A LETTER FROM DEAN CRAWFORD


These are all traits of students in the College of Science. For many students, these traits have been cultivated through undergraduate research.

Over 50 percent of our undergraduates have taken advantage of the opportunity to embark on real projects to address some of the biggest challenges of our world today. Research gives students the opportunity to experience science first-hand beyond the textbook, deepening their knowledge, and developing leadership skills that will be used in careers in research, medicine, business, and beyond. Ultimately, these students are helping to create new knowledge that could have a significant impact on our society. They are the first to see the future with their discoveries.

I am so excited to have such a remarkable group of students who have provided the content for Scientia and managed the production of the journal. I am very proud of their hard work, and I hope you enjoy reading this volume of Scientia as much as I did.

Yours in Notre Dame,

Gregory P. Crawford, Ph.D.
William K. Warren Foundation Dean of the College of Science
Professor of Physics
We are pleased to present the fourth volume of Scientia, the undergraduate journal of scientific research. This year’s edition carries on our proud tradition of presenting top research produced by undergraduates, written by undergraduates, and reviewed by our undergraduate peers.

The very name of this journal, Scientia, is derived from the work of Sir Francis Bacon, who claims that scientia, knowledge of the natural world, is itself the proper partner of potentia, or power. Scientia embodies the mission of the College of Science to prepare tomorrow’s scientific leaders to think big, while also inspiring them to make a difference, to share their knowledge and discoveries in ways that encourage collaboration, advance learning, and contribute to the common good. In the pages of this journal you will discover articles on animal foraging behavior, biomarkers for diabetes, 3-D printing, bacterial clustering dynamics, carbon nanotubes, and hadron colliders. These articles only touch on the vast variety of research done by undergraduates across campus.

One of the goals of Scientia is to drive undergraduate participation in the publication and peer-review process. More broadly, our goal is to foster scientific communication across disciplines and among students and faculty. Beyond the publication of this print journal, we also celebrate the success of our monthly Talk Science seminars. Now in its third year, Talk Science serves as an opportunity for undergraduates and faculty to give talks on their research in a fun and informal setting. We thank all of our student and faculty presenters this year, who are listed on the final page of the journal.

In closing, we thank all of the people whose support has contributed to the continued success of Scientia. In particular, we would like to recognize Greg Crawford, dean of the College of Science; the staff of the dean’s office; and Prof. Dominic Chaloner, our faculty advisor. We gratefully acknowledge all of the students who submitted their papers for review, and well as their faculty mentors. Finally we thank all of our staff members, particularly our layout team and our section editors, for all of their fantastic work throughout the year. Without them Scientia would not be possible.

In Notre Dame,

Rachel Cotton
Scientia Co-Editor-in-Chief

Rebecca Marton
Scientia Co-Editor-in-Chief
New Faculty Join the College of Science

MICHAEL DINH

In 2012, the College of Science welcomed eight new talented faculty members.

Laurie Littlepage, Campbell Family Assistant Professor of Cancer Research in the Department of Chemistry and Biochemistry, is a member of the Harper Cancer Research Institute. Her laboratory is housed in Harper Hall, the new cancer research building located near Eddy Street Commons, south of campus. Littlepage earned her Ph.D. in Cell & Developmental Biology at Harvard University and completed postdoctoral training at the University of California, San Francisco. At Notre Dame, her lab researches biomarkers and therapies of breast and prostate cancers. As described by Littlepage, her research develops and applies in vivo xenograft models, systems biology methods, and both organotypic and cell cultures to study the causes and treatments of breast and prostate cancer.

Siyuan Zhang, Nancy Dee Assistant Professor of Cancer Research in the Department of Biological Sciences and the Harper Cancer Research Institute, earned his M.D. at the Peking University Health Science Center in Beijing, China, and his Ph.D. from the National University of Singapore. He also conducted postdoctoral research at the University of Texas M.D. Anderson Cancer Center. His research focuses on the impact of tumor microenvironments on metastasis and therapeutic resistance in breast cancer. Specifically, he stated that he is studying the interaction between the HER2 protein, which promotes the pathogenesis and progression of breast cancers when overexpressed, and the trastuzumab (Herceptin) antibody treatment that inhibits HER2.

Samaras Li, Roxana Smarandache

Jun Li, assistant professor of applied and computational mathematics and statistics, earned his Ph.D. at Stanford University. He works in the fields of bioinformatics and applied statistics, and is working on developing new methods for modeling biology, medicine, and genetics. His previous research includes modeling RNA sequencing and developing a new method for detecting recombination hotspots in the human genome. Li is a self-described avid fisherman, and his dream is “to become the best angler among statisticians, and the best statistician among anglers.”

Jun Li, assistant professor of applied and computational mathematics and statistics

Roxana Smarandache, associate professor of mathematics and electrical engineering, returned to Notre Dame after completing her Ph.D. here in 2001. Smarandache researches applied mathematics and error control coding theory, which deals with reducing errors that occur when transmitting information over noisy channels. In particular, her research is related to low-density parity-check (LDPC) code, which is a practical class of codes that are implemented nowadays in a variety of applications, like deep space communications, wireless, and more. She teaches coding theory and calculus.

Reginald Hill, Archibald Assistant Professor of Cancer Biology, is also a member of the Department of Biological Sciences and the Harper Cancer Research Institute. He joined the Notre Dame family after earning a Ph.D. in Genetics and Molecular Biology at the University of North Carolina at Chapel Hill and doing his postdoctoral work at the University of California, Los Angeles. His lab is currently the only one at Notre Dame that is studying pancreatic cancer, which is the fourth most common cause of cancer-related deaths in the United States. He uses mouse models, assay systems, and human clinical samples from the nearby Goshen Center for Cancer Care to investigate how specific genes contribute to tumorigenesis. Hill also researches how endoplasmic reticulum stress, which leads to overexpression of the GRP 78 protein, contributes to tumor growth and how certain signals from the tumor microenvironment mediate chemoresistance to conventional treatments such as chemotherapy. Pancreatic cancer has a five-year survival rate of only 6% because it often remains undiagnosed until it has already reached advanced stages. Consequently, Hill stated that one of his goals is to develop a minimally invasive, early detection blood test that can detect the presence of tumor cells circulating in the blood stream.

Adrian Rocha, assistant professor of biological sciences, is a member of Notre Dame’s Environmental Change Initiative. Rocha earned his M.S. in Environmental Science at the Ohio State University and holds a Ph.D. in Earth Systems Science from the University of California, Irvine. His previous research studied the controls on ecosystem carbon cycling and monitored the exchange of carbon between the atmosphere and the biosphere. He is currently conducting field work in Alaska, funded by the National Science Foundation, modeling how carbon cycling in the arctic changes with increased fire frequency in the Alaskan tundra. As described by Rocha, climate warming in the arctic has resulted in drier conditions and increased fire frequency locally, causing stored carbon to be released and decreasing the area’s capacity to take up carbon from the atmosphere.

Justin Crepp, Frank M. Freimann Assistant Professor of Physics, earned a Ph.D. in Physics from the University of Florida, where he worked on developing new technologies and observational techniques to detect planetary systems orbiting nearby stars. He is currently leading a program that combines high-contrast imaging with the Doppler radial velocity method of planetary detection, which measures Doppler shifts in the spectrum of stars to indirectly find planets. He is also developing a new instrument called the Locater. When it is complete, this instrument will identify terrestrial planets orbiting in the habitable zone of nearby stars using the first Doppler instrument that operates behind an adaptive optics system.

Kenjiro Gomes, Frank M. Freimann Assistant Professor of Physics, earned his B.S. and M.S. in Electrical Engineering in Brazil at the Pontifical Catholic University of Rio de Janeiro. He also holds a Ph.D. from the University of Illinois at Urbana-Champaign. He stated that the goal of his research is to engineer electronic systems at the atomic level using a scanning tunneling microscope. This device uses the concept of quantum tunneling to image surfaces to a microscopic resolution of about 0.1 nanometers; Gomes then uses the same device to move individual atoms into a specific arrangement. As a result, this method offers a high level of control that can be used to uncover the physics of new emergent states and create nanoscale devices for energy and information technologies. For instance, this procedure can be used to assemble artificial lifelike structures like graphene, which has many potential applications within materials science.
Translating 3-D Printing to the Clinic

EDITED BY YUKO GRUBER

Ever wonder what it would be like to hold your own skull? Or to check out the twists and turns of your own intestines, exactly as they are in your body? Technology that will allow the creation of such objects is being developed by Evan Doney, a sophomore chemical and biomolecular engineering major, working closely with W. Matthew Leevy, research assistant professor from the Notre Dame Integrated Imaging Facility, and technical developers at Makerbot Industries, a 3-D printing company. Their approach will allow medical scans to be turned into physical objects.

Doney’s research utilizes the rapidly emerging technology of 3-D printing. Lauded as the "next trillion dollar industry" by Business Insider and as "the machine that will change the world" by Wired, the three-dimensional printer promises to revolutionize every industry. 3-D printing or “additive manufacturing” involves a new method for the fabrication of objects, creating them layer by layer instead of using traditional mold and casts. This allows a “printer” the size of a desktop computer to create any object from an array of raw materials, including plastics and alloys. 3-D printing has exploded with popularity in anticipation of the manufacturing breakthroughs that will come in the future.

Although the primary focus of 3-D printing is currently on increasing speed and customizability of manufacturing processes, new 3-D printing technologies offer exciting new possibilities in the medical field. Doney and other students under the mentorship of Prof. Leevy have developed novel applications to bring 3-D printing within the scope of medical diagnostics.

These new methods combine the more customary diagnostic approaches such as X-ray computed tomography (CT) and magnetic resonance imaging (MRI) scans with 3-D printing. By taking data from high resolution in vivo medical scans, the team is able to produce stereolithography files that allow generation of exact copies of the objects originally scanned. “It’s just a cool application at first, but if you apply it in the right way it becomes a powerful tool for diagnostics and doctor-patient communication,” Doney said.

Instead of looking at three-dimensional data on a two-dimensional screen, this method allows the three dimensional data to be represented as a real, full size object. Users also have the ability to separate different organs and organ systems for printing. “We believe the real power here is the ability to take complex three dimensional data off of a two dimensional computer screen and put it in your hand,” Leevy said of the technology.

Their method has been used to conduct studies of skeletal structure, heart valves, and protein folding. The most promising application for this method looks to be in the improvement of surgery procedures. In particular, Leevy and Doney hope to use their method to provide surgeons with a chance to practice complex surgeries on printed plastic models of various organs and tissues. One example involves the human sinuses, a complex maze unique to each patient that can lead to difficulties and complications during surgeries. By 3-D printing an exact copy of these sinuses from routine X-ray scans, surgeons may be able to practice and plan their approach before each patient undergoes surgery.

Moving forward, the team hopes to use the rapidly improving technology to fabricate fluorescent implants that could be used to tag specific organs and regions for tracking during and after surgery. Doney has high hopes for the future of 3-D printing and medical technology, and he said, “this is just beginning of the integration of these two technologies, we hope to continue developing exciting new uses for these machines.”

PaleoEcological Observatory Network (PaleON) is a comprehensive project involving 30 different U.S. and international universities that aims to undertake this challenge. The University of Notre Dame is the leading institution at the forefront of the PaleON project overseen by Jason McLachlan, assistant professor of biological sciences.

This novel project brings together an interdisciplinary group of paleoecologists, statisticians, and modelers whose objective is to reconstruct the forest composition and climate over the past 2,000 years. “PaleON is really unique in that it brings scientists together who never spoke with each other before,” says McLachlan. “It brings different people together to work on a common goal.” PaleON takes an innovative approach by taking a retrospective method of investigation. The primary objective of the project is to use historical data and generate a working global model capable of extrapolating future climate changes. Currently, PaleON relies on three primary paleoecological sources for generating a database: sediment cores, historic surveys, and tree rings. Ice and lake sediment cores trap diverse floral pollen and air bubbles present during a 2,000 year period. Extraction of the pollen and leaves allows identification of species, and the bubbles reveal the CO₂ content in different periods of Earth’s history. Early settlement land surveys and tree rings also shows the environmental changes within the last 300 years. These data records are compared to thirteen different terrestrial ecosystem model systems, ranging from simplistic models based on the carbon cycle to complex population biology models. PaleON aims to determine a model that accurately reconstructs historical forestry and climate confirmed through paleoecological data.

Our world today produces an abundance of CO₂ that is unprecedented in history. Although the contribution of greenhouse gases to global warming is well established, the world’s air is reaching a new milestone for CO₂ levels and continues to increase with accelerating pace. Eight billion tons of CO₂ are produced annually and distributed across the atmosphere, ocean, and terrestrial biosphere. “We will see environmental changes that were never seen before,” says McLachlan. If the PaleON model is shown to accurately predict historical changes, then this model has potential to predict future changes of Earth’s terrestrial biosphere. Global warming may impact the ocean, the atmosphere, and global health. Polar ice caps are melting at an alarming rate, imposing danger on species survival and major coastal cities. Elevation in global temperature may induce a higher risk of heat waves and outbreaks of infectious diseases.

