechanism for this change is still unclear. Future studies will investigate the timing of spindles in relation to slow wave sleep activity. Better understanding of seizure induced sleep changes is key to the development of more effective treatments for seizures and their comorbid sleep disorders.

References

Lanigar, S., & Bandyopadhyay, S. (2017). Sleep and Epilepsy: A Complex Interplay. Missouri medicine, 114(6), 453–457.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 F
Presentation/Poster Number: 22
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating the Role of IgMs in the Immune Response to Factor VIII

York, Elie; Batsuli, Glaivy

Presenter/s: Elie York
Emory Faculty Mentor: Glaivy Batsuli

), an essential protein in the blood-clotting cascade. Such a deficiency causes the inability to form stable blood clots and can lead to spontaneous, trauma-related, or surgical bleeding. The most common treatment for hemophilia A is intravenous infusion of plasma derived or recombinant FVIII. However, treatment may cause inhibitory antibodies (called inhibitors) to form against FVIII in up to 33% of patients with severe hemophilia A. The mechanism through which FVIII inhibitors are formed is not well understood and subsequently patients with hemophilia A who develop inhibitors have limited treatment options. Previous experiments have shown that complexing FVIII and immunoglobulin M (IgM) together against the FVIII C1 domain in a mouse model of hemophilia A produces an overall decreased immunological response to FVIII. Based on these results further investigations on the roles that different subsets of antibodies play in inhibitor development could be beneficial in understanding the immune response to FVIII in human patients. A series of experiments are being performed to characterize the role of IgM in this response. First, NS-1 myeloma cells were fused with hemophilia A mouse splenocytes producing hybridomas that were then selected for anti-FVIII IgM producing hybridoma colonies using an enzyme-linked immunosorbent assay (ELISA). IgM were purified from the array of anti-FVIII antibodies. A Bethesda assay will be utilized to determine the inhibitory effect of IgM on FVIII activity. Binding domains will be determined using ELISAs leading to classification of IgM subclasses. No results have been produced yet, but we anticipate being able to determine the binding site of IgMs against one of the 5 FVIII domains. From these experiments, we hope to characterize murine-derived anti-human FVIII IgM to gain an understanding of their role in propagating the humoral immune response to FVIII.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 7
Presentation/Poster Number: 4 of 6
Presentation Time: 3:00 PM to 4:30 PM
Presentation Link: https://emory.zoom.us/j/97807604820

Understanding the Role of Striatin in Cell-Cell Tight Junctions

You, Victor; Cai, Benjamin; Pallas, David

Presenter/s: Victor You
Emory Faculty Mentor: David Pallas

Cell polarization is vital in human development, and its impairment is implicated in many disorders and most cancers, such as breast, colon, and prostate cancer. In epithelial cells, adherens junctions and tight junctions (TJs) help control cell polarity. Tight junctions are semipermeable, intercellular connectors of epithelial cells that are size and charge selective. Degradation of TJs has negative implications on the epithelial barrier, inner ear, among others. One important enzyme involved in TJ regulation is Protein phosphatase 2A (PP2A). They are made up of a structural A subunit, catalytic C subunit, and a regulatory B subunit. In this study we focused on the regulatory B subunit; where striatin binds to PP2A's A and C subunits and alters their functions. To confirm the presence of striatin in tight junctions, co-immunoprecipitation (Co-IP) was used to identify any striatin interactions with known junctional proteins using human 293 cells. These protein complexes were then separated out and visualized via 1D SDS-PAGE gel, followed by Western Blot. Preliminary results show zinedin, a striatin subtype, is in these TJ protein complexes. However, PP2A has not been detected in some of the Western blots. Future co-IPs and Western Blots are needed in order to confirm these results. Once striatin has been consistently identified in TJ complexes, human 293 cells would be transfected with the plasmids of striatin mutants to investigate how the structures and functions of tight junctions alter. In the long run, once the regulatory role of striatin in PP2A becomes elucidated, the results could be applied to the therapeutic development of disorders caused by TJ dysfunctions.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 6 G
Presentation/Poster Number: 28
Presentation Time: 2:00 PM to 2:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Development of the Partner Touch Task, an in-scanner assessment of sensory perception mechanisms with functional magnetic resonance imaging.

