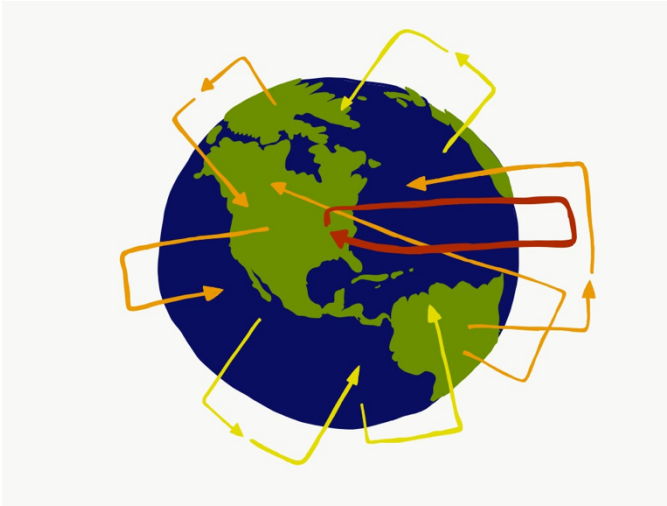


Southeastern Biogeochemistry Symposium




March 14-15, 2020

AGOURON
INSTITUTE



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Georgia Tech  Earth and Atmospheric Sciences
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 EMORY UNIVERSITY

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AL:

Dauphin Island Sea Lab
University of South Alabama

FL:

FAU Harbor Branch Oceanographic Institute
Florida State University
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MS:

iGEM Foundation

SATURDAY MARCH 14, 2020

**9:00-
10:00a**

Welcome & Keynote

*9:00-
9:10a*

Welcome: Dean Susan Lozier
GT College of Sciences

*9:10-
10:00a*

Keynote: **Karen Lloyd, UTK**
“Linking microbial ecology to deep tectonic processes across a subduction zone”

**10:00-
11:30a**

Oral Session I

Chairs: Erin Castorina & Abigail Johnson

*10:00-
10:15a*

Josh Thedford, UGA
“Identifying Patterns In Soil Carbon Dioxide and Reduced Iron Production During Shifts In Atmospheric Oxygen Content”

*10:15-
10:30a*

Nadia Szeinbaum, GT
“A Synthetic Microbial Consortium to Explore Cooperation on Early Earth”

*10:30-
10:45a*

Chad Lloyd, UNC-CH
“Particle-associated Bacteria Use A Versatile Array of Extracellular Enzymes In The Water Column Of The Western North Atlantic”

10:45-11:00a **Faisal Adams, GSU**
“Developing A Surface Complexation Model to Account For Substitution In Minerals: An Analysis Of The Aluminum Substituted Ferrihydrite Structure”

11:00-11:15a **Alireza Merikhi, FSU**
“Three oxygen sensor eddy covariance instruments to measure benthic fluxes with minimum error”

11:15a-11:30p **Jessica Frankle, USC**
“Remarkably concentrated activity of short-lived radium in two hydrothermal systems”

11:30a-1:30p **Break**

1:30p-2:30p **Oral Session II**
Chair: Pan Liu

1:30-1:45p **Qian Wang, GT**
“The Coupled Speciation Transformation of Iron and Phosphorous during Anaerobic Digestion with Hydrothermal Pretreatment of Sewage Sludge”

1:45-
2:00p **Lizbeth Davila-Santiago, GT**
“Diversity of Airborne Bacteria In The Air
Of Metro Atlanta Year-Round”

2:00-
2:15p **Si-Yu Zhang, GT**
“Metagenomics and Metatranscriptomics
Analysis of Paddy Soils with Different
Levels of Arsenic”

2:15-
2:30p **Claire Elbon, UTK**
“Planctomycete Diversity and the Potential
for Anammox in Tennessee Aquarium
Exhibits”

2:30-
2:45p **Break**

2:45-
4:00p **Oral Session III**
Chair: Drake Lee-Patterson

2:45-
3:00p **Victoria Frasier, UTK** “Characterization of
Cave Subaerial Biofilm Carbon Sources
Using Stable Isotope Analysis”

3:00-
3:15p **Ipsita Mohanty, GT**
“Multi-omic Profiling Of Melophlus
Sponges Reveals Diverse Metabolomic And
Microbiome Architectures That Are Non-
overlapping With Ecological Neighbors”

3:15 – 3:30p	Aaron Pital, GT “Boundaries on Abiotic Geochemical Complexity for Earth and Elsewhere”
3:30– 3:45p	Xiaoja He, UGA “Spatially Resolved Electron Transport through Anode-Respiring <i>Geobacter sulfurreducens</i> Biofilms: Controls and Constraints”
3:45– 4:00p	Abigail Johnson, GT “The search for novel gas hydrate inhibitors”
4:00 – 6:00p	Virtual Poster Session

SUNDAY MARCH 15, 2020

**9:00-
10:00a**

Oral Session IV

Chair: Tianze Song

**9:00-
9:15a**

Jack Miklaucic, Emory
“Measuring Soil Ammonia Flux from
Corn Fields in The U.S., Rwanda, And
China”

**9:15 –
9:30a**

Yanyu Wang, Emory
“Agricultural GHG Emissions and
Potential Methane Sinks Under
Different Cover Crop Systems”

**9:30 –
9:45a**

Sydney Bear, ASU
“Methanogen Community Analysis of
Peatlands in North America”

**9:45 –
10:00a**

Katie Stipes, UTK
“Metagenomic Data from Svalbard
Permafrost helps to Infer Microbial
Presence”

**10:00-
10:15a**

Sarah Andrew, UNC-CH
“Differences in the Carbon Fixation
Properties of Southern Ocean Diatoms”

*10:15-
10:30a* | **Break & Point Tallying**

*10:30-
11:00a* | **Award Presentation &
Closing Remarks**

Keynote Speaker

Dr. Karen Lloyd

University of Tennessee Knoxville



Dr. Karen
Lloyd

University
of
Tennessee,
Knoxville

**“Linking microbial ecology to
deep tectonic processes across a
subduction zone”**

ORAL PRESENTATIONS

* - presenting author

ORAL SESSION I

01 **Identifying Patterns in Soil Carbon Dioxide and Reduced Iron Production During Shifts in Atmospheric Oxygen Content**

Joshua Thedford*, Aaron Thompson

When Fe(II) is oxidized to Fe(III) in the presence of dissolved soil organic matter (DOM) it can form Fe-OM co-precipitates; oxidation of Fe(II) by O₂ also generates free radical species that transform into CO₂. However, these processes are rarely studied concurrently. We hypothesized that DOM is rapidly converted to CO₂ during Fe(II) oxidation and that this could be measured as an increase in CO₂. Soil samples were incubated in vials under anoxic conditions to increase [Fe²⁺], then we exposed the samples to an oxygenated atmosphere and resealed them to trap any CO₂ produced. At five-minute increments, the headspace of each replicate was sampled and then the soil was sampled for [Fe²⁺]. In all cases, there was a sudden pulse of [CO₂]. By manipulating water, time, and soil, we were able to vary the amount of [Fe²⁺] present at the end of the incubation. We found that at higher [Fe²⁺], the baseline CO₂ concentrations increased as well as the peak CO₂ concentration of the pulse, and the timing of the pulse. Finally, contrary to our expectations, we found that the [Fe²⁺] did not decrease significantly during the oxidation phase. This research will help flesh out this understudied area of soil chemistry.

02 **A Synthetic Microbial Consortium to Explore Cooperation on Early Earth**

Nadia Szeinbaum*, Christopher T. Reinhard, and Jennifer B. Glass

Introduction: Oxygenic photosynthesis originated on an anoxic Earth and expanded into Fe²⁺-rich oceans and formed reactive oxygen species (ROS) with amplified toxicity due to Fenton chemistry (Swanner et al., 2015). Our research explores microbial interactions that could have safeguarded Cyanobacteria from Fe²⁺-enhanced ROS toxicity, enabling oxygen to accumulate rapidly as the Great Oxidation Event (GOE). We hypothesize that proteobacteria can protect cyanobacteria from ROS toxicity in high Fe²⁺ (pre-GOE) conditions by scavenging H₂O₂. Methods: Synthetic consortia consisting of *Shewanella* species and *Synechococcus* PCC 7002 were tested for growth under pre-GOE conditions.

Synechococcus growth was monitored using flow cytometry. Fe²⁺ and H₂O₂ concentrations were monitored spectrophotometrically. Oxygen consumption rates were measured with optical sensors.

Findings: *Synechococcus* growth was impaired with 500 μM Fe²⁺ compared to growth with 25 μM Fe²⁺, and absent with 1000 μM Fe²⁺. When grown with *Shewanella*, *Synechococcus* reached final cell densities with 1000 μM Fe²⁺ comparable to those of the 25 μM treatment. Our results suggest that Proteobacteria could have protected Cyanobacteria from ROS produced by Fenton chemistry at the upper Fe²⁺ limit estimated for pre-GOE oceans.

03 Particle-associated Bacteria Use A Versatile Array of Extracellular Enzymes In The Water Column Of The Western North Atlantic

Lloyd, C. Chad*, Sarah A. Brown, John Paul Balmonte, Adrienne Hoarfrost, Cherif Ghobrial, Carol Arnosti

Heterotrophic microbes initiate remineralization of complex organic matter by producing a diverse array of extracellular enzymes to hydrolyze complex substrates to smaller sizes that can be taken into the cell. The fate of complex organic matter is therefore dependent on the types of enzymes produced by specific members of bacterial communities. These communities differ in composition, and potentially in their enzymatic tools, at different depths and locations in the ocean. We compared the composition and functional capabilities of particle-associated and whole seawater communities at three depths in the western North Atlantic, at sites from the continental shelf out into the North Atlantic Gyre. At most depths and locations, particle-associated bacteria hydrolyzed a considerably wider spectrum of peptide and polysaccharide substrates than whole water communities. These differences in enzymatic capability between whole water and particle-associated communities were typically greater at offshore locations, and with increasing depths. Higher cell densities and concentrations of organic matter on particles provides a suitable environment for a broader array of enzymatic tools, accounting for the rapid transformation of particulate organic matter sinking in the ocean. Thus, the efficiency of the biological pump is dependent in part on the activities and enzymatic capabilities of these particle-associated communities.

04 **Developing A Surface Complexation Model to Account for Substitution in Minerals: An Analysis Of The Aluminum Substituted Ferrihydrite Structure**

Faisal T. Adams*, Michael Machesky and Nadine Kabengi

Surface Complexation Models (SCMs) have been utilized to describe charging and sorption on numerous mineral surfaces successfully. SCMs have not, for the most part, accounted for site defects and substitutions. Previous attempts to describe sorption on minerals apply to specific scenarios and not varying conditions. In this study, we propose a new approach to building SCMs that considers the location of the substitution and demonstrate its applicability to aluminum (Al) substitution in ferrihydrite (Fh). Fh is a ubiquitous iron oxyhydroxide in natural environments important for its roles in the (bio)geochemical cycling of contaminants. Ferritin, an important protein in plants and animals, is believed to have Fh at its core. The debate around its structure is complicated by impurities such as Al that is known to substitute for Iron in Fh. Our approach situates the Al into octahedrally-coordinated Fe1 sites that are bound to reactive hydroxyl groups and are on the surface of the mineral. We used the Charge Distribution – MultiSite Complexation (CD-MUSIC) model paired with the Basic Stern layer model to describe the zeta potential of pure and Al-Fh as a function of solution pHs. The resulting model produced calculated values that satisfactorily fit the measured empirical data.

05 **3 Oxygen Sensor Eddy Covariance Instrument to Measure Benthic Fluxes with Minimum Error**

Alireza Merikhi*, Peter Berg, Markus Huettel

The eddy covariance method measures oxygen fluxes without interference with natural light and hydrodynamic conditions. We developed and tested a new eddy covariance instrument in which we used three oxygen sensors to minimize time-lag errors that are caused by physical separation of oxygen and velocity sensors and to increase data redundancy. In environments with high hydrodynamic activities or oxygen variations, these errors become significantly larger. The triple O₂-sensor-eddy covariance instrument uses three oxygen sensors positioned in the same horizontal plane and with 120 degrees radial spacing around the center point where current flow is measured. The averaging of the readings of these sensors produces a value with significantly minimized errors that eliminates the need for time-lag correction which is not always easy using data processing. We tested this technique by deploying the new eddy covariance instrument on carbonate sediment of a Florida Keys inner shelf. Model simulations of the synoptic 3 sensors measurements in a known oscillating oxygen distribution field revealed that the time-lag error can be reduced at least five-fold using this method. We conclude that the new system can improve eddy covariance oxygen flux estimates significantly, while simplifying data processing substantially.

