



CCURI

COMMUNITY COLLEGE UNDERGRADUATE
RESEARCH INITIATIVE

Fall 2017 Colloquium

Austin Community College

November 30-December 1, 2017

"What we have to learn to do, we learn by doing"

~Aristotle

www.ccuri.org

Dear Colleagues and Friends,

I would like to personally welcome each of you to Austin, TX and the CCURI Regional Conference and Poster Session. The student poster sessions are our signature events where our undergraduate researchers have the opportunity to share their work with the CCURI community. CCURI's mission is to support the development, implementation, and evaluation of undergraduate research programs at our Nation's community colleges. As many of you already know, CCURI is in its third of four years of funding under NSF's Improving Undergraduate STEM Education (IUSE) program. To date, the National Science Foundation has invested more than \$5.95M in the CCURI program and its network of community colleges.

In 2016-2017, a total of 3,815 students participated in undergraduate research with support of CCURI at our partner and affiliate institutions. Each year, CCURI sponsors two regional student poster sessions to provide students with an opportunity to showcase their work to the CCURI network. Previous events were held in Philadelphia, Phoenix, Washington, D.C., Charlotte, and Portland. This year, we are honored to be holding our event in the great city of Austin, TX with Austin Community College as our gracious host.

We are honored to be co-hosting this event with Austin Community College's AC2 Bio-Link Regional Center. This program was created in 2015 as an NSF-funded ATE Center of Excellence. While the program focuses on the promoting biotechnology education in Texas and Kentucky, the work is being disseminated across the nation. One of the goals of the program is utilize the undergraduate research experience as a way to establish novel student recruitment pipelines into the biotechnology industry.

CCURI believes that the research experience is the most effective way to promote deep learning and advance critical thinking skills, and with close to 50% of our Nation's undergraduates currently pursuing their education at a community college, the CCURI mission is a critical component of this commitment. We hope that you will enjoy exploring the amazing talent on display at this Regional Conference.

Again, welcome to Austin, TX and the CCURI conference. I am glad that you are here, and I look forward to your participation.

Sincerely,

A handwritten signature in black ink, appearing to read "James A. Hewlett". The signature is fluid and cursive, with a long horizontal stroke extending to the right.

James A. Hewlett
Executive Director
CCURI

KEYNOTE ADDRESS
10:00AM – 11:00AM
EASTVIEW CAMPUS 8500

MALCOLM HILL, PH.D.



Dr. Malcolm Hill earned his BA at Colby College, and a Ph.D. at the University of Houston. After post-doctoral work in Boston, he started his academic career at Fairfield University before moving to the University of Richmond where he is the Clarence E. Denoon Jr. Professor of Science. He believes professors should bring student-centered perspectives, growth mindsets, and success models to their classrooms. His goal is to provide transformational experiences to undergraduates, and he uses authentic research experiences in and out of the classroom to achieve that goal. His undergraduate-focused research program emphasizes high-impact pedagogical practices. His research is highly collaborative and interdisciplinary, and is focused on the evolutionary ecology of species interactions in tropical and temperate marine environments. Students in Dr. Hill's lab work on a diversity of questions, most of which use sponges as model organisms, and the work takes place in the field (snorkeling and diving) and in the lab (DNA-based molecular work). A major focus is symbiosis between sponges and their algal and bacterial partners. Work in the Hill lab has been supported by the NSF among other funding agencies. He is steadfast in his belief that the best path forward for humanity involves educating students broadly, ethically, globally, and wholly.

FACULTY PRESENTATIONS
THURSDAY, NOVEMBER 30, 2017
ROOM 8500

New Mexico

Author(s): Gretchen Gürtler

Institution: Mesalands Community College, Tucumcari, NM

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Oral presentation: Room 8500, 2:40pm

New York

Author(s): Maria Entezari, A. Lucia Fuentes

Institution: LaGuardia CC, CUNY

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North Carolina

Author(s): Ashley Hagler, Melissa Armstrong

Institution: Gaston College

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Texas

Author(s): Bridgette Kirkpatrick¹, Daisy Zhang², J. Robert Hatherill², Carole Twichell¹, Linnea Fletcher³

Institution: ¹Collin College, ²Del Mar College, ³Austin Community College

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Oral presentation: Room 8500, 1:00pm

Washington

Author(s): Sandra Porter

Institution: Digital World Biology LLC

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Oral presentation: Room 8500, 1:50pm

New Mexico

UNDERGRADUATE RESEARCH COLLABORATIONS WITH GOVERNMENT AGENCIES

Gretchen Gürtler, Faculty

Mesalands Community College, Tucumcari, NM

Location: **Room 8500, 2:40pm-3:00pm**

The challenges and achievements that a small HSI college had integrating undergraduate research experiences into an existing natural sciences program will be discussed. Like most introductory college science courses, our natural science courses used textbooks, PowerPoint presentations, and lectures to illustrate basic scientific concepts. Though a collective decision was made by our science faculty to incorporate undergraduate research projects into various STEM courses, our greatest challenge was incorporating mandatory research courses into the degree plans of our Natural Science program. We found that students made considerable progress in understanding natural science by critically evaluating primary research articles and undertaking small research projects. Many of these student projects were conducted in cooperation with governmental agencies such as: the Albuquerque District of the US Army Corps of Engineers, United States Geological Survey in Denver, and the National Ice Core Laboratory. These projects illustrated the effects of climate change on the water quality, sediment buildup, and biodiversity at local reservoirs. Other projects involved the analysis of ice core samples from Greenland and Antarctica. Students presented research posters at various research venues including: Community College Undergraduate Research Initiative colloquiums; New Mexico Academy of Science; New Mexico Association of Museums; Western Consortium of Water Analysis, Visualization, and Exploration; and New Mexico Experimental Program to Stimulate Competitive Research.

New York

INTEGRATION OF A SEMESTER-LONG RESEARCH PROJECT THAT PROMOTES SCIENTIFIC INQUIRY AND CIVIC ENGAGEMENT INTO AN INTRODUCTORY BIOLOGY LABORATORY COURSE

Maria Entezari, A. Lucia Fuentes

Department of Natural Sciences, LaGuardia CC, CUNY. Long Island City, NY

Location: **Room 8500, 1:25pm-1:45pm**

Our mission, as educators at community colleges, is to make education relevant for our students' lives and communities, and promote their engagement in finding solutions to challenges and needs of their communities through critical thinking. High attrition rate in STEM majors during the first year of studies makes it difficult to fulfill our objectives. Educational assessments show that introducing scientific research in the first-year science courses lowers these attrition rates in STEM majors. Furthermore, research experiences provide a path for community-college students to understand the process of scientific inquiry and the relevance of science to their communities. A major difficulty in the implementation of this practice lies in integrating the research experiences into first-year courses while ensuring students acquire the basic knowledge and skills set out in the course syllabi. Here we present our approach, including our objectives, pedagogical design strategy and examples, of a series of laboratories that allow students to engage in a research-based, semester-long project. Our model is unique in that it integrates authentic research into the first-year labs; throughout the semester, students perform experiments, gather information, and analyze the data about the physical, chemical and biological characteristics of water samples. The labs are designed and modified so students ask questions and collect information contributing to the final project, while learning concepts and skills outlined in traditional labs, in the context of scientific discovery. Four consecutive assignments, carefully crafted to promote best practices for communicating scientific findings, enable students to gradually build toward the final oral and digital presentation of their results. Importantly, the lab incorporates research into the quality of water bodies close to the communities where students live, work and study, connecting the science to their direct lived experiences and promoting an understanding of the human and social dimensions of scientific practice and insight into possibilities for civic engagement.

North Carolina

IT ALL BEGINS WITH A SPARC3

Ashley Hagler, Melissa Armstrong

Gaston College

Location: **Room 8500, 2:15pm-2:35pm**

Breaking from tradition, Gaston College embarked on a bold initiative in 2009 to increase student engagement and change the culture of learning by redesigning the Associate of Science (AS) program. This initiative, known as SPARC3, embeds inquiry-based instruction and authentic undergraduate research experiences in multiple core science, technology, engineering and mathematics (STEM) courses, incorporates STEM themes in multiple disciplines, establishes learning communities, and provides holistic student services. This presentation will provide an overview of the implementation of the SPARC3 initiative at Gaston College and will focus on the spread of undergraduate research beyond the core STEM courses at Gaston College.

Texas

USING UNDERGRADUATE RESEARCH AS A STUDENT RECRUITMENT TOOL FOR BIOTECHNOLOGY PROGRAMS

Bridgette Kirkpatrick¹, Daisy Zhang², J. Robert Hatherill², Carole Twichell¹, Linnea Fletcher³

¹Collin College, TX

²Del Mar College, TX

³Austin Community College, TX

Location: **Room 8500, 1:00pm-1:20pm**

One of the goals of the AC2 Bio-Link Regional Center is to embed undergraduate research (UGR) projects into feeder courses such as freshman-level biology in order to increase student recruitment into biotechnology programs. Schools such as Del Mar College (DMC) have been doing this for several years, using nationally recognized programs such as HHMI's SEA-PHAGES, The Small World Initiative, and PARE (The Prevalence of Antibiotic Resistance in the Environment). From 2012 to 2016, 30-50% of new biotechnology students at DMC were recruited from freshman-level biology I and II classes that had integrated these research programs. DMC has also seen increases in enrollment, student class retention, and program completion since research experiences have been available to biology students. Austin Community College (ACC) embeds the HHMI SEA-PHAGE Program into their major's freshman biology course, and has also recruited students that have participated in undergraduate research into their biotechnology program. Collin College already integrates UGR into a number of freshman and sophomore courses, and is currently working to adapt all of their freshman biology I labs to be inquiry-based courses. The Panel will discuss best practices, pros and cons of undergraduate research programs, and barriers that must be overcome when transitioning towards an authentic research experience in the classroom.

Washington

DRUG DISCOVERY AND INQUIRY IN BIOINFORMATICS

Sandra Porter

Digital World Biology LLC

Location: **Room 8500, 1:50pm-2:10pm**

Last year, we piloted a research project in our Austin Community College bioinformatics course that is designed to engage students by having them apply their skills and knowledge to the problem of finding drugs to treat Zika virus. In the talk, I will share the process for using protein BLAST to identify drug candidates, discuss how molecular modeling and BLAST can be used to evaluate whether those drugs will work with different proteins, and show how this same process was used to determine that Gilead's anti-hepatitis C drug Sovaldi® might work against Zika virus. This general process for repurposing existing drugs provides a new avenue for students to apply bioinformatics tools to real-life problems and potentially, make discoveries.

STEM CAREER PRESENTATIONS
FRIDAY, DECEMBER 1, 2017
9:00AM – 10:00AM
ROOMS 2208 AND 2209
HIGHLAND CAMPUS

Tyler Drake, Ph.D.

Director

ACC Bioscience Incubator

Location: **Highland Campus, Room 2208, 9:00am**

Dr. Tyler Drake leads ACC Bioscience Incubator's operations. He works with entrepreneurs, economic development interests, faculty and other partners to support the biotech economy. Tyler has experience developing novel technologies in women's health, cancer diagnostics, and HIV/AIDS. He has authored scientific publications, spoken at international conferences, and worked with startups as an engineer and consultant. Tyler completed postdoctoral training, received a PhD in biomedical engineering and MS in medical physics from Duke University. He has a BA in physics from McDaniel College.