Generating a climate model has great importance in evaluating future climate changes and the consequences on our biosphere. PaleON may become the first of many steps in developing a comprehensive global model to predict and make informed decisions regarding the future direction our world is heading towards. The PaleON project has recently completed its first phase in gathering a diverse team of researchers and initiating data collection. The completion of this phase creates the possibility for PaleON to accomplish the ambitious reconstruction of the historical environment. McLachlan hopes to expand the project to reconstruct the historical geography of Northeast America and Alaska in the next phase. “Comparing two different geographies and climates will capture a bigger slice of biodiversity,” says McLachlan.
Notre Dame Science Faculty Play Key Role in 2012’s Top Physics Discoveries
LUQUN SHEN

Notre Dame has made significant efforts to increase its research capacities in recent decades, and this past year Notre Dame faculty proved to be on the cutting edge of physics research. On December 14, 2012, Physics World, a website sponsored by the Institute of Physics, revealed its top 10 list of breakthroughs of 2012.

The discovery of the Higgs boson, on which Colin Jessop, professor of physics, and his team worked extensively, was rated in the number one spot while the violation of time reversal, a project in which John LoSecco, professor of physics, was involved, placed in the top ten. Both experiments are extremely important in the understanding of particle physics and helped reveal insights into the fundamental nature of reality.

The discovery of the Higgs boson generated worldwide interest and excitement when the announcement was made on July 4, 2012. As Jessop explains, the Higgs boson is the observable indicator that can confirm the existence of the Higgs Field, which gives mass to leptons and W/Z bosons. The Higgs field exists everywhere in the universe. Whenever a lepton or W/Z boson interacts with the field, a drag is felt, creating mass. The Higgs boson has often been dubbed the “God Particle” because it interacts with everything and everyone. In an attempt to find it, scientists around the world have been using the Large Hadron Collider at CERN to conduct two experiments, Compact Muon Solenoid (CMS) and Argonne Tandem Linear Accelerator System (ATLAS).

The Notre Dame group was part of the CMS experiment, which featured over 2000 physicists, including Jessop and many other Notre Dame faculty members, postdoctoral researchers, and graduate students. Jessop and his team, which includes research assistant professor Nancy Martielli, post-doctoral researcher Jeff Kolb, and graduate students Douglas Berry, Ted Kolberg, Jamie Antonelli, and Sean Lynch, focused on using the electromagnetic calorimeter, ECAL, which detects photons and electrons that are created when two protons collide. Utilizing the ECAL, researchers were able to determine the energy and the momentum of the photons emitted, enabling them to determine the mass of the former particle. Because the Higgs boson was produced by the collision of two protons before decaying into two photons, Jessop’s team was able to determine whether the resulting decay was in fact a Higgs boson.

Around February of 2012, the group had noted a mass that was extremely similar to that of the Higgs boson. However, the odds of these results being mere chance were about 1/1,000,000. Knowing that more data collection was needed to confirm the discovery. After continued tests coupled with independent discovery of the Higgs boson at ATLAS, the chance of a mistake was reduced to 1/1,000,000.

“This is not the end, but only the beginning,” said Jessop in regards to research surrounding the Higgs boson. Indeed, its discovery ushers in a new era for particle physics that Jessop believes is likely to stretch until 2035. Scientists must now begin mapping out all the properties of the Higgs boson. If the Higgs boson behaves as expected, it will profoundly shape the world’s understanding of particle physics.

While the Higgs boson was declared the biggest physics story in 2012, several other experiments were also conducted, producing ground-breaking results. One of those experiments was the time reversal violation experiment, otherwise known as the BaBar experiment, which featured Notre Dame’s LoSecco. He explains that time reversal is the same as before backward at equal rates, which is one of the fundamental forms of nature. While we may not see this change in the macroscopic world, a single, isolated particle able to go both forward and backwards in time would be expected to look identical going from time A to time B, compared to going from time B to time A. However, it has been indirectly observed that this theory can be violated.

In order to test the hypothesis and produce more concrete evidence for the observing this effect, LoSecco conducted with elementary particles, B mesons. The B mesons were observed in one of four states. Two of the states are of definite charge-parity, + or – (not related to electric charge). As LoSecco elaborates, “By labeling the early state in one of the four flavor or charge-parity states and the later states in a different one of the four flavor or charge-parity states, one can compare forward time conversions to their time reversed conversions, switching the label of the early and late particle.” When these experiments were completed, the results were found to be different, giving strong evidence for a time reversal violation.

Although the primary implications of the experiment related to time reversal, the BaBar experiment also investigated several other symmetry violations. Additionally, the results from this experiment indicate that particles can be produced to be connected to their antiparticles. This experiment’s paper, in which Jessop was a co-author, is one of the final papers of the BaBar experiment. In total, the experiment resulted in the publication of over 500 journal papers. In 2008, Makoto Kobayashi and Toshihide Maskawa were awarded the Nobel Prize for a theoretical prediction that was confirmed by the BaBar experiment. Ikaro Bigi, Grace-Rupley Professor of Physics, won the 2004 Sakurai Prize, which recognizes outstanding achievement in particle theory, for his work which pointed out the process by which this theoretical prediction could be observed.

Jessop and LoSecco both played integral roles in these experiments, and many others worked alongside them. Both experiments were the result of the collaboration of top physicists from around the world. While graduate students, postdocs, and faculty members conduct much of the research associated with these projects, many opportunities are available for undergraduate students to get involved. “Often times,” Prof. Jessop said, “we wish these [undergraduate] students could stay longer.” Working in these labs helps students gain invaluable experience to prepare themselves for the world upon graduation from Notre Dame.

Research in the United States and Hong Kong: An Undergraduate Perspective
CHARLES CONG YANG XU

So far in my undergraduate career, I have been fortunate to have opportunities to conduct research in several laboratories and institutions including the Lodge and Jefrey Feder at the University of Notre Dame, Hopi Koechstra at Harvard University, and Ka Hou Chu at the Chinese University of Hong Kong (CUHK) where I am currently based. While my experiences allow me to compare and contrast undergraduate research experiences across the United States and Hong Kong in a unique way, it is important to note that significant differences do exist between labs within the same culture and even within a single department. My experiences are limited to the ecological and evolutionary sciences, and while generalizations are necessary to draw conclusions, the creation of stereotypes based on my observations should be avoided.

First, there are the obvious differences of location and language. Hong Kong is a port city with the ocean at its doorstep, so research in marine biology is prominent. Similarly, the proximity of Notre Dame to the Great Lakes is advantageous to the study of freshwater aquatic ecology. While one of the official languages of Hong Kong is English, the local Chinese dialect of Cantonese is widely used for daily communication. All conversations in the lab are held in Cantonese, making integration difficult if one does not understand the local language. The same would be true of labs in the United States.
number of research credits that can count toward degree require-
ments). Generally, students are expected to work for six to eight
hours each week per credit hour earned, but each lab has its own
expectations. Undergraduate research positions can be highly
competitive, especially within medically related research fields.
While paid undergraduate technician positions within labs are
common in the United States and serve as another avenue for
students to expose themselves to research, these positions are
filled by full-time staff in Hong Kong.

At CUHK, there does not appear to be much competition
for undergraduate research positions. Students at any point in
their studies wishing to conduct research generally have the
opportunity to do so on a volunteer basis. This is true even at
the beginning of their first year. The fact that medicine is an
undergraduate degree in Hong Kong may be a contributing fac-
tor. All students intending to become doctors have already been
accepted to a six-year medical program as undergraduates. Fur-
ther specializations require more schooling after undergraduate
study, but admission is based on examination rather than appli-
cation. Unsurprisingly, medical students in Hong Kong prefer
university for undergraduate research positions. Students at any point in
the United States conduct research in order to be accepted into
medical school. Typically, undergraduates at CUHK only
receive research credit from a two-semester Final Year Project
(FYP). This project is worth six credits and is largely structured
with proposals, consultations, and presentations, along with a
final report all within the year before graduation. The amount
of time students spend in the lab for their FYP is similar to stu-
dents in the U.S. conducting senior research theses.

Most aspects of lab culture between the United States and
Hong Kong appear to be very similar. The relationships be-
 tween mentors and their students are friendly and casual. Hav-
ing lunch and discussing non-work related topics is common
and almost expected. Socialization in the lab occurs between
tiers of lab hierarchy and anyone can be approached with
questions. All members of the lab, undergraduates included, are
invited to lab meetings and seminars by visiting scholars. How-
ever, certain differences do exist. One personal story I have to
tell regarding the importance of lab culture differences in-
volves something that many would assume insignificant: the
last hold step in a PCR (Polymerase Chain Reaction) protocol. One
of the PCR protocols I have worked in both Notre Dame and Harvard to hold the last step
to ensure that the DNA stays cold, even if the reac-
tions are not taken out of the thermocycler immediately after
the PCR cycle finishes. I had created this protocol several
times in the past and thought it was scientifically universal,
but I was wrong. Apparently, due to the high humidity of
Hong Kong’s climate, holding the last step at the normal 4°C floods
and damages the PCR machine. Although this cultural differ-
ence is not just true of Hong Kong, but other similarly humid
locations as well, it is important to be aware that different rules
can apply in different labs. It is especially true for an under-
graduate researcher, to remember that there is more than one
way for research to be conducted, and that the particular way
students have been trained may not always be ideal for every
situation. It is generally better to assume less and ask more.

Although there are indeed differences in terms of resources
(just compare university endowments), and these differences
don’t affect how research is conducted (just compare
the number of vortexts in a lab), I believe emphasizing the commonalities be-
tween research in these countries is far more important. The
same Eppendorf pipettes and microcentrifuges can be found on
the lab benches of universities in the West and the East. Ameri-
can and Chinese researchers use boxes of German-produced
Qiagen DNA extraction kits with the same exact reagents and
the same Eppendorf pipettes and microcentrifuges can be found on
the lab benches of universities in the West and the East. Ameri-
can and Chinese researchers use boxes of German-produced
Qiagen DNA extraction kits with the same exact reagents and
lab protocols. 70% ethanol will preserve the DNA of nearly
all organisms, whether they are deep-sea crabs from the South
China Sea, apple maggots flies from
Michigan, or the tail clips of deer mice from
the sand hills of Nebraska. Al-
though researchers in Hong Kong have discovered the
phylogeny of marine snails across Southeast Asia while re-
searchers at Notre Dame monitor fish populations in the
Great Lakes using environmental DNA, they use the same
generic methods with the same ultimate purpose of understanding
the world in which we live. No matter the language, the
socio-economic background, or the fact that coffee is the fuel that drives U.S.
labs while tea is preferred in Hong Kong, science provides an international forum
for communication and conversation be-
tween a variety of research groups. As biologists know, life is more similar than different and
the same can be said of the processes with
which these truths are discovered.

Simon F. S. Lee Marine Science laboratory at CUHK

Small Molecules, Big Implications

SARAH OWENS

The desire to serve and the importance of community are
at the heart of the Notre Dame mission. In the laboratory of
Winifred Miller, George and Winifred Clark Professor of
Chemistry and Biochemistry, researchers and collaborating
institutions are bringing both
to the ground-breaking devel-
 ment of a new treatment for
tuberculosis (TB). All levels of
the Notre Dame community, from undergraduates to alum-
ni, are involved in the Miller
lab’s production and develop-
 ment of a new active anti-TB
agent, which they hope will
one day be marketable to peo-
ple in resource-poor areas, es-
pecially developing countries.

The new compound, anti-tuberculosis treatment in the
Miller lab began with an interest in the bacterial assimilation
of iron by molecules called siderophores. “We asked ourselves
if we could interfere with that process or use it to
process to develop new antibacterial agents,” said Miller. “We discovered
that we can synthesize analogs of these iron transporters.
We can attach antibiotics to these, and when the bacteria take
them up, they essentially commit suicide. TB was always in the back
of our minds, because it affects more people than any other bac-
terial disease in the world.”

This idea sparked the large molecule initiative, which in-
volved attaching the anti-malarial agent artemisinin to a TB
inhibitor. While this proved an effective anti-TB agent, the
large molecules were too complicated and expensive to synthesize. “We
found through high-throughput screening that there were some
small molecules that were made by one of our bigger molecules that
had some interesting activity against tuberculosis as well,” said
Miller. The study made the most progress, however, after Gar-
rett Morris joined the lab. An experienced industrial chemist
and Notre Dame graduate, Morris was able to fine-tune
the small molecules into more efficient active anti-tuberculosis in-
hibitors.

The small molecule program is the most groundbreaking
aspect of the current research toward the synthesis of a TB
derug. The small molecules, called imidazopyridines, can be
synthesized relatively easily and, can likely be produced on a
large scale at a reasonable cost. The patent on the
molecules has been licensed by Hsiri Therapeutics, a company owned by
Notre Dame alumns Denny Wilson, which aims to help ad-

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Miller’s group works to develop a novel anti-tuberculosis drug

News

make the subsequent steps of the Miller lab’s work possible.
After the molecules are made at Notre Dame in collaboration with
Jeff Schorey, associate professor of biological sciences, they are
sent off for testing at the University of Illinois, Chi-
cago with Scott Franzblau with funding from Miller’s National
Institutes of Health (NIH) grant. Drug development is further
supported by Eli Lilly & Co. in Indianapolis, an organization
with a tuberculosis drug discovery initiative, and the Infectious
Disease Research Institute in Seattle, which focuses on combat-
ing diseases prevalent throughout the developing world.

