

NH-INBRE
2022 Annual Meeting

**Experience the Art of Biomedical
Scientific Discovery**



New Hampshire Network of Biomedical Research Excellence (NH-INBRE)

William R. Green, Ph.D.
Project Director

Experience the Art of Biomedical Scientific Discovery

ANNUAL NH-INBRE MEETING ITINERARY

August 8, 2022 – August 9, 2022

www.nhinbre.org

Monday, August 8th

8:00am – 9:30am	Registration Desk hours of operation	<i>Great Hall</i>
	<u>Poster set up for Monday Presenters</u>	<i>Grand Ballroom</i>
8:00am – 9:30am	Continental Breakfast	<i>Presidential Foyer</i>
9:30am – 10:00am	State of the INBRE <i>Bill Green</i>	<i>Presidential Ballroom</i>
10:00am – 10:15am	NH-INBRE Alumni Advisory Board Welcome <i>Casey Kimball</i>	<i>Presidential Ballroom</i>
10:15am – 11:15am	Faculty Presentations I	<i>Presidential Ballroom</i>
	<ul style="list-style-type: none">• SEED Grant: <u>RNA from Damaged Cells can Change Proinflammatory Characteristics of Activated Macrophages.</u> Tatiana Jones, Assistant Professor of Biology, Rivier University• Pilot Project: <u>Design, Synthesis, and Preliminary Biological Evaluation of Flufenamic Acid Analogues for Hippo Pathway Inhibition.</u> Jennifer Pace, Assistant Professor of Chemistry, Saint Anselm College	
11:15am – 11:30am	Break	
11:30am – 12:30pm	Student Presentation I	<i>Presidential Ballroom</i>
	<ul style="list-style-type: none">• <u>A multi-omics study of the impacts of Arsenic toxicity on keystone aquatic grazers <i>Daphnia pulex</i>.</u> Sean Cady, Keene State College• <u>Patients vs Providers: Definitions of a Cancer Survivor: A Compare and Contrast Study.</u> Grace Baukus, Saint Anselm College• <u>Isolation and Identification of <i>Borrelia burgdorferi</i> Bacteriophages from New Hampshire <i>Ixodes scapularis</i>.</u> Shoshana Trudel, University of New Hampshire at Manchester• <u>Functional Variation in Flavor Genes Across 459 Yeast Strains Used for Beer and Wine.</u> Bailee Gallant, Plymouth State College	
12:30pm – 1:15pm	Boxed Lunch	<i>Presidential Foyer</i>

Geisel School of Medicine North College Street Vail Building Room 805 Hanover, NH 03755

Colby Sawyer College • Dartmouth College • Franklin Pierce University • Great Bay Community College
Keene State College • New England College • Plymouth State University • River Valley Community College
Saint Anselm College • University of New Hampshire

12:45pm – 1:15pm **NH-INBRE Mentoring Program** *Presidential Ballroom*
How it works, why it's important
Student Session - bring your lunch. Faculty encouraged to attend!

Breakout Sessions

Student Track

1:15pm -2:45pm **Career Mentoring Workshop break-outs** Multiple rooms
NH-INBRE Alumni interactive session *Jefferson, Reagan*

Faculty Track

1:15pm – 2:45pm **Demystifying NIH Grant Submissions and Manuscript Writing** *Presidential Ballroom*

2:45pm – 3:00pm **Break**

3:00pm – 4:15pm **Poster Session I** *Grand Ballroom*

4:15pm – 4:30pm **Break**

Breakout Sessions

Student Track

4:30pm – 5:30pm **Resume and Personal letter writing workshops** *Presidential Ballroom*
Interactive workshop

Faculty/Admin Track

4:30pm – 5:30pm **Science Education Partnership Awards (SEPA)** *Reagan Room*

- *Data to Action: A Secondary School-based Citizen Science Project to Address Arsenic Contamination of Well Water.* **Jane Disney** PI, MDIBL; **Bruce Stanton** co-PI, Geisel
- *Dartmouth Rural STEM Educator Partnership.* **Roger Sloboda** PI, Dartmouth
- *Learning Science Through Research.* **Peter Faletra** PI, NHAS; **Chery Whipple** co-PI, Colby-Sawyer College
- *NH CREATES the Future: The New Hampshire Collaborative for Regenerative Medicine Education and Training for Engineers and Scientists of the Future.* **Carmela Amato-Wierda** PI, UNH; **Kelley Thomas** co-PI, UNH

5:30pm – 6:30pm **Break**

Poster breakdown for Monday Presenters

6:30pm – 7:45pm **Dinner Buffet and Networking** *Presidential Garden*

8:00pm **Networking** *Jewell Terrace*

Tuesday August 9th

Poster set up for Tuesday Presenters

7:30am – 8:30am **Breakfast Buffet** *Presidential Ballroom*
Student networking

Breakout Sessions

Student Track

8:30am – 9:45am **Planning for success after Undergrad** *Presidential Ballroom*
Casey Kimball

Faculty Track

8:30am – 9:45am **Now that you have NIH, Foundation, and/or INBRE funding, inc. RSTG, what comes next?** *Reagan Room*
How to be successful yet avoid pitfalls in science and non-science interactions.

9:45am – 10:15am **Faculty Presentation II** *Presidential Ballroom*

- Pilot Project: Perceptions of Deliberate facial Expressions in People with Parkinson's Disease. **Sarah Gunnery**, Assistant Professor of Psychology, New England College

10:15am – 11:15am **Student Presentation II** *Presidential Ballroom*

- Localization of extraocular opsin in the brain and dermal tissue of the nudibranchs *Berghia stephanieae* and *Hermisenda opalescens*. **Christine Gordon**, New England College
- Bioinformatic analysis of isolate and metagenomic sampling provides insight into bacterial makeup and antibiotic resistance of mastitis in milk producing cows and their environment in organic and conventional farms. **Ethan Edwards**, University of New Hampshire at Manchester
- Faces: Building Bias Awareness in Bioethics Education Through UDL Designed Games. **Hayden Rogers**, Saint Anselm College
- Optimizing Cancer-Specific Antibody Cocktails Using Directed Evolution and Yeast Display. **Nick Genovese**, Colby-Sawyer College

11:15am – 11:30am **Break**

11:30am – 12:45pm **Poster Session II** *Grand Ballroom*

12:45pm **Lunches to Go**

MEETING ADJOURNED

1:00pm – 2:30pm **Steering Committee Meeting** *Reagan Room*

2022 Dartmouth iSURF Class

1:00pm – 2:00pm **Focus Group** *Washington Boardroom*

How to get the Most from the Annual Meeting

For the second straight year, NH-INBRE is using the August annual meeting to focus on student career development. This memo provides an overview of the career development activities at the upcoming meeting and advice on how to get the most from the annual meeting for your own career planning.

First, some preliminary recommendations:

- Sign up for a mentor now and begin working with him or her ASAP. Fill out this [short form](#) and we will match you with a mentor. Each of these mentors is a NH-INBRE alum and has gone through what you are facing.
- Prepare a resume. Check this [link](#) for help getting started. Work with your mentor to refine and improve your résumé. Bring copies of your résumé to the annual meeting so that you can hand them out to NH-INBRE alumni you meet there or to get feedback on how to make it better.
- Get a LinkedIn profile. Check with the career planning resources at your school for help.
- Join the [NH-INBRE LinkedIn group](#).
- Use the annual meeting to speak with as many NH-INBRE alumni attending the meeting as you can. This is a good opportunity to develop your networking skills and to begin building a professional network.
- Create a business card on [HiHello](#) or make a printed one at Staples and bring at least 25 of your cards to the meeting.
- Always carry a notepad and pen to jot down important information and follow-up reminders.

The career-related portions of the annual meeting:

Day 1

10:00am – 10:15am: NH-INBRE Alumni Advisory Board Welcome. Casey Kimball, chair of the advisory board, will provide an overview of the career planning resources being developed by the advisory board.

12:45pm – 1:30pm: Mentoring - Is it for me? Its Importance and Impact. Casey Kimball will explain how the mentoring program works and present data on how the first year of mentoring is going. You will also hear from students who are currently being mentored and from some of the mentors. This is a chance to hear firsthand from your peers about the value of mentoring. *This session is during lunch, so get your boxed lunch and come back to the grand ballroom with your lunch.*

1:30pm -2:30pm: Career Mentoring workshop breakouts. These breakout sessions will be organized by career interest so that you can have a chance to speak with mentors who are in different types of careers including industry, academia, business, and healthcare.

4:30pm – 5:30pm: Resume and Personal letter writing workshops. These interactive workshops will give you a chance to further improve your resume, personal letters/statements and other forms of writing you will need to pursue your career. Bring your resume if you have one! If not, be prepared to sketch one out.

6:30pm – 7:45pm: Dinner Buffet and Networking. You will be seated with NH-INBRE alumni and different faculty members to provide you with more networking opportunities.

8:00pm: Networking. This will be an informal opportunity to continue networking and talk with alumni and faculty at the meeting that you weren't able to speak with earlier in the day – take advantage of this time!

Day 2

7:30am – 8:30am: Breakfast Buffet. Another networking opportunity.

8:30am – 9:45am: Planning for success after Undergrad. Casey Kimball will lead a presentation about how to get your first job out of college and about graduate school strategies. This session will focus on how to prepare for success no matter what year of school you're currently in.



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2022 Annual Meeting Attending Alumni Bios

Name: Mahad Ahmad

Undergraduate: Keene State College - 2020

Current Position: Associate Scientist II, Strand Therapeutics

Bio: Mahad graduated with his BS in biology from KSC where he performed undergraduate research with Dr. Jason Pellettieri. Shortly after leaving Keene, Mahad obtained a job at Pfizer as an Associate Scientist. At Pfizer, Mahad worked on mRNA vaccines for COVID and influenza. After one year, Mahad decided to transition to small biotech and now works at Strand as an Associate Scientist II at Strand Therapeutics where he works on an immuno-oncology mRNA therapeutic.

Fun Fact: In his free time, Mahad enjoys watching and playing competitive video games

Career Breakout Session: Industry

Dinner table: #7



Name: Jason Charbonneau

Undergraduate: Keene State College - 2019

Current Position: Product Specialist – Americas, Fluigent Inc.

Bio: Jason graduated from KSC in December of 2019 with his BS in biology with a minor in chemistry. Shortly after graduating, Jason started an internship at a small biotech company called Aphios. There, Jason spent seven months before transitioning to Perkin Elmer Inc and worked as an R&D application scientist in their Microfluidics department. Jason was at Perkin Elmer for almost two years before starting his new position at Fluigent as a technical/applications representative and sales supporting colleague

Fun Fact: Jason enjoys traveling, scuba diving, training in MMA, conservation biology, and has active applications with the military

Career Breakout Session: Industry

Dinner table: #9



Name: Olivia Economides

Undergraduate: Plymouth State University - 2020

Current Position: MPH Candidate/Research & Admin Assistant, Tufts/Harvard

Bio: Olivia graduated in 2020 with a BA in biology and a minor in business. She participated in iSURF research for two summers, was a Peer Coordinator, and did research with Dr. Arti Gaur. Her research focused on different therapeutic treatments for glioblastomas. Olivia is currently working on her MPH at Tufts University of School of Medicine in Boston. Her degree focuses on Health Services Management and Policy. In addition, Olivia currently helps manage and works for two research labs at Dana Farber and Harvard Medical school where the focus of the research is to identify new treatment options for various blood cancers in relation to lymphoma and leukemia.

Fun Fact: Olivia enjoys surfing, skiing, and taking care of her huge monstera plants

Career Breakout Session: Academia

Dinner table: #4



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Name: Elizabeth Enright

Undergraduate: Franklin Pierce University - 2019

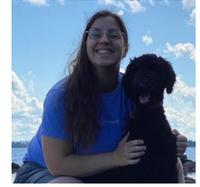
Current Position: Quality Control Associate – Abbott Labs

Bio: Elizabeth graduated from FPU in 2019 with a degree in biology and a minor in chemistry and anthropology. She did undergraduate research in Dr. Jabbour's lab testing for FosB proteins in the brains of opioid overdoses from the NH coroner. Since graduating, Elizabeth has been working in the biotech industry learning about the agricultural and environmental applications to life sciences.

Fun Fact: Liz has been playing rugby for seven years and she loves to backpack and hike in the Maine woods

Career Breakout Session: Industry

Dinner table: #10



Name: Jasmine Huffman

Undergraduate: University of New Hampshire, Manchester, 2019

Current Position: Experiential Learning Coordinator/MBA candidate – UNH-M

Bio: Jasmine graduated from UNH-M in 2019 with a major in psychology and a minor in American Sign Language (ASL) and Deaf studies. She participated in Dr. Nicholas Mian's lab and conducted a study that investigated the relationship between emotional/personal intelligence and deceptive behavior. Jasmine was able to present her studies at the 2019 meeting of the Cancer and Professional Success department. Jasmine currently serves as the Experiential Learning Coordinator for the UNH-M campus while she works on her MBA

Fun Fact: Jasmine is co-directing a Harry Potter short film

Career Breakout Session: Academia

Dinner table: #6



Name: Casey Kimball

Undergraduate: Keene State College Alum – 2017

Current Position: Production Lead, Intellia Therapeutics/MBA Candidate, UNH

Bio: Casey graduated from KSC with a biology degree in 2017. During her time at Keene, she worked in Dr. Jason Pellettieri's lab which focused on evolutionary developmental biology (evo-devo) research. From there, Casey worked at Adimab in Lebanon for 6 months as a Co-Op before obtaining a job at Intellia Therapeutics, a CRISP company in Cambridge, MA. Casey recently transitioned out of the lab and has worked for Intellia for close to 5 years. She is currently working on getting her MBA from UNH.

Fun Fact: Casey's name was legally changed when she was three years old

Career Breakout Session: Industry

Dinner table: #1



Name: Avery Kretschmar

Undergraduate: Norwich University - 2021

Current Position: Cell Culture Manufacturing Technician, Bio X Cell

Bio: Avery graduated from Norwich in 2021 with her BS in neuroscience. During her undergrad studies, Avery worked in Dr. Thomas Shell's lab working on vitamin B12 derivatives as targeted cancer chemotherapeutics. Avery was part of the iSURF program for two years where she was a Peer Coordinator and intern in the fermentation lab at Bio X cell. Avery was offered a position to go to grad school in South Carolina but decided to defer her acceptance and take a full-time position at Bio X Cell. She intends to continue onto graduate school to further pursue her studies in neuroscience.

Fun Fact: Avery volunteers every week at High Horses where she assists with therapeutic riding lessons

Career Breakout Session: Industry

Dinner table: #9



Name: Kate Lu

Undergraduate: University of New Hampshire, Manchester - 2020

Current Position: Process Development, ARMI

Bio: Kate graduate with her BA in biological science in 2020. During her time at UNH-M she worked with Dr. MacLea and Dr. Johnson. She is currently working for ARMI in Manchester, NH as a lab technician.

Fun Fact: Kate can speak Japanese fluently

Career Breakout Session: Industry

Dinner table: #8



Name: Megan Marshall

Undergraduate: Keene State College - 2021

Current Position: Quality Control Associate, Bio X Cell

Bio: Megan graduated from Keene in 2021 with a BS in neuroscience and a BA in psychology and a minor in biology. During her undergrad, Megan worked with Dr. Fichtenholtz in his affective neuroscience lab where she studied the effects of trauma. Megan also took part in the iSURF program in 2020 and 2021. Megan has been at Bio X Cell for a little over a year where she works in their QC department.

Fun Fact: Megan is an amateur photographer and would like to pursue it professionally

Career Breakout Session: Industry

Dinner table: #10



Name: Somer Matar

Undergraduate: Keene State College - 2015

Current Position: PhD Candidate, Dartmouth College

Bio: At Keene, Somer participated in two NH-INBRE projects in microbiology and chemical biology labs. After graduating in 2015, Somer obtained a job at a small biotech company where she researched blood biomarkers for various cancers. She went onto become the lab supervisor and became a board-certified technologist in molecular bio. After spending four years in the industry, Somer entered Dartmouth's MCB graduate program where she is now a PhD candidate studying Molecular Systems biology.

Fun Fact: Somer has never met anyone who can tolerate spicy food as well as she can

Career Breakout Session: Academia

Dinner table: #3



Name: Kayli Neil

Undergraduate: University of New Hampshire, Durham – 2020

Current Position: Associate Scientist II, Atalanta Therapeutics

Bio: Kayli graduated from UNH with a degree in biomedical sciences. Kayli worked in three different undergraduate labs and shortly after graduating, started working in a cell biology lab at Harvard Medical School studying the upregulation of oxidative phosphorylation in regard to platinum based treatments and ovarian cancer tumors. At the same time, Kayli worked as a nursing assistant at St. Elizabeth's Medical Center on the maternity ward and had a plan to apply to PA school. She recently took a position at Atalanta working with siRNA therapeutics for neurodegenerative disorders. She's currently figuring out if she wants to stay in industry attend PA school or obtain a master's in pharmacology!

Fun Fact: Kayli spent 2+ years prepping for med school but is now reconsidering her path, so she very much understands what it's like to switch gears. She also loves to travel and paint.

Career Breakout Session: Industry

Dinner table: #1



Name: Christina Parkinson

Undergraduate: Franklin Pierce University - 2001

Current Position: Vice President of Operations – Boston Analytical

Bio: After graduating from FPU in 2001 with her BS in biology, Christina began working at Charles River Laboratories. During her 20-year tenure at CRL she completed her MBA, Lean Sigma Six Green Belt, and Dynamic Work Design training. Her career developed over time to focus on operations, operational improvements, and people management within the science industry. In 2020 she transitioned from pathogen surveillance and identification to support of the pharmaceutical manufacturing industry. In 2022 she accepted a position as the VP of Operations at Boston Analytical and continues to support the pharmaceutical industry's drug development and release testing needs.

Fun Fact: Christina created a training video which is used on the international space station!

Career Breakout Session: Industry

Dinner table: #5



Name: Brandon Proulx

Undergraduate: Plymouth State University

Current Position: Live Science Consultant (R&D Business Development, talent acquisition), Independent

Bio: Brandon graduated from PSU in 2020 with a BS in biology and a minor in chemistry. Brandon played baseball at PSU and worked in Dr. Doherty's genetics and molecular bio lab. Since graduating, Brandon has worked in several areas of the life science field ranging from research, consulting, and pharmaceutical consulting. Recently, Brandon has worked as a private consultant and contractor for a variety of biotech companies to assist in talent acquisition, business development, and R&D.

Fun Fact: Brandon loves the New England outdoors and has a passion for hiking, skiing, and surfing!

Career Breakout Session: Industry

Dinner table: #6



Name: Eva-Maria (EM) Rudler

Undergraduate: Saint Anselm College, 2021

Current Position: PhD Student, George Mason University

Bio: EM graduated with her BS in 2021 and then moved to D.C area shortly after graduation to start her grad school journey. EM started in one program and school in the fall of 2021 and worked as a full-time assistant to a R&D chemist but ended up switching programs in January 2022 to her current school. EM has now joined a lab and worked as a TA during the spring 2022 semester while taking classes.

Fun Fact: EM was born in Germany and can speak the language fluently

Career Breakout Session: Academia

Dinner table: #7



Name: Leah Schwartz

Undergraduate: University of New Hampshire, Manchester - 2020

Current Position: Research Technician, Tufts University

Bio: Leah graduated from UNH-M in December of 2020 and transitioned directly into working as a medical lab technician in the COVID lab at UNH-M. After that, Leah worked in the Blood Bank laboratory at Mass General as a medical lab technician (MLT). Leah now works in Michael Levin's lab at the Center for Regenerative and Developmental Biology at Tufts University. Her work focuses on studying neural regeneration and calcium signaling.

Fun Fact: Prior to Leah's career in science, she was a professional tap dancer from the age of 16 to 23

Career Breakout Session: Academia

Dinner table: #2



Name: Grace Shaw

Undergraduate: Plymouth State University - 2021

Current Position: QC Microbiologist I, Nova Nordisk

Bio: Grace started at PSU in 2018 and joined Dr. Chris Chabot's lab in the summer of 2019. Her work primarily focused on molecular techniques, early development, and toxicology. During her last two summers in school, she participated in the iSURF program where she remotely studied herd immunity and potential vaccine options for SARS Cov-2. In her second year, Grace was placed at Mascoma LLC working with molecule cloning techniques in yeast. After graduating, Grace started as a temp at Novo Nordisk and went full time in February 2022 in their QC department.

Fun Fact: Grace was in 4-5 music ensembles every semester during undergrad!

Career Breakout session: Industry

Dinner table: #2



Name: Lorna Smith

Undergraduate: Plymouth State University – 2021

Current Position: Process Development, ARMI

Bio: Lorna graduated with her MSc in biology from PSU in 2021 and completed her graduate research with Dr. Heather Doherty. Her research with Dr. Doherty focused on cardiac fibrosis and wound healing. Lorna started at ARMI in February 2022 as a process development associate scientist.

Fun Fact: Lorna learned how to ride the unicycle as a child

Career Breakout Session: Industry

Dinner table: #3



Name: Madison Vigneault

Undergraduate: Saint Anselm College – 2018

Current Position: Principal Associate Scientist (Discovery Research), Affinivax

Bio: Madison graduated from Saint Anselm in 2018 and worked in Dr. Elizabeth Greguske's lab. In addition, Madison was a Dartmouth iSURF fellow in Dr. Cheung's lab in 2017. Shortly after graduating, Madison obtained a job at Affinivax in Cambridge, MA and their work focuses on developing vaccine candidates for C. diff and S. aureus. Madison is also a regular instructor of synthetic biology with the Biobuilder Foundation.

Fun Fact: Madison enjoys brewing her own Kombucha and has a "mini lab" in her home dedicated to all her fermentation projects!

Career Breakout Session: Industry

Dinner table: #8





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Science Education Partnership Award (SEPA)

PI's: Jane Disney, Mount Desert Island Biological Laboratory
Roger Sloboda, Biological Sciences, Dartmouth College
Peter Faletra, NH Academy of Sciences, Inc.
Carmela Amato-Wierda and Kelley Thomas, Materials Science Program and Department of Molecular, Cellular, and Biomedical Sciences, University of New Hampshire

New Hampshire engages in four different NIH SEPA's (Science Education Partnership Awards) that connect the K-12 education system with INBRE researchers and educators across Maine, Vermont, and New Hampshire. Learn how you can participate in these projects during this session.

The four SEPA projects are:

- (1) **Data to Action: A Secondary School-based Citizen Science Project to Address Arsenic Contamination of Well Water**, in which project coordinators and scientist-partners in Maine and New Hampshire support teachers and students in both states as they implement well water monitoring projects in the classroom, analyze data, effectively communicate their data, and work to reduce arsenic exposure in their communities. This is a collaborative project with Geisel School of Medicine, Dartmouth Cancer Center, Maine Center for Disease Control, and Maine and New Hampshire INBRE programs.
- (2) **Dartmouth Rural STEM Educator Partnership** engages middle school teachers in low-income, rural communities to partner with Dartmouth faculty and graduate students and professional science educators at the Montshire Museum of Science to develop sustainable STEM curricular units for their schools.
- (3) **Learning Science through Research** is run by the NH Academy of Sciences, along with its partners, the Fairbanks Museum and Planetarium (FMP) and Colby Sawyer College (CSC), uses its advanced STEM Lab and its connections with mentors in our scientific community to greatly expand its support of middle and high school students and their teachers in experiencing discovery-based science.
- (4) **NH CREATES the Future, or the New Hampshire Collaborative for Regenerative Medicine Education and Training for Engineers and Scientists of the Future**, is a project among NH K-12, Nh INBRE, and ARMI, the Advanced Manufacturing Institute in Manchester, NH. Its goals are to provide teacher professional development, youth projects during the summer and academic year, as well as grow a STEM ecosystem to support the workforce needs of the regenerative manufacturing industry in NH.

