Session N Abstracts

Towards engineering *Azotobacter vinelandii* for characterization of non-canonical nitrogenase

Hanna J. Timek
Mentors: Smruthi Karthikeyan and Zahra Shivji

Current industrial methods of ammonium synthesis are energy-intensive and unsustainable. Hence, the development of bioengineered nitrogen fixation systems is urgently required to sustainably meet global nitrogen demands. A possible solution is engineering nitrogenase enzymes in order to maximize their ammonium output for commercial use. Although the enzyme is found in an immense variety of organisms, current knowledge of nitrogenase comes almost exclusively from the aerobic, soil-dwelling Gammaproteobacteria *Azotobacter vinelandii*. The limited capacity to study nitrogenases outside of *Azotobacter vinelandii*, a culturable diazotroph, creates significant gaps in understanding their diversity, functionalities, and characteristics. In this project, we use CRISPR-associated-transposon machinery to develop a platform to study non-culturable nitrogenases in the model organism *A. vinelandii*. We engineered *A. vinelandii* to be non-diazotrophic by removing the *nifHDKEN* cluster of its nitrogenase gene via homologous recombination. Currently, we are optimizing our protocol for replacing the removed cluster by using a plasmid harboring both the *nifHDKEN* cargo and CAST module. In the future, we hope to use the system to insert cargo of non-canonical nitrogenases and study their capacity to fix nitrogen using acetylene reduction assays and 15N isotope labeling.

The effect of cable bacteria colonization on the marine heat wave tolerance of *Zostera marina*

Quinn J. Hartman
Mentors: Victoria J. Orphan and Magdalene A. MacLean

Marine heat waves are increasingly responsible for large-scale seagrass die-offs worldwide, including a documented loss of eelgrass (*Zostera marina*) at Newport Beach. Heat stress raises sulfide concentrations in marine sediment, and sulfide is toxic to seagrass roots. Cable bacteria, a group of filamentous bacteria that oxidize sulfide in sediment, may reduce this stress and improve seagrass heat tolerance. This project tests that possibility using a laboratory experiment comparing eelgrass grown in sediment with and without an established cable bacteria population, under both normal and simulated heat wave temperatures. Shoot and root length, sediment sulfide levels, and plant dry mass are being measured before, during, and after the simulated heat wave. Early sulfide measurements show a clear difference between sediment with and without cable bacteria, consistent with cable bacteria actively lowering sulfide levels. Seagrass has not yet shown visible signs of heat stress, but temperature and sulfide measurements are ongoing. Results will help clarify whether cable bacteria populations play a meaningful role in helping seagrass meadows withstand future marine heat waves.

Informing photosynthetic model parameterization using solar-induced chlorophyll fluorescence data

Nicolas W. Bartolomeo
Mentors: Tapio Schneider, Katherine Deck, and Oliver Dunbar

In global climate models, photosynthesis is an environmental process integral to accurately modeling the water, energy, and carbon cycles on a global scale. Within ClimaLand, the Climate Modeling Alliance’s land surface model, the fitting of the free parameters of the modeled photosynthesis process is based on matching model-predicted values to a statistically reconstructed global dataset of a measured by-product of photosynthesis that has high bias. This project investigates an alternative dataset, specifically Solar-Induced Chlorophyll Fluorescence (SIF) satellite data, for calibrating photosynthetic parameters within ClimaLand. SIF data are collected globally by measuring photon flux during photosynthesis as plants fluoresce, making observations more direct. With Ensemble Kalman Inversion (EKI), free photosynthetic parameters are estimated from priors informed by the nonlinear

model ClimaLand and TROPOMI SIF Observations, aiming to minimize the misfit function between observed and simulated values. Using daily TROPOMI SIF satellite data collected between 2018 and 2021, we calibrated photosynthetic free parameters with EKI. Using these newly found parameter values, we expect to see improvement within global photosynthesis calculations. The importance of this result is that the various environmental cycles mentioned earlier are now better informed when modeled.