06 **Remarkably concentrated activity of short-lived radium in two hydrothermal systems**

Jessica D. Frankle*, Willard S. Moore, Claudia Benitez-Nelson, and Susan Q. Lang

Hydrothermal circulation influences chemical cycling in the ocean but, to date, most conclusions are based on basalt- and gabbroic-hosted systems. Circulation through mantle rocks results in fluids with distinctly different chemistry, residence times, and impacts on ocean chemistry. The flux and residence time of fluids in the rocky subsurface are reflected in short- and long-lived radium (Ra) isotopes. While these parameters have been constrained in some basalt-hosted systems, no estimates exist for serpentinite-hosted systems that emit fluid with fundamentally different chemistry. We have analyzed Ra isotopes in fluids from three hydrothermal systems hosted on a range of rock types including the Lost City Hydrothermal Field (a nearly pure serpentinite system), Von Damm Vent Field (a mixed serpentinite-basalt system), and Piccard (a purely basaltic-gabbroic system). Preliminary results from Lost City and Von Damm fluids demonstrate that they contain highly elevated ^{223}Ra activities (half-life = 11.4 days), at levels that surpass any previously published data. These substantially elevated ^{223}Ra activities in serpentinite-hosted systems over those in basalt-hosted ones reveal important differences in residence times and circulation, with implications for ocean chemistry.

ORAL SESSION II

- 08 The Coupled Speciation Transformation of Iron and Phosphorus during Anaerobic Digestion with Hydrothermal Pretreatment of Sewage Sludge

Qian Wang* and Yuanzhi Tang

Anaerobic digestion (AD) of sewage sludge with hydrothermal (HT) pretreatment have emerged as sustainable techniques for energy and nutrient recovery. The distinct treatment conditions have impact on elemental speciation transformation. However, the speciation evolution of Fe and P as well as their transformation mechanisms during HT-AD treatments of sewage sludge remain unclear. In this work, Fe and P species in the solids derived from HT treatments with different temperature (90-185 °C) and the subsequent AD process (lasting 74 days) were investigated using X-ray Absorption spectroscopy analysis. Compared with the raw sludge, a large amount of vivianite is formed in the solids after HT treatment at low temperature, while more strengite is precipitated at higher temperature. This suggests that HT treatments at high temperature prohibits Fe(III) reduction. During the subsequent AD process of the derived hydrochars, microbial reduction of strengite and other Fe(III) species produces more vivianite; meanwhile, this process leads to more P release to supernatant and adsorbing on other minerals. These results indicate that the speciation of Fe strongly affects the transformation of P during HT and AD processes. This work has important implications for understanding the nutrients speciation and

availability in sludge-derived hydrochars and AD final solids.

10 **Diversity of Airborne Bacteria in the Air of Metro Atlanta Year-Round**

Lizbeth Dávila-Santiago*, Laura Yang, Casey Erb, Janet K. Hatt, and Konstantinos T. Konstantinidis

Recent estimates seem to agree that airborne bacterial cells are ubiquitous in the atmosphere and their concentration in the lower troposphere is $\sim 10^4$ cells/m³. However, the prevalence and patterns of airborne individual bacterial species and how these are affected by the prevailing physicochemical atmospheric conditions and weather patterns remain understudied. The objective was to test for differences in bacterial diversity between rain and dry-air samples collected at the roof of the FORD ES&T Building on Georgia Tech's campus over the course of one year (n=50) from June 2017 to June 2018. Airborne bacteria in samples were identified using PCR amplification of the V4 variable region of the 16S rRNA gene. Seasonality appeared to be a significant variable for shaping microbial diversity in Metro Atlanta and together with other variables (precipitation, temperature, relative humidity, pollen and mold count) account for >90% of the variation observed among the samples. In addition, dry-air samples showed to have more diversity (e.g., higher counts of Operational Taxonomic Units) than rain samples. *Methylobacterium*, *Sphingomonas*, *Deinococcus*, *Hymenobacter*, *Pseudomonas* and *Massilia* were ubiquitous in all samples. These results have implications for public health (e.g., respiratory

infections) and the role of these taxa in the hydrological cycle in the atmosphere.

11 **Metagenomics and Metatranscriptomics Analysis of Paddy Soils with Different Levels of Arsenic**

Si-Yu Zhang*, Xiao Xiao, Song-Can Chen, Yong-Guan Zhu, Konstantinos T. Konstantinidis

Arsenic (As) metabolism genes are widely present in As-rich environments. However, their abundance and transcriptional activities in response to different As levels remain unclear. To address this issue, we applied metagenomics and metatranscriptomics to investigate eight As resistance genes (ars i.e. arsR, acr3, arsB, arsC, arsM, arsI, arsP, arsH) and As respiratory oxidation (aioA) and reduction (arrA) genes in paddy soils with different As levels. Somewhat unexpectedly, the relative DNA abundances of ars, aioA and arrA were not significantly different between high and low As levels. By comparison to available metagenomes from other studies, geographic distance rather than As levels drive the different composition of microbial communities in soils. Metatranscriptomics revealed a significant increase along the soil As the gradient in the relative transcription of ars and aioA genes, which are induced by arsenite, the usually dominate As species in paddy soils. In contrast, for arrA genes, which are induced by arsenate, no significant increase in relative transcription was found, and these patterns seem to be community-wide as opposed to taxon-specific. Therefore, this study advances our understanding of how microbes respond to high As levels in paddy soils.

12 **Planctomycete Diversity and the Potential for Anammox in Tennessee Aquarium Exhibits**

Claire Elbon*, Matthew Tuttle, Thomas Demas, Christian Keller, Tina Stewart, Gary LeCleir, and Alison Buchan

In commercial large-scale aquaria, microorganisms capable of transforming toxic nitrogen species into more benign species play important roles in system health. Many microbes convert nitrite and ammonium into nitrate via nitrification. However, nitrate is toxic to macrofauna at high concentrations. Some bacteria within the phylum Planctomycetes transform ammonium and nitrite to nitrogen gas via anaerobic ammonium oxidation (anammox). Here, we characterized microbial communities in four habitats at the Tennessee Aquarium and examined the abundance and anammox potential of Planctomycetes using culture-independent approaches. 16S rRNA gene amplicon sequencing revealed distinct yet stable communities between habitats and the presence of Planctomycetes (typically ~1% of community). However, metagenomic analyses identified no known genes diagnostic of the anammox reaction. Given the low relative abundance of these bacteria, a nested Planctomycete specific 16S rRNA gene-based PCR approach was used to (i) enrich amplicons representative of group members and (ii) identify anammox bacteria based on diagnostic genetic signatures. This amplicon enrichment identified highly diverse sequences that share <95% 16S rRNA

gene sequence identity to cultured Planctomycetes, revealing an opportunity to study novel strains within this phylum. These data indicate the potential that anammox organisms are active within these exhibits but requires further study verify.

Oral Session III

13 **Characterization of Cave Subaerial Biofilm Carbon Sources Using Stable Isotope Analysis**

Victoria E. Frazier*, Annette S. Engel

Sub-aerial biofilms (SABs) often form visible, multi-colored colonies on cave walls. Taxonomic profiles of cave SABs reveal high proportions of methane-oxidizers, ammonium-oxidizers, and other chemolithoautotrophs. However, the relative contributions of microbial CH₄ or CO₂ fixation to the cave SAB carbon pool, as opposed to heterotrophic consumption of surface-sourced organic carbon, has not been quantified. Bulk stable carbon isotope analysis of SABs and hypothesized carbon source endmembers was done to determine the proportion of methane-derived carbon in cave SABs. The $\delta^{13}\text{C}$ values of SABs ranged from -42 to -45.6‰ within a cave, while available dissolved organic carbon $\delta^{13}\text{C}$ values were -28 to -31‰. These SAB carbon isotope values are lower than expected if SAB carbon were derived from allochthonous organic carbon alone and suggest that methane may be used as alternative carbon source. Assuming an average atmospheric methane carbon isotope value (which can span $\delta^{13}\text{C}$ values of -85 to -55‰), a two-member mixing model indicated that up to 28% of carbon in some SABs from this cave could be derived from methane. This is the first study to apply stable isotope analyses to cave SABs. Additional research will continue to characterize the isotopic compositions of

other possible carbon sources to the SABs, as well as to evaluate the potential activity of specific metabolic functions.

14 **Multi-omic Profiling of Meloplus Sponges Reveals Diverse Metabolomic And Microbiome Architectures That Are Non-overlapping With Ecological Neighbors**

Ipsita Mohanty*, Sheila Podell, Jason S. Biggs, Neha Garg, Eric E. Allen, Vinayak Agarwal

Marine sponges are benthic sessile filter feeding invertebrates and together with their associated microbiomes, are known to be prolific producers of organic molecules called natural products. The sponge natural product repository is extensive with more than 10,000 natural products reported in literature till date. However, using untargeted mass spectrometry, we have shown that there are many low abundance natural products that have evaded discovery. Considering these low abundance natural products may not be feasible to isolate, insights into their chemical structures can be gleaned by careful curation of their mass fragmentation spectra. Further, sponges are characterized by a complex community comprising of a diverse bacterial population. In order to draw a correlation, if any, between the diversity of sponge metabolome and the diverse microbiome, we overlaid the metabolomes of sponges with their microbiome structures using advanced sequencing technology and analytical metabolomic tools. The multi-omic profiling strategy for sponges that we show enables quantitative comparison of sponge metabolomes

and microbiomes to address, among other questions, the ecological relevance of sponge natural products and for the phylochemical assignment of previously undescribed sponge identities.

15 **Boundaries on Abiotic Geochemical Complexity for Earth and Elsewhere**

Aaron Pital*, Amanda Stockton

The ubiquity of life on Earth deforms every aspect of the geochemical systems that have been well-studied up to this point. Boundaries on what chemical complexity is possible from abiotic reactions can help to inform the contours of metabolic energy landscapes, but the reaction space is enormous and extends across several disciplines. By using data science tools to scrape semantic information from many thousands more papers, we draw connections between studies that may or may not have envisioned geomicrobiological implications and use network analysis to identify which results represent consensus and which may be surprising.

16 **Spatially Resolved Electron Transport through Anode-Respiring *Geobacter sulfurreducens* Biofilms: Controls and Constraints**

Xiaojia He*, Grayson Chadwick, Victoria Orphan and Christof Meile

Understanding the fundamental mechanism of extracellular electron transfer (EET) in electroactive biofilms is critical to develop microbial fuel cells

(MFC) with high metabolic activity and current production. Emerging evidence show that MFC using *Geobacter sulfurreducens* is promising sustainable energy solution to long-existing issues of energy and the environment. However, contradicting observations on metabolic activity stratification within *G. sulfurreducens* biofilms warrant further investigations into the underlying EET mechanisms with high spatial resolution. Here, we present a model that for the first time captures the spatial characteristics of metabolic activity within *G. sulfurreducens* biofilms consistent to experimental observations using nanoSIMS under different anode potentials. We describe the EET using electron hopping through a conductive network of redox-active centers (e.g. multi-heme cytochromes). Our model, together with validation using ^{15}N fractional abundance, reveals the presence of possible inhibitory pH near the electrode and a shifting mechanism of redox-active centers dependent on electric potential. This work provides an in-depth analysis of key parameters that are involved in the EET and suggests that increasing buffering capacity can eliminate pH inhibition on metabolic activity near the electrode, and increasing the biofilm conductivity, abundance of redox-active centers, as well as the conductive network density can reduce potential losses and thus enhance current production in *G. sulfurreducens* biofilms.

- 17 **The search for novel gas hydrate inhibitors**
Abigail M. Johnson*, Dustin J.E. Huard, Jongchan Kim,
Priyam Raut, Anton S. Petrov, Loren Dean Williams,
Sheng Dai, Raquel L. Lieberman, Jennifer B. Glass

Microbial communities are found in gas clathrates, which occur on continental shelves and in permafrost. Because gas clathrates clog natural gas pipelines, companies use clathrate inhibitors, such as synthetic polyvinylpyrrolidone. There is a movement towards greener, biodegradable inhibitors, including antifreeze proteins (AFPs), which evolved to bind ice in eukaryotic and bacterial lineages. We hypothesize that bacteria in clathrate-bearing sediments evolved clathrate-binding proteins (CBPs) that inhibit clathrate more effectively than proteins evolved to bind ice. We synthesized tetrahydrofuran clathrate in the presence of five putative bacterial CBPs from metagenomes sequenced from coastal Oregon and Japan. We tested proteins' effects on clathrate crystal structure, visualized clathrate binding via fluorescence of tagged enhanced green fluorescent protein (eGFP), and quantified protein. Salt solution, cytochrome c, and eGFP were used as negative controls, which formed single, native-like crystals. A fish AFP was used as a positive control, which formed small, platy crystals. CBPs yielded either small, platy crystals or larger, flat crystals. eGFP-tagged CBPs showed evidence of clathrate binding compared to eGFP alone. CBPs were enriched in the clathrate compared to negative controls. These data support bacterial production of CBPs in clathrate-bearing sediments. Future studies include directly assaying CBPs for activity toward methane clathrate.