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Monday, August 8th Oral Presentations

Faculty Presentation Session I

RNA from Damaged Cells can Change Proinflammatory Characteristics of Activated Macrophages

Tatiana Jones – tjones@rivier.edu

Assistant Professor

Department of Biology, River University

An increasing number of publications implicates the role for extracellular RNA (exRNA) in inflammatory pathways. This study has been designed to define the response generated by macrophages activated through either TLR2 or TLR4 agonists and stimulated with self exRNA. We hypothesized that stimulation of cultured bone-marrow derived RAW264.7 activated macrophages with self exRNA would result in upregulation of proinflammatory profile of macrophages. To characterize cells' responses to stimulation, we used FACS analysis to determine expression by CD11b+ cells CD14 co-receptor, and major histocompatibility complex (MHC)II. To examine cytokine production, cultures' supernatants were evaluated by ELISA for Tumor Necrosis Factor-alpha (TNF α) and Interleukin (IL)6. To our surprise, addition of self exRNA to the cultured cells activated by LPS (TLR4 agonist), Pam2CSK4 (TLR2 agonist), or their combination resulted in downregulation of MHCII expression. Moreover, it also resulted in reduced production of TNF α , and IL6 compared to the cells activated with LPS, or Pam2CSK4 alone. At the same time expression of Nuclear Factor kappa B (NF κ B), a regulator of innate immunity, has not been affected by stimulation of activated macrophages with self exRNA, indicating enhanced proinflammatory activity of macrophages in all stimulations' groups. These results require further examination of the changes in macrophages' proinflammatory profile under influence of exRNA. To further investigate the role for self and non-self exRNA in proinflammatory responses of macrophages we intend to evaluate the mechanisms involved in downregulation of MHCII expression and reduced production of TNF α and IL6. Understanding of exRNA influence on proinflammatory phenotype of innate immune cells will enable us to deeper examine the mechanisms of immune tolerance and possible complications related to COVID-19 and other RNA viruses.

Design, Synthesis, and Preliminary Biological Evaluation of Flufenamic Acid Analogues for Hippo Pathway Inhibition

Jennifer R. Pace – jpace@Anselm.Edu

Assistant Professor

Department of Chemistry, Saint Anselm College

The Hippo signaling pathway is a phosphorylation cascade that plays a crucial role in cell proliferation, apoptosis, differentiation, and development. As the Hippo pathway plays a predominant role in cell and tissue homeostasis, dysregulation of the pathway results in uncontrolled cell proliferation and tumorigenesis. Hippo pathway dysregulation has been linked to a variety of human cancers (pancreatic, breast, liver, and prostate) and as a result, this cell signaling pathway has become a novel therapeutic target for cancer treatment. Recently, efforts have been made to inhibit the Hippo pathway with both small molecules and macromolecules. In 2015, a high-throughput screen of FDA-approved and clinical stage drugs identified flufenamic acid (FA), a member of the flufenamates (NSAIDs), as an inhibitor of the Hippo pathway. With this in mind, FA analogues have been designed to probe the scaffold of FA in terms of its novel Hippo inhibitory activity. These FA analogues may serve as potential chemotherapeutic agents as well as biochemical tools for further exploring the role of the Hippo pathway within cancer development, cancer metastasis, and chemotherapeutic resistance. The computational design, synthesis, and preliminary biological evaluation of these FA analogues is reported herein.

Student Presentation Session I

A multi-omics study of the impacts of Arsenic toxicity on keystone aquatic grazers *Daphnia pulex*

Sean Cady - sean.cady@keene.edu

Mentor: Priya Roy Chowdhury, Assistant Professor - pr1043@keene.edu

Department of Biology, Keene State College

Arsenic compounds are prevalent environmental toxicants that are also potent carcinogenic agents to humans. The metabolism of arsenic plays an important role in its toxicity and susceptibility is shown to be higher in malnourished patients. The mechanisms in which nutrition acts as a mediator of arsenic toxicity is however largely unknown. In this study we take a comprehensive look at how different food conditions interact with environmental arsenic supply to mediate organismal fitness, underlying gene expressions, and associated changes in metabolic protein productions in our model organism *Daphnia*. To that end, we first measured life-history endpoints, as surrogates for fitness, in different food conditions and arsenic supply in *Daphnia*. Our results indicated that interaction between arsenic and food influenced growth-related and reproductive-related traits differently, although food does not seem to mediate somatic arsenic accumulation in our study. Supporting this, transcriptomic data indicated differences in expression of several key metabolic genes/pathways that probably facilitate the observed interaction in life-history traits. Further, we measured whole body metabolic protein production (metabolome) under similar treatment conditions that indicated differential expression of several *Daphnia*-lineage specific proteins enabling us to identify the specific metabolic pathways that mediate the observed interactions. Identifying these interactions and in turn the underlying mechanisms of how arsenic susceptibility changes with diet is vital for dealing with arsenic-related health effects, while aiding in the mitigation and management of risks associated with common environmental carcinogens.

Patients vs Providers: Definitions of a Cancer Survivor: A Compare and Contrast Study

Grace Baukus, NH-INBRE iSURF - gbaukus242@Anselm.Edu

Mentor: Elizabeth McGrath, Nurse Practitioner - Elizabeth.B.McGrath@hitchcock.org

Dartmouth Hitchcock Medical Center

Background: According to the National Comprehensive Cancer Network (NCCN) the definition of a cancer survivor is anyone from diagnosis through end of life (EOL). However, not all cancer patients relate to or identify with this designation. The purpose of this study is to compare how patients and health care professionals (HCPs) define a cancer survivor. Methodology: Two surveys were created through an iterative process to ascertain how patients and providers define survivors. Surveys were deployed using a web-based survey tool, using email groups and lists developed by the oncology department. The results were analyzed using qualitative thematic analysis. Results: The patient survey was analyzed and four themes identified. Two unique themes were identified from the patients' responses, personal characteristics and other. The provider survey was analyzed and five themes were identified. The providers' responses coded into three unique themes, completed definitive therapy through surveillance, diagnosis through surveillance and other. The surveys had two shared themes, diagnosis to EOL and completed definitive therapy through EOL. Despite the NCCN standardized definition of a cancer survivor, not all providers or patients utilize this definition. Conclusion: There are distinct perspectives from both patients and providers around the term cancer survivor. It is important to listen to patients to understand how they identify themselves as survivors. Improving patient marketing and counseling will ensure that patients are aware of the designation of a survivor, as well as the resources available to them. It's also essential to ensure HCPs have adequate knowledge of survivorship resources for proper referrals and patient education.

Isolation and Identification of *Borrelia burgdorferi* Bacterial Phages from New Hampshire *Ixodes scapularis*

Shoshana Trudel - shoshana.trudel@unh.edu

Mentor: Kyle MacLea, Assistant Professor - kyle.maclea@unh.edu

Department of Life Sciences, University of New Hampshire at Manchester

Lyme Disease is a condition caused by the bacteria *Borrelia burgdorferi* and is the most common vector-borne disease in the United States. Although antibiotics are currently the primary form of treatment for Lyme Disease, there is great value in exploring the potential for alternative treatments. Like other forms of life, bacteria have natural predators. Bacteriophages are viruses that infect bacteria while possessing an extremely selective host range of target bacteria. Due to this great specificity and concerns of antibiotic resistance, they have many advantages over traditional antibiotics as an antibacterial agent. Phage therapy is the application of bacteriophages in a clinical setting to treat bacterial diseases. An isolated bacteriophage specific for *Borrelia burgdorferi* may have a prospective future in treating Lyme Disease patients who are unresponsive to traditional antibiotics. Previous attempts to isolate bacteriophages for tick-borne bacterial illnesses have been unsuccessful due to the complex conditions needed to culture the bacteria themselves, alongside other factors. We present a novel methodology for *Borrelia* bacteriophage isolation from environmental blacklegged tick (*Ixodes scapularis*) samples using a combination of targeted primers, PEG precipitation, and dilution-to-extinction. Our methodology can be applicable not only for bacteriophages of *Borrelia* species, but for bacteriophages of other challenging to culture bacterial hosts, many of which have clinical significance.

Functional Variation in Flavor Genes Across 459 Yeast Strains Used for Beer and Wine

Bailee Gallant, NH-INBRE iSURF - bjg1031@plymouth.edu

Mentor: Petra Deane, Senior Bioinformatics Scientist - pdeane@lallemand.com

Mascoma LLC

Saccharomyces cerevisiae, better known as baker's yeast, is the main microbial species used in the production of fermented drinks like wine and beer. Genetic diversity in the yeast genome confers unique qualities to fermented drinks affecting their taste, color, and smell, all of which are important for designing commercially successful microbial products for beverage markets. In this study I analyzed the genomes of 134 Lallemand yeast strains and 325 publicly available yeast strains to compare five genes associated with different taste profiles in wine and brewing yeast applications. I performed gene alignments and built phylogenetic trees to characterize functional diversity among strains, identifying cases where a strain in the Lallemand portfolio carries a unique copy of a flavor gene (e.g. FDC1 – ferulic acid decarboxylase) as well as cases where the company portfolio could be expanded to capture more genetic diversity (e.g. BAT1 – branched-chain amino acid transaminase). I also identified several important mutations causing protein truncation and loss of gene function. By performing comparative genomics on such a large scale across different lineages of yeast products, we can understand the value of certain strains from a marketing and consumer standpoint, as well as identifying interesting evolutionary patterns.

Tuesday, August 9th Oral Presentations

Faculty Presentation Session II

The Relationship between Facial Expressivity and Quality of Life in People with Parkinson's Disease and their Care Partners

Sarah D. Gunnery - sgunnery@nec.edu

Assistant Professor

Department of Psychology, New England College

People with Parkinson's disease (PD) often develop difficulties expressing emotion in their face, body, and voice due to motor impairments that are central to the disease. These deficits in nonverbal communication influence the way people with PD are perceived by same aged peers, healthcare providers, and close family and friends. While burnout is well documented in care partners of people with PD, there has been little investigation into how communication challenges relate to quality of life in the dyad. This talk will use the biopsychosocial model of health to frame a discussion of quality of life in people with PD and present original research testing the relationship between care partners' ability to read their partners thoughts and feelings and quality of life in the dyad. Using an empathic accuracy paradigm, we measured care partners' accuracy for the content and valence of their partner's thoughts and feelings during a conversation between 23 dyads. Results showed moderate positive correlations indicating that care partners who are better able to understand what their partner is thinking and feeling have higher quality of life. Care partners with better empathic accuracy also tended to have partners with higher quality of life. This is preliminary evidence for the association between dyadic communication and quality of life in people with PD and their care partners. Future research investigating ways people with PD can compensate for a lack of facial expressivity and improve the accuracy with which they are perceived in their daily lives will be discussed.

Student Presentation Session II

Localization of extraocular opsin in the brain and dermal tissue of the nudibranchs *Berghia stephanieae* and *Hermisenda opalescens*

Christine A. Gordon - cgordon_ug@nec.edu

Mentor: James M. Newcomb, Professor - jnewcomb@nec.edu

Department of Biology and Health Sciences, New England College

Opsin, in conjunction with the chromophore retinal, contributes to photoreception in the eyes, as well as extraocular tissues. While opsin expression has been studied extensively in certain groups of animals, nothing is yet known about its extraocular localization in nudibranchs. In this study, we used immunohistochemistry (IHC) and *in situ* hybridization chain reaction (HCR) to localize extraocular opsin in neural and dermal tissues of two species of nudibranch – *Berghia stephanieae* and *Hermisenda opalescens*. Opsin was expressed throughout the dermis in both species, including the rhinophores, oral tentacles and cerata. In *B. stephanieae*, opsin was also expressed in some peripheral nerves in a few preparations. In the brain, opsin was expressed in a large number of neurons in both species, especially in the posterior region of the pleural ganglia. Furthermore, when comparing opsin expression in *B. stephanieae* with both IHC and HCR, labeling was exhibited in similar areas, suggesting that these two techniques were identifying the same ligand. These results suggest that both of these species have the potential capacity for extraocular photoreception.

Bioinformatic analysis of isolate and metagenomic sampling provides insight into bacterial makeup and antibiotic resistance of mastitis in milk producing cows and their environment in organic and conventional farms.

Ethan Edwards, NH-INBRE iSURF - Ethan.Edwards@unh.edu

Mentor: Kelley Thomas, Director - kelley.thomas@unh.edu

Hubbard Center for Genome Studies, University of New Hampshire at Durham

Mastitis is the inflammation of female breast tissue and subsequent clogging of milk ducts caused by bacterial infection. In humans, this can be remedied by treating mothers with antibiotics and by feeding infants with baby formula. However in the cattle industry, where pathogens are much more diverse and exports rely heavily on milk production, mastitis can cause an annual loss of \$2-billion dollars domestically and \$20- to \$32-billion worldwide. Biological sampling conducted through the joint efforts of Cornell University and the University of New Hampshire have been able to gather and culture bacterial pathogens from over 100,000 farms around the United States in an attempt to uncover a preventative solution to this problem. The aims of this project are to characterize the presence, virulence, and anti-microbial resistance profiles of bacterial strains present in both mastitis samples and stable environments to determine what pathogens are most likely to cause mastitis. This study was conducted simultaneously in farms that subscribe to conventional and organic rearing methods in order to accumulate a larger data set. To identify and quantify the types of bacteria, we used bioinformatics analyses on Illumina-seq data from both mastitis isolates and metagenomic sampling from stable environments to assemble bacterial genomes. The metagenomic data was then mapped to the isolate reads and statistically analyzed for percent coverage across each sample. By doing this, the bacterium present in both the environment and mastitis samples will make themselves known and the density of which will become apparent. Initial analyses suggest that the most likely culprits to be bacteria of the genus *Staphylococcus*, *Streptococcus*, *Escherichia*, and *Klebsiella*. This data, when combined with the anti-microbial profiles of each pathogen, will be able to assist the dairy industry by shining light on potential preventative measures and treatment methods that can be taken to counteract the effects of mastitis.

Faces: Building Bias Awareness in Bioethics Education Through UDL Designed Games

Hayden Rogers - hrogers762@Anselm.Edu

Mentor: Loretta L.C. Brady, Professor - lbrady@anselm.edu

Department of Psychology, Saint Anselm College

Major medical associations, institutes, and schools are now acknowledging and working to address racial, gender, and other biases in medicine is not a new issue. Improvements to curriculum and preparation to understand and address racial disparities in health and care, legacies of institutionalization, and to avoid inhumane practices in human research are underway. However, despite such calls to action, biases still permeate the fields of medicine and this poses specific risks as bioinformatics plays an increasing role in medicine and medical research. Medicalized racism (affecting data inputs) and social determinants of health (affecting data interpretation and synthesis) remain challenges to the effective equitable deployment of bioinformatics. The fields of bioinformatics and bioethics has to become more accessible in order to become more diverse and in order to effectively mitigate the bias systemic to medical and biomedical research preparation. The issues of accessibility can be addressed through Universal Design for Learning (UDL) and game based education is a powerful vehicle for this. This project reports on the construction of such a resource (Faces) drawing from National Institute of Health's (NIH) National Library of Medicine (NLM) archives, the home of bioinformatics and computational medicine for NIH and a repository for important bioethics examples of biomedicine's history. *Faces* is a card deck designed to provide bias awareness and introduce bioethics and bioinformatics principles to players. This card deck enables games to be played in three different play formats that each vary in time commitment and information intensity. They have been designed drawing on NLM resources, infused with bioethics principles, and designed using a UDL-based approach to build bias awareness and interest in the fields of bioinformatics across players. We present the game formats and playtest results from informal youth education settings and college research training settings.

Directed Evolution of Cancer-Targeting Antibodies Via Yeast Display

Nicholas Genovese, NH-INBRE iSURF – nicholas.genovese@my.colby-sawyer.edu

Mentor: Margaret Ackerman, Associate Professor - margaret.e.ackerman@dartmouth.edu

Department of Microbiology and Immunology, Dartmouth College

Targeting cancers with antibodies has proven to be effective. However, the antigens present on cancerous cells often vary, and as such, treatment using a single antibody is ineffective as it cannot target all malignant cells. Using multiple antibodies to fight cancerous growth offers a solution to this problem. Past studies have shown the effectiveness of polyclonal antibodies in treating tumor-bearing mice. We seek to expand upon this success by creating a diverse set of monoclonal antibodies capable of targeting different cancer antigens. We use yeast surface display combined with magnetic- and fluorescence-based selection approaches to enrich our single-chain variable fragment (scFv) yeast library for binders to melanoma antigens. A diverse library of yeast that expresses scFvs is screened against multiple melanoma antigens, creating a new library for each antigen. The sequences of the scFvs undergo error-prone PCR to induce mutations in hopes of increasing scFv binding affinity for the tumor antigen. By performing many rounds of selection and directing the evolution of our scFv libraries, we hope to create a potent cocktail of cancer-specific monoclonal antibodies capable of providing effective cancer treatment.



Monday, August 8th Poster Presentations

Poster Session I

1. **Bacterial Growth on 3D Printed Scaffolds**

*Samrat Adhikari, Md Ahasan Habib, Loren Launen, Slesha Tuladhar
Keene State College*

Being an extension of traditional 3D printing, additive biomanufacturing or bioprinting is a versatile technique that has its applications in regenerative medicine, bioengineering, and the manufacturing industry. Despite having a resemblance to 3D printing, it poses some extra challenges, mainly those mechanical and biological, prominently because it uses biocompatible materials. Among several roadblocks like cell viability, cell proliferation, and maintaining certain cell genetics while printing, the scaffold has a constant probability of being exposed to harmful bacteria. In addition to being biocompatible, it might also serve as a food supply for bacteria like E Coli. and other microorganisms. This research presents the ability of three scaffold compositions to support the 24-hour growth of Escherichia coli (a common bacterial model organism). The results obtained by spectrophotometry provide crucial indications of these scaffolds being intrinsically anti-bacterial given that there is absolutely no food supply. The outcome of this research can help selecting appropriate bio-ink for the 3D bioprinting process.

2. **Connecting Middle School Children to Scientists at all Levels in an Immersive Summer Experience**

*Jeadminas Alexis, Samrat Adhikri, Slesha Tuladhar, Sean Cady, Isabel Garcia, Safiye Yasan, Jacob Carroll, Sam Cook, Sarah McGregor, Md Ahasan Habib, Jason Pellettieri, Denise Junge, Priyanka Roy Chowdhury, Heather Jasmin, Loren Launen
Keene State College*

With funding provided by the NH EPSCoR Biomade program, we designed and implemented an immersive middle school one week summer camp experience at Keene State College offered through the Kids on Campus summer camp program. The camp (entitled Science Explorers) focused on foundational biology, physics, chemistry, and 3D printing as a gateway experience to science broadly and an introduction to concepts important in biomanufacturing specifically. Camp curriculum included hands-on training in the culture and microscopic examination of a variety of microbes and small animals, the physics of light and magnification important in imaging, basics of chemical reactions, the use of a 3D printer and an introduction to a state-of-the-art bioprinter. 12 children attended camp, four through a scholarship program. Six undergraduate students, two high school students, and six faculty members from different STEM disciplines co-designed and taught the camp. We present the curriculum, lessons learned, and our future camp plans.

3. **Utilization of CRISPR Knockout Technologies and FLOW Cytometry with FN14 Cell Surface Trafficking**

*Janelle Annor, Mathew Hayden
Dartmouth College*

CRISPR/CAS9 is an ever growing technological method that is involved in a variety of molecular and genetic screens. For our purposes, we hope to take a list of genes that code for all the genes involved in protein trafficking. From this list we will determine which of the genes result in a high number of Fibroblast growth factor-inducible 14 (FN14), and which genes result in a low number of FN14 on a cell's surface. To do this, we will use CLUE (custom library multiplexed cloning) to create plasmids coding for each gene, with the end result being a pool of plasmids that each contain a single guide RNA (sgRNA), where each sgRNA

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corresponds to a single gene from our original list of genes. Next we will create viruses for infection of CAS9 + sgRNA, this infection will knock out one gene at a time from our original list with the help of CRISPR/CAS9 machinery. Then we will use FLOW Cytometry as our means of coupling antibodies to the FN14 receptors, with the antibodies carrying a fluorescent dye which will serve to highlight the FN14 receptors. In general, FN14 is transiently up-regulated after injury, which is why in states of chronic inflammatory disease and in some solid tumors — most notably melanomas — FN14 is persistently up-regulated.

4. **Genome Annotation of bV_HerculesSTE**

*Ibrahim Ayyash
Franklin Pierce University*

The bacteriophage *bV_HerculesSTE* was discovered and characterized by Evan Bennett in 2021 from a soil sample taken at Franklin Pierce University. An array of computer programs, including NCBI's BLAST software and HHPRED, were used to annotate each gene of this bacteriophages' genome. Annotation included the length, start and stop locations, and potential functions of each gene. The full genomic annotation is currently awaiting publication in GenBank

5. **Culturing Fibroblast and Neural Stem Cells on Crosslinked Bioprinted Methacrylated Gelatin**

*Parker Baumann, John Sardella, Nicholas Mixon, Won Hyuk Suh
University of New Hampshire - Manchester*

Bioprinting is an additive manufacturing process that has found increased usage in recent years to produce tissues, bones, and blood cells. Due to the biocompatibility of polymeric hydrogels, such materials have been utilized to seed cells in multi-dimensional bioprinting procedures in order to construct three-dimensional (3D) soft tissue constructs. In this work, we sought to develop a protocol for rapidly bioprinting gelatin-based hydrogel structures via a Corning Maribot printer in order to potentially develop a high-throughput screening system involving human neural stem cells. The viability of mouse fibroblast cells and human neural stem cells were assessed on gelatin methacrylate hydrogel structures that were crosslinked via a radical polymerization method and an enzyme crosslinking method. Cellular experiments involved resazurin assay, calcein AM staining, immunocytochemistry, and fluorescence microscopy. Morphological analysis of the crosslinked structures was done via electron microscopy. Standard statistical analyses were performed to further assess the acquired data.

6. **Physiochemical Analysis of Crosslinked Gelatin: Photo- vs. Enzyme-Crosslinking**

*Matthew Woodworth, Ofori Mensah, Julia Castimore, David Suh, Won Hyuk Suh
University of New Hampshire – Manchester*

A hydrogel is a three-dimensional (3D) network of hydrophilic polymers that can swell in water, and it can hold a large amount of water while maintaining the structure due to the chemical or physical crosslinking of individual polymer chains. Hydrogels can be produced via synthetic processes, such as poly(ethyleneglycol) (PEG), or they can be harvested from a living organism, such as gelatin a collagen derivative. In this project, the physiochemical properties of crosslinked gelatin via photo-crosslinking vs. enzyme-crosslinking are investigated. Gelatin is a biocompatible and commercially affordable product and popular within the tissue engineering field. Gelatin is chemically cross-linkable; this process involves forming van der Waals interactions, covalent, ionic, or hydrogen bonds. Each chemical crosslinking type has its strengths and weaknesses. However, crosslinking with different methods will cause the gelatin to have different physiochemical properties. The photo-chemical crosslinking method used in this project involved lithium phenyl-2,4,6-trimethylbenzoylphosphinate (LAP) and gelatin methacrylate (GelMA) while (unmodified) gelatin and transglutaminase (TG) were utilized for the enzyme-crosslinking method. This comparison study will further guide us in the development of new bioink formulations involving protein-based biomaterials and human neural stem cells.

7. **An Analysis of the Mycobiome in Children with FPIES**

*Katherine Benjamin, Jeanelle Boyer, Brian Reese
Keene State College*

Food protein-induced enterocolitis syndrome (FPIES) is a non-IgE mediated allergy that primarily affects children ages 4 months to 3 years. Symptoms include vomiting and diarrhea about 1-4 hours after ingestion, which can lead to shock and, in severe cases, be fatal. The bacterial microbiome has been strongly associated

with IgE-mediated allergies, and our group has previously demonstrated associations with FPIES. Very little is known about the associations between the fungal mycobiome and allergy. Our current study examines the association of the mycobiome with FPIES. We analyzed and compared the mycobiome of children with FPIES and children who have outgrown FPIES. DNA was extracted and internal transcribed spacer (ITS) regions were amplified and sequenced. Using QIIME2, we compared diversity and taxonomy between the two groups of children to identify the species present.