Bradley Hall

Sr. Scientist II, Research and Development

Asuragen

Location: **Highland Campus, Room 2209, 9:00am**

Bradley Hall received his Ph.D. at the University of Texas at Austin in 2008 where he focused on the computational and rational design of nucleic acid biosensors under the direction of Andrew Ellington. Brad developed the Aptamer Stream, one of three pilot streams that founded the Freshman Research Initiative at the University of Texas and continued as a Research Educator for the stream until 2010 helping nurture relationships with the local biotech community. During this time, he was also an instructor for ACC's Biotech program for one semester. Brad was recruited by Nobel laureate Kary Mullis to help establish Altermune Technologies, a platform technology start-up venture focused on immune-redirecting therapies utilizing nucleic acid aptamers. There he was instrumental in locating the R&D labs in the UTech Dorm Room at UT, mentoring student researchers in entrepreneurial concepts associated with startups, and developing novel reagents and assays to expand the IP portfolio of the company. Currently, Brad is a Sr. Scientist II in R&D at Asuragen working on diagnostics for genetic diseases. As a nucleic acid scientist for the last 15+ years he is the author of awarded and provisional patents and 15 journal articles.

Jackie Jaskula

Director of Quality Assurance and Regulatory Affairs

OriGen Biomedical

Location: **Highland Campus, Room 2208, 9:30am**

Jackie joined OriGen Biomedical in August 2015 as Director, Quality Assurance and Regulatory Affairs. Jackie has a long history of experience in life sciences reagents and in vitro diagnostic devices. Before joining OriGen, Jackie held the positions of Senior Manager QA/QC at Thermo Fisher and Director of Quality Assurance at Agilent Technologies. Jackie has a Master and a Bachelor of Science in Microbiology from Indiana and Washington State Universities, respectively. Jackie is a long-time member of RAPS and ASQ with a special fondness for regulations. Jackie approaches quality and regulatory compliance in a flexible manner built on partnering requirements of customers and regulators with the needs and culture of the business. In her free time, Jackie enjoys quilting, triathlons, and wrangling her sons. On a good night she'd prefer to end her day with a cup of cocoa and a stack of regulations to be read by the fire!

Sulatha Dwarakanath Ph.D.

Associate Director

IntegenX

Location: **Highland Campus, Room 2209, 9:30am**

Worked in Medical Device Industry for more than 20 years. Currently working as Associate Director at IntegenX, a DNA Diagnostics Company, working in R&D and QC Development. Previously, was founder and CSO of Nano science Diagnostics and Director of Biotechnology at Austin community college. At ACC was instrumental in setting up a CSO at the Biotech Dept. worked as the liaison between the department and industry. Before that worked at Bayer Diagnostics and various startup companies in the Medical devices area. Ph.D. from New York University.

STUDENT PRESENTATION INDEX

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Author(s): A. Brown, K. Casey, A. Eberhard, C. Eslinger, S. Grace, A. Hughes, D. Johnson, A. Kennedy, S. Laughlin, C. Longden, K. Smith, D. Sloan
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Author(s): Tara L. Clancy, Damien Seay, J. Robert Hatherill, D. Zhang

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Author(s): Alexis Custer

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Author(s): Ameen Lalani

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Author(s): Jongsuk Choi
Institution: Edmonds Community College
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STUDENT ORAL PRESENTATIONS
FRIDAY, DECEMBER 1, 2017
ROOMS 2208, 2209 AND 2210
HIGHLAND CAMPUS

10:10am-10:30am

COSMIC RAY MUON FLUX MEASUREMENTS CORRELATED TO ATMOSPHERIC PRESSURE FLUCTUATIONS AND SOLAR FLARE ACTIVITY

David Buitrago

Queensborough Community College, Department of Physics

Raul Armendariz (*Faculty Advisor*)

Location: **Room 2208, 10:10am-10:30am**

Discipline: Physics

When an incoming cosmic ray proton or atom from outer space collides with particles in earth's atmosphere a shower of secondary muon particles is created. Cosmic ray muon flux was measured at the Queensborough Community College using a QuarkNet detector consisting of three stacked polyvinyl-toluene scintillator counters, photomultiplier tubes, and a two-fold coincidence logic trigger. A computer program was created in Python to calculate the muon flux rate and atmospheric pressure sensor readings from the detector's data acquisition board. The program converts the data from hexadecimal to decimal, re-bins it in a more suitable format and then creates plots of muon flux versus atmospheric pressure. Cosmic ray flux was measured over March 13-17, 2017 during an extra-tropical cyclone (winter storm *Stella*, NESIS category 3), and is shown to be inversely correlated with atmospheric pressure. Cosmic rays were measured over September 6-11, 2017 during a period of heightened solar activity, including an X9.3 solar flare; several drops in muon flux were recorded, and are compared here to increased proton and x-ray flux measurements made by GOES space weather satellites.

IMPACT OF WATER QUALITY ON BACTERIAL DIVERSITY IN THE LONG ISLAND SOUND REVEALED BY METAGENOMICS

Sakina Makwana, Sarah Jankowski

LaGuardia Community College, CUNY

Maria Entezari, Ph.D., A. Lucia Fuentes, Ph.D. (*Faculty Advisors*)

Location: **Room 2209, 10:10am-10:30am**

Discipline: Biology

The Long Island Sound estuary is an important resource for NY State. The diverse microbial community in the Sound impacts the ecosystem in surrounding areas. High levels of Enterococci have been reported indicating poor water quality, yet information regarding the unculturable microbial community in these waters is scant. Water of the Sound is a mix of freshwater and ocean water from the east and west. Our study compared microbial communities and physicochemical parameters of East River-ER- (west) and Oyster Bay-OB-(east). Based on EPA data, as well as increases in population and industrial activities in the west side of Long Island Sound, we hypothesized that relative abundance and diversity in bacterial communities would differ in these two areas due to higher pollution in ER and hypoxia in OB. To test our hypothesis, we isolated DNA from samples collected in each area, and 16S DNA was amplified by PCR, sequenced, and analyzed (AREM project). We also determined physicochemical properties, including temperature, pH, salinity, Dissolved Oxygen (DO), and CO₂, using commercial kits. Our findings partially supported our hypothesis; the most abundant bacterial groups were Chloracidobacteria for OB, and Oxalobacteracea, Croptococcus and Xanthomonales for ER. OB presented greater alpha diversity than ER, which could be partially attributed to higher DO in OB. Our data on the bacterial community offer insight into the effects of changes due to pollution and climate change on marine life, underlining the importance of proper legislation to ensure recovery and maintenance of water quality.

TESTING COMPUTATIONALLY PREDICTED ANTIBODY STRUCTURES

Mauricio Tellez

Austin Community College

Nancy Lyon, Tyler Drake (*Faculty Advisors*)

Location: **Room 2210, 10:10am-10:30am**

Discipline: Biotechnology

Experimental antibody design usually involves many time-consuming and labor-intensive steps. Through the use of automated computational design algorithms, it has been shown that an antibody can be designed with no prior experimental data other than the structure of the antigen of interest. Macromoltek, an Austin-based company, has been developing an automated platform to design antibodies aimed at difficult infectious disease and cancer targets. In a collaboration with Macromoltek, the aim of this project is to use their algorithm to create a DNA sequence which when expressed, will synthesize recombinant antibodies with affinity to specific, target antigens. These antibodies will be expressed and subsequently purified from E.coli through standard protein purification methods such as FPLC. Their binding affinity to their target antigens will be tested through binding assays such as ELISA. If affinity to the antigen is observed, we intend on further testing the kinetics involved in their binding through Surface Plasmon Resonance (SPR).

10:35am-10:55am

FINDING NEW ORDER WITHIN CHAOS: SPECULATION ON SYMMETRICAL DOUBLING 3-PERIOD CASCADES BEYOND FEIGENBAUM'S SCALING OF THE LOGISTIC MAP

Jongsuk Choi

Edmonds Community College

Billy D. Jones (*Faculty Advisor*)

Location: **Room 2208, 10:35am-10:55am**

Disciplines: Physics/Mathematics

Chaos refers to dynamical systems that are exponentially sensitive to their initial conditions. In this project, I explore the logistic map, the simplest chaotic system, by characterizing its global nature through Feigenbaum's constants and the relationships between its periods. Using Matlab to code the logistic map, the Feigenbaum constants and existence of the 3-period cycle were verified and explored. Further simulations showed a new pattern of repeating odd-cycle periods stemming from the 3-period cycle - a symmetric doubling cascade of odd-number periods in the chaotic phase of the map which are independent of their initial conditions. The new pattern allows us to see the order that underlies the chaotic system, a meta-pattern based on odd-cycle doubling which shows all odd-number periods in the chaos stemming from the 3-period: with two 5-periods, four 7-periods, eight 9-periods, and presumably sixteen 11-periods, etc., following symmetrically and respectively from the initial 3-period cycle. The discovery of the new ordered pattern can be used to predict the stable state of growth of a population model in its chaotic phase and can be used for population studies in which the initial conditions are known only approximately. This has ramifications for mathematics, population biology, chemistry, physics, and the social sciences.

THE EFFECTS OF LONG TERM SOIL WARMING ON SOIL RESPIRATION AND CARBON STORAGE

States Labrum

Columbia State Community College, Harvard Forest Summer Research Program

Elvira Eivazova, Ph.D. (*Faculty Advisor*)

Location: **Room 2209, 10:35am-10:55am**

Discipline: Biology

Our research objective was to investigate the relationship between long term soil warming and subsequent soil carbon release into the atmosphere, within the context of the impact of global warming. Currently, soil organic matter (SOM) holds the largest carbon pool in the terrestrial ecosystem. The rise of global temperatures accelerates microbial respiration and potentially increases carbon release from the soil. Here, we conducted soil warming experiments to examine how various soil temperatures affect carbon release through soil microbial respiration, and whether the soil microbes may compensate for the effects of rising temperatures by the phenomenon of thermal acclimation. Our field experimental results showed a pattern of decreased soil respiration in the heated plots relative the control plots. To understand what factors drive thermal acclimation, we incubated heated and control soil samples at six separate temperatures (6°C-36°C) in the laboratory. We found that the relationships between temperature and respiration were similar in field and laboratory data. The observed decrease in microbial biomass in heated soils caused the decrease in respiration relative to controls. Additionally, to remove potential bearing of substrate limitation, we amended the soils with sucrose which further minimized the difference in respiration between treatments. The results indicated that microbial biomass and substrate limitations are the factors primarily responsible for thermal acclimation, correlating with the prior conducted 26-year long experimental observations. We hypothesized that structural and functional changes in soil microbial communities drive the patterns of thermal acclimation of SOM decomposition, directly impacting soil carbon release.

GROWTH CHARACTERIZATION OF THE UNICELLULAR GREEN ALGAE,
CHLORELLA VULGARIS, AND CYANOBACTERIA *SYNECHOCOCCUS ELONGATUS* IN A
PHOTOBIOREACTOR

Seemoni Shah, Sandesh Subramanya, Ph.D.