Recently, the small molecule compounds have also become
of interest to global markets and research institutions in the
world. A meeting in París in September about potential TB
treatments proved fruitful, with GlaxoSmithKline revealing re-
lated work further progressing the study of imidazopyridines.
“The worldwide interests and efforts are ongoing, but our disclosures were the first in the
world on this treatment of TB,” says Miller. “The main chemis-
try research was started here and continues here.”

In addition to developing ideal drug properties in the
compound and fine-tuning the molecules to increase their activity,
recent research and discussions have been centered on making
development cost-effective. “You’re not going to get rich de-
veloping a TB treatment agent for the third world,” said Miller.
“but charity won’t fund it either. The goal is to provide a useful
drug, but at the same time, something must be done to cover
the cost.” Miller projects that the solution to the funding issue
will come with a discovery of other uses for the compound. If
the Miller lab can find relevance for the drug in the treatment
of first-world bacterial diseases, it is more likely that they

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It takes between 1.2 and 1.4 billion dollars to take a drug from discovery to market, and studies to develop the most effective derivative of the compound are ongoing. But with nearly two billion people affected by tuberculosis worldwide, Miller and colleagues are determined to continue fighting for an affordable and effective cure.

What was the Christmas Star? An Astronomer’s View

BAILEY MOSER

Each Christmas, the Notre Dame community has wondered if the Star of Bethlehem was one of the hundred million billions of stars in the night sky—or something more spectacular. Could it have been a comet, nova, supernova, or planetary alignment?

Grant Mathews, professor of physics and director for the Center for Astrophysics, presented his research on this revered celestial event in a series of public presentations in the Digital Visualization Theater (DVT) in the Jordan Hall of Science—a time machine containing data of every star and astronomical event known to mankind. The DVT allowed the audience to view the night sky from the Middle East on Christmas Eve 6 A.D., the traditional date of the birth of Christ, and fast forward to a view of the present day in seconds.

The annual lecture entitled “What and When Was the Christmas Star?” added an astrophysics and astronomy perspective to extensive theological and historical research extending from the account in the Gospel of Matthew traditionally used to explain the Christmas Star. In the season of lights, Mathews sought “to remember the birth of the Christ child” by exploring the light that shone above his birth.

According to Mathews, the Star of Bethlehem described by the Magi is most likely one of three plausible cosmological events occurring between 8 and 4 B.C. Mathews believes the Star of Bethlehem was probably an alignment of the Sun, Moon, Jupiter, and Saturn in the constellation Aries, dating the birth of Christ to be April 17, 6 B.C.

Mathews reached this conclusion by carefully considering narratives of where the Star of Bethlehem was observed, its geographical region of Palestine and Judea, Herod’s realm considered the giver of life. The constellation Aries represented the geographical region of Palestine and Judea, Herod’s realm in which Jesus was born. The presence of Venus, Mars, and Mercury in neighboring constellations would have added even more urgency as the Magi traveled through the Silent Night.

The demonstration was followed by a video presentation of “A Season of Lights,” explaining the traditional and historical relation between the Winter Solstice and Christmas season. To learn more about what the Star of Bethlehem could have been, Mathews recommends reading The Star of Bethlehem: The Legacy of the Magi by Michael R. Molnar, available in Hesburgh Library.

For questions about the next presentation of “What and When Was the Christmas Star?” contact Susan Baxmeyer in the Department of Physics.

A Fundraiser Fighting Blindness: The Biology Club’s Vision Walk

JESSICA ZIC

Two years ago, Notre Dame student Maria Sellers, Class of 2011, met with Rev. Theodore M. Hesburgh, C.S.C., and was inspired by the incredible things he has done in his life to help others. She wanted to honor him and show her gratitude for all he has done for the University by starting a fundraiser to help Father Hesburgh and others who are suffering from macular and retinal degeneration and blindness. Maria contacted the Biology Club, led by David Veselik, assistant professional specialist, as well as Notre Dame’s world-renowned retinal degeneration researcher, David Hyde, Rev. Howard J. Kenna, C.S.C., Memorial Director of the Zebralis Research Center, and expressed her “vision” to honor Father Hesburgh. Together, they joined with the Foundation Fighting Blindness (FFB) to sponsor the first Vision Walk at Notre Dame.

The Vision Walk is a signature fundraising event for the FFB, a national eye research organization that acts as a world leader in providing funds for the research and development of treatments and cures for those affected by retinal degenerative diseases. Since 1971, the FFB has raised over $450 million, making it the largest non-governmental source of funding for research in its field. All of the money made from the Vision Walk goes directly towards FFB-sponsored research. The student coordinators of this year’s Vision Walk were Antoinette Pusateri and Nestor Agbayani. Pusateri detailed her hopes for the event, “My personal goal was to raise more money than the last two years combined, which was about $5,000. I also wanted to get a large turnout of students, faculty, and members of the South Bend community.” The results of the 2012 Vision Walk, held on October 28 at Irish Green, exceeded all of Pusateri’s expectations. Thanks to the attendance of numerous students, faculty, South Bend community members, and even families from Chicago, Cleveland, and Columbus, the Vision Walk raised over $7,000 this year. Pusateri said, “the founder of the Foundation Fighting Blindness, Gordon Gund, even sent me an email to thank us for our efforts and express his excitement for the potential of the Notre Dame Vision Walk.”

The Vision Walk holds special significance for the Notre Dame community because Father Hesburgh is one of the millions of people worldwide who suffer from macular degeneration. Notre Dame’s Spirit for this event helped spread the fundraising and awareness-raising efforts of the walk out into the South Bend community. Pusateri says the annual walk “serves as a bridge to bring students, faculty, and community members together for a good cause.” Maria Sellers, local ophthalmologist Dr. Steve Gerber, and Bill Blauvelt, one of Dr. Gerber’s legally blind patients, spoke about their personal connection to the Vision Walk and blindness research. After the walk there was a silent auction and raffle that included prizes such as a free MCAT/LSAT/GRE course and a football helmet signed by Brian Kelly.

The impact of the Vision Walk is apparent in Pusateri’s description of her experience with the walk. “I was amazed by the overwhelming support and cooperation shown to me and the Biology Club during the planning of the walk and during the day of the walk as well. It was incredible to see how people of all ages and backgrounds came together for this cause, and walked in the fight for sight!” It was truly so powerful, and it was just another confirmation for me of how blessed I am to be a part of the Notre Dame family.”
The Honors Program in Biological Sciences will graduate its first cohort of students this May. The goal of the Honors Program is to give students an exceptional background in biological research, increasing research productivity and commitment, in preparation for postgraduate study and a career in research.

“The Honors Program sets a high standard that reflects the goals of the College of Science to help students become creators of knowledge and not merely absorbers,” says Gregory Crawford, dean of the College of Science. “Participants become strong, independent, innovative researchers. They are the first to see the future, and as Marcello Pietro said, ‘The real voyage of discovery consists not in seeking new landscapes but in having new eyes.’ We are so proud to graduate this inaugural class of students who have demonstrated the kind of achievement that holds great promise for a positive impact on the world.”

Since spring of their junior year, students in the Biological Sciences Honors Program have participated in weekly seminars with biological sciences faculty, written 30-40 page theses of their research, taken at least one graduate-level course, and presented their research at a national or regional conference. Most have been working in their respective laboratories for several years, and all have spent at least one summer conducting full-time research at Notre Dame. Michelle Whaley, assisted by Dominic Chaloner and Kristin Hager, is the coordinator for the program. Faculty work with the honors students to hone critical thinking, writing, and presentation skills outside of the students’ time in the lab.

The members of the first class of honors students include Erin Boyle, Alexandra Brumfield, Courtney Currier, Erin Flatley, Patrick O’Hayer, Mike Petravick, Emily Spulak, and Dan-"erel Williams. While all eight are majoring in biological sciences, O’Hayer, Petravick, and Spulak are also in mathematics. All have been recognized and invited to attend the 2013-14 Churchill Scholar program, which prepares students for careers in mathematical research. They are the first to graduate its first cohort of students this May. The goal of the Honors Program is to give students an exceptional background in biological research, increasing research productivity and commitment, in preparation for postgraduate study and a career in research.

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Differentially Expressed Genes in the Pancreas of NOD Mice as Biomarkers for Type 1 Diabetes

JEFFREY HANSEN
Advisor: Kenneth Brayman
1University of Notre Dame, Department of Biological Sciences
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ABSTRACT
Type 1 diabetes (T1D) is an autoimmune disorder that ultimately results in the complete destruction of insulin-producing pancreatic beta cells. By the time of diagnosis, 85-90% of all beta cells have already been irreparably destroyed. In order to predict the onset of disease and provide preventative treatment before cell destruction occurs, high-risk individuals can be screened for biomarkers. Possible biomarkers include genes linked to disease susceptibility, autoantibodies found within the blood prior to disease onset, and genes linked to general inflammation caused by autoimmune disorders. In this study, the relative mRNA expression of GAD2, IL1B, IL18, IFN-γ and CXCL1 was determined by RT-qPCR in the pancreata of non-obese diabetic (NOD) mice at pre-diabetic (3-4 weeks), pre-hyperglycemic (7-11 weeks), and diabetic (>12 weeks) stages of disease. While beta cell destruction due to presumed faulty pancreatic extraction techniques made analysis difficult, an increase in expression of CXCL1, CXCL1 and ICA1 with T1D progression was observed. This investigation sets the stage for future experimentation for enhanced expression analysis and selection of better target genes through microarray reactions.

INTRODUCTION
Type 1 diabetes (T1D) is characterized by an autoimmune response leading to T-cell mediated destruction of an individual’s pancreatic beta cells. These beta cells are normally responsible for the regulation of blood sugar levels through the release of insulin. Without the natural production of insulin by these autoantibodies also have potential to work as biomarkers. Early in the progression of T1D, autoantibodies targeting a islet cell antigens have been detected in the bloodstream. The exact function and mechanism of these autoantibodies is still unknown, but like CXCL1 and CTLA4, these autoantibodies hold predictive value and potential for utilization as biomarkers. These autoantibodies commonly target insulin and a zinc transporter, and are ultimately regulated by negative feedback from receptor-mediated interactions that ultimately result in the T-cell inflammatory response and has been found in higher levels in diabetes compared to their healthy counterparts (4,5). These cytokine interactions eventually lead to T-cell mediated destruction, induced by CD4+ and CD8+ T-cells. Specifically, CD4+ helper T-cells are tasked with activating CD8+ cytotoxic T-cells, the T-cells responsible for releasing granzymes and perforin (1,3).

Genes that have been found to have either increased or decreased levels of expression in the pancreas throughout the progression of T1D are chemokine (C-X-C motif), ligand 1 (CXCL1), and cytokine T lymphocyte antigen 2 (CTLA4) (4,6). CXCL1 is an inflammatory mediator that increases in expression in several autoimmune disorders including T1D. In comparison, RNA isolated from C57BL/6 mice had three to five times higher expression levels of CXCL1 (6). CTLA4, another gene implicated in increasing risk for developing T1D, works as a regulator of immune responses by negatively regulating T-cell activation (4). Lower expression of CXCL4 is therefore strongly connected to T-cell associated autoimmunity. In relation to T1D specifically, there is a 47% increase in risk by possessing all alleles, and a 48% increase in risk by possessing another allele (8). Significant correlations between disease development and gene expression provide the potential for both to be used as biomarkers.

To select for possible biomarkers present during the pathology of diabetes, the mechanism of beta cell destruction must be understood. This mechanism is comprised of a series of receptor-mediated interactions that ultimately result in the T-cell mediated release of granzymes and perforin causing beta cells to undergo apoptosis (1). This process is primarily controlled by macrophages and T-cells, which are both implicated in the activation and recruitment of additional inflammatory cells to the pancreas through the release of cytokines. The primary cytokines involved in disease development are interleukin-6 (IL6) and interleukin-18 (IL18), and their release generates a T-helper type 1 (Th1) inflammatory response (3). Interferon-gamma (IFN-γ) is a cytokine linked to T1D that also initiates a Th1-mediated inflammatory response and has been found in higher levels in diabetes compared to their healthy counterparts (4,5). These cytokine interactions eventually lead to T-cell mediated destruction, induced by CD4+ and CD8+ T-cells. Specifically, CD4+ helper T-cells are tasked with activating CD8+ cytotoxic T-cells, the T-cells responsible for releasing granzymes and perforin (1,3).

Of the experimental genes, only IL18, CXCL1 and ICA1 were upregulated with T1D progression. Of the experimental genes, only IL18, CXCL1 and ICA1 were upregulated with T1D progression. Of the experimental genes, only IL18, CXCL1 and ICA1 were upregulated with T1D progression. Of the experimental genes, only IL18, CXCL1 and ICA1 were upregulated with T1D progression. Of the experimental genes, only IL18, CXCL1 and ICA1 were upregulated with T1D progression. Of the experimental genes, only IL18, CXCL1 and ICA1 were upregulated with T1D progression. Of the experimental genes, only IL18, CXCL1 and ICA1 were upregulated with T1D progression.

RESULTS
RNA was pure and concentrated but significantly degraded
After extracting and cleaning the RNA, two quality control methods were run to measure the purity, concentration, and integrity of the RNA sample. Purity values could be affected by ethanol, phenol or protein contaminations, concentration values could be low if an insufficiently sized piece of tissue was housed in the RNA master mix, and degradation values could be low if the sample was degraded in the RNA. The Nanodrop 2000 revealed that both concentration and purity values were consistently above benchmark values, indicating successful extraction and wash procedures.