Oral Session IV

18 **Measuring Soil Ammonia Flux from Corn Fields in The U.S., Rwanda, And China** **Jack Miklaucic*, Eri Saikawa**

Agriculture is considered a significant contributor to climate change, representing nearly 11% of global greenhouse gas emissions. However, abundant usage of nitrogen fertilizers has also contributed significantly to air pollution. Corn (or maize) is the most widely produced crop in the world and also uses the most nitrogen fertilizers. Thus, changes in agricultural practices can play a prominent role in efforts to address air pollution and climate change. This study analyzes soil ammonia fluxes in Georgia (US), Rwanda, and China and with various treatments to help determine agricultural techniques that can reduce atmospheric ammonia. A living mulch (LM) system is a new method of reducing traditional fertilizer application that involves maintaining a live cover crop year-round, and corn plots in Georgia and China were assigned either traditional application or treatments with nitrogen-fixing plants growing simultaneously while Rwandan plots solely employed traditional fertilizer application. Living mulch plots overall had 39.8% lower mean fluxes than conventional plots. Our results suggest that applying more fertilizer increases ammonia flux even in living mulch plots, and that living mulch plots are a possible way to reduce ammonia emissions. Future studies will

include analyses of greenhouse gases to determine how agricultural practices affect the environment.

19 **Agricultural GHG Emissions and Potential Methane Sinks Under Different Cover Crop Systems**

Yanyu Wang*, Eri Saikawa

Extensive research shows that different land management practices have various effects on GHG emissions. Cover crop establishment could reduce fertilizer inputs by providing accessible N to cash crop from nitrogen-fixing plants. As an interest in investigating which cover crop performs best in minimizing GHG emissions, in this study, trace gas fluxes (CO₂, N₂O and CH₄) from three cover crop systems: crimson clover (CC); cereal rye (CR); white clover (WC) and no cover crop system (traditional) were compared under corn-cropping from 2016-2018. Observational data were collected during growing season once a week for three years from Watkinsville, GA, USA. In 2018, mean CO₂ flux from CC, CR, LMS and Traditional were 99.05, 96.31, 142.20 and 54.44 kg C ha⁻¹ day⁻¹, respectively. The soil served as a sink for CH₄, with a mean flux from CC, CR, LMS and Traditional being -10.72, -10.49, -10.76 and -6.65 kg C ha⁻¹ day⁻¹, respectively. Compared to the traditional system, all the cover crop systems were a larger sink. Although CH₄ uptake among the three different cover crop plots not differ significantly, slightly lower in CR potentially indicates that lack of NH₄⁺ would inhibit methane uptake.

20 **Methanogen Community Analysis of Peatlands in North America**

Sydney Bear*, Jamie Lamit, James Seward, Nathan Basiliko, and Suzanna Bräuer

Peatlands are unique wetlands that play a role in the storage and release of atmospheric carbon in the form of carbon dioxide and methane gas. These peatland environments are estimated to account for one third of Earth's terrestrial carbon. Peatland soil contains communities of archaea, bacteria, and fungi that interact with each other through nutrient cycling and competition. The methanogenic archaea in these peatland communities create methane gas as a product of their metabolism. A community analysis of these methanogen groups and their abundances in varying peatland environments will give insight into their interactions and how the changing environment will affect them. Extracted DNA from peat samples of 19 sites in eastern North America was analyzed through Illumina amplicon sequencing of the *mcrA* gene to observe changes in methanogenic community assemblages in varying environments. It is expected that the community analysis will show preferences of methanogens for depths near the anaerobic/aerobic transition zone as well as the pH, substrate, and environmental preferences of certain orders of methanogens. These data may provide insight into the community make-up and interactions of methanogen communities in peatland environments and are important to consider in the face of climate change.

21 **Metagenomic Data from Svalbard
Permafrost helps to Infer Microbial Presence**
Katie Sipes*, Raegan Paul, Peibo Li, Karen G. Lloyd

Permafrost from Svalbard, 79°N, is rapidly thawing all over the archipelago. Metagenomes from the active layers (where sediments thaw seasonally) were analyzed for microbial metabolic potential and community composition. We retrieved metagenome assembled metagenomes for cultured and uncultured microbial genera. One of the cultured genera was *Pyrinminadacea*, so we used the information from the annotated metagenomic data to try to culture these organisms. For the uncultured representatives, we aimed to elucidate their environmental activities by determining the soil geochemical parameters. We discovered that the permafrost active layer organic fraction in Svalbard is being consumed by organisms, as shown by elemental analysis data. With these different angles; metagenomic analysis, culturing, and geochemistry from Svalbard permafrost active layer, we aim to create a dynamic picture of how the microbial faction is interacting with the environment.

22 **Differences in The Carbon Fixation
Properties of Southern Ocean Diatoms**
Sarah M. Andrew*, Michael J. Ellwood, Spencer M. Whitney

Controls on phytoplankton productivity in the future have been the focus of major research efforts to understand the impact of increasing carbon dioxide (CO₂) emissions but it is still unclear how

phytoplankton will respond to global change. Climate model projections show a large uncertainty regarding how biological productivity will respond to climate change. Here we characterise the CO₂ acquisition kinetics of the RuBisCO enzyme for two polar diatoms (*Proboscia inermis* and *Chaetoceros flexuosus*) and a temperate diatom (*Phaeodactylum tricornutum*). This study characterised the temperature effects on carbon fixation in a warm water diatom and two Antarctic diatoms. The results found that the diatom adapted to the coldest temperatures use a different mechanism for carbon uptake and has evolved a surprisingly efficient carbon fixing properties, compared to the other Antarctic diatom and the warm water diatom. Together these results improve our understanding of biological carbon uptake in the Southern Ocean.

POSTER PRESENTATIONS

* - presenting author

01 Investigating Particle Size-Flux Relationships And The Biological Pump Across A Range Of Plankton Ecosystem States From Coastal To Oligotrophic

Christian K. Fender*, Thomas B. Kelly, Lionel Guidi, Mark D. Ohman, Matthew C. Smith and Michael R. Stukel

Sinking particles transport organic carbon produced in the surface ocean to the ocean interior, leading to net storage of atmospheric CO₂ in the deep ocean. The rapid growth of in situ imaging technology has the potential to revolutionize our understanding of particle flux attenuation in the ocean; however, estimating particle flux from particle size and abundance (measured directly by in situ cameras) is challenging. Sinking rates are dependent on several factors, including particle excess density and porosity, which vary based on particle origin and type. Additionally, particle characteristics are transformed while sinking. We compare optically measured particle size spectra profiles (Underwater Vision Profiler 5, UVP) with contemporaneous measurements of particle flux made using sediment traps and ²³⁴Th:²³⁸U disequilibrium on six process cruises from the California Current Ecosystem (CCE) LTER Program. These measurements allow us to assess the efficacy of size-flux relationships for estimating fluxes from optical particle size

measurements. We find that previously published parameterizations that estimate carbon flux from UVP profiles are a poor fit to direct flux measurements in the CCE and develop new, CCE-optimized parameters for use in an algorithm estimating carbon flux from UVP data in the southern California Current.

02 Manganese (II) Oxidizing Microbes and Mineral Induced Selection

Morgan Smith*, Dr. Suzanna Brauer, Dr. Sarah Carmichael

Manganese oxidizing microorganisms are abundant in nature and play an important role in biogeochemical cycles in the environment. Cave and karst systems are important natural resources because they provide significant sources of the world's drinking water and support unique biological communities. The microbial ecology of Mn oxide deposits is not well understood, and even less is known about the factors that stimulate Mn-oxidizing microbes in situ. Previous studies suggest that biological Mn oxide minerals are strongly oxidative and have highly charged surfaces making them highly reactive. However, the microbes that generate these reactive Mn oxides show a strong preference for some rock/mineral surfaces over others, even when these surfaces are in direct proximity to each other. Based on field observations in a variety of cave, karst, and wetland environments, it is predicted that Mn oxidizers prefer to grow on quartz rather than calcite. The aim of this study is to identify which Mn oxidizing microbes within a local microbial community

preferentially colonize some minerals instead of others. Predicting how and where Mn oxides will grow is a vitally important tool for the production of reactive mineral species, which can be used in a variety of water filtration and bioremediation technologies.

03 Investigating DON Cycling in the Eastern Canadian Arctic Using An Isotopic Approach Holly Westbrook*, Annie Bourbonnais, Cara Manning

The Eastern Canadian Arctic Archipelago (CAA) is a nitrogen limited region with high glacial coverage and relatively little riverine input compared to other Arctic regions. Input of inorganic nitrogen sources such as nitrate, nitrite, and ammonia are expected to increase as climate change causes greater melting of permafrost and glacial sheets. In addition to inorganic forms of nitrogen, dissolved organic nitrogen (DON) could represent a significant source of nutrients for primary producers in Arctic ecosystems. For instance, recent studies in the Arctic reported a DON increase from riverine input which was rapidly consumed as it travelled along the shelves, as well as input of inorganic nitrogen from upwelling caused by glacial melt injections. This project will use stable isotopes to investigate DON cycling in the Eastern CAA, which is not well understood. Findings suggest that more northern regions of the Eastern CAA have DON input from riverine or glacial sources based on a low $\delta^{15}\text{N}$. We hypothesize that, along with inorganic N, upwelling could also bring DON to N-limited surface waters, and support primary productivity. Furthermore, our

data will help establish a baseline to assess future change in nutrient regime for this climate sensitive region.

04 Nitrogen Cycling In South Carolina Lakes in Relation To Harmful Algal Blooms

Julia Raab*, Ioannis Rekleitis, and Annie Bourbonnais

Harmful algal blooms (HABs), which are often comprised of toxin-producing diazotrophic cyanobacteria, have been more frequent all over the world due to increasing temperatures and eutrophication. The production of toxins prevents recreational use of these water bodies and affect drinking water quality. There are still many uncertainties regarding the environmental factors that initiate and sustain HABs, limiting their prediction and management in lakes. The goals of this project are to resolve the influence of 1) spatial and temporal influences of diazotroph N₂ fixation, 2) organic vs. inorganic nitrogen (N) uptake rates, and 3) extreme weather events on HABs in two eutrophic lakes in South Carolina. Biweekly discrete sampling and adaptive sampling after extreme weather events will be conducted in one shallow and one deep site close to the drinking water intakes in both Lake Murray and Lake Wateree from March through October for 4 years (2020 to 2024). To resolve HAB dynamics and nitrogen cycling, we will measure dissolved inorganic and organic nitrogen concentrations, N₂ fixation rates as well as uptake rates of inorganic and organic N using ¹⁵N-labelled incubations. In addition, we will characterize the phytoplankton community composition and deploy

one mini buoy equipped with oxygen and temperature sensors at each sampling site to obtain high resolution temporal measurements.

05 An HPLC Method to Quantify S-Methylmethionine in Marine Samples

Kyle Halstead*, Ronald Kiene

S-methylmethionine (SMM) can be a precursor in dimethylsulfoniopropionate (DMSP) synthesis from the amino acid methionine; therefore, it may serve as an important compound in the organosulfur cycle. While two distinct pathways exist in this synthesis, it is unknown which pathway certain phytoplankton use. To quantify SMM in marine samples (e.g. phytoplankton), a high-performance liquid chromatography with fluorescence detection (HPLC-FLD) was adapted from a published method for SMM detection in non-marine samples (e.g. *Spartina alterniflora*). This method uses precolumn derivatization with o-phthaldialdehyde and 3-mercaptopropionic. Several parameters were tested for development and optimization including derivatization reaction time, derivative stability, and sample salinity. The detection limit of the method is approximately 0.5 nM with variation depending on the sample matrix and injection volume. We applied this to analyze the presence/absence of SMM in certain DMSP-producing phytoplankton, marsh plants, and macroalgae.