Austin Community College, TX

Sandesh Subramanya, Ph.D. (*Faculty Advisor*)

Location: **Room 2210, 10:35am-10:55am**

Discipline: Biotechnology

Algae, a group of highly diverse eukaryotes, are photosynthetic and mainly aquatic organisms. Macro- and micro-algae have been used commercially in food, feed, nutraceuticals, fertilizers, bioremediation, biofuels, with many more in development. Algae have great potential to produce a wide range of valuable compounds, beyond their current exploitation. To date, commercialization of new products, like polyunsaturated fatty acids (PUFAs), has been slow. However, microalgal biotechnology is a relatively new industry, and therefore, it is unsurprising that significant challenges remain to be solved. Here we demonstrate the growth requirements and kinetics of a unicellular green algae, *Chlorella vulgaris*, and a cyanobacterium *Synechococcus elongatus* in a GroFizz photobioreactor. Efficiency of these photobioreactors (2 liters) are being evaluated to achieve optimal growth potential of algae for laboratory scale production.

1:00pm-1:20pm

A STUDY INTO THE FEASIBILITY OF WATER EXTRACTION TO SUPPORT A SUSTAINABLE MARTIAN COLONY

Agnes Mariana Straatman

Kapi'olani Community College

Aaron Hanai (*Faculty Advisor*)

Location: **Room 2208, 1:00pm-1:20pm**

Discipline: Chemistry

The colonization of Mars has become a goal for scientific research and the expansion of human settlement beyond our home planet. However, such an endeavor presents a unique challenge, particularly in the acquisition of a steady source of water. Not only will water be needed for drinking and food cultivation, but it will be used for fuel production, building and housing materials, and so on. While there is water present on the Mars, it is not easily obtainable; the majority of it locked away in the polar ice caps or the hydrated regolith. This research study looks at two prevalent proposed methods of water extraction for Martian Colonies; ice mining and water extraction from the regolith. It examines the applications of both of methods, comparing the advantages and disadvantages on their cost and equipment requirements, and cross-checking the feasibility of each method with proposed colony sites. It explains why research should be focused primarily on these two sources of water extraction as opposed to other methods such as atmospheric water extraction, which cannot provide enough water, or shipping water over long distances, which can become costly. As all aspects of colonization must be considered, it takes a holistic approach of water's use and acquisition methods within Mars' first colony, considering other goals such as soil processing and power production, and evaluate methods to recycle and reuse water efficiently, heeding to as little waste as possible.

THE EFFECT OF WETLAND RESTORATION ON TERRESTRIAL SPECIES DIVERSITY AT THE BLAINE WETLAND SANCTUARY

Sam Mayes

Anoka Ramsey Community College

Kristen Genet (*Faculty Advisor*)

Location: **Room 2209, 1:00pm-1:20pm**

Discipline: Ecology

Wetlands are important components of ecosystems, contributing to biodiversity, water quality, flood prevention, and carbon sequestration. Recent studies show that nearly half of the global wetlands have been lost; less than 9% of earth's land area remains as wetland. One of the issues caused by this loss of wetlands is a reduction in wildlife abundance and diversity. This is due to a decrease in native plant biodiversity that supports life for many terrestrial species. The overall objective of this study was to determine wildlife use in a partially restored wetland in Blaine, MN. The hypothesis was that restoration of wetlands would increase the diversity of terrestrial species present by providing more suitable habitat conditions. The overall methodology of this research was to implement the use of camera traps to sample terrestrial species in the restored and unrestored areas of the Blaine Wetland Sanctuary. The numbers of species at each location were recorded, and statistical analyses were run to determine if there was a significant difference between the disturbed and undisturbed areas. Although the research is still in progress, preliminary analysis of the current data suggests that there are no significant differences between species diversity in restored compared to unrestored wetlands, but does suggest a relationship between specific camera location and diversity. However, these results will contribute to a larger database of wildlife use on a broader geographic scale to identify patterns of species diversity and habitat use. Overall, this was an exciting opportunity to observe wetland habitat degradation's negative side effects being reversed.

1:25pm-1:45pm

COMPARATIVE ANALYSIS OF BACTERIOPHAGE HOST RANGE BETWEEN GORDONIA, MYCOBACTERIUM, AND RHODOCOCCUS

Brendon Ghiringhelli, Tina Slowan-Pomeroy, Laura Briggs

Truckee Meadows Community College

Laura Briggs (*Faculty Advisor*)

Location: **Room 2208, 1:25pm-1:45pm**

Discipline: Microbiology

With the increasing incidence of infection by highly pathogenic, multi-drug resistant microbes, the need for alternative treatments is becoming dire. Bacteriophages, viruses with a typically strict species-specificity capable of rapidly infecting and killing bacteria, are being considered more seriously as an answer to antibiotic resistance. Although phage-based treatment has been used since the early 1900's, recently has it come to the forefront of consideration in the United States as a viable alternative to small-molecule chemotherapy. To date, two phage-based treatments have been FDA-approved. This research analyzes the ability of bacteriophage to cross-infect multiple bacterial hosts. Mycobacteriophage species isolated from northern Nevada soil samples and phage acquired through HHMI SEA-PHAGES were tested for their degree of cross-infection. More than 25 mycobacteriophages known to infect *M. smegmatis* were tested against *Actinobacteria* members *G. terrae*, *R. erythropolis*, and *M. tuberculosis*. Currently, several mycobacteriophage species have been identified as virulent against the latter three hosts.

LARGE DEGREE ASYMPTOTICS AND THE RECONSTRUCTION THRESHOLD OF ASYMMETRIC ISING MODEL ON REGULAR D-ARY TREES

Tengyi Wang, Wenjian Liu

Department of Mathematics and Computer Science, Queensborough Community College, City University of New York

Wenjian Liu (*Faculty Advisor*)

Location: **Room 2209, 1:25pm-1:45pm**

Discipline: Mathematics

BACKGROUND: Determining the reconstruction threshold of a broadcast models on d -ary regular tree, as the interdisciplinary subject, has attracted more and more attention from probabilists, statistical physicists, biologists, etc. However, rigorous reconstruction thresholds have only been established in a small number of models. Liu and Ning have established the critical condition of the asymmetric binary channel to make the Kesten-Stigum bound the reconstruction threshold on regular d -ary trees.

OBJECTIVE: The major purpose of this project is to establish the exact reconstruction threshold of the asymmetric Ising model on regular d -ary trees, when the Kesten-Stigum bound is not tight for the asymmetric channel. The second aim is to apply the numerical analysis to develop an algorithm of determining the concrete reconstruction threshold when the degree d is large enough.

APPLICATION: The reconstruction problem is concerned essentially with a tradeoff between noise and duplication in a tree communication network; phylogenetic reconstruction is a major task of systematic biology; reconstruction thresholds on trees are believed to determine the dynamic phase transitions in many constraint satisfaction problems including random K-SAT and random colorings on random graphs; the reconstruction threshold is also believed to play an important role in the efficiency of the Glauber dynamics on trees and random graphs.

METHODS: The first stage of this project is to show that when degree d is large the interactions between spins become very weak. Then using the Central Limit Theorem, we approximate this collection of small independent interactions to show that the reconstruction function can be approached by a new Gaussian approximation function $f(x)$; the second step is to display the properties of $f(x)$ by the knowledge of Calculus, including its differentiability, monotonicity, convexity, etc.; the third goal is to apply Calculus and MAPLE (math software) to explore first several major terms of the Maclaurin series of $f(x)$. Therefore, with the assistance of MAPLE again, we would be able to figure out the reconstruction threshold by discussing the fixed point of $f(x)$.

RESULTS: We find that, from calculation, as d increases the interactions of nodes on tree become weaker. This allows us to utilize the Gaussian approximation, and the approximation function $f(x)$ is continuously differentiable and increasing on the interval. After expanding the Maclaurin series of $f(x)$, we find that the quadratic coefficient is positive, which guarantees a fixed point near the origin. Eventually, this fixed point will generate the reconstruction threshold of asymmetric Ising model.

CONCLUSION: By means of a refined analysis of moment recursion on a weighted version of the magnetization, concentration investigation, and large degree asymptotics, we conclude that when the deviation of the asymmetric channel is large, the Kesten-Stigum bound is not tight any more. Furthermore, the threshold of the reconstruction is strictly less than 1. Last we develop an algorithm to figure out the exact threshold when the degree d is large enough.

STUDENT POSTER PRESENTATIONS
DECEMBER 1, 2017
11:00AM
HIGHLAND CAMPUS CORRIDOR

Arizona

SYMBIOTIC BACTERIA IN *AGAVE PARRYI*

N. Massoni, A. Bowser, M. Scaff, E. Ramirez, H. Vega, J. Riley, K. Durham

Cochise College, Sierra Vista, AZ

Kari M. Durham, (*Faculty Advisor*)

Display area: 1

For centuries, the cultivation of Agave genus plants in North America has centered around the production of alcoholic beverages. Recent exploration has shown that Agave could be a productive source of alcohol used as biofuel. However, agave plants are slow growing; the practicality of agave-based biofuels depends on the maximization of the plants' total ethanol yield. *Agave parryi* has higher sugar levels than other species of agave, which suggests an increased potential ethanol yield. *A. parryi* is also particularly well suited for arid and saline soils, even at cold temperatures. The yield can be further increased by manipulating and optimizing the composition of the symbiotic microbiome. The purpose of this study is to identify prokaryotic species in and around the roots of *A. parryi* plants that can increase nutrient uptake and accelerate plant growth. Agave root and surrounding soil samples were taken from a total of six *A. parryi* individuals at 2,813 meters elevation and 1,308 meters elevation. Comparisons between the bacteria species found at the two sites will help to deduce the impact of geography and climate on the microbial communities, as well as the microbial impact on the plants' survivability in various ecosystems. After grown and isolated on Tryptic Soy Agar plates, samples from each of the isolated colonies were amplified through polymerase chain reaction (PCR). The PCR primer pairs amplified the 16S region of the bacterial rRNA. The PCR product was then purified and sequenced. The sequence will then be used to run a BLAST in order to identify which species were isolated.

Hawaii

NEST SUCCESS, PARENTAL CARE AND CHICK GROWTH IN A TREE-NESTING SEABIRD ON THE KAPI'OLANI COMMUNITY COLLEGE CAMPUS

Katie Gipson, Wendy Kuntz

Kapi'olani Community College

Wendy Kuntz (*Faculty Advisors*)

Display area: **2**

The White Fairy Tern (*Gygis alba*) or the Manu-o-Kū, is a seabird indigenous to the Pacific and is listed as threatened by the State of Hawaii. In Honolulu, Hawaii the population breeds in urban settings using tree branches as nest sites. This study aims to document and quantify aspects of nest success, chick growth and parental care behavior. Starting in January 2016, nests on the college campus were observed to determine chick fate (n=52). Four chicks were photographed through a spotting scope from the time of hatching to fledging. Reference photos were obtained after fledging using a balloon carrying a cm ruler. Using imageJ software, the chicks' height, bill length, body length, tail length, and wing chord length were measured and growth rates were calculated. To characterize parental care behavior, two chicks were recorded on video; each for 24 hours a day for three weeks totaling over 1,000 hours of video. The majority of nests were successful (75%). Chick growth patterns the body, tail, and wing lengths grew at a steady rate while bill length and height showed a more stepped growth rate. Video recording analysis of parental behavior is ongoing, but a total of ~47 hours of video has been analyzed of one chick at 16 and 35 days old. Understanding the nesting behavior of the Manu-o-Kū will aid in protecting this species from threats in urban environments including feral cat, tree trimming, and overfishing in nearshore areas.

