Welcome to the

GRADUATE + POSTDOCTORAL

RESEARCH SYMPOSIUM

March 18, 2026

UNIVERSITY OF MIAMI

GRADUATE + POSTDOCTORAL

RESEARCH SYMPOSIUM

EVENT OVERVIEW

12:00 - 1:00 P.M.	Registration + Lunch *Third Floor Mezzanine*
1:00 - 2:00 P.M.	Keynote Address: Dr. Gauri Agarwal *Ballroom East*
2:00 - 3:30 P.M.	Poster Session *Ballroom Center*
3:30 - 5:00 P.M.	Oral Presentation Sessions *Activities Room North* *Activities Room South* *Ballroom East* *Ballroom West* *Iron Arrow Room* *Senate Room* *Vista Room*
5:00 - 6:00 P.M.	TED-like Talk Session
6:00 - 6:30 P.M.	Awards Ceremony + Reception *Ballrooms East + Third Floor Mezzanine*

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Keynote Speaker

Dr. Gauri Agarwal

Gauri Agarwal, M.D., F.A.C.P., is the Associate Dean for Curriculum and Associate Professor of Medicine, Medical Education, Informatics & Health Data Sciences at the University of Miami Miller School of Medicine. She also serves as the course director for the Medical Education Senior Elective. She obtained her undergraduate and medical degrees at the University of Miami (UM) as part of the six-year Honors Program in Medical Education. She completed residency training in internal medicine at Northwestern University and the University of Pittsburgh and served as chief medical resident at the University of Pittsburgh. Dr. Agarwal has been on the faculty at the University of Pittsburgh and Harvard Medical School prior to returning to the University of Miami in 2007, where she has been inducted into the Gold Humanism Honor Society, Alpha Omega Alpha, and the Iron Arrow Honor Society. She has developed, directed, and taught numerous courses at the medical school. Dr. Agarwal has an interest in the medical humanities and founded Obliterants, the medical school's first humanities journal. She serves as the faculty advisor for the magazine and for UM's chapter of the Gold Humanism Honor Society. She has won many school, regional, and national teaching awards, including the American College of Physicians (ACP) Medical Educator Award. In 2017, she received the Leonard Tow Award for Humanism in Medicine. Nationally, she chaired the Cell Biology and Physiology Item Writing Committee for the National Board of Medical Examiners and has led national board review courses for practicing physicians for the ACP. Dr. Agarwal's research interests are medical education and medical humanities. In 2023, as a Gold Humanism Scholar for the Harvard Macy Program, she developed a curriculum on the intersection of artificial intelligence and the medical humanities. She recently published the first module on the AAMC's MedEd Portal on artificial intelligence for health professions students, an AMEE guide on implementing medical humanities programs, and a research study on AI ethics in NEJM AI. She is a proponent for thoughtful integration of innovative technology in curricula and recently received a NIH grant to implement a virtual reality curriculum for medical and nursing students.

Poster Presenters

Afshin Asadi

Ph.D. Student in Industrial Engineering

D2LDM: A Dual-Stage Latent Diffusion Framework for Transferable Demand Forecasting

Reliable demand forecasting is essential for efficient resource management and cost optimization, yet remains challenging under nonstationary dynamics, distributional shift, and the need for calibrated uncertainty. Recent diffusion-based forecasters model stochastic temporal behavior effectively, but most operate in the observation space, where high dimensionality and strong cross-variable correlations make noise injection inefficient, sampling slow, and adaptation across domains costly.

This paper presents D2LDM, a dual-stage latent diffusion framework for probabilistic multi-horizon demand forecasting. In Stage I, a statistics-aware temporal autoencoder compresses multivariate time-series blocks, including target and contextual variables into a compact latent trajectory, yielding a structured representation that preserves temporal dependencies while substantially reducing dimensionality. In Stage II, a Transformer-based conditional diffusion denoiser model's future latent trajectories conditioned on historical context and known covariates. By shifting diffusion from the observation domain to a compact latent space, D2LDM enables more efficient noise injection and faster latent sampling, while maintaining expressive stochastic modeling and coherent multi-horizon generation.

Importantly, the same latent manifold learned in Stage I supports domain-invariant representation learning, enabling efficient cross-domain adaptation by fine-tuning only the latent diffusion forecaster under limited target data. Experiments on public benchmarks and cross-user electricity demand forecasting demonstrate improved long-horizon accuracy, calibrated uncertainty, and efficient adaptation compared with observation-space diffusion and standard forecasting baselines.

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Alyssa Cornista

Ph.D. Student in Microbiology and Immunology

Tumoral IL-33/ST2 Signaling Drives Immune Escape through Reduced Antigen Presentation

Immune checkpoint blockade (ICB) therapy delivers promising clinical results in colorectal cancer (CRC), especially in microsatellite instability high (MSI-H) patients; however, the majority of total CRC patients (up to 85%) have a microsatellite stable (MSS) tumor phenotype, which are poor responders to ICB. Therefore, there is a need to identify other checkpoint targets associated with the tumor microenvironment and uncover their mechanism of action. We propose to investigate the IL-33/ST2 pathway expressed on tumor cells as a potential cancer immunotherapy target. Multiplexing was done to define ST2 (Stimulation 2, interleukin-33 receptor) expression in human CRC tissue samples. The inhibitory effects of ST2 were assessed using both patient derived organoids co-cultured with autologous T cells as well as murine subcutaneous and orthotopically transplanted models in WT, TCRbeta^{KO}, and ST2^{KO} mice. Endoscopy-guided injection of tumor cells is used to study microenvironmental changes. We performed single-cell RNA sequencing on orthotopically implanted CRISPR/Cas9-edited tumor cells to identify the mechanism of action. Sequencing results were validated using an array of in vitro experiments. Advanced spectral flow cytometry (CYTEK) was used to study tumoral ST2 expression and its effect on T cells. Our data show that tumor cells have ST2 expression, both in murine and clinical samples. Particularly, we demonstrated ST2 to be prominently expressed on MSS tumors. Activation of tumoral IL-33/ST2 signaling protects tumor cells from T-cell-mediated killing. Functional studies showed reduced antigen presentation, driven by reduced immunoproteasome activity, and leading to the observed T-cell killing escape. Removing tumoral ST2 signaling using CRISPR/Cas9-gene editing leads to significantly reduced tumor growth and increased infiltration of T cells, with a reduced terminally exhausted profile. Our findings suggest that tumoral ST2 signaling drives immune escape through a reduced antigen presentation and could serve as checkpoint target for CRC immunotherapy.

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Amber Balda

Ph.D. Student in Epidemiology

Molecular Subtype-Specific Patterns of Breast Cancer Survival Across Racial and Ethnic Groups in Florida

Background: Distribution of molecular subtypes across racial and ethnic groups differ and have a significant impact on prognosis and treatment modalities. Previous analyses have not fully integrated receptor status, limiting the evaluation of how tumor biology intersects with sociodemographic factors in shaping breast cancer specific survival (BCSS). Consequently, characterization of disparities remains insufficiently understood.
Purpose: This study assessed differences in BCSS among women in Florida, accounting for molecular subtypes.
Methods: Data from the Florida Cancer Registry were used to estimate survival among cases diagnosed between 2011 and 2017. Special attention was given to the four main molecular subtypes defined by hormone receptor (HR+/–; Estrogen/Progesterone) and HER2 status, with an additional focus on the two most common molecular subtypes, HR+/HER2- and triple-negative breast cancer (TNBC). BCSS was assessed using Kaplan-Meier curves and multivariable Cox regression, adjusting for age, race/ethnicity, stage at diagnosis, poverty level, insurance status, tobacco use, surgery, marital status, and urbanicity.
Results: There were 99,919 cases included in the analysis, of which Black women had the highest prevalence of TNBC (22.7%) followed by Hispanics (12%). Compared with White women, mortality risk was higher for Black (HR=1.35; 95% CI: 1.27–1.44), Asian/Pacific Islander (API) (HR=1.19; 95% CI: 1.03–1.37), and Hispanic women (HR=1.08; 95% CI: 1.02–1.15). Elevated risks were observed for current smokers, unmarried women, and patients with TNBC (HR=3.07; 95% CI: 2.91–3.23) compared with HR+/HER2- cases. Disparities were greatest in HR+/HER2– disease, where API and Black women faced 31–46% higher mortality. In TNBC, excess risk persisted for Black women but not for API cases.
Conclusion: With receptor-level data now available, this study shows that disparities are shifting: Hispanic and API women, who previously showed survival comparable or better than White women, now face significantly worse outcomes. Most concerning is that these disparities are greatest in subtypes with better prognosis and effective therapies. Addressing these widening inequities requires equitable access to effective therapies and strategies to mitigate the combined impact of tumor biology and systemic barriers to care. Additional research is needed to better characterize heterogeneity within subgroups and their distinct clinical trajectories.

Author(s): Amber Balda; Hannah M. Cranford; Paulo S. Pinheiro

Annu Joji

Ph.D. Student in Chemistry

Synthesis of Red-Emissive Carbon Dots from Benzothiazoline Salts for Bioimaging

Near-infrared (NIR) fluorophores are indispensable tools in biomedical imaging due to their ability to penetrate deep tissue, minimize background autofluorescence, and enhance signal-to-noise ratios. Despite their utility, conventional organic dyes often exhibit limitations such as photobleaching, poor aqueous solubility, and limited brightness, which restrict their long-term use in biological environments. To overcome these challenges, this study focuses on the design, synthesis, purification, and characterization of benzothiazoline salt derivatives as red-emissive precursors for carbon dot (CD) fabrication.

Benzothiazole-based scaffolds were selected based on their well-documented bioactivity and tunable photophysical properties. A series of benzothiazoline salts were synthesized and structurally modified to achieve red-shifted emission by narrowing the HOMO-LUMO energy gap, thereby enabling fluorescence in the NIR region. These small-molecule fluorophores were then employed as precursors in a bottom-up carbon dot synthesis approach, yielding nanomaterials with enhanced photostability, aqueous dispersibility, and desirable emission characteristics. The resulting carbon dots were subjected to comprehensive characterization using UV-vis spectroscopy, fluorescence spectroscopy, dynamic light scattering (DLS), and transmission electron microscopy (TEM) to confirm their optical properties, size distribution, and surface morphology. Spectral analysis revealed consistent red emission profiles, validating the successful incorporation of benzothiazoline-derived chromophores into the carbon dot. This work expands the molecular toolkit available for red-emissive carbon dot development and demonstrates the feasibility of using benzothiazoline salts as versatile building blocks for bioimaging nanomaterials. The synthesized carbon dots show promise for future applications in fluorescence-guided imaging, in neurosurgery and targeted delivery systems, where stable, observable bright NIR emission is critical.

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Ashfia Tasnim

Ph.D. Student in Chemistry

Designing Stable Gold-Silver Alloy Nanoparticles for Plasmon-Assisted Catalysis

Metal nanoparticles are widely used in catalysis due to their high surface area and tunable optical and electronic properties. Although silver nanoparticles have high plasmonic and catalytic activity, they are easily oxidized in ambient environments, which causes instability and performance degradation. Gold has lower reactivity but better chemical stability. Gold–silver alloy nanoparticles provide a promising strategy to balance catalytic functionality and long-term durability; however, the mechanisms controlling their stability are still not fully understood.

In this study, we use correlated single-particle characterization methods to examine the optical and structural stability of gold-silver alloy nanoparticles. We synthesized gold–silver alloy nanoparticles through citrate mediated co-reduction and characterized them by UV–visible spectroscopy and scanning electron microscopy – electron dispersive spectroscopy (SEM-EDS) to confirm size, morphology, and composition-dependent plasmonic behavior. We validated the stability and characterization methods of the gold-silver alloy nanoparticles using gold nanorods synthesized via seed-mediated growth as stable reference standards.

We monitored the plasmon resonance of individual nanoparticles over time under ambient lab conditions using single-particle dark-field scattering spectroscopy. This approach enables direct assessment of spectral shifts, variability, and aggregation effects that are often obscured in ensemble measurements. In addition, we controlled the particles' exposure to oxygen and water to probe oxidation-induced changes in plasmon response, where resonance shifts and linewidth variations serve as indicators of surface oxidation and charge-transfer processes.

Our results show that 0.5:0.5 Au:Ag mole ratio nanoparticles exhibit noticeable plasmon resonance drift under ambient conditions over the course of many days with particle-to-particle variations. Ongoing work extends this study across multiple alloy compositions, environmental conditions, and correlated optical stability with post-measurement SEM analysis.

This study establishes a solid foundation for assessing oxidation and charge-transfer effects in alloy nanomaterials by combining controlled synthesis with structural and single-particle optical characterization. These insights provide practical design principles for gold–silver catalysts that combine enhanced stability with functional catalytic performance under ambient operating conditions.

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Brandon Leon

Ph.D. Student in Cancer Biology

Glioblastoma Derived Glutamate Drives Tumor-Associated Astrocyte Reactivity

Tumor-associated astrocytes (TAAs) are a key component of the glioblastoma (GBM) tumor microenvironment (TME) and exhibit a reactive phenotype that provides cancer cells with metabolic support, enhances TME immunosuppression, and increases tumor treatment resistance. However, the mechanisms that drive TAA reprogramming remain poorly understood. Previous studies showed that GBM cells secrete supraphysiologic levels of glutamate into the TME via the cystine-glutamate antiporter, SLC7A11, and that autocrine glutamate signaling enhances GBM cell invasion and proliferation. Nevertheless, the potential role glutamate in reshaping the TME remains unexplored. Astrocytes are critical regulators of glutamatergic homeostasis in the brain. They express a range of glutamate transporters, receptors, and metabolic enzymes positioning themselves as a nexus of aberrant glutamate signaling in GBM.

We found that glutamate increases both astrocyte proliferation and the expression of reactive astrocyte markers, including complement component 3 (C3). Additionally, mouse and patient-derived GBM cell models secrete varying levels of glutamate dependent on their SLC7A11 expression. In GBM patients, SLC7A11 expression correlates with reactive astrocyte marker expression. When co-cultured with astrocytes, GBM cell lines that secrete high levels of glutamate more robustly induce reactive astrocyte marker expression and proliferation than those with lower glutamate secretion. Furthermore, pharmacological inhibition of SLC7A11 mitigates reactive astrocyte induction by high- but not low-glutamate-secreting cancer cells. Finally, co-implantation of GBM cells with astrocytes accelerated tumorigenesis, while C3 knockout mice have elongated GBM survival compared to wild-type controls. Collectively, this study defines a novel role for SLC7A11-dependent glutamate signaling in TAA reprogramming and identify therapeutic targets that disrupt GBM–TME interactions to improve patient outcomes. Future studies will investigate how aberrant glutamate signaling endows astrocytes with pro-tumorigenic properties, such as promoting GBM cell proliferation, migration, stemness, and resistance to therapy.

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Charles Gagbe

Ph.D. Student in Nursing Science

How Does Race, Sexual Identity and Sexual Orientation Influence Experiences of Mistreatment and Discrimination of LGBTQ+ Adults in Miami-Dade County?

Background: LGBTQ+ adults continue to experience a disproportionate burden of physical and mental health conditions. Despite being a priority population for HIV prevention and numerous public health initiatives, they continue to experience discrimination and mistreatment when seeking healthcare resulting in poorer health outcomes. Miami-Dade County, is one of the most racially diverse metropolitan areas in the United States and home to a vibrant LGBTQ+ population. This offers a critical context for examining how race, gender identity, and sexual orientation jointly influence experiences of mistreatment and discrimination at healthcare settings.
Methods: An electronic survey as part of a community needs assessment (INCommUNITY- UM IRB Study ID:20231133) was administered to LGBTQ+ adults (n=300) within Miami-Dade County. Percentages and proportions were used to summarize demographic characteristics of participants, Likert-scale measures were used to assess mistreatment and discrimination, and ordinal logistic regression were used to estimate the odds of experiencing mistreatment and discrimination during healthcare encounters.
Results: Participants ranged from 18–71 years (M = 32.13, SD = 9.85). Most identified as gay/lesbian (65.0%) and cisgender male (43.5%); 34.4% were non-Hispanic White. Over one-third (34.1%) reported unfair treatment by healthcare providers, with nearly half attributing these experiences to sexual orientation (49%). Black participants had significantly higher odds of reporting more frequent unfair treatment (OR = 2.087, p = .008) and worse mistreatment (OR = 2.752, p = .008) compared with non-Hispanic Whites. Transgender and non-binary participants had substantially higher odds of unfair treatment (OR = 4.027, p < .001) and mistreatment (OR = 2.990, p < .001) compared with cisgender men. Bisexual participants had lower odds of mistreatment than gay/lesbian participants (OR = 0.575, p = .040).
Conclusion: Healthcare mistreatment and discrimination among LGBTQ+ adults in Miami-Dade are strongly patterned by race, gender identity, and sexual orientation. Black and transgender/non-binary individuals face the greatest burden. Findings underscore the urgent need for culturally responsive, gender-affirming training for healthcare providers to improve care experiences and reduce inequities among LGBTQ+ populations.

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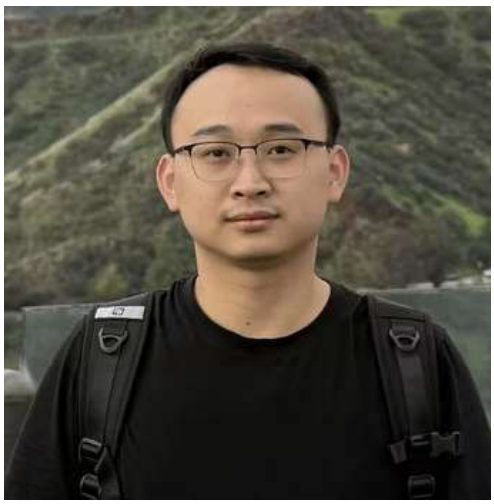

Chengxiang Chen

Ph.D. Student in Chemical, Environmental, and Materials Engineering

Biodegradable Poly-Lysine Crosslinked Multi-Carbonyl Polymers as High-Performance Cathode Materials for Sodium Batteries

As the climate crisis intensifies, developing environmentally friendly, sustainable electrode materials for energy storage has become a global priority. Biomolecules (e.g., proteins, peptides, and amino acids) are attractive alternatives to conventional metal oxides/hydroxides because of their intrinsic safety, low toxicity, abundance, and facile processing. However, many organic electrodes, especially those with aliphatic backbones, remain poorly biodegradable, complicating end-of-life waste management.

Here we introduce a new class of biodegradable cathodes: polylysine-crosslinked polycarbonyl polymers for advanced sodium-ion and potassium-ion batteries (SIBs/KIBs). The key innovation is the simultaneous realization of high electrochemical performance and on-demand degradability enabled by molecular design. These polymers are synthesized by crosslinking biocompatible polylysine (PLL) with polycarbonyl dianhydrides, including PTCDA, NTCDA, and PMDA, forming robust, insoluble networks through imide linkages between PLL amino groups and anhydride functionalities. This architecture mitigates the dissolution issues typical of small organic molecules in electrolytes, while biodegradability arises from controlled hydrolysis of the PLL peptide backbone under mild acidic conditions, yielding environmentally benign amino acids and other non-toxic products. The strategy aligns with circular-economy principles by coupling durable operation with end-of-life decomposition.

The materials were comprehensively characterized by FTIR, solid-state NMR, TGA, SEM, XRD, and XPS to verify structure, stability, morphology, crystallinity, and surface chemistry. Electrochemical properties were evaluated in coin-type half-cells using CV, galvanostatic charge–discharge, rate and long-term cycling tests, as well as GITT and EIS to probe ion transport and charge-transfer kinetics. Future in situ techniques (e.g., in situ XRD/FTIR) will directly track ion–polymer interactions during cycling.

Preliminary results show that PLLPTCDA delivers excellent kinetics and durability: ~125 mAh g^{-1} at 0.05 A g^{-1}, ~75 mAh g^{-1} at 5 A g^{-1}, and stable operation for >1500 cycles at 1 A g^{-1} in SIBs. This performance is attributed to the crosslinked framework, favorable nanostructure, and rapid ion diffusion, leveraging the intrinsically stable redox activity of PTCDA while adding intrinsic biodegradability.

Overall, this work provides a versatile platform for designing high-performance, degradable organic cathodes, advancing truly sustainable battery technologies.

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Christopher Lay

D.N.P. Student in Nurse Anesthesia

Reducing Perioperative Aspiration Risk Using Gastric Ultrasound

Food or liquid in the stomach prior to the induction of anesthesia significantly increases the risk of pulmonary aspiration. Our body can normally prevent aspiration through protective reflexes, but these mechanisms are lost due to unconsciousness and muscle relaxation that occurs with general anesthesia. Despite following recommended fasting guidelines, patients with delayed gastric emptying are at increased risk of having residual contents in their stomach when they arrive to the hospital for surgery. Point-of-care (POC) gastric ultrasound provides real-time assessment of gastric contents and allows anesthesia providers to modify the anesthetic plan to reduce the risk of complications.

The overarching goal of this Doctor of Nursing Practice (DNP) project was to improve preoperative optimization of obese patients with additional risk factors for delayed gastric emptying. Specific objectives included increasing provider knowledge, improving competency in performing POC gastric ultrasound, and increasing provider confidence. The project was conducted at a community-based level II trauma center in South Florida, which is part of a larger academic health system. This facility provides comprehensive surgical care to a variety of patients undergoing both inpatient and outpatient procedures. The primary intervention included a 30-minute didactic lecture followed by hands-on ultrasound-guided training with certified registered nurse anesthetists (CRNAs) and physician anesthesiologists.

The Promoting Action on Research Implementation in Health Services (PARIHS) model is a translational framework used by this DNP project to help guide implementation. The PARIHS model emphasizes the importance of having strong evidence, a supportive context, and knowledgeable facilitators when bringing evidence into clinical practice. Evaluation methods included a pre- and post-education quiz, post-education skills checklist, and post-implementation survey. Data collection and analysis is ongoing with the project currently in the implementation phase. Incorporating POC gastric ultrasound into clinical practice keeps anesthesia providers ahead of the practice curve and allows for objective assessment of aspiration risk in those patients at increased risk for delayed gastric emptying.

Author(s): Christopher Michael Lay

Christopher Roden

Ph.D. Student in Biology

Larval Shape and Swimming Dynamics in Sea Urchin Larvae

Larval sea urchins are a useful system for comparing developmental morphology to whole-organism behavior. However, the extent to which chemically-induced shape changes alter swimming dynamics remains poorly understood. Here, we investigate whether exposure to common environmental chemicals produces quantifiable changes in larval locomotion. Embryos of Lytechinus variegatus were reared under control conditions or treated with Alizarin Red S (45 µM), PFOA (300 µM), or GenX (250 µM) through early development, then washed and recorded in seawater using 2-camera videography. Individual larvae were tracked video analysis software and 3D trajectories were reconstructed to quantify position, velocity, acceleration. Further derived metrics including mean speed, Net to Gross Displacement Ratio (NGDR), and trajectory angle. Analysis showed that exposure produced distinct and treatment-dependent changes in swimming behavior, including changes in velocity magnitude and directionality across axes. This was likely attributed to altered morphology and stability in the water column. Mixed-effects modeling will be used to analyze fixed effects of treatment, axis, and their interaction while accounting for repeated measures within trajectories. Together, these results can demonstrate that morphological perturbations result in quantifiable changes in larval swimming. This work potentially supports a mechanistic link between chemical effects and larval success-relevant behavior.

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Claudia Deveaux Garrido

Ph.D. Student in Civil Engineering

Integrating Biophysical Modeling and Community Codesign to Predict Wave Attenuation Capacity Across Growth Stages of Rhizophora Mangle

Coastal communities face increasing risks from wave-driven erosion and flooding, exacerbated by climate change and intensified locally by human activities such as boat traffic. Ecosystem-based Adaptation (EbA) approaches, including the use of mangrove forests as living coastal defenses, offer flexible and sustainable alternatives to traditional engineered structures. Yet quantitative data on the hydrodynamic performance of mangroves across different growth stages remain limited. The present study evaluates the wave attenuation capacity of Rhizophora mangle (red mangroves) by combining laboratory-scale physical modeling, field-derived structural measurements, and community co-design. Scaled models representing young, intermediate, and mature stands were constructed using structural parameters derived from surveys of 1227 trees across Miami-Dade County (Florida), Belize, and the U.S. Virgin Islands. Prototype geometries, based on allometric relationships, were tested in the SUSTAIN facility under regular waves, JONSWAP irregular waves, storm-surge scenarios, and synthetic boat wakes with a dominant period of 2.0 s. Preliminary results for the youngest age class show that boat wakes are attenuated by up to 18% at 99% stand density and approximately 7% at 33% density. By isolating the effects of stand density, height, and root architecture, this work demonstrates how mangrove development stages shape wave transmission and modify protective function through time. Integrating these hydrodynamic insights with community co-design workshops ensures that EbA strategies reflect local priorities and site-specific needs. Overall, the findings highlight mangroves as dynamic, scalable contributors to hybrid coastal-defense systems, strengthening coastal resilience and supporting sustainable development in an era of growing climate uncertainty.

Author(s): Claudia Deveaux, Sandesh Lamsal, Rafael J. Araújo, Brian Haus, and Landolf Rhode-Barbarigos

Cristina Morales

Ph.D. Student in Music Education

Tracking the Tide: Florida Middle School Chorus Enrollment Trends (2017-2024)

This research poster examines middle school chorus enrollment trends in Florida from 2017 to 2024, exploring potential effects of the COVID-19 pandemic and policy changes. Building on previous studies (Elpus, 2014; Elpus, 2022), this analysis uses county-level data across Florida's 67 counties to provide a comprehensive view of middle school chorus enrollment throughout the state.

The study explores three research questions: (1) What are the overall enrollment trends at the state and county levels, and do these show significant patterns? (2) How did the COVID-19 pandemic and Florida's post-pandemic middle school course requirements affect chorus enrollment patterns? (3) What relationships exist between county demographic factors and chorus program enrollment rates?

The methodology employs quantitative analysis of Florida Department of Education enrollment data covering seven academic years (2017-2024), consistent with prior research examining music enrollments in relation to policy changes (Elpus, 2014) and demographic factors (Salek, 2022). Statistical analysis examines relationships between enrollment patterns and county-level demographic variables, especially socioeconomic indicators from Title I data and free/reduced lunch percentages.

Preliminary findings show that middle school chorus enrollment across the state increased from 2017 to 2019, with changes occurring during and after the pandemic period. The study examines whether counties with higher percentages of economically disadvantaged students experienced different enrollment patterns, which could indicate potential inequalities in access to music education (Abril & Gault, 2008). Geographic disparities are analyzed to determine whether rural counties exhibit different patterns than urban counties. The analysis also evaluates how changes in state policy on elective requirements may have affected chorus participation rates, building on historical observations by Shockley and Irvin (1995).

The findings provide empirical evidence to support targeted advocacy for fair access to music education across Florida's diverse counties. The data may guide how music teacher educators prepare pre-service teachers to sustain programs in various regional settings during disruptions (Cronenberg & Williams, 2023).

By tracking enrollment patterns at the county level over this important seven-year period, this research will add valuable evidence to music education policy discussions and lay a foundation for advocacy efforts to strengthen middle school chorus programs, especially in potentially underserved areas.

Author(s): Cristina Morales

Daniela Neira Fernandez

Ph.D. Student in Nursing Science

Online Information-Seeking and Breastfeeding Beliefs, Intentions, and Practices: A Narrative Review

Background: Breastfeeding is a key public health strategy with well-established benefits for infants and mothers; however, breastfeeding rates in the U.S. remain below national recommendations. While clinical counseling is a primary source of breastfeeding guidance, many mothers increasingly turn to online sources -including social media, websites, mobile applications, and search engines- for breastfeeding information and support. Although prior studies have examined online breastfeeding communities, the ways in which online information-seeking influences breastfeeding beliefs, intentions, and practices remain insufficiently synthesized.
Purpose: This narrative review aimed to examine how online information-seeking is associated with mothers' breastfeeding beliefs, intentions, and practices across diverse populations, using the Health Belief Model as a conceptual lens.
Methods: A narrative review was conducted through a structured search of PubMed, CINAHL, PsycINFO, Web of Science, and Communication & Mass Media Complete, including studies published in English or Spanish with no date restrictions. Quantitative and qualitative primary studies were eligible if they examined mothers' online information-seeking related to breastfeeding beliefs, intentions, or practices.Study selection followed PRISMA guidelines. Thirteen studies met inclusion criteria (five quantitative and eight qualitative studies).
Results: Across studies, Facebook groups were the most frequently examined platform, followed by mobile apps, websites, and Google searches. Findings suggest that online information-seeking is associated with stronger breastfeeding self-efficacy, more positive breastfeeding attitudes, and normalization of breastfeeding through peer reassurance and shared experiences. Sociodemographic differences emerged, with variation in platform use, access, and perceived credibility of information. Studies focusing on African American mothers emphasized the importance of culturally representative online spaces to promote empowerment and reduce stigma. Few studies applied behavioral theory, but findings aligned with HBM constructs, including perceived benefits, barriers, and self-efficacy.
Conclusion: Online information-seeking may function as an accessible extension of breastfeeding support systems by influencing maternal beliefs, intentions, and practices. However, existing evidence is limited by selection bias toward mothers already engaged online and the underrepresentation of emerging social media platforms, highlighting important gaps for future research. These findings have implications for nursing practice and public health efforts to develop equitable, culturally responsive digital breastfeeding support strategies that complement professional care.

