



Undergraduate Research Symposium May 17, 2019 Mary Gates Hall

Online Proceedings

SESSION 1E

ANIMAL BEHAVIOR, ECOLOGY, AND EVOLUTION

Session Moderator: Luke Tornabene, School of Aquatic and Fishery Sciences and the Burke Museum of Natural History and Culture

MGH 231

12:30 PM to 2:15 PM

* Note: Titles in order of presentation.

Data Verification of Counts from Automatic Scales: A Case Study of Magellanic Penguins (*Spheniscus magellanicus*) in Punta Tombo, Argentina

Lexi Wachtell, Senior, Environmental Science & Resource Management

UW Honors Program

Mentor: Dee Boersma, Biology

Automatic scales are designed to weigh and count animals when they step on or cross the device. This means that high quantities of data may be collected when researchers cannot be present, with minimal interference to study subjects. However, remote and automated data collection requires verification of the quality of data before analyses. We use automatic scales in Punta Tombo, Argentina to weigh Magellanic penguins (*Spheniscus magellanicus*). Our scales record the time that each penguin crosses, and if certain conditions are met, they record a weight. We verified our data by comparing counts from automated scales with counts from a video recording of penguins crossing the scales. Over twenty hours of video footage were made during a 17-day period where penguins were recorded crossing automatic scales in the morning, midday, and evening on different days. We then counted the number of times a penguin was present in the video and not recorded by the scale. We expect that the proportion of penguins missed will be higher in the morning and evening when more penguins cross the scales, and lower around midday when fewer penguins cross the scales. The scales are designed to record weights when one penguin is present. When several penguins are on the scale or cross rapidly, the scale does not record a weight and may not record the correct number of penguins. Preliminary results support our prediction, with 75% and 78% of birds crossing the scales recorded during the morning and evening respectively, and

nearly 100% of birds crossing the scales recorded at midday. By comparing the counts and the times between the scale and the video recording, we can determine how many penguins are missed, count the total number of penguins crossing the scales, and identify when most penguin crossings occur.

SESSION 2D

BIOLOGICAL RESPONSES TO ENVIRONMENTAL FACTORS

Session Moderator: Frieda B. Taub, Aquatic & Fishery Science

MGH 234

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

The Influence of Chlorophyll-A and Sea Surface Temperature on Magellanic Penguin Reproductive Success

Anna Sulc, Senior, French, Oceanography

UW Honors Program

Mentor: Dee Boersma, Biology

Organisms in the ocean depend ultimately on phytoplankton as it is the base of the marine food web. Through the use of satellite imaging, indicators of photosynthesis such as chlorophyll-A are used as an index of primary production in the ocean over large areas and variable time scales. Phytoplankton is dependent on large-scale ocean processes such as water temperature and water column mixing. Such estimates might provide insights in food availability for larger predators that eat plankton eating fish such as the Magellanic penguin. Located on the southeast coast of Argentina, Punta Tombo is among the largest breeding colonies for Magellanic penguins. The Boersma Lab at the University of Washington has studied the colony since 1982 and have determined reproductive success for 35 years. Although many factors influence the overall success of the colony, starvation of chicks is responsible for 40% of chick deaths. Through the use of spatial analysis tools, we have looked at chlorophyll-A patterns and seasonal water temperature variation around Punta Tombo and compared these two variables with reproductive success of Magellanic penguins. We expect a strong positive relationship between the two datasets: water temperature and chlorophyll-A. Further we expect that when values are higher

closer to the colony, reproductive success of birds is higher, and parents forage closer to the colony.

SESSION 2J

MEASURING CELL GROWTH AND EVOLUTION

Session Moderator: Kristin Anderson, Immunology

MGH 271

3:30 PM to 5:15 PM

* Note: Titles in order of presentation.

***Staphylococcus Aureus* Strain Switching during Chronic Lung Infections among Cystic Fibrosis Patients Treated with Ivacaftor and Antibiotics**

Madeline Grace Fisher, Senior, Biology (Molecular, Cellular & Developmental)

Mentor: Samantha Durfey, Microbiology

Mentor: Pradeep Singh, Microbiology

In cystic fibrosis (CF), a genetic defect in the CFTR anion channel compromises host defenses and causes chronic lung infections with organisms like *Staphylococcus aureus*. Our lab has been studying the effects of combining ivacaftor, a CFTR modulator which increases CFTR channel activity, with a period of intensive antibiotic treatment. We found that *S. aureus* lung infections generally persisted despite this aggressive treatment. However, most subjects undergoing treatment were found to be infected by different *S. aureus* strains one year after treatment than were present before treatment was initiated. Understanding the dynamics of strain switching provide new knowledge about the natural history of chronic CF infections, help define the effects of CFTR modulators and antibiotics, and inform new approaches that might produce infection eradication. We hypothesize that (1) strain switching is most likely to occur during the period of combined ivacaftor and antibiotic treatment, as sputum bacterial burdens were lowest during combined treatment; and that (2) strain switching is rare in the absence of combined treatment. To test this, we used a new population-based multilocus sequence typing (PopMLST) method we developed to perform strain-level genotyping on *S. aureus*. PopMLST uses PCR amplification and next generation sequencing of housekeeping genes from bacterial isolate pools cultured from sputum. Sequencing determines the number and relative abundance of unique sequence types present, and the data can be used to infer the number of strains present. This analysis was performed on samples obtained before treatment, during treatment with ivacaftor alone, and during combined treatment. We also examined a cohort of subjects receiving usual care. These data improve understanding of strain dynamics during CF infections and suggest new strategies to eliminate infection.