Electropherograms from the Agilent BioAnalyzer 2100 indicated significant degradation of the extracted RNA. An intact sample of RNA would produce an electropherogram with characteristic peaks at 18s and 28s (Fig. 1A). Only one early peak is seen in the electropherograms produced from the extracted RNA (Fig. 1B), indicating a large quantity of short degraded fragments of RNA.

IL18, CXCL1 and ICA1 are upregulated with T1D progression
Of the experimental genes, only IL18, CXCL1 and ICA1 were successfully amplified and sequenced quantitatively. Quantifiable amounts of amplification allowed expression levels of these genes to be measured and compared across time points throughout the progression of T1D. All three of the genes increased in expression from a pre-diabetic time point to a full-onset time point (Fig. 2). If this pattern was more fully developed and substantiated, it could provide data to qualify these three genes as potential biomarkers for T1D and allow one to predict for the onset of T1D if a characteristic change in gene expression is seen in IL18, CXCL1, and ICA1.

DISCUSSION
Of the seven genes experimentally tested for differential expression throughout the development of type 1 diabetes in NOD mice, only IL18, CXCL1, and ICA1 showed observable trends. Each of these three genes increased in expression...
Biology

Preferring Foraging Behavior of Forest Deer Mice (Peromyscus manilacatus gracilis) on Native and Non-native Picea Seeds

LAUREN ECKERT
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University of Notre Dame, Department of Biological Sciences

ABSTRACT
Exotic plant invasions can lead to serious biodiversity and economic losses, with negative effects on many ecosystems. The factors leading to invasive plant success have been well documented and studied, but little is known about the impact of graminoid on invasive plants. Peromyscus manilacatus is the most widely distributed Peromyscus species and has been suggested to cause substantial loss of tree seed crop through seed predation. In this experiment, the preferential feeding behavior of deer mice on the seeds of the non-native, non-invasive blue spruce (Picea glauca) in the Upper Peninsula of Michigan was studied. Captured mice were allowed to feed freely on equal amounts of both seeds, and it was found that they significantly preferred the larger non-native P. pungens seeds to P. glauca. Factors that contribute to invasive plant success are many and complicated, and so further experimentation is necessary to understand the complex aspects of the optimal foraging theory when applied to graminoid. Preference for P. pungens seeds by the widespread deer mice may suggest that seed predators play a more important role in invasive plant establishment. This knowledge would improve our understanding of invasive flora and offer suggestions for future mitigative action.

INTRODUCTION
Exotic plant invasions have become ubiquitous across the United States, and what was once a pristine ecological environment (1). The success of invasive flora can lead to serious biodiversity and economic losses, with negative and far reaching effects on many ecosystems. Invasive flora have been correlated with decreases in both abundance and diversity of native plant species and has been documented and studied, but little is known about the impact of invasive plant species that are large- in size and non-native plants. Invasive plant success are highly complicated and vary with the nature and location of the ecosystem. For this study, “non-native” plants are defined as those that have been introduced with or without attribution as invasive to some states of the Eastern United States as well as southern areas of Canada (11). Blue spruce establishment by wave of seed production in cones every 2 to 3 years, thriving in exposed mineral soil in close proximity to seed trees (12). Trees thrive in climates that are generally cool and humid, with most annual precipitation occurring in the summer. The blue spruce has been introduced into the Upper Peninsula of Michigan and is known throughout the state at commercial nurseries (14, 15). White spruce is native to much of the northern United States and Canada (16). It has been known to grow under highly variable conditions, including extreme climates and soils (17). White spruce is a monocious member of the pine family (Pinaceae) and reproduces by cones every 2-6 years (17, 18). White spruce is an important economic resource, used for timber and wood fiber (20). It is native to the Upper Peninsula of Michigan, and is well-established where this study was conducted (16, 21). Previous studies suggest that P. pungens seeds will avoid consummating non-native invasive species that are largely successful in dominating ecosystems (22). However, blue spruce is not currently considered to be an invasive species, nor does it have a documented history of rapid takeover and success in areas where it is not native but present, as plants labeled “invasive” (4, 11). For this study, “non-native” plants are those which are currently living outside of what has been established as their native range, and “invasive” plants are those non-native species whose introduction, success, and range expansion cause harm to biodiversity and the introduced plants’ resources (14). The blue spruce has been introduced into the Upper Peninsula ornamentally and at nurseries throughout the Upper Peninsula but has not been documented as invasive in the northern United States (11, 14, 15).

Figure 2. Expression Levels of IL18, CXCL1, and ICA1 from Pre-diabetic to Diabetic. The time that symptoms appear, irreversible damage has already been done to the patient. Future expression analysis of genes either located in the pancreas or peripheral blood mononuclear cells of NOD mice may elucidate a set of genes that are characteristically modulated during T1D pathogenesis. This genetic signature would allow for a screen to be carried out in those with a family history of the disease in order to confirm or deny the oncoming disease. If the screening reveals high probability of developing the disease, treatment can be administered early enough to prevent beta cell destruction and consequent T1D development.

ACKNOWLEDGMENTS
I would like to acknowledge Prof. Kenneth Brayman, Prof. Preeti Chhabra, and Prof. Valeria Mas at the University of Virginia for their mentorship and assistance throughout the summer. I would like to thank the College of Science and the Center for Undergraduate Scholarly Engagement for funding this work. Finally, I would like to acknowledge Tom Merrigan, Ethan Seide, and Lawrence Merrigan, members of my family with type 1 diabetes who have provided my motivation since day one.

REFERENCES
would support a prediction that deer mice would feed on larger, more energetically efficient seeds when given a choice between seeds of different species (24). Previous studies have provided overwhelming support that a number of species feed preferentially on larger prey. Among others, swallowing and bluegill sunfish have been strongly suggested to select their food items based on size; in order to optimize energy returns from food acquisition and handling time, they consistently choose the largest food items (25, 26). However, P. maniculatus foraging on other species of seeds (Acer) did not show a preference for size when given free choice between equal amounts of both seed types. Preference towards P. pungens seeds by wild-caught mice may suggest one reason why blue spruce has not been successful in propagating in the Upper Peninsula region and lead to a greater understanding of the factors that influence plant invasions.

METHODS

Study area

All experiments were conducted on the University of Notre Dame Environmental Research Center (UNDERC) property, which comprises approximately 903 hectares of red pine forested land bordering Wisconsin and the Upper Peninsula of Michigan (46° 13’ N, 89° 32’ W). All mice were captured from two randomly located trapping grids, [Storage (46° 13’ 53.75” N, 89° 32’ W) and 5.745° W] and Bono (46° 13’ 6.753” N, 89° 30’ 52.538” W) within second-growth forests that were dominated by sugar maples. Three incidental mice captures were also used for trial purposes.

Experimental Procedure

Seed Preference Trials: Five hours prior to testing, all food was removed from the cages. For each trial, seeds of the following species were presented in plexiglass cages with 5 grams each of Picea glauca and P. pungens seeds, separated into two feeding petri-dishes and placed in the cage. Seeds were obtained from a professional seed company (Sheffield’s Seed Co., Lake NY), and were of the same variety and size. The experimental results were analyzed using a paired t-test to account for statistical differences in addition to seed size (24, 25, 26, 38). Plant residence time, genetic make-up, local ecosystem community structure, mutualisms, resistance to predation, and dispersal strategies are a few factors that have been extensively studied and implicated in the conception of a prosperous invasive species (35, 1, 36). These factors are highly complex and interrelated (35, 1) and were not taken into account in this experiment.

Trapping

All mice used in the experiment were P. maniculatus grallator individuals. We used a multiple-trapping from the UNDERC site in May, June, and July 2012. Trapping grids contained 25 traps in a 5 x 5 configuration with 15 spacing between each trap. Twenty-five mice were used for each set of trials and five of each species. Seed mass was measured and individually marked with ear tags (monel 1; National Band and Tag Co., Newport, KY). Subjects were housed in individual cages with sand as bedding, and provided polystyrene nesting material and water ad libitum. Lactating or pregnant females were not used for any trials. Handling of mice was consistent with guidelines published by the American Society of Mammalogists (29) and the Animal Behavior Society (30), as used and approved by the University of Notre Dame Institutional Animal Care and Use Committee (protocol # 14-047).

RESULTS

Twenty-five mice were tested. There was a significant difference in the selectivity of deer foraging between Wisconsin and the Upper Peninsula of Michigan (46° 13’ N, 89° 32’ W). All mice were captured from two randomly located trapping grids, [Storage (46° 13’ 53.75” N, 89° 32’ W) and 5.745° W] and Bono (46° 13’ 6.753” N, 89° 30’ 52.538” W) within second-growth forests that were dominated by sugar maples. Three incidental mice captures were also used for trial purposes.

DISCUSSION

The experimental results support the hypothesis that deer mice preferentially feed on P. pungens seeds over P. glauca seeds. Preference for P. pungens may indicate that granivores play an important role in the establishment of blue spruce in non-native areas and point towards granivory as an important component of the blue spruce success by blue spruce in the area of study, it was hypothesized that deer mice would preferentially feed on the seeds of the non-native P. pungens over those of native P. glauca when given free choice between equal amounts of both seed types. Preference towards P. pungens seeds by wild-caught mice may suggest one reason why blue spruce has not been successful in propagating in the Upper Peninsula region and lead to a greater understanding of the factors that influence plant invasions.

ACKNOWLEDGMENTS

Immensely thanks is extended to Prof. Michael J. Cramer for his crucial guidance, support, and counseling in both the design and execution of my experiment, as well as the patience and expertise he exuded on early mornings trapping trial mice. Gratitude is also owed to Samantha Driscoll and Cheeza Gaye for their help in trapping and housing mice, as well as Luke DeGroote and Maggie Wisniewska for their hard work and support throughout my time at UNDERC-East. Thanks are due to Gary Belovsky for his mentoring and introduction to the UNDERC program, and of course to the generous Bernard J. Hank Family Endowment for funding my research and stay on the UNDERC property this summer. I also extend a warm thank you to all the faculty, staff, and students in the UNDERC property, whose support was crucial during my experiment. Further experimentation is needed to elucidate the complicated relationships between seed predation, plant invasivity, and community structure.

ENDSCISTRATION

The experimental results support the hypothesis that deer mice preferentially feed on P. pungens seeds over P. glauca seeds. Preference for P. pungens may indicate that granivores play an important role in the establishment of blue spruce in non-native areas and point towards granivory as an important component of the blue spruce success. The experimental results were analyzed using a paired t-test to account for statistical differences in addition to seed size (24, 25, 26, 38). Plant residence time, genetic make-up, local ecosystem community structure, mutualisms, resistance to predation, and dispersal strategies are a few factors that have been extensively studied and implicated in the conception of a prosperous invasive species (35, 1, 36). These factors are highly complex and interrelated (35, 1) and were not taken into account in this experiment.

The family Pinaeae, to which both blue and white spruce belong, has been documented as having the most proportionately invasive species of any conifer family (33). Richardson (2004) propose that the history traits which allow for successful conifer invasion are: small seed mass (< 50 mg), short juvenile period (< 10 year), and short intervals between reproductive cycles. The experimental results were analyzed using a paired t-test to account for statistical differences in addition to seed size (24, 25, 26, 38). Plant residence time, genetic make-up, local ecosystem community structure, mutualisms, resistance to predation, and dispersal strategies are a few factors that have been extensively studied and implicated in the conception of a prosperous invasive species (35, 1, 36). These factors are highly complex and interrelated (35, 1) and were not taken into account in this experiment.

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Figure 1. Selectivity Index of Peromyscus maniculatus individuals on Picea glauca and Picea pungens seeds. Foraging selectivity of P. maniculatus was greater for P. glauca seeds than for P. pungens seeds (paired t-test: t24 = -3.114; p = 0.005).

Figure 2. Differences in Picea glauca and Picea pungens seed size (length, width), Seeds of P. pungens were larger than P. glauca seeds (two-sample t-test: t27 = 0.041; p = 0.970).
The Effects of Varying Cache Depth and Mammalian Predator Scent on the Foraging Behavior of Peromyscus maniculatus

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ABSTRACT
Cache depth and perceived predator risk can affect the foraging behavior of granivorous rodents. Olfaction plays a crucial role in both foraging behavior and assessment of predation risks in many of these species. One factor affecting the strength of olfactory signals is cache depth, which can alter the search time of these rodents. Moreover, the threat of predation can affect the time and induce a trade-off between foraging and vigilance for predators. This laboratory study examined the effects of varying cache depth and mammalian predator scent (mink urine) on the foraging behavior of wild-caught forest deer mice (Peromyscus maniculatus). Mice did not alter the time spent foraging when assigned shallow (1 mm) or control (10 mm) sugar maple seed caches in the absence or presence of mink urine. However, mice did reduce their foraging time when assigned deep caches (20 mm) in the presence of urine. These responses to deep caches and the presence of urine reflected a trade-off between foraging and vigilance for predators. This trade-off affects both predation risk and cache depth on the foraging behavior of granivorous rodents.