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Elka Garcia Rada

Ph.D. Student in Marine Biology and Ecology

Seasonality as a Mechanism Shaping Global Biodiversity Patterns

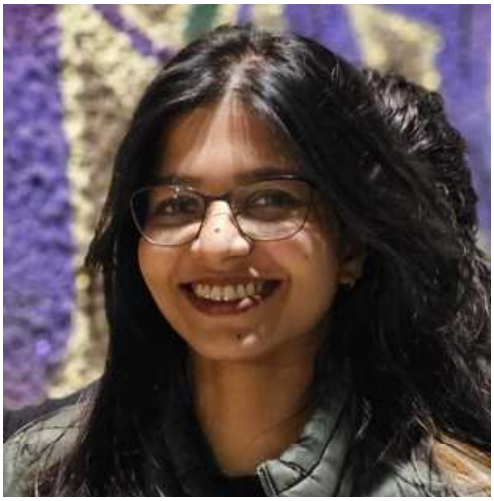
Seasonality, monthly fluctuations in climate and environmental conditions, is one of the fundamental biospheric oscillations shaping life on Earth. It governs species' life cycles, including survival, reproduction, and feeding, and underpins key ecological phenomena such as bird migration, fish spawning, and agricultural timing. While these seasonal patterns are well documented in terrestrial ecosystems, they remain far less understood in the ocean, where environmental signals are more diffuse, highly dynamic, and difficult to observe directly. Consequently, marine biodiversity is still commonly studied using static frameworks based on
long-term environmental averages. In species distribution models (SDMs), this simplification can mask migratory dynamics, seasonal shifts in habitat suitability, and transient ecological functions operating on monthly or seasonal timescales, leading to an incomplete representation of marine biodiversity patterns.

This project evaluates seasonality as a structuring ecological mechanism by extending the AquaX species distribution modeling framework to explicitly incorporate monthly environmental variability. I compare conventional static SDMs with seasonality-aware models calibrated using high-resolution oceanographic climatologies, allowing species–environment relationships to vary through time. Species occurrence data are paired with monthly environmental predictors from Copernicus, including sea surface temperature, chlorophyll a concentration, salinity, mixed layer depth, and zooplankton biomass.

Models are implemented in R using statistical and machine learning approaches and combined to generate robust habitat suitability predictions. This unified modeling framework enables direct comparison between static and seasonal predictions across ecological groups (pelagic or benthic/demersal) and hemispheres. Results reveal temporal structure in habitat suitability that is systematically missed by static SDMs, particularly for highly mobile species, and highlight contrasting seasonal responses across taxa and regions.

Beyond methodological advances, this work addresses a broader macroecological question: how seasonal climate dynamics contribute to the formation of global biodiversity patterns in the ocean. Incorporating seasonality into the SDMs provides a more ecologically realistic representation of species distributions and yields new insights into seasonal richness, turnover, and niche structure at the global scale. These findings have direct implications for understanding marine biodiversity gradients and for informing fisheries management, conservation planning, and dynamic spatial management strategies under climate change.

Author(s): Elka García-Rada, Kristin Kaschner, Yulia Egorova, Juliette Casemajor and Gabriel Reygondeau



Gopika Madhu

Ph.D. Student in Physics

Velocity Correlation Length as a Control Parameter for Emergent Motility in Trichoplax Adhaerens

Coordinated collective motion is a defining feature of animal tissues, yet how tissue-scale coordination arises in living systems without neural control remains an open question. Trichoplax adhaerens, an evolutionary ancient multicellular organism lacking a nervous system, provides a minimal biological system to study mechanically driven collective motility.

We investigate how internal velocity correlations within the tissue control emergent modes of motion, (translation, rotation and pause) in Trichoplax adhaerens. Using time-lapse fluorescence microscopy of the ventral epithelial layer combined with particle image velocimetry (PIV), we extract two-dimensional velocity fields during locomotion. From these velocity fields, we compute isotropic spatial velocity correlation function, , and define a correlation length, , as a quantitative measure of tissue-scale coordination.

Preliminary measurements show distinct correlation lengths associated with different modes of motion. During translational motion, velocity is correlated across the entire organism, with exceeding the organism size, consistent with near-uniform alignment. In contrast, rotational motion exhibits a faster decay of , with limited to approximately 70% of the organism radius, indicating partial coordination. Time-resolved analysis shows that transitions from rotation to translation are accompanied by a pronounced increase in , suggesting that changes in internal correlation precede or accompany changes in overall motion of the organism.

In this work, we propose that the normalized correlation length acts as an effective control parameter governing emergent motility modes. Ongoing work extends these measurements across organisms spanning a wide size range to test scaling relations between , organism size , and motility mode. We further examine whether larger organisms exhibit multiple correlated domains and how inter-domain interactions modify effective correlation lengths.

This work tries to establish that global motion emerges from mechanically mediated correlations and identifies velocity correlation length as a quantitative descriptor linking internal tissue coordination to organism-scale behavior.

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Engineering Enlarged Adeno-Associated Virus (AAV) Capsids

AAVs are ideal vectors for gene therapy and vaccine development due to their minimal pathogenicity and broad infectivity. However, the canonical AAV capsid's limited packaging capacity (<5 kbp) restricts its therapeutic utility. To address this, we have computationally engineered the AAV2 VP3 capsid protein to support larger capsid assembly with a potential genome capacity of up to 25 kbp. VP3 variants were cloned and expressed in E. coli. SDS-PAGE confirmed protein expression at the expected size. Initial transmission electron microscopy (TEM) of purified lysates revealed capsid-like particles, suggesting the possible capsid assembly. However, the identity of the expressed proteins requires validation. Downstream validation assays, including Western blot and ELISA, will be used to assess capsid protein expression and the assembly of small and large capsid phenotypes. Future efforts will focus on structural characterization and evaluating genome packaging capacity. Addressing the critical size constraint may broaden the utility of AAV in gene therapy and vaccination.

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Protein Language Models Reveal Hidden Homology of “Dark” Gene Expression in Ctenophore Phagocytes

Phagocytic cells in the ctenophore Mnemiopsis leidyi express many genes that remain unannotated. This knowledge gap limits our ability to identify explicit cell types with innate immune function. To address this, I tasked structure-based protein language models to explore hidden homology between unannotated Mnemiopsis genes and experimentally characterized proteins in other animals. I annotated protein sets from our whole-animal and phagocyte-enriched cell clusters using FANTASIA, a pipeline that leverages protein embeddings and distance-based matching to assign functions inherited from model-organism embeddings. To further explore relationships in the multidimensional space, I projected low-dimensional spaces using manifold learning approaches such as UMAP. We were able to retrieve >10,000 Gene Ontology terms from Mnemiopsis leidyi´s dark genes expressed by potential immune cells. Our results illustrate that AI methods can enhance functional annotation of ctenophores and the discovery of overlooked cell types, relevant for the evolution of immune repertoires in early-branching animal lineages.

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Escherichia Coli Nissle Bacterial Extracellular Vesicles Modulate Brain Tumor Myeloid Cells

Bacterial extracellular vesicles (bEVs) have emerged as promising immunomodulatory agents for cancer therapy, yet limited understanding of their interaction with the complex tumor microenvironment hampers their clinical translation. We developed a reproducible workflow for the production, characterization, and intracranial administration of immunotherapeutic bEVs in glioblastoma (GBM), the most aggressive primary brain tumor. Escherichia coli Nissle–derived bEVs were isolated using tangential flow filtration (TFF) and size-exclusion chromatography (SEC). Functional potency was quantified using THP-1 Dual Reporter cells. Orthotopic SB28 GBM tumors were established in mice, and bEVs were administered intratumorally via stereotactic injection. Systematic optimization of the bEV production process, yielded consistent and sterile bEV preparations, with 3.84×10^{10} particles and 1.2 mg protein per liter of culture and vesicle sizes of 20–70 nm by electron microscopy. bEVs induced dose-dependent NF-κB and IRF activation in THP-1 cells (ED50 = 5.7 ng/mL, 95% CI: 4.7–7 ng/mL), with responses distinct from heat-killed bacteria and purified endotoxin; one ED50 was defined as a functional bEV unit. In human peripheral blood–derived myeloid cells, bEV exposure increased CD80 and PD-L1 expression while reducing CD163 and CD206. bEV-treated human macrophages exhibited increased expression of CD38 and PD-L1, increased secretion of IL-6, IL-12p40, and IL-12p70 with a profile distinct from heat-killed bacteria. In vivo, maximum tolerated dose was sex-dependent, with 350 bEV units (2 µg) well tolerated and associated with only transient symptoms. A 20% Pluronic F127 / 2% alginate hydrogel enabled sustained bEV release for over three days in vitro and in vivo. Intratumoral bEV delivery altered the GBM immune landscape, increasing inflammatory tumor-associated macrophages and activating tumor-infiltrating $CD8^+$ T cells. This study establishes a reproducible biomanufacturing and potency framework for bEV research and demonstrates the feasibility and safety of intracranial, sustained-release bEV delivery in GBM models. Ongoing studies are evaluating survival outcomes in preclinical GBM.

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Visualizing Multi-Hazard Risk: Design Principles from a Systematic Review

During natural disasters, citizens rely on weather visualizations to make evacuation and preparedness decisions. Visualization design shapes risk understanding and protective behavior: poor design can cognitively overwhelm users, delay action, or lead to unsafe choices. Because weather events often involve multiple threats that co-occur or unfold over time, multi-hazard maps aim to communicate multiple risks simultaneously. Yet, it remains unclear when hazards should be integrated into a single display versus separated across views to best support risk comprehension and protective decision-making. This paper presents a systematic literature review of 11 studies, selected through title, abstract, and full-text screening. Findings were synthesized across three focus areas: hazard relationships, cognitive load, and decision outcomes. Across the literature, there is broad agreement that the effectiveness of integrated displays depends on how hazards relate scientifically and temporally. Integrated maps generally improve comprehension when hazards stem from a shared physical process or co-occur simultaneously (e.g., wind + storm surge during hurricanes). In contrast, combining hazards that unfold over time can introduce temporal bias and misinterpretation, whereas separated formats better support judgment. Cognitive factors further moderate these effects. While dense visuals can increase mental effort and reliance on heuristics, integrating meaningfully related information can reduce cognitive load by minimizing the need for users to mentally synthesize information. Overly salient elements and poorly communicated uncertainty can distort risk perception, diminishing understanding and trust. Importantly, decision outcomes depend not only on visualization structure but also on prior experience and action-oriented guidance. Novices and experienced users respond differently to identical displays, and comprehension alone does not translate into protective behavior without clear cues indicating what action to take and when. Taken together, the literature reveals a key gap: existing studies have not empirically compared integrated versus separate multi-hazard displays while simultaneously accounting for how hazards scientifically relate, cognitive load, and user experience. This review synthesizes findings across these dimensions into design principles for multi-hazard maps, demonstrating that effective integration depends on hazard relationships, how users process information, and what actions the visualization is intended to support. It also provides a foundation for future empirical evaluation.

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Identifying Compositional Effects of Multimetallic Nanoparticles for Catalysis

Nanoparticles play a vital role in catalysis and drug applications because of their unique properties, such as high surface area to volume ratio, quantum effects and tunable properties by adjusting the size, shape and composition of nanoparticles. However, the fundamental understanding of how different metals interact within these nanostructures, particularly as the number of components increases, remains limited. To address this, a series of bimetallic (PdAu, AuAg, PdAg) and trimetallic (AuAgPd) nanoparticles were synthesized using the AuBP1 peptide (WAGAKRLVLRRE) as a biomimetic capping agent. These systems were designed to systematically investigate how varying the composition and combination of gold (Au), silver (Ag), and palladium (Pd) affects nanoparticle formation and catalytic activity. The particles were synthesized via standard approaches and subsequently characterized structurally. The catalytic efficiency of these nanoparticles was then evaluated through the reduction of 4-nitrophenol (4-NP) to 4-aminophenol (4-AP). From this analysis, key compositional criteria have been elucidated to ensure optimized catalytic functionality, which could be exploited for the a priori design of new materials with emergent catalytic properties.

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How Color Shapes Risk Interpretation in Hurricane Hazard Maps

Hazard maps are a critical tool for communicating spatial risk information to both experts and the general public. In hurricane contexts, where decisions must often be made quickly and under stress, visual design choices strongly influence how risk information is perceived and interpreted. Among these choices, color plays a central role due to its pre-attentive processing, strong learned associations, and widespread use in categorical risk systems. However, research on color use in hurricane-specific hazard graphics—such as Hurricane Threat and Impact (HTI) maps—remains fragmented across disciplines and lacks a consolidated evidence base. This paper presents a systematic review of empirical research examining how users comprehend and interpret color-based risk category systems in hazard maps, with a particular focus on implications for hurricane risk communication. A structured literature search across Web of Science, Google Scholar, and institutional library databases identified a final corpus of 16 empirical studies that directly investigate user interpretation of visual risk encodings.

Across the reviewed studies, there is a strong convergence in how color influences the interpretation of risk categories. All studies addressed color perception, and a majority emphasized accessibility and inclusive design, particularly for users with color vision deficiency. The findings indicate that effective color systems rely on perceptual discriminability, monotonic luminance ordering, and semantic alignment with the represented hazard. In contrast, commonly used rainbow color palettes were repeatedly shown to hinder accurate interpretation due to non-monotonic luminance and reduced accessibility. Effective hazard communication requires color to be supported by additional visual and textual cues. Redundant visual cues consistently improved comprehension and reduced misinterpretation, particularly for non-expert audiences. Collectively, these findings support a universal design approach in which color choices are grounded in human perceptual principles and evaluated through empirical user testing.

By synthesizing research across hazard domains, this review provides evidence-based guidance for designing clearer, more accessible color-based risk category systems in hurricane hazard maps. The poster translates these insights into actionable design considerations for improving the effectiveness and inclusiveness of HTI graphics and related hazard visualizations.

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A Qualitative Evaluation on Factors Contributing to LGBTQ+ Community Belonging

A sense of belonging is a key predictor of social well-being and is consistently related to beneficial outcomes such as reduced stress, enhanced satisfaction, and higher resilience. Belonging may be particularly important for marginalized populations such as LGBTQ+ individuals, who face minority stressors such as discrimination that lead to worse mental health outcomes and ostracization. Belonging among LGBTQ+ people can thus act as a significant protective factor against such minority stressors. Individuals who feel belonging within the LGBTQ+ community report higher self-esteem and hope as well as lower depressive symptoms and suicidality. Despite the extensive research on the strong link between LGBTQ+ sense of belonging and well-being, factors that foster the feeling of belonging are not well explored and conceptualizations of belonging vary. In the present study, we qualitatively analyzed the responses from 408 LGBTQ+ participants who indicated the factors they believed contributed to their sense of belonging in LGBTQ+ communities. Using qualitative reflexive thematic analysis, we identified six key themes that participants reported, including mutuality, personal authenticity, active engagement, having an accepting environment, existing relationships in the community, and LGBTQ+ representation. These findings provide specific factors of belonging for future research efforts, and the highlighted themes can promote higher well-being for LGBTQ+ individuals through informing outreach programs and advocating for enhanced belonging in LGBTQ+ spaces.

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Engineering Resilin-Like Peptides Conjugated with Gold-Binding Domain for Nanomaterial Synthesis and Characterization

Resilin, a member of the elastic protein family found in arthropods has recently gained significant attention due to its remarkable elasticity and durability than that of polybutadiene. Resilin peptides produced from natural proteins have attracted a lot of interest in biomaterials research because of their high strain, low stiffness, and effective energy storage.[1] It exhibits remarkable biocompatibility and self-assembly properties, making it an ideal candidate for engineering hybrid biomaterials.[2] In this study, a hybrid peptide composed of a resilin-like peptide (RLP) coupled with a gold-binding peptide (AuBP1)[3] was designed, characterized, and applied to enhance nanomaterial synthesis and biomaterial development. The adsorption behavior and binding kinetics of the conjugated peptide and non-conjugated peptides on gold surfaces were observed using Quartz Crystal Microbalance (QCM) investigations. Additionally, the work delves into the synthesis of gold-based nanomaterials functionalized with resilin peptides, and characterised using UV-Visible Spectroscopy and TEM analysis.

To explore its potential on 3D surfaces, preliminary studies on tyrosine-mediated crosslinking of the hybrid peptide in solution were conducted. These experiments suggest that the peptide can undergo crosslinking, although its behavior on 3D surfaces remains to be fully investigated. This novel approach demonstrates the potential of peptide engineering to create multifunctional materials with enhanced mechanical properties. The findings underline the synergy between resilin-like elasticity and AuBP1's gold-binding specificity, paving the way for innovative bio-nanomaterial designs.

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Associations Between Intimate Partner Violence, Medication Adherence, and Reasons for Missed Medication among Black Women Living with HIV

Background: Black women living with HIV (BWLWH) face structural and interpersonal challenges that shape their medication adherence. Intimate partner violence (IPV), including physical, sexual, and emotional abuse, has been linked to struggles with treatment engagement and adherence to HIV care.
Methods: 258 BWLWH in the Southeastern United States were examined if higher levels of IPV contribute to adherence difficulties and individual reasons for missed medication. Participants completed self-report measures assessing sociodemographics, intimate partner violence, and HIV medication adherence. Intimate partner violence was assessed at baseline using the Woman Abuse Screening Tool (WAST), an eight-item measure capturing physical, sexual, and emotional abuse. Medication adherence and adherence-related psychosocial functioning were evaluated using the AIDS Clinical Trials Group (ACTG) Adherence Baseline Questionnaire, which includes items assessing missed doses and reasons for nonadherence. R-Studio was used to conduct linear regressions examining whether WAST total scores predicted ACTG total scores and individual reasons for missed medication.
Results: Participants' ages ranged from 25 to 83 years (M = 54.37, SD = 10.3). Relationship status varied across women, with a large portion of women being single (n = 113) and others being in a non-cohabiting relationship (n = 29) or not married but living with a partner (n = 23). WAST scores ranged from 1 (min) to 21 (max) (M = 8.73, SD = 3.66; n = 166). ACTG total scores ranged from 0 to 38 (M = 6.28, SD = 7.71; n = 252). WAST total scores significantly predicted ACTG total scores ($b = 0.59$, $SE = 0.16$, $t(164) = 3.71$, $p < .001$), indicating that higher IPV significantly predicted greater non-adherence. Regressions examining individual ACTG items revealed that higher IPV was significantly associated with missing medications due to being away from home, being busy, forgetting, having too many pills, avoiding side effects, changes in routine, falling asleep, feeling ill or depressed, timing difficulties (e.g., with meals), and running out of pills.
Conclusion: Findings show that IPV is linked to practical and emotional barriers broadly, affecting medication-taking behavior among BWLWH. IPV may be a critical barrier to HIV self-management due to its impact on adherence and reasons for missing medications.

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Ocean Circulation as a Missing Driver in Climate-Based Marine Biodiversity Projections

Marine species are rapidly redistributing in response to climate change, reshaping global biodiversity patterns across ocean basins. Species Distribution Models (SDMs) are widely used to project these shifts by estimating habitat suitability based on environmental conditions. However, most SDMs implicitely assume that species can immediately access all newly suitable habitats, neglecting the role of ocean circulation in constraining dispersal and connectivity. Because ocean currents govern transport pathways for most marine organisms, ignoring these physical processes can lead to unrealistic projections of future species distributions.

This study presents a global modeling framework that integrates ocean-driven connectivity into climate-based species distribution projections to be more realistic. Habitat suitability index is first estimated using the AQUAX modeling framework, generating present and future Habitat Suitability Index (HSI) maps under climate change scenatios. Dispersal and connectivity are then simulated using the Connectivity Modelung System (CMS), which tracks particle transport driven by ocean circulation. Connectivity outputs are then used to constrain future habitat suitability by limiting species' potential ranges to areas that are both environmentally suitable and physically accessible.

The workflow is demonstrated using a case study on the Chagos brain coral (Ctenella chagius) highlighting strong differences between potential habitat distributions predicted by SDMs alone and accessible habitats constrained by connectivity. Results show that dispersal limitations substantially restrict future suitable areas, emphasizing the importance of ocean circulation in shaping species redistribution under climate change.

Overall, this framework shifts biodiversity projections from potential to accessible habitats, providing a more realistic representation of marine range shifts. Ongoing work focuses on scaling this approach to over 32,000 marine species to generate improved global biodiversity forecasts. By explicitely incorporating oceanographic connectivity into SDMs, this methodology offers a critical advancement for assessing climate-driven changes in marine ecosystems and informing conservation and management strategies.

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Microporosity-Controlled Carbon Molecular Sieve Membranes for Propylene/Propane Separation: Simulation- and Machine Learning-Enabled Structure-Property Analysis

A series of 6FCDA-based fluorinated copolyimides (FCPs) were synthesized via controlled polycondensation to engineer chain packing and microporosity relevant to propylene/propane separation. Copolymerization of 2,2′-dimethylbenzidine with an ether-linked aromatic dianhydride and a mixed-diamine system (2,4,6-trimethyl-1,3-phenylenediamine and 4,4′-oxidianiline) was used to disrupt segmental packing, increase fractional free volume, and improve solubility in polar aprotic solvents, enabling robust film formation and subsequent conversion to carbon molecular sieve (CMS) membranes via controlled pyrolysis. The resulting copolyimides exhibited high thermal stability, supporting their use as CMS precursors.

Single-gas permeation of C_3H_6 and C_3H_8 at 35 °C revealed pressure-dependent transport consistent with dual-mode sorption and microporosity-mediated diffusion selectivity. To connect chemistry to microporosity quantitatively, we combined experiment-informed modeling with molecular simulation. Dual-mode sorption/transport fitting was applied to permeation trends, while molecular dynamics (MD)–based amorphous polymer models were constructed to extract density, fractional free volume, pore-size and bottleneck distributions, and void connectivity. Gas uptake and solubility descriptors were obtained via grand canonical Monte Carlo (GCMC), and gas diffusivities were estimated from MD mean-squared-displacement analyses, enabling a structure-grounded decomposition of permeability (P = D×S) and selectivity drivers. For aging, accelerated densification states were used to emulate physical aging–induced microporosity evolution and to rationalize permeability–selectivity tradeoffs over time.

A lightweight, uncertainty-aware machine-learning regression integrated monomer-level composition variables with MD/GCMC-derived microporosity descriptors and experimental performance metrics to map structure–property relationships and identify dominant drivers governing permeability, selectivity, and pressure sensitivity. Among the synthesized polymers, the DAM/ODA molar ratio of 3:1 (FCP-31) delivered a C_3H_6 permeability of 271 Barrer and an ideal C_3H_6/C_3H_8 selectivity of 3 at 1 bar, evolving to 199 Barrer and ~4 after 60 days of dry N_2 aging at 25 °C. Carbonization yielded CMS membranes with substantially enhanced selectivity (fresh: ~8 Barrer, ~16 at 1 bar), with pressure-dependent declines up to 6 bar; after 60 days of ambient storage, C_3H_6 permeability decreased to ~5 Barrer while selectivity increased to ~19, consistent with aging-driven ultramicroporosity tightening. Overall, monomer-level backbone design coupled with MD/GCMC-enabled microporosity quantification and ML-based mapping provides a tunable platform for microporosity-controlled CMS membranes targeting efficient propylene/propane separation.

Keywords: Carbon molecular sieve (CMS) membranes, Propylene/propane (C_3H_6/C_3H_8) separation, Microporosity and ultramicroporosity control, Molecular dynamics (MD) and grand canonical Monte Carlo (GCMC), Machine learning–enabled structure–property mapping

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Probing the Iron Center of CthEgtB: A Mössbauer Framework for O2-Dependent Sulfoxide Formation

Ergothioneine biosynthesis relies on the non-heme Fe(II) enzyme CthEgtB, a sulfoxide synthase that catalyzes the oxygen-dependent formation of a C-S bond between trimethylhistidine and L-cysteine. While optical spectroscopy and rapid-mixing kinetics have established that catalysis is tightly coupled to O_2 binding and proceeds on sub-millisecond timescales, the electronic structure, oxidation state, and spin configuration of the catalytically relevant iron species remain unresolved. These questions are central to understanding how CthEgtB activates O_2 and directs selective sulfoxide formation.

Mössbauer spectroscopy provides a uniquely powerful approach for interrogating non-heme iron enzymes, offering direct access to iron oxidation state, spin state, and coordination environment through isomer shift and quadrupole splitting parameters. In related non-heme Fe systems, Mössbauer spectroscopy has been instrumental in distinguishing resting Fe(II) centers from substrate-bound species, identifying Fe-O_2 derived intermediates, and resolving changes in electronic structure with unparalleled site specificity.

Here, we present our motivation for applying Mössbauer spectroscopy to characterize CthEgtB and summarize representative Mössbauer signatures from analogous non-heme iron enzymes to establish benchmarks for data interpretation. Building on our prior spectroscopic and kinetic characterization of CthEgtB, we outline key mechanistic questions that Mössbauer spectroscopy is uniquely positioned to address, including the nature of the resting iron site, substrate-induced electronic rearrangements, and changes in iron speciation upon O_2 exposure. Finally, we describe planned Fe-57 Mössbauer experiments designed to correlate iron electronic structure with defined catalytic states, providing a framework for integrating Mössbauer data with complementary kinetic and spectroscopic measurements to advance mechanistic understanding of CthEgtB catalysis.

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Experimental Investigation of the Coupling of Wind and Wave Loads Under Hurricane Conditions

Understanding the coupled impacts of wind, storm surge, and waves on coastal infrastructure during extreme tropical cyclones remains a major challenge for coastal communities. Current building codes typically evaluate wind and wave forces using independent models that are then combined through factored combinations, which may not fully capture the combined loading that occurs during severe storms. This research aims to experimentally investigate how tropical storm and hurricane winds, storm surge, and waves interact at high wind speeds and their coupled actions on coastal buildings. Experiments are conducted in the Alfred C. Glassell, Jr. SUrge-STructure-Atmosphere Interaction (SUSTAIN) Laboratory wind-wave facility at the University of Miami's Rosenstiel School of Marine, Atmospheric, and Earth Science, capable of simulating Category-5 hurricane conditions with controllable wind and wave forcing. In these tests we simulate wind-only, wave-only, and coupled conditions to measure their effects on a scale house model. Wind speeds are measured with pitot tubes, wave heights are recorded with wave wires, while wind pressures and wave forces are captured using pressure tabs and a load cell mounted on the front face of the model house. To ensure physically valid scaling, the model house height is restricted to one-half of the valid wind profile height, consistent with prior studies. Preliminary results consist of baseline measurements of wind-only and wave-only loads, which establish reference conditions for future coupled testing. The next stage of the work focuses on developing scaling relations based on Reynolds and Froude similarity so that combined wind and wave experiments can be conducted appropriately. Ultimately, this research will help guide on the coupled action of wind and wave loading and support the development of more resilient coastal design practices.