Indiana

ANTIBIOTIC-PRODUCING MICROBES FROM THE SOILS OF NORTH CENTRAL INDIANA

Pamela Arenas, Jayse Cruz, Amy Cuevas, William Drake, Baruch Elias, Kelly Harper, Cody Harrington, Alicia Hozey, Ramanjit Kaur, Michele Mayo, Miriam Lavey, Natasha MaCallister, Jorge Manay, Reva McCoy, Regan Miller, Earl Mullet, Kaitlin Nielsen, John Parroquin, Johnathan Potter, David J. Vega, David S. Vega, Milos Zoric

Kapi'olani Community College

George Twaddle (*Faculty Advisor*)

Display area: **3**

Many microbes have evolved anti-microbial compounds in their competition for resources in the soil. Among the class of antibiotics, some hold promise as the next generation drugs to fight present antibiotic-resistant human pathogens like MRSA. A wide variety of soil types were isolated for the presence of antibiotic producers by selection on soil-conditioned tryptic soil agar and screened for their ability to create zones of inhibition when grown in the presence of surrogates of MRSA (*Staphylococcus aureus*), *Pseudomonas aeruginosa* (*Pseudomonas putida*) and *Escherichia coli* 0157:H7 (*E. coli* C). Candidate antibiotic producers were isolated by streak plating and a tentative identification was performed catabolic pathway identification using the Enterotube II system followed by PCR and sequencing of 16S RNA genes. Non-hazardous microbes were tested for constitutive or inducible production of antimicrobial compounds by growth in regular broth culture or broth culture containing target organism conditioned medium. Each antibiotic was screened against a panel microbes to initially define their range of specificity and to a panel of known antibiotic resistant *E. coli* transformants to tentatively classify the type of antibiotic present. A series of experiments were performed to purify and identify the type of molecule exerting the antibiotic effect. It is our hope that we have isolated a new antibiotic that can prove safe and effective in treating antibiotic resistant pathogens presently threatening human health.

Minnesota

ENTEROBACTERIACEAE AND STAPHYLOCOCCUS FOUND IN MINNESOTA TIMBER WOLF FECAL SAMPLES TESTED FOR ANTIBIOTIC RESISTANCE: COMPARING PRIMARY WILD WOLVES, HUMAN-ADAPTED WILD WOLVES, AND CAPTIVE WOLVES

Taylor Borgman, Scott Danneman

Department of Biology, Anoka Ramsey Community College

Scott Danneman, Kristen Genet (*Faculty Advisors*)

Display area: 4

Wolves are classically said to be the last truly wild species left. Many of the North American Timber Wolves had been locally extirpated and have since been reintroduced in former parts of their range. Some packs, however, have begun to inhabit urban areas beyond their range. Ample ecological research has been conducted on these wolves in attempt to conserve their populations, but little research has been conducted on the antibiotic resistant (AR) bacteria they may carry due to human exposure. Antibiotic Resistance present in wildlife species are scarcely studied, but have suggested a strong correlation with human exposure. The expansion of AR bacteria from humans to wildlife has health implications for wildlife species and natural ecosystems, and requires extended studies. In this study, fecal samples have been taken from primary wild wolves, human-adapted wild wolves, and captive wolves in Minnesota. Bacteria in the family Enterobacteriaceae and genus *Staphylococcus* were collected, and tested for antibiotic resistance using the Kirby Bauer method. The antibiotics tested on these bacteria included Penicillin, Tetracycline, Streptomycin, and Ciprofloxacin. captive and human-adapted wild wolves are predicted be most antibiotic resistant due to previous studies indicating direct correlation between humans, animals, and the expansion of AR bacteria.

THE EFFECT OF BUFFER ZONES, FLOWER VARIETY, AND FLOWER COVERAGE ON BENEFICIAL POLLINATING INSECTS

Meg Gable, Melanie Waite-Altringer

Anoka Ramsey Community College – Department of Biology

Melanie Waite-Altringer (*Faculty Advisor*)

Display area: 5

Over 120 counties realize the important role pollinators have in our global economy; yet the crisis of their decline continues. Combating the negatives effects of pesticides and herbicides along with protecting and restoring habitat is vital to supporting these species into a healthy future. The purpose of this study was to compare the positive effect of various flowering environments on the population and diversity of beneficial pollinating insects. The main question addressed was: “Does the variety of flowering plants, in buffer and non-buffer zone areas, effect beneficial pollinating insect counts?” The prediction was that if the variety of flowering plants in buffer and non-buffer zones influence beneficial insect counts, then a site planted in the buffer zone, with the greatest diversity of flowering plants, would attract a greater variety (eH’) and higher counts of beneficial pollinating insects. Insect counts were gathered at three sites of various acreages every 5-7 days from June 29 until July 31, 2017. Data analysis indicates that an increase of plant variety did not have a significant impact on the quantity or variety of pollinators, but an increase of flowering plant coverage did increase the variety of beneficial pollinating insects with the greatest amount of pollinating insects being at the buffer zone.

THE EFFECT OF WETLAND RESTORATION ON TERRESTRIAL SPECIES DIVERSITY AT THE BLAINE WETLAND SANCTUARY

Sam Mayes

Anoka Ramsey Community College

Kristen Genet (*Faculty Advisor*)

Display area: 6

Wetlands are important components of ecosystems, contributing to biodiversity, water quality, flood prevention, and carbon sequestration. Recent studies show that nearly half of the global wetlands have been lost; less than 9% of earth's land area remains as wetland. One of the issues caused by this loss of wetlands is a reduction in wildlife abundance and diversity. This is due to a decrease in native plant biodiversity that supports life for many terrestrial species. The overall objective of this study was to determine wildlife use in a partially restored wetland in Blaine, MN. The hypothesis was that restoration of wetlands would increase the diversity of terrestrial species present by providing more suitable habitat conditions. The overall methodology of this research was to implement the use of camera traps to sample terrestrial species in the restored and unrestored areas of the Blaine Wetland Sanctuary. The numbers of species at each location were recorded, and statistical analyses were run to determine if there was a significant difference between the disturbed and undisturbed areas. Although the research is still in progress, preliminary analysis of the current data suggests that there are no significant differences between species diversity in restored compared to unrestored wetlands, but does suggest a relationship between specific camera location and diversity. However, these results will contribute to a larger database of wildlife use on a broader geographic scale to identify patterns of species diversity and habitat use. Overall, this was an exciting opportunity to observe wetland habitat degradation's negative side effects being reversed.

Nevada

COMPARATIVE ANALYSIS OF BACTERIOPHAGE HOST RANGE BETWEEN GORDONIA, MYCOBACTERIUM, AND RHODOCOCCUS

Brendon Ghiringhelli, Tina Slowan-Pomeroy, Laura Briggs

Truckee Meadows Community College

Laura Briggs (*Faculty Advisor*)

Display area: 7

With the increasing incidence of infection by highly pathogenic, multi-drug resistant microbes, the need for alternative treatments is becoming dire. Bacteriophages, viruses with a typically strict species-specificity capable of rapidly infecting and killing bacteria, are being considered more seriously as an answer to antibiotic resistance. Although phage-based treatment has been used since the early 1900's, recently has it come to the forefront of consideration in the United States as a viable alternative to small-molecule chemotherapy. To date, two phage-based treatments have been FDA-approved. This research analyzes the ability of bacteriophage to cross-infect multiple bacterial hosts. Mycobacteriophage species isolated from northern Nevada soil samples and phage acquired through HHMI SEA-PHAGES were tested for their degree of cross-infection. More than 25 mycobacteriophages known to infect *M. smegmatis* were tested against *Actinobacteria* members *G. terrae*, *R. erythropolis*, and *M. tuberculosis*. Currently, several mycobacteriophage species have been identified as virulent against the latter three hosts.

SUPERINFECTION IMMUNITY ANALYSIS OF BACTERIOPHAGES USING THE MYCOBACTERIUM SMEGMATIS XENO LYSOGEN

Eric Lundin II, Tina Slowan-Pomeroy, Laura Briggs, Ph.D.

Truckee Meadows Community College

Laura Briggs, Ph.D. (*Faculty Advisor*)

Display area: 8

This research project involves Xeno, a lysogenic Cluster N Bacteriophage (phage), using *Mycobacterium smegmatis* as a host. Xeno encodes for several proteins that are expressed from the latent form of the phage. These proteins may prevent superinfection, an event where multiple phage infect a single bacterial host. Normally lysogens are immune to superinfection by repressor-mediated superinfection immunity. The repressor prevents gene transcription of the latent phage. Xeno is immune to all cluster N phage superinfection discovered to date and several phages that use closely related immunity systems. Lysogens of Cluster N phages, however, have shown defense immunity or resistance to other phages that are not of the same cluster. This could be caused from superinfection exclusion where a putative membrane protein that confers defense against Che9c infection, or from Abortive infection, a Type II Toxin-Antitoxin system. All phages within our database are being evaluated for superinfection immunity or inhibition of 10^4 or greater. Future research would include sequencing and exploring the genomes of the phages to discover the cluster of the inhibited phages, the genes involved in superinfection immunity, and the mechanism of inhibition.

New Mexico

MOLECULAR SYSTEMATICS OF PIÑON PINE, *PINUS EDULIS*, IN CENTRAL NEW MEXICO

Genaro Duran

University of New Mexico – Valencia Campus

Benjamin Flicker (*Faculty Advisor*)

Display area: **9**

We are analyzing DNA from piñon pine, *Pinus edulis*, to find gene regions with greater variability. Piñon pines have economic value, yet the molecular systematics are not well known due to less abundant gymnosperm sampling in comparison to angiosperms. We have so far obtained 16 samples of piñon pines. Six from the western foothills of the Sandia Mountains, three from Water Canyon, three from Jemez Springs, two from Tijeras Canyon Trail, and two from 4th of July Campground in the Manzano Mountains. We will sequence the DNA for five gene regions. Three are from the chloroplast: *ycf1A*, *ycf1B*, and *rpoB-trnC* and two are from the mitochondria: *nad4/3-4* and *nad5* (intron 1). We will perform phylogenetic analysis after sequencing the gene regions to determine the utility of those gene regions for phylogenetic analysis of *P. edulis*. Distribution maps will be provided.