8. Aspergillus-Induced Interferon Production by Dendritic Cells

Evan Bennett¹, Alexander Rapp², Joshua Obar²
¹Franklin Pierce University, ²Dartmouth College

Aspergillus fumigatus is a ubiquitous environmental mold that can cause invasive pulmonary aspergillosis (IPA), a severe respiratory disease, in immunocompromised individuals. There are over 300,000 cases of IPA and has a mortality rate of 30-50%. Due to the major public health concern, it is necessary to understand the pathogenesis of aspergillosis and why certain individuals are more susceptible. Alveolar macrophages that have mutations in RNA-sensing signaling pathways are more susceptible to aspergillus infection. Without these pathways, immune cells are unable to produce interferons which are essential to recruiting adaptive immune cells. These adaptive immune cells will eventually aid in the removal of the fungi thereby improving host survival. My research is aimed at understanding if dendritic cells utilize these RNA-sensing pathways upon infection and how it affects downstream interferon production.

9. The Effects of Chronic Exposure to Polystyrene Microplastics on The Development and Behavior of the American horseshoe crab, *Limulus polyphemus*

Austin Boynton, Christopher Chabot
Plymouth State University

Roughly 300 million tons of plastic waste are produced each year and much of this waste ends up in waterways and oceans where it degrades into “microplastics”, plastic particles (30%) and metamorphosis (>77%; $p < 0.05$). Post hatching analyses of behavior are currently in progress. These findings indicate that, even at low levels, microplastics have a detrimental effect on a species that plays an important role in its environment and economically. This study is the first on its topic and has shown that testing should continue with other plastics, and increased efforts should be made to limit the entry of plastics into the environment.

10. Predicting Suicide Risk in People with Epilepsy: A literature analysis of the use and value of machine learning

Samantha Brooks¹, Matthew Nemesure², Lindsay Schommer³
¹Rivier University, ²Dartmouth College, ³Dartmouth Hitchcock Medical Center

People with epilepsy (PWE) are at a 2.6 to 5 times higher risk of death from suicide. Machine learning (ML) algorithms can predict when patients with epilepsy are at risk of committing suicide. The purpose of this study is to review current literature related to ML and summarize the current use/opinions of ML in neurology, epilepsy, and suicide. A literature search was performed using: “ML and neurology,” “ML and epilepsy,” “ML and suicide” in PubMed, and “ML and suicide and epilepsy” in PubMed and Google Scholar. After MeSH refinement and abstract reviews, the results were narrowed to 18 articles. “ML and epilepsy” identified articles that demonstrated approval by clinicians for diagnosing different types of epilepsy, detecting drug-resistant epilepsy, predicting surgery outcomes, and ranking comorbidities. “ML and suicide” identified articles that determined the most vital risk factors for suicidal ideation (SI) and predicted how many days until someone attempts suicide. “ML and neurology” identified articles that showed excellent diagnostic performance in autism and prediction of stroke survivability. “ML, suicide, and epilepsy” identified articles that showed a need for further research and promising results of current clinical trials. There have been many neurology, epileptology, and suicidology experiments using ML. The current literature points to supporting ML use in the prevention of suicide in PWE and demonstrates the use of many useful tools. It was evident in all fields of research that ML is a promising path toward the prediction of suicide in PWE.

11. The Association Between The CTGF Promoter Variants and Cardiovascular Disease

Emily Carson, Alexandra Walker, Lorna Smith, Heather Doherty
Plymouth State University

Cardiac fibrosis is one of the primary causes of long-term complications of cardiovascular disease. Cardiac

fibrosis occurs when there is excess scarring of the heart tissues. This results in non-viable tissue and impacts the function of the heart. The Connective Tissue Growth Factor (CTGF/CCN2) gene is involved in normal wound healing and fibrotic tissue damage. CTGF promoter variants are thought to be associated with a generalized fibrotic disorder, systemic sclerosis. Although it is unknown whether there is an association between CTGF promoter variants and cardiovascular disease. We predict that there is an association between cardiovascular disease and promoter variants. We investigated this hypothesis by collecting cheek cell samples for DNA and a cardiovascular disease (CVD) family history survey from students and faculty at Plymouth State University. DNA was extracted from the cheek samples, Sanger sequenced, and base variants were mined using PolyPhred. The association between the base variants and risk factors was found using a Kendall's Tau b test. We found two base variants; G-450C (rs34599882) with a frequency of 0.026 and C-745G (rs6918698) with a frequency of 0.319. Preliminary results suggest that G-450C base variant may be associated with a family history of heart attack before 65, whereas C-745G may be associated with overall history of heart disease. Understanding an association between cardiovascular disease and CTGF gene promoter variants can lead to new therapies and personalized treatments to prevent CVD complications such as cardiac fibrosis.

12. Investigating a Novel Use for ddPCR in Melanoma Diagnosis

*Advaita Chaudhari, Jason McFadden, Peter Mikhlin, Edward Hughes, Rachel Barney, Marie Syku, Mirjana Stevanovic, Aravindhan Sriharan
Dartmouth Health, Geisel School of Medicine*

Skin cancer is the most common cancer in the United States; a majority of skin-cancer-related deaths are from melanoma. The current diagnostic assay for melanoma, array comparative genomic hybridization (aCGH), is time-consuming, expensive, and prone to misdiagnosis. Previous literature indicates that gains of MYC and deletion of MYB, also known as copy number variation, are biomarkers of melanoma, so accurately measuring copy number variation in melanocytic tissue biopsied from patients could provide objective evidence to confirm a melanoma diagnosis. Digital Droplet PCR is a technology with the ability to assess the copy number variation of target genes in a large volume of tissue within hours. Copy number data from the ddPCR assay can be compared to data from the aCGH diagnostic assay to assess accuracy and reliability. Our preliminary data indicates ddPCR provides an accurate and reliable copy number analysis of the MYC and MYB genes, in concordance with aCGH data. Using ddPCR technology, we aim to innovate a cheaper and faster diagnostic assay for melanoma.

13. Spatiotemporal Analysis of the Stem Cell Response to Injury in Planarians

*Emily Cornell du Houx¹, Ashley Seel², Shannon Berry², Maggie Rice², Alli Blouin², Haley Zanga², Jason Pellettieri²
¹Southern Maine Community College, ²Keene State College*

Spatiotemporal changes in stem cell division are hallmarks of regeneration in a variety of model organisms, yet the mechanisms governing these responses are not well understood. We are addressing this problem in *Schmidtea mediterranea*, an experimentally tractable planarian flatworm with the remarkable ability to regenerate any lost body part in just over a week. The foundational work of Wenemoser and Reddien revealed that amputation triggers a biphasic increase in the rate of division among the adult stem cells that drive formation of new planarian tissues during both homeostasis and regeneration. In an effort to further characterize these responses, we developed an automated image-analysis script for the open-source Fiji program and used it to quantify dividing stem cells labeled by whole-mount, phospho-histone H3 (H3P) immunostaining. After analyzing the staining patterns in over 2,000 animals fixed at multiple timepoints following a variety of different injuries, we determined that both the early and late mitotic peaks described by Wenemoser and Reddien exhibit pronounced gradation, with a significantly greater increase in cell division occurring proximal to the wound site. Unexpectedly, animals fixed at two hours, the earliest timepoint at which increased proliferation was evident, did not show the same pattern, instead exhibiting a more uniform, systemic response. We speculate that the nervous system may trigger a rapid, body-wide increase in the rate of stem cell division following injury, as has previously been documented in axolotls. Consistent with this scenario, we find that treatment of planarians with anesthetics decreases H3P labeling. In summary, our ongoing work on this project has provided new insight into how stem cell division changes after injury and may support the involvement of deeply conserved regulatory mechanisms.

14. **The Effects of Co-Culture on Antibiotic Production**

*Isabella Darling, Suzanne Cooke
University of New Hampshire - Manchester*

In microscopic ecosystems, many species of bacteria produce antibiotic compounds to give themselves a competitive advantage against other species. By inhibiting the growth of other microorganisms, the antibiotic producer can ensure that it has more reliable access to the resources and space necessary for its survival. Research into naturally-produced antibiotics typically focuses on isolating a bacterial species from its environment. However, this approach frequently results in a loss of antibiotic production over time. This occurs as successive generations of the bacteria species are no longer challenged by other organisms and thus have no need to prevent the growth of others. In a co-culture, two or more species of bacteria are grown together to encourage new interactions. The goal of my work was to examine whether bacteria grown in co-culture would produce antibiotic compounds for a longer time. Over the course of my research, I found that co-culture could be used to encourage antibiotic production in most isolates. An isolate grown in co-culture was found to produce antibiotic compounds longer than the isolate grown in an isolated lawn. This was especially noticeable in weak antibiotic producers which quickly stopped producing their secondary metabolites. Co-culture was also successful at inducing antibiotic production in isolates which had stopped producing antibiotic compounds after being frozen in glycerol stock. More complex co-cultures, where multiple isolates were grown together with an ESKAPE, were also effective at stimulating antibiotic production.

15. **Associations of Lifestyle Factors, Dietary Intervention and Health Conditions with the Skin Microbiome in College Students**

*Jonathan DeJesus, Jeanelle Boyer, Brin Reese
Keene State College*

The human microbiome is of interest because it relates to many health conditions, but previous research primarily focuses on the gut microbiome. The skin microbiome may be equally important and is understudied in comparison. We examined the relationship between a dietary intervention and lifestyle on the skin microbiome in 14 college students. Samples were collected from the (Ears, Back, Forehead). DNA was extracted, sequenced and the resulting data was analyzed using QIIME2 and Songbird. We found moisturizer use, alcohol consumption, season allergies and site of sampling to be significantly associated with the diversity of the skin microbiome. The skin is our largest organ on our body and helps defend our body against numerous infections. Finding out what influences it and how, might help us understand how our lifestyle may impact skin health.

16. **Bioinformatic analysis of isolate and metagenomic sampling provides insight into bacterial makeup and antibiotic resistance of mastitis in milk producing cows and their environment in organic and conventional farms**

*Ethan Edwards¹, Joseph Seigny², Lawrence Gordon², Kelley Thomas²
¹University of New Hampshire – Manchester, ²University of New Hampshire - Durham*

Mastitis is the inflammation of female breast tissue and subsequent clogging of milk ducts caused by bacterial infection. In humans, this can be remedied by treating mothers with antibiotics and by feeding infants with baby formula. However in the cattle industry, where pathogens are much more diverse and exports rely heavily on milk production, mastitis can cause an annual loss of \$2-billion dollars domestically and \$20- to \$32-billion worldwide. Biological sampling conducted through the joint efforts of Cornell University and the University of New Hampshire have been able to gather and culture bacterial pathogens from over 100,000 farms around the United States in an attempt to uncover a preventative solution to this problem. The aims of this project are to characterize the presence, virulence, and anti-microbial resistance profiles of bacterial strains present in both mastitis samples and stable environments to determine what pathogens are most likely to cause mastitis. This study was conducted simultaneously in farms that subscribe to conventional and organic rearing methods in order to accumulate a larger data set. To identify and quantify the types of bacteria, we used bioinformatics analyses on Illumina-seq data from both mastitis isolates and metagenomic sampling from stable environments to assemble bacterial genomes. The metagenomic data was then mapped to the isolate reads and statistically analyzed for percent coverage across each sample. By doing this, the bacterium present in both the environment and mastitis samples will make themselves known and the density of which will become apparent. Initial analyses suggest that the most likely culprits to be bacteria of the genus *Staphylococcus*, *Streptococcus*, *Escherichia*, and *Klebsiella*. This data, when combined with the anti-microbial profiles of each

pathogen, will be able to assist the dairy industry by shining light on potential preventative measures and treatment methods that can be taken to counteract the effects of mastitis.

17. Partner Communication and Disease Progression in Parkinson's Disease

*Keegan Finley, Sarah Gunnery
New England College*

This study investigated how conversation style relates to time since diagnosis in couples with one partner who has Parkinson's disease (PD) with the hypothesis that people who have had PD longer will have smoother conversations styles with their partners. Twenty-three participants with Parkinson's disease and their care partners were videotaped while discussing enjoyable and frustrating activities. These interviews were then coded for how much dyads traded off the conversation between themselves, how much each dyad member helped their partner finish thoughts and find words, and overall talkativeness on a scale from 1 (not at all) to 5 (a great deal). Findings showed a moderate and statistically significant relationship between years since diagnosis and the amount the care partner helped their partner with Parkinson's disease find words and finish thoughts during the conversation. This demonstrates a way that future research can potentially help support communication in dyads with Parkinson's disease by facilitating new tactics for understanding and coping.

18. Functional Variation in Flavor Genes Across 459 Yeast Strains Used for Beer and Wine

*Bailee Gallant¹, Petra Deane²
¹Plymouth State University, Mascoma LLC*

Saccharomyces cerevisiae, better known as baker's yeast, is the main microbial species used in the production of fermented drinks like wine and beer. Genetic diversity in the yeast genome confers unique qualities to fermented drinks affecting their taste, color, and smell, all of which are important for designing commercially successful microbial products for beverage markets. In this study I analyzed the genomes of 134 Lallemand yeast strains and 325 publicly available yeast strains to compare five genes associated with different taste profiles in wine and brewing yeast applications. I performed gene alignments and built phylogenetic trees to characterize functional diversity among strains, identifying cases where a strain in the Lallemand portfolio carries a unique copy of a flavor gene (e.g. FDC1 – ferulic acid decarboxylase) as well as cases where the company portfolio could be expanded to capture more genetic diversity (e.g. BAT1 – branched-chain amino acid transaminase). I also identified several important mutations causing protein truncation and loss of gene function. By performing comparative genomics on such a large scale across different lineages of yeast products, we can understand the value of certain strains from a marketing and consumer standpoint, as well as identifying interesting evolutionary patterns.

19. Directed Evolution of Cancer-Targeting Antibodies Via Yeast Display

*Nicholas Genovese¹, Colin Hartman², Margaret Ackerman²
¹Colby-Sawyer College, ²Dartmouth College*

Targeting cancers with antibodies has proven to be effective. However, the antigens present on cancerous cells often vary, and as such, treatment using a single antibody is ineffective as it cannot target all malignant cells. Using multiple antibodies to fight cancerous growth offers a solution to this problem. Past studies have shown the effectiveness of polyclonal antibodies in treating tumor-bearing mice. We seek to expand upon this success by creating a diverse set of monoclonal antibodies capable of targeting different cancer antigens. We use yeast surface display combined with magnetic- and fluorescence-based selection approaches to enrich our single-chain variable fragment (scFv) yeast library for binders to melanoma antigens. A diverse library of yeast that expresses scFvs is screened against multiple melanoma antigens, creating a new library for each antigen. The sequences of the scFvs undergo error-prone PCR to induce mutations in hopes of increasing scFv binding affinity for the tumor antigen. By performing many rounds of selection and directing the evolution of our scFv libraries, we hope to create a potent cocktail of cancer-specific monoclonal antibodies capable of providing effective cancer treatment.

20. Localization of extraocular opsin in the brain of *Berghia stephanieae*

*Christine Gordon, James Newcomb
New England College*

Opsin is a protein that interacts with the light-sensitive chromophore, retinal, and is used for photoreception in both eyes and extraocular tissues. Preliminary data from immunohistochemistry (IHC) indicates the

presence of extraocular opsin in the brain of the nudibranch *Hermisenda opalescens*. In this study, we used both IHC and in situ hybridization chain reaction (HCR) to investigate the localization of opsin in the brain of another nudibranch, *Berghia stephanieae*. With IHC, opsin protein was expressed in neurons throughout the brain, especially in the posterior region of the cerebropleural and pedal ganglia. Opsin mRNA was localized with HCR in similar regions of the brain. These data indicate that both techniques are likely labeling expression of the same gene. Furthermore, the presence of opsin in many neurons of the brain, which sits immediately below relatively translucent skin, suggests that this species of nudibranch may exhibit extraocular photoreception.

21. NH CLIMBS and the Collaboration with Advanced Solutions Life Sciences and Novo Nordisk

*Kendall Hawkom, Hunter Dupuis
University of New Hampshire – Manchester*

NH CLIMBS, which stands for Collaborative Learning through industry Internships and academic Mentorship in Biotech for Students, is an initiative spearheaded by Doctor Kristen Johnson to provide internship opportunities to students at the University of New Hampshire in Manchester. Internships provide students with the opportunity to gain workplace skills like networking, and to demonstrate skills gained from the classroom. NH CLIMBS specifically allows student-lead research in collaboration with industry partners while working on campus. This summer, NH CLIMBS collaborated with Novo Nordisk and Advanced Solutions Life Sciences on two separate projects. The two projects, one cell culture-based and one protein purification-based, were designed by the students based on the companies' objectives. At the conclusion of the internships, students will have demonstrated the ability to communicate with workplace professionals, develop projects independently, and continue to prepare for the next steps in their careers.

22. Molecular Dynamic Simulations of Hydrogels

*Haley Hildreth, Matthew Young, Harish Vashisth, Arpita Srivastava
New England College*

The purpose of this research is to create a computational model of a hydrogel using molecular dynamics (MD) to provide insight into how particular hydrogel systems capture cationic antimicrobial peptides (CAMPs). This research can help make a more efficient hydrogel for isolating CAMPs from complex mixtures. The monomer system we are using to simulate the hydrogel is comprised of 6-methacrylamidohexanoic acid (MA6AHA) and N,N'-methylene(bisacrylamide) (BIS), with a ratio of 4 to 1. The resulting oligomer is multiplied by 50 to make the polymer. This polymer is then replicated twice along its X, Y, and Z axes to adequately represent the hydrogel. We are using GROMACS, a MD application, to conduct our energy minimizations, and then visualizing the computational results using the VMD (Visual Molecular Dynamics) application. This work provides the basis for further computational work and will later be compared to actual experimental data. The resulting energy minimized model structure can be used to guide the creation of a more efficient hydrogel "net" that isolates the CAMP.

23. SkpA Annotation in Various *Drosophila* Species

*Joshua Hughes, Hannah Johnson, Lauren Pribyl, Forrest Villeaux, Shallee Page
Franklin Pierce University*

SkpA is a gene that is found on the X chromosome in *Drosophila* species. The gene itself is believed to code for ubiquitin ligases (Flybase). These ligases have an influence on the cell cycle progression and chromatin condensation in the X chromosome through nuclear signaling cascades (Flybase) (Natoli & Chiocca, 2008). Through the auspices of the Genome Education Partnership (GEP), the SkpA gene was previously annotated in *D. melanogaster*. This annotation was utilized as a tool for annotating the same gene present in *D. willistoni*, *D. ananassae* and *D. grimshawi*. The gene annotation in these three species was recorded and a gene model was established. Once completed, the gene model has been compared to the GEP model checker. The final part of this protocol involved completing a standardized report form for the annotation which is submitted to GEP. Over the summer research so far, the SkpA gene in *D. ananassae*, *D. willistoni*, and *D. grimshawi* have been successfully annotated. Currently, of these three projects, two have been submitted to GEP. Future analyses would include comparing predicted gene function and additional work annotating regulatory regions of the genes.

24. Using Molecular Dynamics to Explore Hydrogel Structure

*Ty Hunter, Matthew Young
New England College*

This project aims to use molecular dynamics to create theoretical models of N-Isopropylacrylamide (NIPAm) based hydrogel particles and to optimize them to capture cationic antimicrobial peptides (CAMPs). The first steps are to explore the structure of the hydrogel and the process of hydrogelation. Hydrogels are complex systems of three-dimensional colloidal particles made of covalent cross-linked natural or synthetic amphiphilic polymers where water molecules get confined by cohesive forces. Molecular dynamics (MD) is a way to explore how hydrogels are built and how they move and react within a three-dimensional space. The NIPAm-based particle systems can be fine-tuned by adjusting the percentage of cross-linking agent bisacrylamide (BIS). This is explored by using MD software to build the hydrogel and perform simulations that provide a greater understanding of its structure. These simulations will gather data based on temperature, density, pressure, total energy output, radial distribution, and hydrogen bonding. The long-term goal is to optimize hydrogels to improve their ability to capture biomarkers with molecular properties consistent with antimicrobial peptides (AMPs).

25. Gene expression of Δ FosB, EFR3A, SYT4, CX3CR1, and FLT1 in the hippocampus of postmortem human brain from opioid overdose

*Lauren Herrera, Madisyn VanHorn, Leila Jabbour
Franklin Pierce University*

FosB is a transcription factor present in normal cells, while its truncated form, Δ FosB, was reported to be highly expressed following chronic drug exposure. Δ FosB is unique in that it accumulates in response to repeated stimulation due to its unusual protein stability. Animal studies have established the role of Δ FosB in addiction, however, little is known about it in humans with opioid use disorder. In collaboration with the New Hampshire Medical Examiner, a unique human postmortem tissue collection was obtained following opioid overdoses. We dissected hippocampi from both control and opioid cases. Using immunohistochemistry, we assessed the presence of the FosB and Δ FosB proteins. Qualitative analysis revealed a consistent nuclear appearance of Δ FosB protein in the dentate gyrus and cornu ammonis regions of the hippocampus, while FosB was in contrast, barely visible or absent in most cases tested. Therefore, as seen in the rodent model, Δ FosB is the dominant form of the fosB gene expressed in the opioid-exposed human brain and may have a similar role in humans. That is: Δ FosB gradually converts acute drug responses into relatively stable adaptations that contribute to the long-term neural and behavioral plasticity that underlies addiction. Additionally, we used a comprehensive multiplex gene expression analysis assay (Nanostring®), to evaluate gene expression in the hippocampus (control n=4; opioid n=5). We normalized against housekeeping genes and we normalized for batch, sex, and age differences. Following these stringent normalization steps, we identified 9 significantly differentially expressed genes (with a p-value below 0.05). Out of the 9 biologically significant genes, EFR3A, SYT4, CX3CR1, and FLT1 presented with distinct means between control and opioid samples, which is also significant. Transcription factor E2F3a mediates cocaine's effects on gene expression and addiction-related behaviors (Cates, Nestler, 2019), while SYT4 is implicated in synaptic transmission. CX3CR1, a receptor expressed on microglia, may protect against microglial neurotoxicity, while FLT1, which is a receptor implicated in angiogenesis, is modulated by morphine. Our findings provide new insights into gene expression in cases of opioid overdose. Work is underway to better understand the role of these genes in the context of opioid use disorder so that strategies can be applied to the development of therapeutics for the treatment of opioid abuse.

26. Care Partner Perceptions of Parkinson's Disease

*Felicia James, Sarah Gunnery
New England College*

Care partner (CP) burden and burnout are serious concerns for people caring for a spouse with a chronic health condition. This study investigated how CPs' perceptions of their partners with PD are related to their own quality of life (QoL). We found that CPs with lower quality of life thought their partners with PD had more negative thoughts though there was no connection between quality of life and perceptions that their partner was thinking about their disease. These findings give potential avenues for addressing care partner QoL in Parkinson's disease.

27. The effect of FOXN2 gene depletion on the induction of primary cilia in human pancreatic cancer cells

*Dawin Khiev, Jordan Fessenden, Kristen Johnson
University of New Hampshire – Manchester*

Pancreatic cancer has a 5-yr survival rate of less than 10%, and there is a desperate need for a greater understanding of the cellular and molecular underpinnings of this disease in order to allow better diagnosis and treatment. FOXN2, a member of the forkhead domain binding protein family, was identified in a transcriptional profiling screen as a master regulator whose expression and activity are increased in the progression from pancreatic intraepithelial neoplasia (PanIN) to pancreatic ductal adenocarcinoma (PDA). In addition, data from the TCGA database indicates that high levels of FOXN2 are associated with poor overall survival. RNASeq analysis following knock-down of FoxN2 in two human pancreatic cancer cell lines reveals a role for FOXN2 in cilia biology. Knockdown of FoxN2 leads to upregulation of several genes involved in cilia assembly, movement, intraciliary transport, protein localization, and modification. Cell biology studies are underway to determine the presence and function of cilia in FOXN2 deficient cells.