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Engineering Sustainable Concrete with Chemical Modifications to Improve Coral Larval Recruitment on Artificial Reefs

In the wake of intensifying climate change combined with ever-increasing populations in coastal regions, there is a critical urgency in protecting our coastlines and ecosystems. Submerged offshore structures, known as artificial reefs, have emerged as a solution for ecological improvement, habitat preservation, and coastal defense. However, the use of traditional concrete in artificial reef construction raises concerns related to its carbon footprint, poor ecological performance, and susceptibility to erosion. This study investigated the use of modified cementitious materials to enhance natural coral larvae settlement on artificial reefs, leading to increases in biodiversity and coastal protection. The role of chemical cues in larval settlement was explored, motivated by previous evidence that coral larvae exhibit attraction to calcium carbonate-rich substrates in natural reef systems. Experimental cement paste tiles (3 x 3 cm) were developed with various chemical modifications alongside sustainable cement industry practices, including the use of supplementary cementitious waste products and carbonation curing to mitigate carbon emissions. Two approaches were evaluated: (1) uncarbonated tiles incorporating direct mineral additives (limestone, olivine, sodium carbonate), and (2) carbonated tiles combining supplementary cementitious waste products (fly ash, slag) and carbonation curing to precipitate calcium carbonate phases. Tiles were conditioned in seawater and exposed to coral larvae of Colpophyllia natans over a 20-day settlement period in a temperature-controlled chamber. Tiles of each modification were tested in individual glass jars (n = 8) with 50 larvae per jar. Particle tracking methods were also used to quantify larval swimming behavior during the settlement period. Results demonstrated higher settlement on uncarbonated tiles relative to the carbonated tiles. Sodium carbonate-containing tiles exhibited significantly higher settlement than all other tiles. By incorporating minerals that serve as chemical cues in conventional concrete mixes, artificial reefs can be engineered to promote biological recruitment, contributing to reef restoration efforts and coastal resilience.

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Skin Bacterial Dysbiosis and Associated Immune Responses in Hidradenitis Suppurativa

Hidradenitis Suppurativa (HS) is a chronic, inflammatory skin condition leading to the formation of painful nodules, abscesses, and sinus tracts. HS significantly impacts patients' quality of life due to pain, scarring, and drainage. While the currently approved treatments primarily target HS inflammation, the role of associated dysbiosis remains unknown. Our recent findings highlight the emerging significance of anaerobic pathogens including Actinotignum schaalii, abundant in both early and late-stage HS. We hypothesize that A. schaalii functions as an ecological driver at the HS onset by providing microbial fitness for co-colonization of obligate anaerobes.

We developed the first HS bacterial biobank, derived from deep HS tunnel tissue and enriched for clinically relevant slow-growing anaerobic taxa including Actinotignum, Prevotella, Peptinophillus, and Porphyromonas. This resource provides a foundation for mechanistic studies examining bacterial colonization, cooperative survival strategies, and metabolic cross-feeding networks supporting persistent dysbiosis in HS.. We also used C57BL/6 GδT/GFP reporter mice to model early HS-like inflammation by intradermal injection of A. schaalii, commensal Staphylococcus epidermidis was used as a control. Murine lesions were analyzed by bacterial quantification, histopathology, immune infiltration, and metatranscriptomics.

Mice infected with A. schaalii developed abscesses mirroring early HS lesions in humans. CFU analysis confirmed A. schaalii persistence in tissue, while S. epidermidis, was cleared by neutrophils. Metatranscriptomic analyses of colonized murine tissue demonstrated that A. schaalii not only persisted but actively reshaped the murine skin microbiome. Dual RNA-seq and bacterial community analyses showed decreased abundance of murine commensals and enrichment of facultative anaerobes, indicating that A. schaalii reorganizes local microbial networks during early lesion development. The murine inflammatory signature triggered by A. schaalii included robust neutrophil activation, IL-17 and TNF-α pathways, as well as activation of Th17 and γδ T cells, consistent with the chronic inflammation in human HS lesions.

We demonstrate that A. schaalii shows resistance to innate immune clearance, allowing it to drive both microbsial restructuring and chronic inflammation within HS lesion. Ongoing studies explore A. schaalii interactions with Prevotella, Peptinophillus, and Porphyromonas to elucidate cooperative mechanisms that promote microbial persistence and disease progression.

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Cardiometabolic Biomarkers Performance for Early Detection of Metabolic Risk in Hispanic Pediatric Populations

Background:Pediatric metabolic syndrome (MetS) lacks a unified definition and standardized laboratory thresholds, complicating screening and cross-study comparability. Guidelines differ on required components, cut-offs, fasting requirements, demographics and growth trajectories points over childhood. In this context, simple biomarkers and indices (e.g., lipid ratios, insulin sensitivity etc,.) are attractive, but their relative performance and independence remain uncertain.

Methods: We performed a secondary analysis of The Study of Metabolic Syndrome in Hispanic Children in Northeast Tennessee. The sample included 84 participants from 2 -10 years old with complete outcomes, confounders, and biomarkers. The primary endpoint, metabolic risk, was defined as ≥2 abnormal components among waist circumference, blood pressure, glucose, triglycerides, and HDL-cholesterol. We conducted five separate (cholesterol/HDL, Triglycerides/HDL, TyG, AIP, HOMA-IR) logistic models with adjustments made for age, sex, and BMI followed by a final multivariable model including all indices with metabolic risk as the outcome variable. Discrimination was assessed with receiver operating characteristic (ROC) curves; operating characteristics were summarized at a 0.50 threshold.

Results: MetS Risk prevalence was 39.3%. In individually adjusted models (per 1-SD), TG/HDL (odds ratio [OR]15.14, 95% CI 3.54-64.77), AIP (OR 9.87, 95% CI 2.95-33.06), and cholesterol/HDL (OR 6.91, 95%CI 2.64-18.12) were strongly associated; TyG was moderate (OR 3.18, 95% CI 1.45-6.98); HOMA-IR was not significant (OR 2.02, 95% CI 0.76-5.34). In the multivariable model, only cholesterol/HDL retained independent association (OR 4.53, 95% CI 1.10-18.62). The full model showed excellent discrimination (area under the curve [AUC] 0.960, 95% CI 0.921-0.998) and strong performance at 0.50 (sensitivity 87.9%, specificity 92.2%, positive predictive value 87.9%, negative predictive value 92.2%). Individually, lipid-derived biomarkers showed good discriminative performance, with AUCs of 0.875 for TG/HDL and AIP and 0.872 for cholesterol/HDL, while TyG (0.783) and HOMA-IR (0.742) demonstrated acceptable discrimination.

Conclusions: In the context of heterogeneous pediatric definitions and varying laboratory practices, lipid-derived ratios (TG/HDL, AIP, and cholesterol/HDL) demonstrate better discriminative performance for metabolic risk. Notably, cholesterol/HDL emerged as the only independent predictor. Its simplicity and performance suggest that cholesterol/HDL may serve as a practical early-screening marker in pediatric settings.Further research is needed to validate this approach across diverse populations and standardized pediatric thresholds.

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Mucoadhesive Nanoemulsion via Engineered Anionic Surfactant-Chitosan Interactions for Enhanced Delivery of Fucoxanthin

Fucoxanthin (FX) is a marine-derived carotenoid with strong antioxidant and neuroprotective potential, making it a promising candidate for Alzheimer's disease therapy. However, its lipophilic nature and poor aqueous solubility limit its bioavailability. To reach the brain, FX must also bypass the blood-brain barrier (BBB).

Intranasal administration offers a non-invasive route that can bypass the BBB, but its success depends on a formulation that can protect FX and promote efficient nose-tobrain transport. This work focuses on designing a mucoadhesive nanoemulsion (NE) with potential for intranasal delivery of FX, by engineering interactions between an anionic surfactant and the cationic polymer, chitosan at the droplet interface to understand the influence of these interactions on mucoadhesion and colloidal stability. To elucidate the role of interfacial charge dynamics, we use a combination of characterization techniques including UV-vis spectrophotometry, dynamic light scattering, high performance liquid chromatography and zeta potential. Findings guide the preparation of NE systems and ongoing work is focused on optimizing formulation parameters and processing conditions to further reduce droplet size, improve NE stability and FX-NE encapsulation efficiency. Overall, this work advances the development of a nose-to-brain delivery platform for FX, offering a promising therapeutic approach for neurogenerative diseases.

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Engineering Human Fibroblastic Reticular Cell-Based Reticula for Antigen-Specific Tolerance Induction in Type 1 Diabetes

Type 1 Diabetes (T1D) is a chronic autoimmune disease in which dysregulated T cell responses to autoantigens drive the destruction of pancreatic beta-cells. 50% of the genetic risk for T1D stems from specific HLA alleles, specifically HLA class II haplotypes, which mediate antigen presentation and T cell activation in the immune response. Lymph node (LN) Fibroblastic Reticular Cells (FRCs) are non-conventional antigen-presenting cells (APCs). While conventional APCs switch to immunogenic phenotypes under inflammation, FRCs sustain a tolerogenic phenotype contributing to peripheral tolerance in LNs. Harnessing FRCs for specific regulation of autoreactive T cells in T1D could lead to new T1D prevention therapies. Previous work demonstrated that implantable 3D murine FRC-based engineered reticula can regulate diabetogenic T cells via presentation of T1D-relevant antigens. Here, we assess the translatability of these findings for human clinical application. Gelatin scaffolds were generated using our previously reported protocol. Human FRC (hFRC) lines (n=3) were generated by enzymatic digestion of LNs from healthy donors with high-T1D-risk HLA types. 15k hFRCs were seeded onto scaffold sections. Reticula formation and cell viability was assessed by immunofluorescence and confocal microscopy. hFRC lines primed with self-antigens were co-cultured in vitro with antigen-specific CD8+ Jurkat T cell clones for 48hrs and T cell engagement by FRCs assessed by flow cytometry. The macroporous scaffold sections supported hFRC attachment and reticular formation with in vitro survival of hFRCs in scaffolds for at least 7 days. hFRCs maintained a tolerogenic phenotype (CD86low, CD80low, PD-L1hi) and overexpressed antigen-presenting machinery (MHC-I, MHC-II) under inflammation. Auto-antigen–primed hFRCs engaged antigen-specific cytotoxic T cells, as evidenced by upregulation of early (CD69) and late (CD25) activation markers, as well as the exhaustion marker PD-1, indicative of tolerogenic engagement. Ongoing studies are testing 3D engineered hFRC reticula as LN-like microenvironments.

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Socioecological Factors Associated with HIV Risk among Latina Transgender Women in the Americas: A Scoping Review

Background: Latina Transgender Women (LTW) experience a disproportionately high burden of HIV. This HIV risk is not driven solely by individual behaviors but arises from interacting intrapersonal, interpersonal, organizational, community, and structural factors that shape access to prevention and care. While such multilevel determinants have been documented among TW in other global regions and are known to predispose this key population to HIV vulnerability, evidence specific to LTW in the American Continent remains limited, fragmented, and has not been synthesized.

Purpose: To identify and synthesize empirical evidence on HIV risk factors among LTW guided by McLeroy's social ecological model.

Methods: A scoping review was conducted through a systematic search of PubMed, CINAHL Plus, Web of Science, and ProQuest, including studies published between 2016 and 2025 in English or Spanish. Quantitative, qualitative, and mixed-methods studies were eligible if they examined HIV risk factors among Latina transgender women in alignment with McLeroy's ecological model. Eighteen studies met the inclusion criteria, including seven quantitative, two mixed-methods, and nine qualitative studies.

Results: Multilevel factors shaped HIV risk among LTW. At the intrapersonal level, condomless sex, substance use, depressive symptoms, and low risk perception were common. Interpersonal dynamics such as economic dependence, intimate partner violence, sexual coercion, and family rejection undermined autonomy and self-care. Organizational barriers included discrimination in health services, limited gender-affirming care, and misinformation about PrEP, restricting access to prevention. At broader community and structural levels, stigma, labor exclusion, migration challenges, and lack of legal recognition amplified vulnerability and constrained opportunities for HIV protection.

Conclusion: HIV vulnerability among LTW in the American continent reflects interconnected determinants across socioecological levels: behavioral risks intersect with interpersonal violence and economic dependence, while organizational discrimination and structural stigma restrict prevention. These findings underscore systemic drivers beyond individual behaviors and call for multilevel, gender-affirming, and culturally responsive interventions integrated with policy reforms. Strategies that dismantle stigma, expand access to gender-affirming care, and address social inequities are essential to strengthen the HIV response and advance health equity for these women. This scoping review contributes by synthesizing previously fragmented evidence on HIV risk among LTW in the Americas.

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A Novel Extracellular Targeting Strategy for Receptor Tyrosine Kinase Drug Development

Cells communicate with one another through highly coordinated signaling systems that regulate development, tissue maintenance, and responses to injury. Receptor tyrosine kinases (RTKs) are a major class of proteins that span the cell surface and play a central role in these intercellular communication networks. When RTK signaling becomes dysregulated, it can contribute to a wide range of diseases, including cancer, neurodegeneration, and vascular disorders. Although RTKs are important therapeutic targets, most existing drugs focus on blocking their intracellular kinase activity. While effective in some contexts, this strategy often suffers from limited specificity, unintended off-target effects, and the rapid emergence of drug resistance. Here, we present a novel and integrative approach to RTK drug development that instead targets extracellular receptor-ligand interactions to disrupt the initial contact points responsible for enabling cell-cell communication (CCC). Using the Eph-ephrin system, the largest family of RTKs, we establish a rational pipeline for identifying and validating disease-relevant therapeutic targets. Our strategy begins by analyzing single-cell RNA sequencing datasets to infer patterns of CCC, enabling the prioritization of key receptor-ligand interactions active within specific tissues and disease contexts. We then apply computational modeling and structural analysis to characterize the extracellular binding interfaces of these receptors and ligands and infer the critical molecular interactions that can be leveraged in drug design. To experimentally evaluate lead compounds, we developed a live-cell, fluorescent-based approach that directly measures extracellular binding events with high sensitivity and minimal background signal. Unlike other assays commonly used to study RTKs that rely on antibodies or downstream signaling readouts, this platform enables direct and quantitative assessment of binding affinity in a physiologically relevant cellular environment. Together, this workflow provides a scalable framework for discovering extracellular RTK antagonists with improved specificity and translational potential. More broadly, these findings highlight extracellular targeting as an underexplored yet promising strategy for next-generation drug design, offering a complementary and potentially synergistic alternative to the traditional kinase-focused approaches.

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Targeting the OX40 Pathway in Alopecia Areata: Early Clinical Evidence and Therapeutic Implications

Introduction: The co-stimulatory receptor OX40 (CD134) and its ligand OX40L play a key role in alopecia areata (AA) pathogenesis by promoting T cell activation, survival, and memory formation. Inhibition of this pathway has emerged as a biologically rational strategy for downregulating autoreactive T cell activity.

Methods: A narrative review of PubMed and ClinicalTrials.gov (2020-2025) was conducted using the terms "OX40," "OX40L," "CD134," "alopecia areata," "IMG-007," and "OX40 blockade." Sources included mechanistic studies and early clinical development of IMG007, a non-depleting anti-OX40 monoclonal antibody. Key outcomes included severity of alopecia tool (SALT) score change, biomarker modulation, dosing, safety, and tolerability.

Results: In the Phase 2a trial IMG-007 trial (NCT06060977), 29 adults with moderate-to-severe AA received 300mg (n=6) or 600mg (n=23) IV at weeks 0, 2, and 4, with follow-up to week 24 and optional extension to week 36. The higher-dose cohort demonstrated mean SALT reductions of 14.3% at week 24 and 21.7% at week 36, with 25% achieving ≥30% improvement by week 36. Adverse events were mild to moderate and included infections and infusion reactions, with no serious treatment-emergent events. Scalp biopsy biomarker analyses revealed downregulation of Th1, Th2 and CD8+ T cell inflammatory signatures.

Conclusion: OX40 pathway inhibition demonstrates early clinical activity with favorable tolerability in AA. Although regrowth magnitude is modest compared with JAK inhibitors, durability after short induction and mechanistic specificity support continued clinical development and optimization of dosing and patient stratification.

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Multi-Physics Predictive Modeling of Parameter Set Development Framework for Predictive Modeling in Laser Powder Bed Fusion of Titanium Alloys

Parameter set development (PSD) for laser powder bed fusion (LPBF) is often empirical, alloy-specific, and inefficient, limiting both physical insight and transferability across material systems. This project presents a standardized, physics-informed PSD framework applied to Ti-6Al-4V and commercially pure titanium (CP-Ti Grade 2) to identify low-porosity processing windows while generating structured data for predictive modeling. The framework integrates single-track (line), multi-track (sheet), and volumetric (cube) experiments to systematically characterize laser–powder–substrate interactions, track overlap behavior, and three-dimensional porosity formation. Quantitative features extracted from line and sheet experiments, including melt pool geometry, track continuity, and hatch distances, are correlated with volumetric density and pore morphology measured in cube specimens using optical microscopy and micro-computed tomography, enabling objective screening of process stability prior to volumetric validation. Top-performing parameter sets are further evaluated through mechanical testing and detailed microstructural characterization to establish process–structure–property relationships. These experimentally derived features, augmented with material thermophysical descriptors and physics-based constraints, are used to train a physics-informed machine learning model capable of predicting porosity trends and material behavior within the LPBF process space. Model performance is evaluated using holdout experimental data and an inverse-design validation strategy, wherein target material outcomes are used to infer processing parameters that are subsequently fabricated and experimentally assessed. This work demonstrates a data-efficient, physically interpretable PSD methodology that bridges experimental materials science and machine learning, while providing a foundation for transfer learning to additional alloy systems and accelerated LPBF material development.

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Trait Mindful Self-Compassion Buffers Glucocorticoid Resistance and Stress-Related Immune Dysregulation in Women with PTSD

Background: Dispositional self-compassion mindfulness (SCS-M) facilitates psychological regulation and stress management, showing inverse links with PTS symptomology via modulation of HPA axis and immune responses. Alterations in cortisol reactivity to stress predicts PTSD onset and severity. Mindfulness-based interventions can positively influence glucocorticoid receptor (GCR) sensitivity, where immune cells become less responsive to cortisol's anti-inflammatory effects. Yet the role of trait SCS-M in glucocorticoid sensitivity among trauma-exposed populations remains unclear.

Aims: To test whether trait SCS-M predicts GCR-sensitivity changes after trauma recall in women with PTSD, and whether SCS-M moderates the link between cortisol levels and cytokine responses in LPS-stimulated monocytes.

Methods: Seventeen women (mean age 48.6) with PTSD completed the Self-Compassion Scale, including mindfulness subscale, and a standardized trauma recall paradigm. Salivary cortisol was collected at baseline and post-task. Glucocorticoid sensitivity was assessed via the value at which dexamethasone inhibits monocyte IL-6 in LPS-stimulated blood by 50% (IC50). Repeated-measures ANOVA tested time × SCS-M group effects (high vs. low, median = 47.8) on IC50. Covariates (BMI, HIV, ethnicity, age, IES, PCL-5) were included. Multiple regression examined whether trait mindfulness moderates the cortisol-IC50 relationship.

Results: A significant time × SCS-M group interaction on IC50 emerged, $F(1,15) = 6.76$, $p = .020$, $\eta^2 = .311$, indicating that individuals higher in trait SCS-M showed lower IC50 values post-task, reflecting enhanced glucocorticoid sensitivity. Adjusted model confirmed the SCS-M effect; HIV status and IES were also significant predictors. Moderation analysis showed that SCS-M significantly moderated the relationship between variations in cortisol and IC50 ($p = .041$). At higher levels of SCS-M, the negative association between cortisol and IC50 was stronger ($\beta = -0.53$, $p = .011$, 95% CI [−0.90, −0.15]), suggesting a protective effect of SCS-M on immune-endocrine dynamics.

Conclusions: These findings suggest that the balanced awareness of painful thoughts and emotions, i.e., trait SCS-M, may enhance monocyte sensitivity to glucocorticoids in women with PTSD, thereby reducing GCR and mitigating stress-related immune dysregulation. Findings further support extant research highlighting the biological benefits of mindful and self-compassion-based approaches. If replicated, such trait-level factors could inform personalized clinical strategies to improve endocrine-immune functioning in trauma-exposed individuals.

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Polymeric Microneedle Tattoo Patch for Stress-Free Animal Identification, Performance Tracking, and Real-Time Health Monitoring

Animal identification and health monitoring are essential for farm management; however, current methods, like ear notching, tattooing, and rectal thermometry, are invasive, stressful, and poorly scalable. While RFID tags and thermal imaging reduce handling stress, they remain expensive and unreliable. Innovative approaches are needed to enhance animal welfare and provide accurate, low-cost tools. This project proposes a polymeric microneedle (MN) scannable QR-code tattoo patch as a minimally invasive platform for simultaneous animal identification and real-time health monitoring in farm animals.

A patch prototype incorporating multiple MN arrays with uniform distribution and well-defined dimensions was developed. Engraved molds for MN patch fabrication were designed using CAD software and fabricated via laser cutting, enabling the incorporation of patterns such as QR codes, blood type identifiers, the Star of Life, donor symbols, and crosses. The cutting pattern significantly influenced MN geometry and height: cross-cutting produced pyramid-shaped MNs (~680.30 ± 18.77 μm), spiral-cutting yielded conical MNs (~999.83 ± 20.62 μm), and star-cutting resulted in taller pyramidal MNs (~1475.94 ± 19.69 μm) with sharper testator analysis confirmed successful ink incorporation while preserving the chemical composition of both the polymer matrix (polyvinyl alcohol) and the tattoo ink. MN functionality was further validated through an in vitro dissolution assay using ballistic gel, a widely accepted skin-mimicking model, which demonstrated effective ink release. Approximately 70% dissolution occurred within 10 minutes, accompanied by a progressive reduction in MN height from 1000.78 ± 49.87 μm at t_0 = 0 min to 181.38 ± 18.80 μm at t_3 = 10 mi. Additionally, QR-code MN patches incorporating thermochromic powder were fabricated. These MN-based biosensors exhibited a reversible color response, transitioning from pink at 22 °C to yellow at 40 °C and returning to pink upon cooling.

MN patches are a versatile tool for animal management. Scannable QR-code tattoos enable minimally invasive identification, while thermochromic biosensors allow stress-free health monitoring. Their low cost, multifunctionality, and noninvasiveness make MN tattoos a promising solution to improve swine welfare and farm efficiency.

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Genomic Population Connectivity of Reef Fish Abudefduf vaigiensis in the Indo-Pacific Ocean

Coral reef fishes serve as a model group for understanding processes of speciation within marine environments, primarily due to their broad geographic ranges and long pelagic larval stages. Recent advancements in genomic techniques have enabled precise analysis of fine-scale traits that contribute to genetic differentiation among reef fish populations, ultimately influencing their evolution and distribution. The Indo-Pacific Sergeant Major, Abudefdufvaigiensis, is widely distributed across the Indo-Pacific Ocean, despite being a demersal spawner with a relatively short pelagic larval phase. These characteristics make A. vaigiensis an ideal model species for investigating population connectivity. In this study, we analysed patterns among 842 individuals of A.vaigiensis collected from 37 locations across the Indo-Pacific, spanning six biogeographic provinces (the Hawaiian Archipelago, the Indo-Polynesian, the Red Sea, the Western Indian Ocean, the Sino-Japanese, and the Southeastern Australian province). Samples were sequenced using double-digest restriction site-associated DNA sequencing (ddRAD) to generate genome-wide Single Nucleotide Polymorphisms (SNPs). Using SNPs, we aim to identify barriers to dispersal and genetic breaks of A.vaigiensis across the range and to assess patterns among neutral and outlier loci to infer ecological divergence based on local adaptations to environmental and geographic factors. Implementing phylogenetic inference aims to understand lineage divergence among distinct populations.

Specific attention is given to populations in the Red Sea and the Southeastern Australian provinces, where genetic differentiation is expected to correlate with latitudinal environmental gradients. Fine-scale analyses are also conducted across the Hawaiian Archipelago, which represents a non-native range for A.vaigiensis. By leveraging SNPs, this study is expected to reveal strong population structure across the region and identify key ecological and biogeographic drivers of these patterns, offering new insights into the processes influencing speciation and adaptation in the ocean.

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How Does the Type of Waveform Affect Tolerability With Transcutaneous Auricular Vagus Nerve Stimulation?

Purpose: Vagus Nerve Stimulation (VNS) is a promising tool for pain management, with known effects on autonomic balance. However, there are a growing number of available devices, with varying parameters. It is unknown if the waveform used affects the efficacy or the tolerability of VNS, both of which significantly affect outcomes. The purpose of this study was to 1) determine if there is a difference in tolerability between monophasic and biphasic wave forms and 2) examine differences between these waveforms in their effect on heart rate variability (HRV). We hypothesized that (1) the waveforms would be equally tolerable, and (2) the biphasic waveform would produce a greater increase in heart rate HRV due to the continuous cycle which results in twice the amount of energy input.

Methods: A double blinded randomized crossover design was used. Subjects attended 2 sessions, receiving biphasic (continuous) and monophasic (50% duty cycle) VNS. Semi-structured interviews were used to assess subject preference. HRV was assessed pre and post VNS as a measure of autonomic function. Differences between waveform conditions in HRV (pre minus post) were assessed using the Wilcoxon Signed Ranks Test, and sex differences were assessed using the Mann-Whitney test. Investigators who coded the interview transcripts and processed the HRV data were blinded to the condition for each visit.

Results: Overall, there were no significant differences in tolerability or HRV effects between waveform conditions, with 14 out of 30 preferring biphasic. The mean changes ± SD in SDNN were also similar for biphasic and monophasic. However, there were sex differences in HRV response, with males demonstrating a greater increase in SDNN under both conditions.

Conclusions: There was no difference in subject preference or effect on HRV between biphasic and monophasic waveforms with VNS. However, males tended to have a greater increase in HRV than females with both wave forms.

Clinical Relevance: Individual factors and preference may be more important than waveform when choosing devices for VNS, this is encouraging for clinical use as it means more people can effectively use VNS.

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Human Marrow-Isolated Adult Multilineage Inducible Cells-Derived Extracellular Vesicles (MIA-EVs) Exhibit a Conditioning-Resistant miRNA Regulatory Backbone and Enhanced Regenerative and Immunomodulatory Network Pathways Versus Conventional MSC-EVs

Introduction: The origin and physiological state of parental cells shape extracellular vesicle (EVs) cargo and biological activity. Human marrow-isolated adult multilineage inducible (MIAMI) cells represent a defined mesenchymal subpopulation with a pronounced anti-inflammatory phenotype, offering a more standardized EVs source than heterogeneous mesenchymal stem/stromal cell (MSC) populations. Here, we compare the miRNA cargo and regulatory architecture of EVs derived from naïve MIAMI cells (MIA-EVs), irradiation-conditioned MIAMI cells (MIA-IR-EVs), cytokine-primed MIAMI cells (TNFα, IFNγ, and CTGF; collectively referred to as TIC priming factors; MIA-TIC-EVs), and conventional MSCs to define conserved and adaptive regulatory programs.

Methods: MIAMI cells were cultured under low oxygen tension on fibronectin-coated substrates, while MSCs were maintained under standard conditions. MIA-, MIA-IR-, MIA-TIC-, and MSC-derived EVs were isolated by differential ultracentrifugation and characterized by nanoparticle tracking analysis, transmission electron microscopy, flow cytometry, and surface marker profiling in accordance with MISEV2023 guidelines. miRNA cargo was profiled using a 166-miRNA qPCR array (GeneCopoeia) and analyzed using miRNet 2.0 with experimentally validated targets.

Results: MIA-EVs contained 138 detectable miRNAs with 19 highly expressed species, dominated by miR-4466, miR-7975, and miR-4454, converging on networks governing RTK–PI3K–AKT–mTOR survival signaling, growth factor/angiogenic programs, DNA damage control, metabolic homeostasis, immune sensing (TLR/JAK–STAT), and anti-inflammatory regulation (TGF-β/SMAD, PPAR-related nodes). Priming reshaped cargo loading: MIA-IR-EVs (113 miRNAs; 25 highly expressed) were dominated by miR-136-5p, consistent with stress-response programming, while MIA-TIC-EVs (99 miRNAs; 35 highly expressed) were enriched for miR-140-5p and immunoregulatory miRNAs linked to cytokine responsiveness. Despite stimulus-dependent shifts, a conserved 15-miRNA high-abundance module persisted across MIAMI-derived EVs, indicating a conditioning-resistant regulatory backbone. MSC-EVs showed broader detectability (153 miRNAs; 12 highly expressed) but a more restricted shared 9-miRNA core. Although MIA- and MSC-EVs share a mesenchymal miRNA framework, MIAMI-derived EVs amplify expression magnitude and regulatory network connectivity.

Conclusions: MIAMI-derived EVs preserve a conserved, conditioning-resistant miRNA regulatory backbone across naïve, irradiated, and cytokine-primed states, coordinating survival, stress adaptation, and regenerative functions. Conditioning modulates pathway weighting without altering core network identity, indicating refinement rather than reprogramming. Compared with MSC-EVs, MIA-EVs expand regulatory depth across regenerative, cytoprotective, and immune axes, supporting their potential as a robust EVs-based therapeutic platform.