06 Factors Controlling GA Salt Marsh Biomass: A dynamical systems approach

Kadir Bice*, John Schalles, Christof Meile

Coastal ecosystems such as salt marshes are highly dynamic systems with various interacting elements. In this study, we investigate controlling factors on GA salt marsh biomass. For this, we take maximum biomass for each year as a measure of productivity which also helps dealing with the impact of seasonality. As explanatory variables, we consider a number of environmental variables, including air temperature, soil salinity, local precipitation and regional drought indices, and we are interested in their relative and combined importance for determining maximum biomass (i.e. marsh productivity). To test for the causality between biomass and environmental factors, we use Empirical Dynamic Modelling (EDM) which is a specialized method for non-linear time series analysis. Preliminary results on causality show that marsh productivity is being controlled by salinity and drought in the fall and; by precipitation and air temperature in winter. Additionally, we try to predict marsh productivity using a combination of information from different time series. Results show that, combination of salinity, drought, air temperature and precipitation information in spring helps revealing dynamics of the system and gives promising results in estimating marsh productivity.

07 Field Assessments of Novel Benthic Communities Emerging with Changing Coastal Water Quality in the Florida Keys

Zoi Thanopoulou*, Jacob Patus, Kathleen Sullivan Sealey

Water quality parameters such as temperature, salinity, Dissolved oxygen (DO), pH and nutrient concentration have profound impacts on marine benthic community composition. Water quality impacts on benthos are a commonly debated topic in the management of land-based sources of pollution. We address two questions to understand water quality impacts on nearshore benthic communities in the Florida Keys. First, do dredged residential canals serve as point sources of pollution to adjacent benthic communities? Secondly, are the increased nutrient concentrations shifting the dominant benthic organisms in the nearshore benthic communities? We examined 8 study sites in the Florida Keys that included developed residential canals and undeveloped protected shorelines. For each site, a 500m length by 200m width grid was used to randomly sample both the water quality and the benthos. Within each site, water quality components included temperature, salinity, DO, pH, NO_x, TP, TPN, and Chl-a. Benthic communities were evaluated for invertebrate coverage using the point intercept method. The hypothesis was that decreased nutrient concentration values would be found with increased distance from the canals. Concurrently, poor water quality decreases the corresponding species coverage and diversity. Areas that historically supported coral-sponge-octocoral communities are shifting to SAV dominated benthos with lower species diversity.

08 Along For The Ride: Microbial Hitchhikers Associated With An Ice Melting Probe - Implications For Subglacial And Ocean World Exploration

Caleb Schuler*, Dale Winebrenner, Tim Elam, Justin Burnett, Bruce Boles, Jill Mikucki

Deep subglacial lakes on Earth harbor biological ecosystems, however thick ice covers are significant barriers to direct access for sampling. Glaciers are immured with various abundances of microorganisms and debris; the potential for such bioloads to accumulate around and be dragged by instruments used to descend through ice has not previously been investigated. Melt probes are promising tools for reaching and sampling subglacial realms due to their relatively small logistical footprint, ability to transport diverse payloads and ease of cleaning in the field. Here we examined descent strategies for a melt probe and monitored dragging of ice-immured bioloads. We also tested the efficacy of a field-ready cleaning protocol in removing a common spore contaminant, *Bacillus* sp., and the potential for surviving spores to be dislodged during the descent process. We used a synthetic ice block inoculated with bioloads and the Ice Diver melt probe, engineered by the Applied Physics Laboratory at the University of Washington. Results show that our cleaning protocol was effective in removing 99.9% of *Bacillus* spores and the dragging of bioloads during descent was minimal, > 99.9% reduction of bioload after ~48 cm of travel, thus meeting the Antarctic Code of Conduct recommendations for subglacial sampling

09 **Geochemical constraints on the early diagenesis of biogenic silica in reverse weathering**

Simin Zhao* and Yuanzhi Tang

Reverse weathering (hereafter RW) is a process in which clay minerals form via the transformation of biogenic silica, concurrent sequestration of cations (Fe^{2+} , Mg^{2+} , Ca^{2+} , and K^{+}) and release of CO_2 . It is widespread in shallow and deep-sea sediments and deltaic environments. This process plays important roles in global Si flux, coupled ocean nutrient cycling, and CO_2 dynamics. Previous studies have shown that RW significantly affects marine Si flux in global Si cycle and suggested that the unbalanced Si budget be re-visited to consider Si removal by RW.

However, little is known about the geochemical factors controlling the transformation of biogenic silica during RW and the structure of the clay mineral products. Previous study from our group shows that dissolved Fe^{2+} , Al and Fe-containing solid sediment phases suppress Si dissolution from biogenic silica. This research aims to elucidate the roles of major geochemical factors including the cations, anions and dissolved inorganic carbon (DIC) and products of authigenic clay diagenesis by incubating biogenic silica derived from diatom *Thalassiosira pseudonana* with Fe/Al-containing sediment phases. The central hypothesis is that Fe^{2+} and Mg^{2+} play major roles in governing authigenic clay diagenesis from biogenic silica.

10 *Geobacter daltonii* Utilizes a Single Convergent Genetic Pathway During Anaerobic Degradation of Aromatic Compounds

James Bullows*, Alison Kanak, Lawrence Shedrick, Christina Kiessling, Sujay Greenlund, Kuk-Jeong Chin

Geobacter daltonii strain FRC-32 can oxidize various petroleum derived compounds anaerobically as sole carbon sources via a host of unique mechanisms. Our study suggests that degradation of benzene and toluene follow a single metabolic pathway initiated by the enzyme benzylsuccinate synthase (Bss), and its homolog m-hydroxybenzylsuccinate synthase (Mbs). Transcript levels of *bss* and *mbs* were determined using quantitative real-time RT-PCR, revealing *bss* to be upregulated during toluene oxidation, while *mbs* was upregulated during benzene oxidation. Protein profile analysis via SDS-PAGE of cultures grown on toluene, benzene, and benzoate revealed products identified as BbsEFG, the enzyme utilized directly after Bss during toluene degradation, in the benzene- and toluene-degrading culture profiles, demonstrating that benzene degradation continues to follow the toluene degradation pathway after initiation by Mbs. The downstream genetic markers *bamR*, *bamQ* and *bamA* were all upregulated during degradation of benzene, toluene, p-cresol, phenol, and benzoate, while *bamY* was upregulated during degradation of benzoate, phenol, and p-cresol, suggesting a single pathway is being utilized for degradation of all aromatic compounds, converging at the benzoyl-CoA intermediate. Convergence of these pathways represents the unique approach to anaerobic

aromatic degradation employed by *G. daltonii*, demonstrating an unprecedented adaptability in the degradation of these aromatic compounds.

11 Bulk Aerosol Cation and Trace Element Concentrations in the North Pacific Ocean: US GEOTRACES GP-15 Pacific Meridional Transect

Devon Umstead*, Christopher Marsay, William Landing, Clifton S. Buck

The North Pacific Ocean receives aerosol inputs from Asia and North America in the forms of lithogenic, anthropogenic, and pyrogenic sources. In addition to long-range transport of terrestrial aerosols, local sea spray releases ions to the atmosphere in the form of aerosols which may impact local and regional climate. The 2018 US GEOTRACES Pacific Meridional Transect (GP15) traveled from Alaska to Tahiti and provided a platform for the collection of bulk aerosols in the marine boundary layer. Aerosol material was digested with strong acid to characterize chemical composition. Particles were also leached with ultrapure deionized water and filtered surface seawater to investigate trace element fractional solubility. The concentrations of water-soluble Na^+ , K^+ , Ca^{2+} , and Mg^{2+} were measured by ion chromatography. These concentrations (alongside anion and trace metal concentrations) can be used to elucidate the relative sources of the aerosols of the sampling area.

12 Decadal Analysis of Methylmercury Contamination in Fish Subject To Land Use Change In Mobile Bay And Respective Watersheds

Cassandra Bates*, John Lehrter Ph.D., Mark Albins Ph.D.

Land use/cover (LULC) change in coastal watersheds is known to increase many pollutant loads to estuaries. Yet, there have been few studies examining the relationship between LULC and Hg accumulation in fish. This study investigates Hg contamination in differing fish species and trophic levels in relation to LULC changes over four decades in watersheds surrounding Mobile Bay, Alabama. The hypothesis for this study is an expectation of significant differences in Hg levels in fish over time and higher Hg levels in fish in watersheds with predominant LULC of urbanization and agriculture. Preliminary results indicate between 1970 and 2017, 30% of fish sampled by the Alabama Department of Environmental Management surpass acceptable maximum Hg concentrations set by the EPA. Fish in tertiary trophic levels, specifically largemouth bass, comprise 67% of total contaminations, lending this species to potentially act as an indicator. Presence of deciduous forest and woody wetlands, which greatly impact filter capacity and accumulation of Hg in the environment, consistently and significantly declined from 1970-2017 ($7.8 \times 10^{-8}^*$ - 0.00^* and 0.00^* respectively ($p=0.05$)). Results from this study could aid environmental and public health managers in understanding the sources and prevalence of

mercury contamination in the coastal aquatic and estuarine food webs.

13 Nutrient analyses of South Bay Salt Works samples for the Oceans Across Space and Time (OAST) Project

Taylor Plattner*, Jennifer Glass, Sanjoy Som, Alex Pontefract, Britney Schmidt, Peter Doran, Jeff Bowman, and the OAST Team

Exciting discoveries of potentially habitable environments in recent decades on Earth, in our solar system, and beyond have formed the need to understand life detection in various environments, including environments found on ocean worlds like Europa, Enceladus, Titan, and relict ocean worlds like Mars. When we go to an ocean world, we won't know a priori what state it is in: is it habitable? Was it ever? Did life arise? Does it still thrive? And if not, when did it disappear? To answer these questions, we need to first look at similar analog environments on Earth. This has essentially motivated the formation of the Oceans Across Space and Time (OAST) project, part of NASA's Network for Life Detection, which I have joined as a graduate student. OAST is a so-called Ocean Worlds mission to Earth, designed to address gaps in our understanding of habitability in extreme terrestrial environments while simultaneously leveraging these unique analogs to guide upcoming ocean world missions in our solar system. OAST will visit a range of field analogs representative of contemporary, remnant, and relict ocean environments as they progress through stages of wetting, drying, or freezing over

geologic time. My work focuses on the environmental analysis for our first field site, which are the lakes in the South Bay Salt Works in San Diego, California.

Eight lakes were sampled from this field site, and lake samples 4 and 5 were notably higher in MgCl than the rest. As a result, two different types of synthetic field water were made to mimic these brines, one that is high in MgCl and then one that is low in MgCl. After the mimicked brines were made, we conducted nutrient analyses, such as nitrite, nitrate, and ammonium to determine the concentrations in each of the lakes. From the preliminary results, lake 4 and 5 show higher concentrations of nitrate and nitrite. Particularly, lake 4 shows the highest nitrite and nitrate concentration, 2.9 μM and 28 μM , respectively. Thus, higher MgCl in these lakes will result in a higher nitrate/nitrite concentration. The ammonium results are more ambiguous since there is less of a trend, but overall the results show similar concentrations across all samples.

14 Stormwater Runoff Quality from Green Roofs Scout Morgan*

Urban areas increase the quantity of stormwater runoff due to an increase in impervious surfaces such as roads and buildings. Green roofs decrease the quantity of stormwater runoff by providing a temporary permeable storage, though few studies show the effect green roofs have on the quality of runoff. This study investigates the effect of green roofs on stormwater runoff quality in Atlanta,

Georgia. Samples of soil moisture were gathered from three green roofs in downtown Atlanta using suction lysimeters over the course of five months. Samples were analyzed using ion chromatography. Preliminary data analysis suggests that the extensive green roofs in Atlanta increase nutrient levels, such as nitrate and phosphate, in runoff.

15 A modeling approach to clarify the effect of hydrogen peroxide on Prochlorococcus populations

D.K. McCullough* and D. Talmy

The streamlined cyanobacteria, *Prochlorococcus*, dominates the community biomass of surface oligotrophic oceans but cannot survive environmentally relevant concentrations of hydrogen peroxide (HOOH) in monoculture experiments. We used a mathematical model to capture the dynamics of *Prochlorococcus* cultures in published HOOH mortality experiments. The model, accounting for nutrient-dependent growth and HOOH-dependent death, was used to quantify the damage that *Prochlorococcus* experiences from different exogenous HOOH concentrations. The model-derived damage rates covaried with experimental HOOH concentrations indicating that *Prochlorococcus* cells die faster at higher HOOH concentrations. The laboratory study's growth media caused the *Prochlorococcus* cultures became nutrient depleted over time, allowing our model to examine the possible links between nutrient deprivation and HOOH damage. The resulting HOOH damage rates were significantly higher than those of

nutrient-replete cultures. Thus, our model suggests that *Prochlorococcus* experiences higher cell death rates when nutrients are depleted. Preliminary comparisons between our model's predictions and environmental data indicate that laboratory-based models accounting for nutrient and H₂O₂ feedbacks may be capable of explaining an appreciable amount of environmental *Prochlorococcus* death. This project will further explore how nutrient supply and H₂O₂ gradients exert control on marine microbial selection by considering trade-offs between efficient nutrient acquisition and maintaining H₂O₂ detoxification enzymes.