28. Exploring Barriers Experienced by Cancer Patients Enrolling in Clinical Trials

*Maya Langa
Plymouth State University*

When accessing healthcare, experiencing barriers is a typical formality for many individuals despite their healthcare needs. This issue is especially apparent regarding cancer patients enrolling in a clinical trial. Using case examples and an extensive literature review, the barriers that cancer patients face when enrolling in a clinical trial are explored. The literature recognizes that structural, clinical, demographic socioeconomic, and attitudinal (patient and physician) factors are all barriers associated with these low cancer clinical trial accrual rates. With the knowledge that only 5% of cancer patients enroll in a clinical trial, it is significant for cancer institutions and study sponsors to understand the barriers preventing patients from enrolling in a clinical trial. To sustainably change the rate of patient enrollment, it is dependent upon both the provider and health care system to increase patient knowledge of clinical trials, acknowledge the financial burden that enrollment has on patients, implement greater eligibility criteria for diverse populations, and adjust the overall attitude that providers have in regards to clinical trials, among various other needs.

29. Testing a custom-made perfusion bioreactor for 3D Bioprinter scaffolds

*Jack Mankowsky, Connor Quigley, Scott Clark, Md Ahasan Habib
Keene State College*

A Perfusion Bioreactor Is a medical device that simulates an in-vivo environment for cells by flowing complete medium throughout the cell. This medium is designed to give microorganisms the support and nutrients they need to survive. In this work, we will encapsulate living cells with Biomaterials (also known as Bio-ink) for 3D Bio-printing purposes. The patient-specific 3D printed scaffolds will be housed in our custom-designed and prototyped perfusion bioreactor and several tests will be performed such as the viability of different scaffold porosities, shapes, sizes, and finally, the survivability of the encapsulated cells. As a test case, we 3D printed a set of scaffolds using 4% Alginate (A) and 4% Carboxymethyl Cellulose (CMC), i.e. A4C4. The result was proven successful in terms of shape fidelity. For example, the shape fidelity of the A4C4 printed scaffolds were not altered after an hour of perfusion. In the future, we are planning to use various material compositions and living cells to test the effectiveness of our perfusion bioreactor.

30. Examination of NEMO - IκBa interaction in NF-κB pathway

*Grace McLaughlin^{1,3}, Eva Cushai², Maria Pellegrini³, Dale Mierke³
¹Colby-Sawyer College, ² Transylvania University, ³ Department of Chemistry, Dartmouth College*

The nuclear factor kappa-light-chain enhancer of activated B cells (NF-κB) pathway plays an important role in many cellular processes spanning from immune responses to regulation of cellular activity. Aberrant NFKB activity leads to inflammatory diseases, autoimmune diseases, and cancers. NF-κB essential modulator (NEMO) is the scaffolding protein in the NF-κB pathway, which brings the kinases IKKα and IKKβ together. The purpose of this study is to understand how the NEMO works, and to observe protein-protein interactions in the pathway. The Pellegrini Laboratory focuses on designing small molecule inhibitors for therapeutic benefits and is working to understand the importance of structural motifs found throughout NEMO. Pulldown assays and gel electrophoresis on SDS-PAGE gel are used to visualize the protein-protein interactions.

31. **Irradiated Tumor Cell Vaccine to Prevent Ovarian Cancer Relapse**

*Peter Mikhlin, Alexander Misiazek, Steven Fiering
Dartmouth College*

Ovarian cancer is the deadliest gynecological cancer. Occurring mostly in post-menopausal women, ovarian cancer symptoms do not generally occur until the disease has metastasized and then are often dismissed because they present as abdominal pain and distension. Thus, ovarian cancer is typically discovered when it is in stage 3. Surgical debulking and chemotherapy are currently the standard treatments that generally puts the disease into remission. However, the period of remission often leads to relapse. One possible solution to preventing relapse is an injectable vaccine composed of treated tumor tissue from the debulking site and an adjuvant to stimulate immune response against the tumor antigens. We work with an adjuvant of cowpea mosaic virus (CPMV) and combine that with inactivated tumor cells. CPMV is an effective vaccine adjuvant that activates the immunostimulatory response against cancer cells in mouse models. When paired with irradiated cancer cells, the immune system could develop a robust systemic antitumor response and prevent relapse. In this experiment, we will use a mouse model with established disseminated ovarian cancer (aggressive ID8) comprised of four treatment groups: Phosphate-buffered saline (control), irradiated cancer cells, CPMV only, and irradiated cancer cells plus CPMV. These treatment groups, each containing five mice, will be injected with the treatment weekly for 4 weeks. According to previously published literature, a similar strategy of using CPMV as a prophylactic vaccine was an effective treatment that greatly slowed tumor development after live tumor cell inoculation. With our experiment we hope to further establish CPMV as a useful and effective antitumor vaccine adjuvant for stimulating antitumor immune response during the period of remission common in ovarian cancer, especially when paired with irradiated cancer cells.

32. **NH Mountain Soil Bacterial Diversity**

*Raymond Miller, Suzanne Cooke
University of New Hampshire – Manchester*

Soil bacteria diversity is a powerful metric that can show the health and sustainability of an ecosystem. Samples collected in 2019 were processed to isolate as many distinct bacterial species as possible by using research standard Petri dish culture techniques under normal laboratory conditions. Isolated species were processed to extract DNA using a novel technique which reduces plastic and biohazard waste by nearly 75%. DNA was analyzed via Sanger sequencing of the 16S rRNA encoding region and results were compared to data within the National Center for Biotechnology Information Basic Local Alignment Search Tool. Of the 140 currently isolated species, 73 have been tentatively identified as commonly found soil bacteria including *B. mycoides*, *V. arvi*, *S. psychrophila*, and *S. globispora*. Further analysis is required to determine a statistical significance of diversity. Future work includes the completion of all DNA analysis of isolated species and a meta-comparison of diversity between multiple mountains.

33. **Cancer and Marijuana Use: What Do We Know?**

*Madelyn Moedebeck¹, Elizabeth McGrath²
¹Rivier University, ²Dartmouth Hitchcock Medical Center*

Marijuana is the most commonly used illicit substance in the United States. Laws and regulations surrounding marijuana make it difficult to research, leaving its safety and efficacy unclear. Reports show that 25% of cancer patients have turned to marijuana to reduce disease and treatment-related side effects including pain, weight loss, and nausea and vomiting. Providers lack the knowledge to properly advise their patients on the use of marijuana, and many providers don't inquire about use in their patients. A literature review was conducted to see what information has been gathered on marijuana use in cancer patients. Studies are few and far between, but many show potential harm to patients due to the interactions between marijuana and chemotherapy agents. The potential harms associated with marijuana use in cancer patients indicate a need for further research. Due to these findings, the Norris Cotton Cancer Center at DHMC will create and administer a survey to patients regarding use and further details surrounding use if prompted. The goal is to learn about use in cancer patients and provide education to patients regarding potential benefits and harms. Additionally, findings can be used to further educate providers on marijuana use and encourage open discussion between the provider and patient.

34. An Analysis of Coral Metatranscriptomes in States of Health and Disease

*Abigail Peschel, Geoffrey Cook
New England College*

All multicellular organisms are hosts to a vast microbial community. These microbial communities can both help, and harm the host, and to maintain homeostasis of these commensal bacteria, the hosts create anti-microbial peptides or AMPs. These peptides are created through gene expression and are part of the innate immune response. They have the ability to attack bacteria in different ways than antibiotics. Studies have shown that stress can cause microbial dysbiosis, resulting in morbid conditions. The reef-building coral *Orbicella faveolata*, is a holobiont full of many taxa. By studying the metatranscriptome of this holobiont in different states of health, we may see how the gene expression changes, and how this can compare to the levels of AMPs found and the dysbiosis that occurs when under morbid conditions. By collecting the metatranscriptome of coral fragments in states of health, disease, and recovery, and assembling the reads, we may see how gene expression is altered and what that means for the holobiont.

35. Open-Source Medical Device: A Case Study on Manufacturing a Medical Syringe Pump System

*Richard Phipps Jr., Wei Lu
Keene State College*

The recent rise of open-source medical cyber-physical systems has rapidly changed the current healthcare industry mainly due to the technology development in 3D printers and the widely deployed ecosystem of open-source microcomputer systems such as Arduino and Raspberry Pi. Their widespread use in hospitals, however, has also paved a way for a large number of cybercriminal activities targeting these networked devices, raising serious security and privacy concerns when healthcare professionals deal with sensitive and life-critical medical information. In this research, we present how to manufacture an open-source medical syringe pump step by step, using simple hardware parts, a 3D printer, a Raspberry Pi system, and an Arduino microcomputer, where the contributions mainly include (1) the open-source medical syringe pump is validated to cost less than \$300 which is much cheaper than the same commercial products in the market, (2) the pump device can be manufactured in a couple of days, addressing potentially the supply chain issues caused by the COVID-19, and (3) the manufacturing work lays out the foundation for our research in the next phase to investigate a comprehensive intrusion detection system for preventing cyberattacks against these individual open-source medical devices.

36. The Role of Cell Division in Regeneration of Rhinophores in *Berghia stephanieae*

*Lourdes Ricks, James Newcomb
New England College*

Regeneration is exhibited by certain animals, such as the nudibranch *Berghia stephanieae*. The goal of this study was to investigate the role of cell division in *Berghia* regeneration, using phosphorylated histone 3 (H3P) as a marker for cell division. For each animal, the right rhinophore was amputated at the base, while the left rhinophore was left alone, to be used as a within-animal control. Following amputation, cell division was assessed via H3P immunohistochemistry, and then counting the number of H3P-positive cells in the regenerating rhinophore, as well as an equivalent-sized area in the control rhinophore. To see if cell division was more prevalent at various stages of regeneration, each animal was fixed immediately (n=12), or at 4 hours (n=8), 24 hours (n=6), 3 days (n=7), or 7 days (n=8) after amputation of the rhinophore. H3P-positive cells were present in all control rhinophores, indicating a baseline level of cell division. At the initial time point, amputated rhinophores had a significantly lower number of H3P-positive cells than the control rhinophore (p = 0.003). However, by 4 hours, the number of H3P-positive cells was the same between lesioned and control rhinophores. Three days after amputation, the number of H3P-positive cells in the regenerating rhinophores were almost significantly higher than controls (p = 0.057), and by 7 days after lesion, the regenerating rhinophores exhibited a significantly higher number of H3P-positive cells (p = 0.017). These data indicate regeneration of rhinophores in *Berghia* involves cell division, but not until at least several days after injury.

37. Developing a purification scheme for the transmembrane region of Atg32

*Yahira Rivera¹, Devika Andhare², Michael Ragusa²
¹Delaware State University, ²Dartmouth College*

Mitochondria are key component of cellular metabolism. The mitochondria's main role is to maintain cellular respiration which generates most of the cell's energy through ATP production. To maintain a healthy pool of

mitochondria and promote cellular health, the cell has evolved the process of autophagy to degrade and recycle damaged organelles. Atg32 is an autophagy-related protein located on the outer membrane of the mitochondria. Atg32 initiates the process of mitochondrial autophagy (mitophagy), which leads to the engulfment of a portion of the mitochondria within a double-membrane vesicle. Atg32 forms an initiator complex along the mitochondrial surface. Even though Atg32 is known to facilitate the process of mitophagy, information on the three-dimensional structure of the transmembrane region of this protein is lacking. Therefore, we set out to optimize the expression and purification of the transmembrane region of Atg32 (Atg32-TM) for downstream structural and biochemical studies. The purification was achieved via a four-step process. First, we lysed the *E. coli* cells expressing Atg32-TM using a microfluidizer. Second, the isolation of Atg32-TM was achieved via affinity chromatography using a Strep-Tactin XT resin. Third the column was washed with two different wash buffers containing different concentrations of sodium chloride to remove non-specific proteins from the resin. Lastly, an elution buffer was used to release Atg32-TM from the resin. To confirm the purity of the protein, we took multiple samples throughout the purification and analyze them on SDS-PAGE gel. Once the samples are loaded onto the gel, the samples from the elution fractions that display an intense band of the expected molecular weight will be further purified using size exclusion chromatography (SEC). SEC separates molecules based on their size; further purifying Atg32-TM and allowing us to assess the homogeneity of the sample. Successfully purifying the Atg32-TM will allow us to utilize this sample for downstream application to better understand the mechanism of selective autophagy initiation.

38. Circadian rhythms of locomotion in the nudibranch, *Berghia stephanieae*

Maxwell Ross, YaXi Stapp, James Newcomb
New England College

Circadian (~ 24 hr) rhythms are expressed by many living organisms, and help to synchronize behavioral, mental, and physical functions with the environment. This study examines movement of *Berghia stephanieae* (n=18) to investigate circadian rhythms. Animals spent three days in regular light-dark cycles (12 hours of light and dark, respectively) followed by constant darkness for four days. Locomotion was recorded with a digital time lapse camera, and then quantified using Ethovision XT. The output from Ethovision was analyzed in Actogram J to create actograms and identify any significant circadian rhythms. In this experimental setup, 77% of subjects demonstrated nocturnal behavior during regular light-dark cycles, and 56% of the animals exhibited significant circadian rhythms in constant darkness, with an average tau of 26.3 hr. These results suggest that *Berghia* is nocturnal and has an internal clock for circadian rhythms of locomotion.

39. Identifying postsynaptic targets in the zebrafish visual system using trans-Tango

Sona Sahakyan¹, Daria Naumova², Cagney Coomer², Marnie Halpern²
¹Colby College, ²Dartmouth College

There are 86 billion neurons that form intricate circuits in the human brain, not all of which are mapped. Different approaches help study these connections, including optogenetic-assisted circuit mapping and paired recordings from synaptically coupled neurons. Replication-deficient neurotropic viruses can also be used but are limited to genetically defined neurons within the circuit and have a low efficiency of transsynaptic transport. Few of these methods permit genetic access to neural populations of interest. The anterograde transsynaptic tracing system trans-Tango is one successful approach that has been used to trace neural projections in *Drosophila*. It is a synthetic signaling system based on the human glucagon signaling pathway, which has recently been adapted to a vertebrate model, the zebrafish *Danio rerio*. The glucagon ligand is tethered to the presynaptic membrane and binds its receptor across the synapse. Upon activation of the receptor, an Arrestin-protease fusion protein is recruited and induces proteolytic site-specific cleavage, which frees the QF transcription factor at the intracellular tail of the receptor. QF can then move to the nucleus, where it promotes the transcription of genes under the control of its upstream activating sequence (QUAS), such as a fluorescent reporter. Here, we present the use of trans-Tango to label potential postsynaptic targets in the zebrafish visual system. Amacrine cells constitute the most diverse retinal cell type. While their synaptic connectivity with retinal ganglion cells and bipolar cells has been widely studied, the chemical synapses formed between different amacrine cell subtypes have not been well characterized. We used trans-Tango and immunolabeling to help elucidate these circuits in the larval zebrafish retina, specifically focusing on the postsynaptic partners of dopaminergic amacrine cells.

40. **Sex Differences in the Discriminative Stimulus Effects of Nicotine in Rats: Drive State Variation**

Sarah Siudut, Adysn Kilty, Caroline Kukas, Joseph Troisi II
Saint Anselm College

Men and women differ in abstaining from nicotine (i.e., smoking), which may be in part attributed to their separate internal perceptions of the drug effect and withdrawal. We investigated sex differences in the interoceptive stimulus effects of nicotine under high and low drive states (food restriction and adlib feeding, respectively) in 16 Sprague-Dawley rats (8 of each sex). In an operant conditioning procedure, food-restricted rats were first trained to nose poke for food-reward on an intermittent schedule of food reinforcement (variable 30 sec). During interoceptive conditioning, for half of the rats, pre-session subcutaneous administration of nicotine (0.3 mg/kg; base) occasioned food-reward for nose poking (SD); on other sessions, saline occasioned no reward for nose poking (S Δ). The role of nicotine was counterbalanced for the other group and functioned as the S Δ (occasioned no reward) and saline was SD. All rats showed clear nicotine discrimination while food restricted and sated. Nicotine SD response rates fell 50% when rats were maintained on adlib feeding, but such rates remained greater than the SD rates; that is, discriminative control was unaffected by satiety, but motivation to respond decreased. With the rats under continued satiety on adlib feeding, extinction sessions produced a significant decline in responses over time, but females showed higher rates throughout compared to males and took significantly longer for extinction to be attained. Rats in the nicotine SD condition showed a much higher response rate after a recovery session, with a robust recovery in females relative to the males. The data from the reinstatement sessions after extinction training in conjunction with the extinction results suggests sex difference in responses to nicotine under different drive states during extinction training and response recovery. These data are consistent with reports that women have a more difficulty abstaining from nicotine self-administration (smoking) and have higher rate of relapse than men.

41. **Using Quantitative Mass Spectrometry to Compare Protein Expression in Haploid, Diploid, and Aneuploid Yeast (*S. pombe*)**

Angela Slaybe, Anna Michaud, Megan Wozniak, Alexandre Pennell
Saint Anselm College

We used quantitative mass spectrometry (QMS) to identify differences in protein expression among haploid, diploid, and four stable aneuploid strains of the yeast *Schizosaccharomyces pombe*. Since aneuploidy is a characteristic of cancer cells, proteins that play a role in aneuploid yeast survivorship may also be critical to human cancer cell viability. Our results indicate a proteome of 4,090 proteins in *S. pombe*, many of which showed uneven expression levels between haploid, diploid, and aneuploid strains. Some proteins of interest already identified include Upstream frameshift (Upf) proteins, which are expressed at higher levels in the T-5 aneuploid strain compared to haploid and diploid strains. Upf proteins function in nonsense-mediated mRNA decay (NMD), a pathway responsible for destroying aberrant mRNAs and preventing synthesis of the proteins they encode. ISP3 and glucoamylase proteins, which are both involved in ascospore production, were expressed in far greater abundance in diploid cells than in aneuploid and haploid cells. These findings help validate QMS results because only diploid yeast produce ascospores. We await further QMS data, including identities of all phosphorylation sites from experiments with T-1, T-2, T-4, and T-5 aneuploid strains.

42. **Fighting cancer by starving the cancer cell or feeding the immune system**

Trang Tong¹, Ziwei She², Henry Higgs²
¹Plymouth State University, ²Dartmouth College

Today, cancer is one of the most deadly health problems in the world and some cancers still don't have any effective treatments. Oncology has undergone a revolution thanks to immunotherapy, which today offers a special branch of cancer treatment that allows the immune system to eliminate cancer cells. T-cells are a type of white blood cell that can help the body and fight cancer. The main role of T-cell is to directly kill infected host cancer cells, activate other immune cells to produce cytokines and regulate immune response. In this research, we used various treatments including CCCP, Oligomycin and Metformin - which inhibit the proton channel of ATP synthase or complex I within inner membrane, an inhibitor required for the oxidative phosphorylation of ADP to ATP (energy production) to characterize the effect of ADA on cellular metabolism. These drug treatments added into cancer cells can destroy the mitochondria that cause mitochondrial dysfunction and will not generate enough ATP production. Mitochondrial dysfunction can cause perimitochondrial actin polymerization, known as ADA (acute damage-induced actin). ADA is essential for the quick activation of glycolysis, which is a major source of ATP and other metabolic products, when mitochondrial ATP generation is inhibited. Two situations that can happen when treating cells with drugs:

either the glycolysis level of cancer cells increases or they will not be affected. We expect to see whether drugs can stimulate cancer cells and increase the glycolysis level, cancer cells will continue to grow and win the T-cells. Whereas if the glycolysis level of cancer cells does not increase, drugs will raise that level of T-cells and will be able to fight cancer. The long term goal is to figure out which types of cancer cells should be treated with drug treatments and will not increase the level of glycolysis that in turn facilitates T-cells by activating the glycolysis level to inhibit the spread of cancer. Our preliminary cell culture and lactate assay data indicate that three cancer cell types (U2OS, B16 and MC38) react differently with or without treatment at different points of time. My project continues to use in vitro cell culture to test several cancer cell lines for drug response. Key words: cancer cell, T-cell, glycolysis, mitochondrial dysfunction, ADA

43. Tagging Acute Myeloid Anemia cells using Luciferase bioluminescence in Fanconi Anemia patients

*Andy Trinh, Tingting Huang
Dartmouth College*

Fanconi anemia (FA) is a genetic disorder characterized by multiple congenital anomalies and predisposition to a variety of cancers and hematological abnormalities, especially acute myeloid leukemia (AML). Unfortunately, FA-AML is a secondary AML with a very poor prognosis. New therapies are needed for AML in FA patients. It has been established that inhibiting the PD-1/PDL-1 interaction can upregulate T-cells killing AML cancer cells, but because we cannot target where AML cells grow in the bone marrow, thus we are not able to use PD-1 inhibition for treatment. We have hypothesized that firefly luciferase, a light-emitting enzyme responsible for the bioluminescence of fireflies and click beetles, can be used to “tag” AML cells in the bone marrow through lentiviral infection. To construct the lentivirus, we used psPAX2 and MD2.G packaging plasmids along with a pCDH-CMV-MCS plasmid, which contains tdTomato, a bright fluorescent protein. Combined with luciferase, we expect this lentivirus to be able to transduce luminescence of FA-AML cells in the bone marrow of NSG mice and the applications of this research can aid in targeting FA-AML treatment via PD-1 inhibition.

44. Synthesis and Evaluation of Diamide Des-Carboxylate Flufenamic Acid Analogues for Hippo Pathway Inhibition

*Mackenzie Vallely, Jennifer Pace
Saint Anselm College*

The Hippo Signaling pathway plays a crucial role in regulating cell proliferation, differentiation, and apoptosis. In the pathway's inactive state, two homologous transcription factors: Yes-associated protein (YAP) and transcriptional coactivator with PDZ binding motif (TAZ) form a heterodimeric complex with TEA domain transcription factor (TEAD). This transcription complex activates the expression of Hippo-responsive genes responsible for an increase in cell proliferation and inhibition of apoptosis. Due to this mechanism, the Hippo pathway has become a promising target for cancer research as this uncontrolled cell proliferation has been linked to a variety of cancers including pancreatic, breast, and prostate cancer. Flufenamic Acid (FA) is an NSAID that is approved to treat inflammation in various parts of the world and has been studied as a Hippo pathway inhibitor. While FA does inhibit the Hippo pathway, its mechanism of inhibition results in the disruption of TEADs function. To further explore the structure of FA in terms of this novel Hippo pathway inhibitory activity, a series of diamide FA analogues have been designed, synthesized, and studied in preliminary biological assays.

45. Isolation and Characterization of a Bacteriophage for E. coli K-12 from Guano of E. fuscus

*Forrest Veilleux, Shallee Page
Franklin Pierce University*

Bats are known to host a wide array of coliform bacteria, including numerous strains of Escherichia coli. However, little is known about the coliform bacteria of many bat species, nor the bacteriophages specific to them. In this study, a bacteriophage for E. coli K12 was isolated from guano produced by Eptesicus fuscus, the big brown bat. This phage produces large, clear plaques (~7mm); therefore, it was easily purified using standard procedure. The isolation was effected through enriching a sample of guano along with E. coli K12 and conducting three rounds of dilution, followed by the collection of lysate and DNA purification. The guano sample was obtained from a barn inhabited by an individual of E. fuscus. Gel electrophoresis against a lambda marker standard indicated that the genome is >20 KB, and likely ~50 KB.

46. Optimization of Multiplex qPCR to Analyze and Quantify Cytokine Expression in Human-Engineered Tissue Samples

*Sadie Vezina, Monique Gingras
University of New Hampshire at Manchester*

Real-time Quantitative Polymerase Chain Reaction (RT-qPCR) is the selective amplification of genetic sequences via primers and probes designed for the sequence of interest. Multiplex qPCR enables co-amplification and analysis of multiple target sequences in a single reaction vessel. Multiplex qPCR requires less time and materials, enabling increased sample processing capacity, and allows for the analysis of multiple cytokines interacting during a single qPCR reaction. The goal of this project was to design and optimize a multiplex qPCR protocol to improve the efficacy of the quantification of cytokine expression from tissues engineered and studied at Advanced Solutions Life Sciences. RNA from tissue samples was extracted and converted into cDNA for use in qPCR. Multiple rounds of optimization were performed to validate the efficacy of the multiplex assay. The cytokine genes are being analyzed to produce a predictive model for quantifying tolerogenic and immunogenic cytokine expression to determine immune activity in a variety of tissue models.