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Parotid Dose-Response and Xerostomia Risk in Head and Neck Cancer Treated With IMPT and IMRT

Background: Xerostomia (“dry mouth”) is one of the most frequent and debilitating toxicities in head and neck (H&N) radiotherapy, affecting up to 90% of patients. Salivary gland dysfunction results in persistent oral dryness, compromising speech and nutrition and often leading to chronic symptoms that reduce quality of life. Despite the normal tissue sparing advantages of proton therapy, xerostomia remains a major dose limiting toxicity. This study evaluates the incidence of xerostomia in patients treated with intensity-modulated proton therapy (IMPT) and intensity-modulated radiation therapy (IMRT), comparing unilateral (UT) and bilateral (BT) treatment plans while accounting for parotidectomy status, and characterize dose-response relationships using parotid gland dosimetry.

Methods: A total of 172 H&N patients treated at the University of Miami with IMPT or IMRT were included. In patients with parotidectomy, parotid dose data were unreliable, therefore, analyses focused on comparing xerostomia incidence across modalities (IMPT and IMRT). Patients without parotidectomy were further grouped by modality and laterality (UT and BT). UT patients were assessed by analyzing the ipsilateral parotid doses and BT patients were assessed by analyzing the combined parotid doses. Boxplots and normal tissue complication probability (NTCP) curves were generated for each modality and treatment plan for analysis.

Results: Patients with or without parotidectomy do not show a significant toxicity difference when treated with IMPT ($p=0.32$) or IMRT ($p=0.15$). Among parotidectomy patients, 62% treated with IMPT developed xerostomia, compared with 91% treated with IMRT ($p=0.032$). Among BT patients, cumulative mean parotid dose was higher in patients with xerostomia; this difference was significant for IMRT ($p<0.001$) but not for IMPT ($p=0.267$), likely due to limited sample size. NTCP curve analysis demonstrated left-shifted curves for IMPT in both laterality groups, indicating lower tolerance doses for 50% complication probability (TD50) compared with IMRT. The derived relative biological effectiveness (RBE) was 1.55 for the UT cohort and 1.57 for the BT cohort.

Conclusions: QUANTEC-based parotid dose constraints may inadequately classify xerostomia risk. The RBE for salivary gland toxicity in IMPT is substantially higher than the conventional constant value of 1.1.

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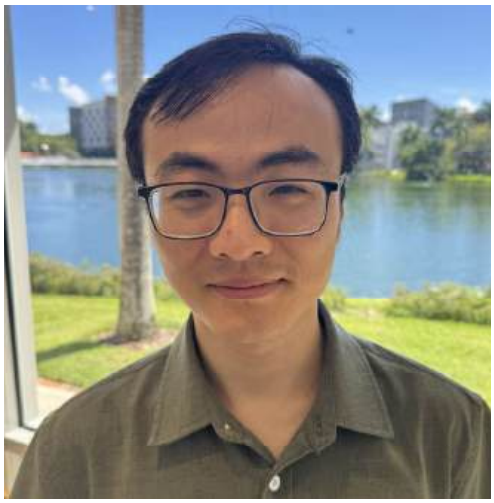

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Experiential Learning Principles in General Music Teaching Approaches: A Content Analysis of the Literature

While theories associated with constructivist learning have long served as frameworks in music education studies, there have been limited systematic efforts to apply constructivist learning methodologies in general music education. Studies indicated that experiential learning, as a constructivist learning methodology, informs general music teaching. Therefore, a systematic exploration of experiential learning principles will guide future research on constructivist learning and general music teaching practices.

This inductive content analysis aimed to explore the principles in experiential learning literature and their connections to general music teaching approaches. The following questions guided the study: (a) What principles underlie experiential learning, and how are they related? (b) How do these principles connect to Dalcroze Eurhythmics and Orff Schulwerk?

The data corpus for analysis consisted of journal articles and book chapters on experiential learning principles, identified through keyword searches and snowball sampling, with inclusion or exclusion based on predefined criteria. The data were coded at the sentence-unit level into themes, and the themes were further grouped into larger categories based on both their meanings and a process that measured their similarities using the Jaccard Index. An experiential learning philosopher evaluated the findings to enhance trustworthiness, and reflexivity was applied to examine the researcher's potential positionality.

Thirty-four themes emerged, of which 31 were identified as experiential learning principles and categorized into 5 groups: Fundamental principles, Psychological process of experiential learning, Student-centered learning, Psychological development and growth, and Individual and society. The researcher then compared the themes with the identified principles in the Orff and Dalcroze literature and found that they aligned with all 31 principles, although differences exist across the principles in Individual and Society.

In contrast with some experiential learning approaches, Orff and Dalcroze sought to change society through aesthetic education rather than through political action. In addition, Orff and Dalcroze are relatively more structured than experiential learning in practice. The 31 identified principles of experiential learning align with the constructivist principles introduced in prior music education literature and will guide further empirical research on their relationships. They also provide general music teachers with a framework for organizing and reflecting on their teaching.

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Targeting the SAGA Chromatin-Modifying Complex as a Therapeutic Vulnerability in Multiple Myeloma

Multiple myeloma (MM) remains an incurable hematological malignancy, underscoring the need for new therapeutic targets. Analysis of CRISPR dependency scores from the DepMap Cancer Dependency Portal shows that several top essential genes in MM encode components of the Spt-Ada-Gcn5 acetyltransferase (SAGA) complex, including EP300, TAF5L, SUPT20H, TADA1, TAF6L, and TADA2B, alongside critical transcription factors such as IRF4, PRDM1, and MAF. These findings suggest an MM-specific dependency on transcriptional activation driven by the SAGA complex, which coordinates transcription factors, enhancer activity, and chromatin architecture to sustain oncogene expression.

We hypothesize that genetic or pharmacologic disruption of SAGA function will selectively impair MM cell survival while sparing non-malignant cells, representing a novel therapeutic strategy that addresses current limitations, including antigen escape and the lack of agents targeting essential transcriptional regulators. To evaluate this, we performed pharmacologic inhibition and siRNA-mediated knockdown of SAGA components and assessed effects on cell viability and oncogene expression across multiple MM cell lines.

Pharmacologic inhibition of the SAGA histone acetyltransferase (HAT) subunit GCN5 using MB-3 was tested in six MM cell lines with diverse chromosomal translocations. IC50 values varied, indicating differential sensitivity. In KMS-11 cells, MB-3 produced a dose-dependent reduction in FGFR3 expression, decreasing from control levels to 0.7-fold at 119 nM ($p = 0.0689$), 0.2-fold at 238 nM ($p = 0.0002$), and remaining low at 476 nM ($p = 0.0041$). NSD2 in KMS-11 and CCND1 in KMS-27 exhibited similar dose-dependent suppression. Conversely, PCM6 cells showed dose-dependent upregulation of MAF and ITGB7, demonstrating cell-line-specific transcriptional responses to GCN5 inhibition.

To further probe transcriptional vulnerabilities, we evaluated the p300 inhibitor Inobrodib and the dual BET/CBP/p300 inhibitor NEO2734 in KMS-11 cells. Inobrodib displayed potent activity with a ~70 nM IC50. NEO2734 yielded an unstable IC50 but induced strong viability loss at lower doses than Inobrodib, suggesting greater potency; validation studies are ongoing.

siRNA knockdown experiments showed that silencing components of the HAT module produced stronger viability reductions than targeting the Core module. Knockdown of SFG29 and TADA2B reduced viability by 41% and 36%, respectively. Silencing IRF4, IKZF1, IKZF3, MAF, and PRDM1 produced the strongest effects, with IRF4 knockdown reducing viability by 60% in KMS-11 cells. Future work will explore combinatorial targeting of SAGA components using dual siRNA approaches and synergistic inhibitor combinations to identify therapeutic strategies with maximal efficacy in MM.

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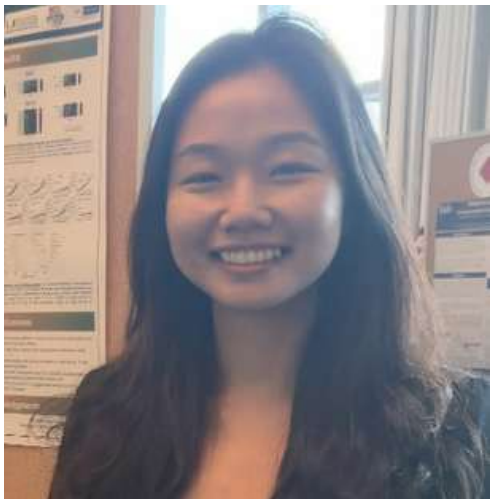

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Role of PNCK in Renal Cell Carcinoma Progression

PNCK is a poorly characterized CaMK family member that has been linked to aggressive tumor phenotypes and poor clinical outcomes in several cancers. Analysis of TCGA data in renal cell carcinoma (RCC) identified PNCK as the most highly overexpressed kinase and showed that its expression is associated with reduced patient survival. In vitro, PNCK overexpression enhances RCC cell growth and cell cycle progression, whereas PNCK inhibition induces growth arrest. This study aims to define the in vivo role and mechanisms of PNCK activation and inhibition in RCC progression.

Two RCC cell models (786-O and ACHN) were used. PNCK overexpression (OE) was achieved by lentiviral transduction, and PNCK knockout was generated using an inducible CRISPR-Cas9 system. PNCK expression was validated by qPCR, Western blotting, and immunofluorescence. For 3D culture, single spheroids were generated by seeding 3000 cells per well in ultra-low attachment 96-well plates with indicated Matrigel concentrations, and growth was assessed by diameter or area. Multiple spheroids were generated by embedding 12000 cells in 75% Matrigel domes. For in vivo studies, control and PNCK-OE cells were injected subcutaneously into the left flank of nude mice. Tumor size was measured, and tumor cells were subsequently isolated and re-cultured.

In vivo, PNCK-overexpressing tumors grew faster than control tumors, and mice bearing OE tumors exhibited reduced survival. Tumor cells isolated from OE tumors maintained elevated PNCK expression compared to controls, supporting a tumor-promoting role for PNCK in vivo. These cells successfully formed spheroids in Matrigel-containing media, with OE spheroids displaying enhanced invasive behavior relative to controls. Consistently, ACHN PNCK-OE spheroids showed increased growth rates compared to control spheroids. Genetic ablation of PNCK in ACHN OE cells using CRISPR-Cas9 reduced spheroid growth, indicating that PNCK is required for tumor growth.

In conclusion, PNCK overexpression promotes tumor growth in vivo, whereas genetic loss of PNCK delayed tumor growth in 3D spheroid models. These findings support a critical role for PNCK in RCC progression. Future studies will focus on elucidating the molecular mechanisms underlying PNCK function.

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Sustainable and Affordable Batteries for Next Generation

The ever-growing demand for electric transportation and grid-scale energy storage underscores the imperative for the development of sustainable energy storage technologies. While lithium-ion batteries dominate the market, their scalability is constrained by limited lithium reserves and reliance on costly transition metals, motivating the exploration of alternative chemistries based on earth-abundant elements. As a result, Na-ion batteries (NIBs) and K-ion batteries (KIBs) are critical for grid-scale energy storage owing to low cost and natural abundance of sodium and potassium resources. However, state-of-the-art cathode materials exhibit limitations in terms of cycling stability, power density, and performance under extreme temperature conditions. To address these challenges, we developed three-dimensional mesoporous polyimides with engineered flexible alkyl chains and rigid conjugation structures to manipulate crosslinked structures and porosity in the polyimides for high structure stability and fast reaction kinetics in NIBs and KIBs. We have a hypothesis that both specific surface area and pore volume are expected to influence electrochemical performance. However, due to their strong interdependence and the limited range accessible in the present material system, it remains challenging to quantitatively decoupling their individual contributions. Our results suggest that their impact may not be governed by a single monotonic trend but instead depend on the specific structural window. Such structural characteristics are expected to affect not only the reversible capacity, but also long-term cycling stability, rate performance, and the initial Coulombic efficiency, particularly through their impact on electrolyte accessibility, interfacial reactions, and ion-transport kinetics. Overall, electrochemical behavior is governed by a complex interplay from surface area, pore volume, structural stability and other chemical interaction rather than a single structural parameter. While moderate porosity can facilitate electrolyte penetration and ion transport, excessive surface area or pore volume may intensify interfacial side reactions and structural degradation, thereby compromising cycling stability and initial Coulombic efficiency. Moreover, the relative contributions of these parameters appear to be highly dependent on the accessible structural window, leading to non-linear and sometimes opposing effects on rate capability and long-term durability. These observations underscore the necessity of optimizing structural balance instead of pursuing maximized porosity, providing important guidance for the rational design of high-performance polymer-based electrode materials.

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Design and Characterization of Cross-Bar Pressure Sensors for High-Resolution Force Mapping

This project advances the development of a wearable ECG “smart shirt” by combining electrode material innovation, impedance characterization, and full hardware–software integration. Novel PEDOT: PSS-CMC hydrogels, carbon fabrics, and silver cloth electrodes were synthesized and tested under stationary and overnight conditions, with crosslinking, ultrasonic treatments, and vapor-barrier or sponge-wick strategies extending hydration and enabling stable ECG signals for over 12 hours. A dedicated Arduino Nano 33 IoT–based impedance measurement device was developed to quantify electrode–skin interactions with ~5% accuracy over 100 Ω–1 MΩ, addressing the limitations of DC-only resistance measurements. In parallel, a complete ECG system was built using an AD8232 front-end and Arduino Nano ESP32, implementing Pan–Tompkins QRS detection and arrhythmia classification with wireless BLE/Wi-Fi data transmission to companion PC and iOS applications for real-time visualization and alerts. Together, these efforts demonstrate a pathway toward a washable, comfortable, and reliable ECG shirt that integrates optimized electrode materials with robust signal processing and communication, enabling long-term monitoring, arrhythmia detection, and timely alerts for at-risk individuals.

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Hexaazatrinaphthylene (HATN) Fused Carboxylate Organic Electrode for Fast Charging and Robust Sodium-Ion Batteries (SIBs)

Organic electrode materials have emerged as sustainable and structurally tunable alternatives to conventional inorganic counterparts for next-generation sodium-ion batteries (SIBs). In this work, we report the rational design and synthesis of a hexaazatrinaphthylene-carboxylate (HATN-COONa) compound as a high-performance organic cathode. The molecular architecture integrates a redox-active hexaazatrinaphthylene (HATN) core with electron-withdrawing carboxylate groups, which not only enhance Na^+ binding capability but also suppress solubility in organic electrolytes. The chemical structure of HATN-COONa material was confirmed by FTIR, solid-state NMR, and mass spectrometry. Electrochemical characterizations reveal a high reversible specific capacity exceeding 300 mAh g^{-1}, excellent rate performance, and long-term cycling stability. The improved performance is attributed to the cooperative Na^+-carboxylate coordination and the extended π-conjugation of the HATN core, which simultaneously facilitate the rapid electron/ion transport and structural integrity during redox cycling. Moreover, the synthesized HATN-COONa can remain outstanding low-temperature performance, demonstrating the fast ion diffusion and good structural integrity of HATN-COONa in low-temperature. This work provides a new molecular-level design strategy for constructing stable and high-capacity organic cathodes, offering valuable insights for the development of sustainable and practical energy storage systems.

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Quantifying Coral Morphology and Turbulence to Understand Microenvironment Carbonate Chemistry Variability

Corals exhibit remarkable architectural diversity, and this morphological variation governs how water moves across the tissue surface and how ions are transported across boundary layers. Although it has long been recognized that morphology can enhance or limit a coral's ability to regulate microenvironment carbonate chemistry, the geometric variables and length scales that mediate turbulence, residence time, and flux remain poorly understood.

We examined skeletons of 32 western Atlantic coral species representing a range of gross morphologies. High-resolution 3D meshes were generated for each colony using a white-light 3D scanner and used to calculate fine-scale morphometric measurements and widely used continuous geometric descriptors, including surface complexity, volume compactness, and top-heaviness. These metrics were then paired with 2D particle image velocimetry (PIV) derived flow fields measured in a controlled laboratory flume to resolve turbulence structure, shear stresses, and boundary-layer thicknesses around the corals. By comparing geometric variables with observed flow characteristics, we elucidated the key geometric variables that structure a coral's capacity to modulate microenvironment carbonate chemistry.

Results indicate that geometric variables capturing fine-scale roughness better predict mass transfer than bulk descriptors alone. When contextualized with literature-derived estimates of species-specific metabolisms, these biophysical models explain some of the variance observed in differential OA sensitivities. Rather than identifying a single predictive geometric measure, this work constrains which morphometric scales matter and how they shape mass transport across coral surfaces. Ultimately, this work advances a form–function framework for forecasting demographic shifts and accretion potential under future ocean conditions.

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Qualitative Analysis of Causes for Religious Withdrawal among Queer People

Affiliating with and participating in religion has been linked with a myriad of positive mental health outcomes, such as a heightened sense of purpose, life satisfaction, and social well-being. Religious affiliation can further act as a protective factor against stressors. However, for minoritized populations such as LGBTQ+ individuals, religion can be a source of conflict, rejection, and stress, particularly among religions where the main doctrines are against same-gender sexual behaviors and/or gender expansive expression. As a result, many LGBTQ+ people choose to change or leave their religions. However, little is known about the specific reasons that LGBTQ+ people give for changing or leaving their religions. To rectify this gap, the present study used thematic analysis among 276 religious or post-religious LGBTQ+ adults who answered the question, “If you have changed or left your religion, what were your reasons for doing so?” We identified seven themes from participant responses: Loss of belief, religious reevaluation, LGBTQ+ identity conflict, interpersonal struggles, religious harm, religious disillusionment, and pursuit of alternative spiritual pathways. Findings from the present study can inform mental health practitioners and religious community leaders regarding the most common reason for religious disaffiliation among LGBTQ+ people, which can lend itself to the creation of complementary interventions to foster a safer and more inclusive religious environment for this population.

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Translation and Validation of the Modern Homonegativity Scale Among Spanish-Speaking LGBTQ Caregivers Sample

Background: Homonegativity refers to the negative attitudes, feelings, or actions directed towards LGBTQ individuals, has been consistently associated with adverse mental health and social outcomes. Modern Homonegativity Scale (MHS) is widely used to assess contemporary forms of homonegativity among diverse populations. Despite Hispanic/Latinx caregivers been a population that faces cultural and religious expectations around caregiving and stress due to the sexual and gender identity of their child, the MHS has not previously been translated or validated for use among Spanish-speaking populations, nor specifically among LGBTQ caregivers. This shows a significant gap, given the cultural, linguistic, and caregiving contexts that shape attitudes toward sexual and gender diversity within Hispanic/Latinx communities.

Purpose: The purpose of this study was to translate the 12-item MHS into Spanish and evaluate the psychometric properties among Spanish-speaking LGBTQ caregivers living in the U.S.

Method: Data were drawn from a sample of 100 Spanish-speaking caregivers who participated in a broader validation study of the LGBTQ Caregiver Acceptance Scale. The MHS-12 was translated from English to Spanish by a native Spanish-speaker. The back translation was from Spanish to English which was done by a native Spanish-speaker and then compared to the original MHS. Analyses were conducted using a Classical Test Theory framework, including descriptive statistics, exploratory factor analysis (EFA), item-total correlations, and internal consistency reliability.

Results: The total sample included 100 Spanish-speaking LGBTQ caregivers with mean age of 38.49 years (SD=9.22). Two items demonstrated weak item-total correlations and poor alignment with the underlying construct in the single-factor solution. The 10-items MHS demonstrated a good reliability (alpha= .936). All retained items showed strong corrected item-total correlations.

Discussion: Our findings suggested that the revised MHS is reliable measure to assess homonegativity among Spanish-speaking LGBTQ caregivers. This study contributes to the development of culturally and linguistically appropriate measurement tools and highlights the importance of examining how caregiving roles and cultural context may shape expressions of homonegativity. Future research should focus on qualitative study to examine why the two removed items did not perform well among this sample.

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Freeze-Dried Macroporous Microparticles as Injectable Cell Scaffolds for Regenerative Medicine

Statement of Purpose: Biomaterial scaffolds are central to regenerative medicine, providing degradable templates for tissue repair and therapeutic cell delivery and physiomimetic 3D in vitro models. Bulk macroporous scaffolds support vascularization and tissue ingrowth but require invasive surgical implantation and are space limited. Injectable scaffolds overcome these limitations but typically require cell encapsulation and they limit host tissue ingrowth necessary for integration. Granular microgels improve upon injectable scaffolds but still restrict tissue ingrowth to the limited packing space of solid particles. Here, we describe a novel freeze-dried injectable macroporous microparticle scaffold that combines injectability with intrinsic macroporosity, enabling cell loading without encapsulation and increasing host integration capability. This platform was evaluated for therapeutic delivery of tolerogenic fibroblastic reticular cells (FRCs), as well as for injectability and biocompatibility in murine models.

Methods: Gelatin type B microparticles were fabricated by dispersing an aqueous gelatin solution in olive oil, followed by glutaraldehyde crosslinking, acetone washing, trehalose resuspension, freezing at −80 °C, and lyophilization. Particle size distribution was measured by laser diffraction, and pore morphology was assessed by scanning electron microscopy (SEM). For cell studies, 200k murine FRCs were seeded onto 2 mg of microparticles under gentle agitation and cultured for 7 days prior to fixation, staining, and confocal imaging. For in vivo testing, 2 mg of cell-free microparticles were injected subcutaneously into 11-week-old non-obese diabetic (NOD) mice and evaluated for biocompatibility using ultrasound.

Results: Microparticles exhibited an average diameter of 499.4 ± 142.9 μm. Microparticle SEM analysis revealed a highly porous architecture with an average pore size of 80.9 ± 24.8 μm. Confocal imaging confirmed FRC infiltration and formation of interconnected 3D reticular networks that persisted over 7 days. Microparticles were successfully injected into mice without analgesics, and no adverse reactions were observed. All injected mice survived 36 days post-implantation and ultrasound imaging confirmed macroporous microparticle suitability for biocompatibility assessment.

Conclusions: Freeze-dried macroporous microparticles function as injectable, biocompatible cell delivery scaffolds that support FRC organization and survival, offering a promising new platform for regenerative medicine applications.

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Social Support and Music Performance Anxiety Among Collegiate Double Bass Students

According to a content analysis of string music education research, the double bass is the least explored instrument among the string family (Sciaroni et al., 2023). This scarcity necessitates for more studies involving the double bass and explore its pedagogy. While performance anxiety has been widely studied, it is important to explore its factors among double bass students because understanding these influences can provide insights into how social environments may contribute to managing performance anxiety. I categorized social support into different sources for this study: family, studio peers, and studio teacher, each of which may play a significant role in having a healthy performance mindset. This study examined the relationship of music performance anxiety and social support in collegiate double bass students. It also investigated how these variables varied by degree level. The following research questions were addressed:

1. How does social support among double bass students vary by degree level?
2. How does music performance anxiety among double bass students vary by degree level?
3. How does social support relate to performance anxiety among double bass students?

The theoretical framework for this study was guided by the Kenny Music Performance Anxiety Inventory (K-MPAI) (Kenny, 2009) and the concept of Multidimensional Scale of Perceived Social Support (MSPSS) (Zimet et al., 1988). K-MPAI, a 40-item scale has demonstrated excellent internal reliability (Cronbach's alpha = .94; Kenny, 2009). MSPSS, a 12-item scale has shown great internal consistency (Cronbach's alpha = .930; Pina et. al, 2025). These frameworks allowed for exploration on how social support may contribute to managing performance anxiety, through correlation and mean scores comparison analyses.

A survey, including K-MPAI and MSPSS that was adapted to align with the double bass studio context was administered to collegiate double bass students in the United States. By investigating the relationship between performance anxiety and perceived social support, this study sought to provide valuable insights for educators and researchers in music pedagogy, focusing on how social relationships influence students' performance psychology. The findings may inform strategies to strengthen social support systems in music programs, that may enhance music students' health and well-being.

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Mapping Single-Strand DNA Break Landscapes in Primary Lateral Sclerosis Using SSiNGLe

Introduction: Single-strand breaks (SSBs) are among the most common forms of DNA damage, yet their genome-wide distribution and relationship to neurodegeneration remain poorly understood. Primary lateral sclerosis (PLS) is a rare neurodegenerative disorder characterized by progressive upper motor neuron degeneration. This study investigates SSB patterns in patient-derived induced pluripotent stem cell (iPSC) neurons from PLS patients compared to isogenic healthy controls using Single-strand break mapping at nucleotide genome level (SSiNGLe).

Methods: SSiNGLe was performed on iPSC-derived neurons from 6 PLS patients and 4 healthy patients. A bioinformatic pipeline incorporating preprocessing, enrichment analysis, and statistical comparisons was developed. SSB enrichment was quantified across five major genomic element types (insulators, promoters, enhancers, exons, and introns) by calculating odds ratios of observed versus expected SSB frequency.

Results: PLS neurons exhibited significantly higher SSB enrichment at transcription start sites (TSS) compared to healthy controls (median 2.01% vs. 1.89%, p=0.016, Cohen's d=2.39). Promoter region analysis (±1000bp from TSS) confirmed elevated SSBs in PLS samples (mean 2.01% vs. 1.81%, p=0.016). Genome-wide enrichment analysis revealed PLS samples showed significantly greater SSB enrichment at insulators (median odds ratio 2.716 vs. 2.382, p=0.031, Cohen's d=1.053), promoters (2.324 vs. 2.074, p=0.039, Cohen's d=1.029), and enhancers (2.179 vs. 2.001, p=0.020, Cohen's d=1.077), with large effect sizes indicating biologically meaningful differences. No significant differences were observed at exons or introns. Gene ontology analysis of genes with SSB enrichment in promoter regions revealed significant enrichment for biological processes related to DNA damage response, neuronal function, and neurodegenerative disease mechanisms, indicating that SSBs occur preferentially in genes functionally relevant to disease pathophysiology.

Discussion: The enrichment of SSBs at regulatory elements in PLS neurons suggests transcriptional dysregulation in genes critical for neuronal function. This pattern indicates SSBs may preferentially accumulate at regulatory regions controlling neurodegeneration-relevant pathways in PLS. These findings establish SSB profiling as a potential biomarker for neurodegenerative disease and highlight the pathogenic role of transcription-coupled DNA damage in PLS pathophysiology.

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Size-Related Physiological Variation in a Sibling Cohort of Aplysia californica

Across species, the fast-slow continuum positions populations along a life-history axis, with fast species showing rapid growth, early reproduction, short lifespan, high mortality, and many offspring, and slow species exhibiting the antithesis of these traits. The pace-of-life-syndrome (POLS) framework explains how evolutionary, ecological, behavioral, and physiological traits are traded off across an organism's lifespan along the fast-slow continuum.

Although the POLS framework has been used to compare and understand life strategies between species, fewer studies test whether these patterns persist among individuals of the same species or even sibling cohort reared under uniform conditions. At National Aplysia Resource which is the only facility worldwide rearing Aplysia californica throughout their life cycle including sibling cohorts, notably, discernible size differences are observed among sibling cohorts raised under facility's standard conditions. Therefore, this study investigates whether there are physiological explanations for the size difference within a cohort of Aplysia and whether these differences are consistent with a slow or fast life strategy within a sibling a cohort. Multiple hypotheses were formulated, predicting that larger individuals would exhibit faster specific growth rates, higher metabolic rates, lower viral loads, and greater reproductive capacity, consistent with a fast life strategy, while smaller individuals would show the opposite, consistent with a slower life strategy.

With our group of experimental animals (n=60), the size ranged between 0.035 kg to 0.137 kg, representing approximately fourfold difference between groups. Despite this, there was no relationship between specific growth rate and body size when Aplysia were maintained on the same diet. In our results, larger Aplysia had larger gonads, while smaller individuals showed higher viral loads, which may reflect differential energy allocation: immunity in smaller individuals and reproduction in larger ones. These studies inform biomedical use of Aplysia as an aging model by linking life-history strategies to aging and disease susceptibility.