Author 1: Youssef, Aya; Author 2: Hackney, Madeleine.

Presenter/s: Aya Youssef
Emory Faculty Mentor: Madeleine Hackney

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 1 G
Presentation/Poster Number: 27
Presentation Time: 9:00 AM to 9:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Visual and Verbal Memory Outcome Following Stereotactic Laser Ablation

Drane, Daniel;

Presenter/s: Joanna Yu
Emory Faculty Mentor: Daniel Drane

Introduction: Stereotactic laser amygdalophippocampotomy (SLAH) is a promising surgical procedure employed in the setting of epilepsy during the past decade. SLAH is nearly as effective as traditional open resection (OR) procedures at controlling seizures, while early results suggest promising cognitive outcomes due to its minimally invasive nature. Nevertheless, memory outcome has not been extensively studied with SLAH.

Methods: We explored memory performance both pre- and post-surgically in medial temporal lobe epilepsy (MTLE) patients (N=40) undergoing either left (n=15) or right (n=25) SLAH using traditional clinical measures. Verbal memory was assessed with the Rey Auditory Verbal Learning Test (RAVLT) and visual memory with the Visual Reproduction (VR) Test. We used a standard metric of change of 1.5 SD to denote significant change, and Fischer's exact tests to explore decline in our sample versus historical base rates associated with traditional OR (e.g., 40-60% of left MTLE and 20% of right MTLE patients decline on RAVLT; 10-30% of all patients decline in visual memory).

Results: There were no significant differences between left and right MTLE patients on relevant demographic and disease-related variables. Left patients performed more poorly than right patients on the RAVLT whereas the opposite pattern was observed with VR performance (t-statistics, p<.01). Only 2/15 (13.3%) left MTLE patients and 3/25 (12.0%) right MTLE patients exhibited a significant decline on the RAVLT, with these numbers far below known baserates with OR (p<.001). Similarly, only 1/15 (6.7%) left and 2/25 (8.0%) right MTLE patients declined on VR, compared to a conservative estimate of 20% of patients declining on similar measures after OR (p<.01).

Discussion: Preliminary results suggest minimally invasive SLAH procedures likely spare verbal and visual memory function to a greater degree than the traditional OR approach. Minimal deficits observed raise questions about the contribution of the hippocampus to learning and memory.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 2 G
Presentation/Poster Number: 26
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Mechanical detection of liquid sorption and evaporation in thin deposited solid films

Zaalishvili, Ana; Gognon, Yannic; Roth, Connie; Burton, Justin

Presenter/s: Ana Zaalishvili
Emory Faculty Mentor: Justin Burton

Nanoscale films deposited on surfaces are widely used in science and industry. The physics of these interfacial layers is often more complex than their bulk or macroscopic counterparts. Due to this difference, properties such as hydrophobicity, absorption, and diffusion need to be investigated at the nanoscale. We used a Quartz Crystal Microbalance (QCM), due to its mass sensitivity and simplicity of use, to investigate two important physical aspects of deposited films. We explored the nanoscale absorption of water into different materials using QCMs. By monitoring the mechanical resonance frequency of a QCM we can detect sub monolayer changes in absorbed mass. These measurements were compared to the corresponding macroscopic contact angle measurements, a traditional way of measuring the hydrophobicity of the surface. We found discrepancies between these measurements, which could be due to the porous nature of our SiO2 coated QCMs. Additionally, we put spin-coated polystyrene films of thickness < 1 micron on the QCMs and found that 10-25% of the residual toluene solvent remained in the film. Part of the solvent left the samples through evaporation, and rest through heating the sample above the glass transition temperature and annealing in vacuum. The presence of residual solvent will affect material properties which are commonly studied in various fields. Both hydrophobicity measurements and solvent evaporation are important characteristics for nanoscale film fabrication and optimization. We are planning on making SiO2 coated QCMs ourselves to avoid porosity and explore this phenomenon further.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 7 F
Presentation/Poster Number: 23
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Identifying Aβ species that induce proinflammatory profiles in mouse microglia in an in vitro model of Alzheimer's Disease pathology