47. Exercise Incontinence Among Average Active Women: Parity, Birth Trauma, and Barriers to Exercise

*Megan Welch¹, Bridget Linehan²
¹University of New Hampshire – Durham, ²Dartmouth Hitchcock Medical Center*

Background: Up to 80% of women experience urinary incontinence (UI). While prior research explores UI in elite athletes, few studies touch on the average active woman. We generated a comprehensive screening tool to assess the rate and experience of UI among active women. Objective: The purpose of this study was to explore the experience of exercise incontinence in average active women including parity (given birth), things women do to manage their exercise incontinence, and the rate of birth trauma among women who experience exercise incontinence. Methods: The Active Women's Incontinence Screening Tool (AWIST) was administered to 143 females who are over age 18 and not currently pregnant. Basic statistics were employed, and, when appropriate, a single-factor ANOVA analysis. Results: Parous women (n=74) have a higher rate of exercise incontinence (P-Value=0.019) compared to nulliparous women (n=69). 79% of parous women who experience exercise incontinence also experienced birth trauma during vaginal delivery. Of the women who experience exercise incontinence (n=67), 45% wear a pad or tampon to decrease leaking during exercise, and 41% worry about what they'll wear during exercise. Conclusion: There are a variety of barriers that inhibit or stop women from exercising. Parous women are more likely to experience exercise incontinence than nulliparous women. Vaginal birth trauma increases the risk of exercise incontinence. Given the vast health benefits of exercise, it is essential that healthcare providers routinely screen women for UI and assess how it affects their quality of life and ability to exercise.

48. Lactate Threshold & Fitness Outcomes in NCAA Rowing Teams

*Allison Wheeler, Tongyu Ma
Franklin Pierce University*

Lactate threshold (LT) has been widely used in fitness testing and the prescription of training zones. More than 20 different types of LT concepts have been developed in the past decades. It has been suggested that the Dmax LT is the most robust predictor of endurance performance among cyclists. However, less is known regarding the best LT concept among rowers. This year we expanded our research to include a larger population. We recruited study participants from the NCAA III Tufts University Men and Women's Rowing Teams. We used a graded exercise test and obtained lactate levels between testing rounds. The data showed that the best methods for determining training zones and rowing performance among collegiate rowers were Dmax and modified Dmax.

49. What is a Shared Resources?

*Christian Lytle, Craig Tomlinson, Robert Gerlach
Dartmouth Cancer Center, Geisel School of Medicine*

Shared Resource laboratories provide researchers with instruments, services, and consultation from experts in their fields. Investigators using the Shared Resources will find they have access to state-of-the-art technology and instrumentation, with the expertise needed to conduct relevant and reproducible research. Dartmouth Cancer Center (DCC) Shared Resource Laboratories are open to all investigators, including those

not part of the Dartmouth research community. These resources include Biostatistics and Bioinformatics, Clinical Pharmacology, Genomics and Molecular Biology, Immune Monitoring and Flow Cytometry, Irradiation Pre-clinical Imaging and Microscopy, Mouse Modeling, Pathology, and Trace Element Analysis. Even if you knew about the DCC Shared Resources, there are new services and equipment about which you will want to learn. No study is too large or too small, and consultation is free. Stop by the poster and find out how we can support your research.

50. **NH CREATES Seeks NH-INBRE Partners**

*Carmela Amato-Wierda, Amy Booth
University of New Hampshire – Durham*

NH CREATES the Future: the NH Collaborative for Regenerative Medicine Education and Training for Engineers and Scientists of the Future (hereafter, NH CREATES) is an NIH Science Education Partnership Award based at the University of New Hampshire. Its vision is to cultivate interest and expertise in regenerative medicine, biomanufacturing and biotechnology among diverse middle and high school students and teachers address current and future workforce needs. The overall goal of NH CREATES is to establish a robust pipeline extending from middle school to higher education and beyond for the burgeoning regenerative medicine and biofabrication (RM&B) industry in New Hampshire. NH CREATES develops partnerships among industry, K-12, and higher-ed partners to carry out this goal. The poster will describe our activities with youth and K-12 teachers, and attendees will learn how they can partner with NH CREATES.

Tuesday, August 9th Poster Presentations

Poster Session II

1. **The Micro in the Macro – Leveraging Foundational Science Curriculum to Introduce Middle School Students to Biomanufacturing**

Jeadminas Alexis, Samrat Adhikari, Md Ahasan Habib, Sarah McGregor, Denise Junge, Slesha Tuladhora
Keene State College

With funding provided by the NH EPSCoR Biomade program, we designed and implemented an immersive middle school one week summer camp experience at Keene State College focusing on foundational microbiology, physics (optics), chemistry, and 3D design and printing as a gateway experience to STEM broadly and biomanufacturing specifically. Camp curriculum included fundamental hands-on training in the culture and microscopic characterization of a variety of microbes, the physics of light and magnification important in microscopy, some basic chemistry focusing on food (for microbes and for humans), and the design and use of a 3D printer followed by an introduction to a more complex bioprinter. 12 children attended camp, four through a scholarship program funded by NH Biomade. Three undergraduate students and four faculty members from different disciplines co-designed and taught the camp making the experience truly interdisciplinary. Here we present the curriculum, lessons learned, and our plans for future offerings.

2. **Up, Up ,and Away: Circatidal vertical migration of larval horseshoe crabs, *Limulus polyphemus***

Emmanuel Alisandro, Faith Schader, Christopher Chabot
Plymouth State University

The American horseshoe crab, *Limulus polyphemus*, is a keystone species in estuaries that act as “bioturbators”, and their eggs provide a crucial food source for migratory seabirds. Their blood is also used biomedically as the most sensitive assay for disease causing bacteria. However, although this species is environmentally and biomedically important, surprisingly little is known about how newly hatched larvae disperse from their nests to their nursery grounds. While other estuarine species such as blue and green crabs exhibit vertical migration rhythms during incoming tides to allow for tidal current transportation to more favorable habitats, this behavior has not been investigated in individual horseshoe crabs. In this study, three groups of freshly hatched larvae were exposed to different environmental stimuli and their behavior tested in vertical migration chambers. Larvae that were raised in constant water levels and then placed into the vertical migration chambers at 27oC exhibited few (3/12) significant circatidal rhythms while more animals tested at 30oC (9/12) exhibited rhythms. A similar number of animals that were exposed to artificial tides for three weeks before being placed into a 30oC migration chamber exhibited circatidal rhythms (8/13). This is the first demonstration that individual larval horseshoe crabs exhibit rhythms of vertical migration. Understanding the patterns of behavior for horseshoe crabs is crucial for maintaining healthy populations of horseshoe crabs, a species that is important environmentally, biomedically, and economically.

3. **A Model System for the Synthesis of 1,3,5,7-tetraethynyladamantane**

Michael Apitz, Carolyn Weinreb
Saint Anselm College

A model system was established to generate a monosubstituted adamantane molecule, 1-ethynyladamantane. The model system will then be used to synthesize a tetrasubstituted adamantane molecule, 1,3,5,7-tetraethynyladamantane. The synthesis of 1-ethynyladamantane was successful with a 32% yield.

4. **Patients vs Providers: Definitions of a Cancer Survivor: A Compare and Contrast Study**

Grace Baukus¹, Elizabeth McGrath²
¹Saint Anselm College, ²Dartmouth Hitchcock Medical Center

Background: According to the National Comprehensive Cancer Network (NCCN) the definition of a cancer survivor is anyone from diagnosis through end of life (EOL). However, not all cancer patients relate to or identify with this designation. The purpose of this study is to compare how patients and health care professionals (HCPs) define a cancer survivor. Methodology: Two surveys were created through an iterative

process to ascertain how patients and providers define survivors. Surveys were deployed using a web-based survey tool, using email groups and lists developed by the oncology department. The results were analyzed using qualitative thematic analysis. Results: The patient survey was analyzed and four themes identified. Two unique themes were identified from the patients' responses, personal characteristics and other. The provider survey was analyzed and five themes were identified. The providers' responses coded into three unique themes, completed definitive therapy through surveillance, diagnosis through surveillance and other. The surveys had two shared themes, diagnosis to EOL and completed definitive therapy through EOL. Despite the NCCN standardized definition of a cancer survivor, not all providers or patients utilize this definition. Conclusion: There are distinct perspectives from both patients and providers around the term cancer survivor. It is important to listen to patients to understand how they identify themselves as survivors. Improving patient marketing and counseling will ensure that patients are aware of the designation of a survivor, as well as the resources available to them. It's also essential to ensure HCPs have adequate knowledge of survivorship resources for proper referrals and patient education.

5. **The Effects of Differential Media on Bacterial Production of Secondary Metabolites**

*Parker Baumann, Suzanne Cooke
University of New Hampshire at Manchester*

Bacterial-acquired antibiotic resistance is one of most pressing problems facing the modern world. Many medical grade antibiotics have been produced via the collection and augmentation of bioactive bacterial secondary metabolites. As such, maximal collection of metabolic products is immensely important for labs hoping to formulate new antibiotic products. One of the most critical factors affecting bacteria metabolism is media composition. It has been shown that polysaccharide-based media has the effect of reactivating dormant bacterial metabolic processes in bacteria previously cultivated on monosaccharide media (Böttcher et al., 2018). To test the effect of polysaccharide media on secondary metabolite production, two polysaccharide media combinations (sweet potato starch and inulin) were formulated and tested alongside media based on less complex sugars (lactose and lysogeny broth). Three soil samples were collected and plated onto the four types of media and their inhibition responses to ESKAPE safe relative bacteria *Mycobacterium smegmatis* and *Bacillus subtilis* were observed. Results indicated that inulin-based polysaccharide media resulted in the most inhibition-producing colonies when exposed to *Mycobacterium smegmatis*, while the three other media combinations produced statistically similar counts of inhibition-producing colonies. Inhibition of *Bacillus subtilis* was low across the board with minor responses being observed on Lactose and Sweet potato starch media. To further clarify the contribution of media type to antibiotic production, additional soil samples should be examined on these and other polysaccharide media, such as xanthan gum, or mixed-nutrient media.

6. **A Nuanced Antimicrobial System Assaying Bacteriophage Against Human Pathogens using *C. elegans***

*Evan Bennett, Shallee Page
Franklin Pierce University*

Antibiotic resistance is a critical problem in medicine, whereby pathogenic bacteria become able to overcome medicinal treatments. One approach to fighting antibiotic resistance is the use of bacteriophages ("phages"), viruses that attack bacteria, a strategy known as "phage therapy". Phages can target specific bacteria, thereby avoiding the problem of antibiotics that kill a wide spectrum of bacteria, including neutral or beneficial bacteria. Phages have been used as antibacterials for a century but suffer from two limitations: a) bacteria acquire phage resistance; and b) phage effects in the test tube were observed to differ from their effects in the body. Thus, we have isolated a bacteriophage against a human pathogen *Salmonella enterica* serovar typhimurium and have fully characterized its growth and annotated its genome. Then, we tested its ability to mitigate *Salmonella* infection in *C. elegans*.

7. **Inducing Disease Alters the Microbiome**

*Michael Bowles, Geoffrey Cook
New England College*

Many diseases are both caused by more than one kind of bacteria and can have chain effects on other kinds of bacteria in an organism's microbiome. The V4 region of the 16S rRNA gene was used to identify the composition of bacteria in the microbiome of *Orbicella faveolata* (Mountainous Star Coral). *Orbicella faveolata* polyps from the same coral medallion are genetically identical. Corals were cut into healthy, diseased and

recovered groups. Bacteria from healthy and diseased corals was extracted via syringe sampling, and vacuum filtered for DNA extraction. Genetic material was amplified through PCR. Bacteria will be extracted from recovered corals once the corals have recovered. The data collected from healthy and diseased groups show a significant difference in the abundance of certain taxonomies. The data collected in this study will help to better determine how an organism's microbiome can change under certain conditions.

8. **Characterizing Antimicrobial Peptides Identified Using Bioinformatics**

*Kelsea Brasseur, Tallia Muller, Olivia Piemonte, Kelly Cunningham
Colby-Sawyer College*

Previously, several peptides identified using a bioinformatics screening method were found to have strong antimicrobial characteristics. In this study, we further determined an accurate MIC for the two 95% pure peptides and conducted assays to characterize their time-kill kinetics against specific microbes. We also explored whether these peptides were hemolytic to mammalian cells. The Cap peptide had a minimum inhibitory concentration (MIC) of $1.75 \pm 0.17 \mu\text{M}$ against *Candida albicans* and the AG2 peptide had an MIC of $13 \pm 1.09 \mu\text{M}$ against *E. coli* BAA-197. In time-kill kinetics assays, the Cap peptide reduced colony forming units (CFU) of *Candida albicans* by more than 95% within 2 hours and the AG2 peptide reduced colony forming units (CFU) of *E. coli* BAA-197 by 95% within the same time frame. The peptides tested showed very little hemolysis against sheep red blood cells even at higher concentrations. Overall, both the AG2 and Cap peptides are very strong AMPs and have potential to be developed into new antibiotics to be used against drug resistant strains of bacteria and fungi.

9. **Decoding COVID-19 Vaccine Hesitancy in the United States by Analyzing Socioeconomic Values**

*Benjamin Burnett, Wei Lu
Keene State College*

With the growth and development of COVID-19 and its variants, reaching a level of herd immunity is critically important for national security in public health. To deal with COVID-19, the United States has implemented phased plans to distribute COVID-19 vaccines. As of the end of April, around 77% of Americans had received their first shot to guard against COVID-19 and 66% were considered fully vaccinated, according to the dataset provided by CDC. However, there are a significant amount of American people who still hesitate to receive a shot of the COVID-19 vaccine mainly because (1) they worry about possible side effects and would like to wait to see if it is safe; and (2) they don't trust the government and don't believe they need it because they think COVID is not a big threat. In this research, we aim to demystify COVID-19 vaccine hesitancy by analyzing various socioeconomic characteristics among individuals and communities so policymakers can make policies accordingly to target vaccine support information and remove this hurdle to end the COVID-19 pandemic effectively.

10. **Investigating Circadian Clock Mechanisms in *Limulus polyphemus*, the American Horseshoe Crab**

*Joshua Chandler, Zoe Clark, Kyle Newton, Christopher Chabot
Plymouth State University*

Endogenous clocks are ubiquitous among living organisms and the dysfunction of clocks that control daily, circadian rhythms can result in disorders that negatively impact human physical and mental health. The clocks that control these circadian rhythms are composed of a transcription-translation feedback loop as well as protein kinases and phosphatases. Although the molecular mechanisms have been worked out in a few model species such as the fruit fly, *Drosophila melanogaster*, and the mouse, *Mus musculus*, little is known about the clocks in many important Arthropoda subphyla, including chelicerates. The American horseshoe crab, *Limulus polyphemus* is an important commercial and biomedical species and has robust circadian rhythms of eye sensitivity. Although both the protein kinase Casein Kinase I ϵ (CK1 ϵ) and the circadian gene period play important roles in the circadian clock of many animals, the importance of the CK1 ϵ and the period paralog (per a, b, and c) is unknown in *Limulus*. When CK1 ϵ inhibitors were applied to juvenile *Limulus*, a significant lengthening of the period of their eye sensitivity rhythms occurred, suggesting that phosphorylation by this protein kinase is an important process for the generation of circadian rhythms in the species. The importance of the period gene is currently being assessed. Thus far, it appears that this species shares similar circadian clock mechanisms with more distant anthropoid relatives.

11. **3D Printed Scaffold Culture in a Custom-Made Perfusion Bioreactor: A Simulation Process**

*Scott Clark, Connor Quigley, Jack Mankowsky, Md Ahasan Habib
Keene State College*

The purpose of this simulation process of our designed and prototyped perfusion bioreactor is to analyze various in vivo conditions to house and cultivate cells in a 3D printed scaffold. Our reactor works by pumping a nutrient rich medium through the scaffolds to nourish the cells while also washing away the cells' waste. Depending on how the medium comes into contact with the cells in the perfusion chamber, the medium may hurt the cells instead. The uncontrolled flow of medium can damage the scaffold and eventually encapsulated cells. Hence, the cells could be washed away by excess turbulence in the chamber. Therefore, before starting the dynamic culture, we conducted various simulations in SolidWorks to see how the medium will behave in the perfusion chamber with the cells. The results of these simulations allow us to identify any potential threats to the cells and change the scaffold shape or perfusion chamber design to protect them. We believe a successful simulation run can help to set up an experiment to get an effective dynamic culture scenario ensuring proper shape fidelity of the scaffold and encapsulated cell growth.

12. **The effect of resistance band training and isokinetic training on strength in college aged females**

*Haleigh Daft, Sophia DeMarco, Charles Graffius, Malik Newcomb, Calie Sorenson
Colby-Sawyer College*

COVID-19 heightened the importance of identifying resistance training exercises that could be completed at home. Resistance band training could provide an affordable and easy way to complete resistance training outside of a gym environment. Additionally, a lack of data exists as to whether resting band training is as effective in improving strength compared to isokinetic weight machine training. **PURPOSE:** To determine the effect isokinetic machines (Keiser A300) training vs. resistance band (Dasking) training had on one repetition maximum (1RM) in college aged females over a four-week period. **METHODS:** Twenty-four college-aged females (19.5 +0.95 years) volunteered for the study. Baseline and post-intervention measurements included height, weight, body mass index (BMI) leg press 1RM (Keiser A300) and chest press 1RM (Keiser A300). The exercise intervention consisted of resistance training exercises that were completed three times per week for four weeks. The program was designed to train all major muscle groups (legs, back, abdomen, chest shoulders, arms). Student research assistants trained all participants on proper form and technique. They supervised training sessions as needed. Each exercise session included a 5-minute warm-up, resistance training consisted of three sets with 8-12 repetitions per muscle group. ANOVA: Two-Factor Without Replication (Excel 16.63) was used to determine whether there were significant ($p < 0.05$) differences between the results of the resistance band group and the isokinetic machine group. When significant differences were not present between the two groups, data was combined, and a T-Test (Excel 16.63) was used to determine whether there were significant differences in 1RM values pre and post resistance training intervention. **RESULTS:** Twenty-four participants successfully completed the study (13 resistance band, 13 isokinetic machines). There were no significant ($p > 0.05$) changes, between the groups, in mean height ($p = 0.62$), weight ($p = 0.20$), BMI ($p = 0.62$), 1RM chest press ($p = 0.06$) and 1RM leg press (0.18) following the 6-week intervention. When data was combined, a significant difference existed in 1RM for chest press ($\Delta = 15.8\%$) ($p < 0.001$) and 1RM for leg press ($\Delta = 14\%$) ($p < 0.001$) after four weeks of resistance training. **CONCLUSION:** Four weeks of resistance training, using either resistance bands or isokinetic machines, significantly increases 1RM for chest press and 1RM for leg press in college-aged females.

Supported by the New Hampshire IDeA Network of Biological Research Excellence (NH-INBRE) with grants from the National Center for Research Resources (5P20RR030360-03) and the National Institute of General Medical Sciences (8P20GM103506-03), National Institutes of Health

13. **Confirming the Effects of FOXN2 on the mRNA Levels of the Genes C9orf116, LMLN, and LRRC6**

*Lauryn Davis, Madisyn Schmanski, Kristine Hayes
NHTI Concord's Community College*

Pancreatic cancer is the 3rd deadliest type of cancer in the United States due to a lack of symptoms in the early stages of pancreatic cancer which often leads too late diagnosis (Yi-Jin, C., 2017). Pancreatic cancer arises from uncontrolled cell growth and division when tumor suppressor genes and proto-oncogenes are mutated (American Cancer Society, n.d.). Minimal research has been conducted about the genes involved in pancreatic cancer, however, mutations in certain genes are known to play a role in some cancers by causing cells to fail cell cycle checkpoints. Research done by the Johnson Lab has targeted FOXN2 to observe its role in pancreatic cancer. In pancreatic cancer, FOXN2 is upregulated in the late stages and appears to act as an

oncogene, thus promoting cancer progression and malignancy (INBRE pilot grant, 2020). When protein levels were quantified with RNAseq and RT-qPCR data, it was found that the expression of FOXN2 when downregulated caused higher mRNA levels of the proteins LMLN, C9orf116, and LRRC6 (Johnson lab, unpublished data). Genetically modifying FOXN2 allows for confirming protein levels using a laboratory technique called western blot, of the three proteins. The hypothesis is that by targeting FOXN2 downstream pathways, the malignancy of human pancreatic cancer tumor cells will be diminished thus providing validation for the concept of therapeutic targeting of FOXN2 or the pathways it regulates (INBRE pilot grant, 2020). The results from the western blot show there is no difference in expression between the control cell lines and the knockdown FOXN2 cell lines of the proteins LRRC6 and C9orf116 and that they are being expressed equally. It was expected to see an increase in the expression of the proteins LMLN, LRRC6, and C9orf116. The results for the protein LMLN were unobtainable. The results did not support the initial data collected from the RNASeq and a RT-qPCR.

14. **Role of SDS-22 in meiosis in C. elegans**

Meredith Ellis¹, Aparna Ravi², Erik Griffin²

¹Colby-Sawyer College, ²Dartmouth College

Meiosis, a specialized cell division that generates haploid gametes, is essential for sexual reproduction. During prophase I of meiosis, homologous chromosomes need to pair with each other to allow for subsequent crossover exchange. In the germline of the nematode *C. elegans*, chromosome pairing is facilitated by the SUN/LINC protein complex. This protein complex spans the nuclear membrane and attaches to chromosomes in the nucleus and to cytoskeletal motor proteins in the cytoplasm. Cytoplasmic motors move chromosomes into a crescent-shaped cluster in one region of the nucleus, which allows the efficient pairing of homologues. Chromosome clustering is stimulated by phosphorylation of the SUN/LINC complex by PLK-2 kinase. While it has been presumed that a phosphatase dephosphorylates the SUN/LINC complex to disperse the chromosome clusters, the responsible phosphatase has not been identified. SDS-22 is an evolutionarily conserved regulatory subunit of serine/threonine phosphatase PP1 (protein phosphatase 1). PP1 plays an active role in mitosis and requires SDS-22 for its activity *in vivo*. Previous preliminary work in the Griffin lab found that chromosome clusters do not disperse normally in *sds-22* mutant worms. To further characterize the role of SDS-22 in regulation of chromosomal clustering, I am using spinning disk confocal microscopy (SDCM) to image DAPI stained germline of wild type and *sds-22* (null) mutants. In the future, we plan to test whether prolonged clustering in *sds-22*(null) worms depends on PLK-2 and on the PLK-2 phosphorylation site on the SUN/LINC complex.

15. **Role of CHRM3 in glioma progression**

Isabella Fox, Sumyuktha Anand, Alexander G. Skorput, Alison L. Young, Allan Gullledge, Matthew C. Havrda
Geisel School of Medicine at Dartmouth

Primary gliomas make up 78% of all malignant tumors arising in the central nervous system and are the deadliest form of brain cancer. The current standard of care is surgical resection followed by chemotherapy with temozolomide and radiotherapy. However, drug-resistant tumors often recur, so glioblastoma patients often have a 5% five-year survival rate. Glioma stem cells (GSCs) are a subset of undifferentiated cells widely believed to drive tumor initiation, therapeutic resistance, and glioma recurrence. Depleting the GSC population could improve current cancer treatments and the survival of glioma patients. Oligodendrocyte precursor cells (OPCs), a type of GSC, have been identified as a cellular origin for glioma. Recent findings indicate that the neurotransmitter acetylcholine (ACh) maintains the primitive state of normal OPCs via muscarinic ACh receptors (mAChRs), preventing both maturation and cell cycle exit. Publicly available data and studies in our lab show high levels of expression of CHRM3 (M3mAChR) in adult and pediatric glioma patients and in primary OPC-like GSCs. We investigated the impact of modulating ACh and mAChRs in malignant OPC-like GSCs. We conducted pharmacologic studies *in vitro* and *in vivo* and found that an FDA-approved anti-muscarinic drug, benztropine (BZT), suppressed OPC proliferation. We also observed that serially passaged patient derived glioma xenografts treated with BZT were unable to re-initiate tumors in subsequently engrafted host mice. These studies suggest that the cholinergic microenvironment may influence OPCs and provide a rationale to investigate widely available antimuscarinics as treatments for glioma.