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Inhibition of Lipid Synthesis Affects Mitochondrial Metabolism Proteins

The biosynthesis of lipids and mitochondrial function are important parts of cellular metabolism which in terms affect the cell cycle regulation. This research investigates how the inhibition of the Fatty Acid Synthesis (FAS) in HEK293 cells affects the mitochondrial metabolism of proteins. The cells were treated using five FAS inhibitors: C75, CP-640186, GSK2194069, ND-630, and Cerulenin. HEK293 cells were cultured using T75 flasks until they were 80-90% confluent. They were then grown on a 24 well plate until they reached 80-90% confluency. The Fatty Acid inhibitors were dissolved, and diluted with phosphate buffered saline (PBS), and were then mixed with the cell culture. The control and treated group experiment used three biological replicates. Upon the addition of the inhibitors, the cells were incubated for five hours at 37° C. The culture medium was removed, and the cells were then washed with PBS. The cells were then scrapped using a cell scraper and collected for a protein extraction. The extracted cells were then analyzed using liquid chromatography-tandem mass spectrometry (LC-MS/MS). The raw data was then analyzed using Proteome discoverer 3.2 (Thermo Fisher Scientific, Waltham, MA). The proteins were then subjected to pathway analysis using Ingenuity Pathway Analysis (IPA). We found that the significant downregulation of the proteins that were involved in the key mitochondrial and metabolic pathways showed impaired energy metabolism. Acylglycerol Kinase (AGK) was downregulated within the Glycerophospholipid Biosynthesis pathway which potentially affects the mitochondrial membrane composition and function. Electron Transfer Flavoprotein, alpha subunit (ETFA) was reduced with the nicotinamide adenine dinucleotide (NAD) signaling pathway meaning that there was compromised lipid-derived energy production and the redox balance. The Prolyl Hydroxylase Domain protein 2 (PDHA2) was downregulated in the Macrophage Activation Signaling Pathway meaning impaired glucose oxidation and the alteration of immune signaling. The inhibitors that were the most effective were C75, GSK-2194069, and CP in downregulating top twenty-five proteins. The inhibition of fatty acid synthesis led to the downregulation of key mitochondrial metabolism proteins which indicated disruptions in energy production, lipid handling, and increased stress response pathway. The level changes of the protein suggest that mitochondrial dysfunction is affected and a broader suppression of oxidative metabolism when the HEK293 cells are subjected to fatty acid synthesis inhibition, consistent with the metabolic stress response.

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Linguistic Translation of the Montreal Cognitive Assessment into Haitian Creole

Alzheimer's disease (AD) and AD-related neurocognitive disorders (ADRD) increasingly impact aging populations, including the rapidly growing Haitian community in South Florida. Between 2010 and 2022, the Haitian immigrant population grew much faster (i.e. 24%) than the overall foreign-born immigrant population, which increased by 16%. Similar to other foreign-born immigrants, one quarter of Haitian immigrants are 65 years and older, but have a much lower proportion of adults with a college degree, and are more likely to work in service occupations. Relevant in this regard, the Haitian community has been severely under-represented in AD/ADRD research. To be effective amongst Haitian Creole-speaking individuals, a widely recognized, sensitive, and valid screening tool for detecting cognitive impairment, the Montreal Cognitive Assessment (MoCA©) must be culturally and linguistically adapted to ensure its accuracy and relevance. This project follows the nuanced linguistic translation process of the MoCA from English to Haitian Creole, as outlined by Sousa and Rojjanasrirat's (2011) translation guidelines for cross-cultural healthcare research. The linguistic translation process is extensive and guided by a group of neuropsychologists and native Haitian Creole speakers to verify linguistic equivalence. First, the assessment is forward translated from English to Haitian Creole. The second step of the translation process is a back translation during which experts will translate the Haitian Creole version from the forward translation back into English to check for linguistic accuracy by comparing it to the original English version of the MoCA. This process of forward and backward translation is continued until a final, linguistically accurate Haitian Creole version of the assessment is yielded. This study offers additional implications for researchers, particularly as a guide for considerations and techniques when translating psychological and neurocognitive assessments across other languages and cultures.

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Collective Cell Movements and Motility in a Simple Marine Animal

Collective cell movements play a crucial role during animal development and their physiology. During these biological processes, cells migrate, divide, differentiate, and rearrange in tissues. Physical forces between cells, such as cell adhesions, play an important role in tissue deformations. How these local collective movements and forces between cells determine the mechanics of tissues and their consequences in biological processes is not yet understood.

To address this question, we study a simple marine animal with a flat body plan, the Trichoplax adhaerens, which is an excellent model system for tissue mechanics. The Trichoplax can exhibit dramatic shape changes, generate fractures within tissue, and undergo stretching while dividing asexually. They feed on the marine algae and exhibit chemotaxis. We observed the motility pattern of Trichoplax over various concentrations of algae (Rhodomonas Salina). We found that the trajectory of the animals varied as the algal concentrations changed. At a maximum algal concentration (C=Cmax), the trajectories were shorter with higher straightness. At maximum starvation (C=0), the trajectories were much longer and more curved (lowest straightness). We also found that at higher concentrations, both the area and the speed of the animal exhibited periodicity, which decreased as the algal concentration decreased. We believe that animals paused frequently to feed, producing plateaus in area and drops in speed, while at starvation (C=0), they moved rapidly and traveled farther. Trichoplax also showed high motility (speed) at lower food concentrations. This higher motility is also reflected in the mean square displacement (MSD) with a higher slope (α=1.8) at starvation and a lower slope at C=Cmax (α=1.3).

So far, we have quantified two key physical parameters involved in the motility of Trichoplax, the area and speed under varying food (algae) concentrations over time. Our preliminary analysis shows that there is an inverse relationship between them, i.e., at higher speed, area is lower and vice versa. We also observed that the animal's motility and shape fluctuations involve the combination of four characteristic modes of motility: pause, run, tumble, and step. We believe that at any algal concentration, the Trichoplax moves using a combination of these four modes.

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The Influence of Immigration and Acculturation on Cancer Risk Profiles: Integrating SNAN and ACGR Epidemiological Data

Introduction/Background: Lifestyle changes that accompany immigration, such as dietary acculturation, reduced physical activity, and increased tobacco and alcohol use, contribute to cancer disparities in the United States. These behavioral shifts drive metabolic and inflammatory changes that elevate cancer risk. The Healthy Immigrant Effect suggests that recent immigrants often have more favorable health profiles, but these advantages weaken with longer residence in the U.S. The Sante Nou Se Avni Nou (SNAN) cohort, the community-engaged arm of the Cancer Health Disparities Registry (CHDR), enrolls predominantly Black and Caribbean-origin immigrants through community partnerships to assess lifestyle factors and social determinants of health. The African Cancer Genome Registry (ACGR) includes U.S.-born and immigrant individuals of African descent and captures detailed epidemiological data on behavioral and contextual cancer risk factors.

Methods: Using harmonized epidemiological data from SNAN and ACGR, we will examine whether time in the U.S. is a strong predictor of lifestyle-related cancer risk behaviors within each registry. Both cohorts administer standardized surveys assessing major cancer risk factors (diet, physical activity, tobacco and alcohol use, body mass index) as well as nativity, age at migration, and duration of U.S. residence. First, in each registry, we will compare the prevalence and clustering of cancer risk behaviors between U.S.-born and non–U.S.-born participants. Second, within each registry, we will model the duration of U.S. residence as a predictor of multiple concurrent cancer risk behaviors, treating it as a proxy for acculturation. Analyses will be conducted separately within SNAN and ACGR to assess consistency and context-specific patterns across these complementary cohorts.

This project will clarify whether and how time spent in the United States predicts the accumulation of cancer risk behaviors among African and Caribbean-origin populations, and whether these patterns are consistent across a community-based registry (SNAN/CHDR) and a broader epidemiological registry (ACGR). The study will also identify subgroups at elevated risk and inform culturally tailored cancer prevention strategies for immigrant and U.S.-born populations of African descent.

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Constructing Resilient Elastomeric Materials using Materials Binding Peptides

Highly elastomeric materials confer exceptional mechanical resilience in nature, facilitating phenomena like energy storage to artificial flights. However, obtaining these kinds of materials that offer high elasticity, and resilience is very challenging to synthesize in the laboratory. In order to achieve excellent and consistent performance at the macro scale, unique materials that bestow great resilience with controllable morphologies at the atomic scale are required. An ideal example of this is resilin, a protein found in specialized regions of the cuticle of most insects. Resilin is characterized by its rubber-like elasticity, low stiffness, great extensibility, effective energy storage, long fatigue life, and outstanding resilience. The rubbery trait of resilin is possibly due to the preorganized conformation of resilin in its natural setting, facilitating Tyr-based cross-linking. Although resilin-like peptides (RLPs) have been established as promising building blocks for biomedical applications like tissue engineering, wound healing, and drug delivery, there have only been very few studies published on the utilization of resilin elastomers capacity for thermal management and energy storage. To accomplish such capabilities, the resilin proteins must be controllably crosslinked via tyrosine residues to form dityrosine. In this work, material binding P1 peptides were conjugated to RLPs to produce P1/RLP conjugates. The binding of these peptides to graphene and h-BN surface was studied using QCM analysis and atomic force microscopy as an initial step towards pre-organization for eventual crosslinking. The binding studies showed that graphene is likely to be a good surface for peptide pre-organization than h-BN. In addition, the tyrosine cross-linking of these peptides in the solution state was studied. The cross-linked products were identified using MALDI and the young's modulus was calculated using AFM.

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Optimizing Phospho-Ester Hydrolysis by Organometallic Catalysts: Beyond Electronic and Structural Modulation

The design of small metal complexes that can efficiently mimic the catalytic activities of natural metalloenzymes remains a significant challenge in the field of chemistry. While considerable progress has been made, existing metal complexes generally demonstrate much slower reaction rates and lower turnover numbers compared to their natural enzyme counterparts. This disparity has driven considerable interest and ongoing efforts toward developing the next generation of molecules with enhanced catalytic performance. In practice, each catalytic system is typically tailored to promote a specific reaction, with its effectiveness determined by its distinct structural, chemical, and electronic properties. As a result, optimizing these parameters is crucial for achieving higher catalytic activity and selectivity in designed metal complexes.

Over the years multiple chemical, structural, and electronic factors have been identified as influencing the catalytic activity of organometallic complexes in phosphor-ester hydrolysis. This work presents a summary of several related projects, focusing on the design of new organometallic complexes through adjustments to these factors to impact the energetics of phosphoester hydrolysis reaction mechanisms. The study begins with previously identified well performing di-Zn metal complexes and examine modifications aimed at improving their chemical reactivity in phosphoester hydrolysis. The findings illustrate how the alterations in chemical, structural, and electronic properties affect the structures and optimize the mechanism. Consideration of these factors may improve the catalytic reaction and facilitate the development of novel catalysts for various chemical transformations.

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Master's Student in Biomedical Sciences

The Role of Target of Rapamycin (TORC1/2) in the Control of the Orb6 NDR Kinase to Regulate Cell Polarized Growth

Schizosaccharomyces pombe yeast cells (S. pombe) is a model used to study cell polarization, which is important in cell morphogenesis, growth, and survival. Nuclear dbf2-related kinases (NDRs) are involved in these pathways and are also conserved across fission yeast and higher eukaryotes. In S. pombe cells, Orb6 is an NDR involved in yeast cell polarized growth. This kinase directly regulates the localization activity of Cdc42 GTPase in yeast cells, the main cell polarity regulator, by phosphorylating Gef1. It has been shown that downregulation of Orb6 leads to chronological lifespan extension. The Target of Rapamycin (TORC1 and TORC2) signaling pathway is also conserved, and its inhibition leads to an extended lifespan in cells. Therefore, the hypothesis is that the TOR pathway interacts with Orb6 kinase, and this study analyzes the effect of inhibiting TORC1/2 on Orb6 activity. To study Orb6 activity, measurements of phosphorylated Gef1-S112 (pGef1-S112) were taken when treated with Rapamicin (TORC1 inhibitor), and Torin1 (TORC1/2 inhibitor). The results show that the pGef1-S112 levels remain similar to the control, but the cells treated with Torin1 show a decrease in pGef1-S112 levels compared to control. When analyzed, the results show that Orb6 activity is dependent on TORC2. Future studies could analyze the effect of only TORC2 on Orb6 activity. These results may provide more insight into current studies related to cancer diseases due to the evolutionary conservation of the kinases and signaling pathways.

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Sumit Kumar

Ph.D. Student in Civil Engineering

Cellular Mechanics for Tensegrity Structures

Tensegrity systems, characterized by their self-equilibrated interplay of continuous tension and discontinuous compression, offer exceptional lightweight efficiency and tunable mechanical behavior through topology and prestress control. However, their application remains constrained by a fundamental disconnect between topology-centric mathematical models and geometry-driven form-finding techniques. To bridge this gap, this study establishes a unified, mechanics-based framework anchored in the concept of the "tensegrity cell"—an infinitesimally rigid unit governed by the theory of cellular morphogenesis. By shifting focus from isolated modules to functional assemblies, this research addresses the critical need for predictable, scalable, and customizable mechanical behaviors in real-world systems.

The study begins with a rigorous parametric study of the fundamental tensegrity cell. By quantifying the influence of prestress levels, axial stiffness, and geometric tuning, the analysis derives precise performance envelopes that define stability conditions, force–displacement behaviors, and failure thresholds regarding cable yielding and strut buckling. Expanding beyond the single unit, the study systematically characterizes the mechanics of multi-cell assemblies formed through distinct processes of adhesion and fusion. This morphogenetic analysis formulates rules for emergent self-stress states, predicting how prestress propagates through shared boundaries to dictate stiffness evolution and guarantee equilibrium feasibility in complex topologies.

Integrating these findings, we propose a generalized design and synthesis methodology capable of generating viable configurations within prescribed spatial domains. This computational approach determines the viable structural compositions -whether single-cell, multi-cell, or fused by simultaneously satisfying load-displacement constraints and material efficiency targets. The framework utilizes an optimization objective that minimizes material volume while mitigating risks associated with structural instability. Validated through numerical case studies, this method provides comprehensive design guidelines that resolve classical compatibility challenges. Ultimately, this work creates a scalable pathway for synthesizing high-performance tensegrity structures that are with different shapes that are mechanically robust, and materially efficient.

Keywords: Tensegrity Structures, Cellular Mechanics, Morphogenesis, Structural Optimization, Adhesion and Fusion, Self-stress States.

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Tarjany Parekh

Ph.D. Student in Biochemistry and Molecular Biology

Inhibition of Lipid Synthesis Affects Fatty Acids and Phospholipids Classes

Lipid synthesis is the metabolic process of producing lipids which is essential for membrane construction, energy storage, and signaling. To examine how inhibition of palmitic acid biosynthesis affects reorganization of cellular lipid composition, we used established human embryonic kidney cells line (HEK293T). The cell line was targeted with five different lipid synthesis enzyme inhibitors: fatty acid synthase inhibitors (FASN): GSK2194069, C75, Cerulenin; and Acetyl-CoA Carboxylase inhibitors (ACC): CP-640186 and ND-630. Cells were plated in 24 well plates, brought to 80-90% confluency and treated with 510µl of inhibitor-containing media for 5 hours at 37℃; these treatments were triplicated. Following treatment, cells were washed with PBS, scraped, pelleted, and stored at -80℃. Lipid extraction was performed using Blight and Dyer method, using 1:1 Chloroform and Methanol followed by 100ul of Chloroform and 50 ul mass spectrometry grade H_2O. Lipidomic Analysis was performed with untargeted mass spectrometry lipid profiling with a Q Exactive Orbitrap Mass Spectrometer coupled with a Vanquish Horizon Binary UHPLC LC-MS system (LC MS-MS). The raw data was analyzed and quantified with LipidSearch 5.0 and the statistical analysis was conducted through Metaboanalyst 5.0 and transformed in GraphPad Prism.

Across all inhibitor treatments, Lipidomic profiles showed lipid depletion in major lipid species, including phosphatidylinositols, phosphatidylethanolamines, and ceramides indicating the influence of fatty acid synthesis inhibition on lipid metabolism. Multivariate Analysis using Partial Least Squares Discriminant Analysis (PLS-DA) revealed major separation between the control and inhibitor-treated groups, with each inhibitor inducing specific lipid composition. Additionally, Variable Importance Plot (VIP), which came from PLS-DA, displayed specific lipid species responsible for the separation; phosphatidylinositols, ether-linked phospholipids, and ceramides were the main contributors to separation highlighted in the VIP. Among the treatments, the fatty acid synthase inhibitor C75 induced the strongest effect manifesting the most pronounced lipid depletion and substantial divergence from control samples suggesting strong shift in lipid composition. Differential abundance analysis between control group and C75 treated groups further disclosed downregulation of the most significantly altered lipids, including phosphatidylinositols and ceramides.

In conclusion, inhibiting fatty acid synthesis at specific enzymatic steps with various inhibitors produced great variance in cellular lipid network. Specifically, with C75, extensive decline in key lipid classes were observed. These discoveries highlight the importance of fatty acid biosynthesis in maintaining lipid production.

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Victor Novara Gennuso

Ph.D. Student in Microbiology and Immunology

TAP and DM Regulation of Antigen Presentation and Human Antibody Binding to Pig SLA-Expressing Cells

The use of genetic modified pig organs could help eradicate the crisis of shortage of organs available for human transplant. More than 100,000 people in the U.S. today are on the transplant waiting list for a kidney, in which few than half will receive an organ. Recent pig-to-human transplants have shown that antibody-mediated rejection (AMR) is still a major immunological barrier for xenotransplantation, despite advances in genetic modified pig donors. The pig major histocompatibility complex (SLA) class I and class II genes play a critical role in rejection, and it is a critical step to study to solve this issue. Different reagents were created to evaluate how the SLA processes peptide antigens that lead to rejection by evaluating class I and class II peptide processing. The transporter of antigen peptide (TAP) supplies peptides to class I molecules to reach cell surface of the human and murine cells. HLA-DM helps peptide “loading” into class II MHC proteins in humans by promoting binding of high affinity peptides. Understanding whether similar accessory molecules help SLA class I/II proteins acquire peptides during their biosynthesis may allow us to create new rejection resistant pigs and understand how the pig MHC works. Methods: CRISPR technology will be used to knockout the TAP, and DM genes in pig renal endothelial cells (pREC) and lymphoma B cell. Then it will be examined whether pig class I and class II protein expression were affected by these genes. Human antibody binding to cells will determine whether these are potential xenoantigens or not. Results: Pig cells made TAP deficient lacked the ability to generate cell surface class I SLA antigens. pREC knocked-out for SLA-DMβ exhibited an accumulation of a peptide derived from the CD74 protein CLIP in class II MHC proteins and an increase in antibody binding for some patients. Conclusions: Accessory molecules TAP and SLA DM are critical for SLA antigen presentation pathways and evaluation of their mechanisms will facilitate development of reagents and new donor pigs for xenotransplantation.

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Yingxi Liu

D.M.A. Student in Vocal Performance and Pedagogy

Self-Reported Vocal Changes Across the Menstrual Cycle in Young Female Classical Singers

Hormonal fluctuations across the menstrual cycle influence multiple physiological systems in the female body, yet their effects on the singing voice remain underexamined in formal singing voice research. Although singers and voice teachers frequently report cyclical changes in vocal function, empirical documentation from the perspective of trained classical singers is limited.

This study investigates self-reported vocal and physical symptoms across the menstrual cycle in young female classical singers. It examines perceived variations in vocal range, flexibility, endurance, vocal quality, and overall physical and emotional condition during different phases of the cycle. In addition, the study explores whether the use of hormonal birth control is associated with differences in perceived vocal stability.

Approved by the University of Miami Institutional Review Board (IRB #20250908), the study has currently recruited and consented fourteen participants. Participants are female classical voice majors or recent graduates from the Frost School of Music, Department of Vocal Performance, aged 20 to 35. Over a 60-day period, participants complete daily questionnaires documenting menstrual cycle phase, physical symptoms, emotional state, and perceived vocal function. The study includes both singers who do not use hormonal birth control and singers who use hormonal contraceptives continuously, allowing for comparison between groups. Data collection emphasizes subjective experience rather than objective acoustic measurement, foregrounding singers' lived vocal experiences within their training and performance contexts.

Existing literature suggests that ovulation may be associated with improved vocal sensations, while the premenstrual and menstrual phases may coincide with increased vocal fatigue, reduced flexibility, and decreased physical energy. This research seeks to determine whether such patterns are consistently reported among young classical singers and how individual variability shapes these experiences.

By documenting singers' self-perceived vocal changes across the menstrual cycle, this study contributes to interdisciplinary dialogue among voice science, vocal pedagogy, and performing arts research. The findings aim to normalize hormonal influences on the singing voice and provide singers and teachers with greater awareness and practical insight for healthy vocal management across the menstrual cycle. Data collection is ongoing and scheduled to conclude on January 30, 2026, followed by data analysis and discussion of pedagogical implications.

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Yulia Egorova

Postdoctoral Associate

Unveiling the Global Marine Biodiversity Hotspot

Efforts to curb marine biodiversity loss have gained momentum through new global agreements extending protections across both national waters and the high seas. However, it remains unclear how to best capture the full range of ecological features encompassed by the term “biodiversity” and, more importantly, how and where to prioritize conservation efforts. Here we use AquaMaps 2.0, a high-resolution global ensemble of species distribution models for 31,370 marine taxa, to map and summarize biodiversity patterns using three complementary metrics: species richness, range-size rarity, and phylogenetic diversity. We identify global marine biodiversity hotspots as the top five percent of values for each metric and assess their exposure to human pressure, existing protection, and future redistribution under climate change. Hotspots are extensive across both coastal and offshore ecosystems and coincide with areas of high cumulative human impact. Under warming scenarios, hotspots contract in the tropics and shift poleward. These results establish a management-ready framework for locating, comparing, and protecting the most irreplaceable concentrations of marine life.

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Yuqing Liu

Ph.D. Student in Epidemiology

Vitamin B6 Supplementation Associates with Lower Sphingosine-1-Phosphate and Altered Sphingolipid Pathways in Early Multiple Sclerosis

Background & Objectives: Sphingosine-1-phosphate (S1P) is a potent signaling lipid that regulates immune cell trafficking, endothelial barrier integrity, glial activity, and oligodendrocyte survival. Several disease-modifying therapies (DMTs) specifically target S1P receptors (S1PR) to prevent lymphocyte egress and CNS infiltration, successfully reducing neuroinflammation and relapse activity. Vitamin B6 is a required cofactor for sphingosine phosphate lyase, the enzyme responsible for degrading S1P. Thus, B6 supplementation may offer a novel, low-risk, DMT-adjuvant strategy to reduce excess S1P at its source, before it can activate S1PRs. In this study, we aim to evaluate if B6 or B-complex (B6BC) supplementation decreases S1P and related species, and alters other metabolic processes in early, untreated relapsing-remitting MS (RRMS).

Methods: Untargeted serum metabolomic profiling (1,100 non-xenobiotic, named metabolites) was performed in 73 RRMS cases who were untreated (96% DMT-naïve) and ≤5 years of symptom onset. Participants reported use and duration of B6BC supplementation. Continuous users (≥1 month) were classified as B6BC users. Empirical Bayes linear models tested metabolite differences between B6BC users and non-users, adjusting for age, sex, BMI, smoking, vitamin D and fish oil supplementation, time of blood draw, and fasting duration. Pathway enrichment evaluated nominally associated metabolites ($p<0.05$).

Results: Participants were 78% female, with mean age 39 ± 10 years and disease duration 1.2 ± 1.2 years; 11% reported continuous B6BC supplementation. B6BC use was validated by elevated pyridoxal (logFC = 1.0, p = 0.01) and pyridoxate (logFC = 0.8, $p < 0.05$). The top association was lower dihomo-linolenoylcarnitine (C20:3n3/6) (logFC = -1.4, p = 0.002), followed by S1P (logFC = -1.1, p = 0.004) and sphinganine-1-phosphate (6th place; logFC = -1.0, p = 0.005), in B6BC users vs non-users. Enrichment analyses revealed overrepresentation of metabolites related to trans-sulfuration and one-carbon metabolism pathways (pFDR = 0.02), extracellular UDP-nucleoside activity (pFDR = 0.008), B6 metabolism (p = 0.004), and sphingolipid metabolism (p = 0.005).

Conclusions: B6BC supplementation was associated with lower circulating S1P and sphinganine-1-phosphate levels in early, untreated RRMS, consistent with enhanced activity of the B6-dependent SPL enzyme and increased S1P clearance. Pathway-level enrichment in one-carbon and trans-sulfuration metabolism further supports a broader biochemical shift linking vitamin B6 status to lipid and redox homeostasis. Together, these findings provide first-in-human metabolomic evidence that B6BC supplementation may modulate endogenous S1P metabolism in MS, offering a safe, low-cost, and upstream adjunct to S1PR-targeted DMTs.

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Zixin Yang

Ph.D. Student in Chemistry

Polypeptide-Based Multivalent Modular PROTACs Toward Enhanced Cancer Therapy

Proteolysis-targeting chimeras (PROTACs) have emerged as a powerful strategy for targeted protein degradation, yet conventional designs are limited by complex linker optimization, rigid stoichiometry, and poor pharmacokinetics. Here, we report a polypeptide-based multivalent PROTAC platform constructed through a modular recombination strategy. By covalently conjugating protein-of-interest binders and E3 ligase ligands onto a polypeptide backbone via CuAAC click chemistry, we obtained self-assembling nanoparticles with programmable ligand ratios and tunable architectures. These nanoparticles exhibited well-defined sizes (30–130 nm), efficient cellular uptake, and enhanced cytotoxic effect compared to the model PROTAC ARV-771. Importantly, the polypeptide-based PROTACs demonstrated potent anticancer activity against multiple tumor cell lines while showing reduced toxicity toward normal cells. This versatile and biodegradable platform provides a generalizable strategy to improve the efficacy, tunability, and drug-like properties of PROTAC-based therapeutics.

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Millie Rogers

Ph.D. Student in Biology

The Role of SLAP75 in Early Motor Neuron Development in Zebrafish

Mutations in the human gene FAM169A were linked by our collaborators to degenerative motor neuron (MN) disease. FAM169A is well-conserved, with duplicate ohnologs in zebrafish. SLAP75A enrichment during early neural development in zebrafish larvae suggests a potential role in establishing spinal circuitry. We created an F0 model to determine whether loss of function in this gene can disrupt MN development. One-cell stage Tg(olig2:dsRed) embryos were injected with sgRNA/cas9 complexes targeting a conserved exon in fam169ab. Frameshift mutations were confirmed via long-read sequencing. We co-injected a complex targeting SLC45A2, a gene critical to melanocyte differentiation, and pigmentation loss served as a selection marker for further assay. Controls received the SLC45A2/Cas9 complex alone. Mosaic slap75ab F0 crispants exhibited disrupted MN morphology and trends toward altered visual motor responses. Together, these findings support a role for SLAP75A in early motor neuron morphogenesis and development of motor system integrity.

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Katie Sanford

Ph.D. Student in English

“How after syr Gawayns ghost apperyd”: Haunting Temporalities of Grief in the Literature of the High and Late Middle Ages

This dissertation explores the specter of grief as it appears in three texts from the High and Late Middle Ages: Sir Orfeo, Pearl, and Le Morte Darthur. By drawing comparison between grief and hauntings as phenomena that warp linear temporality and highlighting the language of spectrality as it is employed in these texts to express this shared characteristic, this project argues that grief permeates each of these texts so thoroughly that it is not only intrinsically entangled with the personal and political strife featured in these narratives, but in the very structure of the narratives themselves. By utilizing perspectives on grief posited by fields of sociology and psychology, psychoanalytic frameworks, and literary analysis, these texts might be understood as historical creations that are haunted by the grief featured therein, as well as texts that bring that haunting forward in time to be felt now, in the present.

I will focus primarily on the material that composes the first chapter of my dissertation, which examines the tragedy of Le Morte Darthur and, more specifically, the instances of anticipatory grief and post-grief recurrence that occur in the narrative. When Merlin imparts onto Arthur the knowledge of his fate, he renders that future as certain as the present. As Arthur goes through the motions of his life with his end assured, we, the audience, know that he has already done so countless times over in the centuries since Le Morte Darthur was written. It is in this way that Le Morte Darthur, with all the instances of loss that it contains, becomes reminiscent of a haunting— a past scene repeating itself once more, the actors therein unable to deviate from course and conclusion while a present-day spectator bears witness. It is already and has always been over for these characters, and the narrative ensures that their losses be felt before they occur and then echoed in the aftermath, a warping of past, present, and future that bleeds throughout the tale and begs to be understood.