Implementation of an observation simulator in ClimaAtmos.jl
Hung-Chih Wu
Mentors: Tapio Schneider and Zhaoyi Shen

Clouds remain a major source of uncertainty in climate projections because many physical processes within clouds occur at scales smaller than a model grid cell. Climate models therefore represent these processes using parameterizations, which must be carefully evaluated. Satellite observations provide broad and consistent measurements of clouds and are therefore valuable for this purpose. However, satellites do not directly measure most geophysical quantities of interest. Instead, they measure electromagnetic signals from which these quantities are inferred using retrieval algorithms, making direct comparisons with model output difficult. Observation simulators address this problem by converting model output into quantities that a satellite instrument would observe. In this project, we implement a simulator for the CloudSat Cloud Profiling Radar (CPR) in ClimaAtmos.jl, the atmospheric model developed by the Climate Modeling Alliance (CliMA). The simulator represents unresolved cloud and precipitation variability, distributes hydrometeors within each model column, and calculates radar reflectivity and attenuation. Comparisons with an established simulator show similar overall reflectivity patterns, with the closest agreement for rain and larger differences for cloud liquid and cloud ice. This implementation enables more direct evaluation of cloud and precipitation parameterizations in ClimaAtmos using CloudSat observations.

Using paleoatmospheric CO_2 to constrain the age and paleoclimate of late Pleistocene Amazonian fossil flora
Nivale E. Baxendell
Mentors: Julia Tejada and Elena Stiles

Although the Amazon is a global carbon sink and regional climate regulator, little is known about how its vegetation responded to glacial–interglacial climate cycles. This knowledge is essential for predicting future environmental change in the region, yet paleobotanical records are scarce. Here, we investigate a late Pleistocene plant fossil deposit in the Peruvian Amazon. Preliminary age estimates place these fossils between 100–150 ka, an interval spanning glacial and interglacial conditions. Because atmospheric CO_2 concentrations vary with climate, reconstructed paleoatmospheric CO_2 constrains the age and climatic setting of fossil assemblages. We analyzed approximately 200 fossil leaf cuticles by combining bulk organic carbon isotope analysis with stomatal anatomical measurements from epifluorescence microscopy in a mechanistic leaf gas-exchange model to reconstruct paleoatmospheric CO_2. Preliminary reconstructions yield an average value of 480 ppm, substantially higher than the 180–280 ppm expected for the late Pleistocene. Ongoing taxonomic identification of fossil morphotypes will allow improved physiological model parameters to be assigned, producing more robust paleoatmospheric CO_2 reconstructions to better determine whether this flora represents glacial or interglacial conditions and improve our understanding of Amazonian vegetation responses to past climate change.

Identifying biomarkers for insect herbivory through stable isotope analysis
Bianca D. Jaramillo
Mentor: Julia Tejada

The evolution of herbivory is one of the most consequential ecological transitions in the history of life. By enabling insects to exploit plants as a food source, it fueled a reciprocal evolutionary arms race with flowering plants that drove extraordinary diversification in both groups and helped shape modern terrestrial biodiversity. Yet despite its evolutionary importance, we still know surprisingly little about the physiological innovations that repeatedly enabled insects to overcome plant defenses and evolve herbivory. I propose to address this question by using compound-specific stable isotope analysis of amino acids to identify biochemical signatures of different herbivorous feeding strategies, providing a physiological perspective that complements and extends beyond traditional morphological approaches. I will then integrate these data with published mammalian and arthropod datasets to determine whether amino acid isotopic signatures of herbivory reflect conserved metabolic processes across animal phyla or lineage-specific evolutionary adaptations. Together, this work will establish a new biogeochemical framework for studying the evolution of herbivory in living insects while laying the foundation for reconstructing plant-insect interactions in the fossil record.

The impact of snow on the Southern Ocean overturning circulation
Jasmine E. Hollis
Mentors: Andrew F. Thompson and Sarah Zhang

The world's oceans are connected by the global overturning circulation, which regulates the storage of heat and carbon dioxide in the deep ocean (Pellichero et al. 2018). In the Southern Ocean, water-masses are lightened and densified through water-mass transformation (WMT) (Abernathey et al. 2016), a key process in setting the strength of the meridional component of this circulation. Sea ice growth and melt dominate WMT rates in the Southern Ocean (Pellichero et al. 2018, Abernathey et al. 2016). However, little is known about the contribution of snow on sea ice to WMT rates due to the complexity of snow-sea ice-ocean interactions and scarce observations (Webster et al. 2018). While ECCO provides a combined freshwater flux including both sea ice and snow atop the ice, we used snow depth to individually estimate the snow freshwater flux. This revealed inconsistencies with the sea ice freshwater flux and observations that improved our understanding of the model's snow-on-sea-ice representation. With that knowledge, we assess how the snow freshwater contribution to WMT evolves with changing sea ice extent, improving understanding of the meridional component of the Southern Ocean overturning circulation.