PALEOCLIMATE INVESTIGATIONS OF PALEOSOLS FROM THE TAOS PLATEAU, NEW MEXICO, USA

Gage R. Lamborn, April R. Bates

University of New Mexico – Valencia Campus

Victor French, M.S., Kevin Hobbs, Ph.D. (*Faculty Advisors*)

Display area: **10**

Paleosols can record the history of the climate conditions under which they formed. We are investigating two paleosols from the Taos Plateau (northern New Mexico, USA) in an attempt to learn what the paleoclimate may have been at the time of soil formation on the Servilleta Basalt, which was erupted at 3.6 to 4.5 Ma. One of the paleosol horizons has a Munsell color of 5YR 5/6, a color normally associated with pedogenesis under more humid conditions than currently exist on the Taos Plateau. To accomplish this, we will determine the chemical and mineral compositions of the samples. We will determine the chemical composition using X-ray fluorescence spectroscopy analysis (XRF). X-ray diffraction analysis (XRD) and optical microscopy will be used to determine sample mineral composition. Here we present data on the physical and morphological properties of two Servilleta Basalt paleosols. To determine the paleoclimate conditions under which the paleosols formed we will perform a geochemical climate analysis. Geochemical climate analyses of basalt-hosted paleosols have been used with success to determine paleoclimate conditions in other settings. Given the geological simplicity and good preservation of these paleosols, we are hopeful that the same analyses will lead to an increased understanding of Taos Plateau paleoclimate conditions during the Pliocene Epoch.

MEDICINAL PLANT EXTRACTION AND ANALYSIS

Shania Sanchez

The University of New Mexico-Valencia

Victor French, M.S., Tracy J. Terry, Ph.D. (*Faculty Advisors*)

Display area: **11**

We have begun a survey of the medicinal properties of common plants of the southwest. Traditional healers have used plants for ages while more recent efforts have yielded the isolation of plant pharmaceuticals such as aspirin, quinine, and paclitaxel. The essential oil industry is expected to double in market value between 2015 and 2022 due to increased consumer awareness of the health benefits of natural personal care products. For this study, steam distillation of essential oils and solvent extractions have been carried out on various locally sourced plants. These extracts have been analyzed for antibacterial properties via Kirby-Bauer assay using *Escherichia coli* and *Staphylococcus aureus* on Mueller Hinton agar and Tryptic Soy agar. Zones of inhibition were measured and compared to controls Ciprofloxacin, Penicillin, and a blank BBL disk. Extracts have shown antibacterial properties via Kirby-Bauer assay. Other assays for biological activity will be conducted in the future. As active agents are found, their compounds will be further isolated, identified, and analyzed for possible synergistic effects.

ANALYSIS OF *SMILODON* SPECIMENS SHOWS EVIDENCE OF PACK LIFE

Eva Sawyer

Mesalands Community College, Tucumcari, NM

Gretchen Gürtler (*Faculty Advisor*)

Display area: **12**

Smilodon fatalis was a felid from the Pleistocene. Despite being abundant throughout the southern part of North America, there is much that is not known about these animals. Comparative analysis to modern felids can improve understanding of how these animals lived. Examination and research helps to determine if *Smilodon* behaved like modern pack felids. Research was conducted using two specimens from Mesalands Community College Dinosaur Museum's (MCCDM) collection. Both specimens were found in the LaBrea Tar Pits of California. Utilizing formulas by Robert Fenerac, the dentition was examined to determine age. Analysis of isotope evidence provided by Blair Van Valkenburg narrowed preferred prey to *Camelops* and *Bison antiquus*. Finally, the comparison of skeletal structure to modern felids gave evidence of animal size and movement. The examination of these specimens determined that these animals were large and stocky, and moved more like bears than cats. It was difficult for them to run long distances; ambush tactics were more effective. Dentition evidence shows that the MCCDM specimens were young adults, at least one under its mother's care. A healed fracture on the scapula of the younger cat, supports the hypothesis that this animal was cared for by others. Lack of enamel wear or breakage on the teeth indicates that these animals did not chew on bone. Since the preferred prey were so sizable, a single cat would have risked great injury if hunting alone. Combined, this evidence supports the idea that *Smilodon fatalis* was a pack animal.

New York

MICROBIOMES ASSOCIATED TO PLANT ROOTS IN NYC SOIL

Edward Nouel, Monica Trujillo, Ph.D.

Biological Sciences and Geology, Queensborough Community College, CUNY

Monica Trujillo, Ph.D. (*Faculty Advisor*)

Display area: **13**

The microbial community in an urban setting can have important implications for human health. The soil can harbor up to 10¹⁰ bacterial cells per gram, and city dwellers use parks for entertainment and outdoor activities. We are interested in characterizing the microbiomes associated to plant roots in NYC parks. On previous work done by our group we characterized the structure of the microbial community associated with roots of plants from three contrasting sites in New York City: the Thain family forest at the New York Botanical Garden which is a pristine forest, the marshes in Newton Creek which are heavily contaminated soil and Central Park a green space exposed to pollutants. The diversity and composition of the soil community were analyzed using primers specific to the 16S rRNA gene. As a preliminary assessment of the possible implications for human health, we have characterized each microbiome by analyzing the distribution of antibiotic resistance genes using PCR. We are also interested in studying the distribution of metal resistance genes using PCR. We have used degenerated primers for the *czcA* gene to identify the bacterial communities that carry this gene. To identify the bacterial species coding for this gene, we have cloned the PCR fragments and will sequence them. To correlate the presence/absence of metal resistance genes with the metals present in the soil samples we will chemically determine the concentration of certain metals in the soil. This project has already shed light on the influence of human activity on the distribution of both antibiotic and heavy metal resistance genes. Additionally, the determination of the metal concentration in soil and the identification of the bacteria species that carry the corresponding resistance gene will identify the bacterial species present in soil that can tolerate the metal concentration associated with urban sites.

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Tengyi Wang, Wenjian Liu

Department of Mathematics and Computer Science, Queensborough Community College, City University of New York

Wenjian Liu (*Faculty Advisor*)

Display area: **14**

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RESULTS: We find that, from calculation, as d increases the interactions of nodes on tree become weaker. This allows us to utilize the Gaussian approximation, and the approximation function $f(x)$ is continuously differentiable and increasing on the interval. After expanding the Maclaurin series of $f(x)$, we find that the quadratic coefficient is positive, which guarantees a fixed point near the origin. Eventually, this fixed point will generate the reconstruction threshold of asymmetric Ising model.

CONCLUSION: By means of a refined analysis of moment recursion on a weighted version of the magnetization, concentration investigation, and large degree asymptotics, we conclude that when the deviation of the asymmetric channel is large, the Kesten-Stigum bound is not tight any more. Furthermore, the threshold of the reconstruction is strictly less than 1. Last we develop an algorithm to figure out the exact threshold when the degree d is large enough.

North Carolina

FRESHWATER SPONGES IN THE PIEDMONT REGION OF NORTH CAROLINA

Ellie Armstrong

Gaston College

Joshua Mays (*Faculty Advisor*)

Display area: **15**

Freshwater sponges are an invertebrate found in clean, slow-moving bodies of water. They are filter feeders and use gemmules as a form of asexual reproduction. They are believed to be bio-indicators of water quality. It is unclear if they have previously been found in our region. We are working to determine if the waterways in the western piedmont of North Carolina can maintain a population of freshwater sponges. Using a continuous flow system to grow gemmules, we will determine which water samples from our area are conducive to the growth of sponges. Sponges collected in our region will be analyzed using PCR and DNA sequencing to identify their species. Water quality testing will be conducted in regions where sponges are observed.

HAIR PIGMENTATION IN CONNECTION WITH THERMAL SENSITIVITY: REDHEADS FEEL MORE INTENSE COLD

Natalie Belcher, Hisayo Tokura-Gallo

Gaston College

Hisayo Tokura-Gallo (*Faculty Advisor*)

Display area: **16**

The purpose of this research is to investigate whether the proteins that cause hair color have an effect on pain tolerance. Melanocortin-1 Receptor is a receptor involved in pigmentation control. There are two pigments, Eumelanin (darker pigmentation) and Pheomelanin (blonde and red). The color of hair is determined by the amount of these pigments. When MC1R is mutated, the receptor sends signal for a large amount of Pheomelanin. This overflow pigmentation is what causes red hair. This mutation also affects pain perception by sending altered signals along neural pathways, and increasing stimuli in redheads. To test this, subjects placed their hands in 40 degree ice water until they could not tolerate the pain. The results of the tests was that brunettes have the highest pain tolerance, followed by blondes with a wide margin, and redheads had the lowest thermal pain tolerance. The redhead's thermal pain intolerance may be caused by either heightened pain perception or heightened sensitivity to temperature change. The sequential study focused on finding out whether hair pigmentation is related to thermal sensitivity. The results will show that redheads overestimate how cold the water is or brunettes underestimating the cold temperatures.

EFFECTS OF HABITAT ON THE LIFE HISTORY TRAITS OF BLUEGILL SUNFISH (*LEPOMIS MACROCHIRUS*)

Keyla Davis, Nicholas Zuleg, Shannon Stephens, Joshua Mays, M.S.

Gaston College

Joshua Mays, M.S. (*Faculty Advisor*)

Display area: **17**

Phenotypic plasticity (morphological variance based on environmental pressures, including habitat) is a well-documented phenomenon. This research was conducted to quantify phenotypic plasticity for bluegill sunfish (*Lepomis macrochirus*) across habitat types as well as to document its occurrence in Southcentral North Carolina. Bluegill were collected via sport fishing from Jan-April, 2017 from two different habitat types: a river and a pond. Specimens were divided into like-age groups and analyzed for length, mass, and body depth. Data indicate that there is a significant difference in length, mass, and depth ($p < 0.05$) across habitat types. These results may be useful for fisheries managers in policy development. Future research may focus on variance in the development of bluegill taken from similar habitats.

QUALITY OF ROMANTIC RELATIONSHIPS AND WELL-BEING

Hannah Matthews, Hisayo Tokura-Gallo, M.S.

Gaston College

Hisayo Tokura-Gallo, M.S. (*Faculty Advisor*)

Display area: **18**

Many research on marital relationship quality and its effect on stress report that there is a high correlation between how one feels about their partner in marriage and their overall stress level. In general, the more negative they feel about their partner, the higher their stress level is. However, it is often difficult to discern what types of romantic relationships tend to exhibit higher stress. In this research, participants are asked to identify their romantic relationship type based on Gottman's five relationship types and to take Cohen's Perception of Stress Scale. The correlation will be analyzed. In addition, this research will include non-married couples (i.g., boyfriend/girlfriend and cohabitating couples), since many millennials choose to delay getting married, but are in romantic relationships, and homosexual couples. We expect to find higher perceived stress in hostile couples and volatile couples, while validating couples showing lower perceived stress. Conflict-avoiding and hostile detached couples may show somewhat in-between stress level. We'll also analyze whether sexuality of the couple (heterosexual vs. homosexual) show different stress level.

