The Midstates Consortium for Math and Science presents

Undergraduate Research Symposium

Biological Sciences and Psychology

November 1-2, 2024
University of Chicago

Beloit College - Carthage College - Colorado College
Grinnell College - Gustavus Adolphus College - Hope College
Knox College - Lawrence University - Macalester College
St.Olaf College - University of Chicago
Washington University in St. Louis

Midstates Consortium for Math and Science Undergraduate Research Symposium for the Biological Sciences and Psychology at the University of Chicago		
November 1-2, 2024		
	Program Schedule	
Friday, November 1		
1:00 – 4:00 pm	Registration at Hyatt Place 5225 S Harper Ave, Chicago, IL 60615	Hyatt Place Lobby
3:45 - 4:15 pm	Shuttles to University of Chicago campus	Hyatt Place Lobby
4:30 - 5:25 pm	Graduate Student Panel How to Apply to Grad School Life in Grad School	Biological Sciences Learning Center (BSLC) 115
5:30 pm – 5:40 pm	WELCOME Navneet Bhasin Senior Instructional Professor Biological Sciences Collegiate Division University of Chicago Pamela Kittelson, Director Midstates Consortium for Math and Science Professor, Biology Gustavus Adolphus College	Biological Sciences Learning Center (BSLC) 115
5:40 pm – 6:30 pm	KEYNOTE LECTURE Nicholas Hatsopoulos **Wired Minds: The Age of Brain-Computer Interaction** Professor, University of Chicago	BSLC 115
6:40 pm – 7:45 pm	Dinner Buffet	Gordon Center for Integrative Science (GCIS) Atrium
8:00 pm – 8:40 pm	JANET ANDERSON AWARD LECTURE Shane Heschel **Living with an invasive species in riparian systems of the Southwest – *Tamarix*** Professor, Colorado College	BSLC 115
Following lecture	Group Picture and shuttles back to hotel	

Saturday, November 5		
Begins at 7:00 am; avoid the 7:45 rush	Breakfast and coffee Check out; bring luggage There will be a secure room for luggage and posters at the meeting; no coffee at the meeting until 10:15	Hyatt Place Lobby
8:15 - 8:30 am	Vans and shuttles depart for University of Chicago Those with vans or cars will drive to campus Others will take the shuttle	Hyatt Place Lobby
8:30-9:00 am	Set-up for poster session 1 Check set-up and load Session I oral presentations	Gordon Center for Integrative Science (GCIS) Atrium
9:00 – 10:15 am	Session 1 Poster Presentations (n=21)	GCIS Atrium
10:15 – 10:30 am	Break. Remove posters Check set-up and load Session I oral presentations	Coffee & tea in Atrium
10:30 -11:30 am	Session I Oral Presentations	Kersten
	Session I.A: Moderator: Kim Kandl	Room 101
	Session I.B: Moderator: Tawnya Cary	Room 103
	Session I.C: Moderator: Anthony Smith	Room 105
	Session I.D:Moderator: Naomi Rushing	Room 120
11:30 am - 12:30 pm	Lunch	Baker Dining Hall
12:30 – 12:45 pm	Set-up posters for Session 2 Check set-up and load Session II oral presentations	GCIS Atrium
12:45 – 2:00 pm	Session 2 Poster Presentations (n=21)	GCIS Atrium
2:00 – 2:15 pm	Break. Remove posters. Check set-up and load Session II oral presentations	Coffee & tea in Atrium
2:15 – 3:15 pm	Session II Oral Presentations	Kersten
	Session II.E: Moderator: Vince Eckhart	Room 101
	Session II.F: Moderator: Pamela Kittelson	Room 103
	Session II.G: Moderator: Navneet Bhasin	Room 105
3:15 -3:30 pm	Break. Set-up for Poster Session 3	GCIS Atrium
3:30 – 4:45 pm	Session 3 Poster Presentations (n=22)	GCIS Atrium
4:45 – 5:00 pm	Meeting Concludes. Remove posters Take boxed dinners to go. Depart Complete online evaluations	GCIS Atrium

2024 Keynote Lecture

Wired Minds: The Age of Brain-Computer Interaction

Dr. Nicholas Hatsopoulos
Professor of Organismal Biology and Anatomy
Professor of Neuroscience Institute
University of Chicago

Abstract: A fundamental challenge in developing useful brain machine interfaces (BMIs) is to augment BMIs with kinesthetic and tactile feedback. We have attempted to provide kinesthetic feedback by using cortically-controlled exoskeletal robots to provide naturalistic kinesthetic feedback. This approach could be practical for subjects with residual sensation which is common in spinal cord-injured patients. To provide tactile feedback, we are using electrical stimulation of somatosensory cortex (S1) to deliver artificial tactile feedback. While successful in providing localized tactile percepts, we have documented that electrical stimulation in S1 can disrupt BMI decoding from motor cortex due to anatomical connections between these two areas. I will present our attempt to address this challenge.

About: Nicholas G. “Nicho” Hatsopoulos, Ph.D. is currently running a laboratory with graduate students, postdoctoral fellows, and technicians, funded in part by the National Institutes of Health.In 2001, he co-founded a company, Cyberkinetics Neurotechnology Systems, which took the basic scientific research he and his colleagues conducted to develop neural prosthesis technology to assist people with severe motor disabilities.His research focuses on the neural basis of motor control and learning. He is investigating what features of motor behavior are encoded and how this information is represented in the collective activity of neuronal ensembles in the motor cortex. Dr. Hatsopoulos earned a B.A. in Physics from Williams College, M.S. in Psychology and a Ph.D. in Cognitive Science from Brown University. Dr. Hatsopoulos completed two postdoctoral research fellowships, one in the Department of Neuroscience at Brown University and the other in the Computational Neuroscience Program at the California Institute of Technology.

2024 Janet Andersen Award Lecture

Living with an Invasive Species in Riparian Systems of the Southwest – *Tamarix*

Dr. Shane Heschel
Professor of Organismal Biology and Ecology (OBE)
Colorado College

Abstract: Whether plants can adapt to a commonly experienced stress such as drought is a matter of contention. Species may tolerate drought without adapting to it. Moreover, drought response traits are notoriously interconnected and tradeoffs with growth can limit adaptability. One approach to better understand the adaptive nature of drought response traits is to examine physiological traits such as photosynthesis and transpiration. An evolutionary response at the physiological level could have sweeping effects on fecundity and viability. Over the past 18 years, Colorado College students and I have been exploring the nature of stress adaptability in plants. We have documented genetic differences in drought- response plasticity for model populations like *Impatiens capensis* and *Arabidopsis thaliana*. Our work also has focused on drought response physiology of invasive species of the Southwest. Invasive species can have a profound impact on plant communities by altering the local environment or by out-competing local taxa. The invasive, *Tamarix ramosissima*, a deciduous shrub native to southeastern Europe and Asia, has caused massive morphological changes to riparian ecosystems and their bank structures over the last century throughout the southwestern U.S. My students and I have conducted studies (the focus of this presentation) to analyze *Tamarix* water-use efficiency, stomatal conductance, and photosynthetic rates in various environmental conditions to understand the impact of drought and light stress on this species' fitness. With an ecophysiological lens, my students and I have provided data to assist with the management of this invasive species.

About Professor Heschel: The nomination letter for Dr. Heschel cited his accessibility as a teacher – his enthusiasm for biology, especially the green organisms that make life on this planet possible, his sense of humor and capacity to explain complex concepts in an understandable way. The letter lauded the collaborations he fosters with peers and undergraduates, which have resulted in 36 papers and many presentations. Our speaker also avidly supports undergraduate research students by being a frequent faculty chaperone to the Midstates symposia. Dr. Shane Heschel is a Professor from Colorado College, his lab investigates how plant physiological traits may evolve to local conditions or stressful environments like drought– the subject of tonight's lecture. Shane also helps manage the Carter Herbarium on CC's campus. Dr. Heschel earned his Ph.D. from Brown University, his B.S. and M.S. degrees from the University of Illinois, Urbana- Champaign. In his spare time, he hikes, plays blues guitar or watches baseball while indulging in pie and cheese.

About the Janet Andersen Award Lecture: Professor Janet Andersen was a beloved faculty member in the Hope College Mathematics Department and served as the Midstates Consortium Director for five years before her life ended tragically in an automobile accident in 2005. As a teacher and scholar, Janet was devoted to providing creative, high quality learning experiences for her students, and she was always learning as she was teaching. As Consortium Director, she looked for ways to connect with and support natural science faculty, both new and experienced. To honor Janet's work in her teaching, research and service to the Consortium, the Janet Andersen Lecture Award was established in 2008. Each year, nominees from the Consortium are selected by the Executive Committee to present the Janet Andersen Lecture at the fall Undergraduate Research Symposia on a topic of his or her expertise.

WiFi: Campus visitors can access the University of Chicago's wireless network by selecting the uchicago-guest network from a wireless device. Enter the username: MURS-wifi@uchicago.edu and password: **dpr8m.** If a sponsor's name is needed, it is **rcarter**

Oral Session I Schedule

SESSION I.A: 10:30-11:30 a.m. Room: Kersten 101 Moderator: Kim Kandl			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.A.1	Lowell Finster	Washington University in St. Louis	Determining the Role of RUNX1 in Driving Mesenchymal Features in Early-Stage Melanoma
I.A.2	Ana Welge	St. Olaf College	Using Tumor-Specific Transposable-Element-Chimeric Antigens (TS-TEAs) to Initiate an Anti-Cancer Immune Response
I.A.3	Lara Bencsics	University of Chicago	Modulation of mTORC1 and Lipid Metabolism by BNIP3 in HCC.
I.A.4	Zoe Zizzo	Colorado College	Characterization of Extracellular Vesicles from Human Chordoma Cell Lines and their Impact on Recipient Cells

SESSION I.B: 10:30-11:30 a.m. Room: Kersten 103 Moderator: Tawnya Cary			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.B.1	Unitas Vang	Macalester College	First Report of Cave-Adapted Mite-Harvesters (Arachnida, Opiliones, Cyphophthalmi) from Aotearoa New Zealand
I.B.2	Maddie Chaplin	Gustavus Adolphus College	Induction of Rapid Cold-Hardening in *Drosophila melanogaster* by Ecologically-Relevant Diurnal Temperature Fluctuations: Is It Promoted by Transcriptomic Changes?
I.B.3	Alekya Dantam	Washington University in St. Louis	Impact of Early to Mid-Gestational Testosterone Excess on Maternal Cardiometabolic Outcomes in Late Gestation
I.B.4	Satirtha Saha Protya	Beloit College	Alterations in Neuropeptide Distribution in Blue Crab, *Callinectes sapidus,* Under Hypoxia

SESSION I.C: 10:30-11:30 a.m. Room: Kersten 105 Moderator: Anthony Smith			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.C.1	Nathan Lin	Washington University in St. Louis	Investigating the Differential Roles of ClpXP in Classical and Hypervirulent *Klebsiella pneumoniae*
I.C.2	Manu Redah	Lawrence University	Development of a Novel PCR Assay for Detecting Enterovirus D68
I.C.3	Cameron Lian	Grinnell College	Mitotic Regulation by Tricellulin at Tricellular Tight Junctions (tTJs)
I.C.4	Kashi Bhagat	University of Chicago	Opposing Mechanisms of lncRNA Glacier Mediate Neighboring Gene Expression

SESSION I.D: 10:30-11:30 a.m. Room: Kersten 120 Moderator: Naomi Rushing			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
I.D.1	Lina Mo and Matias O'Hara	Hope College	Identifying Factors Affecting College Students' Perceptions of Differently Accented English Language Audio Clips
I.D.2	Jean Pateman	Macalester College	The Impact of Prenatal Alcohol Exposure on Addiction Behavior in Young Adults and Dams
I.D.3	Ahmad Ayyeh	Grinnell College	Effects of Rock Climbing and Running on General Mood, Arousal, and Anxiety levels
I.D.4	Cara Conforti	Washington University in St. Louis	Enhanced Behavioral Feedback: A Novel Synchronization Engineering Technique Reveals Photoperiod-Dependent Organization of the Mouse Circadian System

Oral Session II Schedule

SESSION II.E: 2:15 – 3:15 p.m. Room: Kersten 101 Moderator: Vince Eckhart			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.E.1	Shae Johnston	Hope College	Impacts of Air Pollution on the Auditory Physiology of House Sparrows (*Passer domesticus*)
II.E.2	Ava Vaccarella	Knox College	Have Microplastics Made Their Way to Green Oaks?
II.E.3	Vu-Anh Le	Beloit College	Assessing the Site Closure Time Frame for Soil and Groundwater Contaminated Sites
II.E.4	August Angulo	University of Chicago	The Role of Histotripsy-Induced Hemolysis in Terms of Platelet Aggregation

SESSION II.F: 2:15 – 3:15 p.m. Room: Kersten 103 Moderator: Pamela Kittelson			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.F.1	Kent Schechter	University of Chicago	Novel Cancer Cell-Specific Stress Signature Predicts Poor Prognosis and Highlights Racial Disparities in Breast Cancer
II.F.2	Grace Matsumoto	Washington University in St. Louis	Age-related Differences in Acute Kidney Injury Pathogenesis
II.F.3	Autumn Kim	Washington University in St. Louis	Chondrocyte Volume in Cartilage Pericellular Matrix as a Potential Early Sign of Osteoarthritis
II.F.4	Ava Doty	Hope College	Origins of the Milk Microbiome Pre-colostral to Mature Milk: A Feasibility Study

SESSION II.G:2:15 – 3:15 p.m. Room: Kersten 105 Moderator: Navneet Bhasin			
Session #	**Presenter Name**	**Institution**	**Title of Presentation**
II.G.1	Naeun Kim	Knox College	A comparative Analysis of Jaw Kinematics of Rats, Pigs, and Monkeys
II.G.2	Alyssa Stringer	Knox College	On the Clinical Relevance of Animal Variation
II.G.3	Julia Mastracci	University of Chicago	Characterizing *C. elegans* Actin Cytoskeletal Dynamics
II.G.4	Prithi Srinivasan	University of Chicago	Investigating the Mechanism of Actin Transport into the Nucleus by Importin 9

Poster Sessions Schedule

Poster Session P1: 9:00 – 10:15 a.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.01	Halla Elmore	Washington University in St. Louis	Chronic Intermittent Sleep Deprivation Drives Supercompensation in Sleep's Restorative Impact on Neural Circuit Function
P1.02	Rahaf Qarabsa	St. Olaf College	REM Sleep without Atonia Levels in Community Dwelling Adults in the Rochester Epidemiology Project
P1.03	Reyna Ngu	University of Chicago	Evaluating the Impact of the I-SLEEP Intervention on Memory and Sleep Quality in Hospitalized Patients
P1.04	Ram Guruprasad	Macalester College	Subcortical Sensitivity to Facial Identity but not Facial Expression in Humans
P1.05	Lauren Rocheford	Gustavus Adolphus College	Evaluation of Sexual Function in Spinal Cord Injury Patients in the Epidural Stimulation after Neurological Damage (ESTAND) Study
P1.06	Pierce Hoenigman	University of Chicago	Elucidating the Protein Design Space Using Variational Autoencoders
P1.07	Fuxuan Liu	Macalester College	Engineering Dye-Decolorizing Peroxidase Activity into an Artificial LmrR-hemin Enzyme
P1.08	Peter Zhao	Grinnell College	Single-Cell Encapsulation Using Flipchip Design and Surface Tension-Induced Droplet Formation
P1.09	Xingchen Liu	Carthage College	Force-Time and Velocity Differences between Ballistic Partial Squats and Ballistic Partial Step-Ups
P1.10	Elinor Parry	Gustavus Adolphus College	Meaning-Making Strategies in Emerging Adult Narratives of a Federal Election
P1.11	Jocelyn Cottrell	Macalester College	Predictors of Follow-Up Survey Non-response in a Longitudinal Study of National Guard Soldiers
P1.12	Helena Wu	University of Chicago	Change in Screen Time and Overuse: Psychological Well-being among US-Wide Children during Pandemic Years 2018–2021
P1.13	Chisom Okogbue	Hope College	The Impact of Iron Oxide Nanoparticle Exposure on Bioaccumulation in House Sparrows (*Passer domesticus*)
P1.14	Liam Hanlon	Hope College	Antipredator Behavior Changes in House Sparrows Exposed to Iron Oxide Nanoparticles
P1.15	Jill Coleman	Colorado College	*Tamarix ramossisma* ABA sensitivity at Fountain Creek, CO

Poster Session P1: 9:00 – 10:15 a.m. - Continued			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P1.16	Cecelia Kivell and Olivia Chapman	St. Olaf College	Prairie Restoration in a Changing Climate
P1.17	Emily Mathew	Hope College	Comparison of Experimental and Predicted Carbon Utilization of Escherichia coli from a Hypereutrophic Watershed
P1.18	Tisya Goel	Knox College	Comparison of Soil in the Agroforestry Region and the Forest at Finca Las Piedras
P1.19	Rachel Lester	Gustavus Adolphus College	Impact of Northern Wild Rice (Manoomin, *Ziziana palustris*) Site History on Soil Nutrient Composition
P1.20	Riley Kadis	Colorado College	Characterizing the Soil Microbiome of Invasive Halophytes in Disturbed and Non-Disturbed Sites
P1.21	Alexander Puch and Eric Zhai	University of Chicago	High Throughput Isolation and Identification of Soil Microbiota

Poster Session P2: 12:45 - 2:00 p.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.01	Damanpreet Khaira and Grace Krueger	Carthage College	Genome Analysis of a Novel Genus of Bacteria
P2.02	Meena Kim	Colorado College	Long-Read Genome Assembly and Identification of Heterochromatin in the Yeast *Ogataea angusta*
P2.03	Yannik Leuz	University of Chicago	Structural Characterization of PEX19 by NMR
P2.04	Brendon Wang	Washington University in St. Louis	Crystal Structure of Glutamate-1-Semialdehyde 2,1-Aminomutase from *Stenotrophomonas maltophilia* K279a in Complex with PLP
P2.05	Ian Knowles	St. Olaf College	Purification of Predicted Tetrahymena Lipase Protein TTherm_00013720
P2.06	Alexander Johnson	Gustavus Adolphus College	Isolation and Purification of MS2-MBP for Investigating sRNA Hierarchical Regulation of mRNA in *Escherichia coli*
P2.07	Karen Wong	University of Chicago	Defining the Interaction Between the ZAP70 Proline-Rich Motif and Lck.
P2.08	Emma Clift	St. Olaf College	Faster Detection of Microsatellite Instability in Cancer Transcriptomics Using K-mer Methods
P2.09	Reeshi Bhattacharjee	Lawrence University	Development of a Universal Prokaryotic Expression and purification System for Human Ribonuclease Inhibitor (RNH1)
P2.10	Taylor Elliott	University of Chicago	Polyelectrolyte Complex Micelles for the Targeted Delivery of Aptamers to Inhibit TXNDC5 and Treat Atherosclerosis
P2.11	Gabriel Seaver	Hope College	Using Molecular Dynamics to Determine the Mechanism of Chloride Dependence in System xC-
P2.12	Lydia Osborn	University of Chicago	Quantifying Modifications to Lysozyme Structure and Function after High and Low Dose Rate Irradiation
P2.13	Veronica Torres-Bermudez	St. Olaf College	Epigenetic Acetylation of Histone3Lysine9 (H3K9ac) Promotes Hepatic Stellate Cell Activation
P2.14	Sophie Juethner and Kelly Paek	Grinnell College	Role of Tricellulin and Cdk1 in Spindle Orientation and Mitotic Progression in *Xenopus laevis* Epithelium
P2.15	Chris Lohmeier	Macalester College	Cell-Specific Removal of Perineuronal Nets in Mouse Olfactory Bulb Using a Novel Modified Adeno-Associated Virus

Poster Session P2: 12:45 - 2:00 p.m. - Continued			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P2.16	Alexander von Kumberg	University of Chicago	4-NQO Induced Mouse Tongue Epidermal Organoid Transformation as a Model for Oral Squamous Cell Carcinoma
P2.17	Laura Sullivan	Macalester College	Central Sensitization in a Mouse Model of Chronic Vulvar Pain
P2.18	Amelia Butler and Joe Ream	Gustavus Adolphus College	Bacterial Regulation & sRNA Gene Expression in Escherichia Coli
P2.19	Elizabeth McArthur	Lawrence University	G Protein Coupling Selectivity in Parathyroid Hormone 1 Receptor
P2.20	Brian Chen	University of Chicago	Gene Editing in *Staphylococcus aureus* for Deletion of Colonization Factors
P2.21	Tim Sun	University of Chicago	Connection Between Ribosome Biogenesis and the Heat Shock Response

Poster Session P3: 3:30- 4:45 p.m. Room: GCIS Atrium			
Poster #	**Presenter Name**	**Institution**	**Title of Presentation**
P3.01	Michael LaPorte and Jacob Caballero	Hope College	Leaves or Not Leaves: Differentially Expressed Genes in Leafy Structures of *Tilia americana* (Malvaceae)
P3.02	Irene Wang	Washington University in St. Louis	The Role of Transposable Element-Derived Promoters in Tissue-Specific Gene Expression and Phenotype in Zebrafish Testis
P3.03	Kaia Meyer	Gustavus Adolphus College	Histological analysis of the U11-Null Growth Plate Reveals Contributions of Defective Chondrocyte Proliferation to Micromelia
P3.04	Annabelle Swenson	Colorado College	*Acinetobacter baylyi* Biofilm Formation Assay for Type IV Pili Mutants
P3.05	Monica Gould	University of Chicago	Epigenetic Signatures in Placental Tissues are Associated with in Utero Environments
P3.06	Shreya Chilukuri	Washington University in St. Louis	Evaluating the Role of Neonatal Murine Roseolovirus (MRV) Infection in Systemic Lupus Erythematosus After TLR Stimulation
P3.07	Gloria Adeola	University of Chicago	Insulin Resistance in Hypercalciuric Calcium Kidney Stone Patients
P3.08	Grace McFarlane	Gustavus Adolphus College	Therapy-Induced Senescence in ERα+ Breast Cancer
P3.09	Juliana Geronazzo and Abby Heimerl	Colorado College	Assessing *Drosophila melanogaster* as a Model Organism for Fatty Acid Oxidation Disorders
P3.10	Tamara Dandreamatteo	Washington University in St. Louis	Targeting the Hematopoietic Niche to Treat Rett Syndrome
P3.11	Kassidy Thomas	Gustavus Adolphus College	Impact of Ploidy on Antifungal Drug Resistance
P3.12	Aurora Ferrell	University of Chicago	Mapping the Evolutionary Trajectory of Dendritic Complexity in Cerebellar Purkinje Neurons
P3.13	Siem Tsegay	Macalester College	Effect of the Gut Microbiome on the Adolescent Brain
P3.14	Elizabeth Clarkson, Saniya Kelkar and Nikki Ware	Grinnell College	Now You See it... Now What's the Pattern? Developing a New Task to Study Statistical Learning
P3.15	Richie Ogura	Knox College	Influence of Absolute or Relative Math Exam Score on Self-Efficacy

Poster Session P3: 3:30 - 4:45 p.m. - Continued			
P3.16	Noah Parker	Lawrence University	Preliminary Results of a Mindfulness Meditation Mobile App Intervention for Adolescents Awaiting Mental Health Treatment
P3.17	Mai Hasegawa	Knox College	The Role of Positive Feedback when Japanese Elementary School Children Engage in "Acts of Kindness" Intervention
P3.18	Sophia Schultz	Lawrence University	Inclusive Revision of the Brief Multidimensional Measure of Religiousness/Spirituality for Use in Health Research
P3.19	Giang Pham	Lawrence University	Utility of Child and Parent Reports of Mental Health Risk in Middle Childhood
P3.20	Wendy Wang	Washington University	Improving Retention of People with Disabilities in Clinical Trials: A Systematic Review
P3.21	Hadley Groom	University of Chicago	Decoding Mouse Posture: An Analysis of Behavioral Syllables with Keypoint-MoSeq
P3.22	Emily Xu	University of Chicago	Differentiating Healthy Aging, Early, and Intermediate Age-Related Macular Degeneration via Retinal Thickness in Optical Coherence Tomography - ALSTAR2 Baseline

Abstracts
Biological Sciences and Psychology
MCMS Undergraduate Research Symposium, University of Chicago
November 1-2 2024

All abstracts (poster and oral) are listed alphabetically by presenter last name.