Hormonal control of calcium isotope signals in humans: A mechanistic model of kidney handling, skeletal balance, and dietary restriction
Kyra Y. Jun
Mentors: François Tissot and Theo J. Tacail

Calcium isotopes in blood and urine have been proposed as early markers of bone loss, but recent literature shows that kidney handling and dietary calcium can dominate these signals, limiting their use as direct readouts of skeletal balance. We developed a mechanistic model in which parathyroid hormone and active vitamin D regulate calcium exchange among diet, intestine, blood, kidney, and fast- and slow-exchanging bone pools. Isotopes are propagated along these regulated fluxes, including progressive fractionation during tubular reabsorption. Under simulated dietary restriction, the model maintains blood calcium near its set point by increasing fractional intestinal absorption and renal conservation. The urinary signal shows an immediate kidney-driven response followed by a slower shift that tracks blood, suggesting that a single sample may conflate distinct physiological processes. Across simulated individuals varying in calcium intake and filtration rate, urinary isotope variability is approximately threefold greater than blood variability and decreases with increasing calcium excretion, consistent with published cohort patterns. Continuing work will further develop vitamin D storage and activation to examine deficiency, malnutrition, and skeletal growth. Paired urine and fingernail measurements will then help narrow plausible model parameters by informing short-term renal handling and longer-term isotope integration, improving inference of hormone-regulated calcium fluxes.

Deconvolving vital effects from paleoceanographic signals using stable isotopes, clumped isotopes, and metal/Ca ratios in deep-sea scleractinian corals
Jesse M. Benitez
Mentor: Jess F. Adkins

Deep-sea corals are a useful archive of thermocline and deep ocean conditions, with the potential of providing century-long records of deep ocean change at sub-decadal resolution. However, offsets from isotopic and trace-element equilibrium in coral skeletons, termed “vital effects”, have complicated the application of these archives, as well as those of other biomineralizing organisms, to paleoclimate reconstructions. Deep-sea corals are ideal candidates for the study of biological overprinting mechanisms due to the large tracer gradients within individual corals, their independence from photosynthesis, and relatively stable growth conditions. Insights into the biomineralization mechanisms of these corals might be used to develop a generalized understanding of biomineralization in other Scleractinia and marine calcifiers. In this study, we present stable isotope, clumped isotope, and trace-metal (Me/Ca) data in a suite of *Desmophyllum* d*ianthus, Caryophyllia*, *Lophelia*, and *Enapsollamia* coral specimens, performing multi-proxy analyses on the same samples when possible. Both genera were selected due to their large tracer variability, wide environmental range, and availability in the fossil record. Data to come. Additionally, based on initial indications of consistent tracer variability and correlation and the suggestions of control by a single universal biomineralization process, we aim to build a biomineralization model that incorporates all three tracer classes. To do this, we incorporate Me/Ca differential equations (Chen, 2022) into a stable and clumped isotope model for biomineralization (Watkins, 2025). The outputs of this model are compared to the stable isotope, clumped isotope, and trace-metal data from the coral samples. Data to come. These findings illuminate the mechanisms of biological overprinting of isotopic and trace element composition in deep-sea coral skeletons, which is essential to the improved use of these specimens as paleoceanographic archives of temperature, pH, carbonate chemistry, and other environmental parameters.

Fiber-optic sensing of seismic velocity change in urban settings

Lela R. Hanson
Mentors: Zhongwen Zhan and Elijah Bird

Seismic velocity change is a powerful tool to measure changes in temperature and water content in the subsurface. The ambient seismic wavefield can be used to sample the Earth continuously and at depth, with potential to provide important data for sustainable groundwater management. The technology remains underdeveloped because existing studies of seismic velocity change have been limited by sensor density. In this exploratory study, we leverage Distributed Acoustic Sensing (DAS) to measure surface wave velocity change beneath a 40-kilometer commercial telecommunications cable in Los Angeles at high spatial resolution. We gather pairs of channels in common offset and common midpoint patterns to locate the signal robustly in space and establish sub-seasonal temperature fluctuations at this site. We also identify the effects of noise source variations on our signal. Our methods and findings offer guidance for other researchers attempting similar methods in urban settings and highlight the ongoing potential of DAS to extend the range and density of ambient seismic field interferometry.