Introduction
Granivorous rodents rely on their ability to successfully forage and cache seeds. By caching seeds when they are plentiful, rodents convert their intermittent food supply into a more reliable one, enabling them to have better control over food supplies (1). The ability to control food supplies becomes increasingly important, especially in the fall and winter months, when food supplies become limited. Therefore, increased success in recovering caches and making accurate cache decisions during the seasonal harvest is essential for survival (2).

Olfaction plays an important role in seed procurement for many of these species such as hedgehogs (Erinaceus europaeus), snowshoe hares (Lepus americanus), mountain beaver (Aplodontia rufa), mice (Mus musculus), and ground squirrels (Spermophilus beldingi). Rodents can detect volatile organic compounds (i.e., volatilized organic molecules) emitted from seeds as they are being eaten (1). Therefore, the signals perceived by rodents should be stronger for shallower caches than for deeper ones of the same size (1). Given these observations, it is hypothesized that buried seeds (>10 mm) will require a longer search time than those seeds buried in shallower depths or on the surface.

Co-investigators, other factors such as predation can also influence foraging behavior as well. For many systems, the threat of predation may be more important than the threat of predation. (2). When an increased risk of predation is perceived, a variety of responses can occur, including avoidance of riskier habitats and reduced foraging activity (3). For example, in response to the presence of small rodents such as gerbils (Gerbillus alleni and Gerbillus pyramidum) shift foraging activity to safer bush microhabitat and spend less time foraging in resource patches (4). These responses in behavior are often coupled with an energy trade-off between foraging efficiency and predation risk (5).

Many mammalian graniwores rely on olfaction not only during foraging, but also when assessing predation risk. They exhibit a variety of behavioral responses to predator odors found in urine, feces and anal gland secretions (5). Prey species such as hedgehogs (Erinaceus europaeus), snowshoe hares (Lepus americanus), mountain beaver (Aplodontia rufa), mice (Mus musculus) and ground squirrels (Spermophilus beldingi) exhibit a variety of behavioral responses to predator odors found in urine, feces and anal gland secretions (5). Prey species such as hedgehogs (Erinaceus europaeus), snowshoe hares (Lepus americanus), mountain beaver (Aplodontia rufa), mice (Mus musculus) and ground squirrels (Spermophilus beldingi) exhibit a variety of behavioral responses to predator odors found in urine, feces and anal gland secretions (5).

The objective of this study was to investigate the effects of both predator risk and cache depth on the foraging behavior of forest deer mice (Peromyscus maniculatus gracilis). Both predation risk and cache depth on the foraging behavior of forest deer mice (Peromyscus maniculatus gracilis) were observed during the seasonal harvest (1). When an increased risk of predation is perceived, a variety of responses can occur, including avoidance of riskier habitats and reduced foraging activity (3). For example, in response to the presence of small rodents such as gerbils (Gerbillus alleni and Gerbillus pyramidum) shift foraging activity to safer bush microhabitat and spend less time foraging in resource patches (4). These responses in behavior are often coupled with an energy trade-off between foraging efficiency and predation risk (5).

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Shaker traps (0.17 m x 0.054 m x 0.065 m) were baited with rolled oats, sunflower seeds and peanut butter and were set at dusk in each grid the night prior to experiments. Individuals were housed at the UNDERC Aquatic Laboratory facility for approximately 24 hours in separate plastic cages (0.1905 m x 0.21 m x 0.1270 m) lined with sand. Mice were provided with food, water, shelter, and nesting materials prior to experimentation. Mice were starved approximately five hours before each trial. All experimental protocols adhered to animal care and use guidelines endorsed by the American Society of Mammalogists and the Animal Behavior Society (7, 8). All experimental protocols were approved by the University of Notre Dame Institutional Animal Care and Use Committee (14-047).

**Cache Depth**

Each trial was performed in a standard 15-gallon glass aquarium (0.62 m x 0.30 m x 0.30 m) filled with a set amount of sand that corresponded to each cache depth treatment – shallow (1 mm), control (10 mm), and deep (20 mm). Using latex gloves, seed caches were prepared, consisting of three sugar maple seeds each. Mice were randomly assigned one of six different treatments – shallow cache depth (1 mm), control cache depth (10 mm), or deep cache depth (20 mm) – and either the presence or absence of mammalian predator scent (mink urine). Mice were tagged upon capture to ensure that no mouse was used more than once during the experiment.

**Mammalian Predator Scent**

For trials with simulated predators, urinated-saturated cotton balls were placed in perforated film canisters positioned in the corners of the aquarium tank. If urine was not present, then water was used to saturate the cotton balls. Each trial was conducted separately according to its randomly assigned variables (e.g., control with predation vs. control without predation) and fresh sand was used for each trial. In addition, aquaria were cleaned with a 10% bleach solution and thoroughly dried between trials. Trials were conducted at night and recorded using infrared lights and a Sony Handycam DCR-DVD610E infrared sensing camera. The search time (the amount of time it took an individual to uncover the seed cache) was measured for each trial.

**Data Analysis**

Data were analyzed with a two-way analysis of variance performed using SYSTAT v. 13.0 to determine if there were significant effects of cache depth and/or the presence of mammalian predator scent on the search time of mice (9). The data were analyzed using a two-way ANOVA to determine if there was a significant interaction between the two factors. The data were then analyzed using a post-hoc hypothesis test indicated a non-significant difference between the presence and absence of urine in the deep cache treatments \( F_{1,36} = 3.041; \ p = 0.0897; \) Fig. 3. However, when deep caches were contrasted with shallow and control caches in the presence of urine, there was a significant interaction with respect to search time \( F_{1,36} = 18.547; \ p = 0.0001; \) Fig. 3. Incidentally, in the absence of urine, this same contrast yielded a non-significant result with respect to search time \( F_{1,36} = 0.622; \ p = 0.882; \) Fig. 3.

**DISCUSSION**

There was a significant interaction effect between cache depth and the presence of urine \( F_{1,36} = 3.958; \ p = 0.0279; \) Fig. 3. Foraging behavior at different cache depths and the presence of urine \( F_{1,36} = 3.958; \ p = 0.0279; \) Fig. 3. Foraging behavior was measured by search time(s) to the seed cache. There were no statistically significant differences among varying cache depths \( F_{1,36} = 0.112; \ p = 0.990; \) Fig. 3. The error bars represent the standard errors of the mean.
that mice preferentially chose to spend more time being vigilant and less time foraging when seed caches were buried deep and urine was present. Correspondingly, the relatively short search times may be explained by the same time-cost trade-off between vigilance and foraging. When urine was absent, mice utilized time that might have been used for vigilance as prime foraging time. Overall, given these observations, it is assumed that the interaction effect between seed cache depth and urine was due to the time-cost or trade-off between vigilance and foraging behaviors. An increase in the number of seeds per cache may provide a more accurate assessment of the role of olfaction in seed detection. Gelsó (2005) found that the ability of Ord’s kangaroo rats to detect caches was significantly influenced by the size of caches (1). As cache size increased, kangaroo rats removed greater percentages of caches. In addition, Vander Wall (2003) found that as caches became smaller and deeper, they were more difficult for rodents to detect. Thus, increasing the number of seeds per cache would provide mice with greater opportunity to find and uncover the caches at deeper depths (3).

Although there are many more possibilities for future experimentation, this experiment provided an opportunity to explore the effects of varying cache depth and mammalian predator scent on the foraging behavior of P. maniculatus. While this experiment did not reveal significance in the two main effects, cache depth and mammalian predator, independently, the interaction between the effects of cache depth and mammalian predator scent provided valuable insight into the foraging behavior of granivorous rodents. Overall, these results reflect an important trade-off between foraging and vigilance, a fundamental behavior of granivorous rodents. Overall, these results highlight an important trade-off between foraging and vigilance, a fundamental behavior of granivorous rodents. Overall, these results reflect an important trade-off between foraging and vigilance, a fundamental behavior of granivorous rodents.

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I would first like to thank my advisor, Prof. Michael J. Craemer, for his guidance, encouragement, and patience throughout this experiment and my committee members Prof. Jensen, Prof. Watt, and Prof. Fogle at Saint Mary’s College. In addition, I thank Lauren Eckert, Samantha Driscoll, Nick Kales, Kevin Creamer, and Mary Chivetta for assisting me in trapping, baiting, setting grids, and taking care of mice while I was away. I also extend my gratitude to the UNDERC class of 2012 for their help, support, and sense of humor, making this experience truly unforgettable. Others who deserve my gratitude include the UNDERC Director, Prof. Gary Belovsky and our teaching assistants, Luke Degroote and Maggie Wisniewski. Finally, I thank the Bernard J. Hank Family Endowment for their generosity in providing me with this incredible research opportunity.

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ABOUT THE AUTHOR

Chelsea Gyure was born in Crown Point, Ind., and is a senior biology major with a minor in Chemistry at Saint Mary’s College. She conducted her research in the summer 2012 at the University of Notre Dame Environmental Research Center (UNDERC), and had been anticipating this research opportunity, in particular, since her freshman year. Chelsea was immediately drawn to this experiment as it echoed her passion for animals and research into their behaviors. She will be attending veterinary school as it echoed her passion for animals and research into their behaviors. She will be attending veterinary school.

Cluster Dynamics of the Myxococcus xanthus Bacteria

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ABSTRACT

The Myxobacteria Group of the Department of Applied and Computational Mathematics and Statistics at the University of Notre Dame studies how bacteria clusters are formed or diminished during the swarming processes of Myxococcus xanthus. In order to study the collective motion of the bacteria, the group uses a computational model to measure the effects of parameter changes on the formation of clusters.

INTRODUCTION

On a fundamental level, the Myxobacteria Group of Notre Dame’s Department of Applied and Computational Mathematics and Statistics is studying collective motion. By collective motion we refer to coordination of motility as seen in birds flocks and bee swarms. Collective motion is a topic often studied in different scales in biology, and the Myxobacteria Group is studying collective motion at a smaller scale with the swarming of Myxococcus xanthus, a gram-negative and rod-shaped soil bacterium. Swarming is the coordinated and collective motion of bacteria through a surface. Bacteria swarm through surfaces from which they are extracting nutrients (1). Even though bacteria have no central nervous system, they have developed the ability to swarm because it is the most efficient mechanism to acquire nutrients (2). In order to spread efficiently, M. xanthus forms coordinated clusters by both periodically reversing direction and engaging in social interactions (3).

First, the reversal of the bacteria’s direction is necessary for efficient swarming, because it aligns cells and generates clusters of cells parallel to each other (1). It is theorized that reversal is necessary for cells to move to the edges of the colony where there is less competition for nutrients (1). It takes 8 ± 2.1 min for bacterial cells to reverse their direction (1). The importance of directional reversal cannot be underestimated, because when the reversal period is set to zero cells cannot swarm (1). This suggests that without reversals, cells are unable to align and create cluster arrangements.

Second, myxobacteria have two gliding motility mechanisms that allow cells to interact. These two motility systems are the A-motility (or A-motility) and the S-motility (or Social-motility). The S-motility needs other bacteria in order to function. Without reversals, cells are unable to align and create cluster arrangements. The S-motility mechanism is not fully understood, but it is known that it enables the bacteria to move without the help of other bacteria. The Myxobacteria Group uses the slime gun model to explain the A-motility mechanism. The slime gun model’s basis is that the slime comes out of roughly 150 pores or nozzles at the tail ends of the cells (4). The slime secreted from cells pushes the bacteria forward and leaves a slime trail behind which influences the trajectory of other bacteria. It is important to note that the two motility mechanisms are independent from each other and that the cells move back and forth, but never sideways.

The Myxobacteria Group is particularly interested in knowing how the individual motilities lead to collective motion. Therefore we want to model the motion of single bacteria and try to determine how collective motion forms from the individual systems.

MODEL AND CLUSTERING

We use a version of the Subcellular Element Model (SCEM) developed by Newman in his “Modeling Multiscale Systems Using Subcellular Elements.” The subcellular elements are simply a series of nodes connected by springs, which form bacterial cells in the model. The springs connecting the nodes allow us to measure quantitatively the stretching and bending of the bacteria cells (5). There are N nodes connected by (N–1) segments with between these segments (4, 5). The motion of an individual cell is modeled by letting the head-node move in an arbitrary direction, and then using the Monte Carlo method to position the rest of the nodes (4).

When implementing the model, the following parameters all come into play: factors that should be taken into account to lower computational costs. In the model, bacteria have a standard fixed length of 5μm and width of 0.5μm although in real life these dimensions vary. Secondly, we use the A-motility instead of the S-motility. Thirdly, the slime trail factor is not included in the algorithm because it would add a dimension of interactions that would increase the computational cost exponentially. Finally, our computational model is developed in a 2-D surface, since z is small and the cells do not overlap in the model (biologically, cells do not overlap during swarming, but may do so in other occasions).

The equations that govern the Myxobacteria Group’s model using subcellular elements are as follows. The bending energy equation controls the length of the stretching. The bending energy equation controls the length of the stretching. The bending energy equation controls the length of the stretching. The bending energy equation controls the length of the stretching.
of cells; a high value makes the cell very stiff, and a smaller value allows it to bend easily (5). Even though bacteria are able to bend, complete U turns are extremely infrequent. Instead, during reversal, the tail becomes the head and the head becomes the tail (3, 6).