Presenter(s): Adeola, Gloria
School: University of Chicago
Session: P3.07
Title: Insulin Resistance in Hypercalciuric Calcium Kidney Stone Patients
Co-Author(s): Megan Prochaska, Noah Vetter, Raghavendra G Mirmira, Fredric Coe, Elaine Worcester
Advisor(s): Megan Prochaska

Abstract: While current research does suggest that diabetic patients are at a higher risk of developing kidney stones, there is a gap in knowledge on the theorized predisposition for calcium kidney stone formers to develop diabetes. Thus, we analyzed key metabolic markers in the serum and urine samples of 42 calcium kidney stone formers against 27 healthy matched controls. Stone formers were characterized by type of stone formation and the presence of idiopathic hypercalciuria with no other medical conditions; ineligible patients were excluded using a sensitivity analysis. Sample collection began with study participants arriving at the clinical research center in a fasting state, after which they were periodically fed prepared meals and had samples taken to obtain raw data on glucose metabolism and insulin resistance for both fasted and fed indices. The results of multivariate linear models showed that stone formers had higher fasting serum insulin values (24 (3 to 46pmol/L), p=0.03), higher fed serum glucose values (10 (2 to 18mg/dL), p=0.01), and higher homeostatic model of insulin resistance (HOMA-IR) values (1.0 (0.2 to 1.8), p=0.02). Fed serum insulin, C-peptide, glucagon like peptide-1, and glucagon values were similar across groups, and HOMA-IR analysis showed no differences in urine composition.

Presenter(s): Angulo, August
School: University of Chicago
Session: II.E.4
Title: The Role of Histotripsy-Induced Hemolysis in Terms of Platelet Aggregation
Co-Author(s): Leonora Rodriguez, Erik Saucedo, Kenneth B. Bader
Advisor(s): Kenneth B. Bader

Abstract: Histotripsy is a focused ultrasound therapy that relies on the mechanical action of bubble clouds for noninvasive tissue ablation. It is a technique that can be clinically beneficial due to its ability to treat deep vein thrombosis and tumors. Studies suggested extended exposure of the vasculature may create prothrombotic conditions. In this paper, we will investigate histotripsy-induced hemolysis as a potential mechanism for platelet activation and aggregometry. During investigation, we established a protocol that effectively separates plasma from whole blood. We have also found a difference in platelet functionality based on given data.

Presenter(s): Ayyeh, Ahmad
School: Grinnell College
Session: I.D.3
Title: Effects of Rock Climbing and Running on General Mood, Arousal, and Anxiety Levels
Co-Author(s):
Advisor(s): Elizabeth Queathem

Abstract: Effects of top rope and bouldering rock climbing on general mood, arousal, and anxiety levels were examined and compared to those of indoor running. Participants were asked to assess their general mood, arousal, and anxiety levels before and after a 30-minute exercise session, with half of them rock climbing and the other half running. Rock climbing significantly increased arousal levels relative to running, while rock climbing also had a trend of improvement in general mood and anxiety levels. Further studies are needed to better understand the meaning behind the heightened arousal levels in rock climbers.

Presenter(s): Bencsics, Lara
School: University of Chicago
Session: I.A.3
Title: Modulation of mTORC1 and Lipid Metabolism by BNIP3 in HCC
Co-Author(s): Althea Bock-Hughes, Hardik Shah, Niamh Whalley, Kay Macleod
Advisor(s): Kay Macleod
Abstract: Hepatocellular Carcinoma (HCC) is a growing health concern. Poor nutrition and diet have led to increasing rates of obesity and HCC diagnoses worldwide. BNIP3 (BCL-Interacting Protein 3) is a mitochondrial cargo receptor that promotes mitophagy in response to stress. Loss of BNIP3 causes lipid accumulation in HCC tumor cells but the mechanism explaining how BNIP3 loss causes lipid accumulation is not understood. BNIP3 binds to Rheb GTPase and modulates mTORC1 signaling, a central regulator of cellular responses to nutrient availability, promoting cell growth by stimulating lipid synthesis and trafficking. We hypothesize that loss of BNIP3 stimulates mTORC1 due to the de-repression of Rheb contributing to lipid accumulation, altered cell size, and enhanced growth. I examine mTORC1 activity via western blot, quantifying mitochondria, and lipid droplets via immunofluorescence, and perform lipidomic analysis of human HepG2 cells, WT, and CRISPR/Cas9 deleted for BNIP3 in the presence or absence of oxygen and/or Torin (mTORC1 inhibitor). I harness flow cytometry to determine if mTORC1 activity and lipid profile explain changes in cell size when BNIP3 is lost. This novel mechanistic insight into the relationship between BNIP3 and mTORC1 is relevant to understanding how diet contributes to the incidence and progression of HCC.

Presenter(s): Bhagat, Kashi
School: University of Chicago
Session: I.C.4
Title: Opposing Mechanisms of lncRNA Glacier Mediate Neighboring Gene Expression
Co-Author(s): Gabriela Haddad
Advisor(s): Alexander J. Ruthenburg
Abstract: Transcription factors selectively bind regions of the genome, which make them extremely important regulators of cell identity. In the cardiomyocyte systems, surprisingly, transcription factors mainly bind non-coding regions of the genome, which may generate ncRNA. I focus on one long non-coding transcript dependent on transcription factor Tbx5, henceforth referred to as Glacier. The Glacier locus has been shown to engage in

throughspace contacts with the locus of transcription factor Gata4. Furthermore, knocking down Glacier with siRNAs has reduced levels of proximal factor Gata4, suggesting that Glacier may be promoting the transcription of Gata4. Luciferase assays conducted using the promoter region of Glacier have shown evidence to the contrary, as tethering the first part of Glacier (involving regions that are in contact with Gata4's locus) results in significantly reduced downstream gene expression. To look at potential trans mechanisms of regulation, we expressed Glacier under a strong promoter, which resulted in no change to the levels of Gata4. Further investigation of the trans mechanism under a knockout condition, as well as using transient CRISPRa to overexpress the entire RNA, is necessary to further characterize the mechanism by which Glacier regulates gene expression.

Presenter(s): Bhattacharjee, Reeshi
School: Lawrence University
Session: P2.09
Title: Development of a Universal Prokaryotic Expression and purification System for Human Ribonuclease Inhibitor (RNH1)
Co-Author(s): Kimberly Dickson
Advisor(s): Kimberly Dickson

Abstract: The Human Ribonuclease Inhibitor (RNH1) is an essential mammalian protein with a complex horseshoe-shaped structure and a broad range of functions including ribonuclease (RNase) A inhibition, transcriptional and translational control, and oxidative stress responses. The structure of RNH1 features leucine-rich-repeats (LRRs) and a remarkably high portion (7%) of reduced cysteine residues, which upon oxidation leads to structural collapse. The long-term goal of this work is to construct variants of RNH1- where oxidation-sensitive cysteines are replaced by leucine, thereby enabling us to dissect the role of oxidation sensitivity from the structural stability and ribonuclease binding activity of the protein. However, a universal and function-independent expression and purification system for RNH1 does not exist due to the biochemical attributes of the RNH1 protein. My work is aimed at assessing multiple prokaryotic expression and purification systems to facilitate biochemical studies of RNH1 and its variants. I will present my work with eight different expression systems and report the theoretical and experimental efficacy of subsequent purification schemes of the RNH1 protein.

Presenter(s): Butler, Amelia and Ream, Joseph
School: Gustavus Adolphus College
Session: P2.18
Title: Bacterial Regulation & sRNA Gene Expression in Escherichia Coli
Co-Author(s): Alexander Johnson
Advisor(s): Jane Frandsen

Abstract: *Escherichia coli*, a bacteria commonly found in human intestines, relies on regulatory mechanisms, such as small RNAs (sRNAs), to maintain homeostasis. sRNAs bind with multiple messenger RNAs (mRNAs), collectively a targetome, to manipulate their expression. Because each sRNA typically regulates multiple mRNAs, there is likely a hierarchy in which the mRNAs are bound. A regulatory hierarchy has been identified for the targetome of the sRNA SgrS, which is assumed to be true for other sRNAs. Yet to be determined are which features dictate the hierarchy. Our research focuses on how the accessibility of sRNA binding sites in mRNAs affects prioritization. We are establishing a

pull-down assay to determine the order in which an sRNA binds to each target mRNA. Additionally, we are working to optimize a dual reporter assay that measures the order in which the expression of mRNA targets changes. Together, these assays will help determine if accessible mRNA is favorable in the hierarchy and if accessible mRNA initiates faster cellular changes. Ultimately, we can make informed assumptions about the function of similar cellular processes in other organisms and take steps towards influencing these processes in bacteria with small molecules to mitigate detrimental effects and encourage beneficial ones.

Presenter(s): Caballero, Jacob and LaPorte, Michael
School: Hope College
Session: P3.01
Title: Leaves or Not Leaves: Differentially Expressed Genes in Leafy Structures of *Tilia americana* (Malvaceae)
Co-Author(s): Jianhua Li, Jacob Caballero, Erik Keisling, Michael LaPorte, Emily Dougherty
Advisor(s): Jianhua Li

Abstract: Leafy structures in plants originated from the same stem cells. However, they have evolved into different shapes, sizes, textures, and colors, etc. for a specific function or functions over millions of years. The changes manifest the fundamental interactions between genes, morphology, and their environment. Therefore, studies on mechanisms causing the changes in time and space help elucidate the complex evolutionary history and will benefit the global society in food security and medicinal needs and development. In this study we use *Tilia* (Basswood) as an example to explore the differential gene expressions in the production of leaves, bud scales, and floral bracts. We documented morphological and anatomical similarities and differences among the leafy tissues through field observations and anatomical section technologies. Genes expressed in different tissues were obtained using the transcriptomics and differentially expressed genes (DEGs) were identified using a series of transcriptomic analysis programs including Trinity, RSEM, MMSEQS, and DESEQ2. The DEGs were annotated using the TAIR (The Arabidopsis Information Resource) database and the interactions were built using the STRING database online. Our results showed that both bud scales and floral bracts are much smaller than the leaves, they lack marginal teeth and stomata, and their mesophyll cells do not differentiate into spongy and palisade cells, and they may have a smaller number of cell layers. Mature bud scales and floral bracts are brown or yellowish green, while leaves are dark green. We observed the largest numbers of DEGs between bud scales and other leaf structures, implying a dramatic change and highly adaptive values for plants to evolve the protective layers against climate changes and/or herbivory. There were more spongy mesophyll-specific DEGs than the palisade-specific genes in the differentiation of leaves, bud scales, and floral bracts, consistent with previous studies. Both bud scales and floral bracts, in comparison with leaves, had more upregulated DEGs for functions such as mechanical support, anti-pathogen, anti-herbivory, and more down-regulated DEGs for growth and metabolism. In floral bracts, we have found a few highly upregulated DEGs (e.g., AP1, SEP1, TCP1, and LSH3) that are involved in floral development in flowering plants. This is consistent with the idea that floral bracts in basswood facilitate pollination due to their yellowish color, and further suggests that floral tissue boundaries in basswood may have initiated from the bracts subtending the inflorescence.

Presenter(s): Chaplin, Madeline
School: Gustavus Adolphus College
Session: I.B.2

Title: Induction of Rapid Cold-Hardening in *Drosophila melanogaster* by Ecologically-Relevant Diurnal Temperature Fluctuations: Is It Promoted by Transcriptomic Changes?
Co-Author(s):
Advisor(s): Yuta Kawarasaki

Abstract: Rapid cold-hardening (RCH) describes the ability of insects to swiftly adjust their physiological states to a changing condition. In *Drosophila melanogaster*, RCH is traditionally induced by exposure to 5ºC for 2 hours. However, gradual cooling can also induce RCH. We examined the effects of RCH by gradual cooling, and compared them against "classic" RCH and acclimation in *D. melanogaster*. Compared to a control group directly exposed to -5.4ºC for 2 hours, individuals that experienced gradual cooling from 23 to 9ºC before the same cold shock had a greatly enhanced survival rate (6.1±3.4% vs.100%); this effect was similar to "classic" RCH and acclimation. Additionally, multiple exposures to temperature cycles further enhanced the cold tolerance of flies (0% to 32.7±6.7% at -6.4ºC). Interestingly, flies exposed to 7 cycles of thermoperiodic fluctuations were still able to significantly enhance their cold tolerance with "classic" RCH (32.7±6.7 to 66±6.7% at -6.4ºC). These results suggest that RCH induction by gradual cooling might involve a different set of mechanisms than "classic" RCH induction. Consequently, I propose to analyze the transcriptomic data to compare the underlying mechanisms of RCH by gradual cooling against "classic" RCH induction and acclimation.

Presenter(s): Chapman, Olivia and Kivell, Cecelia
School: St. Olaf College
Session: P1.16
Title: Prairie Restoration in a Changing Climate
Co-Author(s): Cecelia Kivell, Naomi Rushing
Advisor(s): Naomi Rushing

Abstract: Tallgrass prairie is one of the most complex, diverse, and endangered ecosystems on the planet (U.S. National Parks Service). Over 96% of North America's tallgrass prairie has been lost; in Minnesota, less than 1% of the once abundant ecosystem remains (MN Department of Natural Resources). Though restoration efforts have increased, tallgrass prairie still exists in isolated fragments which are vulnerable to rapidly changing climatic conditions. Key to prairie plant resilience is the symbiotic relationship that exists between plant roots and the microbes living around them. We are seeking to identify techniques which could strengthen prairie restoration efforts under current and altered climatic conditions. In this study, we investigate the impact of Arbuscular Mycorrhizal Fungi (AMF) and Rhizobia microbial treatments on the fitness of partridge pea, an annual native prairie legume. We conducted this research at a restored prairie site in Southeastern Minnesota using 16 plots of approximately 10 partridge pea seedlings. We treated each plot with either AMF, rhizobia, both, or plain water as a control, and harvested seedlings after five weeks of growth. We collected fitness data throughout the growth period and took final measurements post-harvest. Ultimately, combined AMF/rhizobia inoculation improved root nodulation; subsequently, root nodulation improved plant fitness. Extreme herbivory presented a challenge for our study. Results suggest that inoculation with AMF and rhizobia may improve plant fitness under current and altered climatic conditions; therefore, the addition of inoculation could strengthen current and future prairie restoration efforts.

Presenter(s): Chen, Brian
School: University of Chicago
Session: P2.20
Title: Gene Editing in *Staphylococcus aureus* for Deletion of Colonization Factors
Co-Author(s): Yunys Perez-Betancourt
Advisor(s): Dominique Missiakas

Abstract: *Staphylococcus aureus* is a gram-positive bacterium that can persistently colonize the skin and nares of humans. Infections caused by *S. aureus* are among the deadliest of any bacteria. The development of a human vaccine has become a major priority due to the growing frequency of antibiotic resistance, however these attempts so far have seen limited success due to *S. aureus*' wide range of immune evasion factors. Our research is focused on developing a vaccine targeting S. aureus' ability to colonize the nasal cavity via the use of a colonizing mouse model. This is accomplished by deleting surface protein genes to observe their effects on colonization and adhesion both in vivo and in vitro. Our method of gene editing involves the plasmid pKOR1, a shuttle vector of *E. coli* and *S. aureus* which contains multiple antibiotic and counter selection markers. This method allows for quick generation and identification of successful *S. aureus* mutants while avoiding false positives.

Presenter(s): Chilukuri, Shreya
School: Washington University in St. Louis
Session: P3.06
Title: Evaluating the Role of Neonatal Murine Roseolovirus (MRV) Infection in Systemic Lupus Erythematosus After TLR Stimulation
Co-Author(s):
Advisor(s): Tarin Bigley

Abstract: Viruses have long been hypothesized to be a cause of autoimmune disease. Recently, Dr. Bigley's lab has shown that neonatal infection with the beta-herpesvirus, Murine Roseolovirus, (MRV) induces autoimmune disease. Specifically, neonatal MRV infection has been shown to induce autoimmune gastritis in adult mice when there is no other ongoing infection. This seems to be happening through the disruption of the development of the thymus along with a disruption in central tolerance, the process by which autoreactive T cells are removed during development in the thymus to reduce the risk of autoimmunity. These disruptions have led to an increase in autoreactive CD4+ T cells in the mice. We are studying lupus, an autoimmune disease in which the immune system attacks its own tissue and organs. To do this, we are utilizing neonatally infect MRV mice and stimulating TLR7, a protein involved in pathogen recognition and the activation of the innate immune system via R848, a synthetic agonist. We are then analyzing T and B cell responses prior to and after this stimulation and its impact on the development of lupus in the mice.

Presenter(s): Clarkson, Elizabeth; Kelkar, Saniya; Ware, Nikki; Crowe, Maile
School: Grinnell College
Session: P3.14
Title: Now You See it... Now What's the Pattern? Developing a New Task to Study Statistical Learning
Co-Author(s): Nichole Henning, Saniya Kelkar, Nikki Ware, Christopher Conway
Advisor(s): Christopher Conway

Abstract: Implicit learning is the ability to acquire new information without selective attention. Within implicit learning is statistical learning, which is the ability to perceive patterns in the environment over time. These patterns can be based on dependencies within a pattern such as nonadjacent dependencies (NAD), which are statistically reliable relationships between two items separated by intervening elements, and adjacent dependencies (AD), which have no intervening elements between items. The present study sought to develop a new task to study statistical learning in NADs versus ADs and to investigate the role of personality trait levels, musical experience, stress levels, learning disabilities, attention disorders, and multi-language ability in learning ADs and NADs. The task consisted of a familiarization phase where participants were shown sequences of visual stimuli that followed a pattern, or "grammar," followed by a testing phase where participants were shown sequences of visual stimuli and had to indicate if the sequences were familiar based on the previous pattern. The results showed some learning for predictable stimuli and some correlations between learning and individual differences, specifically correlations with the personality traits Openness to Experience and Neuroticism. Moreover, participants with learning and attention disorders tended to perform worse than those without, and there were some correlations between the level of awareness of the patterns and learning of ADs. The results suggest that some of these individual differences, like levels of personality traits, may relate to a stronger statistical learning ability and awareness and attention may be necessary for learning. Contrarily, other individual differences, like learning disabilities, may inhibit implicit learning ability. Future studies could clarify the role of individual differences in implicit learning and continue this research to better understand the level of necessity of attention in learning. This may give insight into how various skills that are thought to be learned implicitly, like language ability, are acquired.