16 Dynamics of Porewater Flow at Cold Seeps Inferred from Conservative Tracer Profiles and Modeling

Jurjen Rooze*, Leigha Peterson, Richard N. Peterson, Christof Meile

Rising fluids entering the water column at cold seeps form the basis for diverse biological communities, fueled by the oxidation of reduced chemicals in the surficial sediments. The porewater flow velocity is a key parameter controlling oxidation rates. In brine seeps, it is often constrained by fitting vertical porewater chloride profiles with a one-dimensional, steady-state model. Here we applied this approach to 226-Ra profiles retrieved from non-brine seeps. The velocities obtained with this method were similar to previous estimates based on chloride. Monte Carlo simulations revealed considerable error margins, motivating an investigation into the effect

of spatiotemporal variable flow at seeps on tracer distributions.

To determine magnitude and variability of seepage and to identify the factors controlling it, reaction-transport simulations of cold seep surface sediments were carried out. Lateral variability of flow at the meter scale indicated that velocities obtained from conservative tracer profiles depend on the coring location and the core diameter. In the model the formation of carbonates and hydrates is most pronounced at high flow velocities and along preferential flow paths and constitutes a negative feedback on flow, which may help explain the relatively narrow range of velocities obtained from various seep locations.

17 Weathering the Extremes: Survival Strategies of Clathrate-Dwelling Bacteria

Dustin J. E. Huard*, Abigail M. Johnson, Jongchan Kim, Priyam Raut, Anton S. Petrov, Loren Dean Williams, Sheng Dai, Jennifer B. Glass, Raquel L. Lieberman

Gas clathrates are found on Earth in permafrost and in sediments underlying continental shelves and are extreme habitats due to low temperatures, high pressures, low water activity and high salinity. Despite their hostile living environs, gas clathrates still foster life, and survival strategies employed by gas clathrate-dwelling microbes could provide clues for detecting life elsewhere in our solar system, such as on icy moons, comets, and possibly the subsurface of Mars. We hypothesize that bacteria inhabiting gas

clathrates utilize clathrate-binding proteins (CBPs) in a pro-survival manner analogous to cold-water fish and other species that express ice-binding proteins (IBPs) to inhibit ice crystal growth. IBPs have been successfully tested for their efficacy to inhibit gas clathrate formation, with those from Antarctic fish being the most potent. To test our hypothesis, we engineered a temperature-controlled chamber in which to synthesize tetrahydrofuran (THF) clathrate in the presence of recombinantly-expressed hypothetical CBPs of bacterial origin; THF clathrate is an accessible and structurally similar stand-in for natural gas clathrates. We chose seven potential CBP sequences that were predicted to be IBPs identified from clathrate-bearing sediment from Hydrate Ridge off the coast of Oregon, USA and one from clathrate-bearing sediment off the coast of Japan. The predicted CBPs were expressed as C-terminal fusions to enhanced green fluorescent protein (eGFP), purified with and without the eGFP fusion, and biophysically characterized. Five proteins have been identified as CBPs with the THF clathrate experimental setup based on (1) green fluorescence observed with the THF hydrate crystals when grown in the presence of eGFP fusion proteins, (2) morphological impact on the THF clathrates and (3) partitioning of protein mass between the THF hydrate crystals and the remaining solution. Our results validate the hypothesis that organisms express CBPs to enable survival in the extreme environment of gas clathrates. Future work includes testing the five identified CBPs for their ability to interact with methane clathrate and structural characterization of the CBPs toward the goal of developing a mechanism of interaction of the proteins with gas clathrate.

18 FUS-Ribosomal RNA Interaction Triggers Phase Separation in Eukaryotic Cells

Sara Fakhretaha-Aval*, Santi Mestre-Fos, Chieri Ito, Amanda Bagwell, Roger Wartell, Jennifer Glass, Loren Dean Williams

Liquid-liquid phase separation is one of the eukaryotic sophisticated mechanisms which provides different biochemical inner cell microenvironments. Currently, amyotrophic lateral sclerosis/frontotemporal dementia-related proteins such as Fused in Sarcoma (FUS) and RNA are thought to form liquid-liquid phase separation in the cell without any membrane involvement. However, a direct link between proteins-RNA dynamics and phase separation is not well understood. Here, we report that FUS is able to interact with ribosomal RNA (rRNA) through rRNA specific expansion segment on the large subunit surface and their interaction promotes the formation of cellular liquid compartments. The results also demonstrate ribosome-FUS droplets formation is a RNA sequence-specific dependent phenomenon. We believe that FUS-ribosome interaction and the phase transition prepare a suitable microenvironment for protein synthesis in eukaryotic cells.

19 Evidence for Genes Related to Sulfonate and Sulfate Ester Metabolism in Sediments of the White Oak River, NC

Maryn F. Miles*, Taylor M. Royalty, Andrew D. Steen

In anoxic estuarine sediments, sulfate derived from seawater serves as an electron acceptor for the oxidation of organic carbon. Estuarine environments are unique in the fact that they have large quantities of dissolved sulfate because of their interaction with seawater, but they also receive high quantities of organic matter derived from both terrestrial and marine sources. This organic matter contains other forms of oxidized sulfur, such as sulfonates and sulfate esters. Sulfoquinovose (SQ) is one of the most abundant forms of organic sulfur found in these environments. It is possible that heterotrophic microbes could use this abundant form of oxidized sulfur as an electron acceptor in the place of sulfate, to oxidize organic carbon to CO₂. To understand if this pathway is being utilized in estuary environments, we conducted a bioinformatic study to search for genes that encode for the entire sulfo-EMP and sulf-ED pathways in a metagenome from the White Oak River estuary of coastal North Carolina. If many of the organisms that are present in the White Oak River estuary sediments can carry out this pathway, this could be an important new aspect of the sulfur and carbon cycles of estuarine sediments.

20 Mineral Surface Chemistry of Hydroxyapatite and Urea-Rich Solutions

Estefania Garcia*, Katerina Slavicinska, Anna Nastase, Christian Luda, Altug Poyraz, and Heather Abbott-Lyon

Phosphorus in biological systems is significant through its involvement in metabolic functions (e.g., ATP, Coenzyme A), cell structure (i.e., phospholipid membranes), and genetic storage/transfer (i.e., phosphodiester bonds in DNA and RNA). However, an ambiguity remains with the assimilation of phosphorus into biological systems, caused by its presence in the geological record as insoluble phosphates. Recent research has found that insoluble phosphate minerals when combined with urea-rich solvents, can release sequestered phosphate into solution and promote mineral transformation to more soluble secondary minerals. Our study investigates surface interactions of hydroxyapatite minerals with prebiotically plausible urea-rich solvents and magnesium sulfate. Infrared studies of the mineral surface were conducted via polarization reflection-absorption infrared spectroscopy (PM-IRRAS). Thin hydroxyapatite films were analyzed before and after reaction with scanning electron microscopy (SEM), energy-dispersive x-ray spectroscopy (EDX), x-ray diffraction (XRD), and PM-IRRAS. Surface analysis revealed depletion of phosphate, and results were further confirmed with detection of free phosphate in solution by nuclear magnetic resonance spectroscopy (NMR). Additionally, film corrosion was observed by SEM, and depletion of Ca and P was monitored by EDX for prebiotic solutions containing ammonium formate, urea, and water. Our study

revealed that ammonium formate, rather than urea causes a release of free phosphate.

21 Biogeochemical Interactions in the Hyporheic Zone of a Contaminated Wetland and their Effect on the Transformation and Mobilization of Uranium

Anthony D. Boever*, Daniel I. Kaplan, Eryn Eitel, Martial Taillefert

Decades since the accidental release of 44 metric tons of legacy waste at the Savannah River Site (SRS) near Aiken, SC, a significant fraction of uranium contamination remains in soil and ground water. Previous studies hypothesized that SRS wetlands function as a net uranium sink through sequestration in the rhizosphere and sediment. However, the extent to which the wetlands function in this capacity is not well-established. In this preliminary study, electrochemical profiling of sediment cores from an uranium-contaminated stream rich in iron floc revealed correlated increases in Fe^{2+} and organic Fe(III) complexes with depth below the sediment-water interface followed by a sharp decrease within 5 cm of the sediment surface. Aqueous molecular clusters of FeS (FeS(aq)) which represent geochemical tracers for FeS precipitation followed a similar pattern and were also present in overlying water. Total dissolved uranium increased by more than three orders of magnitude from overlying water to ~19 cm below the sediment surface. The observed trends in Fe(II) species suggest a flux of reduced iron from the sediment to the overlying waters where it is oxidized by putative

iron-oxidizing bacteria to form the floc, while the presence of FeS(aq) suggests an active sulfate-reducing bacterial community. The flux of reduced iron coupled to the fact that uranium was detected in highest concentrations at depth challenges the view of the SRS wetlands functioning as a net sink and points instead to hyporheic regions in gaining parts of streams functioning as sources of uranium at local and possibly regional scales.

22 Sulfur Cycling Beneath Microbial Mats of Guaymas Basin

Christopher Chambers*, Andreas Teske

The sulfur cycle in hydrothermally active sediments of Guaymas Basin (Gulf of California, 27° 20' N, 111° 15' W) was examined using sulfate, sulfide, and isotopic measurements. Sulfur, through both sulfide oxidation and sulfate reduction, forms the base of the chemosynthetic community living in Guaymas. The sediments beneath microbial mats in particular are active areas of sulfur cycling. Cores of mat and the sediments beneath were taken during two research cruises in 2016 and 2018 on R/V Atlantis (AT37-06, AT42-05) using HOV Alvin. Profiles show large variation over small spatial scales, ranging from cores that have no appreciable sulfide and seawater sulfate concentrations (~28mM) throughout, to complete sulfate reduction and a maximum of ~2-3 mM of sulfide. $\delta^{18}\text{O}$ of sulfate shows large variation as well, and even within one core, with a 5‰ difference over ~10cm, and several regions of potential oxidation and reduction. $\delta^{34}\text{S}$ profiles were also measured. Cores can be effectively classified by their temperatures and mat coverage, from cores that remain bare and similar to

background temperatures, up to cores that max out the thermal probe used. These measurements allow a greater understanding of which processes are contributing to sulfur cycling beneath Guaymas microbial mats.

23 iGEM: Training the next generation of scientists in biogeochemistry and beyond
Holly Bowman* and Nannan Jiang

The sustainability of biogeochemistry, along with all other fields of study, depends on our students. In addition to coursework, students benefit greatly from hands-on opportunities such as undergraduate research and internships. The International Genetically Engineered Machine (iGEM) Competition offers a unique experiential learning opportunity that introduces students to the world of synthetic biology. This training spans beyond the bench, incorporating societal impacts, collaboration, fundraising, and science communication experience. Additionally, iGEM instructors gain valuable experience in mentoring and project management. In this work, we summarize the impacts of iGEM on the southeastern region, including but not limited to the Georgia Institute of Technology, Georgia State University, Emory University, and University of Tennessee. Furthermore, we introduce the outcomes of the iGEM Competition, and offer resources and connections for both students and mentors to foster past, present, and future iGEM teams.

25 **Searching for the formate dehydrogenase enzyme outside of Hydrothermal Vents**

John J. Freier* and Susan Q. Lang

Hydrothermal vent systems that circulate seawater through the ocean floor are host to unique ecosystems. Due to high concentrations of reduced chemicals coming from the water-rock interactions, a rich and diverse community of organisms are able to thrive at extreme depths and temperatures. Even more impressive than the animal community is a taxonomically vast microbial community that some researchers believe could have been the 'Garden of Eden' for evolutionary life on earth. Serpentinite-hosted hydrothermal systems are chemically different from basalt-hosted systems. One of the distinct products of serpentinization is the organic acid formate, which is present in elevated concentrations in most serpentinite-hosted systems. Microbial communities can utilize formate as a source of carbon, which may be particularly important in alkaline serpentinization systems where concentrations of dissolved inorganic carbon (DIC) are minimal. Recent work has shown formate can be readily converted into DIC in these serpentinite systems by the formate dehydrogenase enzyme. Surprisingly, this same conversion happens in nearby deep seawater where microbes should not be adapted to carry out the same process. In this study, we explored the extent of ecosystems in which formate is converted into carbon dioxide, far from hydrothermal systems that are elevated in formate. Samples were spiked with ^{13}C -labeled formate and its conversion was detected as ^{13}C - CO_2 . Water samples were taken from multiple ecosystems, including salt-pan estuaries, man-made

lakes, mountain rivers, and soil samples. Even though these systems are not known to have elevated formate concentrations, the biological conversion of formate to CO₂ was universally detected. This data suggests the ability to utilize formate may be extremely widespread.