The number of neighbors a bacterium cell has is governed by the adhesion between two cells, and this is modeled using the Lennard-Jones potential (5).

\[ E_{\text{rep}}(\text{nodi}, \text{nodi}) = \epsilon_{ij} \left( \frac{\sigma_{ij}}{\|\mathbf{r}_{ij}\|} \right)^{12} - \left( \frac{\sigma_{ij}}{\|\mathbf{r}_{ij}\|} \right)^{6} \]

In the equation, \( \sigma_{ij} \) is the distance between nodes i and j of two cells, \( \epsilon_{ij} \) is the strength of adhesion, and \( \sigma_{ij} \) is the width of the cell. When in contact, if the distance between the nodes of two cells is less than \( \sigma_{ij} \), there is a repulsion force that prevents the cells from overlapping (5). On the other hand there is an attraction force when the distance between two cells is close enough. Of course, if the cells are not close enough there will be no attraction force. In our simulation, SCE's are repulsed if the distance of \( \sigma_{ij} \) is less than 0.5 \( \mu \text{m} \), and attracted when \( \sigma_{ij} \) is between 0.5 \( \mu \text{m} \) and 0.7 \( \mu \text{m} \).

The velocity of the bacteria in the surface is modeled using Langevin’s equation of motion (5).

\[ \frac{d}{dt} \mathbf{v}(t) = \frac{1}{m} (F - \gamma \mathbf{v}(t)) \]

In this equation \( \gamma \) is the friction coefficient, and \( F \) is the vector sum of all the forces acting on the node (5).

\[ F = F_{\text{slime}} + \sum_{k \in N_{\text{neighbors}}} F_{\text{adh}}(\mathbf{v}(t)) \]

More generally, the velocity is provided by the force exerted by the expulsion of slime from the nozzle of the A-motility (5). The slime force is assigned to an arbitrary tail end of the cell and switches after reversal. The velocity of the M. xanthus bacterium is approximately 4 \( \mu \text{m/min} \), which is a result of a slime force of 0.12 \( \text{nN} \) and a friction coefficient 1.8x10^{-6} \( \text{N.s/m} \) by the force equation \( F = \gamma \mathbf{v}(t) \). The surface of the bacteria cells is covered by polysaccharide slime, which is what gives the adhesive interaction between cells during swarming (1). The peptidoglycan sacculus, a layer characteristic in Gram-negative bacteria, defines the particular shape and bending ability of the cell (1). We want to know how parameters such as adhesion and flexibility affect the formation of clusters during bacterial swarming.

RESULTS

The simulations are run in a GPU (Graphical Processing Unit), which is efficient for the processing of our algorithms because the data is processed in parallel rather than in series (CPU) (7). However, even though GPU algorithms allow us to better simulate biological phenomena, we must take into account that the Subcellular Element Model is one of the most demanding computationally (7). Therefore, it is important to note that due to computational restrictions in the model we are not able to consider all interactions between all cells; instead we select a particular neighborhood around a cell and analyze the interactions of that area to a particular cell (4, 8). While the computational model can effectively run simulations of up to 1024 cells over a different parameter set, I used 256 cells in my simulations in order to lower computational costs.

Thereafter, I created MATLAB programs that analyze data for the adhesive parameter and tried to understand how this parameter affects the clustering dynamics. My MATLAB programs used the raw data generated by the simulations and clustering analysis algorithms; the first program calculated the distance traveled by a cluster of bacteria, and the second calculated the speed at which the cluster moved. The raw data generated by the simulations can also be visualized in a 3-D environment using the Visual Molecular Dynamics (VMD) software. Figure 1 illustrates the typical fact that by increasing the adhesion of cells, more clusters are formed. The two values given to \( \epsilon_{ij} \) namely [0.0025,0.05], will serve as our boundary points, and are the minimum and maximum plausible values that bacteria in a real biological environment could hold.

My first program provides a scatter plot that illustrates the distance traveled by different-sized clusters. It is important to note that since clusters are dynamic (bigger clusters can divide into smaller clusters and vice versa), my program takes the average of all the cluster-sizes to which a particular cell belonged and the average distance it traveled (2).

First, I wanted to compare the clustering dynamics of a small adhesive value versus a large adhesive value. The results are shown in Figure 2. As shown in the VMD illustration of Figure 1, my program confirms that as the adhesive value of cells, the more neighbors it is expected to have. We can also note that there is a negative correlation between the distance traveled and the cluster size. The higher the number of neighbors there are the less far the cluster will travel. We can also note that when given an adhesive value of \( \epsilon_{ij} = 0.0025 \) the cells behaved in a quasi non-biological manner, cells did not have more than three neighbors, and uniformly traveled a long distance.

When looking for a threshold for more realistically behaved clusters, I noticed that this behavior remained constant when the adhesive value is increased from 0.0025 to 0.01. However, given values greater than 0.01, the variance increases quickly, as shown in Figure 2. From this observation we can conclude that the optimal adhesive value for bacterial cells should be greater than 0.01 in order to more accurately replicate the clustering dynamic of the model bacterias.

My second program calculates the average speed for different-sized clusters. As shown in Figure 3, average speed decreases as the adhesive value increases. My results are counter to a statement made in Zhang’s “Collective motion and density fluctuations in bacterial colonies” (2). He states that the average speed of a cluster increases proportionally with its size. However, from my previous two plots we can see that as we increase the adhesive value the cluster size increases, but this in turn decreases the average speed of cells. A major difference between the two models is that Zhang used only experimental data to make his observations; so while looking at bacteria in a microscope there is a constant flux of bacteria in and out of the perimeter being analyzed, which leads to a constant density. In our simulations, however, the perimeter we are analyzing might increase (since we do not have boundary conditions in the model) while the number of bacteria in the simulation stays constant. This leads to a less densely populated system. Therefore it can conclude that the average speed of a cluster is a very density-dependent measure.

CONCLUSION

We are currently working on comparing our data from simulations to experimental data. The group has developed an algorithm that can track the bacterial cells from the experimen tal movies created in the lab. Figure 4 shows how the image processing algorithm tracks cells in a particular frame. Even though the program is fairly accurate, there still corrections that need to be done manually before we run the cluster analysis for the experimental data.

At large, we are using mathematics as a tool in modeling how biological systems work. The group will continue working on understanding better complex biological systems such as collective motion with the hope of providing insight into how we can better contain the spread of bacteria. If we can understand more deeply the spread of bacteria we would be better equipped to control and even prevent infections.
An Analysis of Neural Spike Trains

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ABSTRACT
Spike trains encode a vast amount of information. The analysis of spike trains is useful for the understanding of communication between excitable cells. The interspike interval, or the time in between spikes, is a critical facet of encoding information. From the interspike interval, the frequency of cell firing can be determined. Using Monte Carlo simulations, bifurcation analysis, and stability theory with the Morris-Lecar model, type I and type II membrane excitability were analyzed. A bifurcation refers to a point of qualitative change in a system, in this case, a change in stability. Stability analysis showed that the type I system has three equilibrium points, which give rise to a saddle-node bifurcation and a Hopf bifurcation. The single equilibrium point in the type II system is stable and marks a Hopf bifurcation. Critical bifurcation values of the primary parameter, applied current, were found for both systems.

INTRODUCTION
The Action Potential
Action potentials, or spikes, are brief electrical impulses that have a fundamental role in communication between excitable cells, particularly neurons. An action potential occurs when a stimulus triggers the opening of ion channels in the cell membrane, allowing a rush of sodium or calcium ions into the inner cell. This influx of positively charged ions creates a new electrical state in the cell membrane, allowing a rush of sodium or calcium ions into the inner cell. This influx of positively charged ions causes the negatively charged inner cell to become briefly positively charged, which marks the peak of a spike. This change in polarity triggers the opening of voltage-gated potassium channels, which allow positively charged potassium ions to leave the cell, restoring the cell membrane to its original negative state.

Spike Trains
A sequence of action potentials over a given period of time is called a spike train. Action potentials adhere to a phenomenon called the “all-or-nothing” law, which states that spikes can either occur or not occur at all, reaching a peak voltage of some arbitrary positive magnitude. This means there is no critical voltage at which a spike is considered to have occurred. Further, the magnitude of an action potential is independent of the stimulus intensity and encodes no information relevant to spike train analysis (2). Therefore, properties such as the frequency and temporal correlation of spikes are crucial to analyzing the coding mechanisms of excitable cells.

ABSTRACT
The analysis of spike trains has been an area of interest for decades (3, 4, 5, 6). The temporal correlation of spikes has been likened to a code that relays information from one cell to another; in muscle cells, spike trains convey things like how much muscle tension is required to lift an object and when a muscle contraction is necessary (7). In sensory cells, spike trains can communicate whether a stimulus takes the form of sound, smell, light, touch, or taste, as well as determine how the stimulus is perceived (8). In the brain, the synchronization of spike trains is associated with levels of mental functioning; a decrease in synchronization has been linked to mild cognitive impairment (9).

Membrane Excitability
Cells can be classified in a variety of ways, one of which involves the excitability of axons — the cellular structure through which an action potential travels. When an external current is applied, type I membranes fire spikes at some arbitrarily low frequency with a potential minimal firing rate of zero. Conversely, type II membranes fire repetitively at a non-zero frequency when a current is applied (10).

Bifurcation Theory
The spiking, or firing, of a neuron can be described as a dynamical system to illustrate the change from state to state over time. Bifurcation theory, which studies variations in the qualitative structure of a system, is commonly applied to the analysis of dynamical systems. A bifurcation marks the sudden qualitative change in the nature of the solution as a parameter is varied. The two major classifications of bifurcations are local, in which the behavior around a single point is dependent on a varied parameter, and global, in which equilibria collide with a more general behavior of the system, such as periodic orbits (11).

MATHEMATICAL MODELS
The Hodgkin-Huxley Model
The original mathematical model of the initiation and propagation of action potentials was described in 1952 by Alan Lloyd Hodgkin and Andrew Huxley based on experiments using a giant axon from the Loligo squid (12). This four-dimensional model describes sodium-based action potentials, i.e., action potentials initiated by an initial influx of positively charged sodium ions into the cell, and is an example of Type II excitability (10):

\[
\frac{dV}{dt} = \frac{1}{C} \left( I - g_N(V-V_N) - g_L(V-V_L) - g_K(V-V_K) - g_L(V-Y_L) \right)
\]

where \( C \) is the membrane capacitance, or the amount of electrical charge that can be stored in the cell membrane, \( V \) is the membrane potential, \( I \) is the applied current, \( g_N \) is the sodium conductance, \( g_K \) is the potassium conductance, \( g_L \) is the leak conductance, \( V_N \), \( V_L \), and \( V_K \) are the resting potentials for sodium and potassium, respectively, and \( V_Y \) is the leak reversal potential.

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potential. The values of the sodium and potassium conductances, $g_{Na}$ and $g_{K}$, are determined by the following:

$$ \frac{dV}{dt} = -\frac{g_{Na}V}{C_m} + g_{Ca} (V - V_{Ca}) + \frac{g_K (V - V_{K})}{C_m} $$

with $g_{Na}$ and $g_{K}$ as the maximum sodium and potassium conductances and $m$, $h$, and $n$ as gating variables which indicate the probability that a sodium channel is open ($m$), closed ($h$), or a potassium channel is open ($n$). The rate functions of which are defined in Peter Rowat’s 2007 paper, “Interspike Interval Statistics in the Stochastic Hodgkin-Huxley Model” (13).

### The Morris-Lecar Model

In 1981, Catherine Morris and Harold Lecar developed a three-dimensional model that would eventually be reduced to a two-dimensional system (14). The Morris-Lecar model, originally used to describe the dynamical membrane potential of the barnacle Balanus balanoides, depicts calcium-based action potentials.

The parameters are defined as they were in the Hodgkin-Huxley model with the addition of $g_{Ca}$ and $V_{Ca}$ the maximum conductance and Nernst potential for calcium, respectively, and $w$ as the probability that a potassium channel is conducting. The functions form $\nu(V)$, $\omega(V)$, and $\lambda(V)$ are defined by the following:

$$ \nu(V) = 0.5 \left[ 1 + \tanh \left( \frac{V - V_T}{\Delta V} \right) \right] $$

$$ \omega(V) = 0.5 \left[ 1 + \tanh \left( \frac{V - V_T}{\Delta V} \right) \right] $$

$$ \lambda(V) = \frac{\nu(V) - \omega(V)}{2} $$

where the parameters and functions $\nu(V)$ and $w(V)$, and $\lambda(V)$ are defined by the same equations used in the Morris-Lecar model, and $\lambda(V)$ is defined by:

$$ \lambda(V) = \frac{1}{3} \tanh \left( \frac{V - V_T}{2\Delta V} \right) $$

### METHODS

#### Ordinary Differential Equations

When analyzing the system from a deterministic approach, it is appropriate to treat the equations as ordinary differential equations. Using MATLAB’s collection of ODE solvers, the Hodgkin-Huxley, Morris-Lecar, and the non-dimensional model were evaluated at initial conditions specified in Rowat 2007 (13) and Ermentrout 1996 (10). These solutions were plotted in MATLAB and show the rise and fall of membrane potential over time, depicting the firing of action potentials, or the spike train.