16. mTOR signaling regulates porphyrin biosynthesis in a planarian model of acute porphyrias

Isabel Garcia, Elijah Trepanier, Lucy McGrade, Leanna Landfair, Mahad Ahmad, Kaleigh Powers, Jason Pellettieri, Keene State College

Porphyrias are rare disorders characterized by extreme light sensitivity and neurological symptoms ranging from anxiety and confusion to seizures or paralysis. These conditions are caused by inherited mutations in enzymes of the eight-step heme biosynthesis pathway, leading to the accumulation of toxic heme precursors. Porphyrins, for example, are ring-shaped compounds that react with oxygen to form free radicals when exposed to light. In 'acute' porphyria patients, symptoms can be brought on suddenly by triggers like medications or reduced calorie intake. We previously showed that planarian flatworms produce porphyrins in the pigment cells of their skin due to a physiological heme biosynthesis bottleneck, resulting in rapid pigment cell death when animals are exposed to light. Remarkably, starvation leads to increased porphyrin levels, just as it does in acute porphyrias. These observations prompted us to conduct an RNAi screen in an effort to identify novel metabolic pathways regulating porphyrin/heme biosynthesis. Our preliminary results show knockdown of genes in either the PI3K-PTEN-AKT-mTOR or RAS-RAF-MEK-ERK signaling pathways result in changes in porphyrin levels and consequent photosensitivity. To our knowledge, we are the first to link the former pathway to the metabolic control of porphyrin/heme biosynthesis. Thus, our work is not only advancing our understanding of basic science, but also stands to reveal new avenues for developing porphyria treatments.

17. Headwater streams continue to provide important cold-water refugia for brook trout

*Abigail Halterman, Barry J. Wicklow, Bridget Monaghan, Shannon J. O'Leary
Saint Anselm College*

Brook trout are found throughout eastern North America, from as far west as Minnesota to the Atlantic Ocean where they are a popular game fish. Brook trout thrive in streams with high dissolved oxygen levels, and cool waters not exceeding 18°C. Thus, headwater streams have become important cold water refugia for brook trout as stream temperatures rise due to climate change across their habitat. Here, we used environmental DNA (eDNA), DNA from blood, mucus, or tissue of a species left behind in aquatic systems to test for the continued presence of brook trout in 13 headwater streams in New Hampshire. Ten of these streams were identified as refugia for brook trout during summer months via electrofishing in 2010-2012. We collected one liter of water at each site from May to August in 2021. Samples were filtered using 0.45µm nitrocellulose filters to trap and extract the eDNA. Finally, we used a fluorescently labeled species-specific probe to quantify relative abundance using qPCR. We detected brook trout eDNA in all but one of the 10 streams, indicating that headwater streams continue to provide important climate refugia as stream temperatures continue to warm.

18. Synthesis and Evaluation of Flufenamic Acid Analogues as Hippo Pathway Inhibitors

*Larissa Havey, Jennifer Pace
Saint Anselm College*

The Hippo pathway is a phosphorylation cascade that controls tissue growth and organ size through the regulation of the homologous downstream transcription factors Yes-associated protein (YAP) and transcriptional coactivator with PDZ motif (TAZ). Genes that control cell proliferation, differentiation and apoptosis are expressed when YAP/TAZ form a heterodimeric complex with the TEA domain transcription factors (TEADs) in the nucleus. When the pathway is dysregulated, it leads to tumorigenesis induced by uncontrolled cell proliferation, making this pathway a central target for cancer research. Flufenamic acid (FA) is a small molecule that has been proven to prevent palmitoylation in TEAD, destroying the transcription factor's stability and functionality and therefore inhibits gene expression. This research focuses on designing and synthesizing FA analogues in hopes of extending the small molecule deeper into the central, hydrophobic pocket of TEAD in order to interrupt YAP's ability to bind. The discovery of a small molecule to selectively inhibit the downstream processes in the Hippo pathway would be significant for future exploration in cancer research, metastasis and chemotherapeutic resistance. Several analogues have been successfully synthesized, isolated and characterized that have comparable, predictive binding affinities to FA, suggesting that the modified scaffold does not interrupt the analogues ability to bind to TEAD.

19. **Survival of *C. elegans* After Knocking Down the bir-2 Gene**

*Justin Haynes, Shallee Page
Franklin Pierce University*

This experiment sought to determine whether the bir-2 gene in *C. elegans* is involved in the organism's immunity. To investigate the gene's role in immunity we measured the survival between wildtype and apoptosis resistant mutant of *C. elegans* with and without the knockdown of the bir-2 gene. Survival rates over one generation were tracked to determine if the gene affected immunity.

20. **Synthesis and Evaluation of Flufenamic Acid Analogues as Hippo Pathway Inhibitors**

*Noelle Honan, Jennifer Pace
Saint Anselm College*

The Hippo Pathway is a crucial point of cancer research. This pathway controls cell proliferation and tumorigenesis. Dysregulation of this pathway has been observed in a significant portion of patients suffering from liver, breast, pharynx, pancreatic, and prostate cancers. This pathway mediates the activity of the two transcription factors called Yes-associated protein (YAP) and transcriptional coactivator with PDZ-binding motif (TAZ). Both YAP and TAZ interact with TEA domain transcription factors (TEADs) to form a complex that results in expression of the Hippo Pathway target genes. The expression of these target genes leads to uncontrolled cell growth. One therapeutic approach to treating this dysregulation would be disrupting YAP and TEADs interactions. Previous studies have shown that the compound Flufenamic Acid inhibits Hippo Pathway target gene expression through the destruction of TEAD. Synthesis of Flufenamic Acid analogues is a promising area of research because it would allow for the inhibition of the Hippo Pathway without the loss of TEAD function. These analogues were synthesized through a one-step amide coupling reaction and purified through column chromatography. A total of five Flufenamic Acid analogues were successfully synthesized and assessed for purity using HPLC. These compounds will be analyzed for efficacy using a cancer cell line (MDA-MB 231).

21. **Investigation of GP-88 in bV_HerculesSTE using Synthetic Biology**

*Joshua Hughes, Ibrahim Ayyash
Franklin Pierce University*

bV_HerculesSTE is a recently discovered kuttervirus bacteriophage that infects the pathogenic bacteria *Salmonella enterica*. Hercules was found to have several genes of unknown function. One of these genes was GP-88 which according to BLAST and HHPred codes for an electron transport chain (ETC) complex known as NADH dehydrogenase as part of the aerobic respiration process used by the host *S. enterica*. GP-88 is a gene that is 99 percent conserved in Hercules from *S. enterica* and maintains 99 percent coverage across other facilitative anaerobe bacteriophages (BLAST). This would suggest that the gene is functional in these bacteriophages. GP-88 is around 675 base pairs in length and is located on the minus strand of Hercules' DNA at 57292- 56618. This experiment aimed to investigate and confirm the function of GP-88 using BRED to remove the gene in Hercules. BRED stands for Bacteriophage Recombineering through Electroporated DNA. This is the process where genes in a plasmid (pJV53, in this case) are transformed into host bacterial species (*S. enterica*) from *E. coli* through electroporation. The genes were first edited to exclude GP-88 using a kinase/ ligase treatment of the two gene ends and were extended using PCR techniques. GP-88 is then incorporated into the replicated bacteriophage DNA using the pJV53 plasmid. pJV53 encodes for a nuclease and which is induced with exposure to acetamide. Once the pJV53 is expressed, the extended GP-88 gene is taken up by the host bacteria and is replicated in the bacteriophage as a nonfunctional gene.

22. **Effects of Common Contaminants, PFOA and PFHxA on Apoptosis, Proliferation and the Cell Cycle on Placental Cells**

*Finn Husband, Alycia Ashby, Chery Whipple
Colby-Sawyer College*

Water-resistant products like Teflon, firefighting foam, and food packaging contain manmade chemical perfluoroalkyl and polyfluoro-alkyl substances (PFASs). PFAS are uniquely comprised of a carbon chain unnaturally surrounded by fluorine molecules (2) which enable the chemical to be hydrophobic. These hydrophobic substances are extremely durable giving them a long half-life and rendering them unrecognizable to the body and nature. The biological response to PFAS is to secrete the chemical through urine and breast

milk while the excess binds to proteins and are stored in the blood, liver and kidneys (1). When the body is exposed to accumulating concentrations of PFAS it can result in heart disease, thyroid irregularities, cancer and high blood pressure (2). When this information came to light, companies combatted the problem by switching from an 8-carbon chain (PFOA) to a 6-carbon chemical (like PFHxA) stating it would be less harmful due to it's faster half life. The primary goal of the research has been to determine if 6-carbon PFAS are less detrimental to the human body at the same concentrations as the original 8-carbon PFOA by utilizing assays testing for the chemical's effect on apoptosis, proliferation, and the cell cycle.

23. **Determining Relative Gene Expression and Efficiency in *C. elegans* Using qPCR**

*Hannah Johnson, Shallee Page
Franklin Pierce University*

Using qPCR, it is possible to compare gene expressions between different genes, primer sets and worm strains amongst *C. elegans*. We were interested in examining changes in gene expression in the innate immune response upon an immune challenge. The worms used in these experiments were N2 which is the wild-type and IG10 which is a strain lacking the *tol-1* receptor gene which is suspected to have a role in the innate immune response. Worms were washed and then isolated from bacteria, then their RNA was harvested and purified. Each sample then undergoes reverse transcription to obtain cDNA. Using cDNA, qPCR amplified the DNA and provided a Ct value. Using the Ct, or cycle threshold data from qPCR runs, relative gene expression was calculated using the $2^{-\Delta\Delta Ct}$ which compares the Ct values between different genes and worm strains. Serial dilutions of N2 wild-type samples were used to create standard curves to determine primer efficiency and accuracy of qPCR runs. We have analyzed the gene expression of the following genes: *act-1*, *ced-3*, *ikb-1*, and *pik-1*. We have performed primer efficiency standard curves on *act-1* and *pik-1*. Next, we will be investigating how gene expression changes in *C. elegans* upon challenge with a pathogenic bacterium as well as refining qPCR techniques and analysis.

24. **Assessment of Sous Vide Water Baths for Acute Rewarming of Frostbitten Extremities**

Kara Keiper¹, Jessica Chevalier², Elizabeth Hamilton³, William Galvin³, Amalya Wilson⁴, Nicholas Daniel³
¹Colby-Sawyer College, ²Dept of Medicine, Dartmouth-Hitchcock Medical Center, ³Dept of Emergency Medicine, Dartmouth-Hitchcock Medical Center, ⁴Dartmouth College

The prevalence of frostbite is unknown as there is no standardized reporting system or database for frostbite. However, children, the elderly, and homeless populations are especially vulnerable to frostbite. To treat mild cases of frostbite, a warm bath maintained between 37° to 39° Celsius is used. However, there is no standardized method for consistently maintaining the temperature of the water baths. The purpose of the study is to investigate the effectiveness of sous vide cooking devices in maintaining a warm bath between 37° to 39° Celsius. The need for this study was determined by the strain that water temperature regulation puts on healthcare providers while treating frostbite. One frostbite patient was treated last year using two sous vide devices set to 38° Celsius. The temperature of the water was read and recorded every two minutes. Results showed that the sous vide devices were able to maintain water temperature at $\pm 1^\circ$ degree Celsius from the set point. The study is expanding across multiple hospitals to collect more data to support the benefits of sous vide devices in water bath management.

25. **Isolation and Characterization of Cancer Stem Cells from C6 Rat Glioma Cells**

*Nicole Lezon, Micayla Bourski, Hye Young Shin
Rivier University*

Glioblastoma (GBM) is the most malignant and metastatic brain cancer, and the average survival time of the patients is limited to 15 months despite deep understanding of its genomic mutations and advanced medical therapeutics. Recent studies revealed that a unique subpopulation of cancer stem cells (CSCs) is the major cause of resistance to radiotherapy and chemotherapy and its recurrence of GBM. In this research, our goal is to compare differential cytokine expression of the CSCs versus differentiated cancer cells. To this end, we employed the C6 rat glioma cell line since it has been mostly used in neuro-oncology due to its abilities to simulate overall the high growth rate, the high vascularization, and the highly infiltrative character of GBM. We successfully isolated CSCs from the main population of C6 by utilizing conventional neurosphere assays, and properties of these CSCs were confirmed with immunofluorescence staining for a typical CSC marker, SOX2. The expression of SOX2 was observed only in C6-derived CSC spheroids but not in the adherent differentiated cells. We, in the further study, will work on cytokine expression study of CSCs versus differentiated glioma cells to find potential targets for therapeutics of GBM.

26. Production and Purification of Anti IL-8 Monoclonal Antibody

*McKenna Malone, Gwendolyn Tupman, Deb Audino
Manchester Community College, Great Bay Community College*

Interleukin-8 (IL-8), a proinflammatory mediator chemokine, is categorized as a neutrophil chemoattractant. The over expression of IL-8 in cancer cells leads to poor prognosis due in part to the IL-8 increasing tumor cell proliferation, angiogenesis, and metastasis of tumors. This poster describes the production of an anti-IL8 monoclonal antibody to reduce levels of IL-8 as a potential treatment for cancer. Monoclonal antibodies are a rapidly advancing type of biologic medicine for cancer treatment. CHO cells recombinant for the anti-IL-8 monoclonal antibody were grown in a spinner flask for 1 week then scaled up into a 1L benchtop bioreactor for an additional 2 weeks. The media contained the monoclonal antibody as confirmed by an ELISA. The anti-IL-8 monoclonal antibody was purified by affinity chromatography. SDS-PAGE showed successful purification of the protein.

27. Patient-Derived Glioma Xenograft MR Images Demonstrates Reduction in Tumor Volume Post ent-28 Treatment

*Bamlak A. Messay, Carmen Del Genio, Zachary Shallit, Glenn Micalizio, Arti B. Gaur
Dartmouth College, Norris Cotton Cancer Center*

Gliomas are the most aggressive primary brain tumors deriving from glial cells in the central nervous system (CNS), the most lethal and severe (Grade IV) of which are known as glioblastomas (GBM). GBM are detected magnetic resonance imaging (MRI) and diagnosed by histological analyses of the patient's tumor. GBM are incurable as the median survival rate of patients with GBM is 15 months following treatment, and only four months if the patient does not receive treatment. Studies that have examined Erβ's role to suppress tumor progression had found that in GBM, Erβ expression levels are less than normal. Ent-28, a synthetic Erβ-agonist, stops the progression glioma-patient derived cells in in vitro studies, making a Erβ a viable chemotherapeutic target. To assess the efficacy of ent-28 treatment in reducing the tumor burden in glioma-patient derived xenograft mice, MR images have been analyzed using part of the clinical NANO criteria for tumor enhancement and disease progression with appropriate scaling and procedural modifications for murine models. The control group of mice that received propylene glycol (PG) survived for a maximum of 20 days after the establishment of orthotopic tumors from patient-derived glioma cell line. The ent-28-treated group had a significantly higher survival rate when compared to PG-treated mice, surviving for up to 150 days. Additionally, the tumor size (mm³) significantly increased in control group mice, while ent-28 treated mice tumor size decreased post-treatment.

28. Comparing CCND1 Gain in Melanoma Patients to Literature Data

*Peter Mikhlin, Advaita S. Chaudhari, Jason McFadden, Edward Hughes, Rachael Barney, Marie Syku, Mirjana
Dartmouth College, Dartmouth Health, Geisel School of Medicine at Dartmouth*

Most deaths from skin cancer are due to melanoma. It occurs when UV radiation triggers mutations in melanocytes, resulting in uncontrolled cell growth. It can arise in existing moles, but more frequently appears as a new lesion. To diagnose melanoma, analysis of microscopic morphology is the gold standard. In certain cases, however, analysis of specific genetic markers can serve as indicators of malignancy. Genes that when amplified, deleted or mutated, contribute to oncogenesis, are known as proto-oncogenes. CCND1 is one such protooncogene. When CCND1 is amplified, the protein it encodes, Cyclin D1, is overexpressed, which can lead to chemotherapeutic resistance and evasion of apoptotic mechanisms. Currently, CCND1 amplification is used to help distinguish nevi from melanoma in cases where morphology is not decisive. In the literature, CCND1 gain is recorded in about one-third to one-half of cases, although frequency depends on anatomic site and subtype. Our subset of thirty melanoma cases showed completely different results, with only 4.2% of cases showing evidence of CCND1 gain as determined via chromosomal microarray (CMA), the current gold standard in the detection of copy number variation. We explore the discrepancy between the rate of CCND1 gain in the literature versus our cohort through an analysis of CMA data collected over six years. We hypothesize reasons for this discrepancy, discuss the potential impact on patient care, and outline directions for future research.

29. Testing irradiated tumor cells as antigen source for therapeutic ovarian cancer vaccine

Alex Misiaszek, Jennifer Fields, Steven Fiering
Dartmouth Geisel Medical School

The goal of this project is to develop an intraperitoneal model for colon cancer (CT26 cell line) in mice to be treated with a therapeutic vaccine containing irradiated cancer cells as an antigen source and the Cowpea Mosaic Virus (CPMV) as an adjuvant. Recent findings have supported the use of CPMV as an effective adjuvant, and there has been work involving a subcutaneous model for this cell line, so this project will further the current research by investigating the treatment of carcinomatosis in the peritoneum with an established adjuvant. The use of irradiated cancer cells as a source of antigens should enhance the response of the model organism to the treatment. Research techniques will involve culturing CT26, irradiating cancer cells, intraperitoneal injections, and tumor measurement. It is expected that mice treated with irradiated CT26 and CPMV will have the best response, likely exhibiting the greatest tumor reduction compared to mice treated with PBS, irradiated cancer cells alone, and CPMV alone.

30. Pelvic Floor Physical Therapy: An Insight into Utility and Availability

Madelyn Moedebeck¹, Bridget Linehan²
¹Rivier University, ²Dartmouth Hitchcock Medical Center

The goal of this project is to explore the role pelvic floor physical therapy (PF PT) plays in pelvic floor health and identify PF PTs in New Hampshire and Vermont to strengthen referral relationships for DHMC. A search was done to learn more about PF PT and to identify PTs by name and location. A spreadsheet was created, and PTs were called to gather more information. A survey was sent to inquire about their education and limitations they may have. The PT survey and the Active Women Incontinence Screening Tool (AWIST) was used for analysis. The survey sent to PF PTs indicates a desire to strengthen the PF PT network, so next steps include hosting a zoom meeting with all interested PF PTs. The AWIST shows that pelvic floor health is gaining attention, but women lack the skills to be able to perform beneficial exercises correctly on their own. There is a limited number of PF PTs and a stigma surrounding pelvic floor health, therefore making general knowledge surrounding the topic and assistance in learning techniques difficult to achieve.

31. Comparative Analysis on the effects of long and short chain PFAS on the development, viability, and motility on *Caenorhabditis elegans*

Patrick Murphy, Meredith Ellis, Chery Whipple
Colby-Sawyer College

Perfluorooctanoic acid (PFOA) and perfluorohexanoic acid (PFHxA) are both types of PFAS (Per and polyfluoroalkyl substances), a group of manmade chemicals that are used within a variety of consumer and industrial products. These chemicals can persist and accumulate within the environment and humans. An abundance of evidence has shown that these chemicals have toxic effects on human health. PFOA and PFHxA are structurally similar except PFHxA is shorter by two carbons within its carbon backbone. Companies have now been transitioning to new shorter PFAS claiming they pose fewer health risks. In this study, we test this by comparing the toxic effects of PFOA and PFHxA on the model organism *Caenorhabditis elegans* (*C. elegans*). *C. elegans* were exposed to a range of chemical concentrations (0.5 mg/L, 1 mg/L, 1.5 mg/L, 2.5 mg/L, 5 mg/L, 10 mg/L) within their environment through the agar and their food (*Escherichia coli*). Three different health markers were examined: viability, mobility, and development after 24, 48, and 72 hours of exposure. We found that PFAS chemicals at these concentrations have not shown a significant impact on the health of the *C. elegans*. This range of concentrations was tested to encapsulate the varying levels of PFAS exposure within the natural environment. Further research is necessary to investigate the chemicals' impact on *C. elegans* fecundity and identify specific cellular pathways triggered by high dose PFAS exposure.

32. Exploration of the Molecular Mechanisms Controlling Circatidal Rhythms in the American Horseshoe Crab, *Limulus polyphemus*

Kyle Newton, Emmanuel Alisandro, Christopher Chabot
Plymouth State University

Biological rhythms are ubiquitous to virtually all life forms and play a key role in human health as they regulate sleep-wake cycles and metabolic functions. Although much is known about the molecular processes that regulate circadian rhythms, little is understood about the mechanisms of the clocks that control important

secondary rhythms such as circatidal rhythms. While a few dozen proteins have been identified as part of the circadian clock in many species, only the enzyme Casein Kinase I, has been found to play a role in regulating circatidal rhythms thus far. In the current study, pharmacological agents known to affect circadian rhythms were administered to juvenile American horseshoe crabs, *Limulus polyphemus*, under constant conditions to assess their possible role in the generation of their circatidal rhythms. The application of an activator of Cryptochrome, a core circadian protein, caused a significant lengthening of period, indicating that this protein is part of the circatidal mechanism. However, neither inhibition of Glycogen Synthase Kinase-3 (a circadian enzyme that causes phosphorylation) or exposure to Neuropeptide F (a circadian output signal peptide), affected circatidal period significantly. Interestingly, they did appear to induce arrhythmicity suggesting a role for these proteins in circatidal rhythms. Lastly, inhibitors of histone acetylation/deacetylation also had no significant effect on period suggesting that epigenetic modifications to histone proteins are not involved with these clocks. Further work with other known circadian proteins such as post-translational regulators, Casein Kinase II, and protein phosphatases are currently underway.

33. **Forget about your speakers, I found some cool AMPs**

*Nyah Piper, Amy Carfagno, Barney Bishop, Geoffrey Cook
New England College*

Antimicrobial peptides (AMPs) are all organisms' first line of defense for illness/disease. Specific to each organism, AMPs are produced by the host's innate immune system. Native to the Caribbean sea, *Orbicella faveolata* is the research subject for this following report. With the rise of global temperatures, a shift in the coral holobiont may lead to an imbalance of health or dysbiosis. The findings will abet more information regarding the AMPs of *Orbicella faveolata* that hope to relieve some of the deathly attributes of dysbiosis. Mass spectrometry was implemented upon samples to receive data concerning the properties of coral in a state of health and disease. Of the 1,792 de novo sequences peptides identified with an average local confidence percentage (ALC%) of greater than or equal to 50% (within both states of health and disease), 1600 peptides bear two or more characteristics of antimicrobial properties. With the steadfast growth of antibiotic resistance, antimicrobial peptides may be able to flatten the curve of these 'superbugs' and help fight off infirmity with the introduction of novel therapeutic agents. The discoveries of this study will help to demonstrate the importance of AMPs; maintaining the health of an organism while slowing the rate of illness/disease.

34. **C. elegans Optimization**

*Lauren Pribyl
Franklin Pierce University*

Caenorhabditis elegans (*C. elegans*) are microscopic nematode worms. These worms are a model organism for research because they are cost-efficient, have a fully annotated genome, and can be frozen. Additionally, *C. elegans* reproduce quickly and have a short 2-week life span. Previous work performed by our lab focused on the physiological role of Bir-2 and its relationship to Bir-1 and the human Bir family. The research completed focused on experimentation on the survivability of the bir-2 gene in *C. elegans* against pathogens and various stresses. This investigation with *C. elegans* focused on optimizing systems for worm tracking and multiwell survival assays to optimize our data on *C. elegans* motility and survivability.

35. **The Relationship Between Social Anxiety and Performance on SpeechMatch**

*Hannah Prinz, Larry Welkowitz, Harlan Fichtenholtz
Keene State College*

The goal of the current project is to understand the relationships between social anxiety, verbal communication, and heart rate variability. It was hypothesized that participants with greater social anxiety would have difficulty matching speech patterns when using SpeechMatch (a linguistic communication tool) and decreased heart-rate variability. Participants in this study completed the Liebowitz Social Anxiety Scale (Liebowitz, 1987), matched happy, sad, and neutral phrases in SpeechMatch, and had ECG recorded during a 10-minute resting period. The results showed that there is a significant relationship between social anxiety and overall volume matching. When looking at the emotions individually, the correlations between social anxiety and all three measures of speech (pitch, rhythm, and volume) were significant for the neutral phrase. Heart rate variability showed no relationship to social anxiety scores or SpeechMatch performance. A next step in this research could be determining if volume matching was too low or too high. The study allowed us

to determine that volume had a lower percent match for those more socially anxious, but it did not determine how the volume was not a good match.