26 DNA Extraction and elemental analysis of Svalbard permafrost

Peibo Li*, Katie Sipes, Karen G. Lloyd

The permafrost active layer in Svalbard is increasing in depth every year due to the warming climate. The newly thawed permafrost is thought to make new organic materials available for the microbes in the soil. We analyzed the geochemistry of two active layer permafrost sites with an elemental analyzer to determine the carbon and nitrogen percentages in the soil. We combined this with an acidification treatment to differentiate the inorganic from the organic carbon fraction in the soil. We then extracted DNA from every depth in the sample for metagenomic sequencing. The stable carbon isotope ratios of organic and inorganic carbon show that there is microbial activity in these active layer permafrost soils. Furthermore, a large degree of heterogeneity was observed in the stable carbon isotope ratios, total amount of carbon, and carbon to nitrogen ratios between adjacent boreholes drilled from the same site.

27 Dissolved gases (O₂/N₂/Ar) concentrations in the Eastern Canadian Arctic

Darcy Perin*, Melissa Shugart, Cara Manning, Robert Izett, Holly Westbrook and Annie Bourbonnais

Climate change is affecting the biogeochemical cycling of carbon and other dissolved gases within the Arctic Ocean. It is expected that climate warming and sea ice melting will increase the amount of Arctic Ocean primary productivity. Dissolved gases (N₂/O₂/Ar) are used as tracers for primary productivity and respiration processes in aquatic environments. O₂ is a tracer of net photosynthetic production and N₂ is a tracer of denitrification, the conversion of nitrate to N₂ by heterotrophic microbes in anoxic waters and sediments. Noble gases (such as Ar), which are chemically and biologically inert, are used to determine the influence of physical processes on observed excess or deficit relative to equilibrium gas concentrations at in-situ temperature and salinity. Physical processes include bubble injection as well as rapid warming and cooling.

We measured N₂/Ar and O₂/Ar ratios by membrane inlet mass spectrometry (MIMS) at several stations in the Eastern Canadian Arctic as part of the ArcticNet expedition in summer 2019 (legs 2a and 2b). We generally observed an increase in the N₂/Ar in deeper waters due to sedimentary denitrification, and a decrease in O₂/Ar levels with depth due to respiration in aging waters. In this presentation, we will discuss our data at a few stations, taking into account the physical circulation in Baffin Bay and Nares Strait.

28 Cutting in-line with Iron: Uncovering Fe²⁺-RNA relationships

Rebecca Guth-Metzler*, Jennifer B. Glass, Loren Dean Williams

Metals are intimately involved in life's oldest conserved system, protein translation. Central to translation is the ribosome, a massive macromolecular machine comprised of catalytic ribosomal RNA (rRNA) and protein. The ribosome has evolved by accreting new material onto old, preserving signatures of ancient life, including RNA structure, protein structure, and the use of metals as cofactors. Mg²⁺ is ubiquitous in the modern ribosome, yet the ribosome evolved in a time of high Fe²⁺ prior to the Great Oxidation Event. We propose that iron was readily used by early life and the ribosome and predict that modern ribosomes have a latent ability to incorporate Fe²⁺. Here, we employ in-line cleavage, a reaction specific to RNA and divalent or trivalent metal cations, to probe modern ribosomes for Fe²⁺ association. In-line cleavage reveals a strong interaction of rRNA and iron, with Fe²⁺-induced cleavage more than two orders of magnitude faster than cleavage with Mg²⁺. Our demonstration of Fe²⁺ rRNA in-line cleavage shifts the paradigm that Fe-induced rRNA cleavage, tied to illnesses such as Alzheimer's disease, occurs by iron oxidation pathways alone. Moreover, we believe our study to be the first demonstration of Fe²⁺ in-line cleavage and that this cleavage extends to all RNA.

29 Carbon Fixation Within the Costa Rican Subduction Zone

Timothy J. Rogers*, Joy Buongiorno, Matthew Schrenk, Maarten de Moor, Peter Barry, Marco Basili, Donato Giovannelli, Karen G. Lloyd

The carbon flux between the surface and subsurface has a substantial impact on the atmospheric CO₂ budget. Subduction zones play a major role in the recycling and storage of this carbon. As the oceanic plate subducts below the overriding plate, it releases volatiles rich in reduced compounds that can stimulate microbial activity within hydrothermal systems. However, the interaction of microbes and deep tectonic processes is unknown. We hypothesize that microbes are heavily involved CO₂ cycling. Chemoautotrophs fix dissolved inorganic carbon into biomass, potentially altering the carbon flux. There are six known carbon fixation pathways (CFPs) utilized by chemoautotrophs. Each CFP has key enzymes specific to itself and signature carbon isotopic fractionation values due to faster reaction of ¹²C over ¹³C in the carbon species being fixed. The Costa Rican subduction zone, with its wide range of hot spring environments influenced by tectonic forces, offers a novel opportunity to examine microbial carbon fixation within subsurface ecosystems. Through bioinformatic analysis of annotated metagenome assembled genomes (MAGs), we describe the variety, geographic distribution, and frequency of CFPs across the subduction zone. We found that MAGs containing CFPs were widespread, suggesting that subsurface chemoautotrophy is an important process for carbon transformations in the subsurface.

30 Induced respiratory pathway controls on the degradation of harmful organic contaminants in marine sediment

Matthew Quinan*, Christoph Aeppli, Michael Martinez-Colon, Jordon Beckler

Terrestrially derived iron minerals may safeguard marine ecosystems from eutrophication and sulfidization, but the full extent of their ecosystem benefits has not been established. Iron redox cycling can generate hydrocarbon-degrading hydroxyl radicals, with reactions probably occurring more frequently in sediments with elevated iron content such as those in the RiOMars (River-dominant Ocean Margins). To determine if iron in marine sediment affects the degradation of hydrocarbons, we augmented sediments with iron and Deepwater Horizon crude oil to simulate conditions similar to those of a post-spill seafloor environment. Significant differences in the redox environment and oil degradation result as a function of sediment composition. These results could have significant implications for environmental policy decision making.

31 **Constraining photochemical production rates of dissolved inorganic carbon in seawater using the moderate dissolved inorganic carbon (DI13C) isotope enrichment (MoDIE) method**

Kun Ma*, Jay Brandes, Leanne Powers, William Miller

Dissolved organic carbon (DOC) photochemistry is thought to be a major abiotic process in the surface ocean, yet production rates of photoproducts, such as dissolved inorganic carbon (DIC), are poorly constrained. The analytical challenges posed by determining rates in the order of nM/h to uM/h, against a high DIC background of ~2 mM, have resulted in the lack of direct measurements of DIC photoproduction. Previous methods used DIC-stripped samples or proxies such as CO. The moderate dissolved inorganic carbon (DI-13C) isotope enrichment (MoDIE) method was developed to directly measure DIC photoproduction rates in seawater with minimal sample manipulation. Preliminary photochemical experiments with open ocean seawater using MoDIE showed DIC rates of change of irradiated samples indistinguishable from those of dark controls, and pose the question of whether open ocean seawater DOC has limited to no DIC photoproduction. Here we present results from photochemical experiments where solid-phase extracted DOC from coastal and open ocean seawater were added to 0.2 um-filtered open ocean seawater, resulting in samples with 3-10 times concentrated DOC, to test the photoreactivity of marine carbon sources, and the utility and validity of optical extrapolations of nearshore results to open

ocean photochemical rate estimates for DIC production.

32 Modeling biogeochemical dynamics in porous media under various flow conditions and reaction kinetics

Heewon Jung*; Christof Meile

Biogeochemical reactions in natural porous media such as soil, sediments, or aquifers, determine global elemental cycling and the fate of contaminants. Microorganisms are of central importance as they mediate many near-surface geochemical processes. However, quantitatively describing microbial processes is a daunting task because of the challenge to resolve the scales relevant to microbial activity, and because of dynamic interactions between microbial communities and their surroundings. Here, we present our efforts to describe complex microbial dynamics within a range of environmentally relevant conditions using reactive transport modeling.

We studied the variability in macroscopic rate estimates under heterogeneous microbial distribution conditions. Pore scale reactive transport analysis revealed that the macroscopic rate estimates are largely determined by flow conditions and reaction kinetics, and to a lesser extent by the distribution of microbial aggregates. We further evaluated physicochemical conditions effectively coordinating microbial phenotype expression mediated by signaling molecules. Modeling results show that advection dilutes signaling molecules so that faster flow conditions require higher microbial

densities, faster signal production rates, or higher sensitivities for effective communication through signaling molecules. As a consequence, the induction of quorum sensing is no longer a simple function of cell densities.

33 Identifying Ecophysiological Regimes of Phytoplankton Communities in the Mississippi Sound System

Blair Morrison*, Jessica Jones, Joie Horn, Clark Gerken, Drew Sheehan, Jeffrey W. Krause

The Eastern Mississippi Sound System (EMSS) is a spatially and temporally diverse estuary driven by freshwater discharge from Mobile Bay and marine water exchange from coastal Alabama. Due to the prevalence of local freshwater inputs, salinity gradients structure ecological regimes for phytoplankton. During 2019, salinities ranged from 4 ppt – 31 ppt in the EMSS, largely due to riverine discharge and the opening of the Bonnet Carré spillway in Louisiana. To determine how freshwater dynamics impact the composition of phytoplankton communities after spring bloom conditions, plankton samples were collected from June-October of 2019 at 10 sites in the EMSS. During this period, 18 genera were observed, with dinoflagellates having the most diversity. Preliminary data suggests that the EMSS hosted three distinct salinity-associated phytoplankton community regimes. Using a checkerboard-score approach, closely associated co-occurring species were identified for each community regime. Each regime was characterized by the predominance of a single species: two

dinoflagellates, *Akashiwo sanguinea* (10 ppt) and *Prorocentrum micans* (22 ppt), and one diatom *Pseudo-nitzschia* spp. (29 ppt). Continued analysis may allow for greater understanding of factors that influence phytoplankton communities in the EMSS, resulting in enhanced abilities to predict future community regime shifts from more frequent low-salinity events.

34 Thallium Isotope Evidence For Cryptic Oxygenesis On The Archean Earth

Zijian Li*, Kyle Rybacki, Jeremy Owens, Noah Planavsky, Sean Newby, Frantz Ossa Ossa, Alex Hofmann, Christopher Reinhard

Biogeochemical models predict that Earth's ocean-atmosphere chemistry can remain pervasively reducing despite vigorous local biological oxygen production in localized regions of the surface ocean. This potential for ocean-atmosphere redox disequilibrium raises the possibility that oxygenic photosynthesis emerged on Earth long before significant amounts of oxygen accumulated in the atmosphere, and would render potential geochemical fingerprints of the earliest oxygenesis an intrinsically local phenomenon. Here, we use stable thallium (Tl) isotopes to fingerprint the stabilization of manganese (Mn) oxide phases in the shallow Archean ocean at ~3 billion years ago (Ga). Specifically, we observe positive Tl isotope signatures in Fe- and Mn-rich siliciclastic marine sediments of the Mozaan Group, South Africa, indicative of local Mn oxide burial and incorporation, which are difficult to explain without local water oxygen to stabilize Mn oxides against

reduction during water column settling and early sediment diagenesis. We suggest that these signatures provide evidence for the presence of oxygenesis in shallow marine environments by at least ~3 billion years ago, implying Earth's ocean-atmosphere system remained pervasively reducing on timescales of ~100 million years despite the presence of an oxygenic biosphere.

35 Comparing Environmental Enzyme Assay Protocols Using The ezmmek R Package

Christopher L. Cook* and Andrew D. Steen

Extracellular enzyme assays are a widely-used method to probe the interactions between microbes and complex organic matter. While environmental enzyme assays are popular techniques, there remains a need to standardize the exact methodologies used by practitioners. Here we describe ezmmek (Easy Michaelis-Menten Enzyme Kinetics), an R package designed to compare common environmental enzyme assay protocols. ezmmek is capable of calibrating, calculating, and plotting enzyme activities as they relate to the degradation of synthetic substrates. At present, ezmmek contains functions to compare two enzyme assay protocols. The first, as outlined by German et al. (2011), accounts for quenching by considering the contribution of each individual component, such as enzyme substrate, buffer standard and homogenate. The second protocol, used by Steen and Arnosti (2011), assumes that the interaction between fluorophore/chromophore standard and homogenate will approximately equal the

interaction between that standard's corresponding substrate and homogenate, and result in the same bulk quenching. Both protocols will be employed on the same water, sediment, and soil samples prior to analysis in ezmmek. As a reliable platform to compare protocols, ezmmek aims to stimulate further discussion about how to best optimize environmental enzyme assays.