#### Monte Carlo Simulations

Monte Carlo simulations are useful in simulating systems under conditions that emulate the randomness of real-life, relying on repetitive random sampling to determine the general behavior of a system over time. This method evaluates the same systems of differential equations from a stochastic approach. In order to construct stochastic differential equations from the original ODEs, a Wiener process (Standard Brownian motion) was added to the system of equations defined in the Morris-Lecar model (5, 16). The system was then evaluated using Itô’s lemma:

$$ V = V_0 + a(V, w) dt + \sigma(V, w) dB_t $$

where $a$ is a constant or function with respect to $V$ and $w$ that describes the diffusion of the process. The resulting solutions were plotted in MATLAB to produce the stochastic spike train.

#### Bifurcation Analysis

As the primary parameter $I$ is varied, type I fixed points and $b$ conform to the saddle-node bifurcation phenomena, growing closer as $I$ increases before colliding to form the critical equilibrium, then disappearing as $I$ increases further, as depicted in Figure 3A. The critical saddle-node bifurcation point occurs around an $I$ value of approximately 0.07. After this critical parameter value, the Hopf bifurcation at point $c$ reflects a change in stability, with the real part of the complex conjugate eigenvalue pair transitioning from positive to negative. This change from a subcritical Hopf bifurcation to a supercritical Hopf bifurcation reflects the system’s shift from unstable to stable after the point of bifurcation.

#### Non-dimensional Model

In the early ‘90s, Bard Ermentrout developed a system of dimensionless equations based on the Morris-Lecar model for the purpose of analyzing the system near criticality, i.e., the point at which the behavior or stability of the system changes with a change in external stimuli. The stability of a fixed point is determined by evaluating the eigenvalues of the system at that point; real negative eigenvalues, or the negative real part of a complex eigenvalue indicate stability. A fixed point in two dimensions that has one positive and one negative eigenvalue is called a “saddle” and is unstable. A fixed point with two real negative eigenvalues is called a “node” and is asymptotically stable. When a parameter is varied, the number of fixed points changes and the “saddle” and “node” points are brought together and collide, giving rise to a saddle-node bifurcation. This phenomena shows the two points colliding, forming a critical saddle-node equilibrium, then disappearing as the given parameter is increased.

**Figure 3A-B. Equilibrium of a Type I (A) and Type II (B) neuron at varied $I$.**

By definition, $a$ is a node, $b$ is a saddle, and $c$ marks a Hopf bifurcation point. Since the real part of the complex conjugate eigenvalues in point $c$ is positive, the point is unstable and is a subcritical Hopf bifurcation.

The type II membrane has one equilibrium point $d$ with a complex conjugate eigenvalue that has a negative real part, corresponding to a stable supercritical Hopf bifurcation.

**Bifurcation Analysis**

**Stability at Fixed Points**

In order to evaluate the stability of the non-dimensional system, the partial derivatives of the non-dimensional equations were taken with respect to $V$ and $w$.

$$ \frac{\partial V}{\partial I} = \lambda + \frac{g_{Ca} (V - V_{Ca})}{C_m} $$

$$ \frac{\partial V}{\partial w} = \frac{\nu(V) - \omega(V)}{2} $$

These equations form the Jacobian matrix $J$:

$$ J = \begin{bmatrix} \frac{\partial V}{\partial I} & \frac{\partial V}{\partial w} \\ \frac{\partial w}{\partial I} & \frac{\partial w}{\partial w} \end{bmatrix} $$

The fixed points were determined by finding the roots of the equations with no applied current ($I = 0$). Three equilibrium points were found for the type I membrane and their corresponding eigenvalues are as follows:

<table>
<thead>
<tr>
<th>Fixed Point</th>
<th>$\lambda$</th>
<th>$\mu$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$a$</td>
<td>-1.4300</td>
<td>-1.4650</td>
</tr>
<tr>
<td>$b$</td>
<td>-1.4350</td>
<td>-1.3650</td>
</tr>
<tr>
<td>$c$</td>
<td>-1.2500</td>
<td>-1.2500</td>
</tr>
<tr>
<td>$d$</td>
<td>-1.2500</td>
<td>-1.2500</td>
</tr>
</tbody>
</table>
Conversely, the type II membrane was able to retain stability over a wider range of stimulus values because of the type II membrane, which is more stable over a broader range of applied current $I$. This difference in stability can explain the difference in excitation between type I and type II membranes. The ability of the type II membrane to consistently fire at a non-zero rate independent of stimulus intensity not only allows SWNTs to have different “chirality” depending on the angle at which the graphene sheet is rolled. Chirality is designated by a unit of vectors $(n, m)$, which determines the nanotube’s electronic properties, such as semiconducting or metallic. The three main categories of SWNT chirality that occur in CVD growth experiments are “armchair” $(n, n)$, “zigzag” $(n, 0)$ and “chiral” $(n, m)$ (6). At this time, the ability to control chirality from the moment of SWNT nucleation (7, 8). Within a given sample of SWNTs, it was theorized and later experimentally shown that one third will end up being metallic $(n - m = l/3)$, and the other two thirds will be semiconducting (9).

The particular focus of this investigation was to grow SWNTs for THz spectroscopy. THz radiation is an underdeveloped region of the electromagnetic spectrum corresponding to a wavelength range of 300 μm – 1 mm, in between electronics and optical frequency ranges. Metallic SWNTs in this length range have been shown to polarize THz radiation, and semiconducting SWNTs may be used in the first THz sensors, detectors, emitters, and modulators (10, 11). Such devices may be used to replace harmful X-rays, to detect the presence of water in objects, or to characterize ancient artifacts (3). In previous experiments, SWNTs for THz applications were first grown vertically and then transferred to a horizontal surface to take measurements (12). This resulted in reduced density of SWNTs, however. Therefore the ability of dense SWNTs in the desired length range grown directly onto a horizontal surface to be used for THz spectroscopy is being investigated.

The most important characteristic of horizontal SWNTs is their ability to form highly aligned arrays. Higher alignment increases the density of the SWNT arrays and reduces bundling. Therefore, a high degree of alignment is desired for most electronic and spectroscopic applications of SWNTs (3, 8). Horizontal SWNTs can be grown on a number of different substrates, but the most common include crystal quartz, sapphire, or silicon. SWNTs can be grown with macroscopic alignment on substrates using the gas-flow method, in which alignment direction is determined by the direction of the gas flow during CVD, so the SWNTs are effectively “floating” above the surface of the substrate (13). Alternatively, micro-scale and even nanoscale alignment can be achieved by growth on a crystal quartz (14, 15) or sapphire (16) substrate, in which the SWNTs are adsorbed to the substrate surface due to Van der Waals forces.

In our experiment, all SWNTs were grown on 0.3 mm-thick crystal quartz. SWNT alignment on crystal quartz arises from the electronic structure of the crystal’s “R face” (17, 18, 19). The R face is characterized by parallel potential wells along which SWNTs can grow, causing them to have a high degree of alignment. Although the R face is the theoretically perfect surface for this type of growth, a similar type of cut, called ST cut, has a small offset from R cut but is used much more frequently in CVD growth experiments. This is simply because ST cut is commercially available as for some transistor applications, whereas R cut has no other mainstream uses and is difficult to obtain. Highly aligned SWNTs can be grown on ST cut despite the fact that experiments have shown (20).

In our experiment, SWNTs were grown both on R cut and ST cut. Although we were able to grow SWNT arrays on
imprint patterns of lines either 50, 100, or 300 μm apart. Vacuum deposition was used to vaporize a metal wire and deposit it onto the substrate at a fixed rate for a fixed period of time to create a nominal thickness. Finally, a process called “lift-off” was used to remove all the photosresist except for that on the lines formed by photolithography. In the wet method, the sample was covered with a layer of scotch tape and a stripe pattern was imprinted by hand onto the tape using a razor blade (21, 22), which produced a pattern lacking in uniformity compared with the dry method, shown in Figure 2A. Catalyst solutions were deposited onto the sample, the scotch tape acting as a physical mask. After the solution evaporated the tape was removed, leaving catalyst nanoparticles deposited only where the razor had imprinted lines. Solutions used were ethanol-based and contained different concentrations of copper salt and PVP (polyvinylpyrrolidone), a polymer whose purpose was to reduce nanoparticle aggregation.

CV conditions were for the most part kept constant during the experiment. CVD parameters of pressure, sample position within the vacuum tube, and growth time were adjusted to investigate whether ideal conditions differed between the catalysts. It was found that initial CVD conditions are mainly characteristic of the system proper rather than characteristic of different catalysts. It was established in a previous experiment (23) that adjusting pressure alters the carbon-feeding rate and that within each CVD system, an optimum pressure exists to maximize density while minimizing bundling, which can occur when SWNTs grow too quickly (23, 24). Moreover, adjusting growth time affects SWNT length and an optimum time exists to maximize length and minimize “etching” of SWNTs due to unwanted byproducts produced during the breakdown of ethan-ol (23).

RESULTS AND DISCUSSION

Catalyst type is thought to be the most important CVD growth parameter (26, 27). In our experiment, the choice of catalyst depended on the deposition method. Initially only iron metal was deposited using the dry method. When this failed to grow SWNTs in the desired length range, we began investigating other catalysts with the hypothesis that they may employ other growth mechanisms and hence grow longer CNTs. For instance, iron may employ a base-growth mechanism, meaning that during growth, the entire nanotube must be pushed along the surface of the quartz as additional carbon atoms are added to its base. Copper, on the other hand, is may use a tip-growth mechanism, meaning that only the catalyst particle moves as carbon atoms are added to its tip (8, 18). This was hypothesized by multiple research groups, including Manyama’s, after previous experiments which showed copper to be capable of growing SWNTs in the 1 mm range (28). It is thought that tip-growth catalysts can achieve greater lengths because less material is being pushed along the quartz surface, hence there is less resistive force for the CNT to overcome as it grows.

Copper was initially deposited using vacuum deposition (dry method) but failed to grow any SWNTs. It was hypothesized that this may have been due to the fact that copper has a narrower range of nanoparticle sizes from which CNTs can nucleate. Figure 1B shows that the vacuum deposition method produced relatively uniform particle sizes. We believe that the copper nanoparticles deposited by vacuum deposition were too large to grow SWNTs, even though the same method grew SWNTs successfully for iron, which we deem to be a more “flexible” catalyst. We wished to decrease the size of depos-ited nanoparticles in order to potentially grow copper-based SWNTs. Since this appeared difficult to achieve using vacuum deposition, we switched to the wet method. Figure 2A-b shows that catalyst deposited using the wet method produced a much broader range of nanoparticle sizes than the dry method. Our hope was that if the copper catalyst could only grow SWNTs from a narrow range of particle sizes, this ideal range would be easier to obtain using the wet method. For copper, four different solutions using different concentra-tions of CuCl2 :PVP (mmol/L) in 10 mL of ethanol were test- ed: 1:10, 1:100, 10:10, 0.1:1 nmol/L respectively, the first of these having been used to successfully grow Cu-based SWNTs in the experiment of Liu’s group. In our CVD sys-tem, the first three solutions failed to produce any SWNTs. The fourth solution, however, which contained the lowest concen-tration of copper salt, produced a dense, highly aligned array of SWNTs within the desired length range for THz spectroscopy (> 300 μm), shown in Figure 4. We believe that reducing copper concentration reduced nanoparticle aggregation and produced nano-particles small enough for copper-based SWNTs to nucleate.

After SWNTs in the desired length range were successfully grown, more in-depth analysis was required to further charac-terize the copper-based SWNTs. Cobalt, a catalyst similar to iron but more compatible with the wet method, was used as a control (29). The cobalt catalyst produced arrays with density, alignment, and length comparable to that of copper. Copper and cobalt-based SWNTs were grown on ST cut and analyzed using AFM imagery and Raman spectroscopy. AFM was used to calculate SWNT density and diameter distribution. Density
for copper-based SWNTs was found to be on average 7 - 8 SWNTs/μm. Density for cobalt was 5 - 6 SWNTs/μm. Figure 4 shows an example image of cobalt-grown SWNTs on ST cut used to calculate SWNT density. These results were comparable to densities calculated using AFM for iron-based SWNTs using the same CVD system and parameters. The results from AFM diameter distribution calculations were more informative for characterizing SWNTs. An example of an AFM diameter profile used to collect diameter data is shown in Figure 5. Copper was shown to have a relatively narrow diameter distribution in the 1 - 2 nm range (Fig. 6A), whereas the diameter distribution for cobalt was much broader (Fig. 6B). It was assumed that SWNTs with diameters larger than 2 nm were either bundled or multi-walled (1, 3, 18). This finding coincided with the previously discussed belief that copper is a more “selective” catalyst than cobalt and iron in terms of the size of nanoparticles from which SWNTs can nucleate. This further suggests that due to the fact it only grows from selectively small catalyst nanoparticles, copper may be used more successfully than other catalysts to grow purely single-walled nanotubes.

In addition, AFM, Raman spectroscopy was used to detect a G-band and RBM of the SWNT sample. For both ST cut samples, a G-band was detected with a slight up-shift compared to what is normally seen for R cut, in the 1591-1594 cm\(^{-1}\) range (30). This suggests there may be some small differences in the interaction between SWNTs and the surface lattice of the quartz for R cut and ST cut that are not yet well understood.