Presenter(s): Clift, Emma
School: St. Olaf College
Session: P2.08
Title: Faster Detection of Microsatellite Instability in Cancer Transcriptomics Using K-mer Methods
Co-Author(s): Jamie Davilla
Advisor(s): Jamie Davilla

Abstract: A subset of cancers can occur from a condition called microsatellite instability (MSI-H) that results in increased insertions and deletions (indels) in repeated DNA sequences. MSI-H is used clinically for tumor detection and classification of cancer, potentially resulting in genetic counseling. Current MSI-H detection methods using genomic data are computationally intensive and take hours. A k-mer is a subsequence of size k from a genomic read. K-mer-based methods are increasingly popular and have faster processing times. Our goal is to assess microsatellite stability status in transcriptomic sequencing data leveraging k-mer methods. We designed and implemented a method using KMC by intersecting the set of k-mers from the cancer sample against a synthetic reference consisting of indels in transcriptome regions with a repeated base. We decreased the number of k-mers considered for analysis from 10^8 to 10^4, reducing the calculation time from hours to minutes. We tested our method on 10 samples with an optimal synthetic reference. The mean number of indels in MSI-H cases was 37.6 and 20 in the samples without. We present a novel method for detecting microsatellite instability in transcriptome data using k-mer techniques that take minutes while preserving accurate detection of microsatellite status.

Presenter(s): Coleman, Jill
School: Colorado College
Session: P1.15
Title: *Tamarix ramossisma* ABA sensitivity at Fountain Creek, CO
Co-Author(s): Shane Heschel
Advisor(s): Shane Heschel

Abstract: The invasive shrub *Tamarix ramosissima* poses a threat to riparian ecosystems throughout the southwestern United States. Due to its ability to establish and persist in stressful conditions, in part ascribed to its extensive and plastic root biomass allocation, Tamarix is able to outcompete native species and alter water table depths (Lovell et al. 2009; Robinson 1965; Cleverly et al. 1997). Furthermore, an understanding of water-use traits, especially in drought prone environments, is essential in understanding this plant's competitive relationships and water system impacts. Stomatal conductance, an index of water vapor loss, is a trait regulated by the plant hormone abscisic acid (ABA) (Glenn et al. 2013). Although ABA concentration has been found to increase in Tamarix as a response to water and foliar stress from a biocontrol agent (Craine et al. 2016), ABA sensitivity has never been studied in this system. To understand differentiation in Tamarix populations' water use traits based on varying growing conditions, we asked the following questions: 1) How does Tamarix population site morphology impact stomatal conductance? 2) How does ABA application impact stomatal conductance and water use efficiency (WUE)? 3) Does population growing condition impact its sensitivity to ABA?

Presenter(s): Conforti, Cara
School: Washington University in St. Louis
Session: I.D.4
Title: Enhanced Behavioral Feedback: A Novel Synchronization Engineering Technique Reveals Photoperiod-Dependent Organization of the Mouse Circadian System
Co-Author(s): Nikhil Lokesh, Erik Herzog
Advisor(s): Erik Herzog

Abstract: Circadian rhythms in rodents are orchestrated by a network of ~20,000 neurons in the primary circadian pacemaker – the Suprachiasmatic Nucleus (SCN). SCN neurons harbor endogenous molecular clocks, and synchrony among these clocks (driven by intercellular coupling) is crucial for robust circadian rhythm generation and seasonal adaptation. However, how such a large complex network of SCN cells encodes photoperiod and functionally organizes to drive coherent circadian rhythms remains largely unknown. To probe this, we developed a novel technique — Enhanced Behavioral Feedback (EBF) – inspired by concepts from synchronization engineering (a theoretical framework to modulate synchrony of large, coupled oscillator networks). EBF monitors activity levels in real-time and delivers strategic light feedback to the animal after a predetermined delay to modulate synchronization of the circadian clocks by light. Here we demonstrate that EBF reorganizes mouse circadian activity rhythms into two anti-phasic activity bouts (splitting) which consolidate to a single bout on feedback removal. We next hypothesized that if photoperiod-dependent coupling of SCN drives seasonal adaptation, splitting of circadian rhythms should be light-history dependent. We predicted that mice exposed to long days (LD18:6) would split faster than those exposed to short days (LD6:18). We observe that mice adapted to long days and short days split 91% faster than those adapted to equinox days.

These results indicate that EBF induces splitting in mice consistent with two circadian oscillators that adjust their coupling depending on their prior light history.

Presenter(s): Cottrell, Jocelyn
School: Macalester College
Session: P1.11
Title: Predictors of Follow-Up Survey Non-response in a Longitudinal Study of National Guard Soldiers
Co-Author(s): Melissa Polusny
Advisor(s): Melissa Polusny

Abstract: Loss to follow-up is a major methodological challenge for longitudinal studies, especially if there are systematic differences between survey respondents and non-respondents. Such non-response bias can lead to inaccurate conclusions. This is of special concern in military studies, as prior research has documented certain demographics (e.g. young men) predict non-response. This study aimed to identify baseline predictors of loss to follow-up in a longitudinal study of military recruits. A sample of 1082 National Guard soldiers completed computerized self-administered questionnaires and cognitive performance measures before Basic Combat Training (BCT) and were followed up at multiple time points following BCT. Baseline assessments included demographics (e.g. sex, age), psychological factors (e.g. mental health, personality), and military characteristics (e.g. AFQT score). Predictors of nonresponse to the initial post-BCT follow-up survey were identified using multivariable logistic regression. Results indicated participants who endorsed a history of past suicidal behavior were more likely to respond to follow-up, while greater rule-breaking behavior was associated with non-response. Demographics, neurocognitive performance, personality, and other mental health variables were not significantly associated with non-response. Findings from the current study can inform how missing data is handled in future analyses to obtain unbiased estimates and make accurate conclusions.

Presenter(s): Dandreamatteo, Tamara
School: Washington University in St. Louis
Session: P3.10
Title: Targeting the Hematopoietic Niche to Treat Rett Syndrome
Co-Author(s): Tamara Dandreamatteo, Jose A. Mazzitelli Perez, Sebastian Lares, Nora Abduljawad, Igor Smirnov, Jasmin Herz and Jonathan Kipnis
Advisor(s): Jose Mazzitelli Perez

Abstract: Rett syndrome is a neurodevelopmental disorder caused by mutations in the X-linked methyl-CpG binding protein (MeCP2). Rett syndrome is characterized by a regression in motor and cognitive abilities. Research has typically focused on neuronal mechanisms of disease. However, little is known about non-neuronal mechanisms. Bone marrow transplants (BMT) have been shown to slow progression of disease in MeCP2 deficient mice. However, the mechanism underlying the therapeutic benefit and possible phenotype is not well understood. By performing flow cytometry experiments on an MeCP2-deficient mouse model, we found that the hematopoietic stem cell (HSC) compartment is impaired in Rett mice. Targeted replacement of the HSC pool increases survival in Rett mice, suggesting this bone marrow phenotype is important for disease progression. Adoptive transplant experiments show that the aberrant hematopoiesis observed in Rett mice is largely driven by the MeCP2-deficient environment. Protein

expression data within the bone marrow niche stromal compartment revealed leptin receptor positive mesenchymal stromal cells (LepR+ MSC) and endothelial cells as high expressors of MeCP2. Conditional knockout of MeCP2 within these two cell types suggests endothelial cells, but not LepR+ MSCs, are contributing to the aberrant hematopoiesis phenotype. This uncovers a novel potential contributor to Rett pathogenesis.

Presenter(s): Dantam, Alekya
School: Washington University in St. Louis
Session: I.B.3
Title: Impact of Early to Mid-Gestational Testosterone Excess on Maternal Cardiometabolic Outcomes in Late Gestation
Co-Author(s): Alekya Dantam, Bashar Alkhatib, Arpita Vyas
Advisor(s): Arpita Vyas

Abstract: Cardiovascular disease contributes to over 33% of pregnancy-related deaths in the U.S. We have previously reported that gestational hyperandrogenism, a pregnancy insult, can lead to adverse postpartum cardiac outcomes in sheep. Utilizing a validated ovine model of gestational hyperandrogenism, we hypothesize that gestational testosterone (T) excess will adversely impact maternal heart during pregnancy culminating in the reported postpartum pathological cardiac remodeling. From gestation day (GD) 30-90 (full term GD147), pregnant ewes were injected with 100 mg of T intramuscularly twice weekly. On GD 120, maternal body weight (BW), left ventricles (LV) and right ventricles (RV) weights were measured, and LVs were processed for molecular analyses. Body weight and cardiac weights were unchanged in T ewes compared to C. Analysis of the amniotic fluid showed significantly increased expression of pro-inflammatory cytokines IL-8 and TNF-α and anti-inflammatory cytokine IL-10 in T ewes. At a molecular level, markers of cardiac hypertrophy p-mTOR/total mTOR protein ratio were significantly increased in T vs C, while cardiac stress markers atrial natriuretic peptide and brain natriuretic peptide were unchanged. Altogether, our preliminary data demonstrates T-induced increased amniotic pro-inflammatory milieu and increase in molecular marker of cardiac hypertrophy that could contribute to pathological cardiac remodeling in postpartum period.

Presenter(s): Doty, Ava
School: Hope College
Session: II.F.4
Title: Origins of the Milk Microbiome Pre-colostral to Mature Milk: A Feasibility Study
Co-Author(s): Brian Yurk, Lauren M. Cribbs, Aaron A. Best, Anita Esquerra-Zwiers
Advisor(s): Anita Esquerra-Zwiers

Abstract: Little is known about the colonization of human milk. The gut-mammary axis pathway proposes that bacteria are selectively transferred to the bloodstream when gastrointestinal tight junctions are altered. Analogous tight junction changes throughout pregnancy and lactation occur within mammary epithelial cells, which hypothetically transfer healthy bacteria. This study compared the changes in the HM microbiome during late pregnancy (38 weeks) through the early phases of lactation (days 2 and 10) during presumed changes in mammary tight junction permeability. The sodium and potassium concentrations of the samples were used to confirm the period of mammary epithelial development. The DNA of the microbiome was sequenced and analyzed; the three most abundant bacterial phyla over the three milk collections included Firmicutes, Proteobacteria, and Bacteriodota.

PCoA and NMDS plots illustrated distinct bacterial community groupings for the sampling times. There were no significant differences in bacterial communities by permeability. However, the PERMANOVA identified a significant difference in the bacterial communities at different sampling times, p = 0.01. This feasibility study provides evidence of a significant difference in bacterial communities during lactation stages. However, additional investigation with corresponding maternal fecal and infant oral and fecal samples will strengthen these findings.

Presenter(s): Elliott, Taylor
School: University of Chicago
Session: P2.10
Title: Polyelectrolyte Complex Micelles for the Targeted Delivery of Aptamers to Inhibit TXNDC5 and Treat Atherosclerosis
Co-Author(s): Ha Ram Kim, Kai-Chien Yang, Yun Fang
Advisor(s): Matthew V. Tirrell

Abstract: Atherosclerosis is a subset of cardiovascular disease and a leading cause of human mortality. Current therapies are suboptimal, focusing on controlling systemic and unspecific risk factors rather than targeting the regions of vessel branching or bifurcations where atherosclerotic plaques preferentially form. We present a targeted nanomedicine approach that uses polyelectrolyte complex micelles (PCMs) to efficiently target inflamed vascular endothelium for nucleic acid drug delivery. These PCMs encapsulate aptamers – synthetic nucleic acids with high binding specificity and affinity – designed to inhibit TXNDC5, an endoplasmic reticulum protein proposed to play a role in the inflammatory mechanosensing pathway. We have successfully formulated aptamer-encapsulating PCMs that are stable, monodisperse, and small in diameter. Transfection studies suggest that the PCM delivery system significantly increases aptamer uptake to endothelial cells. Ongoing studies focus on assessing the therapeutic effect of PCM-delivered aptamers in vitro utilizing a cone and plate flow system to mimic biological conditions. Aptamers have been frequently used as targeting moieties on nanocarriers but limited studies assess aptamers' therapeutic potential when delivered by nanocarriers, which are crucial for protecting small molecule drugs from degradation and rapid clearance in biological systems. Here, we integrate them to propose a targeted nanomedicine platform for atherosclerosis treatment.

Presenter(s): Elmore, Halla
School: Washington University in St. Louis
Session: P1.01
Title: Chronic Intermittent Sleep Deprivation Drives Supercompensation in Sleep's Restorative Impact on Neural Circuit Function
Co-Author(s): James N. McGregor, Zach Berriman Rozen, Samuel J. Brunwasser, Keith B. Hengen
Advisor(s): Keith Hengen

Abstract: A daily sleep deficit leaves adults at a higher risk for obesity, diabetes, cancer, and overall poorer quality of life, and continuous sleep deprivation is eventually lethal (Liew & Aung, 2021). Sleep deprivation is also known to drive impairments in several areas of neurophysiological function (Xu et al., 2024), which may lead to impaired cognition. Following intermittent sleep deprivation, animals undergo periods of sleep rebound, where the duration and depth of sleep are enhanced to compensate for the prior deficit (Borbely, 1982). Whether

this mechanism is sufficient to fully compensate for sleep-deprivation-induced perturbation of neurophysiological processing over long timescales is unknown. Here, we designed an experimental protocol for automated, chronic sleep deprivation over many days while simultaneously performing electrophysiological recordings of neural activity. We measured three properties of neural activity: slow wave oscillations, sharp-wave ripples, and critical network dynamics, all of which are associated with optimal brain function and are impaired by sleep deprivation. Our results demonstrate that the custom sleep deprivation chamber effectively deprives sleep over a long-term period. Chronic intermittent sleep deprivation (CISD) drives increased NREM delta power, increased sharp-wave ripple frequency, and nearness to criticality. These findings suggest that CISD can induce significant changes in neurophysiological activity, potentially impacting brain health and function.

Presenter(s): Ferrell, Aurora
School: University of Chicago
Session: P3.12
Title: Mapping the Evolutionary Trajectory of Dendritic Complexity in Cerebellar Purkinje Neurons
Co-Author(s): Silas E. Busch, Madison Hillegas, William Hopkins, Chet Sherwood, Christian Hansel
Advisor(s): Christian Hansel

Abstract: The cerebellum is an evolutionarily conserved brain structure often considered structurally and functionally well-defined. However, recent studies reveal substantial heterogeneity in the dendritic morphology of the cerebellum's primary cell type, the Purkinje cell (PC). This morphological variation has functional implications: PCs with multiple primary dendrites can host non-canonical climbing fiber multi-innervation, generating functionally distinct dendritic compartments. While multi-dendritic PCs are uncommon in mouse, they are nearly universal in human—is this a human-specific trait, or did it emerge gradually throughout evolution? We investigated this question using immunolabeling (calbindin) and high-resolution confocal imaging to compose the first-ever comparative analysis of PC morphology across primates (macaque, gibbon, siamang, orangutan, gorilla, chimpanzee, bonobo, and human) and non-primates (mouse, elephant). PC reconstructions revealed significant inter-species differences in dendritic size, shape, and compartmentalization, likely indicating increasingly complex cellular computation. In primates, phylogenetic proximity to humans (not allometric factors) predicts increased PC compartmentalization: dendrites ramify more proximally and horizontally, exhibiting an increasingly "poly-dendritic" morphology with 2+ dendritic compartments emerging directly from the PC soma. Distinct from primates, elephant PCs are more poly-dendritic but less horizontally oriented. We conclude that throughout evolution the cerebellum is characterized not by a canonical stereotyped anatomy, but by immense morphological—and, likely, physiological—variation.

Presenter(s): Finster, Lowell
School: Washington University in St. Louis
Session: I.A.1
Title: Determining the Role of RUNX1 in Driving Mesenchymal Features in Early-Stage Melanoma
Co-Author(s): Paola Angulo Salgado, Eva Hernando, Markus Schober
Advisor(s): Markus Schober

Abstract: Melanoma is the deadliest skin cancer due to its propensity to metastasize from early-stage tumors, attributed to its transcriptional heterogeneity. To identify molecular links between these transcriptionally distinct melanoma cell states and their metastatic potential, we analyzed tumors of a melanoma mouse model that recapitulates human disease progression with single-cell RNA-seq at different timepoints. Bioinformatic approaches for this dataset predict that a subset of melanoma cells that undergo an epithelial-to-mesenchymal transition (EMT) emerge at an early timepoint and that this phenotype is governed by expression of transcription factor RUNX1. We hypothesize that RUNX1 establishes this EMT state, granting metastatic potential for early dissemination. To address this hypothesis, I inhibited RUNX1 expression in EMT-like MM099 human melanoma cells and ectopically expressed RUNX1 in melanocytic (non-invasive) MM074 human melanoma cells. I will define changes in the RUNX1 chromatin binding patterns and transcriptional changes in these RUNX1 loss- and gain-of-function studies and link them to RUNX1-regulated gene expression changes. If RUNX1 establishes and/or maintains mesenchymal features, I expect to identify changes in EMT-related gene sets and cell proliferation, migration, and metastasis-defining functional features. Long-term, these results can help identify prognostic factors for early-stage patients and inform individuals who can benefit from adjuvant therapy.

Presenter(s): Geronazzo, Juliana and Heimerl, Abby
School: Colorado College
Session: P3.09
Title: Assessing *Drosophila melanogaster* as a Model Organism for Fatty Acid Oxidation Disorders
Co-Author(s): Abby Heimerl, Meredith Course
Advisor(s): Meredith Course

Abstract: Fatty acid oxidation disorders (FAODs) are a large category of metabolic disorders that vary in severity from asymptomatic to causing sudden infant death syndrome (SIDS). These disorders are largely understudied, and establishing a model organism is essential to understand their molecular mechanisms. CRISPR/Cas9 was used to produce *Drosophila melanogaster* with knocked out genes predicted to be the orthologs of human genes implicated in FAODs. Mcad, CG4860, and Etf-QO are Drosophila genes that are predicted to be involved in the MCAD, SCAD, and ETFQO proteins respectively. The presence of homozygous frameshift deletion mutations in Mcad and CG4860, and a heterozygous mutation in Etf-QO after CRISPR/Cas9 were confirmed through Sanger sequencing, and the metabolic profile of these mutants were analyzed through acylcarnitine analysis. The acylcarnitine profile of the Mcad knockout flies resembled that of humans with an MCAD deficiency. The profile of CG4860 knockout flies did not align with that of humans with an SCAD deficiency, and the Etf-QO profile was not significantly different from the control flies. These experiments will be continued with other genes involved in the FAO pathway to establish Drosophila as a model organism for FAODs.

Presenter(s): Goel, Tisya
School: Knox College
Session: P1.18
Title: Comparison of Soil in the Agroforestry Region and the Forest at Finca Las Piedras
Co-Author(s):
Advisor(s): Joana Duran

Abstract: Knowing the quality of soil is essential for plant growth and therefore human nutrition. The Alliance for a Sustainable Amazon is a non-profit organization in the Amazon rainforest based in Puerto Maldonado, Peru. Three major components of soil health were tested — soil texture, structure and pH. Two areas in the property were compared. One sample was taken from the forest, and another from an agroforestry region. Tests and visual assessments were conducted to quantify the ratios of sand, slit, and clay to determine the type of the soil. Baking soda and vinegar were used for an approximate pH of the soil. The agroforestry region has a slightly acidic sandy loam type of soil, with good structure. The soil in the forest is a neutral sandy clay loam type of soil, with poorer structure. This information can be used as a baseline for further tests with advanced equipment, like an analysis on the minerals present in the soil. Camera trapping, phenology of trees, handling butterfly traps, bird surveys, using QGIS and R script, off-trail navigation, reforestation of Castania, aiding PhD students with data collection are some of the other things I got the chance to do in the rainforest.

Presenter(s): Gould, Monica
School: University of Chicago
Session: P3.05
Title: Epigenetic Signatures in Placental Tissues are Associated with in Utero Environments
Co-Author(s): Emma E. Thompson, Brittney M. Snyder, James E.Gern, Christopher G. McKennan, Tina V. Hartett, Carole Ober
Advisor(s): Carole Ober

Abstract: Maternal asthma is a significant risk factor for asthma in her children, yet the mechanisms through which risk is conferred are unknown. The placenta forms the interface between the maternal environment and the fetus throughout pregnancy. We hypothesized that the effects of in utero exposures on child health outcomes are mediated through DNA methylation (DNAm) changes in the placenta. Placentas from pregnancies with and without an asthmatic mother were collected as part of the Childhood Allergy and the NeOnatal Environment study at Vanderbilt University (n=37). Paired placental cores were collected from the basal plate (maternal side) and the chorionic plate (fetal side) of each placenta. DNAm was measured at 45,227 CpG sites using the Asthma&Allergy array. An empirical Bayes approach to factor analysis defined 10 factors, or signatures. DNAm signatures were associated with maternal asthma ($p=3.68\times10-3$), child's sex ($p=9.43\times10-4$), and location (basal vs. chorionic plates) ($p=3.74\times10-8$). These results suggest that epigenetic patterning in the placenta reflects in utero exposures and differs between placenta cells from the maternal and fetal sides. We are currently analyzing RNA-sequencing data from these samples to identify gene regulatory networks associated with the DNAm signatures to provide insights into the biological processes perturbed by these exposures.

Presenter(s): Groom, Hadley
School: University of Chicago
Session: P3.21
Title: Decoding Mouse Posture: An Analysis of Behavioral Syllables with Keypoint-MoSeq
Co-Author(s): Elizabeth de Laittre, Jason MacLean
Advisor(s): Jason MacLean

Abstract: Decoding the representation of animal posture in the primary motor cortex (M1) continues to remain a challenging objective in neuroscience. Researchers have implemented

a variety of methods to track animal movements, often aiming to reduce dimensionality of keypoint data and to identify behavioral patterns that align with neural data. To address the inconsistencies in postural data extraction, we first utilized DeepLabCut, a software package for animal pose estimation. We labeled 24 key points along the mouse body, tail, and digits to accurately capture kinematic data for further computational analysis. We then applied Keypoint-MoSeq, a motion sequencing method, to capture “syllables” or motion trajectories in mice during a trained reach task. We hypothesized that fewer poses would be identified due to the repetitive nature of the task. However, our results revealed 23 distinct syllables, indicating that the mouse movements are more nuanced than expected. These findings suggest the presence of subtle postural variations with potential implications for M1 neuron activity. The next phase of this research will focus on correlating these behavioral syllables with neural activity in the primary motor cortex, which could offer insights into motor control and planned behavior.