Zeng, Hollis ; Bowen, Christine ; Santiago, Juliet ; Xiao, Hailian ; Rangaraju, Srikant

Presenter/s: Hollis Zeng
Emory Faculty Mentor: Srikant Rangaraju

Alzheimer’s disease is a progressive neurological disease that afflicts over 6 million Americans. One of the hallmark features of Alzheimer’s disease is β-Amyloid (Aβ) protein aggregates that form plaques. Aβ adopts various states, ranging from oligomers to fibrils, with distinct effects on neurons and glial cells. Microglia, the immune cell of the brain, enter a disease associated state, known as disease associated microglia (DAM). A subset of these DAMs have a proinflammatory phenotype, where they fail to phagocytose Aβ, release cytokines, and promote neuronal death. Our lab has found that proinflammatory DAM in the brain upregulates expression kv1.3, a potassium channel. Modeling this response in vitro has been challenging. In order to investigate how Kv1.3 impacts microglial functions, my goal is to determine which form of Aβ (oligomer, fibrils plaques) maximally influence microglial immune response, particularly expression of Kv1.3 potassium channels and proinflammatory cytokine Il1b. We cultured immortalized mouse microglial cells (MMCs) with three aggregation states of Aβ (oligomers, fibrils, plaques) at three concentrations (1 μM, 100 nM, 10 nM) for 24h and 48h. We confirmed the aggregation of Aβ using transmission electron microscopes (TEM). We used lipopolysaccharide (LPS) as a positive control and saline as a negative control. RNA was extracted using a trizol extraction followed by quantitative reverse transcriptase polymerase chain reaction (qRT-PCR) to measure expression of Kv1.3 (Kcna3), a pro-inflammatory gene (Il1b)and housekeeping gene (Gapdh). The data shows LPS exposure shows a robust Il1b response and no significant changes across any of the time points or concentrations of Aβ for the Il1b gene or Kcna3. Our results could indicate unsuitability of MMCs to model Abeta induced immune responses or the lack of immune effects of our Abeta preparations. We are now performing optimization studies in primary microglia and additional microglial cell lines.

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 7
Presentation/Poster Number: 5 of 6
Presentation Time: 3:00 PM to 4:30 PM
Presentation Link: https://emory.zoom.us/j/97807604820

Synthesis, Characterization, and Coordinative Reactivity of Novel Copper Complexes with a Tripodal Amidate Ligand

Zhang, Yiran; Liu, Elaine; Bacsa, John; MacBeth, Cora

Presenter/s: Yiran Zhang
Emory Faculty Mentor: Cora MacBeth

Copper-centered oxidases and oxygenases existing in nature are crucial models for the development of new catalysts for oxidation reactions. In order to better understand their working mechanisms and reveal any structure-activity relationships at the protein active-site, Cu complexes bearing various ligand scaffolds have been synthesized and investigated. Particularly, tripodal ligands with four coordinating nitrogen atoms have been widely employed to simulate the non-planar coordination environment around the metal center and the coordinating histidine moieties. In this study, a tripodal, redox-active, anionic amidate ligand N(o-PhNHC(O)CF3)3 is utilized to synthesize two novel Cu complexes (PPh4)2[Cu(N(o-PhNC(O)CF3)3)] and PPh4[Cu(N(o-PhNC(O)CF3)3)]. Both complexes are structurally, spectrally, and electrochemically characterized. In the investigation of the coordinative reactivity of (PPh4)2[Cu(N(o-PhNC(O)CF3)3)] with Et4NCN, the unexpected involvement of the countercation PPh4+ is detected, as evidenced by the formation of P(O)Ph3.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 2 G
Presentation/Poster Number: 27
Presentation Time: 10:00 AM to 10:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Intersectionality: Remodeling Affirmative Action for Justice