Oklahoma

VIABILITY ASSAY & POTENTIAL EFFECTS OF E-JUICE ON CHO-K1 CELLS

A. Brown, K. Casey, A. Eberhard, C. Eslinger, S. Grace, A. Hughes, D. Johnson, A. Kennedy, S. Laughlin, C. Longden, K. Smith, D. Sloan

Tulsa Community College, Biotechnology

Dusti Sloan (*Faculty Advisor*)

Display area: **19**

Electronic cigarette (E-cigarette) use has dramatically increased in recent years, and in-depth studies testing the toxicity of E-liquid components have not been performed. Given the lack of data to support the safety of E-cigarettes, the goal of our project was to determine if E-liquid components are detrimental to the growth of Chinese hamster ovary (CHO) cells. CHO Cells were plated and incubated for 48 hours in control media, media containing E-liquid base, nicotine, or cinnamon flavoring. An MTT viability assay was used to determine the cytotoxicity of E-liquid components on cells. There was a significant difference in the viability of cells grown in the different E-liquid components. Results were inconclusive, however, because there were differences in viability between the two control wells; viability values for identical treatments should not be different. Additionally, there were similar differences in viability in the two wells containing the same nicotine media. Upon further investigation, we found a direct correlation between cell death and proximity to cinnamon flavoring; cell viability improved with increasing distance from wells containing the cinnamon flavor. Additional testing will need to be performed to determine if E-liquid base and nicotine are toxic cells. In summary, E-liquid cinnamon flavoring is toxic to CHO cells and additional testing on E-liquid components should be carried out given the substantial use of E-cigarettes.

UTILIZING CYTOCHROME C OXIDASE I (*COI*) FOR MICROGENOMIC IDENTIFICATION OF OSTEICHTHYES OBTAINED FROM RURAL AND URBAN PONDS IN THE OKLAHOMA CENTRAL PLAINS

A. Brown, A. Eberhard, C. Eslinger, M. Gates, M. Hilton, D. Johnson, A. Kennedy, A. Platt, S. Sandoval, D. Spencer

Tulsa Community College

Diana Spencer, Dusti Sloan (*Faculty Advisors*)

Display area: **20**

DNA barcoding provides an effective method for individual identification of species using specific molecular tags derived from the mitochondrial cytochrome c oxidase I (*COI*) gene. Taxonomists are only able to identify 0.01% of the 10-15 million species on the planet. DNA barcoding, or microgenomic identification, is an alternative to using morphology in taxonomy. The aims of the study included: i) analysis of number and diversity of individuals and species in the two ponds; ii) lab process analysis of sample loss and concentration of extracted DNA for successful PCR; iii) and an evaluation of fresh water and salt water fish phylogenetic divergence using freely available software. Biodiversity information was used as a monitoring tool for the area on the Southeast Campus of Tulsa Community College. Specimens were collected from two locations, both a rural and urban pond, and identified by national wildlife conservation workers before being harvested. The collected sample DNA was obtained through a lysing procedure, then amplified using published primers for PCR. The product was verified on an agarose gel, then purified using the EZNA Cycle Pure Kit. Nine samples, three of each species of fish, were sent to be bi-directionally sequenced. Sequences were trimmed using FinchTV and aligned using Muscle in Mega7. Each of the 3 species included in the experiment possessed a different amino-acid sequence at *COI* and diverged from the salt water specimens. While 87% of the total number of fish were found in the smaller rural pond, a greater variety of fish were located in the urban pond. Two successful PCR amplifications were derived from less than 50% of the published concentration needed, and in our hands, only four samples were lost from 24 secured in the field.

STUDENT POSTER PRESENTATIONS
DECEMBER 1, 2017
2:00PM
HIGHLAND CAMPUS CORRIDOR

Arizona

THE EFFECT OF HUMAN PRESENCE ON WILDLIFE ACTIVITY ALONG THE ARIZONAN U.S.-MEXICO BORDER

M. Scaff, N. Massoni, A. Bowser, M. Buono, H. Vega, J. Riley E. Priddis

Cochise College, Sierra Vista, AZ

Edmund Priddis (*Faculty Advisor*)

Display area: **1**

Southeastern Arizona is one the most biodiverse areas in all of North America due to its unique position at the convergence of four major deserts and the presence of mountain ranges scattered throughout the semi-arid landscape called “sky islands.” The unique biodiversity is enhanced as the region sits on the border between two countries. Many of the species found here are at the northernmost reach of their range, and within this region are a number of waterways that transverse the border and may act as an important corridor for species movements. Human activity along the border between the two countries could potentially have significant impacts on the wildlife in this area. This study compares the activity of species “captured” at sites on federal conservation lands in the U.S. and sites in Mexico, that lie within the border region, to the human activity also “captured” in these locations. High output covert infrared detecting camera traps were deployed at each of the sites in the U.S. and Mexico. Pictures were gathered from March 2015 through November 2017. The relative abundance of species at each location, seasonal variations in species’ abundance, and species pair activity similarity was examined.

New York

IMPACT OF WATER QUALITY ON BACTERIAL DIVERSITY IN THE LONG ISLAND SOUND REVEALED BY METAGENOMICS

Sakina Makwana, Sarah Jankowski

LaGuardia Community College

Maria Entezari, Ph.D., A. Lucia Fuentes, Ph.D. (*Faculty Advisors*)

Display area: **2**

The Long Island Sound estuary is an important resource for NY State. The diverse microbial community in the Sound impacts the ecosystem in surrounding areas. High levels of Enterococci have been reported indicating poor water quality, yet information regarding the unculturable microbial community in these waters is scant. Water of the Sound is a mix of freshwater and ocean water from the east and west. Our study compared microbial communities and physicochemical parameters of East River-ER- (west) and Oyster Bay-OB-(east). Based on EPA data, as well as increases in population and industrial activities in the west side of Long Island Sound, we hypothesized that relative abundance and diversity in bacterial communities would differ in these two areas due to higher pollution in ER and hypoxia in OB. To test our hypothesis, we isolated DNA from samples collected in each area, and 16S DNA was amplified by PCR, sequenced, and analyzed (AREM project). We also determined physicochemical properties, including temperature, pH, salinity, Dissolved Oxygen (DO), and CO₂, using commercial kits. Our findings partially supported our hypothesis; the most abundant bacterial groups were Chloracidobacteria for OB, and Oxalobacteracea, Croptococcus and Xanthomonales for ER. OB presented greater alpha diversity than ER, which could be partially attributed to higher DO in OB. Our data on the bacterial community offer insight into the effects of changes due to pollution and climate change on marine life, underlining the importance of proper legislation to ensure recovery and maintenance of water quality.

North Carolina

BACTERIAL ANTIBIOTIC SECRETIONS TESTED FOR EFFECTIVENESS AGAINST COMMON PATHOGENIC BACTERIA

Brandon Miles, Cliff Grimsley, M.S.

Gaston College

Cliff Grimsley, M.S. (*Faculty Advisor*)

Display area: **3**

Antibiotic resistance is a rapidly growing issue not just here in the United States, but around the world. This is due to the abuse of antibiotics, and with this comes a lack antibiotics that can effectively kill bacteria. With the prominent issue of antibiotic resistance getting worse, we believe a possible answer can come from the bacteria itself. Our hypothesis states the next highly effective anti-biotic could be synthesized from a bacterium. To test our hypothesis, we selected several soil samples from around the base of two different species of trees. We cultured the bacteria from the soil and tested the cultured bacteria against four common pathogenic bacteria: *Staphylococcus aureus*, *Pseudomonas putida*, *E. coli* and *Klebsiella pneumoniae*. Antibiotic secretors were found in several of our diluted soil samples. We subjected the cultured bacteria to a barrage of test with the intent of finding their Genus and species. Our results show there could be an untapped abundance of antibiotics in the bacteria themselves.

ANTIBIOTIC RESISTANCE IN PRIMARY AND SECONDARY EFFLUENT WASTEWATER

Mersadie Moore, James Young, Paris Covington

Gaston College

Susan Whittemore (*Faculty Advisor*)

Display area: **4**

Through the testing of wastewater from two wastewater treatment facilities in Gastonia, North Carolina, Long creek and Crowders creek, we hypothesize that the bacteria in Long Creek will have a higher resistance of antibiotics, including Ciprofloxacin, Ampicillin, Erythromycin, Streptomycin, and Tetracycline, than Crowders Creek because Long Creek receives wastewater from a hospital. Currently, both sites do not test for or remove antibiotics in the wastewater. After diluting several solutions of wastewater on both Primary and Secondary effluent sample from both sites, we plated the samples on LB broth agar and treated them with the antibiotics. The samples were then places on Master spread patch plates for continues observation. All of the samples were analyzed using PCR and RFLP in order to isolate the 16S rRNA of the microbes. Afterwards, 1492R and 27F primers were added and the samples were amplified using PCR. The samples were streaked onto plates containing one of the antibiotics. The Zones of inhibition were measured for each of the bacterial species. Comparisons were made between both the Crowders Creek and Long Creek sites in order to determine significant differences in the resistance of antibiotics. Upon completion, all of the samples that contained pure DNA product were sent to Yale University in order for the DNA to be sequenced and identified.

IDENTIFYING THE ANTIBIOTIC RESISTANT FACTORS OF *E. COLI*, *S. AUREUS*, AND *K. PNEUMONIAE* AGAINST ERYTHROMYCIN

Jessica Speckman, Zoe French, Grace Goins

Gaston College

Ashley Hagler (*Faculty Advisor*)

Display area: 5

Current antibiotics, such as Erythromycin, are becoming ineffective against major bacterial strains as the bacteria develops factors of resistance either in the genome or an additional plasmid. The antibiotic Erythromycin will be used with the bacteria *Escherichia coli*, *Staphylococcus aureus*, and *Klebsiella pneumoniae* chosen for this experiment. The purpose is to determine the factors and mutations that develop in the chosen bacteria when placed in increasing increments of antibiotic concentration in the self-made agar. The first set of bacteria colonies are controls which will be incubated then placed into a broth, then further incubated for more growth to easily observe the DNA of the control set. Increments will increase by .1% starting at .1% Erythromycin in the LB agar, the colonies of each respective bacteria being pulled from the preceding step. 3 plates of antibiotic increments, 1 broth of the same antibiotic increment, and 1 control plate of 0% antibiotics are incubated for each bacteria at each step up in increments. The broth created for each increment will be used to grow a large amount of that strain of bacteria, allowing for a large sample when testing for DNA. After being tested, each bacteria increments will be separately compared to the other samples of the same type of bacteria. The segments of the genome, or in alternative cases the plasmid, of each bacteria known to mutate in the presence of an antibiotic will be specifically compared to simplify the scope of the genome comparison. In the case where a mutation is located outside of that commonly mutated genome or plasmid, further observations of the data and research will be performed to identify another common, or possibly new, form of mutation in the bacteria selected against Erythromycin.

ANTIBIOTIC RESISTANCE IN WASTEWATER

Nicholas M. Tallent, Matthew Moore, Susan Whittemore, M.S.

Gaston College

Susan Whittemore, M.S. (*Faculty Advisor*)

Display area: 6

Our observations, have led us to the hypothesis that due to the larger human population that utilizes the Long Creek treatment plant in contrast to Crowders Creek, they will have a higher concentration of anti-biotic resistant bacteria within their wastewater. Due to the fact that these antimicrobial compounds do not metabolize completely within humans, they are passed into the wastewater treatment plants. Both Primary and Secondary wastewater samples were obtained from these treatment plants and tested for anti-biotic resistant bacteria. After several dilution trials were conducted on the Primary and Secondary effluent samples from both treatment plants, they were plated and incubated. Water samples were analyzed from each site, while being plated on LB broth agar plates that have been treated with cycloheximide. Master spread patch plates were created for the water samples taken. Individual colonies underwent extraction of the 16S region of ribosomal DNA, samples underwent PCR for amplification. During the study, the bacteria colonies were tested for resistance against the following antibiotics: Ampicillin, Erythromycin, Streptomycin, and Tetracycline. After the observations were completed, samples were sent to the DNA analysis facility in Yale University for Sanger sequencing. The samples were applied to plates containing antibacterial disc including: Ciprofloxacin, Streptomycin, Erythromycin, Tetracycline, and Ampicillin. The bacteria species were measured for their zones of inhibition and recorded. A statistical analysis was used to see if the difference in anti-biotic resistance between the plants was statistically significant.