Presenter(s): Guruprasad, Ram and Benevento Zahner, Silas
School: Macalester College
Session: P1.04
Title: Subcortical Sensitivity to Facial Identity but not Facial Expression in Humans
Co-Author(s): Silas Benevento Zahner, Ram Guruprasad, Moura Saad, Darcy Burgund
Advisor(s): Darcy Burgund

Abstract: Research on facial recognition at the cortical level has revealed a network of regions involved in facial processing. Recent studies also indicate that at the subcortical level certain brain structures play a more rudimentary role in facial perception. These subcortical structures have been shown to be more sensitive to face identities than to non-human objects. This research aimed to determine whether these face-sensitive subcortical structures are tuned solely to identity or also to facial expression. Sensitivity to facial expressions would suggest that lower-order systems are integral to processing facial expressions. To investigate this, we presented faces to the same or different eye, exposing the monocular-subcortical structures to faces with the same or different identities, each having either sad or neutral expressions. We then measured efficiency (response time divided by accuracy) at identifying these faces. Efficiency for the same identity was greatest when stimuli were presented to the same eye, indicating that monocular cells are sensitive to face identities. However, efficiency did not differ when the subsequent face had a different expression but was still the same identity. This finding implies that subcortical structures are sensitive to coarse facial information but not to differences in facial expression.

Presenter(s): Hanlon, Liam
School: Hope College
Session: P1.14
Title: Antipredator Behavior Changes in House Sparrows Exposed to Iron Oxide Nanoparticles
Co-Author(s): Shae Johnston, Chisom Okogbue, Kelly Ronald, Natalia Gonzalez-Pech
Advisor(s): Kelly Ronald

Abstract: The past 50 years have led to a significant increase in urbanization to accommodate increasing human populations which have created many environmental issues, including a decrease in North American bird populations by 29%. Loss of habitat, predation from cats, and agricultural chemicals are just some of the previously studied

causes for the observed loss, but air pollution has been neglected as a potential cause. The solid portion of air pollution is called particulate matter (PM). PM can have a diameter as small as 2.5 μm or even smaller (i.e., PM2.5). Nanoparticles within PM2.5 are small enough to bypass the blood-gas barrier, and once in the bloodstream can additionally bypass the blood-brain barrier. Once in the brain, these nanoparticles can functionally alter species-appropriate behavior. We predicted that house sparrows (*Passer domesticus*) exposed to aerosolized iron oxide nanoparticles would show less antipredator responses (e.g. scanning and fleeing) and less exploration (i.e. movement) compared to controls. These results will help shed light on the drastic decrease in bird populations and help to determine the effects that pollution has on avian species. House sparrows, in particular, may serve as a sentinel species for other downstream consequences of urbanization.

Presenter(s): Hasegawa, Mai
School: Knox College
Session: P3.17
Title: The Role of Positive Feedback when Japanese Elementary School Children Engage in "Acts of Kindness" Intervention
Co-Author(s):
Advisor(s): Heather Hoffmann

Abstract: Counting acts of kindness is one of the Positive Psychology Interventions (PPIs) that has been shown to be effective in increasing people's happiness level and fostering well-being. Previous studies have shown that in a collectivist culture such as Japan, simply being aware of one's contribution to the collective can make people happier. People may also increase their sense of well-being by helping people, especially when they can see how their help is actually making a difference. Therefore, I hypothesized that Japanese children who receive positive feedback for acts of kindness would improve their happiness level more than those who do not get feedback about their acts. I then conducted an experiment with Japanese elementary school children from grade 5 to 6. The happiness level of the participants were measured before and after the experiment. During the experimental period, the participants were asked to list three acts of kindness everyday for five days, and the participants in the experimental group received positive feedback whilst the ones in the control group did not. However, the results did not support the hypothesis and getting positive feedback did not make the intervention more effective for the Japanese children. The limitations of this study were the test-retest reliability of the well-being scale and ceiling effects. In addition, some future improvements of the experimental design were discussed.

Presenter(s): Heimerl, Abby and Geronazzo, Juliana
School: Colorado College
Session: P3.09
Title: Assessing *Drosophila melanogaster* as a Model Organism for Fatty Acid Oxidation Disorders
Co-Author(s): Juliana Geronazzo, Meredith Course
Advisor(s): Meredith Course

Abstract: Fatty acid oxidation disorders (FAODs) are a large category of metabolic disorders that vary in severity from asymptomatic to causing sudden infant death syndrome (SIDS). These disorders are largely understudied, and establishing a model organism is essential to understand their molecular mechanisms. CRISPR/Cas9 was used to produce *Drosophila*

melanogaster with knocked out genes predicted to be the orthologs of human genes implicated in FAODs. Mcad, CG4860, and Etf-QO are Drosophila genes predicted to be involved in the MCAD, SCAD, and ETFQO proteins respectively. The presence of homozygous frameshift deletion mutations in Mcad and CG4860, and a heterozygous mutation in Etf-QO after CRISPR/Cas9 were confirmed through Sanger sequencing, and the metabolic profiles of these mutants were analyzed through acylcarnitine analysis. The acylcarnitine profile of the Mcad knockout flies resembled that of humans with an MCAD deficiency. The profile of CG4860 knockout flies did not align with that of humans with an SCAD deficiency, and the Etf-QO profile was not significantly different from the control flies. These experiments will be continued with other genes involved in the FAO pathway to establish Drosophila as a model organism for FAODs.

Presenter(s): Hoenigman, Pierce
School: University of Chicago
Session: P1.06
Title: Elucidating the Protein Design Space Using Variational Autoencoders
Co-Author(s):
Advisor(s): Rama Ranganathan

Abstract: Protein design is a long-standing goal of synthetic biology and medicine, but until recently we have lacked sufficient data and computational power. Variational autoencoders are a deep learning architecture which have proven useful in learning the amino acid sequence patterns to generate novel proteins by first compressing large sequences into a low-dimensional latent space. Yet despite their ability to replicate the sequence patterns of protein families, the models are overfit to evolutionary noise and thus are not able to produce diverse proteins. Additionally, the functional properties of the protein are not well separated in the latent space, and therefore using the models for more precise protein engineering is infeasible. Statistical coupling analysis is a method which has shown great utility in disentangling the functional properties of a protein family. This project aims to connect the functional awareness of statistical coupling analysis with the generative capability of variational autoencoders to create a more diverse, interpretable, and controllable protein generative model.

Presenter(s): Johnson, Alexander
School: Gustavus Adolphus College
Session: P2.06
Title: Isolation and Purification of MS2-MBP for Investigating sRNA Hierarchical Regulation of mRNA in *Escherichia coli*
Co-Author(s):
Advisor(s): Dr. Janie Frandsen

Abstract: In the well-studied and abundant model organism *Escherichia coli*, small RNAs (sRNA) preferentially bind to and regulate target mRNAs, thus influencing the cell's gene expression. Due to the varying accessibility of sRNA binding sites in target mRNAs, we sought to investigate if that characteristic promotes a hierarchical binding tendency for sRNA. mRNA target binding site accessibility was predicted based on the amount of single-strandedness of the region found in vivo. Pull-down assays will be used to explore sRNA/mRNA binding at various time points. The isolation and purification of the marker protein MS2-MBP were necessary to facilitate such assays examining sRNA hierarchical

regulation of mRNA. Growth and competency of the BL21 cell line with select plasmids led to the induction of MS2-MBP protein, which was further isolated and purified using a nickel-affinity and a maltose-binding column. These efforts will provide insight into sRNA's overall target prioritizations, potentially correlating with mRNA binding site accessibility.

Presenter(s): Johnston, Shae
School: Hope College
Session: II.E.1
Title: Impacts of Air Pollution on the Auditory Physiology of House Sparrows (*Passer domesticus*)
Co-Author(s): Kelly Ronald, Natalia Gonzalez-Pech, Chisom Okogbue, Peyton Hallemann, Olivia Sprys-Tellner
Advisor(s): Kelly Ronald

Abstract: Urbanization has drastically increased in the past several decades; with this there has been a matching increase in air pollution. Air pollution consists of several compounds of varying sizes, but the smallest type of particle is the nanoparticle. Nanoparticles are able to bypass the blood-gas barrier and the blood-brain barrier, with one potential mechanism for this being through sensory nerves. Nonetheless, it is unknown whether exposure to nanoparticles alters hearing sensitivity directly. Songbirds are particularly unique because they have thin blood-gas barriers and are particularly sensitive to airborne contaminants. The aim of this project was to determine the impact of chronic iron oxide nanoparticle (IONP) exposure on the auditory sensitivity of the house sparrow (*Passer domesticus*). Birds were captured from locations around Holland, MI, USA. Pre-exposure auditory brainstem response (ABR) tests were performed, and then exposure to aerosolized IONPs consisted of 50 hours of exposure over 10 days. Following exposure, hearing was assessed again in a pre vs post-test design. We predicted that exposure to iron oxide nanoparticles would reduce hearing sensitivity. Changes in the ABR have the potential to disrupt the comprehension of auditory signals during communication. This communication disruption could impact the survival and fitness of urban birds.

Presenter(s): Juethner, Sophie and Paek, Suhyeon
School: Grinnell College
Session: P2.14
Title: Role of Tricellulin and Cdk1 in Spindle Orientation and Mitotic Progression in *Xenopus laevis* Epithelium
Co-Author(s): Suhyeon Paek
Advisor(s): Joshua C. Sandquist

Abstract: Proper orientation of the mitotic spindle is crucial for maintaining tissue architecture and preventing tumorigenesis during cellular division. It has not yet been discovered how information about spindle positioning is linked to how the cell progresses through mitosis. We propose that Cdk1, a cell division regulator, and tricellulin, a protein at tricellular tight junctions (tTJ), could potentially act as a signaling link that influences cell cycle regulation, as suggested by their colocalization in the *Xenopus laevis* epithelium. To investigate the potential binding of tricellulin with Cdk1, a biochemical pulldown assay using GST-tagged portions of tricellulin and extracts from *X. laevis* embryos was conducted, along with an immunoprecipitation assay using GFP-tagged tricellulin in *X. laevis* embryos. Additionally, we explored the effect of tricellulin on spindle orientation and mitotic length with

live cell imaging. So far, we have demonstrated that overexpression of full-length and truncated tricellulin disrupts the correlation between cell shape and spindle orientation, leading to randomized division axes. Furthermore, we observed a dose-dependent effect of tricellulin overexpression on the mitotic duration, suggesting its involvement in cell cycle regulation.

Presenter(s): Kadis, Riley
School: Colorado College
Session: P1.20
Title: Characterizing the Soil Microbiome of Invasive Halophytes in Disturbed and Non-Disturbed Sites
Co-Author(s):
Advisor(s): Jesus Peña

Abstract: *Tamarix* sp. of the Tamaricaceae are an invasive tree common in riparian areas across the South West United States which can outcompete native Salicaceae trees. *Tamarix* sp. are drought-adapted halophytes with the capacity to concentrate salt in their foliar tissue. At the end of a growing season, the senesced leaves contribute to increased salinity in the topsoil giving this organism an advantage over native plants. In order to examine the effect of *Tamarix* sp. on the soil microbiota we collected soil along a gradient of distance from *Tamarix* sp. trunks in areas with different disturbance history and shade aspects. Soil samples were tested for macronutrient content and salinity. Serial dilutions of the soil were used to observe culturable microbes. While fungi appeared consistent along the gradient, we found differences in bacterial community composition. Additionally we have employed ITS/16S metabarcoding to characterize the full microbial communities associated with each site.

Presenter(s): Kelkar, Saniya; Clarkson, Elizabeth; Ware, Nikki; and Crowe, Maile
School: Grinnell College
Session: P3.14
Title: Now You See it... Now What's the Pattern? Developing a New Task to Study Statistical Learning
Co-Author(s): Elizabeth Clarkson, Nichole Henning, Saniya Kelkar, Nikki Ware, Christopher Conway
Advisor(s): Professor Christopher Conway

Abstract: Implicit statistical learning is the ability to perceive patterns in the environment without intending to do so and without being consciously aware of what was learned. However, very little research has investigated what cognitive or psychological factors predict statistical learning abilities. The present study sought to develop a new task to study statistical learning of both simple and complex patterns and to investigate the role of individual differences in statistical learning ability. Participants engaged in a statistical learning task in which they responded as quickly as possible to visual stimuli that were either predictable or not based on the structure of the covert patterns. We also measured participants' personality traits, chronic stress, and other demographic variables. The results showed learning of both simple and complex patterns, with certain measures of individual differences being correlated with performance, specifically the personality traits Openness to Experience and Neuroticism. Moreover, learning and attention disorders were associated with worse performance, and awareness of the patterns related to learning. Finally, there was a

positive correlation between dwelling on stressful events scores and learning. These findings provide insight into what factors can predict and even promote the ability to implicitly learn new information.

Presenter(s): Khaira, Damanpreet and Krueger, Grace
School: Carthage College
Session: P2.01
Title: Genome Analysis of a Novel Genus of Bacteria
Co-Author(s): Grace Krueger
Advisor(s): Emily Wollmuth

Abstract: Understanding the function of bacteria from the hindgut of *Kyphosus sydneyanus*, a herbivorous fish native to Australasia, can provide further insights into the mechanisms behind the digestion of seaweed in the fish diet. Using Nanopore and Illumina sequencing data, we produced several genome assemblies to recreate and analyze the genome of a novel bacterial species isolated from the gut of *K. sydneyanus*. Our final assembly contains 3,009 genes and is 98.68% complete. To determine evolutionary relationships and relatedness of the novel bacterial species to other organisms, phylogenetic trees were developed and analyzed. Following genome assembly, the genome was annotated to predict gene functions in relation to metabolism. We also identified carbohydrate-active enzyme encoding genes potentially involved in breaking down seaweed, targeting substrates including carrageenan, beta-galactan, and cellulose, which are found in the cell walls of seaweed and other plants. This suggests the novel bacterial species is involved in breaking down brown seaweed, including the invasive seaweed *Undaria pinnatifida*, which is part of the diet of *K. sydneyanus*. This research is part of a large collaborative project which aims to use these bacteria to break down seaweed in a bioreactor to create natural fertilizers, vitamin supplements, and animal feeds.

Presenter(s): Kim, Naeun
School: Knox College
Session: II.G.1
Title: A comparative Analysis of Jaw Kinematics of Rats, Pigs, and Monkeys
Co-Author(s): Nicholas J Gidmark, Saxon Alvarez, Naeun Kim, Sonia Lopez, Emily D McParland, Rosalie Ross, Amira Siddique, and Alyssa Stringer
Advisor(s): Nicholas J Gidmark

Abstract: Temporomandibular disorders (TMD) encompass a range of conditions affecting the jaw joint, muscles, and associated structures, leading to pain and dysfunction. Different model organisms are used to study TMD due to the challenges of studying it directly in humans. This study aimed to compare jaw kinematics in rats, pigs, and monkeys, commonly used models, to assess their suitability for studying specific aspects of TMD. We employed a standardized Joint Coordinate System (JCS) for objective and direct comparison of jaw movements during the grinding phase of chewing. The findings revealed significant variations in jaw movement patterns across these species. Pigs and monkeys primarily utilized a mediolateral grinding motion, similar to the hypothesized side-to-side movement in humans. Rats, in contrast, exhibited an anterior-posterior movement for grinding. This highlights the diverse biomechanical adaptations for mastication in different mammals. Interestingly, the condylar motion did not always directly reflect jaw movement, suggesting a complex interplay

between these factors during grinding. The variability observed in rat chewing kinematics data warrants further investigation.

Presenter(s): Kim, Autumn
School: Washington University in St. Louis
Session: II.F.3
Title: Chondrocyte Volume in Cartilage Pericellular Matrix as a Potential Early Sign of Osteoarthritis
Co-Author(s): Nancy Steward, Yu Seon Kim
Advisor(s): Farshid, Guilak

Abstract: Osteoarthritis (OA) is a chronic joint disease characterized by articular cartilage degradation and inflammation, leading to pain, stiffness, and swelling. The lack of disease-modifying drugs has led to a demand for a deeper understanding of OA. One of the earliest signs of OA is the degradation and softening of the pericellular matrix (PCM), a thin layer of matrix that surrounds chondrocytes. Previous studies indicate that in situ chondrocytes exhibit increased cell volume in areas of cartilage degradation, however, the mechanism behind this increased cell volume is unclear. To investigate the relationship between PCM softening and cell volume, agarose hydrogels of varying concentrations—0.75%, 2%, and 3.25% w/v— were used to assess cellular changes. Human iPSC-derived chondrocytes were differentiated and encapsulated in the three groups. Biochemical analysis, via DNA content, measurements revealed a weak trend toward decreased matrix secretion in softer constructs. Additionally, cell volume measurements indicated significantly larger cell volumes in the 0.75% w/v group compared to the 2% and 3.25% w/v groups, suggesting a positive correlation between cell volume and PCM degradation in OA. Current experiments on exploring different cell densities and imaging techniques (e.g., DIC) are being conducted to better understand these dynamics. Developing a model representative of PCM degradation will further studies of the matrix's influence on gene expression to better understand OA.

Presenter(s): Kim, Meena
School: Colorado College
Session: P2.02
Title: Long-Read Genome Assembly and Identification of Heterochromatin in the Yeast *Ogataea angusta*
Co-Author(s): Gena Blumencwejg, Sara Hanson
Advisor(s): Sara Hanson

Abstract: Chromosome segregation is vital for the reproduction of all cells. The centromere is the binding site for the kinetochore and plays an essential role in cell division. Across budding yeast clades, centromere and heterochromatin structures have evolved over time. Following the loss of typical eukaryotic heterochromatin machinery in an early ancestor in Saccharomycotina, a transition from epigenetically-defined regional centromeres to genetically-defined point centromeres has also been observed. Yeast species that have regional centromeres but have lost typical heterochromatin mechanisms have also been shown to have altered distributions of heterochromatin, such as the CUG-Ser1 yeast *Candida lusitaneae*, which lacks pericentromeric heterochromatin. Here, we investigate the genomic distribution of heterochromatin in the distantly related Pichiaeceae yeast *Ogataea angusta* to identify whether pericentromeric heterochromatin loss is generalizable to other yeasts in this

evolutionary transition. We used RNA-seq data and an improved genome assembly to find that *O. angusta* has subtelomeric heterochromatin and lacks pericentromeric heterochromatin. These data suggest that loss of pericentromeric heterochromatin may have occurred in the common ancestor of the CUG-Ser1 and Pichiaceae yeasts. Studying centromeres and telomeres of different species can help to better understand the evolution of heterochromatin and the new mechanisms used to carry out chromosome segregation.

Presenter(s): Kivell, Cecelia and Chapman, Olivia
School: St. Olaf College
Session: P1.16
Title: Prairie Restoration in a Changing Climate
Co-Author(s): Olivia Chapman, Naomi Rushing
Advisor(s): Naomi Rushing

Abstract: Tallgrass prairie is one of the most complex, diverse, and endangered ecosystems on the planet (U.S. National Parks Service). Over 96% of North America's tallgrass prairie has been lost; in Minnesota, less than 1% of the once abundant ecosystem remains (MN Department of Natural Resources). Though restoration efforts have increased, tallgrass prairie still exists in isolated fragments which are vulnerable to rapidly changing climatic conditions. Key to prairie plant resilience is the symbiotic relationship that exists between plant roots and the microbes living in and around them. We are seeking to identify techniques which could strengthen prairie restoration efforts under current and altered climatic conditions. In this study, we investigate the impact of Arbuscular Mycorrhizal Fungi (AMF) and Rhizobia microbial treatments on the fitness of partridge pea, an annual native prairie legume. We conducted this research at a restored prairie site in Southeastern Minnesota using 16 plots of approximately 10 partridge pea seedlings. We treated each plot with either AMF, rhizobia, both, or plain water as a control, and harvested seedlings after five weeks of growth. We collected fitness data throughout the growth period and took final measurements post-harvest. Ultimately, combined AMF/rhizobia inoculation improved root nodulation; subsequently, root nodulation improved plant fitness. Extreme herbivory presented a challenge for our study. Results suggest that inoculation with AMF and rhizobia may improve plant fitness under current and altered climatic conditions; therefore, the addition of inoculation could strengthen current and future prairie restoration efforts.