Zhang, Emil; Huseyinzadegan, Dilek

Presenter/s: Emil Zhang
Emory Faculty Mentor: Dilek Huseyinzadegan

The word “intersectionality” has become mainstream and widely used in conversations surrounding diversity and inclusion. Although definitions of intersectionality vary, the concept of intersectionality centers around the compounding nature of discrimination that affects people who are vulnerable to multiple structural oppressions. Intersectionality is useful to analyze how social identifiers such as race, gender, and class interact; and it was originally developed with the normative goal to eradicate interlocking oppressive structures. However, many current usages of this term misconstrue the original vision and diminish the powerful potential of intersectionality. Tracing back its roots to Black feminism, I investigate the appropriation of this term while reinforcing the true conceptualization of intersectionality as an analytical tool to redress historic and current inequalities stemming from systemic prejudice of identity. By close reading contemporary texts that have developed out of the Black feminist tradition such as authors Kimberlé Crenshaw, Vivian May, and Jennifer Nash, I reaffirm a more accurate depiction of intersectionality. I develop that one method intersectionality can promote justice lies in the ability to improve equal opportunity in education. I argue that intersectionality must be taken into account for affirmative action policies in higher education admissions in order to open opportunities to the most marginalized of people. My viewpoint defends affirmative action on the primary basis of reparations, the duty to rectify historical oppression that continues to affect the lives of people who have been exploited. My critical analysis of texts from political philosophy, critical race theory, and feminist theory leads to the conclusion that effective affirmative action programs are essential to a more equitable society, and that intersectionality must be taken into account to model these programs.

Research Discipline: Humanities
Presentation Type: Oral Presentation

Session: 1
Presentation/Poster Number: 5 of 5
Presentation Time: 9:00 AM to 10:30 AM
Presentation Link: https://emory.zoom.us/j/92988928818

The Neurobiology of Adult Caregiving

Zhang, Jiajin (Molina); Rilling, James K.

Presenter/s: Jiajin (Molina) Zhang
Emory Faculty Mentor: James Rilling

Abstract not available.

Research Discipline: Natural and Physical Sciences
Presentation Type: Oral Presentation

Session: 7
Presentation/Poster Number: 6 of 6
Presentation Time: 3:00 PM to 4:30 PM
Presentation Link: https://emory.zoom.us/j/97807604820

Dual experimental manipulation of size and color in monarch butterflies (Danaus plexippus)

Zhao, Ella; Protil, Karl; Villa, Scott; de Roode, Jacobus

Presenter/s: Ella Zhao
Emory Faculty Mentor: Scott Villa

Both body size and wing color are thought to play fundamental roles in monarch butterfly mating success. However, the functional role of these presumably important traits has yet to be tested. In some populations, monarchs have evolved differences in both size and color. For example, monarchs found in Puerto Rico are smaller and have darker wing patterns than those found in Eastern North America. Thus, it is possible that both size and color work together to influence mating success. While monarch size and color can be experimentally manipulated separately, it is unclear if both traits can be altered together. To test the interaction of body size and color manipulation, we first experimentally manipulated monarch size by restricting their diet immediately when they entered the 5th instar developmental stage. Then we injected heparin solution, which results in darker wing patterns, with three different concentrations (1%, 2%, 4%) in 45 smaller-bodied monarchs and 45 normal-sized monarchs. For control, water or saline solution was injected in 15 smaller-bodied monarchs and 15 normal-sized monarchs. Our data showed that size and color manipulation can function together in monarchs. We further showed that the monarchs injected with 1% heparin solution bore the closest resemblance to the Puerto Rican phenotype. This study paved the way for further research on the functional roles of size and color in monarch mating behavior.