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Oral Presenters

Social Justice, Policy & Identity

Activities Room North

Carlie Dario

Postdoctoral Associate

Designing Criteria for Urban Coastal NbS: Restoration and Engineering Perspectives in Miami, Florida

Coastal nature-based solutions (NbS), such as mangroves and corals, offer a sustainable and effective approach for mitigating coastal hazards and protecting shorelines and infrastructure. Despite their potential, the implementation of coastal NbS faces challenges on the lack of design guidance and expert consensus. In this study, we conducted interviews with 19 coastal engineers and ecological restoration experts with expertise in the coastal environment of Southeast Florida and Miami. Our study applies a design-thinking framework to capture perspectives across disciplines (designers), understand the objectives of coastal NbS in Miami (design product), and identify appropriate priorities for Miami that need to be addressed for coastal NbS to be successful in Miami (design criteria and challenges). While we found similarities in defining the objectives of NbS, we capture nuances in criteria across disciplines, such as aesthetics and accessibility considered by coastal engineers, and survivability and scale, prioritized by ecological restoration experts. Our interviewees also defined time-bound challenges to overcome in Miami, particularly addressing urgent environmental issues in the short-term (e.g., water quality), policy-related discussions in the medium-term (e.g., permitting exceptions to advance NbS), and social concerns in the long-term (e.g., public perception of mangroves). We integrate our findings to create an initial road map of recommendations to reconcile a growing yet conflicting demand of NbS situated within coastal metropolitan areas like Miami.

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Lovelyn Isiani

Master's Student in Sociology

Fundamental Cause Theory and Public Health Interventions: Urban–Rural Variations in ITN Use Among Women of Reproductive Age in Nigeria

Malaria remains one of the most persistent drivers of preventable morbidity and mortality among women of reproductive age in Nigeria, yet preventive behaviors such as consistent insecticide-treated net (ITN) use remain unevenly distributed across social and spatial contexts. Rather than treating these disparities as a function of awareness alone, this paper interrogates how social conditions and flexible informational resources shape women's capacity to translate malaria knowledge into preventive practice, particularly across Nigeria's urban–rural divide. Drawing on secondary data from the 2021 Nigeria Malaria Indicator Survey (NMIS), a nationally representative survey conducted under the Demographic and Health Surveys (DHS) Program, the study analyzes responses from 14,476 women aged 15–49. The analysis examines how wealth, education, and exposure to malaria-related information, at both individual and community levels, interact to influence ITN use. The paper asks not only whether urban and rural women differ in preventive behavior, but how unequal access to information infrastructures mediates these differences, even when formal knowledge of malaria is widespread. Findings reveal pronounced urban–rural variation in both preventive practices and pathways to information. Urban women are more likely to encounter malaria prevention messaging through digital and institutional channels, while rural women rely more heavily on interpersonal and community-based sources that vary widely in quality and reach. These differences shape not only ITN ownership but the consistency of use, suggesting that information functions as a flexible resource that amplifies or constrains preventive agency depending on social location. The results complicate assumptions that increased awareness alone leads to behavior change, highlighting instead the importance of how information circulates, who controls it, and under what conditions it becomes actionable. The paper argues that malaria prevention strategies must move beyond uniform messaging toward interventions that recognize uneven information ecologies across space. Strengthening community-embedded health communication in rural areas, integrating malaria education into maternal health services, and expanding adolescent-focused prevention initiatives are critical to reducing persistent inequalities in vector-borne disease burden. Beyond Nigeria, the findings offer broader insight into how inequitable access to information sustains health disparities, underscoring the need for gender-responsive and context-specific approaches to preventive health in low- and middle-income settings.

Keywords: malaria prevention; women's health; information inequality; ITN use; urban–rural disparities; Nigeria; global health.

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Nolan Jekich

Master's Student in Public Administration

Addressing Masculinity: An Interdisciplinary Approach Toward Strengthening Identity Development Among Young Men

Recent public health data and sociological research has indicated a rising prevalence of loneliness , social isolation, and disengagement among many young men in the United States, alongside declines in educational attainment, workforce participation, and involvement in intimate relationships.

Although institutions and state governments (i.e. Utah, Maryland) across the country are beginning to recognize and address this prevailing issue through downstream programs and initiatives (i.e. educational attainment, workforce participation, family formation, etc.), this research argues that initiatives, policy or otherwise, must also adopt an upstream focus on relational and emotional development that fosters a strengthened identity formation. Without such upstream attention, programs risk producing short-term or partial gains, leaving many underprepared to cultivate the emotional and relational skillsets to succeed in an evolving world. Prior studies have often independently examined this phenomenon through siloed economic, technological, or evolving cultural lenses. This research proposes adopting an interdisciplinary approach that addresses the root causes many have termed - the masculinity crisis.

This research seeks to advance two core questions:

1. Does an interdisciplinary analysis incorporating emotional regulation, relational literacy, and identity formation contribute to a strengthened understanding of the masculinity crisis?
2. What strategies and programs are needed to cultivate a blueprint that provides the foundation to enhance young men's social, emotional, and relational wellbeing?

Previous research has provided the foundation that re-conceptualizes masculinity and femininity as independent but integrable dimensions of identity, and further calls for a conscious integration of masculine and feminine emotional and relational competencies as central to healthy development6. Prior generations' constructions of masculinity were often anchored in sole, traditional provider-centric frameworks, wherein economic provisions function as the primary maker of male identity and value. However, as cultural shifts and labor-markets have led many young women - particularly those under 30 - to attain higher socioeconomic statuses than their male counterparts , these frameworks have become increasingly m 7 isaligned with contemporary realities. This divergence underscores the need for a re-articulated model of masculinity that moves beyond narrow provider-based definitions and rather integrates relational, emotional, and identity-based competencies better suited for present-day social and economic conditions.

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Courtney Amaro

Ed.D. Student in Applied Learning Sciences

Bridging the Science of Reading and Teacher Practice: An Iterative Evaluation of a K–3 Professional Learning Course

The Science of Reading (SoR) has generated increasing consensus around evidence-based literacy instruction, yet gaps remain between research knowledge and consistent classroom implementation. This study presents the design and evaluation of a professional learning course developed to support K–3 teachers in translating SoR principles into instructional practice.

Using a design-based and iterative evaluation approach, the course was implemented across multiple cohorts of early-elementary educators. The professional learning model emphasized explicit instruction, application to classroom contexts, and opportunities for reflection and revision. Evaluation data were collected through validated survey instruments, including the Teacher Efficacy and Self-Efficacy for Literacy Instruction (TESLI) and the Questionnaire for User Interaction Satisfaction (QUIS), alongside qualitative feedback from participants.

Findings indicate growth in teachers' self-reported confidence in applying Science of Reading strategies, particularly in areas related to phonological awareness, decoding, and instructional decision-making. Participant feedback also informed ongoing revisions to course structure, pacing, and instructional supports, strengthening alignment between research-based content and teacher needs.

This presentation highlights how iterative evaluation and practitioner feedback can be leveraged to refine professional learning experiences and support instructional transfer. Implications are discussed for designing scalable, responsive Science of Reading professional development that balances research fidelity with classroom realities.

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Kate Arnold

Ph.D. Student in Teaching and Learning

"It Would Have Only Taken 527 Different Votes": Analyzing the Justifications for English as Official Language

This study examines how US lawmakers publicly justify official-English language policy through political rhetoric, focusing on the English Unity Act as a case study. Although English has been the dominant language in the United States since the British American colonial period, the United States has never had an official language at the federal level. Recent political developments highlight the continued salience of official-English debates. This study investigates how sponsors of the English Unity Act construct and legitimize official-English policy through public discourse.

Drawing on Critical Discourse Analysis and the Economies of Worth framework, I analyze congressional transcripts from years in which full records were available: 2005 and 2009 (Rep. Steve King) and 2013 (Sen. Jim Inhofe). Using a qualitative approach, I identified 80 distinct phrases in which the speakers explicitly articulated justifications for supporting the bill. These phrases were first coded into 13 inductive themes and subsequently categorized within Boltanski and Thévenot's six orders of worth: civic, market, industrial, domestic, inspiration, and fame.

The findings reveal that civic justifications dominate the rhetoric surrounding the English Unity Act. Lawmakers consistently frame English as essential to national unity, democratic participation, and civic legitimacy, positioning linguistic conformity as a prerequisite for full membership in the political community. Market-based justifications present English proficiency as a form of individual capital necessary for economic mobility, while simultaneously framing non-English speakers as economically deficient or dependent. Industrial justifications depict multilingualism as a source of inefficiency and fiscal waste, shifting responsibility for systemic failures onto individuals with limited English proficiency. Domestic and inspirational appeals further naturalize English dominance by tying it to heritage, tradition, and moral or religious authority.

Taken together, these justificatory strategies construct English as a symbolic boundary marker that delineates belonging, legitimacy, and worth. The analysis demonstrates how official-English rhetoric obscures structural barriers to language acquisition, reinforces raciolinguistic ideologies, and legitimizes exclusionary policies. By revealing how language policy is rhetorically framed, this study contributes to broader conversations about language ideology, citizenship, and the role of discourse in sustaining inequality in the United States.

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Harleen Kaur

Postdoctoral Associate

Obesity and Nutrition and Exercise Knowledge Drive Risk Stratification in a Tailored Lifestyle Intervention for Cancer Survivors: The OnPOINT Trial

Lifestyle behaviors, such as maintaining a healthy diet and engaging in regular physical activity, can reduce the risk of cancer recurrence and mitigate comorbid conditions among cancer survivors. However, individual needs for nutrition and exercise programs may vary based on medical, environmental, and psychosocial factors. To date, few studies have focused on evaluating a clinical decision-making framework that enables risk stratification to generate tailored referrals for nutrition and exercise programs, addressing the distinct needs of cancer survivors. The purpose of the OnPOINT trial is to evaluate the feasibility, acceptability, and retention of a tailored nutrition and exercise referral program for cancer survivors, while developing, assessing, and refining a risk-based complexity stratification model that assigns cancer survivors to low, moderate, or high-intensity programs. To better understand how the algorithm captures complexity levels, we examined key factors driving risk-stratification. Among the n=24 participants in the intervention arm, the distribution across complexity levels was 8% low, 50% moderate, 42% high. Adiposity primarily drove high-complexity classification, with 69% of participants assigned to this arm due to elevated body mass index ($\bar{x}$ ≥30 kg/m^2), body fat ($\bar{x}$ =46%), and visceral fat level ($\bar{x}$ ≥12), whereas lower nutrition and exercise knowledge (89%) and/or moderate symptom burden (67%) were predominant in the moderate and low-complexity arm. Findings highlight the burden of obesity and limited lifestyle knowledge among cancer survivors, supporting the need for tailored lifestyle programs to improve treatment-related symptom burden.

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Oral Presenters

Neuro, Public Health & Policy

Activities Room South

Carolina De La Pena Fernandez

Ph.D. Student in Cancer Biology

Horizontal Mitochondria Transfer Epigenetically Reprograms Glioblastoma

Horizontal transfer of intact mitochondria has been identified as a key driver of tissue homeostasis, cell differentiation, and intracellular signaling. Moreover, recent research highlights how cancer cells co-opt this process and exploit it as a mechanism of bidirectional metabolic communication with cells in the tumor microenvironment. Notably, mitochondria transfer has been shown to be a prevalent phenomenon in glioblastoma (GBM), the most frequent and malignant brain tumor. With less than 5% long term survival and a 90% recurrence rate, GBM is amongst the deadliest cancers in humans. Our group previously demonstrated that, in the context of GBM, mitochondria transfer from astrocytes perpetuates cancer onset and tumor progression. We specifically saw that transfer-mediated metabolic reprogramming resulted in increased proliferation, tumorigenicity, and stemness of GBM cells. However, the underlying mechanism by which transfer changes cancer cell behavior remains unclear. I hypothesize that mitochondria transfer serves as a master metabolic/epigenetic regulator that induces a stem-like GBM phenotype.

I observed that GBM cells that acquired astrocyte mitochondria in co-cultures have higher 5mC methylation levels, an indicative DNA hypermethylation. Additionally, previous metabolomics data indicates that transfer positive GBM cells have a distinct metabolite pool; particularly significantly lower levels of succinate to alpha-ketoglutarate ratio, which serve as co-factors for histone and DNA modifying enzymes. To further evaluate whether this phenotype is driven by host mitochondria, I used MitoTimer, a reporter that exhibits a time-dependent shift from green to red fluorescence, and thereby allows tracking the age of transferred mitochondria. My results indicate that younger mitochondria, usually linked to more efficient energy production and a higher capacity for one-carbon metabolism, are getting preferentially transferred to GBM. Collectively, my observations highlight that transferred mitochondria are inherently different and identify subsequent epigenetic regulation as a driver for phenotypic changes in GBM cells. My future studies will elucidate the mechanisms by which mitochondria transfer maintains the stem cell epigenetic program and its downstream impacts.

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Nathan Becker

Ph.D. Student in Human Genetics and Genomics

Multiomic Evidence of Coordinated Complex Rearrangements, Enhancer Hijacking, and Epigenomic Signatures in the First Whole-Chromosome-Phased Myeloma Genomes

Introduction: Genomic analysis of multiple myeloma has advanced rapidly, yet traditional short-read sequencing remains limited in examining complex genomic events. Chromosome-scale haplotype phasing, integrated with multiomic datasets, has enabled the resolution of complex genomic and epigenomic states across entire chromosomes, providing a more complete view of tumor architecture.

Methods: Fourteen multiple myeloma patient-derived xenografts were used to generate multiomic data, including short- (Illumina) and long-read (PacBio) whole genome sequencing (WGS, average depths of 92x and 16x) to identify single nucleotide variations (SNVs), copy number (CN) abnormalities, structural variation (SV), and DNA methylation, as well as expression (>124 million reads), chromatin states (CUT&Tag-IT; >10M reads per mark), and Micro-C/LinkPrep (Dovetail Genomics; >900M reads) and HiChIP (Dovetail, H3K27ac mark) to identify 3D chromatin architecture/folding and enhancer-target gene interactions. Micro-C interaction reads were leveraged for chromosome-scale haplotype phasing, onto which genomic, epigenomic, and transcriptional features were integrated using heterozygous SNPs.

Results: For the first time, complete haplotype-resolved assemblies at the chromosomal level have been generated in multiple myeloma. Our approach resulted in an average of 96.3% haplotype phasing per autosome generating chromosome length haplotypes up to 241.9 Mb. In comparison, HiFi long-read WGS (PacBio) was able to generate phase-blocks of up to 4.6 Mb (median 44.1 kb). Haplotype-specific interaction heatmaps were generated allowing us to examine the interaction of complex SVs across chromosomes. In one sample, we identified a primary t(11;14) that was linked to additional SV events on chromosomes 3 and 17. The pattern of interactions combined with breakpoint analysis indicated a four-way complex reciprocal translocation between chromosomes 3,11,14 and 17. Integration of epigenetic data within this complex SV revealed haplotype-specific spreading of activating epigenetic domains from the IGH super-enhancer to CCND1 and SKIL, driving oncogene activation across multiple chromosomes.

Conclusion: We have generated the first chromosome scale haplotype-resolved genomes in multiple myeloma and integrated them with epigenetic states. We have shown that it is possible to identify interactions across chromosomes to resolve complex SVs as well as their epigenomic consequences to understand the intricate nature of how the multiple myeloma genome is organized.

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Marco Marchi

Postdoctoral Associate

Stabilizing the Mitochondrial Genome in Depletion Syndromes

Mitochondrial DNA depletion syndromes (MTDPS) are rare and severe neuromuscular disorders characterized by a critical loss of mitochondrial DNA (mtDNA), leading to failure of oxidative phosphorylation and early-onset muscle and neurological dysfunction. Current therapeutic options are extremely limited and largely gene-specific, highlighting the urgent need for strategies that can stabilize mtDNA across different genetic causes.

Recent unbiased genetic screens in yeast have identified conserved genes whose overexpression suppresses mtDNA loss, even in the presence of severe mitochondrial defects. These findings suggest that mtDNA stability can be enhanced by modulating cellular pathways beyond the core mitochondrial replication machinery. However, the relevance of these suppressors in human neuromuscular disease models remains largely unexplored.

Our aim is to validate conserved mtDNA-stabilizing suppressors in complementary human cellular models of mtDNA depletion. Using pharmacological and genetic models that recapitulate distinct pathogenic mechanisms -impaired nucleotide supply (DGUOK deficiency) and dysregulated mitochondrial quality control (FBXL4 deficiency)- we will test whether selected suppressors preserve mtDNA copy number, support mitochondrial function, and improve stress tolerance in iPSC-derived neuromuscular cells.

By focusing on rapid functional validation rather than mechanistic dissection, this project aims to identify and prioritize mtDNA-stabilizing modifiers with therapeutic potential. The results will provide a translational bridge between genetic discovery and therapy-oriented research, establishing a foundation for future intervention strategies applicable across multiple forms of MTDPS.

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Allie Stiffler

Ph.D. Student in Biology

Mass Induction of Sargassum-Associated Prophages Shifts Algal Biofilm Community Dynamics

The pelagic seaweed Sargassum (S. natans and S. fluitans) has undergone significant range expansion and super bloom events in the equatorial Atlantic Ocean over the past 15 years. Mass beaching of these blooms has negative ecological, economic, and human health impacts. This seaweed's microbiome provides symbiotic functions, including novel nitrogen and phosphorus acquisition mechanisms, which are believed to contribute to its ecological success. Recent research shows that Sargassum-associated bacteria are enriched in prophages, viruses that have integrated into their genome, compared to the surrounding seawater. Further, these prophages are inducible, capable of excision from the genome, and subsequent lysis of their bacterial host, by chemical and ultraviolet treatment.

Here, we investigated a Sargassum-derived in vitro multispecies biofilm encompassing dominant heterotrophic microbial members associated with Sargassum to probe the impacts of prophage induction on the composition of Sargassum biofilms. Induction was quantified by coverage-based virus-to-host ratios in chemically induced treatments with Mitomycin C and non-induced controls, and the community composition and metabolic profiles were analyzed after a period of recovery post-induction. Chemical induction led to a significant increase in virus-to-host ratio of viral genomes linked to Vibrio metagenome-assembled genomes. This was accompanied by altered biofilm community composition, with a reduction in Vibrio abundance, creating niche space for other biofilm members in the genera Pseudoalteromonas, Alteromonas, and Cobetia. The induced Vibrio-associated phages encoded genes involved in quorum sensing, biofilm formation, and virulence. Induction led to a relative decrease of 17 metabolic modules, including functions related to energy metabolism and nitrogen utilization. Due to the high frequency of lysogeny in the Sargassum microbiome and the susceptibility of prophages to chemical and ultraviolet light induction, these results suggest that prophage integration and induction contribute to structuring the Sargassum microbiome and its functional profiles, potentially aiding microbiome flexibility in changing environmental contexts.

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Abdul-Manaf Mutaru

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Healthy Mothers-Healthy Children: A Randomized Controlled Trial for Obesity Prevention Among Hispanic Mothers and Children

Objective: Hispanic women and their young children face disproportionately high rates of overweight and obesity, contributing to long-term cardiometabolic and psychosocial health risks. The aim of the Healthy Mothers Healthy Children (HMHC) trial was to evaluate a 12-week, culturally tailored intervention to improve the nutrition and physical activity behaviors for Hispanic mothers and their children aged 3 to 5 years.
Methods: A total of 287 Hispanic mother–child dyads were randomized to the HMHC intervention or an equal-attention control group. HMHC is one of the few randomized trials focused exclusively on Hispanic families, offering culturally tailored, bilingual programming for both mothers and children. The cultural specificity and depth of the HMHC dataset provided a rare opportunity to examine behavioral and anthropometric change in an underrepresented, high-risk population. The intervention included weekly education, structured physical activity, and coping-skills training for mothers, alongside a parallel child curriculum, with monthly booster sessions for both groups. Data was collected at baseline, post-intervention, and six-month follow-up. Primary outcomes included changes in BMI, weight, height, and adiposity indicators, with secondary outcomes assessing diet, physical activity, and exercise self-efficacy. Descriptive statistics and mixed-effects models were used to evaluate longitudinal differences.
Results: Primary adiposity outcomes showed small, non-significant differences between groups ($P > .05$). Mothers' waist circumference remained comparable, with an estimated difference (-0.73cm [-2.15, 0.70]). Children's growth patterns were similar across groups, and skinfold measures showed no meaningful divergence, including subscapular thickness (-0.56 [-2.11, 0.98]). Secondary outcomes related to physical activity, lifestyle behaviors, and self-efficacy also followed parallel trends; exercise self-efficacy scores showed a non-significant difference of (-2.63 [-8.90,3.63]). No statistically significant group effects emerged over 12 months.
Conclusion: Although the HMHC intervention did not yield significant differences in adiposity or weight trajectories, the study demonstrates the feasibility of delivering a culturally tailored, theory-driven intervention for Hispanic families, even amid the COVID-19 pandemic. Findings highlight the promise of nurse-led, bilingual, community-embedded strategies to support weight maintenance, address social and environmental barriers to healthy behaviors, and promote maternal self-efficacy and intergenerational health.

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Spatial and Environmental Drivers of Fish Community Structure and Diversity in Seagrass Meadows Across the Florida Reef Track

The Florida Reef Track represents the only barrier reef system in continental North America, functioning within an interconnected mosaic of seagrass meadows, mangroves, and coral reefs. Seagrass beds are critical marine ecosystems providing essential fish habitat, nursery grounds, and feeding areas for numerous species. In the Florida Bay (FB), Florida Keys National Marine Sanctuary (FKNMS), and the Dry Tortugas National Park (DT) these ecosystems are the predominant benthic community type, supporting both commercially and ecologically important, as well as cryptic fish species.

We examined fish community structure across 62 permanent seagrass sites spanning FB, FKNMS and DT by conducting underwater visual censuses using 200 m^2 belt transects during winter and summer seasons to characterize the complete fish community. Our surveys documented 144 fish species from 51 families. The most important families in terms of a richness were Gobiidae, Labridae, Serranidae, Syngnathidae and Scaridae. Labridae, Haemulidae, Gobiidae, Lutjanidae and Gerreidae were the most important families in terms of abundance.

Diversity metrics showed no significant seasonal variation; however, they revealed significant spatial heterogeneity. Offshore seagrass beds exhibited higher species richness and Shannon diversity compared to Bay habitats, with community composition significantly structured by spatial location (PERMANOVA: $R^2 = 0.15$, $p < 0.001$). Multivariate analyses (distance-based Redundancy Analysis and General Linear Models) were conducted to assess which environmental variables drive the diversity and composition patterns in fish communities in seagrass meadows across the surveyed area. Spatial zone, type of seagrass meadow, and sediment type (categorical variables); temperature, depth, distance to the closest reef, distance to shore, and canopy height (continuous variables), emerged as critical predictors of fish diversity and community composition.

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Aswathy Joji

Ph.D. Student in Chemistry

Engineering Oligonucleotide Heterodimers for Upregulation of SCN1A to Combat Dravet Syndrome

Dravet syndrome (DS) is a severe developmental epileptic encephalopathy caused by haploinsufficiency of SCN1A, which encodes the α-subunit of the voltage-gated sodium channel Nav1.1. Therapeutic strategies that selectively increase SCN1A expression therefore represent a promising disease-modifying approach. Antisense oligonucleotides (ASOs) enable targeted gene modulation through diverse mechanisms and have emerged as powerful therapeutic tools. Previously, our group developed a 21-mer MOE gapmer ASO that targets and inhibits a long non-coding antisense transcript (Scn1A-NAT) that represses SCN1A transcription, resulting in increased SCN1A mRNA levels. In parallel, splice-switching oligonucleotides (SSOs) designed to enhance production of productive SCN1A transcripts are currently under clinical evaluation. Leveraging these complementary mechanisms, we demonstrated that co-administration of the NAT-targeting ASO and the SSO produces synergistic upregulation of productive SCN1A mRNA.

Despite this promise, regulatory and pharmacological challenges associated with administering multiple investigational agents complicate clinical translation. To address this limitation, we explored the feasibility of engineering a single bifunctional oligonucleotide heterodimer capable of recapitulating the synergistic effects of combination therapy. Given the increased steric bulk of the heterodimer and the need to engage two distinct RNA targets in different nuclear contexts, we hypothesized that intracellular cleavage of the linker would be required for optimal activity.

Accordingly, ASO heterodimers were synthesized using a non-cleavable carbon linker, nuclease-cleavable deoxythymidine linkages, and glutathione-responsive disulfide linkages. Functional studies revealed that the non-cleavable heterodimer failed to induce significant Scn1A upregulation, while nuclease-cleavable constructs showed only partial activity. In contrast, disulfide-linked heterodimers achieved robust upregulation of productive Scn1A mRNA. These studies further highlighted the importance of directionality of conjugation and productive uptake in achieving the expected pharmacological effect of the oligonucleotide combination. Collectively, this work demonstrates that rational linker design enables effective oligonucleotide heterodimers and supports the potential of engineered conjugates to serve as a viable strategy for combination gene-upregulation therapies.

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Oral Presenters

Arts, Culture & Performance

Ballroom East

Stacey Swanson

Ph.D. Student in Music Education

Who Played That? College Music Education Students' Accuracy in Detecting AI-Generated Piano Performance

This study examines whether college music education students can distinguish between human and AI-rendered performances of piano pieces, and whether confidence in detection judgments corresponds to accuracy. Seventeen participants evaluate six piano excerpts representing three musical styles (classical, folk, and ragtime), with each piece presented in both human-performed and AI-rendered versions created using the CFE+P expressive performance system. Participants make binary detection judgments, provided confidence ratings, and evaluated performance quality using rubric criteria. Results reveal that detection accuracy ($M = 51.96$) is not significantly different from chance, $t(16) = 0.46$, $p = .651$. No individual excerpt is detected at above-chance levels, and accuracy does not vary by musical piece or performance source. Confidence ratings show no significant correlation with accuracy ($r = .16$, $p = .530$), indicating poor metacognitive calibration. Participants rate human and AI-rendered performances equivalently on quality dimensions ($p = .775$). Neither prior AI exposure nor MIDI familiarity predict detection success. These findings suggest that college music education students cannot reliably distinguish AI-rendered from human piano performances, with implications for assessment validity and teacher preparation in an era of increasingly sophisticated generative AI.

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Alannah Egan

Master's Student in Musicology

"Atomic Age Renegades": Punk, Hip Hop, and Afrofuturism in Rage Against the Machine's "Renegades of Funk"

"They ain't gonna send us campin' like they did my man Fred Hampton... a ballot's dead so a bullet's what I get."
Los Angeles-based rock-rap group Rage Against the Machine called their audience to revolutionary arms against the United States government in their 1996 song "Down Rodeo."1 The band carried the spirit of 1960s racial equality movements into the 1990s, disillusioned by events such as the beating of Rodney King (1991) and fatal shooting of Amadou Diallo (1999). The band had close family members who introduced and connected them to 1960s-1970s progressive organizations. Frontman Zack de la Rocha's father is Mexican-American Berto de la Rocha of the 1970s East L.A. arts collective Los Four.2 Guitarist Tom Morello's mother is a Civil Rights activist and his father was a Black Kenyan liberation activist.3 This connection to the 1970s Californian revolutionary culture is demonstrated in Rage's modernized, multicultural approach to the Black Panthers' ideological foundations. Rage Against the Machine's participation in an Afrocentric musical lineage is emphasized in their cover of Afrika Bambaataa & the Soulsonic Force's song, "Renegades of Funk" (1983). Bambaataa's upbringing and philosophy were distinctively defined by the Black Panthers and the Nation of Islam.4
Drawing on Mattius Rischard's theories on performance as protest and Errol A. Henderson's work on Black Nationalism in rap and hip hop, this paper analyzes Tom Morello's punk/hip-hop do-it-yourself (DIY) approach, creating electric-guitar-adaptations of DJ musical techniques in Rage Against the Machine's cover of "Renegades of Funk" by Afrika Bambaataa & the Soulsonic Force. In doing so, Rage Against the Machine created an innovative and distinctive sound that actively engages with Afrocentric politics and ideologies of activist groups such as the Black Panther Party. In this light, DIY becomes a mode of critical thinking and reflection that can encourage political engagement.

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Chelsea McBride

D.M.A. Student in Jazz Composition

The Lone Arranger: Carla Bley's Singular Humor

Putting on any Carla Bley recording requires signing up for a journey to the unexpected. While she was primarily a jazz composer and arranger, her music incorporates classical, rock, raga, and instrumental extended techniques and sound effects not typically found in a concert hall. Bley's music upends traditional expectations of serious jazz, and incorporates both cerebral, referential humour and slapstick sound effects in her music to create a wild and wacky musical experience.