Presenter(s): Knowles, Ian
School: St. Olaf College
Session: P2.05
Title: Purification of Predicted Tetrahymena Lipase Protein TTherm_00013720
Co-Author(s):
Advisor(s): Laura Listenberger

Abstract: *Tetrahymena thermophila* is a single-celled ciliated organism that has contributed to key biological discoveries such as telomerase, histone acetyltransferase, and dynein. Lipase proteins are enzymes that catalyze the hydrolysis of lipids. It is known that Lipases are critical for the survival of the cell but not much is known about individual lipases. This summer, our lab has been predicting a protein's function, designing plasmids for the predicted protein's expression, using nickel affinity chromatography to purify the protein, and performing enzyme activity assays to recognize its function. We were specifically interested in

triglyceride lipase as they will be used in further studies on the metabolic pathways in *Tetrahymena thermophila.*

Presenter(s): Krueger, Grace and Khaira, Damanpreet
School: Carthage College
Session: P2.01
Title: Genome Analysis of a Novel Genus of Bacteria
Co-Author(s): Damanpreet Khaira
Advisor(s): Emily Wollmuth

Abstract: Understanding the function of bacteria from the hindgut of *Kyphosus sydneyanus*, a herbivorous fish native to Australasia, can provide further insights into the mechanisms behind the digestion of seaweed in the fish diet. Using Nanopore and Illumina sequencing data, we produced several genome assemblies to recreate and analyze the genome of a novel bacterial species isolated from the gut of K. sydneyanus. Our final assembly contains 3,009 genes and is 98.68% complete. To determine evolutionary relationships and relatedness of the novel bacterial species to other organisms, phylogenetic trees were developed and analyzed. Following genome assembly, the genome was annotated to predict gene functions in relation to metabolism. We also identified carbohydrate-active enzyme encoding genes potentially involved in breaking down seaweed, targeting substrates including carrageenan, beta-galactan, and cellulose, which are found in the cell walls of seaweed and other plants. This suggests the novel bacterial species is involved in breaking down brown seaweed, including the invasive seaweed *Undaria pinnatifida*, which is part of the diet of *K. sydneyanus*. This research is part of a large collaborative project which aims to use these bacteria to break down seaweed in a bioreactor to create natural fertilizers, vitamin supplements, and animal feeds.

Presenter(s): LaPorte, Michael and Caballero, Jacob
School: Hope College
Session: P3.01
Title: Leaves or Not Leaves: Differentially Expressed Genes in Leafy Structures of *Tilia americana* (Malvaceae)
Co-Author(s): Jianhua Li, Jacob Caballero, Erik Keisling, Emily Dougherty
Advisor(s): Jianhua Li

Abstract: Leafy structures in plants originated from the same stem cells. However, they have evolved into different shapes, sizes, textures, and colors, etc. for a specific function or functions over millions of years. The changes manifest the fundamental interactions between genes, morphology, and their environment. Therefore, studies on mechanisms causing the changes in time and space help elucidate the complex evolutionary history and will benefit the global society in food security and medicinal needs and development. In this study we use Tilia (Basswood) as an example to explore the differential gene expressions in the production of leaves, bud scales, and floral bracts. We documented morphological and anatomical similarities and differences among the leafy tissues through field observations and anatomical section technologies. Genes expressed in different tissues were obtained using the transcriptomics and differentially expressed genes (DEGs) were identified using a series of transcriptomic analysis programs including Trinity, RSEM, MMSEQS, and DESEQ2. The DEGs were annotated using the TAIR (The Arabidopsis Information Resource) database and the interactions were built using the STRING database online. Our results showed that both

bud scales and floral bracts are much smaller than the leaves, they lack marginal teeth and stomata, and their mesophyll cells do not differentiate into spongy and palisade cells, and they may have a smaller number of cell layers. Mature bud scales and floral bracts are brown or yellowish green, while leaves are dark green. We observed the largest numbers of DEGs between bud scales and other leaf structures, implying a dramatic change and highly adaptive values for plants to evolve the protective layers against climate changes and/or herbivory. There were more spongy mesophyll-specific DEGs than the palisade-specific genes in the differentiation of leaves, bud scales, and floral bracts, consistent with previous studies. Both bud scales and floral bracts, in comparison with leaves, had more upregulated DEGs for functions such as mechanical support, anti-pathogen, anti-herbivory, and more down-regulated DEGs for growth and metabolism. In floral bracts, we have found a few highly upregulated DEGs (e.g., AP1, SEP1, TCP1, and LSH3) that are involved in floral development in flowering plants. This is consistent with the idea that floral bracts in basswood facilitate pollination due to their yellowish color, and further suggests that floral tissue boundaries in basswood may have initiated from the bracts subtending the inflorescence.

Presenter(s): Le, Vu-Anh
School: Beloit College
Session: II.E.3
Title: Assessing the Site Closure Time Frame for Soil and Groundwater Contaminated Sites
Co-Author(s): Haruko Murakami Wainwright
Advisor(s): Haruko Murakami Wainwright

Abstract: Monitored Natural Attenuation (MNA) is an increasingly recognized remidiation method for its cost-effective and minimally invasive approach to managing soil and groundwater contamination. By extending the PyLEnM machine learning framework, we developed a data-driven model to estimate the time for contaminants like Sr-90 and I-129 to reach regulatory safety standards. The study integrates linear regression, random forest regression, and an ensemble LSTM model to analyze trends in contaminant concentrations, accounting for the site's complex hydrostratigraphic units and geochemical conditions. Preliminary results indicate a significant downward trend in contaminant levels, with the maximum time to reach safety thresholds being 320 years for Sr-90 and 258 years for I-129 amongst decreasing wells. Our findings highlight the importance of specific hydrological factors, such as total depth and screen zone, in enhancing the predictability and effectiveness of MNA strategies, ensuring long-term groundwater protection. The study scope covers the Savannah River Site (SRS), a Department of Energy-owned Superfund site contaminated with radionuclides that plans to apply MNA.

Presenter(s): Lester, Rachel
School: Gustavus Adolphus College
Session: P1.19
Title: Impact of Northern Wild Rice (Manoomin, *Ziziana palustris*) Site History on Soil Nutrient Composition
Co-Author(s): Wesley A. Bickford
Advisor(s): Wesley A. Bickford

Abstract: Northern wild rice (*Zizania palustris*, manoomin) is an integral plant to the culture and livelihood of local indigenous populations, but Michigan manoomin populations have declined heavily, impacted by industrialization activities over the past 150 years. Thus,

investigations into ways to improve conservation efforts for this species are of prime importance to tribal communities. A previous growth chamber study at the USGS Great Lakes Science Center observed significant differences in manoomin germination rates based upon the soil's manoomin history. As both horizontally transferred microbiota and soil nutrient availability are important factors in successful seed germination, this follow-up study aimed to characterize the nutrient availability of each site history's soil (manoomin-naive, restored, and healthy) and determine if significant differences existed between them. We sampled six sites of each manoomin history in wetlands of northern Michigan. No significant differences were found in mean macronutrient and SOM concentrations between samples of different site histories. These data will be important in the context of manoomin microbial community data, currently in the process of being obtained at GLSC, which will allow us to verify how influential horizontal transfer of soil microbes may be to manoomin germination.

Presenter(s): Leuz, Yannik
School: University of Chicago
Session: P2.03
Title: Structural Characterization of PEX19 by NMR
Co-Author(s): Sebastian Metzler, Stefan Gaussmann, Michael Sattler
Advisor(s): Sebastian Metzler

Abstract: Peroxisomes are essential organelles for a variety of metabolic functions. They import all their enzymes from the cytosol through a highly dynamic pore formed by PEX proteins. PEX19 acts as a putative chaperone for the post-translational insertion of key pore component PEX14 into the peroxisomal membrane. PEX19 contains an N-terminal intrinsically disordered region (NTR) which is hypothesized to solubilize PEX14 by "hugging" its hydrophobic membrane span. However, the structural details remain elusive due to the flexibility of the NTR. Here, we use nuclear magnetic resonance (NMR) spectroscopy to get first molecular insights of PEX19 in solution. We purified full-length PEX19 and a middle region of the NTR, PEX19 MR, with immobilized metal ion chromatography and size exclusion chromatography, achieving high yields and purity. We acquired well resolved NMR fingerprint spectra of both constructs and determined that full-length PEX19 conformation was not concentration dependent. Additionally, when comparing spectra of full-length PEX19 with NTR subregions, we determined that there were only few chemical shift changes, suggesting that analysis via "divide and conquer" faithfully reports on the structural properties of the PEX19 NTR. Our work provides the basis for the structural analysis of full-length PEX19 through point mutations and interactions with PEX14.

Presenter(s): Lian, Cameron
School: Grinnell College
Session: I.C.3
Title: Mitotic Regulation by Tricellulin at Tricellular Tight Junctions (tTJs)
Co-Author(s): Dingyuan Hu, Kelly Paek, Joshua Sandquist
Advisor(s): Joshua Sandquist

Abstract: Anaphase in epithelia typically does not commence until mitotic spindles achieve a characteristic position and orientation, but how cells link it to anaphase onset remains unknown. Given that Wee1 inhibition, or Cdk1 activation, accelerates the metaphase-anaphase transition and that Cdk1 accumulates at tricellular tight junctions (tTJs), we hypothesized that tTJs-localized Cdk1 serves as anchors to guide proper spindle

orientation and subsequently signal anaphase onset. Unpublished data revealed that Cdk1 colocalizes with tricellulin, a MARVEL protein exclusively residing at tTJs, suggesting that tricellulin may help recruit Cdk1 to tTJs for its mitotic functions. Here, we demonstrated that perturbing tricellulin expression disrupts spindle positioning and delays the metaphase-anaphase transition using live-cell imaging on Xenopus embryonic epithelia. By expressing truncated versions of tricellulin, we identified the tricellulin-N205 fragment as the critical region responsible for its role in mitotic regulation. Additionally, fluorescence recovery after photobleaching (FRAP) analysis measured Cdk1 dynamics across different mitotic stages and showed that tricellulin perturbation affects Cdk1 localization. Our findings highlight tricellulin's central role at the spindle checkpoint by ensuring a proper spindle positioning before anaphase initiation.

Presenter(s): Lin, Nathan
School: Washington University in St. Louis
Session: I.C.1
Title: Investigating the Differential Roles of ClpXP in Classical and Hypervirulent *Klebsiella pneumoniae*
Co-Author(s):
Advisor(s): David Rosen

Abstract: *Klebsiella pneumoniae* is an opportunistic bacterium identified by the CDC as an urgent public health threat, necessitating studies on its virulence to improve therapeutic development. Utilizing a transposon-mutant library, I identified clpX, clpP, and clpXP as potential virulence genes and created knockouts in both a classical (TOP52) and hypervirulent (43816) strain of *K. pneumoniae* using a modified Red recombinase mutagenesis method. Initial growth assays showed no significant deviations, but uronic acid assays revealed that clpX and clpXP knockouts in 43816 significantly reduce capsule production, a key virulence factor. While India Ink staining was used to evaluate capsule production and morphology but results were inconclusive. An invasion assay of lung epithelial cells showed that disruption of clpX, clpP, or clpXP in 43816 significantly impairs adhesion and invasion. In addition, it showed that 43816 primarily adheres to lung epithelial cells rather than invading them. These findings suggest that these genes play a more critical role in 43816 virulence, particularly through capsule production. Future studies in animal models and other virulence factors such as fimbriae are needed to further elucidate their roles.

Presenter(s): Liu, Fuxuan
School: Macalester College
Session: P1.07
Title: Engineering Dye-Decolorizing Peroxidase Activity into an Artificial LmrR-hemin Enzyme
Co-Author(s): Liz Ortiz, Kathryn Splan
Advisor(s): Kathryn Splan

Abstract: Artificial metalloenzymes (ArMs) combine the properties of natural enzymes with catalytically active, abiological metal cofactors. ArMs enable “new-to-nature” reactions, offering sustainable chemical synthesis. Designing ArMs involves two key factors: substrate binding to the protein scaffold and incorporation of the transition metal complex. The scaffold must stabilize the transition state and accommodate both the substrate and metal cofactor. Roelfes et al. identified lactococcal multidrug resistance regulator (LmrR) as a promising scaffold due to its large hydrophobic pore, which binds and stabilizes hydrophobic molecules.

Metal cofactors can be incorporated into LmrR through covalent attachment or supramolecular assembly.The Splan lab has focused on the incorporation of heme into LmrR, which is a form of supramolecular assembly. Compared to covalent attachment, supramolecular assembly is more dynamic and self-adjustable. The LmrR-hemin enzyme exhibits a wide range of capabilities, including the catalysis of abiological carbene transfer reactions and the oxidation of anthraquinone, demonstrating dye-decolorizing peroxidase activity. Certain LmrR variants, specifically LmrR_A11H_A92H and LmrR_A11H_N14E_A92H_F93H (LmrR_HEHH), have been identified to enhance catalytic activity. UV-Vis oxidation assays with hydrogen peroxide (H2O2) as the oxidizing agent are used to monitor oxidation reactions. These assays measure absorbance at specific wavelengths over time, reflecting the concentration changes of the species involved in the reaction.

Presenter(s): Liu, Xingchen
School: Carthage College
Session: P1.09
Title: Force-Time and Velocity Differences between Ballistic Partial Squats and Ballistic Partial Step-Ups
Co-Author(s): Tony Pustina
Advisor(s): Tony Pustina

Abstract: The purpose of this study is to examine how the force-time and velocity characteristics change when performing bilateral and unilateral ballistic (explosive) partial movements across assisted and loaded conditions. Participants will attend four, 40-minute sessions over a 10-day period. The sessions will consist of:
1. 1RM Squat (parallel) and ¼ Squat, Height, Weight, Age
2. 1RM Step-up (parallel), ¼ Step-up,
3. ¼ Squat @ Assisted, 0, 60, 80, 100% 120%of 1 Repetition Maximum
4. ¼ Step-up @ Assisted, 0, 60, 80, 100% 120% of 1 Repetition Maximum
Measures taken will include:
Mean Force, Peak Force, Duration, and Impulse are measured by the force plate.
Mean Barbell Velocity and Peak Barbell Velocity are measured by a linear position transducer.

Presenter(s): Lohmeier, Chris; Guruprasad, Ram; Chang, Yuelia; Baman, Sonya
School: Macalester College
Session: P2.15
Title: Cell-Specific Removal of Perineuronal Nets in Mouse Olfactory Bulb Using a Novel Modified Adeno-Associated Virus
Co-Author(s): Chris Lohmeier, Sonya Baman, Yuelia Chang, Juan Pineda, Sylvia Choi, Ram Guruprasad, Morgan Houlihan, Clara Lo, & Michelle Tong
Advisor(s): Michelle Tong

Abstract: A recent interest in the role of extracellular matrix structures, like perineuronal nets (PNNs), has led to a boom in experiments using infusions of bacterial enzyme chondroitinase ABC (ChABC) to degrade PNNs. However, this method relies on diffusion and cannot be targeted to specific cell types, which limits our ability to fully understand PNNs. In this project, we pilot a novel adeno-associated virus (AAV) that targets ChABC to specific neuron populations under the control of the Cre-LoxP system. Previous work in the lab found PNNs

around the axon initial segment (AIS) of mitral cells (MCs) in the olfactory bulb (OB). To target the MCs, we used the SLICK-H transgenic mouse line, an inducible Cre line that co-expresses CreERT2 recombinase and YFP behind a Thy-1 promoter. We injected a novel cre-dependent AAV encoding ChABC and mCherry into the OB of SLICK-H mice, and harvested their brain tissue after 7 days of tamoxifen injections. Preliminary findings show that, using the ChABC-AAV method, in vivo, targeted PNN removal to specific brain regions and cell types is possible, facilitating experiments to characterize the function of extracellular matrix structures in learning and memory.

Presenter(s): Mastracci, Julia
School: University of Chicago
Session: II.G.3
Title: Characterizing *C. elegans* Actin Cytoskeletal Dynamics
Co-Author(s): Kash Baboolall, Rachel Kadzik, Cristian Suarez, David R. Kovar
Advisor(s): David R. Kovar

Abstract: The actin cytoskeleton facilitates various crucial functions in the cell by using actin-binding proteins to organize itself into functionally distinct filamentous actin (F-actin) networks. The C. elegans zygote is emerging as a model organism to study the regulation, dynamics and organization of F-actin networks. The actin-binding protein profilin (PFN-1) is necessary for cell division in the embryo. Though fixed imaging of profilin's localization in the embryo is possible, live in vivo imaging has not yet been achieved, leaving gaps in understanding of profilin's regulatory mechanism. Outlined here are the first steps in an ongoing process to transgenically express GFP labeled PFN-1 in the C. elegans zygote. Additionally, fundamental dynamic properties have not yet been characterized for ACT-2, the primary actin isoform in the C. elegans embryo. The polymerization and depolymerization rates of purified ACT-2 were collected using Total Internal Reflection Fluorescence Microscopy and compared to chicken muscle actin, which is widely used for in vitro experiments. Over the range of monomer concentrations tested, chicken actin polymerized roughly 5.6 subunits per second faster than ACT-2, but the elongation rates of both isoforms increased linearly with concentration. Additionally, ACT-2 depolymerized approximately 2.8 times faster than chicken actin.

Presenter(s): Mathew, Emily; D'Lamater, Jacqueline; Melges, Fredrick
School: Hope College
Session: P1.17
Title: Comparison of Experimental and Predicted Carbon Utilization of Escherichia coli from a Hypereutrophic Watershed
Co-Author(s): Clayton G. Piehl, Lauren M. Cribbs, Benjamin N. Turner, Natalie L. Huisman
Advisor(s): Aaron Best, Michael Pikaart, Brent Krueger

Abstract: Public agencies routinely monitor recreational waters for levels of *Escherichia coli* as part of public safety measures and indicators of water quality based, in part, on the assumption that *E. coli* is an indicator of recent fecal contamination. Through ongoing monitoring of the Macatawa Watershed, we have isolated >10,000 water-derived *E. coli* strains, sequencing the genomes of >500 of these strains. Results suggest that subpopulations are native to the watershed environment. To characterize differences between animal-derived and water-derived strains, 32 watershed strains and a reference strain were tested for growth on 190 carbon-based substrates using BiologTM plates. Genome-scale

metabolic models of sequenced strains were generated using ModelSEED2 and compared with experimental results, revealing 68% model accuracy. We used comparative genomics approaches to examine discrepancies. For example, significant variation in growth/no-growth phenotypes on D-Serine was observed; corresponding genomic variation of the D-Serine operon correlated well to observed phenotypes. Combining genomic observations of strain-level variation with metabolic models improved prediction accuracy (27% to 79%) for this substrate. Our results indicate significant metabolic diversity among water-derived strains, supporting the hypothesis that some *E. coli* populations are native to recreational waters, independent of fecal contamination, with temporal factors influencing functional diversity.

Presenter(s): Matsumoto, Grace
School: Washington University in St. Louis
Session: II.F.2
Title: Age-related Differences in Acute Kidney Injury Pathogenesis
Co-Author(s): Aidan Leckie-Harre
Advisor(s): Dr. Monica Chang-Panesso

Abstract: Acute Kidney Injury (AKI) is a sudden, often reversible, decrease in kidney function ranging from minor loss to kidney failure. AKI has a rising incidence amongst hospitalized patients, specifically the elderly. These patients are at greater risk for developing chronic kidney disease, needing dialysis, and dying. Our current incomplete knowledge of AKI's pathogenesis has delayed the development of therapeutic interventions. It is essential to continue AKI research to understand the molecular pathways driving tubular epithelial repair after injury to promote better health outcomes for older patients. My research is focused on identifying key differences in the age-related injured tubular epithelial cell recovery process, specifically regarding transcriptional response differences in proximal tubule (PT) cells. Kim1, a PT injury marker, has been used in a Kim1-GCE; R26-EGFP-L10a mouse line to trace and compare injured epithelial cells in young and old mice. Through statistical analyses on Kim1 labeled injured cells that have been pulled down through translating ribosome affinity purification (TRAP), we were able to find two genes, Jun and DUSP1, that may have age-dependent roles in the AKI recovery pathway. Further analyses must be conducted to find more genes of interest and explore transcription factors and secreted proteins. Experiments involving in vitro testing with siRNA gene knockdown and immunofluorescence staining will be conducted to validate Jun and DUSP1. The overarching goal is to reveal age-dependent transcriptional signatures that can be utilized to find therapeutic targets to determine biological differences in the recovery pathways to enhance overall kidney repair in AKI patients.

Presenter(s): McArthur, Elizabeth
School: Lawrence University
Session: P2.19
Title: G Protein Coupling Selectivity in Parathyroid Hormone 1 Receptor
Co-Author(s): Kelly Culhane
Advisor(s): Kelly Culhane

Abstract: G-protein coupled receptors (GPCRs) are the largest family of membrane proteins, responsible for mediating cellular responses to stimuli. Parathyroid Hormone 1 Receptor

(PTH1R), a class B GPCR, regulates calcium homeostasis and plays an important role in kidney function and bone density, as well as diseases such as osteoporosis and other calcium imbalance caused diseases. PTH1R is activated by two endogenous hormones: parathyroid hormone (PTH) and parathyroid hormone-related peptide (PTHrP). When bound to a hormone, the receptor has distinct conformations that couple with different G protein subtypes and trigger various signalling pathways. Therefore, transfecting PTH1R into mammalian cells and isolating the receptor using Giant Plasma Membrane Vesicles (GPMVs) containing nanoluciferase biosensors allows the response to different hormone binding and G protein selectivity to be measured. The results show that different variations of PTH, including wildtype PTH, PTHrP and E19A/E22A double mutant PTH, show different G protein coupling profiles. Distinct G protein coupling profiles indicate that different hormone interactions stabilize specific PTH1R conformations. Understanding these interactions further and which G protein subtypes bind with higher affinity is a crucial step in working towards drug development to target PTH1R to treat osteoporosis and other bone diseases.