Research Discipline: Natural and Physical Sciences
Presentation Type: Poster Presentation

Session: 8 G
Presentation/Poster Number: 27
Presentation Time: 4:00 PM to 4:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

The Effects of Glutamine Deprivation on Cancer Cell Survival and Protein Expression Following Radiation

Zhou, Grace; Shin, Jenna; Punyala, Amith; Hou, Sean; AbuSalim, Jenna; Kesarwala, Aparna

Presenter/s: Grace Zhou
Emory Faculty Mentor: Aparna Kesarwala

Cancer cells undergo altered metabolic processes, including glycolysis and the tricarboxylic acid (TCA) cycle, to support growth and survival. In cancer cells, an alternative car1b1o1n1 1s1o1u1r1c1e1 1f1o1r1 1t1h1e1 1T1C1A1 1c1y1c1l1e1 1c1o1m1e1s1 1f1r1o1m1 1g1l1u1t1a1m1i1n1o1l1y1s1i1s1,1 1w1h1i1c1h1 1p1r1o1d1u1c1e1s1 1±————————————-1k1e1t1o1g1l1u1t1a1r1a1t1e1,1 1a1 1T1C1A1 1c1y1c1l1e1 1i1n1t1e1r1m1e1d1i1a1t1e1,1 1f1r1o1m1 1t1h1e1 1a1m1i1n1o1 1a1c1i1d1 1g1l1u1t1a1m1i1n1e1.1 1T1h1i1s1 1s1t1u1d1y1 1e1x1a1m1i1n1e1s1 1t1h1e1 1e1f1f1e1c1t1s1 1o1f1 1r1a1d1i1a1t1i1o1n1 1o1n1 1g1l1u1t1a1m1i1n1e1 1d1e1p1r1i1v1e1d1 1c1o1l1o1r1e1c1t1a1l1 1c1a1n1c1e1r1 1c1e1l1l1s1 1c1o1m1p1a1r1e1d1 1t1o1 1t1h1o1s1e1 1w1i1t1h1 1g1l1u1t1a1m1i1n1e1.1 1W1e1 1u1s1e1d1 1l1a1c1t1a1t1e1 1d1e1h1y1d1r1o1g1e1n1a1s1e1 1(1L1D1H1)1,1 1a1n1 1e1n1z1y1m1e1 1t1h1a1t1 1c1a1t1a1l1y1z1e1s1 1t1h1e1 1l1a1s1t1 1s1t1e1p1 1o1f1 1g1l1y1c1o1l1y1s1i1s1,1 1a1s1 1a1n1 1i1n1d1i1c1a1t1o1r1 1o1f1 1g1l1y1c1o1l1y1s1i1s1 1a1n1d1 1p1r1o1b1e1d1 1f1o1r1 1t1h1e1 1e1n1z1y1m1e1 1u1s1i1n1g1 1W1e1s1t1e1r1n1 1b1l1o1t1t1i1n1g1.1 1R1e1l1a1t1i1v1e1 1L1D1H1 1e1x1p1r1e1s1s1i1o1n1 1i1n1c1r1e1a1s1e1d1 1f1o1l1l1o1w1i1n1g1 1r1a1d1i1a1t1i1o1n1 1i1n1 1c1a1n1c1e1r1 1c1e1l1l1s1 1w1i1t1h1 1c1o1m1p1l1e1t1e1 1g1l1u1t1a1

Research Discipline: Biomedical Sciences
Presentation Type: Oral Presentation

Session: 5
Presentation/Poster Number: 6 of 6
Presentation Time: 12:00 PM to 1:30 PM
Presentation Link: https://emory.zoom.us/j/99538389212