TOXICITY OF ROBENACOXIB TO *DAPHNIA MAGNA*

Christian J. Williams, Joshua Mays, M.S.

Gaston College

Joshua Mays, M.S. (*Faculty Advisor*)

Display area: 7

The effect of veterinary medications—specifically antibiotics—on the environment has become a big issue over the past several years. Research focused on this issue suggests that antibiotics in the environment help create antibiotic-resistant bacteria, which are a danger to the health of humans and animals alike. Although steps are being taken to mitigate or prevent these indirect adverse effects of antibiotics, there remains a need to assess alternate environmental risks associated with new veterinary medications as they come on the market. Our research aims to quantify the direct threat that Robenacoxib, a veterinary non-steroidal anti-inflammatory drug (NSAID) used for post-operation inflammation and pain control, poses to aquatic environments. The ecological significance of *Daphnia magna* as well as their use as an indicator species for environmental health is well established in the literature. In this experiment varying concentrations (0, 30, 60, 120, and 150 mg/L) were prepared by dissolving oral Robenacoxib tablets into distilled water. In each solution, 10 juvenile *Daphnia* were selected at random from a controlled environment and placed into test solutions for 48 hours. Reactions of *Daphnia* to the treatment were monitored and recorded every 24 hours. Percent survival was recorded at the conclusion of each trial and was used to calculate LC50 values for *Daphnia*. The results of this study suggest that Robenacoxib is lethal to ecologically important aquatic organisms at relatively high concentrations. Future research should focus on realized environmental effects caused by increased mortality to important aquatic organisms.

Tennessee

DOCUMENTATION OF WILDLIFE IN MIDDLE TN: A LIFE CYCLE OF THE WHITE TAIL DEER *ODOCOILEUS VIRGININUS*

Matthew Hayden, States Labrum, Levi Guzman

Columbia State Community College

Elvira Eivazova, Ph.D. (*Faculty Advisor*)

Display area: **8**

The aim of this project was to examine the life cycle of white tail deer in the Middle Tennessee area using multiple infrared camera traps. The data was collected during spring, summer and fall of 2017. We analyzed the frequency of visits, time of attendance during day and night, the age and gender representation, and inter-species behavioral characteristics. We also investigated the effects of weather and presence of food, such as natural vegetation and shell corn bates, on deer activities. At the start of the project, we observed the newborn deer, called fawns, born in the spring or early summer. It was noted that a fawn is covered in white spots and able to walk after birth. The spots help camouflage the fawn from predators and remain for the duration of the first year. Male deer, called bucks, and female deer, called does, stayed with the mother for most of the observation period. Young males have very small or nonexistent antlers, but grow them fast; we were able to monitor their rapid development. The feeding of the deer took place mainly at dawn and dusk. We didn't observe a lot of deer activity during daylight hours. A female and her fawns usually stay together as a unit or graze together with other females, but bucks grazed together in herds of 3-5. The rate of antler growth was the most prominent feature of the buck's developmental changes.

THE EFFECTS OF LONG TERM SOIL WARMING ON SOIL RESPIRATION AND CARBON STORAGE

States Labrum

Columbia State Community College, Harvard Forest Summer Research Program

Elvira Eivazova, Ph.D. (*Faculty Advisor*)

Display area: 9

Our research objective was to investigate the relationship between long term soil warming and subsequent soil carbon release into the atmosphere, within the context of the impact of global warming. Currently, soil organic matter (SOM) holds the largest carbon pool in the terrestrial ecosystem. The rise of global temperatures accelerates microbial respiration and potentially increases carbon release from the soil. Here, we conducted soil warming experiments to examine how various soil temperatures affect carbon release through soil microbial respiration, and whether the soil microbes may compensate for the effects of rising temperatures by the phenomenon of thermal acclimation. Our field experimental results showed a pattern of decreased soil respiration in the heated plots relative the control plots. To understand what factors drive thermal acclimation, we incubated heated and control soil samples at six separate temperatures (6°C-36°C) in the laboratory. We found that the relationships between temperature and respiration were similar in field and laboratory data. The observed decrease in microbial biomass in heated soils caused the decrease in respiration relative to controls. Additionally, to remove potential bearing of substrate limitation, we amended the soils with sucrose which further minimized the difference in respiration between treatments. The results indicated that microbial biomass and substrate limitations are the factors primarily responsible for thermal acclimation, correlating with the prior conducted 26-year long experimental observations. We hypothesized that structural and functional changes in soil microbial communities drive the patterns of thermal acclimation of SOM decomposition, directly impacting soil carbon release.

Texas

IDENTIFICATION OF ANTIBIOTIC RESISTANT *OCHROBACTRUM INTERMEDIUM* AND THE UTILIZATION OF BACTERIOPHAGE IN CELL LYSIS

Tara L. Clancy, Damien Seay, J. Robert Hatherill, and D. Zhang
Natural Science Department, Del Mar College, Corpus Christi, TX
Daisy Zhang (*Faculty Advisor*)
Display area: **10**

Ochrobactrum intermedium, a gram-negative, rod shaped, and non-lactose fermenting opportunistic pathogen, has long been known to infect animals and immunocompromised humans, especially those that are hospitalized and/or have recently undergone surgical procedures. In the hopes of discerning potential antibiotic resistance and bacteriophage susceptibility as an alternative to current infection treatment, a number of assays were performed on an *O. intermedium* isolate obtained from soil located near the Animal Rehabilitation Keep (ARK) in Port Aransas, Texas, including 16S rRNA sequencing to determine the species, Kirby-Bauer antibiotic resistance assays, predatory phage isolation and purification, phage DNA isolation, restriction digests of phage genetic material, and lysogeny assays. Moreover, transmission electron microscopy (TEM) was performed in order to visualize the isolated phage which use *O. intermedium* as a host for replication. As a result of these experiments, various degrees of resistance were observed to six of the eight antibiotics used, and the isolated bacteriophage was shown to produce lysogens that incorporate viral genetic material into their own genome. Continued research will allow for the sequencing and annotation of the aforementioned phage genome and the potential development of a bacteriophage solution to help combat *O. intermedium* infections in both humans and animals – particularly native aquatic species – as an alternative to traditional antibiotic treatments.

COULD TYPHOID MARY HAVE BEEN A CARRIER FOR CYSTIC FIBROSIS

Alexis Custer
Lone Star College
Julie Harless (*Faculty Advisor*)
Display area: **11**

Cystic Fibrosis is a genetic disorder that causes the mucosal lining of the organs to become thick and sticky, potentially blocking the airways and causing respiratory problems. But it also has an evolutionary advantage: when a person has only one copy of the mutant CFTR gene, it stops the binding of typhoid bacteria to the intestinal wall, thus blocking *Salmonella typhi* infection. (American Lung Association, 2010; Poolman & Galvani, 2006; Pier, 1998). I propose that Typhoid Mary may have had cystic fibrosis. I have taken an interdisciplinary approach to researching this question by looking at the genetic, biological, and historical evidence.

ANALYTICAL OPTIMIZATION OF PHARMACEUTICAL TREATMENT FOR GLIOBLASTOMA MULTIFORME USING FLOW CYTOMETRY

Mike Delisi

Austin Community College

Nancy Lyon, Tyler Drake, Lindsay Sulzer (*Faculty Advisors*)

Display area: **12**

Glioblastoma Multiforme (GBM) is one of the most aggressive forms of brain cancer, with a 97% mortality rate within the first five years. Treatment of GBM is typically limited to alleviation of symptoms, brain surgery, or aggressive chemotherapy. The goal of this project is to assist in the analysis of the effects of the transcription-disrupting pharmaceutical CT179 on glioma tumor initiating cells (GTICs) via flow cytometry. GTICs are stem cell-like bodies that are responsible for GBM tumor formation, and CT179 is currently undergoing FDA New Drug Application studies with proposed human clinical studies in mid-2018. Multiple cell lines pre-treated with CT179 will be dissociated, fixed, permeabilized, stained, and run on a flow cytometer. The expression of several proteins thought to be affected by the drug will be analyzed via flow cytometry to help discern the mode of action of CT179.

INTERACTIONS OF CELL DIVISION PROTEINS FtsA AND FtsN IN *E. COLI* – WHEN AND WHERE?

Erica L. Duncan¹, Steven L. Distelhorst², William Margolin²

¹Natural Science Department, Del Mar College, Corpus Christi, TX

²UTHealth Center, University of Texas, Houston, TX

Daisy Zhang (*Faculty Advisor*)

Display area: **13**

Cell division is a critical biological process in *Escherichia coli* and it is imperative that it is accomplished precisely. Within the *E. coli* cell, the subcomplex controlling cell division is called the divisome. The divisome contains 12 essential division proteins and numerous other proteins whose main primary functions remain unknown. The essential cell division protein FtsA assists in anchoring FtsZ to the membrane and recruiting the downstream cell division proteins to the septal ring. FtsN, a late division protein, which activates septal peptidoglycan synthesis and constriction of the cell, is known to interact with FtsA. It has been shown that FtsN binds to residues within the FtsA 1c subdomain, comprised of 77 amino acids, but which specific amino acids are responsible for this interaction is not known. By using a ‘cut and paste’ method of mutagenesis, we targeted five potential FtsA residues -- 127, 128, 129, 130, and 131. A series of deletions and alanine substitutions were examined using bacterial two-hybrid analysis to determine if FtsA-FtsN interactions were interrupted by these mutations. The preliminary results suggest that residues 127 and 128 are involved in this important interaction. We will continue to probe this interaction with single amino acid substitutions.

MEDICINE ON MARS

Minerva Gillis, Marilyn Shaughnessy

Lone Star College – Montgomery

Anitha Iyer (*Faculty Advisor*)

Display area: **14**

Colonizing Mars is NASA's next objective. One of the obstacles in long-term space travel is the availability and viability of medications. Logic turns the examination of this issue to the source of most of our current medication: fungi. Fungal secondary metabolites have been the source of medicines such as penicillin. In our study, we plan to explore if fungi can be cultured under Martian environmental conditions. Some of the conditions that we plan to explore are nitrogen levels, temperature, pressure and inorganic substrates. We hypothesize that exposing a fungus to the stressful conditions on Mars could trigger secondary metabolites that have yet to be studied. We will also examine the growth pattern of Lichens under Martian conditions. While the mechanism for survival of Lichens is not clearly understood, it is known that they are quite hardy and grow in environments inhospitable to other organisms. Since they grow on different materials, they secrete unique secondary metabolites to help them break down the substrates for nutrients. We plan to analyze the secondary metabolites produced using HPLC. If the lichen culture is successful under Martian conditions, the fungi may be used for pharmaceutical purposes while the algae could be harvested to create nutraceuticals and biofuels, which could prove vital in colonizing a barren environment.