Presenter(s): McFarlane, Grace
School: Gustavus Adolphus College
Session: P3.08
Title: Therapy-Induced Senescence in ERα+ Breast Cancer
Co-Author(s): Lena Batoon, John Hawse
Advisor(s): John Hawse

Abstract: Approximately 80% of breast cancers (BC) express estrogen-receptor alpha (ERα+) and proliferate through estrogen signaling. ERα+ BC is treated using CDK4/6 inhibitors or endocrine therapies, which block cell cycle progression or prevent estrogen signaling, respectively. CDK4/6 inhibitors, such as abemaciclib, cause cancer cells to enter a state of cell cycle arrest known as senescence. Recent evidence suggests that senescent cancer cells can exit this state, leading to tumor progression. Senescence is well-characterized in non-ERα+ BC contexts. However, it is unclear if these characteristics exist in ERα+ BC. Gaining a better understanding of senescence in BC therapy will allow for more targeted treatment of senescent cells. MCF7 and T47D cells were treated with abemaciclib in combinations of endocrine therapies. Western blot analysis and immunofluorescence were used to investigate if abemaciclib treatment altered senescence markers. Combination treatment resulted in increased BCL-XL expression in MCF7 and increased MCL-1 expression in T47D. Abemaciclib treatment resulted in increased nuclear LaminB1 in MCF7 and a decrease in T47D. There was decreased nuclear HMGB1 in MCF7 and an increase in T47D. Thus, the characteristics of therapy-induced senescence differ between common ERα+ BC models and suggest that even larger variability likely exists in patients.

Presenter(s): Meyer, Kaia
School: Gustavus Adolphus College
Session: P3.03
Title: Histological analysis of the U11-Null Growth Plate Reveals Contributions of Defective Chondrocyte Proliferation to Micromelia
Co-Author(s): Saren Springer, Abigail Boria, Rahul Kanadia
Advisor(s): Rahul Kanadia

Abstract: The minor spliceosome, which catalyzes the removal of less than 0.5% of introns from pre-mRNAs, has a demonstrated role in development and disease. The minor spliceosome contains five small nuclear RNAs (snRNAs) including the U11 snRNA. Previous research suggests inhibition of the minor spliceosome through loss of the U11 snRNA in the mouse limb results in micromelia and delayed limb development. Previously, mutations in the U4atac snRNA have been linked to rare skeletal conditions such as Microcephalic osteodysplastic primordial dwarfism type 1 (MOPD1), Roifman syndrome, and Lowry-Wood syndrome. An essential component in embryonic bone development is the formation of the growth plate which occurs through the proliferation of three different types of chondrocytes (round, columnar, and hypertrophic) and replacement of cartilage by bone. Thus, the central aim of this project was to perform histological analysis for proliferative chondrocytes and molecular markers involved in growth plate formation at embryonic day (E)15.5 to explore the cause of stunted bone growth. Our data reveals the mutant growth plate has a decreased number of proliferative cells and that cell cycle defects, specifically defective S phase, could be driving the delay in bone formation.

Presenter(s): Mo, Lina; Matias O'hara, Juan
School: Hope College
Session: I.D.1
Title: Identifying Factors Affecting College Students' Perceptions of Differently Accented English Language Audio Clips
Co-Author(s): Juan Matias O'hara, Yew Meng Koh
Advisor(s): Yew Meng Koh

Abstract: In this study, students in a West Michigan Liberal Arts college listened to short audio clips in differently accented English. These clips were on technical, as well as non-technical, subjects. The listeners were asked to rate (on a continuous scale) their perceived clarity of each speaker they listened to. They also rated their confidence in each speaker's subject matter knowledge, as well as their likelihood of continuing to listen to each speaker if a possibly longer clip of that speaker were presented. The listener's sex, whether or not they were fluent in a language other than English, as well as the main language they were exposed to in childhood were recorded. The aim of this study is to identify the effects of those factors on the perceptions the listeners had of each speaker on the audio clip, as measured by the variables described above. We also investigated whether there were significant differences in perceptions of speaker clarity across the different English accents of the speakers. The possibility of interacting factors within a listener’s own language background was also considered. This presentation will discuss the statistical models we used, as well as highlight the conclusions the analyses led us to.

Presenter(s): Ngu, Reyna
School: University of Chicago
Session: P1.03
Title: Evaluating the Impact of the I-SLEEP Intervention on Memory and Sleep Quality in Hospitalized Patients
Co-Author(s): Aashna Sunderrajan, Vineet Arora
Advisor(s): Aashna Sunderrajan, Vineet Arora

Abstract: This study investigates the effectiveness of the I-SLEEP (Inpatient Sleep Loss: Educating and Empowering Patients) intervention in improving sleep quality and cognitive

function in hospitalized patients. I-SLEEP, comprising an educational brochure, video, and sleep kit with earplugs, an eye mask, and a notecard of questions to reduce nighttime disruptions, aims to enhance patients' ability to advocate for uninterrupted sleep. 192 hospitalized adults were randomly assigned to either the I-SLEEP intervention or control group. Cognitive function was assessed using the USC Repeat Episodic Memory Test and sleep quality was measured with wrist actigraphy monitors. Data were collected before the intervention and daily during hospitalization. Results showed that the I-SLEEP and control groups had significant improvements in recall ability over the hospital stay, with no significant changes in sleep duration. Sleep efficiency increased significantly in the I-SLEEP group, although the correlation between sleep quality and cognitive function was weak. These findings suggest that while I-SLEEP improves sleep efficiency and recall, sleep duration remains unaffected, and the relationship between sleep and cognitive function is complex. The study's limitations include its single-center design and short follow-up period. This study highlights the potential benefits of sleep interventions in hospital settings to improve sleep quality and cognitive function.

Presenter(s): Ogura, Schoichiro
School: Knox College
Session: P3.15
Title: Influence of Absolute or Relative Math Exam Score on Self-Efficacy
Co-Author(s):
Advisor(s): Patricia Xi

Abstract: For students to succeed academically, academic self-efficacy exerts considerable influence. It is beneficial to find factors that improve students' self-efficacy. As one of the factors, grading seems to influence students' decisions on whether they should keep or drop classes. This leads to the assumption that whether students feel they can deal with a study topic is influenced by how many points they get in recent course. Also, the difference in grading style, which is grading compared to others (relative grading) and grading based on predefined criteria (absolute grading), also seems to affect students' performance later. Thus, both the grades that students received and the grading style seem to influence students' self-efficacy. This research aimed to investigate if students' mathematics exam scores and percentages given after taking mathematics exams affect their self-efficacy toward mathematics. For ease of study, fake exam scores or percentile ranks were given to students after students took exams, and their self-efficacy was measured based on the difference between the self-reporting before and after the exam. The result did not support the hypothesis and the floor effect seemed to have affected the result.

Presenter(s): O'Hara, Juan; Mo, Lina
School: Hope College
Session: I.D.1
Title: Identifying Factors Affecting College Students' Perceptions of Differently Accented English Language Audio Clips
Co-Author(s): Lina Mo, Yew Meng Koh
Advisor(s): Yew Meng Koh

Abstract: In this study, students in a West Michigan Liberal Arts college listened to short audio clips in differently accented English. These clips were on technical, as well as non-technical, subjects. The listeners were asked to rate (on a continuous scale) their

perceived clarity of each speaker they listened to. They also rated their confidence in each speaker's subject matter knowledge, as well as their likelihood of continuing to listen to each speaker if a possibly longer clip of that speaker were presented. The listener's sex, whether or not they were fluent in a language other than English, as well as the main language they were exposed to in childhood were recorded. The aim of this study is to identify the effects of those factors on the perceptions the listeners had of each speaker on the audio clip, as measured by the variables described above. We also investigated whether there were significant differences in perceptions of speaker clarity across the different English accents of the speakers. The possibility of interacting factors within a listener's own language background was also considered. This presentation will discuss the statistical models we used, as well as highlight the conclusions the analyses led us to.

Presenter(s): Okogbue, Chisom
School: Hope College
Session: P1.13
Title: The Impact of Iron Oxide Nanoparticle Exposure on Bioaccumulation in House Sparrows (*Passer domesticus*)
Co-Author(s): Kelly Ronald, Shae Johnston, John Wenderski, Liam Hanlon, and Natalia Gonzalez-Pech
Advisor(s): Kelly Ronald, and Natalia Gonzalez Pech

Abstract: Air pollution from urban areas poses serious threats to both human health and the environment. One particularly harmful aspect of this pollution is the presence of tiny solid particles known as iron oxide nanoparticles (IONP). These nanoparticles are so small that they can easily pass through various biological barriers in the body, including the blood-gas barrier and the blood-brain barrier. This capability raises concerns about their potential to cause a range of health issues. Avian species, such as house sparrows, are especially vulnerable to airborne contaminants due to their thinner barriers, which allow more harmful substances to enter their systems. The aim of this project was to investigate whether chronic exposure to IONP leads to excessive iron bioaccumulation in house sparrows (*Passer domesticus*). House sparrows are an appropriate model for this study because they can be found in both rural and urban environments, making them relevant for understanding the effects of urban pollution. Birds were captured from various locations around Holland, MI, and were divided into two groups: one group was exposed to aerosolized clean water (the control group), while the other group inhaled aerosolized IONP over a ten-day period. We examined several key organs—such as the brain, heart, lungs, liver, kidney, gastrointestinal tract, and blood—using an Inductively Coupled Plasma spectrometer to measure iron levels. Analyzing these organs will provide insight into whether chronic exposure leads to harmful iron buildup and how this accumulation might impact the birds' health and behavior. The findings from this project will enhance our understanding of how air pollution affects wildlife and may inform better urban planning and air quality standards to protect both human populations and biodiversity. Ultimately, this research aims to contribute to the development of strategies that minimize the harmful effects of urban air pollution on avian species and other organisms.

Presenter(s): Osborn, Lydia
School: University of Chicago
Session: P2.12
Title: Quantifying Modifications to Lysozyme Structure and Function after High and Low Dose Rate Irradiation

Co-Author(s): Savannah Kidd, Simruthi Subramanian
Advisor(s): Corie Ralston

Abstract: The FLASH effect uses high dose rate radiation (HDR) to kill cancerous cells but spare healthy cells, preventing many side effects of conventional radiotherapy (CRT) that uses low dose rates (LDR). One hypothesis for the mechanism is that our immune response varies based on dose rate. This poster investigates the effects of FLASH HDR and conventional LDR radiation on the activity and structure of lysozyme, a hydrolytic immune enzyme. We found that with clinically relevant doses (5-25 Gy), the activity of lysozyme is not significantly different between high and low dose rates, indicating that lysozyme is unlikely to be central to the body's radiation response. Doses of 1000 Gy were necessary to see a drop in activity and increased dimerization. Peptide-level LCMS analysis of irradiated lysozyme revealed that FLASH treatment caused lower percent modifications than CRT. On an active site peptide, FLASH treatment caused three times less oxidation than CRT. Dose-response curves showed an increase in modification between 1000 and 5000 Gy, supporting the conclusion that neither HDR nor LDR treatment at clinically relevant doses affects lysozyme enough for it to be a direct contributor to the FLASH effect; however, it is remarkably resistant to radiation damage.

Presenter(s): Paek, Suhyeon and Juethner, Sophie
School: Grinnell College
Session: P2.14
Title: Role of Tricellulin and Cdk1 in Spindle Orientation and Mitotic Progression in *Xenopus laevis* Epithelium
Co-Author(s): Sophie Juethner
Advisor(s): Joshua C. Sandquist

Abstract: Proper orientation of the mitotic spindle is crucial for maintaining tissue architecture and preventing tumorigenesis during cellular division. It has not yet been discovered how information about spindle positioning is linked to how the cell progresses through mitosis. We propose that Cdk1, a cell division regulator, and tricellulin, a protein at tricellular tight junctions (tTJ), could potentially act as a signaling link that influences cell cycle regulation, as suggested by their colocalization in the Xenopus laevis epithelium. To investigate the potential binding of tricellulin with Cdk1, a biochemical pulldown assay using GST-tagged portions of tricellulin and extracts from X. laevis embryos was conducted, along with an immunoprecipitation assay using GFP-tagged tricellulin in X. laevis embryos. Additionally, we explored the effect of tricellulin on spindle orientation and mitotic length with live cell imaging. So far, we have demonstrated that overexpression of full-length and truncated tricellulin disrupts the correlation between cell shape and spindle orientation, leading to randomized division axes. Furthermore, we observed a dose-dependent effect of tricellulin overexpression on the mitotic duration, suggesting its involvement in cell cycle regulation.

Presenter(s): Parker, Noah
School: Lawrence University
Session: P3.16
Title: Preliminary Results of a Mindfulness Meditation Mobile App Intervention for Adolescents Awaiting Mental Health Treatment
Co-Author(s): Milciades Gonzalez Medina, Justus Wahl, Layne Eklund, Lori M. Hilt

Advisor(s): Lori M. Hilt

Abstract: Background: There are currently long wait times for youth to receive mental health treatment. In previous work, we found that the CARE mobile app, which provides mood monitoring and mindfulness exercises, was helpful in reducing rumination as well as symptoms of depression and anxiety in community samples. For the present study, we tested whether the app would also be helpful for adolescents awaiting mental health treatment. Participants: We aimed to recruit 30 participants, and thus far, 16 have completed the study. Participants (ages 13-17) were recruited from an outpatient mental health clinic that has a wait time for treatment of approximately six weeks. Methods: Adolescents and a parent/guardian completed surveys regarding rumination and mental health symptoms at baseline and after three weeks. During the three week intervention period, adolescents were asked to use the app three times daily. Results: Data are still being collected, but all outcomes are trending in the expected directions with small-to-medium effect sizes for adolescent-reports, and medium-to-large effect sizes for parent reports. Conclusions: Based on preliminary data, the CARE app appears to be helpful for adolescents waiting for mental health treatments and may potentially be a useful tool to help manage wait times.

Presenter(s): Parry, Elinor
School: Gustavus Adolphus College
Session: P1.10
Title: Meaning-Making Strategies in Emerging Adult Narratives of a Federal Election
Co-Author(s):
Advisor(s): Marie Walker

Abstract: How do young or emerging adults (EAs) make meaning of a divisive, racially charged, and polarizing political event such as the 2020 federal election that occurred at an essential time in their political identity development? Previous researchers identified linguistic strategies used to make sense of a specific socio-historical event within EA personal narratives. In the present study, 209, 18-24 year olds were asked “What does the 2020 federal election mean to you?” Through coding, meaning-making linguistic strategies of self-positioning, counterfactual thinking, metaphor, perspective shifting, contrast, emotional expression, and self-identification were identified. Self-positioning or placing oneself within a greater cultural narrative was used most frequently to create meaning of the 2020 federal election. Typical self-positioning narratives employed by EAs were realization of a need to counter fascism, recognition of the unique/unprecedented socio-historical circumstances of the election, understanding that the fate of the world rested on the election, and the obligation to choose the lesser of two political evils. Additional frequently employed meaning-making strategies by EAs were shifting their perspective from the individual to the collective, expressing emotion and invoking a relevant social identity to personalize their experience of a federal election.

Presenter(s): Pateman, Jean
School: Macalester College
Session: I.D.2
Title: The Impact of Prenatal Alcohol Exposure on Addiction Behavior in Young Adults and Dams
Co-Author(s): Anna Rakowski, Naomi Singer, Petar Elenkov, Phillip Rivera
Advisor(s): Phillip Rivera

Abstract: Postpartum depression (PPD) is experienced by 1 in 7 women and a recent study suggests that maternal alcohol consumption can increase the likelihood of developing PPD. There is a dearth of information on how alcohol consumption during pregnancy can affect the postpartum period(Px). To better understand these behaviors, mouse dams were subjected to drinking in the dark (DID), a four day paradigm that assesses the likelihood to binge on alcohol. This occurred during the human equivalent of the first trimester (embryonic day 0.5-10). A second round of DID took place during a period of PPD (PND21-28) in dams. We hypothesized that during the second binge, dams would binge more alcohol than water control dams. Water control dams will also receive alcohol during the second binge. In order to further understand the impact of previous in-utero alcohol exposure, adolescent offspring went through DID (PND45). Based on preliminary results we expected that female adolescents exposed to alcohol during gestation would binge more than their male counterparts, and all water control dams. In conclusion, a better understanding of how alcohol exposure during gestation influences addiction behavior during the postpartum period will help develop better treatment plans for mothers and young adults who suffer from substance abuse disorders.

Presenter(s): Pham, Thao Giang and Matthews, Daryian
School: Lawrence University
Session: P3.19
Title: Utility of Child and Parent Reports of Mental Health Risk in Middle Childhood
Co-Author(s): Daryian Matthews, Thao Giang Pham, Lori Hilt
Advisor(s): Lori Michelle Hilt

Abstract: The Samaritan Wellness Screen Program (CCWS; Hilt et al., 2018) was designed to screen students from various middle and high schools in Northeastern Wisconsin, aiming to identify youth at risk for suicide and refer them to mental health services. This study evaluated the accuracy of caregiver reports in assessing younger children's mental health, particularly in relation to suicide risk. The Wellness Screen includes several measures, including the Youth Pediatric Symptom Checklist (PSC-Y; Jellinek et al., 1995). This checklist is an adaptation of the original Pediatric Symptom Checklist (PSC) to a self-report format for children and adolescents. Additionally, the screen incorporates other items that assess clinical variables correlated with suicide risk, such as rumination, self-harm, and belongingness. In the 2023-2024 school year, the screening tool was adapted and extended to younger students in grades 4-6. Caregivers reported on their children's mental health, and students were given the option to self-report. A total of 95 caregivers completed the screening for their children, while 50 students opted to self-report. Students meeting specific criteria based on their responses or those of their caregivers advanced to an interview with a clinician who determined whether referral to mental health resources was necessary. Results revealed that caregivers generally underestimated their children's scores across various clinical subscales, except for externalizing behaviors. Caregivers especially underreported self-injurious behaviors, suicidal ideation, and attempts Results demonstrate the importance of integrating self-reports in mental health assessments, even for younger children, as they provide a more comprehensive picture of children's mental health risks, which may go unnoticed by caregivers.

Presenter(s): Protya, Satirtha Saha
School: Beloit College

Session: IB.4
Title: Alterations in Neuropeptide Distribution in Blue Crab, *Callinectes sapidus,* Under Hypoxia
Co-Author(s): Thao Duong, Penghsuan Huang, Ashley Phetsanthad, Vu Ngoc Huong Tran, Lingjun Li
Advisor(s): Lingjun Li

Abstract: Hypoxia, characterized by inadequate oxygen levels in tissues, represents a significant stressor in aquatic ecosystems and can lead to severe physiological disturbances. In crustaceans, such as the blue crab *Callinectes sapidus*, neuropeptides play a pivotal role in regulating stress responses and maintaining physiological balance. This research aims to elucidate how hypoxic conditions affect the distribution and abundance changes of neuropeptides in hemolymph and various tissues, including the central ganglion (CoG), stomatogastric nerve (STN), stomatogastric ganglion (SG), thoracic ganglion (TG), and pericardial organs (PO). We exposed blue crabs to varying oxygen levels: early controls (2 days before hypoxia), control (80% Oxygen), moderate hypoxia (50% Oxygen), and severe hypoxia (10% Oxygen). Hypoxia conditions were prepared by purging nitrogen gas into the tanks. Advanced mass spectrometry techniques, including MALDI imaging and mass spectrometry, were employed to analyze the neuropeptide profiles. Neuropeptides were extracted from hemolymph following standard lab protocol for mass spectrometry. For imaging, tissues were de-sheathed, washed, and transferred to ITO slides, and a DHB matrix was applied. For spotting, samples were prepared by homogenizing tissues in chilled methanol, extracting neuropeptides, and desalting using C18 Ziptips. This research enhances our understanding of stress-induced physiological adaptations in crustaceans by providing a comprehensive analysis of neuropeptide changes under different oxygen levels.

Presenter(s): Puch, Alexander and Zhai, Eric
School: University of Chicago
Session: P1.21
Title: High Throughput Isolation and Identification of Soil Microbiota
Co-Author(s): Eric Zhai, Maryam Adebisi, Rohanna Hasselkus
Advisor(s): Seppe Kuehn

Abstract: Current literature highlights bacterial recruitment by plants in the rhizosphere under stress, yet it remains unclear whether this recruitment is a deliberate selection of specific bacterial strains or simply an attraction of bacteria with similar niches based on the plants' secreted metabolites. Addressing this question requires the ability to construct diverse microbiomes for study. Traditional methods for isolating monoclonal bacterial cultures from soil, such as streak plating, are often inefficient and low-throughput. To address this, we adapted a previously developed protocol for isolating bacteria from plant roots, creating a workflow that allows for the rapid acquisition of a diverse bank of monoclonal bacterial cultures within two weeks. Additionally, this workflow utilizes Sanger sequencing enabling a cost-effective way to identify bacteria. This approach facilitates the construction of bacterial strain banks, which can be utilized to assemble representative synthetic communities for studying the diversity and function of the soil microbiome. Future work will apply this method to investigate the bacterial recruitment mechanisms of *Chlamydomonas reinhardtii* under stress. Beyond this, our methodology opens avenues beyond the recruited microbiome, such as exploring the contributions of soil microorganisms to global carbon emissions, as well as elucidating the effect of various soil conditions on microbial diversity.

Presenter(s): Qarabsa, Rahaf
School: St. Olaf College
Session: P1.02
Title: REM Sleep without Atonia Levels in Community Dwelling Adults in the Rochester Epidemiology Project
Co-Author(s): Rahaf Qarabsa, Besna Erol, Waadaa Daka, Amanda Cesarone. Mahmoud Elawady, Laura McLees, Kaiden Rivera, Olivia Cesarone., Thomas Finstuen RPSGT, Jack Jagielski, Makayla Kelleher, Stuart McCarter, Bradley Boeve, Michael Silber MBChB, Erik St. Louis.
Advisor(s): Erik St. Louis M.D, M.S.