36 Microbial Population and Distribution at a Mars Analog Alluvial Plain Dyngjusandur, Iceland 2016

Scot Sutton*, Gigi McGaughey, Anna Simpson, Diana Gentry, George Tan, Morgan Cable, Thomas Cantrell, Zach Duca, David Cullen, Wolff Geppert, Amanda Stockton

Earth analogs of extraterrestrial environments can provide insight into the potential habitability of the locations while also providing information about the terrestrial biota at terrestrial extremes. The limited nutrient availability, extreme temperatures, and desiccation of Arctic volcanic regions provide a unique opportunity to study environments with multiple similarities to extraterrestrial systems. In July 2016, FELDSPAR conducted a field campaign to Dyngjusandur, Iceland, an alluvial plain of nutrient-poor volcanic basaltic tephra with spectroscopic similarities to analogous geological features observed on Mars. Sample collection was conducted using a system of nested triangular grids beginning at the 10 cm scale and increasing to the 1 km scale. A portable near-IR reflectance spectrometer provided in situ mineralogical analysis of samples at time of

collection. After return to the Georgia Institute of Technology, biological analyses included bacterial copy quantification by qPCR and analysis by 16S rRNA sequencing. Geophysical assays included grain size and moisture content measurements. Correlations have been observed between grain size and bioactivity, and sampling distance appears to play a critical role in microbial distribution. Continued analysis of the Dyngjusandur samples will inform our sampling on future Mars missions, and act as a starting point for temporal analysis at this location.

36 Isolating Cultures from Svalbard Permafrost and Analyzing the Morphology Variations on Different Media

Raegen Paul*, Katie Sipes, Karen G. Lloyd

Microbial ecosystems have been classified within permafrost in a variety of ways including culturing, metagenomics, 16S rRNA amplicon sequencing and thawing experiments. We combined metagenomic inferences with culturing work from the active layers of permafrost in Svalbard. By referencing metagenomic results from two different active layer sites we were able to comprise a list of what organisms may grow in culture. These organisms were then evaluated on the basis of nutrients needed and the growth period based on other researchers' results. To begin selecting for specific microorganisms, general nutrient rich agars (TSA and R2A) were used to begin colony formation. As colonies formed in communities, each was mechanically separated to obtain a unique colony.

These colonies were Sanger sequenced to identify the microorganism. We were able to grow nearly 15 unique isolates on 3 different media enrichments. To further research on this, microbes cultured will be compared to previous cultures from similar permafrost environments.

38 Understanding Containment: Life Unbounded?

Brooke Rothschild-Mancinelli* and Loren Williams

There are few features that occur in all domains of life. Those universal features include the translation system and cell membranes. The translation system is conserved across all domains but membrane composition is not, suggesting that LUCA (Last Universal Common Ancestor) had an alternative membrane that does not exist in life today, or perhaps life existed in a different sort of container. Membranes and their constituents play many key roles in extant life including importing nutrients and exporting waste, chemotaxis, and coordinating DNA replication. Yet, current models of early life membranes indicate their main roles were passive, without transport proteins, and selectively permeable. In addition, phospholipids were unlikely to have been the building blocks of these membranes. This project aims to re-create the roles of early membranes without lipids, using alternative forms of containment, bridging the gap between the non-living (cell-free systems) and the decidedly living (bacteria and L-form bacteria).

39 Effects of Benthic Macrofaunal Bioturbation on the Preservation of Diatom Silica and Formation of Authigenic Products

Dylan Cole*, Nils Volkenborn, Jeffrey W. Krause

Bioturbating macroinfauna can be considered ecosystem engineers; however, the long-term impact of particle reworking and bioirrigation on elemental cycles is not well constrained. We analyzed sediment samples collected from 400 m² experimental plots in the German Wadden Sea, where lugworms (*Arenicola marina*) have been permanently excluded from intertidal sandflats over the last 17 years by a 1-mm polyethylene mesh buried at 10 cm depth in 2002. The mesh prevented adult lugworms from establishing J-shaped burrows which typically are 20-30 cm deep. The experiment therefore offered a unique opportunity to investigate the long-term consequences of bioturbation by adult lugworms on sediment silicon cycling. Samples from different sediment depths were analyzed for both biogenic silica and acid-leachable silica —the latter being associated with early diagenetic products. Initial data reflect a statistically significant elevation of biogenic silica and metal-oxide-associated silica in lugworm exclusion plots compared to areas where adult lugworms were present. This suggests that adult lugworms have the capacity to significantly modify local silicon cycling. Specifically, their presence reduces sedimentary retention of silicon, which can potentially increase diatom productivity in surficial sediments and the overlying water by enhancing mobilization and benthic flux of silicate.

40 Nitrogen Sources and Sinks: Spatial Relationships Impact Coastal Resilience

Anne Margaret Smiley*

Persistent nutrient enrichment can be considered a chronic disturbance that erodes coastal resilience, potentially compromising a system's ability to respond to an acute disturbance (i.e. a hurricane). Coastal habitats including salt marshes, oyster reefs, and seagrasses are substantial nitrogen sinks that may be able to buffer against coastal eutrophication, but the extent of which is still unclear. Using New Bern, NC post-Hurricane Florence as a case study, this work aims to understand the spatial relationships between nutrient sources (wastewater and storm water discharge points) and sinks (coastal habitats) and how those relationships impact biogeochemical cycling. One aspect of this study is examining the denitrification process in the context of both chronic and acute disturbances; whether habitats continually exposed to nutrient enrichment are equipped to handle an additional pulse of nutrients following an extreme weather event. Furthermore, this work will explore demographic distribution as it relates to these sources, sinks, and processes. In our current state of rapid coastal population growth and elevated storm activity, increased nutrient supply to coastal waterbodies is almost guaranteed. Understanding how our coastal habitats will respond will enable us to make decisions and develop strategies that maximize coastal resilience.

41 Deep North Atlantic Carbon Cycling Across the Mid-Brunhes Event

Kathleen Harazin*, Bradley Opdyke, Jimin Yu

The Mid-Brunhes Event (MBE) occurred about 430 kyr ago and represents a climatic transition to higher atmospheric $p\text{CO}_2$ during interglacial periods. The cause of the transition is unknown, but the decoupling of atmospheric CO_2 variation and sedimentary carbonate preservation suggests dynamic shifts in oceanic carbon cycling over the past 550 kyr. A record of $[\text{CO}_3^{2-}]$ derived from foraminiferal B/Ca from the deep Northeast Atlantic (MD01-2446; $39^\circ 03' \text{N}$, $12^\circ 37' \text{W}$; 3547 m) is presented to investigate changes in the Atlantic Meridional Overturning circulation and deep ocean carbon inventory across the MBE. The record of $[\text{CO}_3^{2-}]$ shows clear glacial-interglacial trends, with generally lower $[\text{CO}_3^{2-}]$ during glacials and higher $[\text{CO}_3^{2-}]$ during interglacials, indicating a strong control by water mass circulation and/or geometry on $[\text{CO}_3^{2-}]$. Notably, interglacial $[\text{CO}_3^{2-}]$ is similar during both high- and low- $p\text{CO}_2$ interglacials. An examination of $\delta^{13}\text{C}-[\text{CO}_3^{2-}]$ systematics indicates an increased $\text{CaCO}_3:\text{C}_{\text{org}}$ rain ratio during the glacial cycles surrounding the MBE. The elevated $\text{CaCO}_3:\text{C}_{\text{org}}$ is likely the effect of a global proliferation of coccolithophore blooms (e.g. *Gephyrocapsa*) during $\sim 200\text{-}600$ kyr. These results suggest that an enhanced carbonate pump played a role during the atmospheric CO_2 increase of the MBE.

42 **Functional Characterization of Two-Component-Signaling System bamVW in Anaerobic Aromatic Degradation by *Geobacter daltonii* Strain FRC32**

Christina Kiessling*, James Bullows, Hao Sun, Kuk-Jeong Chin

Anaerobic iron- and uranium-reducing *Geobacter daltonii* FRC-32 has been shown to initiate oxidation of aromatic compounds through a single mechanism. Genome annotation revealed the presence of a two-component-signaling system, bamVW, which initiates degradation of various aromatic compounds via a universal binding site on the sensing domain. The regulatory kinase domain is activated via phospho-transfer which upregulates expression of the first gene of the aromatic degradation cascade, bamY. The expression of a gene encoding a universal aromatic transporter protein was upregulated during the degradation of all tested aromatic compounds by *G. daltonii*, indicating facilitated influx of aromatic compounds. These compounds bind to bamVW's binding domain, thereby initiating transcriptional regulation of their subsequent aromatic degradation pathways. The objective of this study is to elucidate the two-component-signaling system bamVW that binds to a plethora of aromatic compounds, thereby facilitating transcriptional regulation. Preliminary results suggest that degradation of plastics such as cellulose-acetate-butyrates is also initiated via bamVW's concerted up-regulatory mechanism. The findings of this study indicate that *G. daltonii* is a suitable candidate for novel bioremediation strategies in contaminated environments and

fundamentally improve our understanding of anaerobic degradation of crude oil derivatives including plastics.

43 Comparing Carbon Sources of Microbes in The Chimneys Of The Lost City Hydrothermal Vent Field: Does Location Matter?

Jessica C. Rodgers*, Susan Q. Lang

The Lost City Hydrothermal Field hosts distinctive microbial communities supported by the products of serpentinization reactions. Chimney interiors are characterized by an anoxic environment, while the exteriors are mixing zones of hydrothermal fluid and seawater. The anoxic environment of the chimney interior should promote microbial communities that differ in energy and carbon sources from those living on the exterior. We collected a large, intact chimney from Lost City during the 2018 expedition with distinct interior and exterior sections. We have analyzed lipid biomarkers from both interior and exterior sections of the chimney to investigate the spatial distribution of microbial communities, focusing on the fatty acid synthesizing bacterial community. The distribution of long-chain fatty acids are distinctly different between the interior and exterior of the chimney. The interior section contained saturated fatty acids while the exterior contained both saturated and partially unsaturated fatty acids. These differences provide insight into the spatial distribution of the microbe communities inhabiting chimneys. This spatial distribution implies that each community is utilizing distinct carbon and energy sources. Identifying these

sources could offer insight into the ability of similar serpentinite environments to host microbial communities.

44 Microbial Community Characterization of the Peatland Root Microbiome

Sarah Verlander*, Caitlin Petro, Colleen Iverson, Joel Kostka

Peatland ecosystems constitute the greatest meter for meter repository of terrestrial carbon on the planet. As climate change progresses, the fate of this carbon repository remains undetermined. The key to understanding the fate of these ecosystems remains with the driving force of microbial activity. The soil closely surrounding the root tissue, referred to as the rhizosphere microbiome, constitutes a hotspot of microbial activity due to release of root exudates and the production of an aerobic microbiome. The root endosphere refers to the presence of microbial symbionts within the root tissue. Careful characterization of the vascular plant (trees and shrubs) microbiomes is integral to the understanding and future projections of nutrient dynamics in peatland ecosystems. The microbial communities of the soil rhizosphere and the plant endosphere of typical peatland shrubs and trees were characterized using the amplification and sequencing of the 16S rRNA gene. The plant endosphere and rhizosphere represents unique microbiomes that differ from the community of the typical peat soil. This study gives a first insight into the microbial dynamics of a changing peatland ecosystem.

**45 N Cycling prokaryotes in alpine meadows:
AOA drive ammonia oxidation in dry
meadows of the PNW**

Anna Simpson*, Darlene Zabowski

Sensitive low-nutrient ecosystems such as alpine meadows are threatened by both the effects of climate change and by increases in nitrogen (N) pollution from lowland industrialization, overfertilization of agricultural fields, and population growth. Changes or increases in microbial ammonia (NH₄⁺) oxidation to nitrate (NO₃⁻) is of particular concern to land managers because NO₃⁻ is mobile in soils and easily leached into lakes and streams. Specialized bacteria are thought to perform most bulk ammonia oxidation in soils, while specialized archaea perform background very low-level ammonia oxidation that does not significantly contribute to the soil nitrate pool. We simulated N deposition using fertilization at levels of 0, 0.3, 0.5 and 1g m⁻² NH₄NO₃-N in order to study the effects of N pollution on three PNW alpine ecosystems: two mesic heath meadows and one dry mixed heath/graminoid meadow. We found that at the dry meadow site, both N mineralization from soil and counts of ammonia-oxidizing archaea were orders of magnitude higher than at the heath meadow sites, and that the presence of heather inhibited ammonia-oxidizing archaea populations. Soil inorganic ammonia availability during the growing season strongly correlated with copies of archaeal, but not bacterial, ammonia monooxygenase.