In this presentation, I will build on the work of Amy Beal and Charles Hiroshi Garrett to place Carla Bley squarely at the intersection of humour - in its myriad forms - and jazz. I describe Bley's unorthodox musical training and early life, establishing the context for her move to New York City, and describe her entry into composition and collaboration. Then, I look at her most notable recordings, and examine the concepts she used to create that humour. Lastly, I draw from interviews to describe her compositional process, and how she feels about composing and arranging.

Whether the band is getting on and off the horse ("The Lone Arranger"), teaching the bassist to sing ("Very Very Simple"), lamenting singing or piano lessons ("I Hate To Sing," "The Piano Lesson"), or simply mimicking the chaos of New York City traffic ("Fast Lane"), Bley's music always brings a laugh or a chuckle to an otherwise serious art form. Even her political commentary is steeped with a sense of humour: "Circus '68 '69" features multiple songs played at the same time, and "The National Anthem" is a wild take on the American national anthem (and some other songs). Bley's music manages to take the things we know and understand about American culture and jazz, take them apart, and put them back together - hilariously - in a way we didn't expect.

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Euge Stumm

Ph.D. Student in Literary, Cultural, and Linguistic Studies

Body as Language, Language as Body: Marico Carmona's Mutant Poetics

This study examines how the Argentinian poet Marico Carmona (1998–present) reimagines gender and body through their poetry slam performances. My hypothesis is that Carmona's poetry utilizes the poet's body as a central element for bringing visibility to their non-binary identity and experiences when assembling language. Carmona is one of the prominent new voices in Argentinian literature of gender and sexual dissidence, as the country witnessed over the last decade the largest number of cultural productions made by trans, travesti, and non-binary writers. I closely read selected poems from the anthology Futuro Problema, taking into consideration the poetry slam context to understand Carmona's linguistic and formal innovations. This anthology was published as part of Carmona's award for winning the 2019 Ciudad Emergente poetry slam in Buenos Aires. I break down my argument into three main theoretical axes of analysis: First, I utilize Brian Richardson's poetics of lists to examine how Carmona mixes narrative and non-narrative writing to bend poetic spatiotemporality, not only multiplying their body materiality but also simultaneously defying the binaries of genre and gender. Second, I take up sociolinguistic scholarship on gender-inclusive Spanish to examine how Carmona's use of the gender-inclusive neomorpheme "-e" in poetry slams emphasizes pronunciation deliberately, centering the poet's body as the locus of enunciation. Third, I dialogue with the queer critique of Édouard Glissant's framework of opacity, transparency, and relation to claim that difference in Carmona's poetry is a product of the relation with their body rather than language alone. Carmona's mutant poetics establish body and language as mutually constitutive through relationality, rejecting a binary separation or hierarchy between body and language. I conclude that the political force of gender-inclusive Spanish in Carmona's poetry should not be reduced to language as a purely abstract linguistic system but rather as the product of the relation between the body of the poet and language itself.

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Sarah Blakney

Master's Student in Musicology

Sound Foundations: Music Practices of the Institute in Basic Life Principles

The Institute in Basic Life Principles (IBLP), based in Big Sandy, Texas, runs an annual program known as Sound Foundations. This summer camp takes the course of three weeks and includes lessons in Music History, Hymnology, and Orchestra. Founded by evangelist Bill Gothard, the IBLP is a Christian fundamentalist group with an established set of moral and behavioral standards. These standards include guidelines pertaining to gender roles, obedience to authority, and musical expression. Scholarship on the IBLP has thus far focused on the interpretation of religious text and connections to larger political movements. However, there have been no major studies of the role of music in this organization.

In this presentation, I provide a glimpse into the musical life of the IBLP. I focus on how members of this community, particularly participants in Sound Foundations, use music and faith to navigate their professional careers. The performance practices and religious themes in this Christian coalescence reflect their purported values as well as the image they wish to portray to the public. I examine Bill Gothard's homeschool curriculum, The IBLP official website, and the book Quivering Families by Emily Hunt McGowin, who explored Gothard's doctrine. I also drawn on correspondence with camp alumnae Alissa Wilkinson and Cherith Hendrich. Wilkinson attended Sound Foundations in her teens and wrote an article about her experience in 2014. Hendrich is professional harpist who lives on the campus of Sound Foundations. Both musicians exemplify how women within an insular Christian organization operate within gender guidelines often regarded by outsiders as restrictive while carving out fulfilling careers. My goal is to understand how this community organizes musical activities at Sound Foundations and how members currently reflect the values of the group. My work contributes to the literature of Protestant music making and considers how musical activities align with the established doctrine of the IBLP.

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Victor Bento

D.M.A. Student in Vocal Performance and Pedagogy

Reintroducing the Songs of Elizabeth Turner (d. 1756) in Voice Training Today: Modern Performers Edition and Pedagogical Guide

Very little is known about the personal life of Elizabeth Turner (d. 1756). No letters, diaries, or personal accounts survive. What remains instead is her professional footprint: published music, documented performances, and clear evidence of an active career as a singer and composer in mid-eighteenth-century London. Despite this visibility in her own time, Turner's music has largely disappeared from modern performance and from the repertoire used in collegiate voice instruction.

This doctoral research examines six songs from Turner's A Collection of Songs with Symphonies and a Thorough Bass (1756) with the specific objective of evaluating their usefulness in undergraduate voice training today. The project does not attempt to reconstruct Turner's biography or to produce a critical edition. Instead, it asks a practical question: how do these works function when assessed through the priorities of contemporary voice pedagogy?

Each song is examined using a consistent pedagogical framework that addresses five areas central to studio teaching: vocal technique, diction and historical pronunciation, stylistic features, expressive content, and pedagogical utility. These categories are applied flexibly, allowing the analysis to focus on the most relevant learning challenges presented by each piece. Through this approach, Turner's songs are considered not as historical artifacts, but as functional teaching material.

A central component of the project is the preparation of a modern performer's edition of the six songs. Intended specifically for studio use, this edition includes a realized basso continuo, complete text underlay for all verses, and editorial markings designed to support rehearsal and instruction. The edition functions as a practical extension of the analytical work, enabling instructors and students to engage directly with the repertoire in applied settings.

By focusing on how Turner's songs operate within modern voice pedagogy, the project clarifies the instructional value of eighteenth-century English song for developing singers. More broadly, it offers a discipline-specific case study in how historically overlooked repertoire can be evaluated through functional criteria and thoughtfully reintroduced into contemporary educational practice, allowing music long confined to the archive to be heard, taught, and studied once again.

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Oral Presenters

Cellular & Molecular Mechanisms

Ballroom West

Abelardo Aguilar Camara

Ph.D. Student in Biology

Small Viruses Reveal Multiple Transitions Between HK97-Fold Viruses and Cellular Compartments

The HK97-fold is an ancient protein structure that forms shells. It is the building block of viruses infecting all domains of life. It is also the building block of encapsulins, cellular compartments that confine biochemical reactions. Recent studies have hypothesized that encapsulins evolved from viral capsids. However, this evolutionary pathway is challenging to justify biophysically, as these viruses form larger, more complex shells. We addressed this paradox by searching for smaller, simpler viral capsids across ecosystems. Our analyses yielded a group of viral entities that encode HK97-fold proteins with molecular similarities to encapsulins. Phylogenetic analysis revealed multiple evolutionary transitions between encapsulins and viruses. A mechanism for such transitions was proposed based on the structural and molecular parallels between encapsulins and procapsids, the immature state of viral capsids. We concluded that procapsids are akin to the common HK97-fold protein shell ancestor and might still facilitate transitions between modern viruses and encapsulins.

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Benjamin Minch

Ph.D. Student in Marine Biology and Ecology

Giant Viruses Commit Widespread Key Fraud Using Genomic Islands

Giant viruses (phylum Nucleocytoviricota) possess massive genomes that challenge the traditional definition of viral life. While their "chimeric" nature implies rampant gene theft, the structural mechanisms driving this acquisition have remained unclear. Using long-read metagenomics, we uncovered the landscape of "genomic islands", large, mobile DNA segments, across 369 giant virus genomes. We found that these genomic islands are widespread among giant viruses, with many even having multiple islands. Functional analysis reveals these islands are significantly enriched in surface adhesion proteins, effectively acting as stolen "keys" to pick cellular "locks" during infection. Phylogenetic reconstruction indicates many of these keys are of bacterial origin. This suggests a tripartite model of gene exchange where viruses steal entry mechanisms from bacteria within the "melting pot" of the protist host. By adopting these bacterial surface proteins, the viruses likely utilize molecular mimicry to trick hosts into engulfing them. Furthermore, these island regions function as hypervariable hotspots, shuffling genes even among closely related viral strains. This plasticity allows viruses to rapidly swap their surface adhesion proteins to evade host defenses or expand their host range. Ultimately, we establish that genomic islands are essential engines of adaptation, enabling giant viruses to gain an advantage in the host-virus arms race.

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Deema Abayawardena

Ph.D. Student in Biology

Specification of the Primary Embryonic Axis in Metazoan Embryos: Insights from Sea Star Development

An essential event in embryonic development in bilaterians (bilaterally symmetrical animals) is the establishment of the anterior-posterior axis (AP). This process is strongly influenced by the maternally determined animal-vegetal (AV) axis of the oocyte. AP axis formation involves localized Wnt/β-catenin (cWnt) signaling in vegetal-blastomeres.We have shown that, in echinoderms, cWnt activation requires the localized activation of Dishevelled (Dvl), a critical cWnt regulator; however, the maternal regulation of Dvl activity remains unknown. To identify maternal factors regulating Dvl and cWnt activity in vegetal blastomeres, I applied RNA-seq and mass spectrometry analysis to isolated Patiria miniata oocyte halves and identified various mRNAs, long non-coding RNAs, and proteins enriched at the two poles. Candidate factors are being functionally tested for their roles in regulating AP axis specification. This research sheds light on maternal mechanisms in axis specification and their evolution in animal eggs.

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Ina Niroula

Ph.D. Student in Molecular and Cellular Pharmacology

Regulation of Mitochondrial Biogenesis in T Cells

In the evolving field of oncology, understanding metabolic requirements of immune cell is essential to fuel effective antitumor immunity. T lymphocytes are essential players of the adaptive immune system and are central to tumor surveillance and immune homeostasis. Upon encountering tumor antigens, T-cell receptor (TCR) signaling reprograms T cell metabolic landscape, including rapid increase in mitochondrial mass. This mitochondrial expansion enables T cells to meet the bioenergetic and metabolic demands required for proliferation, clonal expansion, and cytotoxic function. Yet, the molecular mechanisms by which antigen-induced TCR engagement initiates the mitochondrial biogenesis program remain unknown.

To investigate how TCR signaling governs mitochondrial programs, we performed temporal gene expression analysis of early T cell activation. Surprisingly, this analysis revealed that PGC-1α, a transcriptional coactivator, a master regulator of mitochondrial biogenesis, is absent in T cells. Moreover, its close paralog PGC-1β is not induced during T-cell activation, suggesting that the canonical mitochondrial biogenesis program is not operative in T cells. Instead, we identified a lesser-understood paralog of PGC-1α, called PPRC1, which is rapidly and transiently upregulated following TCR engagement. We hypothesize that PPRC1 drives a unique translational and metabolic program that supports mitochondrial biogenesis and effective antitumor immunity.

To define the functional role of PPRC1, we generated T-cell-specific PPRC1 knockout mouse models, as its whole-body deletion is embryonically lethal. Loss of PPRC1 disrupted mitochondrial organization, including altered cristae architecture, reduced mitochondrial membrane potential, and increased mitochondrial reactive oxygen species. These mitochondrial defects coincide with reduced T-cell viability, altered activation dynamics, and pronounced T-cell lymphopenia phenotype in vivo, implicating PPRC1 as a critical regulator of mitochondrial function during the T-cell life cycle.

Our ongoing work aims to define the specific transcriptional programs coordinated by PPRC1 that fuel mitochondrial metabolism and function. For its role in tumor, we are using co-culture killing assays and in vivo tumor xenograft models to evaluate whether loss of PPRC1 or engineering PPRC1-armored chimeric antigen receptor (CAR) T cells alters antitumor efficacy. In summary, we have discovered PPRC1 as a novel regulator of mitochondrial biology in T cells. These findings open new avenues for modulating mitochondrial mechanisms for cancer therapy.

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Mariana Viso

Ph.D. Student in Biomedical Engineering

Modeling Dynamic Myeloid Fibroblast Crosstalk in Pancreatic Cancer Within a Microfluidic Platform

Pancreatic cancer adenocarcinoma (PDAC) is one of the deadliest types of cancer, with 90% of its patients succumbing to this illness within five years after diagnosis. The effectiveness of most chemotherapy in PDAC is limited by the development of chemoresistance. This motivates the need for tools to study chemoresistance development and novel treatments.

Chemoresistance arises from the inflammatory polarization of cancer-associated fibroblast (iCAF) within the PDAC microenvironment, driven by interactions with myeloid-derived suppressor cells (MDSCs). However, not much is understood about the mechanisms that govern immune-driven iCAF polarization. We set to uncover these gaps by developing a microfluidic platform capable of showcasing the dynamic MDSC-CAF interactions that promote tumor development in-vivo.

Spheroids were formed with pancreatic tumor cells and dual-reporter CAFs that fluoresce green when they become inflammatory. The spheroids were seeded on the concaved wells of the platform and allowed to interact with MDSCs that are fluidically introduced for 48 hours. Positive and negative controls for polarization were conducted by flowing in cytokines that stimulate an inflammatory (TNF-α) or non-inflammatory (TGF-β) phenotype. After 48 hours, the spheroids were imaged and then extracted from the chip for single cell RNA sequencing analysis.

MDSC and TNF-α groups had the highest levels of fluorescent iCAF polarization compared to the media control, demonstrating the role of MDSCs in inducing an inflammatory microenvironment. Gene analysis revealed transcriptional changes in both CAF and tumor cells after interacting with MDSCs. CAFs exposed to MDSCs exhibited upregulation of inflammatory and hypoxic pathways, suggesting a shift toward a pro-tumorigenic and inflammatory phenotype. KPC tumor cells from the same group showed enrichment of basal-like gene signatures, linked to more aggressive tumors with worse patient outcomes. These findings demonstrated the role of MDSCs beyond immune suppression, as they induced CAF and tumor configurations that promote tumor progression.

This study demonstrated the role of MDSCs in driving inflammatory and basal-like transitions in PDAC and validated our novel platform as a powerful tool for interrogating cell-to-cell interactions. Thorough understanding of the role of MDSC in tumor progression will provide insight into the mechanisms that govern chemoresistance development, and possible targets for attenuation.

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Michael Cioffi

Postdoctoral Associate

Rational Design of Enlarged AAV Capsids to Enhance Gene Therapy Cargo Capacity

Adeno-associated virus (AAV) is a leading gene therapy vector, yet its therapeutic potential is limited by a small packaging capacity (~4.7 kb), restricting applications requiring large transgene delivery. While dual AAV vectors have shown promise in preclinical models and clinical trials, they face many challenges including requiring efficient co-transduction, potential incomplete reconstitution, and higher vector doses. Here, we propose a complementary approach: engineering an enlarged AAV capsid adopting the next possible icosahedral capsid architecture, T=3, theoretically increasing internal volume 5-fold to yield approximately 25 kb packaging capacity. Computational rational design of AAV capsid proteins integrated the geometrical theory of viral capsids, AI-based protein folding, molecular dynamics simulations, and molecular visualization software. Capsid protein multimers were folded to identify optimal oligomeric tiles compatible with icosahedral tiling theory, then assembled into T=1 and T=3 architectures. Geometrical constraints at oligomer interfaces determined mutation sites for T=3 compatibility. VP3 trimers were identified as optimal building blocks, with the AAV2 VP3 parent mutant requiring 15 deletions to accommodate T=3 curvature. The parent mutant was coarse-grained with the Martini model (~5 Å per bead) and subjected to molecular dynamics simulations assessing stability and thermodynamic properties. Molecular dynamics yielded stable T=3 capsids (~45 nm diameter) under physiological conditions, though mutants also remained stable in a T=1 architecture, suggesting T-number competition during assembly. Comparative analyses confirmed the predicted 5-fold volume increase versus wild-type T=1 capsids. Homologous mutants in AAV1, AAV5, AAV8, and AAV9 required 10-20 residue deletions. The computational design approach proposed here resulted in AAV capsid protein mutants that, in silico, yielded stable T=3 capsids. However, mutants also remained stable in a T=1 architecture. We are currently investigating second-generation designs to selectively destabilize smaller capsids while testing predictions experimentally. Additionally, this computational strategy is generalizable and could be used to modify other viral vectors. To our knowledge, the work presented here represents the first publicly shared effort to reengineer the icosahedral T-number architecture of AAV vectors.

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Lea Wilson

Ph.D. Student in Biomedical Sciences

Herpes Simplex Virus 1 Manipulates Chromatin During Infection for Viral Benefit

Herpes Simplex Virus 1 (HSV-1) has infected an estimated 64% of the global population under 50. The virus is mainly known to cause oral cold sores, but it can cause severe illness in immunocompromised patients. Additionally, it has the ability to go dormant and reactivate, allowing another round of symptomatic infection and spread. Currently, treatments are only available for symptomatic infections, which makes understanding how HSV-1 infects cells critical for the development of future treatments. HSV-1 replicates in the nucleus of a host cell, leading to extensive nuclear remodeling. Chromatin, formed by DNA wrapping around proteins called histones, is manipulated by the virus to allow escape of newly formed viral particles through gaps in the nuclear membrane. Here, we use a combination of microscopy and chromatin profiling techniques to investigate how HSV-1 exploits chromatin dynamics. Understanding precisely how the virus manipulates chromatin will aid in the development of future treatments and help identify intrinsic vulnerabilities of the cell.

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Oral Presenters

Clinical Medicine & Outcomes

Iron Arrow Room

Alex Hu

Postdoctoral Associate

A Mitochondrial Regulator of Your Skin: Defining the Role of MPZL3 in Sebaceous Gland Growth, Homeostasis, and Inflammation

Sebaceous glands (SGs) are specialized skin appendages that produce sebum, a lipid-rich substance essential for skin barrier function and hair health. Dysregulation of SG growth or activity contributes to common dermatologic conditions, including acne and inflammatory skin disease, yet the molecular mechanisms governing SG homeostasis remain incompletely understood. Our previous work identified Myelin Protein Zero-like 3 (MPZL3), a mitochondrially localized protein, as a negative regulator of SG size; however, how MPZL3 functions during SG development and maintenance in vivo has not been fully defined.

In this study, we investigated the role of MPZL3 in SG morphogenesis and function using keratin 14 promoter-driven, epithelium-specific Mpzl3 knockout mouse models. We analyzed both constitutive epithelial knockout (epiKO) mice and an inducible epiKO model to distinguish developmental from postnatal roles of MPZL3. Histological analysis, indirect immunofluorescence, RT-qPCR, and bulk RNA sequencing were used to assess SG size, sebocyte number, proliferation, differentiation, and gene expression changes across postnatal development and hair cycle stages.

Constitutive Mpzl3 epiKO mice were born grossly indistinguishable from littermate controls, and early postnatal skin development appeared normal. However, beginning at postnatal day 12, coinciding with completion of SG morphogenesis, epiKO mice developed markedly enlarged SGs. This phenotype persisted into later hair cycle stages and was accompanied by increased sebocyte number, enhanced sebocyte proliferation and differentiation, elevated sebum production, increased inflammation, and a visibly greasy hair coat. Transcriptomic analysis of anagen skin revealed significant alterations in pathways related to lipid metabolism, epidermal differentiation, and inflammation.

In contrast, inducible deletion of Mpzl3 after early postnatal development resulted in a milder SG enlargement phenotype, suggesting that MPZL3 plays a particularly important role during SG morphogenesis rather than exclusively in adult tissue maintenance.

Together, these findings identify MPZL3 as a key regulator of sebaceous gland growth and homeostasis in vivo and highlight a previously underappreciated link between mitochondrial regulation and skin appendage biology.

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Caleb Calaway

Ph.D. Student in Exercise Physiology

Comparison of Upper vs. Lower Limb Movement Asymmetries in Persons with Parkinson's Disease

Movement asymmetry is a common symptom experienced by persons with Parkinson's Disease (PD) due to the unilateral nature of the condition as well as sarcopenia and bradykinesia. PURPOSE: To determine if differences in neuromuscular power exist across numerous training loads relative to maximal strength for the leg press (LP) and chest press (CP) exercises in PD persons. METHODS: 33 individuals diagnosed with PD completed 1-repetition maximum (1RM) and power testing at 30 – 80% of 1RM in 10% increments. Data on peak and average power were collected at each load for both limbs. Multiple 2 (limb) x 6 (load) ANOVAs were conducted to detect main effects and interactions. LSD pairwise comparisons were used to determine where differences occurred (Mdiff ± SE; 95% CI; p value) and Cohen's d values were calculated as effect sizes. RESULTS: For LP peak and average power, no main effects or interactions were seen by limb. However, pairwise comparisons for peak power asymmetries by load were significant at 30% (17.9 ± 6.8 W; 4.1 W, 31.7 W; p = .011, d = .11) and 40% 1RM (20.8 ± 9.2 W; 2.0 W, 39.6 W; p = .033, d = .12) alone; for average power, differences were seen only at 30% 1RM (12.2 ± 6.0 W; .1 W, 24.4 W; p = .050, d = .45). Main effects by limb were seen for CP peak (F (1,39) = 8.024, p = .008, np^2 = .211) and average power (F (1,30) = 5.827, p = .022, np^2 = .163). CONCLUSIONS: While upper limb asymmetry was significant across nearly the entire loading spectrum, lower limb asymmetries were seen only at lower %'s of 1RM, where movement speed is a critical determinant of power production. These data may warrant unique loading protocols for PD persons in the upper and lower limbs when reduction in asymmetries is of great importance to the individual; while lower limbs may benefit from lower load training at high speeds, the upper limbs may improve further when training the entire loading spectrum.

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Luiza Waechter Severo

Postdoctoral Associate

Global Functional Homogenization of Plant and Bird Assemblages Across Island Archipelagos

Island archipelagos are often considered natural laboratories for studying ecological and evolutionary processes, as they have historically experienced lower levels of anthropogenic disturbance than continental systems. However, increasing rates of species introductions are reshaping insular biodiversity worldwide, with potentially profound consequences for ecosystem structure and functioning. Here, using a globally extensive dataset, we investigate taxonomic and functional patterns of native and introduced plant and bird assemblages across island archipelagos. We compiled present-day species distribution data for plants and birds, including migratory bird species, across 19 archipelagos encompassing 138 islands worldwide. We quantified taxonomic and functional beta diversity for native and introduced assemblages to assess patterns of compositional turnover among islands. In addition, we evaluated how key geological and geographic attributes of archipelagos such as age, elevation, total area, number of islands, and isolation shape richness patterns of native, introduced, and migratory species. Our analyses revealed a pronounced global pattern of homogenization across island archipelagos, characterized by reduced functional turnover in both plant and bird assemblages. Archipelago age emerged as the main driver of native and introduced plant richness, while the number of islands influenced native plant richness only. In contrast, elevation was the sole variable positively associated with introduced bird richness, suggesting that topographic complexity may facilitate the establishment of non-native bird species. Despite marked differences in dispersal ability between plants and birds, both taxonomic and functional compositions showed increasing similarity across islands. Our findings demonstrate that functional homogenization is a pervasive process in insular systems, transcending taxonomic groups with contrasting life histories and dispersal strategies. Even in some of the most isolated ecosystems on Earth, characterized by distinct geological and geographic contexts, human-mediated species introductions are eroding biodiversity patterns and potentially compromising ecosystem functions and processes. These results highlight the vulnerability of island ecosystems to biological invasions and underscore the need for conservation strategies that explicitly consider functional diversity alongside species richness.

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Julianna Darcy

Master's Student in Architecture

Biophilia as Clinical Infrastructure: Rethinking the Healthcare Campus

Historically, healthcare campuses have prioritized efficiency over psychological restoration, yet they are among the most emotionally and cognitively demanding environments people encounter. This research examines how biophilic design can foster meaningful connections between people and nature when systematically integrated into healthcare campuses, supporting patient recovery, reducing stress, and enhancing staff well-being. This study is grounded in the Biophilia Hypothesis and Attention Restoration Theory, focusing on how natural elements, spatial configuration, and sensory experiences influence the nervous system and attentional capacity in clinical settings.

By using a mixed-methods approach, the research combines theoretical frameworks with site-based observation and user-experience mapping conducted within a Cleveland Clinic infusion bay. Extra attention was given to visual access to nature, daylight, materiality, acoustic conditions, and spatial prospect and refuge. The analysis revealed that environments offering naturalistic materials, natural light, and greenery support emotional regulation and mental restoration during treatment, while sterile, visually barren spaces increase perceived stress and cognitive fatigue.

These findings suggest that biophilic strategies must extend beyond decorative elements to become core organizational elements of the healthcare campus, shaping circulation, waiting areas, treatment rooms, and outdoor spaces. If a campus can carefully balance prospect, refuge, and natural stimuli with healthcare environments, it would allow for that space to function not only as places of medical intervention but also as therapeutic landscapes that actively participate in healing.

This research argues for a shift from the typical sterile healthcare environment to a more nature-centered campus design. This is proven to be a critical component of patient-centered care, offering architects and healthcare planners evidence-based strategies to create environments that support both physiological and psychological recovery.

Author(s): Julianna Darcy

Jordan Walker

Postdoctoral Associate

Metabolic Impacts of Bacteriophages on Anaerobic Phototrophic Bacteria in Early Earth Analogs

The structure of microbial communities and the stable anoxic, sulfidic conditions in meromictic lakes make them powerful analogs for conditions in ancient oceans and potential extraterrestrial environments. The dominant primary producers in these systems are purple sulfur bacteria (PSB) and/or green sulfur bacteria (GSB), which leave characteristic carbon and sulfur isotopic signatures and diagenetic products of their pigments in the geologic record. Observations from meromictic lake ecosystems reveal a decoupling between biomarkers produced by sulfide-oxidizing bacteria and bulk carbon isotope signatures, suggesting the influence of additional ecological controls. Viruses infecting bacteria, or phages, are known to alter host metabolism and have been hypothesized to contribute to the observed decoupling. Here, we utilize a suite of meta'omics techniques to characterize virus-host interactions and their metabolic impacts at three meromictic lakes in the North American Pacific Northwest. In PSBdominated lakes, PSBs account for 73% of the community gene expression, which is significantly higher than their relative abundance of 30%. In a GSB-dominated lake, GSBs represent 30% of the community and only 20% of the activity. We show that PSB lakes have significantly higher abundance of temperate viruses, those that establish dormant and long-term infections, and bacteria containing viral defense systems. Furthermore, we show that all viruses infecting PSB were classified as temperate, while those linked to GSB were lytic, i.e., causing cell death upon infection. Viruses in both lake types encoded genes implicated in sulfate reduction to sulfite and pathways for heme incorporation into pigments. Our results provide evidence that differences in viral lifestyles influence the decoupling of host abundance and activity and demonstrate the potential for viruses to directly alter host metabolic pathways involved in pigment production and isotopic biosignature formation. This study was funded by the NASA Exobiology Program (80NSSC23K0676 to C.B.S), the JGI Community Science Program (508870 to C.B.S. and W.G.), and the NSF Emerging Mathematics for Biology Program (2424579 to C.B.S).

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Ariel Leyte-Vidal

Ph.D. Student in Biochemistry and Molecular Biology

Numerous Clinically-Detected Asciminib-Resistant BCR::ABL1 Mutations Disrupt Allostery and Confer Cross-Resistance to the Novel Clinically-Active Allosteric TKI Tgrx-678

Objectives: Asciminib is a first-in-class potent and selective allosteric inhibitor of BCR::ABL1 that has demonstrated substantial clinical efficacy and excellent tolerability in patients with Philadelphia chromosome positive chronic myeloid leukemia in chronic phase (Ph+CML-CP) who exhibit resistance or intolerance to prior TKI therapies that target the ATP binding site, and in newly diagnosed patients. Asciminib has received accelerated approval by the US FDA as a treatment option for Ph+CML-CP in any line of therapy. Asciminib inhibits BCR::ABL1 kinase activity via a unique mechanism of action that involves binding to the allosteric regulatory myristoyl binding pocket (MBP) and inducing an assembled, autoinhibited confirmation. This aspect of asciminib enables a reduced propensity for off-target inhibition in patients, thereby potentially enhancing its therapeutic index. However, an increasing number of asciminib-resistant mutations are emerging clinically and have been identified both within the MBP and elsewhere in the kinase domain. We previously demonstrated that mutations in the kinase N-lobe unexpectedly confer in vitro and clinical asciminib resistance despite retaining binding affinity for asciminib and provided indirect evidence for disruption of allostery as a candidate mechanism for one mutation (Leyte-Vidal et al, Blood 2024). We now present a comprehensive analysis of 25 asciminib-resistant mutations recently identified in clinical isolates, including in regions outside of the kinase domain.