Abstract: Background: REM Sleep Behavior Disorder (RBD) is a parasomnia diagnosed by dream enactment and REM sleep without atonia (RSWA), which can be quantified. We were interested in exploring RSWA amounts in community participants in the Rochester Epidemiology Project (REP) who completed the Mayo Sleep Questionnaire (MSQ), a previously validated instrument for ascertaining RBD symptoms.
Aim: To assess quantitative RSWA in probable RBD (pRBD) participants within the REP who responded to the MSQ, and who had previously underwent polysomnography (PSG).
Hypothesis: Probable RBD (pRBD) subjects will have greater RSWA than control subjects (non-probable RBD).
Methods: MSQ dream enactment symptoms were dichotomized as controls (i.e., without probable RBD) or probable RBD (i.e., endorsed dream enactment) participants. RSWA measures in probable RBD vs. Controls were then compared using Mann Whitney non-parametric tests, with alpha set at p=0.05.
Results: Phasic RSWA weakly trended greater in probable RBD than no RBD (control) participants in the SM muscle. Interestingly, some controls also demonstrated RSWA consistent with RBD despite absent symptoms (aka isolated RSWA).
Conclusion: This first North American study of community dwellling participants demonstrated similar RSWA between pRBD and controls. Further large-scale polysomnographic analysis are needed in larger community population cohorts to expand these preliminary findings.

Presenter(s): Ream, Joseph and Butler, Amelia
School: Gustavus Adolphus College
Session: P2.18
Title: Bacterial Regulation & sRNA Gene Expression in Escherichia Coli
Co-Author(s): Amerlia Butler
Advisor(s): Jane Frandsen

Abstract: *Escherichia coli*, a bacteria commonly found in human intestines, relies on regulatory mechanisms, such as small RNAs (sRNAs), to maintain homeostasis. sRNAs bind with multiple messenger RNAs (mRNAs), collectively a targetome, to manipulate their expression. Because each sRNA typically regulates multiple mRNAs, there is likely a hierarchy in which the mRNAs are bound. A regulatory hierarchy has been identified for the targetome of the sRNA SgrS, which is assumed to be true for other sRNAs. Yet to be determined are which features dictate the hierarchy. Our research focuses on how the accessibility of sRNA binding sites in mRNAs affects prioritization. We are establishing a pull-down assay to determine the order in which an sRNA binds to each target mRNA. Additionally, we are working to optimize a dual reporter assay that measures the order in

which the expression of mRNA targets changes. Together, these assays will help determine if accessible mRNA is favorable in the hierarchy and if accessible mRNA initiates faster cellular changes. Ultimately, we can make informed assumptions about the function of similar cellular processes in other organisms and take steps towards influencing these processes in bacteria with small molecules to mitigate detrimental effects and encourage beneficial ones.

Presenter(s): Redah, Manu
School: Lawrence University
Session: I.C.2
Title: Development of a Novel PCR Assay for Detecting Enterovirus D68
Co-Author(s):
Advisor(s): Dr. Bart De Stasio

Abstract: First discovered in 1960, the enterovirus D68 is a disease causing Acute respiratory infection and Accute Flaccid Myelitis and is known to have outbreaks every 2 years of even years since 2014. To this day, no assay is capable of distinguishing the EV-D68 from other enteroviruses or rhinoviruses. The aim of this study was to develop a real-time reverse transcriptase PCR and retrospectively test patients aging from 19 to 75 years old. Out of 155 samples, 19 were tested positive compared to 16 positive that was tested with the previous assay. These results potentially showed that the new design assay is more precise and more efficient in order to detect the enterovirus D68.

Presenter(s): Rocheford, Lauren
School: Gustavus Adolphus College
Session: P1.05
Title: Evaluation of Sexual Function in Spinal Cord Injury Patients in the Epidural Stimulation after Neurological Damage (ESTAND) Study
Co-Author(s): Ria Koppikar, Elizabeth Bottorff, Tara Nash, Srinidhi Satish, David Darrow, Sam Cramer
Advisor(s): Elizabeth Bottorff

Abstract: Sexual dysfunction has a significant impact on quality of life, leading to other health problems. The ESTAND trial aims to optimize the use of eSCS to restore functions that enhance patient quality of life. In this study, sexual function is assessed using the Orgasm Rating Scale (ORS), a list of adjectives describing orgasm experiences. The adjectives are categorized into physical sensations (PS), emotions (E), and interpersonal relations (IR). Patients undergo surgical implantation of the spinal cord stimulator and attend 13 follow-up visits. Average female and male ratings for each category of the ORS were calculated for the first visit and final visit and a paired t-test was conducted. The data we obtained from the ORS does not indicate any improvement in sexual function in females or males over time. Previous studies done on the effects of eSCS on female sexual function using two alternative scales demonstrates improvement over time with each patient visit, this data does not reflect similar trends. We question if the ORS accurately captures the sexual experiences of individuals with a spinal cord injury (SCI)? In the future, we aim to secure IRB approval to reach out and interview our ESTAND participants for further insights.

Presenter(s): Schechter, Kent
School: University of Chicago
Session: II.F.1

Title: Novel Cancer Cell-Specific Stress Signature Predicts Poor Prognosis and Highlights Racial Disparities in Breast Cancer
Co-Author(s): Long C. Nguyen, Geetha P. Yerradoddi, Rania Bassiouni, John D. Carpten, Marsha R. Rosner
Advisor(s): Marsha R. Rosner

Abstract: Triple-negative breast cancer (TNBC) is the most aggressive subtype of breast cancer. TNBC displays exceptional transcriptional heterogeneity, both between patients and intratumorally, and disproportionately affects underserved women. Hypoxia, a state of low oxygen levels, is often present in the solid tumor microenvironment. In TNBC, hypoxia is a key driver of aggressiveness and therapeutic resistance. Past bulk RNA sequencing (RNAseq) studies in cancer research have lacked spatial resolution, failing to uncover precise transcriptional differences within tumor regions. This spatial limitation has been especially problematic for studying transcriptional heterogeneity of the cellular hypoxia response within tumors. By integrating single-cell RNA sequencing and spatial transcriptomic analyses in a TNBC xenograft tumor model, our research has uncovered a novel hypoxia gene signature, specific to cancer cells. Elevated expression of this hypoxia signature predicts poorer prognosis in breast cancer patients, especially within TNBC patients and those of African ancestry. This suggests that hypoxia may play a role in the racial disparities observed in TNBC prognosis, potentially informing treatment strategies. This workflow introduces a novel framework for translating general spatial transcriptomics data into clinically relevant and accurate gene signatures.

Presenter(s): Schultz, Sophia
School: Lawrence University
Session: P3.18
Title: Inclusive Revision of the Brief Multidimensional Measure of Religiousness/Spirituality for Use in Health Research
Co-Author(s): Kristina Pagel-Martinez
Advisor(s): Kristina Pagel-Martinez

Abstract: Researchers have been using the same questionnaires since they began examining the relationship between religiosity/spirituality and physical health in the 1990's. One such questionnaire is The Brief Multidimensional Measure of Religiousness/Spirituality (BMMRS). The working group that developed the BMMRS aimed to create a multi-dimensional measure of religiosity/spirituality that distinguishes between religion and spirituality, measures potential unhealthy effects of religion on well-being, and identifies domains of religiosity/spirituality relevant for health research. The authors of the BMMRS acknowledge that many of the items have a strong Judeo-Christian focus, arguing that it is appropriate, "given the current distribution of religious preference in the U.S." (Fetzer Institute, 2003). The present study argues that employing a Judeo-Christian focus is not appropriate and that minorities should be represented in research. Due to the heterogeneity of results and the underrepresentation of minority groups in this research, measures of religiosity/spirituality need to be updated. Adjustments were made to the BMMRS to create an inclusive, multi-dimensional measure of religiousness & spirituality. The adjustments made included changing wording of questions to break away from monotheistic terminology and quasi-Protestant narratives, remove questions that represent specific beliefs, and add questions that consider additionally important religious context (e.g., religious mismatch, spiritual struggles, belonging, support).

Presenter(s): Seaver, Gabriel
School: Hope College
Session: P2.11
Title: Using Molecular Dynamics to Determine the Mechanism of Chloride Dependence in System xC-
Co-Author(s): Leah Chase-Wallar, Brent Krueger
Advisor(s): Brent Krueger

Abstract: The human transmembrane protein system xC-, an antiporter of glutamate and cystine, has been targeted in the treatment of a wide array of neurodegenerative disorders due to its roles in glutamate signaling and combating oxidative stress through cystine regulation. In vitro experimentation has shown system xC- activity to be dependent on chloride concentration. In this work, we use molecular dynamics simulations as a tool to examine the mechanism by which chloride ions enable cystine uptake in system xC-. To begin this examination, we have built several simulation systems of system xC- embedded in a 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine and 1-stearoyl-2-arachidonoyl-sn-glycero-3-phosphoethanolamine lipid bilayer with explicit solvent and potassium chloride. We have analyzed properties of the system such as total system energy, membrane area, and diffusion of water, ions, and lipids to examine system equilibration (relaxation of the system into a more realistic state which occurs over simulation time) and for comparison to experimental properties.

Presenter(s): Srinivasan, Prithi
School: University of Chicago
Session: II.G.4
Title: Investigating the Mechanism of Actin Transport into the Nucleus by Importin 9
Co-Author(s): Amanda J. Keplinger
Advisor(s): Alexander J. Ruthenburg

Abstract: The cytoskeletal protein actin plays canonical roles in the cytoplasm, maintaining structure and supporting cell motility. It also plays an important role in the nucleus, interacting with RNA polymerases, chromatin-remodeling complexes, and transcription factors to modulate gene expression. It follows that nuclear actin dysregulation is correlated with aberrant gene expression, contributing to cancer and neurodegeneration. Hence, it is critical to understand the factors underlying actin's entry into the nucleus. Actin is brought into the nucleus by importin 9 (IPO9), one of eleven mammalian proteins responsible for nuclear import. The established model for actin's import suggests that cofilin, an actin-depolymerizing protein, is required to "anchor" actin to IPO9 so it can be brought into the nucleus. However, in the first biochemical examination of this model with purified components, we demonstrate with immunoprecipitation assays and analytical size exclusion chromatography that cofilin is not required for actin to bind IPO9; it may even antagonize actin-IPO9 binding. Furthermore, we find that IPO9 preferentially binds monomeric actin, likely recognizing it at a region known as its "barbed face." Our findings contradict the established model for actin's import, suggesting a novel mechanism for the import of actin monomers driving their profound role in maintaining gene expression.

Presenter(s): Stringer, Alyssa
School: Knox College

Session: II.G.2
Title: On the Clinical Relevance of Animal Variation
Co-Author(s): Saxon Alvarez, Naeun Kim, Sonia Lopez, Emily D McParland, Rosalie Ross, Amira Siddique, and Nicholas J Gidmark
Advisor(s): Nick Gidmark

Abstract: The mammalian jaw joint — the temporomandibular joint (TMJ) — is complex in its anatomy and motion, and facilitates many critical everyday activities such as speech and mastication. Pathologies of the joint in humans — known as temporomandibular disorders (TMD) — are widespread and often painful. Clinical studies of TMD are dedicated to elucidating its development as well as possible therapies and treatments. Because studies of the TMJ and its disorders are difficult, costly, and invasive in humans, many pre-clinical and clinical studies utilize model species including mice, rats, rabbits, monkeys, sheep, and pigs. The diversity of jaw joint anatomy and motion across this group of animals is immense, causing the direct comparison of results between studies to be difficult. Here, we use XROMM (x-ray reconstruction of moving morphology) to comparatively quantify these differences. We found that only some species were tenuously comparative when quantifying healthy chewing kinematics. Instead, joint size and shape, articulation topology, muscle length and mechanics, and ligament length dynamics varied more between species groups than across the chew stroke. These findings suggest that, moreso than variation in chewing kinematics, inter-species variation in anatomy is the most important factor to consider when translating findings from model species to human TMJ health.

Presenter(s): Sullivan, Laura
School: Macalester College
Session: P2.17
Title: Central Sensitization in a Mouse Model of Chronic Vulvar Pain
Co-Author(s): Laura Neal
Advisor(s): Elena Tonc

Abstract: Vulvodynia is a chronic pain condition with unclear etiology and limited treatment options. Understanding the mechanisms contributing to the persistent pain in this condition is crucial for better therapeutics. Our lab has developed a murine model where repeated methylisothiazolinone (MI) skin-exposure is correlated with increased inflammation and long-term tactile sensitivity in the vulvar region. Chronic pain is maintained, in part, by central sensitization, leading to the question of whether central sensitization is occurring in our model of chronic vulvar pain. The goal of my research is to investigate the ways in which central sensitization is involved in our model, focusing on microglial cell populations and neuroinflammation as possible pathways through which central sensitization is established. Targeting the lumbar spinal cord of mice exposed to MI, I have been optimizing immunofluorescent staining to quantify and categorize macrophage and microglial cells present. I am also measuring the level of inflammation in the spinal cord by assessing gene expression changes for common, pro-inflammatory mediators and markers associated with with activated microglia by qPCR analysis . The results of these experiments will elucidate the possible pathways through which chemical-provoked repeat local tissue inflammation can lead to changes in the central nervous system, increasing our understanding of how the immune and nervous systems interact in patients with vulvodynia and chronic pain more broadly.

Presenter(s): Sun, Tim
School: University of Chicago
Session: P2.21
Title: Connection Between Ribosome Biogenesis and the Heat Shock Response
Co-Author(s):
Advisor(s): David Pincus

Abstract: The heat shock response (HSR) involves the transcription of heat shock proteins, including Hsp70, that help to maintain protein homeostasis under stress. Hsf1, the master regulator and transcription factor of the HSR, is repressed by Hsp70 under normal conditions. Upon heat shock, elevated temperatures halt rRNA transcription, leading to the formation of orphan ribosomal proteins (oRPs) that cannot assemble into ribosomes due to the lack of rRNA. These oRPs titrate Hsp70 away from Hsf1, which allows Hsf1 to activate the HSR. Ifh1 and Sfp1, key transcription factors for ribosomal protein (RP) and biogenesis genes, were tagged with an auxin-inducible degron and degraded via the OsTIR1 ubiquitination pathway and the proteasome. This degradation reduced RP and oRP levels, thereby downregulating HSR gene expression. To further establish the link between oRP and HSR activation, the constitutively active kinase Iks1-CA, which disrupts rRNA processing, was shown to activate HSR even in the absence of heat stress.

Presenter(s): Swenson, Annabelle
School: Colorado College
Session: P3.04
Title: *Acinetobacter baylyi* Biofilm Formation Assay for Type IV Pili Mutants
Co-Author(s):
Advisor(s): Dr. Pheobe Lostroh

Abstract: The Gram negative soil bacteria Acinetobacter baylyi (ADP1) utilize type IV pili. These dynamic appendages are required for interaction between both biotic and abiotic surfaces as well as various behaviors including biofilm formation. Here we present an biofilm formation assay for both biotic and abiotic surfaces, with the goal of testing which pilin subunits, which comprise extracellular filament components of the pili, are required for this process. ADP1 bacteria control strains inoculated for 72 hours formed biofilm on various surfaces including krill, navy beans, and surprisingly, the glass test tubes. Our proposed protocol maximizes reproducible results while minimizing resource utilization, optimizing it for the quantification of biofilm formation for multiple type IV pili mutants.

Presenter(s): Thomas, Kassidy
School: Gustavus Adolphus College
Session: P3.11
Title: Impact of Ploidy on Antifungal Drug Resistance
Co-Author(s):
Advisor(s): Laura Burrack

Abstract: Antifungal drugs treat invasive fungal infections that kill millions of people a year. One issue resulting in mortality is the development of antifungal drug resistance. Resistance originates from mutations within the genome. Fungal pathogens can have haploid genomes (one set of chromosomes per cell) or diploid genomes (two sets of chromosomes per cell). In previous studies, haploid cells have been shown to develop resistance due to mutator alleles.

However, it is unknown if there is a mutator allele effect in diploid cells. This project tested if there was a difference in rate of resistance between haploids and diploids, with and without mutator alleles. We tested the effect in *S. cerevisiae* because of its ability to to exist stably in haploid and diploid forms. The effect of ploidy on antifungal drug resistance to fluconazole was tested using evolution experiments through 96-well plating and replica plating for 10 passages. Evolved strains were tested through an MIC (minimum inhibitory concentration) assay to determine any differences in resistance between initial and evolved strains. Results showed that both of the control strains(BY4741 and BY4742) and one of each of the haploid and diploid strains(MATalpha mlh1 and MLH1/MLH1) evolved resistance. Overall, *S. cerevisiae* strains were shown to have evolved resistance towards fluconazole through evolution experiments. However, a strong ploidy-dependent mutator phenotype was not observed.

Presenter(s): Torres-Bermudez, Veronica
School: St. Olaf College
Session: P2.13
Title: Epigenetic Acetylation of Histone3Lysine9 (H3K9ac) Promotes Hepatic Stellate Cell Activation
Co-Author(s): Alexander Washington, Enis Kostallari
Advisor(s): Enis Kostallari

Abstract: Hepatic stellate cells (HSCs) in a healthy liver are typically inactive, playing a key role in vitamin A storage and liver development. When the liver is damaged due to factors like genetics, alcohol, obesity, or viruses, these HSCs become activated and transform into myofibroblasts, which produce extracellular matrix proteins, leading to fibrosis. Histone acetylation, an epigenetic modification, influences gene expression and cell behavior. This study focuses on how epigenetic regulation affects HSC activation. First liver samples from healthy individuals and patients with fibrosis/cirrhosis were analyzed for H3K9ac using immunofluorescence (IF). Primary HSCs were also examined for H3K9ac levels. Then HSCs were stimulated with platelet-derived growth factor (PDGF) and analyzed by western blot. CPTH6, a lysine acetyltransferase inhibitor, was used to block H3K9ac, with varying concentrations tested to find the optimal dose. Increased H3K9ac levels were found in liver samples from fibrosis/cirrhosis patients compared to healthy controls. PDGF-stimulated HSCs showed a significant increase in H3K9ac expression, peaking at 2 hours. Inhibition of H3K9ac with CPTH6 reduced collagen production and cell proliferation. These studies suggest that H3K9ac is important for HSC activation and there is a correlation between H3K9ac and chronic liver fibrosis.

Presenter(s): Tsegay, Siem
School: Macalester College
Session: P3.13
Title: Effect of the Gut Microbiome on the Adolescent Brain
Co-Author(s): Guadalupe Herrera and Santiago Cuesta
Advisor(s): Santiago Cuesta

Abstract: Adolescence is a time of dramatic structural and functional changes for the brain, making adolescents vulnerable to environmental factors that can have profound and long-lasting effects on an individual’s mental health. One important environmental factor is the gut microbiome, a community of microorganisms residing within the gut, which is

constantly changing during this time. Yet, the mechanism by which alterations in the gut microbiota affect brain development in adolescents is poorly understood. This study seeks to understand the relationship between gut microbiome alterations and dopamine circuitry maturation, particularly the mesocortical pathway. To do this, we altered the normal gut microbiome of mice by treating them with *E. coli* HS, ran several behavioral tests on them, performed a Western Blot of the PFC and NAc, and then compared their results with the control group with a normal gut microbiome. Results showed that *E. coli* HS mice expressed less NMDA R1 and Grin 2B than control mice in NAc tissue and less TH and NMDA R1 than control mice in PFC tissue. E. coli HS mice also exhibited more locomotion activity following AMPH treatment than control mice. This study's findings could have significant implications for combating adolescent mental health disorders.

Presenter(s): Vaccarella, Ava
School: Knox College
Session: II.E.2
Title: Have Microplastics Made Their Way to Green Oaks?
Co-Author(s):
Advisor(s): Katherine Adelsberger

Abstract: Microplastics are starting to gain more attention as scientists discover their increasing existence in many ecosystems, such as our own bloodstreams. There has not yet been a clear connection between microplastics and human health, but the research has increased to try connecting the dots between microplastic pollutant concentrations rising and certain diseases become more prevalent. This ten week independent research project aimed to produce a methodology to extract and identify microplastics from inoculated soil standards to then apply to soil samples at the Knox College Biological Field Station, Green Oaks. The process followed five broad steps in the following order: sieving, digestion, density separation, filtration, dying, and examination through a stereo fluorescence microscope. After examination of the microplastic standards, the recovery rates were 106.5%, 102.8%, 93.1%, 100%, and 86.3%. Unfortunately, the 1.0 micron glass filters fluorescence under the microscope, as well as the designated non-fluorescing PCTE filter. However, based on geometric patterns of the standards with known plastic, there was evidence of microplastics in the soil samples from Green Oaks. Further modifications of filters, dyes, and microscope would help to support or reject this finding.

Presenter(s): Vang, Unitas
School: Macalester College
Session: I.B.1
Title: First Report of Cave-adapted Mite-Harvesters (Arachnida, Opiliones, Cyphophthalmi) from Aotearoa New Zealand
Co-Author(s): Sarah Henderson, Rachel Christensen, Anna Stewart, Phil Sirvid, Sarah Boyer
Advisor(s): Sarah Boyer

Abstract: Mite harvesters (suborder Cyphophthalmi) are a type of tiny arachnid known to be extremely poor dispersers with species ranges typically no larger than 50km in any dimension. These animals commonly inhabit leaf litter environments throughout New Zealand, one of the world’s biodiversity hotspots. In 2021, mite harvesters in the genus Aoraki were collected from a cave in the northern South Island; these, along with a poorly

documented specimen from 1973, represent the first ever record of cave-dwelling mite harvesters in New Zealand. A comparison of ratios taken from appendage measurements of the cave animals and thirteen other Aoraki species showcases trends characteristic of cave-adapted arthropods. Specifically, the elongated appendages of the cave specimens suggest adaptation to subterranean environments. We sequenced the mitochondrial loci COI and 16S from one of the cave populations and populations of the closely related species A. westlandica in order to better define the cave population's phylogenetic position and assess the possibility that it represents a new species.