Fitness Estimation for Viral Variants in the Context of Cellular Coinfection

Zhu, Julie; Allman, Brent; Koelle, Katia

Presenter/s: Julie Zhu
Emory Faculty Mentor: Katia Koelle

Animal models are frequently used to characterize the within-host dynamics of emerging zoonotic viruses. More recent studies have also deep-sequenced longitudinal viral samples originating from experimental challenges to gain a better understanding of how these viruses may evolve in vivo and between transmission events. These studies have often identified nucleotide variants that can replicate more efficiently within hosts and also transmit more effectively between hosts. Quantifying the degree to which a mutation impacts viral fitness within a host can improve identification of variants that are of particular epidemiological concern and our ability to anticipate viral adaptation at the population level. While methods have been developed to quantify the fitness effects of mutations using observed changes in allele frequencies over the course of a host's infection, none of the existing methods account for the possibility of cellular coinfection. Here, we develop mathematical models to project variant allele frequency changes in the context of cellular coinfection and, further, integrate these models with statistical inference approaches to demonstrate how variant fitness can be estimated alongside cellular multiplicity of infection. We apply our approaches to empirical longitudinally sampled H5N1 sequence data from ferrets. Our results indicate that previous studies may have significantly underestimated the within-host fitness advantage of viral variants. These findings underscore the importance of considering the process of cellular coinfection when studying within-host viral evolutionary dynamics.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 3 G
Presentation/Poster Number: 28
Presentation Time: 11:00 AM to 11:50 AM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium

Investigating the Role of LCMT-1 in Monocytes

Zhu, Jedidiah; Pallas, David; Tam, Duncan

Presenter/s: Jedidiah Zhu
Emory Faculty Mentor: David Pallas

LCMT-1 is an enzyme that methylates the catalytic subunit of PP2A, a major mammalian protein that regulates cell growth, apoptosis, and other cellular and organismal functions. Previous research has shown that a global knockout of LCMT-1 results in defects in fetal hematopoiesis. From studying a different mouse model with a pan-hematopoietic conditional knockout of LCMT-1, it has been shown that deletion of LCMT-1 from hematopoietic cells results in various phenotypical changes and disorders, such as hyperactive T-cells, a swollen spleen, and an apparent invasion of immune cells to the lungs, suggesting a possible link between LCMT-1 and autoimmune disorders. This research builds on previous findings and investigates the effect of LCMT-1 conditional pan-hematopoietic knockout on monocytes, an important class of leukocytes involved in immune response.

Using flow cytometry, we stained splenocytes in LCMT-1 knockout and control mice with external and internal phosphoantibodies to determine differences in cell-type proportions and phosphorylation activation levels. CD11b (Mac-1) and Gr-1 are antibody markers for various types of monocytes and granulocytes. We find that the proportions of CD11b+ cells among all splenocytes are statistically different for knockout and control mice (p<0.001,n=24,t=7.50). Furthermore, the proportions of all CD11b+ cells that are Gr-1+ (p<0.001,n=24,t=4.75) or Gr-1- (p<0.001,n=24,t=9.74) are also statistically different. These results suggest that LCMT-1 has a significant effect on different types of monocytes, and further research can be performed to distinguish between the effects on different monocytes.

Preliminary results also suggest that the internal phosphorylation of activation sites at various proteins (including MEK, S6, and ERK) are different; further experimentation can demonstrate whether these differences are significant, which would imply that certain pathways are more activated in LCMT-1 knockout mice. These results could begin to explain the physiological effects of LCMT-1 knockout, with implications towards understanding how LCMT-1 and PP2A pathways influence various medical disorders.

Research Discipline: Biomedical Sciences
Presentation Type: Poster Presentation

Session: 7 F
Presentation/Poster Number: 24
Presentation Time: 3:00 PM to 3:50 PM
Presentation Link: https://spatial.chat/s/EmorySummerSymposium