Methods: BCR::ABL1 mutants were created in MSCVpuro by site-directed mutagenesis and transduced into Ba/F3 cells, which were selected for growth factor independence and tested for sensitivity to asciminib and a second clinically active allosteric TKI, TGRX-678. Drug binding assessments were conducted utilizing an in cellulo nanoBRET assay with full length BCR::ABL1. Limited proteolysis experiments were performed to assess for evidence of global alteration of purified kinase protein in vitro. Mutants were cloned into MSCVpuro ABL1b, transduced into Ba/F3 cells, and assessed for growth factor independence/kinase activation.

Results: Twenty-five BCR::ABL1 mutations identified in asciminib-resistant patients were assessed. These substitutions are located in or near the MBP (n=8), in the kinase C-lobe/hinge region but removed from the MBP (n=4), in the kinase activation loop (n=4), in the kinase N-lobe (n=4), in the SH2-kinase linker region (n=2), SH3 domain (n=2) and in the SH2 domain (n=1). All assessed mutants conferred resistance of varying degrees to asciminib in vitro. Relative resistance to asciminib highly correlated with in vitro resistance to the novel clinically-active allosteric TKI TGRX-678. Only a minority of the 22 mutations, primarily those in the MBP, substantially altered the binding affinity of asciminib. Partial proteolysis studies of several mutants demonstrated evidence of global structural alterations. Most mutations activated the kinase activity of ABL1b in cellulo, as reflected by their ability to confer growth factor independence in Ba/F3 cells associated with elevated levels of phosphotyrosine.

Conclusion: Asciminib is clinically susceptible to a substantially larger number of drug-resistant mutants than 2G or 3G TKIs. All 22 BCR::ABL1 mutations tested conferred varying degrees of resistance to asciminib, with a majority retaining asciminib binding affinity. Several mutants displayed activation of kinase activity and alteration of kinase structure, providing the first direct evidence for disruption of allostery as the most common resistance mechanism of asciminib resistant-mutations. Notably, this study also marks the first report of a clinically-detected asciminib-resistant SH2 domain mutation, further expanding the spectrum of resistance mutations and demonstrating the need to assess regions of BCR::ABL1 outside of the kinase domain in patients with asciminib resistance. The high degree of cross-resistance observed between asciminib and TGRX-678 suggests a class-like effect of mutations that confer resistance to allosteric TKIs, primarily through disruption of allostery. These findings underscore the need for continued investigation into resistance mechanisms to inform the development of next generation therapies and treatment strategies for CML patients.

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Oral Presenters

Physical Science, Engineering & Ecology

Senate Room

Luis Alvarez Garcia

Postdoctoral Associate

Using a Heterogeneous Graph Transformer to Repurpose Drugs for the Treatment of Nipah Virus Infectious Disease

Nipah virus (NiV) is a bat-borne pathogen whose infection in humans causes disease with a very high observed mortality rate, with the NiV-M lineage having a case fatality of 39% while NiV-B lineage reporting a much higher mortality range of 60% to 100% in different outbreaks. Since the identification of the first cases of NiV infection in humans in Malaysia in 1998, several outbreaks have occurred in South East Asia . Due to its high mortality rate and lack of effective therapies or vaccines, it is currently listed as a select biological agent by both the US Dept. of Health and Human Services and US Dept. of Agriculture. Therefore, it is crucial to develop treatments for care of infectious cases in order to reduce the health impacts and public health concerns. In this work we leverage a heterogeneous graph transformer model in order to repurpose drugs for the treatment of NiV infectious disease. By using the model in a heterogeneous Knowledge Graph (KG) we hope to harness different varied forms of interactions between different biological entities - such as interactions between drugs and gene/proteins, diseases and gene/proteins, diseases and effect/phenotype (symptoms), drugs and effect/phenotype, etc - in order to predict novel indications between already existing, approved drugs and the disease from NiV infection. This KG based drug repurposing capitalizes on the known heterogeneous interactions between relevant biological entities to overcome the time and costs associated with drug development. Our goal is the attention mechanism will extrapolate from newly-observed genes affected by the NiV infectious disease to perform link-prediction on the KG, by learning from the existing topology of relations in the KG and how these predict existing indications. Previous similar methods for drug repurposing by link-prediction on biological networks mostly relied on simplified homogeneous networks, e.g. similarity-matrix based collapses of heterogeneous data into homogeneous versions, thus losing some information. By utilizing an attention mechanism that is able to process a graph with different types of interactions, and between different types of nodes, our link-prediction model exploits the full breath of available information.

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Opeyemi Isaac

Ph.D. Student in Chemistry

Exploring PGRMC1 Dimerization and Stability: Biophysical Insights into Heme Interactions in Phospholipid Nanodiscs

Progesterone Receptor Membrane Component 1 (PGRMC1) is a heme-binding protein that is expressed in heme-rich organs like the breast, liver, and ovaries, indicating its involvement in various biological functions, drug metabolism, cytochrome P450 activity, and cancer cell proliferation. Previous reports have shown that it is the heme-dependent PGRMC1 dimers that interact with cytochrome P450 enzymes (CYPs) and epidermal growth factor receptors (EGFRs), exhibiting promising functional activity compared to monomeric form. In a recent study from our lab on the cytosolic domain of PGRMC1, we identified two routes to form the dimer: heme-mediated and disulfide-bond-mediated pathways. Despite these advancements, significant knowledge gaps remain regarding the physiological relevance and the functional dynamics of the full-length, membrane-bound PGRMC1. Therefore, investigating full-length PGRMC1 in a membrane-like system, and characterizing the influence of heme binding following incorporation, is crucial to understanding its behavior, oligomerization trends and structural stability. Such insights could pave the way for novel therapeutic approaches that leverage PGRMC1's role in cellular signaling and cancer proliferation, ultimately improving treatment options for various malignancies.

So far in this work, we have utilized various spectroscopic techniques, such as size exclusion chromatography to evaluate the oligomeric state of the protein, nanoDSF to monitor the thermal stability and unfolding behavior of PGRMC1 in nanodisc, and circular dichroism in the far UV and visible region for secondary structural analysis of full length PGRMC1. Our goal is to (i) explore full-length PGRMC1 homodimerization dynamics in the presence of nanodiscs, to (ii) investigate the nuanced effects of heme binding and characterization of its downstream interactions with other enzymes, and (iii) it uses in informing design of targeted therapeutic strategies to disrupt dimerization and mitigate tumor progression.

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Jordan Grant

Ph.D. Student in Biomedical Engineering

Inflammasome Inhibition Mitigates Neuroinflammation and Neurovascular Unit Dysfunction in Intracortical Microelectrode Array Implantation

A vast user population with neural injury or neurodegenerative disease gains function and independence in their everyday lives with the recent strides in brain-computer-interface (BCI) technology. BCIs provide direct communication with a patient's own nervous system to control an output device, such as a neuroprosthetic. However, BCIs require invasive microelectrode (ME) implantation into the central nervous system (CNS) to have proximity to neuronal units and obtain signal at a high resolution, and a major limitation is the foreign body response (FBR). The innate immune response proceeds acutely after ME implantation and chronically the FBR leads to glial encapsulation, blood-brain-barrier (BBB) permeability, and neurodegeneration that all contribute to neurovascular unit (NVU) dysfunction and electrophysiological signal decay. In this study, we target the inflammasome complex, a key element of the innate immune system found in neuroinflammatory conditions and the FBR that leads to pyroptosis, a lytic form of cell death. We evaluated the effects of inflammasome inhibition in a rodent model of intracortical ME implantation through gene expression and immunohistochemistry (IHC) analysis at the acute and sub-acute phases of injury. We treated subjects with the inflammasome inhibitor IC100, a monoclonal antibody targeting the adaptor protein of the inflammasome complex. We found significant acute downregulation of inflammasome components and products' gene expression, as well as decreased caspase-1 activity, the effector protein of the inflammasome complex that downstream leads to pyroptosis. We also show decreased gene and protein expression of the potent pro-inflammatory cytokine and inflammasome product interleukin-1β (IL1β), which propagates neuroinflammation by promoting further cytokine production and recruiting immune cells, exacerbating BBB permeability and NVU dysfunction. We also evaluated the presence of IgG, a plasma protein, and cells of the NVU at the tissue-electrode interface as metrics of BBB permeability and NVU dysfunction. Finally, we show changes in ME performance with inflammasome inhibition with in-vivo electrophysiological recordings. These results highlight the therapeutic potential of inflammasome inhibition to alleviate pyroptosis, neuroinflammation, BBB permeability, and NVU dysfunction in the FBR of chronic neural implants to maintain the clinical function of BCI systems.

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Gabriella Berman

Ph.D. Student in Environmental Science and Policy

Using International Law to Protect Marine Biodiversity from Deep-Sea Mining

Deep-sea mining, the extraction of minerals from the seabed, is likely to have major environmental impacts. Studies point to possible impairment of key ecosystem functions through pollution and biodiversity loss. Notwithstanding the inability to predict the full extent of spatiotemporal environmental impacts, negotiations are underway at the International Seabed Authority to finalize regulations for commercial extraction of critical minerals in the international seabed. The regulations under negotiation would permit deep-sea mining to proceed despite significant scientific uncertainty; however, international law prohibits deep-sea mining unless science demonstrates that it can be conducted while adequately protecting biodiversity and preserving ocean health. To comply with international law, a moratorium on deep-sea mining is required until a greater understanding of its environmental impacts is reached.

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Sofiane Amroun

Ph.D. Student in Civil Engineering

Towards Sustainable Concrete - Mechanochemical Activation of Supplementary Cementitious Materials

Cement is often partially replaced with supplementary cementitious materials (SCMs) to reduce CO_2 emissions caused by its production, while improving concrete's performance. The shortage of conventional SCMs allowed the exploration of new materials to produce alternative SCMs. Materials that can satisfy market needs for producing SCMs are typically inert and require processing. Mechanochemical activation (MCA) is one way of activation. It is performed by exposing materials to high-energy grinding, altering crystalline structure and particle morphology. In this work, we focus on the effect of MCA on different materials, with an emphasis on basaltic fines (BF), a widely available resource. BF was exposed to different grinding conditions with varied grinding time (GT) and ball-to-powder ratio (BPR). BF showed increased reactivity with increases in GT and BPR. Partial amorphization was evident from X-ray diffraction (XRD). Scanning electron microscopy (SEM) revealed the formation of rounded particles, aggregates, and agglomerates. Reactivity strongly correlated with the amorphous content in the case of BF, but not with the BET specific surface area. In this work, 16 materials and SCMs were also exposed to MCA at the same GT and BPR. The increase in reactivity after MCA was found to logarithmically correlate with the initial reactivity of the SCMs, suggesting that the Modified R^3 reactivity test is an efficient screening test for MCA. Finally, we investigated the effects of MCA on the performance of mortar and cement paste specimens. This was done by replacing 30% of the cement with the tested materials. The SCMs used were BF, low-grade clay, dredged sediments, and bottom ash. The cumulative heat release from the paste specimens decreased in all cases after MCA. In general, compressive strength and bulk resistivity increased after MCA, which was attributed to increased reactivity. Except for BF, the mortar flow increased after MCA. In summary, our work showed the great potential of using MCA as an alternative activation method for inert materials.

Keywords: Mechanochemical activation, supplementary cementitious materials, reactivity.

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Amir Sharafudin

Ph.D. Student in Chemical, Environmental and Materials Engineering

Effect of Particle Concentration on Collection Efficiency in a Condensational Growth Tube

Condensational growth of aerosol particles is widely used in aerosol measurement devices and bioaerosol collection. While it is anticipated that particle concentration plays a crucial role in determining the size of the droplets formed, the effect of this parameter on the collection efficiency of the Viable Virus Aerosol Sampler (VIVAS) is still unknown. The objective of this study was to investigate how variations in aerosol concentration affect aerosol growth dynamics and collection performance in the VIVAS, using computational fluid dynamics (CFD) modeling with COMSOL Multiphysics®. Simulation results demonstrated that the release of latent heat during droplet growth and the depletion of water vapor associated with particle activation reduce peak supersaturation within the growth tube, thus reducing the droplet size. As the particle number concentration increased, the resulting droplet sizes decreased. Based on a 3-µm cut-off size, as the VIVAS was operated at an 8 LPM flow rate, four inlet particle concentrations were tested, ranging from 10^3 to 10^6 particles/cm^3. The mean diameter of the final particle size decreased from 7.9 µm to 2.75 µm, and the corresponding collection efficiency decreased from 98% to 78%. These findings underscore the significance of thermodynamic and vapor mass-transfer effects in condensational growth tubes. These results provide a foundational step toward optimizing operational conditions. Future work will extend this study by evaluating how temperature gradients and particle residence time influence condensational growth and collection efficiency. Such analyses will enable more precise control over droplet growth and enhance the reliability of bioaerosol sampling across a wide range of environmental conditions.

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Oral Presenters

Multidisciplinary High Impact

Vista Room

Taylor Dutil

Ph.D. Student in Business

Adrenaline and Sorrow: How Python Hunters Manage Values Conflicts

This research investigates how python hunters navigate persistent values conflicts inherent in their work. Python hunters catch and remove invasive Burmese pythons that are wreaking havoc on the local ecosystem in the South Florida Everglades. They experience a stark tension between valuing the environment and valuing snakes, because to protect the environment, they are required to euthanize the pythons they catch. We draw on ethnographic fieldwork, including over 130 hours across 24 hunts, supplemented by nine semi-structured interviews. Our ongoing grounded theory analysis revealed that python hunters manage this tension through a process of temporal bracketing, in which they divide their hunting experiences into distinct temporal segments and attend to those segments differently. Namely, they bracket off the value-violating act of euthanasia and instead focus their attention on other segments of their work, including hunting for and catching pythons. Several mechanisms fortify their ability to engage in this temporal bracketing. First, they employ emotional buoying practices during the hunting portions of their work. These practices, such as intentionally pausing their hunts to appreciate wildlife and nature, elicit positive emotional experiences that redirect their attention away from the act of euthanizing. Second, the experience of catching pythons triggers intense bodily reactions such as thrills and adrenaline rushes. These overwhelming embodied reactions completely absorb attention—further psychologically distancing them from the act of euthanasia. Our findings hold promise to extend research on occupational values conflicts by foregrounding the role of emotional and embodied mechanisms—such as adrenaline rushes and habitual appreciation practices—in managing dissonance. Also, by highlighting the significance of micro-level routines in everyday work and explaining how hunters' physical bodies respond to the strains and joys of their occupation, our research shines new light on how workers live with and tolerate, rather than resolve, value tensions.

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Karissa Coady

Ph.D. Student in Community Well-Being

Together, We Have Power: Navigating University-Community Partnerships in an Ever-Changing Context

This project examines what participatory action research (PAR) requires in an era of profound instability—when the social, political, and economic conditions shaping urban life are in flux, and grassroots organizations face ongoing precarity. We ask: How can PAR remain responsive and relational when both the world and our partner institutions are undergoing rapid change? Grounded in critical community psychology and urban participatory research, our multi-year collaboration is currently centered on a universal childcare campaign. Together, we co-created a plan for a PAR project that used a variety of methods to understand how Miamians are experiencing the current early childhood education system. This paper will not focus on the empirical outcomes of the campaign research, but reflect on the process instead. Methods used for this paper include memos, field notes, and co-authored debriefs documenting how shifting organizational structures, campaign priorities, and external crises reshaped the work. Findings suggest that in unstable contexts, PAR must be practiced as a dynamic negotiation rather than a linear method. Organizational change and campaign pressures often conflicted with research timelines, demanding continual decisions about when to slow down for reflection and repair, and when to speed up to meet urgent community needs. Embracing not knowing became an essential part of our ethos both in research and campaign work. Most critically, trust was sustained through showing up beyond research and campagin—participating in organization-wide activities, listening during moments of tension, and centering relationships over deliverables. By the time of presentation, we will share co-authored reflections and strategies for navigating instability through care, presence, and shared power. In alignment with adrienne maree brown idea's that "Small is beautiful," we argue that even though our time together has been far from perfect, we have built power for change in the process.

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Sreejeta Mondal

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Recurrent Non-Coding Mutational Hotspots Reveal Regulatory Drivers in Multiple Myeloma

Multiple myeloma (MM) is a hematologic malignancy driven by complex genetic alterations in terminally differentiated plasma cells. However, most genomic analyses and therapeutic strategies focus on protein-coding regions, which comprise only ~3% of the genome, potentially overlooking pathogenic alterations in non-coding regulatory elements. We performed whole-genome sequencing of 157 patient samples to identify significantly recurrent non-coding regions in the multiple myeloma genome. We identified 1,284 hypermutated regions (mutational hotspots) across the genome, whose significance was ranked using a negative binomial model accounting for hotspot length, mutation burden, and background mutation rate. Enrichment analysis showed that hotspots annotated to promoters and intergenic regions were significantly enriched, suggesting recurrent mutational activity in regulatory elements with potential functional relevance. As expected, most high-confidence mutational hotspots were mapped to immunoglobulin loci undergoing somatic hypermutation and class-switch recombination in mature B cells. These 125 hotspots were enriched for canonical and off-target AID mutational signatures, consistent with physiological B-cell mutagenesis rather than oncogenic selection and were therefore excluded from further analysis. The remaining 1,159 identified hypermutated hotspots included known multiple myeloma driver genes, such as NRAS, KRAS, BRAF, TP53,and DIS3, as well as additional candidates that will be assessed for functional significance using a high-throughput lentiviral massively parallel reporter assay (Lenti-MPRA). Among the top 40 hotspots, we identified an understudied region within the 3′UTR of the BMP6/TXNDC5 locus that overlaps a super-enhancer. This region is recurrently affected by both translocation breakpoints and hypermutations. Mutations were detected in 40 samples, out of which 25 of them did not have translocations, suggesting that solely small variations might play a role in disrupting this superenhancer region. To investigate the functional impact of mutations in this region, we introduced patient-derived variants into myeloma cell lines using homology-directed repair–mediated CRISPR–Cas9 editing. These mutations led to reduced gene expression and chromatin interaction activity at the locus compared to wild-type controls. This pattern is consistent with TXNDC5 RNA-seq profiles from mutated patient samples and indicates transcriptional deregulation. Ongoing studies of local DNA topology in vitro and in PDX models will further define the regulatory dynamics of the TXNDC5 super-enhancer hotspot.

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The Importance of Monte Carlo Simulations in Proton Therapy for Cancer Treatment

Background: Proton therapy is increasingly adopted in clinical oncology as an alternative to conventional X-ray radiotherapy due to its superior dose conformity, which enables improved tumor targeting and the sparing of surrounding normal tissues, potentially reducing treatment-related toxicities. Clinically, it is often assumed that only protons are present in the tumor region. However, proton interactions generate secondary particles within the body, and their contribution to side effects remains uncertain. Although these processes cannot be directly measured in patients, Monte Carlo simulations provide a robust framework to model particle transport, secondary particle production, and energy deposition.

In this study, we focus on oral mucositis, a debilitating toxicity affecting most head and neck (H&N) cancer patients treated with proton therapy, and investigate whether its occurrence may be partially explained by the presence of secondary particles in the oral cavity, the organ-at-risk associated with mucositis.

Methods: We used openTOPAS (Open TOol for PArticle Simulation), a Monte Carlo simulation tool incorporating detailed electromagnetic and hadronic physics models to describe proton interactions with matter. This enabled modeling of secondary particle production, including their type, energy spectra, and spatial distribution.

Our cohort included 87 H&N cancer patients treated at the University of Miami. For each patient, we simulated secondary particle production in the oral cavity and evaluated its relationship with the incidence and severity of oral mucositis.

Results: In patients who developed oral mucositis, simulations revealed a diverse spectrum of secondary particles in addition to protons within the oral cavity. These particles, due to their physical properties, exhibit higher interaction probabilities with tissues and a higher likelihood of cellular damage. Our findings suggest that secondary radiation components may contribute to tissue toxicity beyond the primary proton dose alone.

Conclusion: Secondary particle production in the oral cavity, often overlooked in routine proton therapy planning, appears to play an important role in the development of oral mucositis in H&N patients. Incorporating secondary particle modeling into clinical workflows could improve toxicity prediction and treatment optimization, providing a foundation for broader toxicity modeling across disease sites and advancing safer proton therapy with improved patient quality of life.

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Predictors of the Divided Self among Black Women in South Florida

Background: Black women (BW) in the United States continue to experience disproportionate HIV vulnerability, shaped by intersecting psychosocial and relational stressors. One of these stressors is the divided self, a construct within the Silencing the Self Theory that reflects an internal conflict between outward compliance with social standards and suppressed emotional needs. When women feel unable to express authentic emotions or concerns, particularly within intimate partner violence (IPV) relationships, they may internalize distress in ways that impair communication, erode self-worth, and limit their ability to negotiate safer sex practices.

Purpose: To examine the associations between the divided self, depressive symptoms, self-esteem, IPV, substance use, and social support, and identify predictors of the divided self among BW living in South Florida.

Methods: A cross-sectional design was used to enroll 100 BW. A survey was administered to assess the study variables. Analysis included descriptive statistics, correlations, and hierarchical linear regression.

Results: Participants' mean age was 34 years (SD = 9), and 38% reported being in a relationship with a male. The mean self-esteem score was 20.1 (SD = 5.7), indicating moderate self-esteem, and 66% reported mild to severe depressive symptoms. Participants reported substance use in the past three months (M = 14.63, SD = 7.6); 17% reported IPV, and 60% reported having social support. The divided self mean score was 17 (SD=6.4), indicating moderate divided self experiences. Social support, self-esteem, and depression were significantly correlated with the experience of a divided self. In the regression model, lower self-esteem scores ($B = -0.504$, $\beta = -.446$, $p < .001$) and higher IPV experience ($B = 0.576$, $\beta = .360$, $p < .001$) significantly predicted higher divided-self scores.

Conclusions: Findings suggest that self-esteem and IPV are significant contributors to the divided self among BW. Interventions that prevent IPV, enhance communication skills, and facilitate emotional expression may strengthen HIV prevention efforts and support psychosocial well-being. Understanding the determinants of the divided self is critical for improving HIV-related health outcomes among BW.

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Ted-like Talk Presenters

Ted-like Talk

Anya Sondhi

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Making the Invisible Visible: Brightening the Target to Reveal and Treat Blood Cancers

Cancer is clever. Even when we build immune cells that are trained to hunt it down, cancer can learn how to disappear.

For patients with mantle cell lymphoma, an aggressive blood cancer, CAR T-cell therapy can feel like a miracle: engineered immune cells that seek out and destroy tumor cells. But too often, that miracle fades. The cancer survives not by becoming stronger, but by becoming harder to see. It turns down the molecular “flare” (called CD19) on its surface that alerts immune cells to its location. When the flare disappears, the immune system is left searching in the dark.

Our work began with a simple idea: instead of making better immune cells, what if we stopped cancer from hiding? Inside every cell is a genetic control system that determines which signals appear on the surface. We focused on one switch, a transcription factor called IKZF1, that helps regulate CD19. By increasing IKZF1, either directly using gene delivery or indirectly using a drug that prevents its breakdown, we were able to force mantle cell lymphoma cells to turn their CD19 flares back on.

In two human cell lymphoma models, boosting IKZF1 increased CD19 levels by more than two-fold. This change transformed how immune cells behaved. CAR T-cells recognized cancer cells faster, killed them more efficiently, and released stronger anti-tumor signals such as IFNg, TNFa, and IL-2. In killing experiments, cancer cells with higher IKZF1 were eliminated more quickly and completely.

Importantly, the drug approach worked as well as genetic engineering, pointing to a translational and realistic way this strategy could be used in patients. This research highlights a powerful idea: immune therapies do not fail because immune cells are weaker. They fail because cancer becomes invisible.

By targeting the IKZF1 pathway, a newly identified, druggable control system for tumor visibility, we show that it may be possible to keep cancer “lit up” for the immune system to find. Instead of chasing an ever-hiding enemy, we can hold it in the spotlight. And that shift, from building stronger hunters to revealing hidden targets, could help turn short-lived remissions into lasting cures.

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Ted-like Talk

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Application of Generative Artificial Intelligence in Teaching Prevention Science

Introduction:AI-assisted tools have greatly expanded university instructors' capabilities to teach, assess, and innovate. The use of AI in the university-level teaching is ubiquitous across all departments, schools, and fields, and is a priority area in University of Miami scholarship, as demonstrated by recent initiatives supported by the Platform for Excellence in Teaching and Learning (PETAL) and the Miller School of Medicine (MsoM)'s Academy of Medical Educational Scholars (AMES).
As part of an AMES-funded project, we created a Generative AI-based chatbot ("PreventionX") to assist in the teaching of Prevention Science to students in the Department of Public Health Sciences (DPHS). The chatbot was developed using course materials and lectures from a DPHS graduate course in prevention science, professional organization materials, and published articles, and it sought to shift classroom instruction from deductive- to inductive-based learning using applied case studies. The chatbot engaged students in interactive real-world scenarios prompting students to strengthen their knowledge and application of prevention science; including risk, promotive, and protective factors, health theory, and intervention strategies.
Methods / Process:Ninety-five graduate-level students were given access to PreventionX to (a) create exam questions based on course content for use during class and on exams and (b) develop and assess real world scenarios for students to apply prevention science concepts, and (c) interact with simulated personas within case-based scenarios in order to extract relevant contextual information and propose evidence-informed prevention strategies.
Results / Outcomes: Survey results showed that students were very open to the use of the chatbot as a teaching tool; however, satisfaction with the use of the chatbot varied greatly by type of AI provider, type of instructional approach, and type of student. For example, medical students responded less favorably than non-medical students to tasks. Development and assessment of prevention science case studies were better received than exam question generation.
Our findings demonstrate the strong potential of AI to enhance classroom instruction by supporting real-world application of concepts; however, identified limitations indicate that our current use of AI represents only an early stage in the integration of this technology as an effective, practice-oriented teaching tool.

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When the Placenta Turns Hostile: Decoding Oxidative Stress in Preeclampsia

Hypertensive disorders of pregnancy, particularly preeclampsia, remain one of the most pressing challenges in maternal health worldwide. Affecting up to 8% of pregnancies and responsible for nearly 75,000 maternal deaths each year, this condition continues to puzzle researchers and clinicians despite decades of investigation. Preeclampsia typically develops after 20 weeks of gestation in women who were previously healthy, characterized by high blood pressure and organ dysfunction that can place both mother and fetus at severe risk. At the heart of this condition lies the placenta, an extraordinary but often under-investigated organ that sustains the fetus throughout pregnancy. Under normal circumstances, the placenta maintains an intricate balance of oxygen exchange, nutrient transfer, and vascular communication between mother and baby. However, when this balance is disturbed, it can transform from a nurturing interface into a trigger for inflammatory-related disease. Our research focuses on understanding how oxidative stress, caused by an excess of reactive oxygen species (ROS), disrupts placental function and drives the onset of preeclampsia. Using placental trophoblast cells and tissue explants, we discovered that elevated ROS levels initiate an endoplasmic reticulum (ER) stress response that alters protein folding and activates the unfolded protein response (UPR) pathway. This stress cascade interferes with cellular homeostasis, leading to trophoblast dysfunction and vascular inflammation, key hallmarks of preeclampsia. Through molecular analyses and ultrastructural studies, our findings illuminate how oxidative and ER stress together compromise placental health early in pregnancy, setting the stage for disease progression. By decoding these molecular signals, we can identify new biomarkers and therapeutic targets that could aid in early detection and intervention. This work not only highlights the placenta's central role in pregnancy complications but also underscores an important message: understanding the biology of this remarkable organ offers a window into improving maternal and fetal outcomes worldwide. Our goal is to translate this knowledge into preventive strategies that can help ensure every pregnancy remains a safe and healthy journey.

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