36. What are children's worldviews?

*Madison Puglisi, Shailee Woodward
Keene State College*

Worldviews (individuals' core beliefs, values, and attitudes) have been linked to significant social, behavioral, and health outcomes. However, there is very little research on how worldviews develop. In the present research, we developed and evaluated the first measure of children's worldviews, the Unified Worldview Measure – Child Form (UWM-CF). Twenty items were taken from the Unified Worldview Measure (UWM; Woodard, 2019) and “translated” into child-friendly language to create the UWM-CF. The UWM-CF was then administered to 83 children ages 7-9 years and 249 adults, including 44 parents of the participating children. Exploratory factor analyses of the adult data revealed four factors of the UWM-CF: Religion, Humanism and Harmony, Determinism and Mechanism, and Self-Reliance. Exploratory factor analyses on the child data revealed three factors: Religion, Determinism, and Growth/Learning/Self-Reliance. . We conducted analyses to evaluate the 20 worldview questions to see whether there are differences in children's and adults' responses. Further evaluation will help determine if there is a relationship between parents' religious/political affiliations and their children's responses. This research data reveals how parents' worldviews influence their children and is an important step in developing the first measure of children's worldviews. The next steps in this line of research include (1) refining the UWM-CF by adding additional items and administering the revised measure to children and adolescents, and (2) asking parents of participating children about their children's physical, mental, and socioemotional health to assess relationships between children's health and their worldviews.

37. Mountains Yet to Climb in the Search for Novel Antibiotics

*Fiona Rodrigue, Suzanne Cooke
University of New Hampshire at Manchester*

The discovery of novel antibiotic compounds produced by soil bacteria is a strategy being utilized to combat the rise in antibiotic resistance. The location, diversity and required growth conditions of soil bacteria collected and isolated for our research is crucial information needed for the discovery of new antibiotics. Mountain soil bacterial isolates were tested for antibiotic production against known safe relatives of ESKAPE pathogens. Previously collected and isolated mountain soil bacteria were revived from preserved glycerol stock and maintained on specific media. Mountain soil isolates from three different elevations were tested and compared for antibiotic production. The effect of different bacterial growth media on the isolates' ability to inhibit ESKAPE safe relatives was also analyzed and presented. Isolates collected from the middle and top locations of the mountain were found to effectively inhibit multiple ESKAPE safe relatives on lactose and LB media. Future directions include the use of novel experimental growth media containing complex polysaccharides to further test the antibiotic potential of these isolates.

38. Evaluating Soil Sample Storage Conditions for Maximum Bacterial Recovery

*Sydney Rollins, Benjamin Beane, Suzanne Cooke
University of New Hampshire at Manchester*

Soil bacteria are integral to research in antibiotic discovery, ecological studies, agricultural research and development, and other fields of research. However, only about 1% of bacteria from soil can be successfully cultivated in the lab using current methods, and further, some of that 1% is lost when soil is stored incorrectly before processing. This study aimed to find the ideal sample storage temperature for maximum recovery of soil bacteria as measured by colony counting, and found no significant difference between storage at room temperature, at 4°C, and at -20°C over seven days of storage. Further studies will compare diversity as well as density of recoverable bacteria and test a larger temperature range, the addition of storage buffers, and the manipulation of oxygen exposure.

39. Developmental and Behavioral Effects of Chronic Exposure of Permethrin, Bifenthrin, and Perfluorooctane Sulfonic Acid (PFOS) on the American horseshoe crab, *Limulus polyphemus*

*Faith Schader, Christopher Chabot
Plymouth State University*

Insecticides and per- and polyfluoroalkyl substances (PFAS) are chemicals frequently used by humans that enter marine environments worldwide. Two insecticides, permethrin and bifenthrin, are regularly used for mosquito and other pest control, while the PFAS chemical, perfluorooctane sulfonic acid (PFOS), is commonly found in household items and firefighting foam. Permethrin and bifenthrin cause acute behavioral and developmental effects on aquatic organisms, however little is known about chronic effects on marine species. Likewise, PFOS causes delays in development and reproduction but few studies have been conducted on possible behavioral effects, especially in marine species. In this study, a keystone marine species, *Limulus polyphemus*, was used to assess the effects of these compounds. Newly developing eggs were exposed to these chemicals at 1X and 10X environmental levels for 45 days. The PFOS high treatment caused a two-week delay and 97% reduction in metamorphosis and the PFOS low treatment caused a 44% reduction ($P < 0.05$), while neither permethrin nor bifenthrin had significant effects at any concentration. Neither hatching rate or success were significantly affected by any treatment. Post-hatching activity levels and circadian rhythms of both larvae and juvenile horseshoe crabs are being analyzed. These results will help to highlight the impacts of these common environmental toxicants on a species of economic and medical importance as well as on the ecosystem at large and could also help to inform further appropriate legislation for limiting the release of these compounds into the environment.

40. CBEC Cell Block for Cell Cycle Analysis

*Ashna Siddiqui, Kellie Mathewson
University of New Hampshire at Manchester*

Analyses of the cell cycle and the process of cell adhesion in mammalian cells will be discussed. Explanations on the significance of flow cytometry in gathering data for effects on a cell cycle will also be present, as well as a discussion of how different drug treatments affect different cell types and their ability to adhere to ECM components as well as their overall impact on cell adhesion. The experiment began by subculturing human embryonic kidney 293 cells and Madin-Darby canine kidney (MDCK) cells.

41. An Evidence-Based Collection of Dos and Don'ts in Motion-Induced Blindness Research

*Vishnu Soni
University of New Hampshire at Manchester*

Ever since it was brought to the limelight of vision research by Bonneh and colleagues in 2001, the phenomenon of Motion-Induced Blindness (MIB) has spawned a great deal of scholarly activity. This line of research has many possible objectives; some seek to understand the intricacies of MIB itself, while others leverage it to unravel the inner workings of vision and attention in the brain. However, when it comes to 'how' to appropriately use the MIB stimulus, many studies have without hesitation followed the footsteps of other articles such as Bonneh et al.'s (2001) article. In other words, the past 21 years of MIB research seem to have occurred without a clearly defined, up-to-date, and agreed-upon set of guidelines for using the MIB stimulus. Thus, this study set three objectives. First, the most common methods of data collection in MIB research were identified, including the various constituent elements of a MIB stimulus and their common configurations found in the literature. Second, the often overlooked implications of using those methods and configurations were discussed. New empirical findings from this study's authors will be used to support this discussion, along with findings from previous studies as well. And third, novel and effective methods of MIB-related data collection were drawn from past studies and compiled as a set of recommendations for future studies using MIB.

42. Localization of Kv2.1 potassium channels in the soma and axons of the sea hare *Aplysia californica*

*Cade Stewart¹, Michael B. Hoppa², James M. Newcomb¹
¹New England College, ²Dartmouth College*

The endoplasmic reticulum (ER) makes junctions with the plasma membrane (PM) of cells in many different species, such as mammals and various invertebrates. In neurons, it was recently discovered that the PM-bound potassium channel, Kv2.1, forms junctions with ER-bound VAMP-associated proteins (VAPs), to form ER/PM junctions. Preliminary evidence from our labs suggests that Kv2.1 is present in the cell bodies of neurons in the sea slug *Aplysia californica*, which is the species where VAPs were first discovered. The goal

of this current study was to test the hypothesis that Kv2.1 is located in the axons of neurons as well. Western blots and immunohistochemistry, using a custom Aplysia anti-Kv2.1 antibody, were used to determine where Kv2.1 is located in the brain. The Western blots used protein samples extracted from just the ganglia (containing cell bodies), or just the nerves and connectives (containing axons). Results indicated that Kv2.1 was present in both the soma and the axons, with a band at the appropriate size (~96 kDa) for Kv2.1 in both tissue samples. These data were supported by immunohistochemistry, with Kv2.1 labeling exhibited in all ganglia and connectives. Together, these results provide evidence that ER/PM junctions may be present in both the soma and the axons of Aplysia, similar to other recent studies in mammals. Therefore, wide distribution of ER/PM junctions throughout neurons may be a highly conserved feature of animal nervous systems.

43. **Isolation and Identification of *Borrelia burgdorferi* Bacteriophages from New Hampshire *Ixodes scapularis***

Shoshana Trudel, Fardeen Siddiqui, Raunak Vijay, Monique Gingras
University of New Hampshire at Manchester

Lyme Disease is a condition caused by the bacteria *Borrelia burgdorferi* and is the most common vector-borne disease in the United States. Although antibiotics are currently the primary form of treatment for Lyme Disease, there is great value in exploring the potential for alternative treatments. Like other forms of life, bacteria have natural predators. Bacteriophages are viruses that infect bacteria while possessing an extremely selective host range of target bacteria. Due to this great specificity and concerns of antibiotic resistance, they have many advantages over traditional antibiotics as an antibacterial agent. Phage therapy is the application of bacteriophages in a clinical setting to treat bacterial diseases. An isolated bacteriophage specific for *Borrelia burgdorferi* may have a prospective future in treating Lyme Disease patients who are unresponsive to traditional antibiotics. Previous attempts to isolate bacteriophages for tick-borne bacterial illnesses have been unsuccessful due to the complex conditions needed to culture the bacteria themselves, alongside other factors. We present a novel methodology for *Borrelia* bacteriophage isolation from environmental blacklegged tick (*Ixodes scapularis*) samples using a combination of targeted primers, PEG precipitation, and dilution-to-extinction. Our methodology can be applicable not only for bacteriophages of *Borrelia* species, but for bacteriophages of other challenging to culture bacterial hosts, many of which have clinical significance.

44. **Prediction of Viscosity of Bio Ink using Machine Learning Tools**

Slesha Tuladhar, Md. Ahasan Habib
Keene State College

3D Bioprinting has been forwarded as technical progress of 3D printing that might be a possible solution to tissue engineering and regenerative medicine. However, unlike the traditional 3D printing process, additive bio-manufacturing has a lot of challenges like cell survivability, proliferation, and the mechanical properties of the biomaterials that involve printability and the ability to hold the structural integrity which are the key subjects of this research. With the help of appropriate design of experiments with a series of rheological investigations, one can identify the physical and mechanical properties of 3D bio-printed scaffolds directly related to their geometric fidelity. Using a machine learning tool, various compositions of Alginate and CMC were tested under a rheometer to generate an estimation equation. In the future, this equation will help predict the behavior of the compositions as well as help us generate the composition with desirable viscosities. Maintaining a constant parameter, a steady sweep test for 18 compositions was done that reflected the shear thinning behavior of the compositions and provided a viscosity region that helps to make the selection of compositions for printing easier.

45. **Hierarchical Tracing of T Cells Responding to Infection**

Alexandra Walker¹, Leena Abdullah², Yina Huang²
¹Plymouth State University, ²Dartmouth College

The adaptive immune system, comprised of T cells and B cells, provides protection to our body from infections by generating specific immune responses and by forming immunological memory. T cells have the capacity to directly kill infected cells or tumor cells. They develop in a specialized organ called the thymus where they differentiate into mature CD4 helper T cells, or CD8 killer T cells. Once fully developed, T cells are ready to respond to infection. Upon exposure to an antigen, naïve T cells differentiate into effector T cells to fight off pathogens. After antigen clearance, most effector cells die while some differentiate into memory T cells. Upon

secondary exposure the memory T cells quickly expand and differentiate into specific effector T cells to provide faster and bigger immune responses. While we know effector T cells become memory T cells, we remain unclear about the exact pathway taken by them. In this study we used CRISPR/Cas9 dependent lineage tracing tool GESTALT^{2,3} (genome editing of synthetic target arrays for lineage tracing) along with single cell RNA-seq to capture information on T cell type and lineage hierarchy, to better understand this pathway. Our current data focuses on optimizing the conditions to introduce GESTALT machinery into primary murine naïve and activated CD8 T cells. This study will look at lineage relationships to understand the differentiation of endogenous naïve CD8 T cells into memory T cells in response to infection.

46. The Effects of Chronic Exposure to Organophosphate Pesticides on the Development and Behavior of the American Horseshoe Crab, *Limulus polyphemus*

Cristian Will, Christopher Chabot

Plymouth State University

Organophosphates are a class of pesticides that are among the most heavily used in agriculture with 80 million tons used annually in the United States alone. These pesticides have been found in several coastal environments worldwide at concentrations that can negatively impact marine organisms. Exposure to these pesticides has induced changes in circadian rhythms in Manila clams and growth rates in lobsters while liver and gill damage has been observed in some fishes. However, little is known about the effects of these pesticides on estuarine keystone species such as the horseshoe crab, *Limulus polyphemus*. In addition, few studies have included behavioral assessment of any species, arguably the most sensitive assay of a toxin's effect. Here, horseshoe crab eggs, larvae and juveniles were chronically exposed to two organophosphate pesticides, chlorpyrifos and diazinon, at environmentally relevant levels (10 and 100ng/l) beginning within one week of egg fertilization. While this exposure had no effect on hatching rate, metamorphosis was significantly impacted (p -value < 0.05) causing up to a 75% reduction in metamorphosis rates. Behavioral analysis to determine potential impacts on movement and rhythms are ongoing. Since delayed development of keystone species such as horseshoe crabs could have compounding effects in the environment, this study may be used to help develop better recommendations for regulatory agencies and legislators.

47. Influence of Bacterial RNA on Characteristics of Macrophages

Alexandria Williams, Brian Patenaude and Tatiana Jones

Rivier University

Proinflammatory profile of macrophages plays a crucial role in the outcome of inflammation. Others showed that extracellular (ex)RNA derived from either damaged cells (self), or from a pathogen (non-self), can alter inflammatory properties of macrophages. We previously showed that proinflammatory responses of cultured RAW264.7 macrophages activated by agonists of toll-like receptors (TLR)4 or TLR2 can be altered by self-exRNA in a dose-dependent manner. Stimulation of macrophages activated by either TLR4 agonist lipopolysaccharide (LPS) or by TLR2 agonist Pam2SC4 with 5µg/mL of self exRNA, resulted in a downregulation of major histocompatibility complex (MHC)II and reduced tumor necrosis (TNF)α and interleukin (IL)6 production leaving NFκB upregulated, suggesting an active proinflammatory response. Those results prompted us to further research the mechanisms by which exRNA can alter the proinflammatory profile of macrophages. One of the questions we asked was about the influence of self- vs. non-self exRNA on macrophages. To answer this, we studied influence of non-self exRNA (derived from *E.coli*). We hypothesized that stimulation of activated through either TLR4 or TLR2 macrophages with non-self exRNA in contrast to stimulation with self exRNA, results in upregulation of MHCII expression and increased production of TNFα and IL6. To test this hypothesis, we stimulated macrophages activated with LPS or Pam2 with 5µg/mL of *E.coli*-derived exRNA. Our preliminary results showed that addition of 5µg/mL of non-self exRNA to LPS, Pam2, or both leads to increase in production of TNFα and IL-6. In addition, in single experiment we observed reduced expression of MHCII and interferon receptor A1 with exRNA alone. Thus, compared to self exRNA, addition of non-self exRNA to activated macrophages has opposite changes in TNFα and IL6 production, however, it might have similar to self exRNA downregulating effect on MHCII expression.

48. Human Neural Stem Cell Biocompatibility Study of Fmoc-Dipeptide Hydrogels

Matthew Woodworth, Ofori Mensah, Julia Castimore, Won Hyuk Suh

University of New Hampshire at Manchester

Peptide gelators are peptides that can form 3D supramolecular crosslinked structures. An interesting dipeptide peptide generator is Fmoc-Phe-Phe-OH. This molecule has been in the spotlight for being a potential scaffold

for tissue regeneration. Fmoc-FF gels can be formulated using the solvent switch and pH switch method. In this project, we replicated the conditions for formulating the gel using the solvent switch method. This method involves dissolving the dipeptide in an organic solvent dimethyl sulfoxide (DMSO), then mixing the solution with a controlled amount of water to form hydrogel structures. Once the hydrogels were prepared, they were exposed to human neural stem cells derived from the ventral mesencephalon region of the brain. Biocompatibility studies involved the usage of resazurin assays and live/dead cell assays plus fluorescence microscopy. Rheological testing was also performed to study the physiochemical properties of the as-prepared gels. We hope to utilize the finding from this study to further develop peptide-based hydrogels for developing new bioink formulations.

49. What is a Shared Resources?

*Christian Lytle, Craig Tomlinson, Robert Gerlach
Dartmouth cancer Center, Geisel School of Medicine*

Shared Resource laboratories provide researchers with instruments, services, and consultation from experts in their fields. Investigators using the Shared Resources will find they have access to state-of-the-art technology and instrumentation, with the expertise needed to conduct relevant and reproducible research. Dartmouth Cancer Center (DCC) Shared Resource Laboratories are open to all investigators, including those not part of the Dartmouth research community. These resources include Biostatistics and Bioinformatics, Clinical Pharmacology, Genomics and Molecular Biology, Immune Monitoring and Flow Cytometry, Irradiation Pre-clinical Imaging and Microscopy, Mouse Modeling, Pathology, and Trace Element Analysis. Even if you knew about the DCC Shared Resources, there are new services and equipment about which you will want to learn. No study is too large or too small, and consultation is free. Stop by the poster and find out how we can support your research.

50. NH CREATES Seeks NH-INBRE Partners

*Carmela Amato-Wierda, Amy Booth
University of New Hampshire – Durham*

NH CREATES the Future: the NH Collaborative for Regenerative Medicine Education and Training for Engineers and Scientists of the Future (hereafter, NH CREATES) is an NIH Science Education Partnership Award based at the University of New Hampshire. Its vision is to cultivate interest and expertise in regenerative medicine, biomanufacturing and biotechnology among diverse middle and high school students and teachers address current and future workforce needs. The overall goal of NH CREATES is to establish a robust pipeline extending from middle school to higher education and beyond for the burgeoning regenerative medicine and biofabrication (RM&B) industry in New Hampshire. NH CREATES develops partnerships among industry, K-12, and higher-ed partners to carry out this goal. The poster will describe our activities with youth and K-12 teachers, and attendees will learn how they can partner with NH CREATES.

MEETING ATTENDEES

Bonnie Ackerman

Faculty
Community College System of New Hampshire
bakerman@ccsnh.edu

Samrat Adhikari

Undergraduate Student
Keene State College
sba1018@usnh.edu

Mahad Ahmad

Alumni
Strand Therapeutics
mahad.chrome@gmail.com

Jeadminas Alexis

Undergraduate Student
Keene State College
jeadalexis713@gmail.com

Emmanuel Alisandro

Undergraduate Student
Plymouth State University
ea1082@plymouth.edu

Carmela Amato-Wierda

Science Education Partnership Award (SEPA)
University of New Hampshire - Durham
carmela.amato-wierda@unh.edu

Janelle Annor

POWERED Student
Dartmouth College
Janelle.E.Annor.24@dartmouth.edu

Michael Apitz

Undergraduate Student
Saint Anselm College
mapitz122@anselm.edu

Lynn Arnold

Staff
Keene State College
larnold@keene.edu

Debra Audino

Faculty
Community College System of New Hampshire
daudino@ccsnh.edu

Ibrahim Ayyash

Undergraduate Student
Franklin Pierce University
ayyashi19@live.franklin Pierce.edu

Grace Baukus

iSURF Student
Saint Anselm College
gbaukus242@Anselm.Edu

Parker Baumann

Graduate Student
University of New Hampshire - Manchester
parker.baumann@unh.edu

James Beeby

Administration
Keene State College
james.beeby@keene.edu

Katherine Benjamin

Undergraduate Student
Keene State College
katherine.benjamin@keene.edu

Evan Bennett

iSURF Student
Franklin Pierce University
Bennette18@live.franklin Pierce.edu

Autumn Berlied

Undergraduate Student
Keene State College
Autumn.Berlied@keene.edu

Donald Bix

Administration
Plymouth State University
dlbix@plymouth.edu

MEETING ATTENDEES

Amy Booth

Science Education Partnership Award (SEPA)
University of New Hampshire - Durham
Amy.Booth@unh.edu

Michael Bowles

Undergraduate Student
New England College
mbowles_ug@nec.edu

Jeanelle Boyer

Faculty
Keene State College
jboyer@keene.edu

Austin Boynton

Undergraduate Student
Plymouth State University
aeb1126@plymouth.edu

Loretta Brady

Faculty
Saint Anselm College
lbrady@anselm.edu

Kelsea Brasseur

Undergraduate Student
Colby-Sawyer College
kelsea.brasseur@my.colby-sawyer.edu

Samantha Brooks

iSURF Student
Rivier University
samantha.brooks1024@gmail.com

Benjamin Burnett

Undergraduate Student
Keene State College
benjamin.burnett@keene.edu

Sean Cady

Undergraduate Student
Keene State College
sean.cady@keene.edu

Jenna Campbell

Undergraduate Student
Community College System of New Hampshire
jcampbell@ccsnh.edu

Emily Carson

Undergraduate Student
Plymouth State University
ec1242@plymouth.edu

Julia Castimore

Graduate Student
University of New Hampshire - Manchester
julia.castimore@unh.edu

Chris Chabot

Faculty
Plymouth State University
chrisc@plymouth.edu

Joshua Chandler

Undergraduate Student
Plymouth State University
jechandler@plymouth.edu

Jason Charbonneau

Alumni
Fluigent Inc.
jascharb@verizon.net

Advaita Chaudhari

POWERED Student
Dartmouth College
Advaita.S.Chaudhari.24@dartmouth.edu

Jennifer Chretien

Administration
Dartmouth College
Jennifer.J.Smith@Dartmouth.edu

Zoe Clark

Undergraduate Student
Plymouth State University
zc1048@plymouth.edu

MEETING ATTENDEES

Scott Clark

Undergraduate Student
Keene State College
Cscotty734@gmail.com

Lindsay Coats

Staff
New England College
lcoats@nec.edu

Chuck Cole

Administration
Dartmouth College
Charles.N.Cole@Dartmouth.edu

Bridget Conley

Faculty
Community College System of New Hampshire
bconley@ccsnh.edu

Geoff Cook

Faculty
New England College
gcook@nec.edu

Sue Cooke

Faculty
University of New Hampshire - Manchester
suzanne.cooke@unh.edu

Pat Corbett

Administration
New England College
pcorbett@nec.edu

Emily Cornell du Houx

Undergraduate Student
Keene State College
emilycornellduhoux@smccme.edu

Steven Cornish

Administration
Colby-Sawyer College
steven.cornish@colby-sawyer.edu

Debra Costa-Nino

Faculty
Community College System of New Hampshire
dcostanino@ccsnh.edu

Mark Cronin

Administration
Saint Anselm College
mwcronin@anselm.edu

Kelly Cunninham

Undergraduate Student
Colby-Sawyer College
kelly.cunningham@my.colby-sawyer.edu

Haleigh Daft

Undergraduate Student
Colby-Sawyer College
haleigh.daft@my.colby-sawyer.edu

Isabella Darling

Undergraduate Student
University of New Hampshire - Manchester
igd1005@usnh.edu

Lauryn Davis

Undergraduate Student
Community College System of New Hampshire
ldavis241@students.ccsnh.edu

Petra Deane

iSURF Mentor
Mascoma LLC
pdeane@lallemand.com

Jonathan DeJesus

Undergraduate Student
Keene State College
jdejesus31570@gmail.com

Kristen Deleault

iSURF Mentor
Mascoma LLC
kdeleault@lallemand.com

MEETING ATTENDEES

Rob DeLong

Faculty
University of New Hampshire - Manchester
rkdelong@gmail.com

Sophia DeMarco

Graduate Student
Colby-Sawyer College
sdemarco1129@gmail.com

Danny DeSousa

Undergraduate Student
Plymouth State University
dfdesousa@plymouth.edu

Jane Disney

Science Education Partnership Award (SEPA)
Mount Desert Island Biological Laboratory
jdisney@mdibl.org