Presenter(s): von Kumberg, Alexander
School: University of Chicago
Session: P2.16
Title: 4-NQO Induced Mouse Tongue Epidermal Organoid Transformation as a Model for Oral Squamous Cell Carcinoma
Co-Author(s): Elena Jochum, Joseph Kainov, Alka Singh, Nishant Agrawal, Evgeny Izumchenko, Le Shen
Advisor(s): Evgeny Izumchenko

Abstract: Oral cavity squamous cell carcinoma (OCSCC) is the most common subtype of head and neck cancer, the seventh most prevalent type of cancer worldwide. With few targeted therapies, OCSCC causes substantial morbidity and mortality. Thus, developing in vivo and in vitro models for OCSCC is crucial in order to study its progression and identify novel therapeutic targets. Here we describe an organoid model suitable for studying the mechanisms of OCSCC carcinogenesis by exposing normal tongue epidermal organoids to long-term treatment with the carcinogen 4-nitroquinoline 1-oxide (4NQO). While 4NQO at doses higher than 6 μM cause significant cell death, lower doses at 1 and 3 μM 4NQO exhibit only slightly reduced growth without widespread cell death. These doses are sufficient to produce genetic and phenotypic changes which mimic OCSCC transformations. While further characterizations such as mutational analysis and the ability of these 4NQO treated organoids to grow in vivo are warranted, our study provides a pipeline establishing a useful in vitro model for both OCSCC modeling and drug screening.

Presenter(s): Wang, Brendon
School: Washington University in St. Louis
Session: P2.04
Title: Crystal Structure of Glutamate-1-Semialdehyde 2,1-Aminomutase from *Stenotrophomonas maltophilia* K279a in Complex with PLP
Co-Author(s): Thomas Yuan, Craig Smith
Advisor(s): Craig Smith

Abstract: *Stenotrophomonas maltophilia* is an emerging Gram-negative bacterium commonly associated with respiratory diseases such as COPD and cystic fibrosis. While *S. maltophilia* has low pathogenicity, the bacteria are associated with a high fatality rate due to high antibiotic resistance. One approach to treatment of *S. maltophilia* involves inhibition of the protein Glutamate 1-semialdehyde-2,1-aminomutase (GSAM), an integral protein that converts glutamate 1-semialdehyde (GSA) into aminolevulinic acid (ALA), an intermediate required in the formation of the metal-binding tetrapyrrole core of important metabolic cofactors such as chlorophyll and vitamin B12. GSAM lacks a human homolog, making it an ideal target for therapeutic interventions. Structural alignment with GSAM from other bacteria

reveals the conservation of the GSG motif, important in opening and closing the gating loop which controls access to the active site. Analysis of the homodimer also reveals the importance of PLP, a cofactor related to amino acid metabolism, and K267 in the formation of a Schiff base. Interactions identified provide insights into selection of a potential competitive inhibitor, namely 2,3-diaminopropyl sulfate, or DAPS, that could disrupt co-factor binding to GSAM by forming an enzyme-inhibitor complex through hydrogen bonding patterns with the active site, mimicking the structure of glutamate 1-semialdehyde.

Presenter(s): Wang, Irene
School: Washington University in St. Louis
Session: P3.02
Title: The Role of Transposable Element-Derived Promoters in Tissue-Specific Gene Expression and Phenotype in Zebrafish Testis
Co-Author(s): Yujie Chen, Ting Wang
Advisor(s): Ting Wang

Abstract: Transposable elements (TEs) are repetitive sequences that constitute a substantial portion of eukaryotic genomes, including zebrafish (*Danio rerio*). Growing evidence suggests that TEs serve as essential regulatory elements due to the existence of abundant transcription factor binding sites, enabling TEs to act as tissue-specific enhancers, insulators, and promoters. Emerging studies suggest that TEs can act as cis-regulatory elements, offering alternative promoters for gene regulation. Previous work from our lab demonstrated that 37% of TEs are associated with active regulatory states in adult zebrafish tissues, particularly in the testis. Additionally, we confirmed that novel TE-derived promoters have the capacity to initiate testis-specific transcription of alternate gene isoforms. However, it remains unclear whether these TE-derived promoters play a crucial role in testis development. In this study, we selected a promising candidate, rasgrp4, from a pool of 413 novel TE-derived promoters identified using nanoCAGE and RNA-sequencing analyses. Employing CRISPR-Cas9 technology, we performed targeted deletion of the TE-derived promoter and generated a homozygous mutant zebrafish line. We used RNA-sequencing to delve into the functional significance of TE-derived promoters on testis-specific gene expression. This investigation will shed light on the essentiality of TE-derived promoters in zebrafish development and tissue-specific gene regulation.

Presenter(s): Wang, Wendy
School: Washington University in St. Louis
Session: P3.20
Title: Improving Retention of People with Disabilities in Clinical Trials: A Systematic Review
Co-Author(s):
Advisor(s): Parisa Parsafar

Clinical trials play a vital role in medical research, in determining the safety and effectiveness of various medical, surgical, and behavioral interventions, in improving treatments and in understanding the impact of diseases on different populations. However, inequities persist regarding which populations are represented within clinical trials, leading to skewed results that do not generalize to other populations and contribute to health disparities. People with disabilities (PWD) constitute approximately 18.7% of the U.S. population, making them the largest minority group. Inclusion of PWD in clinical trials is limited – they experience many barriers to participating in research and are frequently overlooked in clinical research even

though they are at high risk for health disparities and are significant users of healthcare and social services. While there are numerous recommendations to increase PWD's access to clinical trials, few studies have sought to understand how to improve their retention.

Goal: This systematic review sought to identify common themes in the barriers and facilitators to retention of PWD in clinical trials, to increase awareness and improving the inclusivity of clinical research. We included peer-reviewed qualitative and mixed-methods studies from 1950 to present. The databases searched included Academic Search Complete, APA PsycInfo, and CINAHL Plus. The search was conducted in August 2024 using terms focused on disability, retention, and clinical trials/interventions. Out of 384 initial studies, 15 studies met inclusion criteria, including 7 focused on older populations, 4 on physical disabilities, 2 on developmental disabilities, and 2 on cognitive disabilities.

Results: Thematic analysis revealed the most frequently mentioned barrier to retaining participants in clinical trials is burnout resulting from the ongoing demands of maintaining the study treatment. These included long study duration, frequent study visits, and difficulties accessing the study site. Individual-level factors such as transportation, caregiver availability, and participant fatigue, also contributed to and interfered with retention in clinical trials. Additional challenges encompassed perceptions of the study, including experiences of dismissal as well as a general lack of motivation and interest in continuing.

Presenter(s): Ware, Nikki; Kelkar, Saniya; Clarkson, Elizabeth; Crowe, Maile
School: Grinnell College
Session: P3.14
Title: Now You See it... Now What's the Pattern? Developing a New Task to Study Statistical Learning
Co-Author(s): Elizabeth Clarkson, Nichole Henning, Saniya Kelkar, Nikki Ware, Christopher Conway
Advisor(s): Christopher Conway

Abstract: Implicit statistical learning is the ability to perceive patterns in the environment without intending to do so and without being consciously aware of what was learned. However, very little research has investigated what cognitive or psychological factors predict statistical learning abilities. The present study sought to develop a new task to study statistical learning of both simple and complex patterns and to investigate the role of individual differences in statistical learning ability. Participants engaged in a statistical learning task in which they responded as quickly as possible to visual stimuli that were either predictable or not based on the structure of the covert patterns. We also measured participants' personality traits, chronic stress, and other demographic variables. The results showed learning of both simple and complex patterns, with certain measures of individual differences being correlated with performance, specifically the personality traits Openness to Experience and Neuroticism. Moreover, learning and attention disorders were associated with worse performance, and awareness of the patterns related to learning. Finally, there was a positive correlation between dwelling on stressful events scores and learning. These findings provide insight into what factors can predict and even promote the ability to implicitly learn new information.

Presenter(s): Welge, Ana
School: St. Olaf College

Session: I.A.2
Title: Using Tumor-Specific Transposable-Element- Chimeric Antigens (TS-TEAs) to Initiate an Anti-Cancer Immune Response
Co-Author(s):
Advisor(s): Ting Wang; Mitchell Grinwald

Abstract: Transposable elements are repetitive sequences in our DNA that do not code for proteins in healthy cells. They make up nearly half of the human genome and sometimes act as alternative promoters which initiate transcription of a given gene. Typically, they are transcriptionally silenced. However, in cancerous cells, they can be transcribed into what are called "TE-chimeric transcripts." These atypical transcripts can be translated into a class of proteins called "tumor-specific, transposable-element antigens" or TS-TEAs. TS-TEAs are displayed to the immune system on a type of cell surface molecule that informs the immune system about what is occurring inside the cell. TS-TEAs are exclusive to tumor cells, which means that if the immune system was prompted to target TS-TEAs, somatic cells would emerge unscathed. TS-TEAs are also shared among cancer patients, which means that a treatment could extend across patient pools and potentially across cancer types as well. TS-TEAs are being explored as a form of next generation cancer immunotherapy. The hope is to identify antigens that can aid in developing a TS-TEA-based treatment that could treat many patients who are battling the devastating disease that is cancer.

Presenter(s): Wong, Karen
School: University of Chicago
Session: P2.07
Title: Defining the Interaction Between the ZAP70 Proline-Rich Motif and Lck.
Co-Author(s): Indrani Biswas, Yuan-Li Tsai, Arthur Weiss, Lin Shen
Advisor(s): Lin Shen

Abstract: The protein tyrosine kinase ZAP70 interacts directly with the T cell antigen receptor (TCR) complex and is essential of TCR signaling. Dysfunctional ZAP70 has been associated with immunodeficiency or autoimmune diseases. The proline-rich motif within ZAP70 was found to be highly conserved within 26 mammals. Preliminary data showed that mutations in this motif decreased ZAP70 phosphorylation, leading to impaired T cell activation. Structural analysis suggested that the SH3 domain of Lck, specifically, W97 and F115, directly interact with the proline-rich motif of ZAP70. To further understand the interaction between the ZAP70 proline-rich motif and Lck, we introduced two mutants, W97A and F115A, into the Lck SH3 domain, and assessed how these mutations affect ZAP70 phosphorylation and TCR signaling. Our cell line data showed that compared to wild type Lck, these mutations resulted in decreased phosphorylation of ZAP70 Y493 and Y292. Additionally, the mutated Lck SH3 domain and ZAP70 proline-rich motif together resulted in decrease in LAT phosphorylation. Our results suggested that the interaction between the ZAP70 proline-rich motif and Lck SH3 domain play a positive role in TCR signaling. Our study will further our understanding of ZAP70 function and regulation and its impact on TCR signaling and immune-dysregulatory disorders.

Presenter(s): Wu, Helena
School: University of Chicago
Session: P1.12

Title: Change in Screen Time and Overuse: Psychological Well-being among US-Wide Children during Pandemic Years 2018–2021
Co-Author(s): Amy Tsurumi, Jiandong Li
Advisor(s): Amy Tsurumi

Abstract: Previous research on screen use and children's mental health during the COVID-19 pandemic primarily focused on a limited timeframe, narrow age ranges, or children facing severe family economic hardship. Additionally, these studies often did not differentiate between instructive and recreational device use. To address these gaps, we examined trends related to recreational screen use and psychological well-being (PWB) before and during the pandemic, across a broad age range of school-aged children nationwide. Using data from the National Survey of Children's Health (NSCH) from 2018-2021, we analyzed a random sample of 88,823 children aged 6-17 years. We developed psychological well-being issue scores (PWBIS) based on self-reported measures and constructed regression models to assess the pandemic's impact on recreational screen use and PWB. Our findings reveal a significant increase in both screen overuse and PWBIS during the pandemic compared to prior years. Moreover, the pandemic strengthened the association between screen time and PWBIS ($p<0.01$). These results highlight the pandemic as an independent risk factor for screen overuse and its adverse effects on PWB among school-age children. Future research should evaluate whether these effects persist post-pandemic to further understand long-term implications.

Presenter(s): Xu, Emily
School: University of Chicago
Session: P3.22
Title: Differentiating Healthy Aging, Early, and Intermediate Age-Related Macular Degeneration via Retinal Thickness in Optical Coherence Tomography - ALSTAR2 Baseline
Co-Author(s): Emily Xu1, Kenzie Megid1, Sophia Xu1, Sohaib Fasih-Ahmad1, Ziyuan Wang1, Zubin Mishra1, Mark E, Clark2, Thomas A. Swain2,3, Christine A. Curcio2,3, Cynthia Owsley2,3, SriniVas R Sadda1, Zhihong Jewel Hu1*
Advisor(s): Zhihong Jewel Hu

Abstract: Retinal layer thickness features may be affected by age-related macular degeneration (AMD) processes. The purpose of this project is to investigate associated retinal layer thicknesses in optical coherence tomography for differentiation of healthy aging, early, and intermediate AMD. The study included 371 total eyes (133 early AMD, 17 intermediate AMD, and 221 normal from subjects ≥ 60 years) [1]. An automatic segmentation algorithm was applied [2-4] to obtain internal limiting membrane boundary, inner nuclear-outer plexiform junction, and inner and outer choroidal boundaries [5-6]. Each B-scan was manually inspected and refined if needed. The analysis was with 3-6mm, 1-3mm ring, and within 1mm ETDRS rings in inner retinal, outer retinal, and choroid. With an ANOVA test, there was a significant ($p<0.05$) difference among AMD stages within 1mm and 1-3mm ring of inner retinal. With a T-test between normal and early AMD, there was a significant difference in all inner retinal and 3-6mm ring of choroid. Likewise, when comparing normal to intermediate AMD and intermediate to early AMD, there was a significant difference in outer retinal within 1mm ring. Overall, most significant differences were found in all inner retinal, within 1mm ring of outer retinal, and 3-6mm ring of choroid.

Presenter(s): Zhai, Eric and Puch, Alexander

School: University of Chicago
Session: P1.21
Title: High Throughput Isolation and Identification of Soil Microbiota
Co-Author(s): Alexander Puch, Maryam Adebisi, Rohanna Hasselkus
Advisor(s): Seppe Kuehn

Abstract: Current literature highlights bacterial recruitment by plants in the rhizosphere under stress, yet it remains unclear whether this recruitment is a deliberate selection of specific bacterial strains or simply an attraction of bacteria with similar niches based on the plants' secreted metabolites. Addressing this question requires the ability to construct diverse microbiomes for study. Traditional methods for isolating monoclonal bacterial cultures from soil, such as streak plating, are often inefficient and low-throughput. To address this, we adapted a previously developed protocol for isolating bacteria from plant roots, creating a workflow that allows for the rapid acquisition of a diverse bank of monoclonal bacterial cultures within two weeks. Additionally, this workflow utilizes Sanger sequencing enabling a cost-effective way to identify bacteria. This approach facilitates the construction of bacterial strain banks, which can be utilized to assemble representative synthetic communities for studying the diversity and function of the soil microbiome. Future work will apply this method to investigate the bacterial recruitment mechanisms of *Chlamydomonas reinhardtii* under stress. Beyond this, our methodology opens avenues beyond the recruited microbiome, such as exploring the contributions of soil microorganisms to global carbon emissions, as well as elucidating the effect of various soil conditions on microbial diversity.

Presenter(s): Zhao, Peter
School: Grinnell College
Session: P1.08
Title: Single-Cell Encapsulation Using Flipchip Design and Surface Tension-Induced Droplet Formation
Co-Author(s): Edgar Ruiz Bello, Julea Vlassakis
Advisor(s): Julea Vlassakis

Abstract: Current single-cell encapsulation strategies aiming to recapitulate the in vivo 3D microenvironment struggle to be applied to single-cell analysis due to complicated setups and low encapsulation efficiency. This study introduces a simple single-cell encapsulation method by integrating the Flipchip design with surface tension-induced droplet formation. The Flipchip utilized a hydrophilic chip with cell-sized microwells for single-cell isolation and a hydrophobic chip with micromolds for droplet formation, allowing for rapid single-cell settlement into individual micromolds. Droplet formation with cell encapsulation was achieved through a micromold-based technique using surface tension-induced droplet formation with a wetting fluid. This method was validated using 30μm polystyrene microspheres, which mimicked the size and density of real cells, and poly(ethylene glycol) diacrylate (PEGDA), a biocompatible hydrogel commonly used in bioprinting. We achieved single-microsphere encapsulation in 100μm PEGDA droplet in 30 minutes on a microscope slide-sized chip. Tunability of droplet size and higher throughput (~6000 droplets) could be achieved by optimizing the micromold design. This method provides high throughput, improved encapsulation efficiency, and a simple setup, enhancing current single-cell encapsulation approaches. The Flipchip can be applied to single-cell proteomic measurements, such as single-cell western blot, to more accurately assess cellular proteomic behavior in physiologically relevant conditions.

Presenter(s): Zizzo, Zoe
School: Colorado College
Session: I.A.4
Title: Characterization of Extracellular Vesicles from Human Chordoma Cell Lines and their Impact on Recipient Cells
Co-Author(s): Michael Graner
Advisor(s): Phoebe Lostroh

Abstract: Chordoma is a rare, aggressive bone cancer with poorly understood immune interactions and limited treatment options. We hypothesize that extracellular vesicles and particles (EVPs) from chordoma cells contribute to immune evasion and tumor progression. To investigate this, we cultured two chordoma cell lines, ARF-8 and N11-2, isolated EVPs using differential ultracentrifugation, and reintroduced them to their cell of origin. We then conducted proteomic and cytokine "secretome" analyses. Proteomic results indicated that TGFβ1 and oncostatin M (OSM) in ARF-8 exosomes may be involved in epithelial-to-mesenchymal transition (EMT). We aimed to confirm the presence of TGFβ1 and OSM in/on chordoma EVPs using ELISA and Western blotting. TGFβ1 was found at higher concentrations in ARF-8 EVPs compared to conditioned media, suggesting TGFβ1 is bound to EVPs instead of just free in solution. TGFβ1 was undetectable in N11-2 cells, and OSM was absent from both cell lines and their conditioned media. Treatment of N11-2 cells with their own EVPs led to a generally increased and differential release of cytokines and chemokines, underscoring the immunomodulatory role of EVPs. Our findings demonstrate the autocrine effects of EVPs on tumor cells, and ongoing proteomic analyses aim to uncover new biological targets for potential treatments of these malignancies.

All Students Presenting at
MCMS Undergraduate Research Symposium,
University of Chicago
Biological and Psychological Sciences
November 1-2, 2024

Beloit College: Vu-Anh Le, Satirtha Saha

Carthage College: Grace Krueger, Damanpreet Khaira, Xingchen Liu

Colorado College: Jill Coleman, Juliana Geronazzo, Abby Heimerl, Riley Kadis, Meena Kim, Annabelle Swenson, Zoe Zizzo

Grinnell College: Ahmad Ayyeh, Elizabeth Clarkson, Saniya Kelkar, Cameron Lian, Kelly Paek, Sophie Juethner, Nikki Ware, Peter Zhao

Gustavus Adolphus College: Amelia Butler, Maddie Chaplin, Alexander Johnson, Rachel Lester, Grace McFarlane, Kaia Meyer, Elinor Parry, Joe Ream, Lauren Rocheford, Kassidy Thomas

Hope College: Jacob Caballero, Ava Doty, Liam Hanlon, Shae Johnston, Michael LaPorte, Emily Mathew, Lina Mo, Chisom Okogbue, Matias O'Hara, Gabriel Seaver

Knox College: Tisya Goel, Mai Hasegawa, Richie Ogura, Alyssa Stringer, Ava Vaccarella

Lawrence University: Reeshi Bhattacharjee, Beth McArthur, Noah Parker, Giang Pham, Manu Redah, Sophia Schultz

Macalester College: Jocelyn Cottrell, Ram Guruprasad, Fuxuan Liu, Chris Lohmeier, Naeun Kim, Jean Pateman, Laura Sullivan, Siem Tsegay, Unitas Vang

St Olaf College: Olivia Chapman, Emma Clift, Cecelia Kivell, Ian Knowles, Rahaf Qarabsa, Veronica Torres-Bermudez, Ana Welge

University of Chicago: Gloria Adeola, August Angulo, Lara Bencsics, Kashi Bhagat, Taylor Elliott, Aurora Ferrell, Monica Gould, Hadley Groom, Pierce Hoenigman, Yannik Leuz, Julia Mastracci, Reyna Ngu, Lydia Osborn, Alexander Puch, Kent Schechter, Prithi Srinivasan, Tim Sun, Alexander von Kumberg, Karen Wong, Helena Wu, Emily Xu

Washington University in St, Louis: Shreya Chilukuri, Brian Chen, Cara Conforti, Tamara Dandreamatteo, Alekya Dantam, Halla Elmore, Lowell Finster, Autumn Kim, Nathan Lin, Grace Matsumoto, Brendon Wang, Irene Wang, Wendy Wang, Eric Zhai

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MCMS Undergraduate Research Symposium, University of Chicago
Biological and Psychological Sciences
November 1-2, 2024

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