In Memoriam:
Prof. Ron P. Kiene
(1959–2019)

Prof. Ron Kiene passed away on 19 January 2019. It is a great loss to academia as Ron was truly one of the great biogeochemists of the last half century. Ron obtained his Ph.D. at the State University of New York at Stony Brook (Kiene 1986). His early work concerned the impact of metal ions on methanogenesis and sulfate reduction in anoxic marine sediments (Capone, Reese and Kiene 1983). He then studied DMS, methanethiol (MT) and dimethyldisulfide (DMDS) reduction to methane in a marine methanogenic member of the *Archaea* (Kiene *et al.* 1986). This strain (GS-16) was later characterised (Oremland *et al.* 1989) and was designated as the type strain of a new

species: *Methanlobus taylorii* GS-16^T (Oremland and Boone 1994) in the class "*Methanomicrobia*" of the *Archaea*. He demonstrated the production of MT, DMS and methane from methionine and DMSP in anoxic sediments from *Spartina alterniflora* Loisel. marshes (Kiene and Visscher 1987). He showed demethylation of DMSP to yield MT and 3-mercaptopropionate in sediments from *Thalassia testudinum* Banks ex. König and *Syringodium* spp. Kütz (Kiene and Taylor 1988). He went on to publish on the impact of biological DMS catabolism in seawater (Kiene and Bates 1990) and its impact on climate control and the biogeochemistry of sulfur. In the same year, he demonstrated the production of DMS from DMSP in bacterial cultures and in seawater samples (Kiene 1990). Ron's first foray into the *FEMS* journals came with Kiene (1988), studying the role of DMS metabolism in *Spartina* spp. Schreb. sediments, followed by Visscher, Kiene and Taylor (1994) on DMSP catabolism in sediments and Visscher, Taylor and Kiene (1995) on DMS and MT degradation. It was almost 10 years before he published again in a *FEMS* journal with Stets, Hines and Kiene (2004) on thiol methylation to yield DMS in acidic wetland sediments. To even attempt to cover every one of Ron's subsequent publications beyond his earliest work would take me many months as there are so many to cover—including a large number of publications in *Nature* and *Science*.

Excerpt and adapted from: Rich Boden, *In Memoriam: Prof. Ron P. Kiene (1959–2019)*, *FEMS Microbiology Letters*, Volume 366, Issue 14, July 2019, fnz178, <https://doi.org/10.1093/femsle/fnz178>

Code of Conduct

This code of conduct outlines our expectations for participants of the Southeastern Biogeochemistry Symposium, as well as steps to reporting unacceptable behavior. We are committed to working to provide a welcoming, safe, and inspiring community for all and expect our code of conduct to be honored. Anyone who violates this code of conduct may be asked to leave the symposium.

1. Participation Guidelines
2. Anti-Harassment Policy
3. Harassment Definitions
4. How to Report a Code of Conduct Violation
5. How We Respond to Reports
6. Questions

1. **Participation Guidelines**

In following code of conduct, you should keep the following expectations about behavior in mind, which are essential for creating a welcoming and safe environment:

- Physical, sexual, and verbal harassment are unacceptable.
- Do not discriminate against people because of their identity (e.g. race, gender, sexuality, age, class background, ability, religion, and more).
- We expect participants to work together to create a welcoming, inclusive, and safe(r) environment for people from diverse backgrounds.

You should take the time to read about what constitutes harassment and discrimination in our full Code of Conduct (below). However, here are some rules of thumb to keep in mind when checking whether you are putting the Code of Conduct into practice:

Ask for consent (i.e. permission) and respect people’s boundaries.

Ask for permission before you engage in physical interactions with participants. This applies to everything from friendly interactions, such as asking “Can I hug you?” before you hug someone, to sexual attention and/or sexualized physical contact at conference social events or after hours, off-site. If you ask someone’s permission and they indicate no, respect that and don’t continue. Sexual harassment (including verbal comments or gestures) is unacceptable, including online, at conference social events, and after-hours at the conference.

Be considerate in your interactions with others and careful about the words you use. Is the language that you’re using discriminatory?

There is a lot of everyday language which discriminates against people, and interactions that seem harmless from one perspective may perpetuate bias when viewed from another. We ask that participants be thoughtful in the language you use and avoid using terms or phrases that—overtly or implicitly—discriminate against minorities such as people of color, LGBTQ+ people, or those with disabilities. We also ask that community members are sensitive to microaggressions[i] and unconscious bias. If someone calls you out for using problematic language or microaggressions, please take the time to listen, apologize, and put effort into not using the language again. You may be asked to leave the community for using this kind of language.

Be mindful of how much time and space you’re taking up. Be aware of the dynamics of power and privilege, and whether you’re taking advantage of it.

Are you taking up a disproportionate amount of time for questions or discussion? Are you giving a chance for participants from an underrepresented country or a marginalized group to speak? Are you attempting to engage in a physical or intimate interaction with someone

who doesn't have the capacity to consent (e.g. at an evening social event with alcohol)? Are you taking the time to listen to the perspectives of those who are different from you? We ask that participants be considerate of how their actions shape the community and create space for others to participate fully themselves.

2. Anti-Harassment Policy

We value your participation. We do not tolerate harassment of SBS members in any form. SBS members asked to stop any harassing behavior are expected to comply immediately.

Our Code of Conduct and Anti-Harassment Policy extend to all aspects of SBS where individuals' behavior affects the ability of others to participate. This includes online interactions (e.g. conference hashtag, interacting on conference-related platforms such as Facebook), as well as "after hours" at the conference, including evening social events. All conference participants, including sponsors, are subject to the anti-harassment policy.

If needed, conference hosts will provide information for participants to contact local law enforcement. Hosts will also make efforts to provide escorts or otherwise assist those experiencing harassment to feel safe, at the request of a participant. A full list of potential sanctions is provided below.

3. Harassment Definitions

For purposes of this code of conduct, sexual harassment is defined as unwelcome sexual advances, requests for sexual favors, or other verbal or physical conduct of a sexual nature when such conduct interferes with an individual's

ability to participate at SBS or creates an intimidating, hostile, or offensive environment.

Some examples of sexual harassment include (but are not limited to):

- Unwelcome and repeated flirtations, propositions, advances, or other sexual attention—including gratuitous or off-topic sexual images or behavior
- Unwelcome physical contact
- Whistling
- Looking at someone in a way that makes them uncomfortable
- Improper gestures
- Use of stereotypes
- Offensive, insulting, derogatory, or degrading remarks
- Unwelcome comments about appearance
- Sexual jokes or use of sexually explicit or offensive language
- Gender- or sex-based pranks
- Display of sexually suggestive objects or pictures
- Demands for sexual favors in exchange for favorable or preferential treatment

Other harassment is defined as verbal or physical conduct that denigrates or shows hostility or aversion toward an individual because of their race, color, religion, national origin, sex, age, sexual orientation, gender identity or expression, personal appearance, political affiliation, marital status, family responsibilities, veteran status, matriculation, disability, mental illness, neuro(a)typicality, or any other legally protected status, and that creates an intimidating, hostile, or offensive environment for participation or unreasonably interferes with an individual's ability to participate in the community.

Some examples of other harassment include (but are not limited to):

- Offensive comments related to gender, gender identity and expression, sexual orientation, disability, mental illness, neuro(a)typicality, physical appearance, body size, race, age, regional discrimination, lifestyle, political or religious affiliation
- Using epithets or slurs
- Mocking, ridiculing, or mimicking another's culture, accent, appearance, or custom
- Deliberate misgendering. This includes deadnaming^[ii] or persistently using a pronoun that does not correctly reflect a person's gender identity. Address people by the name on their name tag (or by their username or handle, if appropriate) unless they invite you to refer to them by another name.
- Threats of violence, both physical and psychological
- Deliberate intimidation
- Incitement of violence towards any individual, including encouraging a person to commit suicide or to engage in self-harm
- Physical contact and simulated physical contact without consent or after a request to stop
- Stalking or following
- Harassing photography or recording, including logging online activity for harassment purposes
- Continued one-on-one communication after requests to cease
- Deliberate "outing" of any aspect of a person's identity without their consent except as necessary to protect others from intentional abuse

- Publication of non-harassing private communication

We will not act on complaints regarding reverse-isms (e.g. reverse racism, reverse sexism), reasonable communication of boundaries (such as “leave me alone”), refusal to explain or debate topics, or criticism of ‘tone’ or oppressive behavior.

4. Reporting Issues

If you experience or witness unacceptable behavior—or have any other concerns—please report the issue by the means described below.

If you experience or witness behavior that violates the code of conduct at the SBS meeting or online, please either **speak directly** to one of the SBS organizing committee members or submit a report to the SBS Conduct Committee at **THIS FORM**. Alternatively, you may also submit reports directly to the staff representatives on the committee at:

Jennifer Glass: jennifer.glass@eas.gatech.edu

If you are more comfortable submitting a report anonymously, simply do not include your name and contact information in the form linked above. We will do our best to respond to the situation, and reports submitted anonymously are taken seriously; however, submitting anonymously may inhibit the committee’s ability to take specific action.

The SBS Code of Conduct Committee is composed of the SBS organizing committee. All reports will be handled with discretion by the Code of Conduct Committee.

In your report, please do your best to include:

- Your contact information

- Identifying information of the participant who has violated the code of conduct
- The behavior that was in violation
- The approximate time of the behavior (if different than the time the report was made)
- Where the code of conduct violation happened
- The circumstances surrounding the incident
- Other people involved in or witness to the incident
- If you believe the incident is ongoing, please let us know
- If there is a publicly available record (e.g. mailing list record), please include a link, or any relevant documentation
- Any additional helpful information

5. How We Respond to Reports

Responses to reports are decided by the SBS Code of Conduct Committee.

After a report is submitted related to the SBS meeting, the incident will be documented, the Code of Conduct Committee will be notified, and the person making the report will be contacted (if possible) to confirm the report, gather more information, and determine how the person making the report can be best supported. All reports will be investigated to the extent the details provided allow. The Code of Conduct Committee will meet to discuss the report and decide what actions to take, in consultation with the person making the report, if known, and in as timely a manner as possible. During this part of the process, we will do our best to protect your confidentiality, if you wish your report to be confidential; however, reporting an incident anonymously or wishing not to disclose key details (e.g. the name of the person being reported) may inhibit the committee's ability to take action. Once appropriate actions are determined by the

committee, they'll be communicated to the person who violated the code of conduct and the person making the report.

Actions in response to reports can range from warnings with instructions on how to correct behavior that violated the code of conduct to immediate removal from SBS events, online communities (e.g. email lists, Facebook), and future engagement.

If you have concerns with the process provided (or if the process is unclear), you can contact SBS Code of Conduct Committee at the means described above, and the committee will make efforts to provide support.

Sanctions

The following is a list of potential sanctions for anyone who violates the code of conduct, depending on the severity of the violation. The sanctions will be decided by the Code of Conduct Committee:

- Warning the accused to cease their behavior and that further reports may result in sanctions
- Ending a talk that violates the policy early
- Not allowing a speaker who violated the policy to give (further) talks at the event
- Immediately ending any event volunteer responsibilities and privileges the accused holds
- Requiring that the accused not volunteer for future events (either indefinitely or for a certain time period)
- Requiring that the accused immediately leave the event and not return
- Banning the accused from future events (either indefinitely or for a certain time period)

- Being banned or blocked on online community platforms, e.g. Facebook
- Being reported to the proper authorities

6. Questions

For additional guidance of codes of conduct in general, you may find Ashe Dryden's introduction to [codes of conduct and frequently asked questions helpful](#).

This Code of Conduct was adapted from the OpenCon2018 code of conduct: https://www.opencon2018.org/code_of_conduct

[i] Microaggressions are the brief and commonplace verbal, behavioral, and environmental indignities, whether intentional or unintentional, that communicate hostile, derogatory, or negative racial, gender, sexual-orientation, and religious slights and insults to the target person or group.

Adapted from Sue, D. (2010). *Microaggressions in everyday life*. Hoboken: John Wiley & Sons, p.5.

[ii] Deadnaming refers to someone who has changed their name by their previous name