Heather Doherty

Faculty
Plymouth State University
hedoherty@plymouth.edu

Debra Dunlop

Administration
New England College
ddunlop@nec.edu

Hunter Dupuis

Graduate Student
University of New Hampshire - Manchester
Hunter.Dupuis@unh.edu

Olivia Economides

Alumni
Tufts University
olivia.economides@tufts.edu

Ethan Edwards

iSURF Student
University of New Hampshire - Manchester
Ethan.Edwards@unh.edu

Meredith Ellis

Undergraduate Student
Colby-Sawyer College
meredith.ellis@my.colby-sawyer.edu

Elizabeth Enright

Alumni
Abbott
enrightel333@gmail.com

Brian Ernsting

Administration
Rivier University
bernsting@rivier.edu

Peter Faletra

Science Education Partnership Award (SEPA)
New Hampshire Academy of Science
peter.faletra@gmail.com

Jordan Fessenden

Undergraduate Student
University of New Hampshire - Manchester
jordan.fessenden@unh.edu

Harlan Fichtenholtz

Faculty
Keene State College
harlan.fichtenholtz@keene.edu

Steve Fiering

Administration
Dartmouth College
Steven.N.Fiering@Dartmouth.edu

Keegan Finley

Undergraduate Student
New England College
keegan.finley.2020@gmail.com

Isabella Fox

POWERED Student
Dartmouth College
Isabella.B.Fox.24@dartmouth.edu

MEETING ATTENDEES

Bailee Gallant

iSURF Student
Plymouth State University
bjg1031@plymouth.edu

Isabel Garcia

Undergraduate Student
Keene State College
isabel.garcia@keene.edu

Nicholas Genovese

iSURF Student
Colby-Sawyer College
Nicholas.genovese@my.colby-sawyer.edu

Monique Gingras

iSURF/CLIMB Student
University of New Hampshire - Manchester
monique.gingras.29@gmail.com

Shaun Golding

Staff
Dartmouth College
Shaun.A.Golding@dartmouth.edu

Christine Gordon

Undergraduate Student
New England College
cgordon_ug@nec.edu

Charles Graffius

Undergraduate Student
Colby-Sawyer College
charliegraffius@gmail.com

Natalie Gravelle

Undergraduate Student
Plymouth State University
nlg1014@plymouth.edu

Bill Green

Administration
Dartmouth College
William.R.Green@Dartmouth.edu

Louise Griffin

Staff
University of New Hampshire - Durham
louise.griffin@unh.edu

Sarah Gunnery

Faculty
New England College
sgunnery@nec.edu

Christine Gustafson

Administration
Saint Anselm College
cgustafson@anselm.edu

Md Ahasan Habib

Faculty
Keene State College
md.ahasan.habib@keene.edu

Jeffrey Hall

Staff
University of New Hampshire - Durham
jeffrey.hall@unh.edu

Abigail Halterman

Undergraduate Student
Saint Anselm College
ahalterman393@anselm.edu

Larissa Havey

Undergraduate Student
Saint Anselm College
lhavey845@anselm.edu

Kendall Hawkom

Graduate Student
University of New Hampshire - Manchester
kendall.hawkom@unh.edu

Kristine Hayes

Undergraduate Student
Community College System of New Hampshire
Kristine1818@live.com

MEETING ATTENDEES

Justin Haynes

Undergraduate Student
Franklin Pierce University
justinhaynes2525@gmail.com

Daniel Henderson

Consultant
Director of Workforce Development
Daniel.Henderson@dartmouth.edu

Haley Hildreth

Undergraduate Student
New England College
haleyhildreth@gmail.com

Noelle Honan

Undergraduate Student
Saint Anselm College
nhonan165@anselm.edu

Yina Huang

Administration
Dartmouth College
Yina.H.Huang@dartmouth.edu

Jasmine Huffman

Alumni
University of New Hampshire - Manchester
JasmineAlexisHuffman@gmail.com

Joshua Hughes

Undergraduate Student
Franklin Pierce University
hughesj20@live.franklin Pierce.edu

Ty Hunter

Undergraduate Student
New England College
thunter1_ug@nec.edu

Warren Hurd

Faculty
Keene State College
warren.hurd@keene.edu

Finn Husband

Undergraduate Student
Colby-Sawyer College
husbandfinn@gmail.com

Leila Jabbour

Faculty
Franklin Pierce University
jabbourl@franklin Pierce.edu

Felicia James

Undergraduate Student
New England College
FJames_UG@nec.edu

Kristen Johnson

Faculty
University of New Hampshire - Manchester
kristen.johnson@unh.edu

Hannah Johnson

Undergraduate Student
Franklin Pierce University
johnsonh19@live.franklin Pierce.edu

Tatiana Jones

Faculty
Rivier University
tjones@rivier.edu

James Jukosky

Faculty
Colby-Sawyer College
james.jukosky@colby-sawyer.edu

Karrie Kalich

Administration
Keene State College
kkalich@keene.edu

Kara Keiper

iSURF Student
Colby-Sawyer College
kara.keiper@my.colby-sawyer.edu

MEETING ATTENDEES

Saron Ketema

POWERED Student
Dartmouth College
Saron.S.Ketema.24@dartmouth.edu

Dawin Khiev

Graduate Student
University of New Hampshire - Manchester
dawin.khiev@unh.edu

Casey Kimball

Alumni
Intellia Therapeutics
casey.kimball11@gmail.com

Erin Kopeski

Undergraduate Student
Keene State College
kopeskie16@gmail.com

James Kraly

Administration
Keene State College
jkraly@keene.edu

Avery Kretschmar

Alumni
Bio X Cell
Averykretschmar@gmail.com

Isabelle Laizure

Graduate Student
University of New Hampshire - Manchester
isabelle.laizure@unh.edu

Maya Langa

POWERED Student
Plymouth State University
mjlanga1@plymouth.edu

Loren Launen

Faculty
Keene State College
llaunen@keene.edu

Gordon Leversee

Consultant
Keene State College
gleverse@gmail.com

Nicole Lezon

Undergraduate Student
Rivier University
nlezon@rivier.edu

Bridget Linehan

Faculty
Dartmouth Hitchcock Medical Center
Bridget.A.Linehan@hitchcock.org

Sheila Liotta

Administration
Saint Anselm College
sliotta@anselm.edu

Wei Lu

Faculty
Keene State College
wlu@keene.edu

Kate Lu

Alumni
Advanced Regenerative Manufacturing Institute
kate.lu0530@gmail.com

Chris Lytle

Faculty
Dartmouth College
Christian.H.Lytle@dartmouth.edu

Kyle MacLea

Faculty
University of New Hampshire - Manchester
kyle.maclea@unh.edu

Mary Mader

Administration
Saint Anselm College
mmader@anselm.edu

MEETING ATTENDEES

McKenna Malone

Undergraduate Student
Community College System of New Hampshire
Mmalone738@students.ccsnh.edu

Jack Mankowsky

Undergraduate Student
Keene State College
jam1273@usnh.edu

Megan Marshall

Alumni
Bio X Cell
mmarshall0598@gmail.com

Priscilla Marsicovetere

Faculty
Franklin Pierce University
marsicoveterep@franklinpierce.edu

Somer Matar

Alumni
Dartmouth College
Somer.M.Matar.GR@dartmouth.edu

Elizabeth McGrath

Faculty
Dartmouth Hitchcock Medical Center
Elizabeth.B.McGrath@hitchcock.org

Grace McLaughlin

iSURF Student
Colby-Sawyer College
grace.mclaughlin@my.colby-sawyer.edu

Ofori Mensah

Graduate Student
University of New Hampshire - Manchester
ofori.mensah@unh.edu

Bamlak Messay

POWERED Student
Dartmouth College
Bamlak.A.Messay.23@dartmouth.edu

Anna Michaud

Undergraduate Student
Saint Anselm College
annamichaud3@gmail.com

Peter Mikhlin

POWERED Student
Dartmouth College
Peter.Mikhlin.23@dartmouth.edu

Raymond Miller

Graduate Student
University of New Hampshire - Manchester
Raymond.Miller@unh.edu

Alexander Misiaszek

POWERED Student
Dartmouth College
Alexander.J.Misiaszek.25@dartmouth.edu

Nicholas Mixon

Undergraduate Student
Community College System of New Hampshire
njm1122@usnh.edu

Madelyn Moedebeck

iSURF Student
Rivier University
mmoedebeck@rivier.edu

Jessica Morgan

Staff
Plymouth State University
jpmorgan2@plymouth.edu

Krystalynne Morris

Staff
University of New Hampshire - Durham
krystalynne.morris@unh.edu

Dianne Moschitta

Grad Student
University of New Hampshire - Manchester
des1023@wildcats.unh.edu

MEETING ATTENDEES

Talia Muller

Undergraduate Student
Colby-Sawyer College
talia.muller@my.colby-sawyer.edu

Patrick Murphy

iSURF Student
Colby-Sawyer College
patrick.murphy@my.colby-sawyer.edu

Kayli Neil

Alumni
Atalanta Therapeutics
kneil9716@gmail.com

Jim Newcomb

Faculty
New England College
jnewcomb@nec.edu

Malik Newcomb

Undergraduate Student
Colby-Sawyer College
maliknewcomb@icloud.com

Kyle Newton

Undergraduate Student
Plymouth State University
kjn1018@plymouth.edu

Daria Naumova

Faculty
Dartmouth College
Daria.Naumova.GR@dartmouth.edu

Sharon O'Connor

Administration
Dartmouth College
Sharon.O'connor@dartmouth.edu

Jen Pace

Faculty
Saint Anselm College
jpace@anselm.edu

Shallee Page

Faculty
Franklin Pierce University
pages@franklinpierce.edu

Christina Parkinson

Alumni
Boston Analytical
Christina.Parkinson@gmail.com

Jason Pellettieri

Faculty
Keene State College
jpellettieri@keene.edu

Alexandre Pennell

Undergraduate Student
Saint Anselm College
apennell772@gmail.com

Abigail Peschel

Undergraduate Student
New England College
apeschel_ug@nec.edu

Richard Phipps Jr.

Undergraduate Student
Keene State College
rhp1012@keene.edu

Olivia Piemonte

undergraduate Student
Colby-Sawyer College
olivia.piemonte@my.colby-sawyer.edu

Nyah Piper

Graduate Student
New England College
Npiper_ug@nec.edu

Lauren Pribyl

Undergraduate Student
Franklin Pierce University
pribyll19@live.franklinpierce.edu

MEETING ATTENDEES

Hannah Prinz

Undergraduate Student
Keene State College
hannahprinz@comcast.net

Brandon Proulx

Alumni
Median LLC
bproulx33@gmail.com

Madison Puglisi

Undergraduate Student
Keene State College
madison.puglisi@keene.edu

Brian Reese

other
Keene State College
brian.reese@keene.edu

Lourdes Ricks

Undergraduate Student
New England College
Lricks_ug@nec.edu

Yahira Rivera

iSURF Student
Delaware State University
ymrivalopez18@students.desu.edu

Hayden Rodgers

Undergraduate Student
Saint Anselm College
hrogers762@Anselm.Edu

Fiona Rodrigue

Graduate Student
University of New Hampshire - Manchester
Fiona.Rodrigue@unh.edu

Sydney Rollins

Graduate Student
University of New Hampshire - Manchester
sydney.rollins@unh.edu

Maxwell Ross

Undergraduate Student
New England College
mross_ug@nec.edu

Priya Roy Chowdhury

Faculty
Keene State College
pr1043@keene.edu

Eva-Maria (EM) Rudler

Alumni
George Mason University
evamariarudler@gmail.com

Sona Sahakyan

iSURF Student
Colby College
ssahak24@colby.edu

Kirk Sanger

Faculty
Keene State College
kirk.sanger@keene.edu

John Sardella

Graduate Student
University of New Hampshire - Manchester
john.sardella@unh.edu

Faith Schader

Undergraduate Student
Plymouth State University
fes1008@plymouth.edu

Madisyn Schmanski

Undergraduate Student
Community College System of New Hampshire
mschmanski851@students.ccsnh.edu

Lindsay Schommer

Faculty
Dartmouth Hitchcock Medical Center
Lindsay.M.Schommer@Hitchcock.ORG

MEETING ATTENDEES

Leah Schwartz

Alumni
Tufts University
leah.schwartz@tufts.edu

Joseph Sevigny

Staff
University of New Hampshire - Durham
joseph.sevigny@unh.edu

Grace Shaw

Alumni
Novo Nordisk
gracetshaw@gmail.com

Hye-Young Shin

Faculty
Rivier University
hshin@rivier.edu

Fardeen Siddiqui

Undergraduate Student
University of New Hampshire - Manchester
fardeensiddiqui19@gmail.com

Ashna Siddiqui

Undergraduate Student
University of New Hampshire - Manchester
ashna.siddiqui@unh.edu

Stephen Simpson

Staff
University of New Hampshire - Durham
stephen.simpson@unh.edu

Sarah Siudut

Graduate Student
Saint Anselm College
ssiudut860@anselm.edu

Angela Slaybe

Undergraduate Student
Saint Anselm College
aslaybe299@anselm.edu

Roger Sloboda

Science Education Partnership Award (SEPA)
Dartmouth College
Roger.D.Sloboda@dartmouth.edu

Lorna Smith

Alumni
Advanced Regenerative Manufacturing Institute
lsmith@armiusa.org

Vishnu Soni

Undergraduate Student
University of New Hampshire - Manchester
Vishnu.Soni@unh.edu

Calie Sorenson

Undergraduate Student
Colby-Sawyer College
calie.sorenson@my.colby-sawyer.edu

John Sparrow

Faculty
University of New Hampshire - Manchester
john.sparrow@unh.edu

Ben Steele

Administration
Colby-Sawyer College
bsteeler@colby-sawyer.edu

Cade Stewart

Undergraduate Student
New England College
cadestew3@gmail.com

Sadie Stimmell

Administration
Community College System of New Hampshire
sstimmell@ccsnh.edu

Kerstin Stoedefalke

Faculty
Colby-Sawyer College
kstoedefalke@colby-sawyer.edu

MEETING ATTENDEES

Annika Stone

Undergraduate Student
Keene State College
Annika.Stone@keene.edu

David Suh

High School Student
Bedford High School

Won Hyuk Suh

Faculty
University of New Hampshire - Manchester
WonHyuk.Suh@unh.edu

W. Kelley Thomas

Administration
University of New Hampshire - Durham
kelley.thomas@unh.edu

Devin Thomas

Staff
University of New Hampshire - Durham
devin.thomas@unh.edu

Steve Tobin

Faculty
Saint Anselm College
stobin@anselm.edu

Trang Tong

iSURF Student
Plymouth State University
tongthuytrang3112@gmail.com

Elijah Trepanier

Undergraduate Student
Keene State College
elijah.trepanier@keene.edu

Andy Trinh

POWERED Student
Dartmouth College
Andy.Trinh.24@dartmouth.edu

Joseph Troisi

Faculty
Saint Anselm College
jtroisi@anselm.edu

Shoshana Trudel

Undergraduate Student
University of New Hampshire - Manchester
shoshana.trudel@unh.edu

Slesha Tuladhar

Undergraduate Student
Keene State College
slesha.tuladhar@ksc.keene.edu

Gwendolyn Tupman

Undergraduate Student
Community College System of New Hampshire
gtupman015@students.ccsnh.edu

Danielle Vaclavik

Administration
Dartmouth College
Danielle.S.Vaclavik@dartmouth.edu

Robert Vallari

Faculty
Saint Anselm College
rvallari@anselm.edu

Mackenzie Valley

Undergraduate Student
Saint Anselm College
mvalley412@anselm.edu

Forrest Veilleux

Undergraduate Student
Franklin Pierce University
veilleuxf18@live.franklinpierce.edu

Sadie Vezina

Graduate Student
University of New Hampshire - Manchester
sadie.vezina@unh.edu

MEETING ATTENDEES

Madison Vigneault

Alumni
Affinivax
mkvigneault@gmail.com

Raunak Vijay

Undergraduate Student
University of New Hampshire - Manchester
raunak.vijay@unh.edu

Lexi Walker

iSURF Student
Plymouth State University
asw1029@plymouth.edu

Megan Welch

iSURF Student
University of New Hampshire - Durham
Megan.Welch@unh.edu

Larry Welkowitz

Faculty
Keene State College
lwelkowi@keene.edu

Allison Wheeler

Undergraduate Student
Franklin Pierce University
Wheelerallison@outlook.com

Chery Whipple

Faculty
Colby-Sawyer College
chery.whipple@colby-sawyer.edu

Derk Wierda

Administration
Saint Anselm College
dwierda@anselm.edu

Beth Wilkes

Faculty
Community College System of New Hampshire
bwilkes@ccsnh.edu

Christian Will

Undergraduate Student
Plymouth State University
cjw1091@usnh.edu

Alexandria Williams

Undergraduate Student
Rivier University
awilliams1@rivier.edu

Shailee Woodard

Faculty
Keene State College
shailee.woodard@keene.edu

Matthew Woodworth

Undergraduate Student
University of New Hampshire - Manchester
matthew.woodworth@unh.edu

Megan Wozniak

Undergraduate Student
Saint Anselm College
mwozniak167@anselm.edu

Nancy Wray

Administration
Dartmouth College
Nancy.J.Wray@dartmouth.edu

Matt Young

Faculty
New England College
MYoung@nec.edu



Center for Program Design & Evaluation

CPDE at Dartmouth College

We are NH-INBRE's internal evaluation team. Our role is to measure and assess NH-INBRE's impact on students, faculty, staff, and institutions. We work closely with the Administrative Core but are objective evaluators, situated outside the program's leadership and implementation structure.

We gather the experiences of students, faculty, alumni, and other key stakeholders, through:

- Surveys
- Interviews
- Focus groups
- Metrics on the utilization of INBRE infrastructure

CPDE adheres to national guidelines for data privacy and security, and we take confidentiality very seriously. When we ask you for feedback or program improvement ideas, we aggregate that information, never sharing identifiable responses.

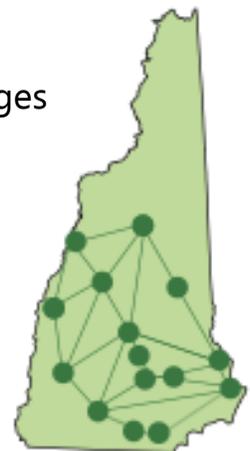
Danielle Vaclavik, Ph.D.

Shaun Golding, Ph.D.

Building a network of research excellence in a rural state takes effort, and evaluation helps gauge program effectiveness to better inform efforts moving forward.

Our work is used to track and measure progress toward enhancing the following components of New Hampshire's biomedical infrastructure:

- Scientific & scholarly interactions within the network of colleges
- The research infrastructure & training at each institution
- Research opportunities for students & faculty
- The research culture at NH-INBRE institutions
- New Hampshire's biomedical workforce



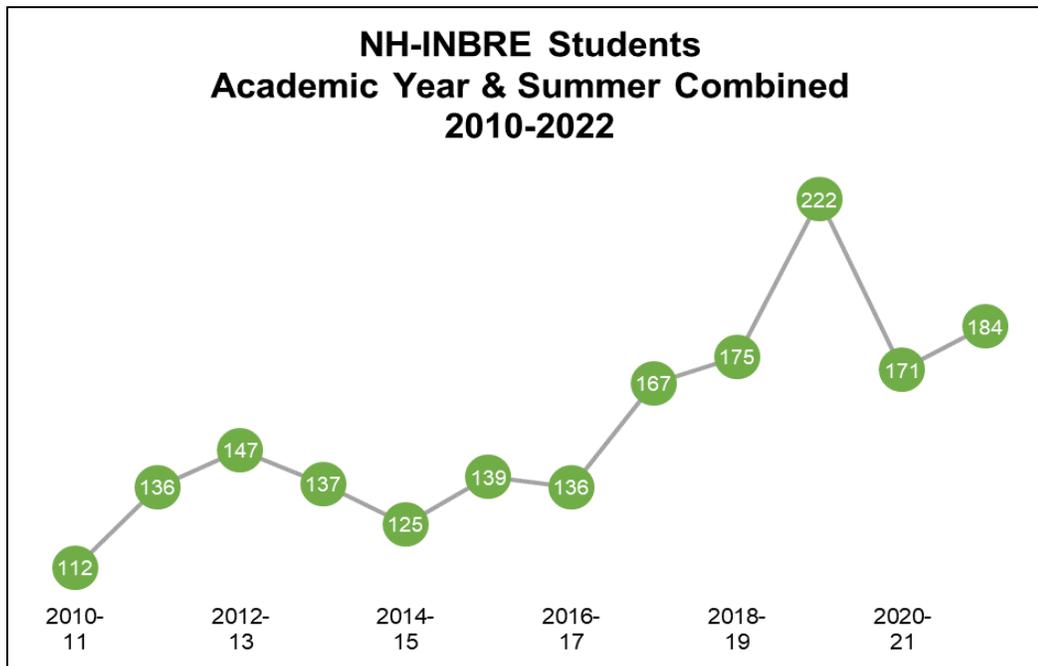
»»»»» Turn over to see the latest NH-INBRE alumni metrics »»»»»



Center for Program Design & Evaluation

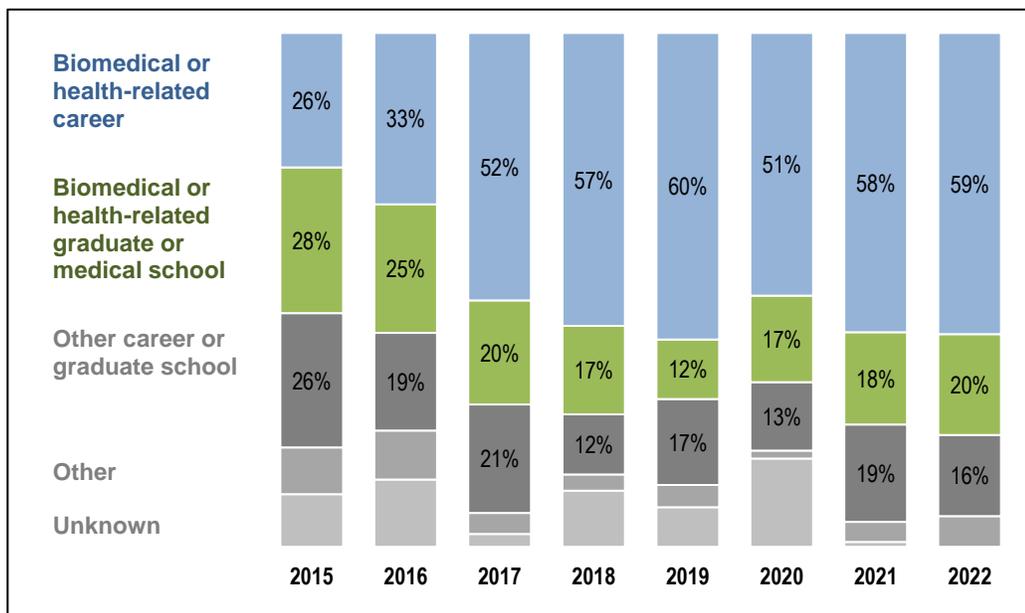
CPDE at Dartmouth College

Tracking Student Participation in NH-INBRE...



Averaging 154 students per year, the number of students impacted by NH-INBRE has grown to over 1,300 since inception.

What NH-INBRE Alumni are up to within 5 years of graduation...



Annual surveys show that a growing share of NH-INBRE alums are working in **Biomedical or Health-related careers**, and more than a third have pursued **higher degrees in biomedical disciplines and beyond**.

Looking into the future: Efforts are underway to build a NH-INBRE alumni community with opportunities to network with each other and mentor current students. Our surveys facilitate this by keeping tabs on NH-INBRE students after they complete their degrees.



Tell us about your experience

Use **ONE** of these options to access the feedback survey.

1. Scan this QR code:



2. Type this link into your web browser:

<https://tinyurl.com/INBREannualmeeting2022>

3. Ask for a paper survey at the registration table

Thank you for sharing your feedback,

~ The Evaluation Team

Danielle Vaclavik & Shaun Golding