GENOMIC DARK MATTER: EXAMINING MECHANISMS OF RESTRAINT & REPRESSION OF MOBILE GENETIC ELEMENTS IN *DROSOPHILA*

James T. Gonzalez, John M. Abrams, Bhavana Tiwari, Candace Caillet

UT Southwestern Medical School, Dallas, TX

Del Mar College Dept. of Biotechnology, Corpus Christi, TX

Daisy Zhang (*Faculty Advisor*)

Display area: **15**

Transposable Elements (TE's) are mobile genomic components conserved across all domains of life. TE's have lately been identified as components of genomic evolution, innovation, and destabilization. They're implicated as catalysts for numerous diseases and Elevated levels of de-repressed transposons have been tied to over 75 diseases; half all human cancers contain a mutated copy of the p53 tumor suppressor gene, normally inhibiting retroelement (RE) mobilization. Given their propensity for host pathogenicity, it's imperative we develop a better understanding of retrotransposition into novel genomic loci. *Drosophila Melanogaster* (DM) provides an elegant, practical archetype in which to examine the mechanisms of TE classes due to both DNA Transposons and RE's being active throughout its genome. Examining DM regulation of retrotransposition in vivo can serve in furthering the understanding of RE interactions in humans due to methods of TE repression being widely conserved in eukaryotes. It's fundamental RE mobilization be repressed in the DM germline during oogenesis to mitigate compromising germline stem cells during differentiation. Once GSC's terminally differentiate, piRNA and p53 function together responding to cellular stressors ensuring genomic fidelity. Our aim is to examine DM germline differentiation, elucidating how RE's such as TAHRE target GSC's and if localization is pertinent in germline formation. We intend to induce mislocalization of RE's via integration vectors, analyzing interactions of DM's GSC regulatory network. RE's selectively target the developing germline and GSC's; mechanisms allowing target specificity remain uncertain along with what functions RE's such as TAHRE serve in constructing germline components; this experiment addresses these inquiries.

BQUAT SIPHOVIRIDAE BACTERIOPHAGE GENOME ANNOTATION AND ANALYSIS

Lydia Flores, Elana Dike, Marcus Shank, Sophia Hines, Johnathan Lawson, Carole Twichell, Bridgette Kirkpatrick, Ph.D.

Collin College, Plano, TX

Bridgette Kirkpatrick, Ph.D. (*Faculty Advisor*)

Display area: **16**

In 2010, mycobacteriophage BQuat was directly isolated from soil collected on the campus of Washington University in St. Louis, Missouri. BQuat was identified to be a unique Siphoviridae that infects *Mycobacterium smegmatis* (*mc*²*155*). DNA extraction was performed and the DNA was sent to the McDonnell Genome Institute at Washington University for sequencing, making it ready for annotation. BQuat's genome is 41893 bp in length and is a member of the G1 Cluster. Through analysis of BQuat's genome, we will assign putative functions to BQuat proteins utilizing various bioinformatic resources. BQuat's bacterial host *M. smegmatis* (*mc*²*155*) is genetically similar to *Mycobacterium tuberculosis*. Through analysis of BQuat's genome, the goal is to identify genes that likely contribute to viral fitness through interaction with described proteins of *M. smegmatis* (*mc*²*155*), and in turn, *M. tuberculosis*. Identification of these proteins will progress the aim of finding alternative treatments for humans infected with tuberculosis, as well as adding to the growing knowledge of viral and bacterial interactions and the relationships between the two pathogens.

GENOMIC AND FUNCTIONAL ANALYSIS OF A SOIL-ASSOCIATED B4 SUB-CLUSTER MYCOBACTERIOPHAGE ZEMANAR

Ameen Lalani

Austin Community College, Austin, TX

Sandesh Subramanya, Ph.D. (*Faculty Advisor*)

Display area: **17**

Mycobacteriophage, a genetically diverse group of double-stranded (ds) DNA viruses, infect mycobacterial hosts like *Mycobacterium tuberculosis* and the non-pathogenic *Mycobacterium smegmatis*. Increased prevalence of antibiotic resistance in bacterial pathogens has spurred renewed interest in the therapeutic use of these bacteriophages. Genomic characterization and bioinformatics analysis through next generation sequencing techniques has the potential of identifying novel viruses that can cross-infect hosts. Although more than 1400 genomes have been sequenced, these still poorly represent the likely diversity of the broader population of phages that can infect the host. We describe here the isolation and analysis of *Mycobacterium* phage Zemanar which belongs to the sub-cluster B4. Contiguous sequence is 71,076 bp and contains 107 predicted protein-coding genes arranged in non-canonical genomic architecture. The genome is replete with novel genes not present in other mycobacteriophage genomes, and although most are of unknown function predictive analysis is currently being investigated.

THE DISCOVERY OF NOVEL INHIBITORS FOR *K. PNEUMONIAE* CARBAPENEMASE (KPC-2) USING VIRTUAL SCREENING

Tu Nguyen

University of Texas at Austin

Josh Beckham (*Faculty Advisor*)

Display area: **18**

EXPLORATORY USE OF TRANSPOSON AIDED CAPTURE OF MOBILE GENETIC ELEMENTS

John F. Ramirez^{1,2}, Ankita Kothari², Aindrila Mukhopadhyay², J. Robert Hatherill¹

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Daisy Zhang (*Faculty Advisor*)

Display area: **19**

The inability to culture many different species of bacteria has confounded attempts to better understand the microbial ecosystem. Many of these bacterial species carry small subunits of DNA called plasmids. Plasmids are attributed with being one of the primary sources of survival factors for a bacterial colony. These factors can include antibiotic resistance or even heavy metal resistance. Furthermore, when needed the plasmids are capable of being shared throughout the bacterial population. The study of these plasmids could help researchers better understand the microbial populations they originated from. JBEI researchers wishing to elucidate microbial ecosystems determined that it would be possible to capture the broad range of plasmids by way of transposon insertion and thus reveal information about the bacterial hosts of origin. They first selected ideal target plasmids that were previously sequenced and studied thoroughly. After a number of target plasmids were selected the plasmids were categorized according to their length and selection factor, antibiotic resistance. Researchers then captured each plasmid individually to confirm that the system would work as intended on the target plasmids. The individual plasmids were then combined into two mixes. One mix held each plasmid in equimolar ratio while the other was skewed more heavily towards the larger plasmids. A capture of each of the two mixes was performed with results recorded. Full plasmid sequencing was performed to ensure that the insertions were in-fact successful. It was found that the transposon capture method was able to be successfully transformed into a surrogate strain of EPI300 *E. coli*. Additionally, each of the transformed cell lines was able to grown as an overnight culture with the exception of the 16kb plasmid. However, even though the 16kb plasmid did not grow as an overnight culture, it was confirmed to have been successfully transformed via plasmid sequencing of the transformed colonies. The equimolar ratio mix of plasmids yielded results with zero to three plasmids captured. The skewed molar ratio mix of plasmids yielded an expected outcome heavily favoring the largest plasmids. It is unclear why the overnight culturing of the 16kb plasmid was unsuccessful. Future studies hope to elucidate the full extent to which transposon aided capture systems are capable of identifying microbes within environmental samples.

GROWTH CHARACTERIZATION OF THE UNICELLULAR GREEN ALGAE,
CHLORELLA VULGARIS, AND CYANOBACTERIA *SYNECHOCOCCUS ELONGATUS* IN A
PHOTOBIOREACTOR

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Algae, a group of highly diverse eukaryotes, are photosynthetic and mainly aquatic organisms. Macro- and micro-algae have been used commercially in food, feed, nutraceuticals, fertilizers, bioremediation, biofuels, with many more in development. Algae have great potential to produce a wide range of valuable compounds, beyond their current exploitation. To date, commercialization of new products, like polyunsaturated fatty acids (PUFAs), has been slow. However, microalgal biotechnology is a relatively new industry, and therefore, it is unsurprising that significant challenges remain to be solved. Here we demonstrate the growth requirements and kinetics of a unicellular green algae, *Chlorella vulgaris*, and a cyanobacterium *Synechococcus elongatus* in a GroFizz photobioreactor. Efficiency of these photobioreactors (2 liters) are being evaluated to achieve optimal growth potential of algae for laboratory scale production.

TESTING COMPUTATIONALLY PREDICTED ANTIBODY STRUCTURES

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Experimental antibody design usually involves many time-consuming and labor-intensive steps. Through the use of automated computational design algorithms, it has been shown that an antibody can be designed with no prior experimental data other than the structure of the antigen of interest. Macromoltek, an Austin-based company, has been developing an automated platform to design antibodies aimed at difficult infectious disease and cancer targets. In a collaboration with Macromoltek, the aim of this project is to use their algorithm to create a DNA sequence which when expressed, will synthesize recombinant antibodies with affinity to specific, target antigens. These antibodies will be expressed and subsequently purified from E.coli through standard protein purification methods such as FPLC. Their binding affinity to their target antigens will be tested through binding assays such as ELISA. If affinity to the antigen is observed, we intend on further testing the kinetics involved in their binding through Surface Plasmon Resonance (SPR).

Washington

FINDING NEW ORDER WITHIN CHAOS: SPECULATION ON SYMMETRICAL DOUBLING 3-PERIOD CASCADES BEYOND FEIGENBAUM'S SCALING OF THE LOGISTIC MAP

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Chaos refers to dynamical systems that are exponentially sensitive to their initial conditions. In this project, I explore the logistic map, the simplest chaotic system, by characterizing its global nature through Feigenbaum's constants and the relationships between its periods. Using Matlab to code the logistic map, the Feigenbaum constants and existence of the 3-period cycle were verified and explored. Further simulations showed a new pattern of repeating odd-cycle periods stemming from the 3-period cycle - a symmetric doubling cascade of odd-number periods in the chaotic phase of the map which are independent of their initial conditions. The new pattern allows us to see the order that underlies the chaotic system, a meta-pattern based on odd-cycle doubling which shows all odd-number periods in the chaos stemming from the 3-period: with two 5-periods, four 7-periods, eight 9-periods, and presumably sixteen 11-periods, etc., following symmetrically and respectively from the initial 3-period cycle. The discovery of the new ordered pattern can be used to predict the stable state of growth of a population model in its chaotic phase and can be used for population studies in which the initial conditions are known only approximately. This has ramifications for mathematics, population biology, chemistry, physics, and the social science



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The CCURI model of incorporating undergraduate research (UR) into community college curricula, engages students from the moment they enter the classroom. The model employs active learning methods of instruction in the first year coursework, which teaches basic scientific concepts within the context of an ongoing research project. Students are then given an opportunity to explore those projects as either a CURE (Course Undergraduate Research Experience), a SURE (Summer Undergraduate Research Experience) or a PURE (Program Undergraduate Research Experience). The growing CCURI network has become a rich source of collaboration on both the curricular and research sides of the CCURI model. With over 50 community colleges implementing the CCURI undergraduate research model; thousands of students are connected to research and opportunities that are vital to the successful pursuit of a STEM career.

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