RBM were very difficult to detect due to the low ratio of graphitic material to quartz. The quartz produced a much reduced background noise, but introduced other difficulties. Since samples were grown using the wet method in which lines of graphitic material to quartz. The quartz produced a much reduced background noise, but introduced other difficulties. Since samples were grown using the wet method in which lines of graphitic material to quartz. The quartz produced a much reduced background noise, but introduced other difficulties. Since samples were grown using the wet method in which lines of graphitic material to quartz. The quartz produced a much reduced background noise, but introduced other difficulties. Since samples were grown using the wet method in which lines of graphitic material to quartz. The quartz produced a much reduced background noise, but introduced other difficulties. Since samples were grown using the wet method in which lines of graphitic material to quartz. 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Analysis of a Potential Tracking Algorithm for the SLHC Upgrade

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ABSTRACT

This work studies a triggering algorithm for the proposed 2020 upgrade to the Compact Muon Solenoid (CMS), one of the main detectors in the Large Hadron Collider (LHC) in Geneva, Switzerland. This upgrade will begin the era of the Super Large Hadron Collider (SLHC). The luminosity of the collider will increase by roughly a factor of 10, allowing for observation of extremely rare events. The large number of interactions, however, would overwhelm the current trigger system, making it impossible to select interesting events from the background. The SLHC will thus include an upgrade to the silicon tracker for CMS, which will use high-speed electronics to track particles in the lower layers of the detector. By reconstructing a particle’s trajectory in the detector’s magnetic field, the Level-1 trigger identifies events containing high-energy tracks to be processed by the software trigger. This work focuses on the optimization of the tracking algorithm for the Level-1 trigger using simulated collision data. Specifically, track finding efficiency must increase while simultaneously avoiding fake tracks. It has been shown that this algorithm successfully maintains this balance and would make a good foundation for the SLHC Level-1 trigger.

INTRODUCTION

Located about 100 meters underground in Geneva, Switzerland, the Large Hadron Collider (LHC) is the largest and most powerful particle accelerator in the world. The LHC consists of three main parts: the 27-kilometer circular accelerator tunnel, four different detectors, and the Worldwide LHC Computing Grid.5 By colliding protons or heavy ions, physicists use the LHC to study some of the most fundamental questions in particle physics. The LHC is designed to accelerate protons up to an average energy of 7 TeV, or about 7500 times the rest mass of a proton. This will result in a maximum collision energy of 14 TeV. However, reaching a high energy is not enough to guarantee results; the particle beams must also be very tightly packed to increase the probability of collision. The LHC is currently designed to reach a maximum luminosity (or particles per unit area per unit time) of 1034 cm−2 s−1 (1). The current LHC design has produced important results, especially the recent discovery of the Higgs-like particle.

The Compact Muon Solenoid (CMS) is one of the two major detectors at the LHC. CMS gets its name from the large superconducting solenoid magnet it uses to generate a 3.8 T magnetic field in the detector. CMS is 21 meters long, 15 meters in diameter, and weighs about 12500 tonnes (2). It is divided into five layers: the solenoid layer and the four different detector layers. The innermost layer, the silicon tracker, is the focus of this study. The tracker is made of layers of silicon strip and pixel detectors arranged into barrels with endcaps. The silicon tracker tracks the curved paths of charged particles. Therefore, the silicon tracker cannot track photons or other neutral particles. The second layer, the Electromagnetic Calorimeter (ECAL), is made of lead tungstate (PbWO4) crystals, which produce a small amount of light when any type of particle passes through them. This light is then detected by silicon avalanche photodiodes (APDs) in the barrel and by vacuum photodiodes (VPTs) in the endcaps. Because photons, electrons, and positrons cannot pass through the ECAL, it is designed specifically to track these particles. The third layer, the Hadron Calorimeter (HCAL), consists of brass plates with scintillator sheets sandwiched between them. When hadrons pass through the HCAL, they interact with the nuclei in the detector and produce charged particles. The HCAL is used to detect protons, pions, and neutrons, which are stopped at this layer. The fourth layer is the solenoid magnet, which creates the magnetic field necessary to calculate the momentum of charged particles in CMS. The final detector layer consists of muon detectors, which include three different types of detectors: drift tubes (DT), cathode strip chambers (CSC), and resistive plate chambers (RPC). Since all other particles have been stopped before reaching these detectors, muons are the only type of particles tracked at this layer.

CMS uses a two-part trigger system to determine which events to reprocess further. The first part, the Level-1 trigger, reduces the readout rate from about 40 MHz to 100 kHz. This trigger is currently implemented in the hardware of the HCAL, ECAL, and muon detectors. The second part of the trigger system, the High Level Trigger (HLT), uses a computer farm to reduce the readout rate further from about 100 kHz to 300 Hz.

In about 2020, the LHC will be shut down for a period of time in order to perform the SLHC upgrade. After the upgrade, the luminosity of the collider will increase by about a factor of 10 (4). This will lead to a dramatic increase in the number of collisions per crossing. The CMS trigger system is not designed to handle this level of collisions, which would overwhelm the current HLT. To deal with this, the upgraded Level-1 silicon trigger must be able to more effectively reduce the number of events to be processed by the software trigger. Currently, the silicon tracker cannot output information quickly enough to be used by the Level-1 trigger. When the LHC is shut down for the upgrade, the silicon tracker must be replaced due to radiation damage. This is the perfect opportunity to replace the silicon tracker with a more advanced detector. Specifically, the proposed design for the silicon tracker would be able to output information quickly enough to be used by the Level-1 trigger. When the LHC is shut down for the upgrade, the silicon tracker must be replaced due to radiation damage. This is the perfect opportunity to replace the silicon tracker with a more advanced detector. Specifically, the proposed design for the silicon tracker would be able to output information quickly enough to be used by the Level-1 trigger.

In the current CMS detector, the Level-1 trigger does not include any form of track reconstruction (1). The algorithm being analyzed, however, does include basic tracking. This has the potential to improve the trigger system by incorporating information from the track as well as the properties of the particle’s transverse momentum, or px. Particles from background events tend to have low px while particles from interesting events tend to have high px. Many of these background events come from pileup, events resulting from glancing collisions of particles in the detector. Track reconstruction thus allows the algorithm to weed out a much higher percentage of the background than is possible with the current Level-1 trigger.

EXPERIMENTAL SETUP

When a particle of charge q travels perpendicular to a magnetic field B at velocity v, it experiences a force Bqv perpendicular to its motion. This force moves the particle along a circular path with radius r (called the radius of curvature). This motion can be described by the following equation (3):

\[ Bqv = mv^2 \]

This can be used to obtain the following equation for the transverse momentum of a particle (pT):

\[ p_T = Bqr \]

where B is given in Tesla, r in meters, and pT in GeV/c. Since the strength of the magnetic field is set at 3.8 T, only the radius of curvature r needs to be calculated.

One way to calculate the radius of curvature for a particle is by using “stubs.” The figure below is a basic diagram of the detector:

\[ r = (R/2)/\sin(\theta - \phi) \]

where R is the radius of the detector, \( \phi \) is the angular position of the stub within the detector, and \( \theta \) is the angular direction of the stub. It was hoped that this formula would give better accuracy in stub pT than the local formula, since it incorporates more information about the track. However, the overall performance of the two different formulas was very similar. Since the separation between the hits in a stub is so small, the errors in pT are too high to use stub pT alone for triggering.

ANALYSIS

To investigate the source of pT error, the plots of the transverse momentum (pT) of stubs from a set of 50000 muons all with pT = 2 GeV were analyzed:

![Image 1. Detector terminology](image1.png)

Each layer of the detector consists of a “stack,” a pair of two sensors separated by about 1 mm of silicon. A particle passing through the detector is recorded by both sensors. Such a pair of hits is called a “stub.” The relative positions of the hits give a direction for the stub. This direction can be used to calculate the transverse momentum pT of the stub.

Two methods of calculating \( r \) from the stubs were tested. Locally, radius of curvature is given by \( r = (R/2)/\sin(\theta - \phi) \). This is done by approximating the change in arclength and angle of the stub.

Additionally, a calculation, which uses the global position of the hits within the detector and the fact that the track must have begun at the origin of the detector, was tested.

![Image 2. Geometry of radius of curvature calculation](image2.png)

This leads to:

\[ r = (R/2)/\sin(\theta - \phi) \]

To focus the study, the momentum measurements were limited to a small region of the detector (small \( \phi \) and \( \theta \) range). Instead of finding a smooth distribution over a small range, several distinct peaks in momentum measurement were found.
Looking at the $\phi$ dependence of the stub $p_T$, a pattern was found and given the name “cat scratches.” The cat-scratch pattern is the cause of the peaks in the $p_T$ spectrum: a small $\phi$ slice overlaps with approximately three of these cat scratches per layer, giving a few discrete $p_T$ values. It was found that each of these peaks correspond to one $\phi$ value, confirming the hypothesis. The directional resolution of individual stubs is quite poor, and there is significant discretization of the directional measurements. Thus, much of the error in $p_T$ measurements is likely due to the low precision in the measurement of stub direction. Because of the high error in $p_T$ calculation, it is not suitable for initial track reconstruction. Therefore, the algorithm uses the position of the stubs to reconstruct the particles’ trajectories. The algorithm works by first identifying the stubs in the sixth layer. The assumption was made that any particle that makes it to the sixth (outermost) layer of the detector began its path at the center and left and left hits in each of the five lower stub layers. To determine the momentum of the particle that made the track, the algorithm searches through different ranges of $p_T$ and looks for stubs along a trajectory consistent with that $p_T$ and sixth layer stub, represented by the thick lines in the diagram. To check these locations, the $p_T$ ranges are converted into $\phi$ ranges using the layer radii and the $p_T$ calculation formula. These ranges are called “$\phi$ windows.” The width of the $\phi$ windows depends on the range in $p_T$, it is checking. In this algorithm, $p_T$ windows can be defined in two ways: equal separation in $p_T$ and equal separation in curvature (the inverse of radius of curvature). Since low $p_T$ tracks are more curved, it is easier to distinguish between tracks of different $p_T$, so smaller $p_T$ windows are used. High $p_T$ tracks are straighter, so it takes a greater difference in $p_T$ to tell them apart and wider $p_T$ bins are required. If the algorithm finds stubs in each layer for a particular $p_T$, then that $p_T$ range corresponds to a “found” track. All of the found tracks for a particular sixth layer stub are stored for further analysis. Although most particles fall in the middle of the $\phi$ windows, a stub that is found at the border between two $\phi$ windows will not be found properly by the algorithm. To account for this, a percent overlap value called “slop” was added. A high value of slop will allow the algorithm to pick up all particles that would otherwise be missed, but will also cause the algorithm to pick up particles that do not actually correspond to that $\phi$ window.

**RESULTS**

Any triggering algorithm must strike a balance between efficiency and fake rate. Efficiency describes the rate at which the trigger correctly identifies a track. Conversely, the fake rate is the rate at which the trigger incorrectly reconstructs a track. An ideal trigger would pass all interesting events while rejecting all uninteresting ones. Unfortunately, changes that increase efficiency tend to increase fake rate as well, and vice versa. In the analysis of the code, a system was developed to measure these parameters, and used it to tune the track finding algorithm. A particle is declared “found” if the algorithm reconstructed a track with $p_T$ and $\phi$ close to the actual values of the particle. If not, it is labeled a fake. The width of this window is $p_T$ dependent, based on the typical spreading for single-track events. If the algorithm found a close track for a high percentage of the particles, it is said to have good efficiency. Figures 7A-F shows the effect of changing slop on the efficiency and fake rate of the algorithm. The efficiency plots show the percentage of muons that were found by the algorithm in 300,000 single-track events. With zero slop, tracks near the edges of $p_T$ bins have reduced efficiency, as discussed above. Increasing slop to 10% gives fairly uniform efficiency of about 93% across the tested $p_T$ range. Further increasing slop to 50% has a negligible effect on the efficiency. The fake rate was tested using a sample of 240 events with 100 pileup (low-momentum background) interactions per event. With 0% slop, the algorithm found no fake tracks, but fakes started to appear as slop was increased, with higher rates for higher slop. This is a good illustration of the trade-off between efficiency and fake rate.
CONCLUSION AND FURTHER WORK

This algorithm provides a good basis for the design of a Level-1 tracking trigger. Various adjustable parameters such as the $\phi$ windows and slope can be changed to optimize the algorithm. The values for these parameters lead to high efficiencies and low fake rates.

Much work still remains to be done on this project. Minor tweaks to the current algorithm, such as changing the implementation of slope or stub finding, might help performance. The performance of the algorithm should be evaluated for non-muon particles such as electrons or pions. The algorithm could also be tested with other proposed upgrade geometries. Finally, since the Level-1 Trigger will be implemented in FPGA hardware, further work will need to investigate the feasibility of coding the algorithm directly into high-speed electronics.

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Rachael Creager is a member of the Class of 2014 and currently lives in Breen-Phillips Hall. Rachael grew up in Clemson, S.C. and is a honors physics and mathematics double major. She has been a part of the Lannon-Hildreth trigger group since September 2011. This summer, Rachael will be at the Large Hadron Collider (LHC) in Geneva, Switzerland with the University of Michigan REU program performing research and learning more about high-energy physics. Rachael has a wide variety of academic interests, but hopes to pursue a Ph.D. in high-energy theory at a top research university after graduation.