

# SCIENTIA

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Undergraduate Research Journal for the Sciences  
University of Notre Dame

# A LETTER FROM DEAN CRAWFORD

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The College of Science at Notre Dame has every reason to be proud of its undergraduate researchers. The quality of the work they perform in labs and the quality of their publications give me confidence that they will go on to excel in their respective disciplines after they graduate from this University.

The pages of this journal offer glimpses into the many fascinating topics of research in the fields of mathematics, chemistry and biochemistry, biological sciences, and physics carried out by our undergraduate students. In discussing their research, they highlight various novel facilities and initiatives around campus, such as the Digital Visualization Theater, the new particle accelerator, the “green” approach to chemistry and even the Department of Applied and Computational Mathematics and Statistics.

The Scientia students join me in expressing gratitude to the Charles Edison Fund for supporting the printing of this publication. Many thanks to all the researchers for their hard work, and many thanks, likewise, to the team that has fashioned the results of the research into this attractive and informative publication.

Yours in Notre Dame,

Gregory P. Crawford, Ph.D.,  
William K. Warren II Foundation Dean of the College of Science

The Charles Edison Fund has generously supported the printing of this journal. The Fund is an extension of the benefactions and aspirations of its founder, Charles Edison, the son of Thomas Alva Edison, a man of discerning foresight, rare achievement and background.

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# FROM THE EDITORS

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We are pleased to present the second edition of *Scientia*, the journal of undergraduate science research at the University of Notre Dame. The journal brings together, over the course of the academic year, a dynamic group of undergraduates from every department in the College of Science to organize and edit the research of their peers.

With this issue, we hope to spotlight some of the scientific research being conducted by Notre Dame undergraduate students. From the mathematics of knots to malaria, leaf decomposition to supernovae, *Scientia* gives you a taste of the rich and diverse work of Notre Dame students. Additionally, our news articles spotlight just a few of the many exciting new developments in the College of Science, such as the construction of a second particle accelerator in Nieuwland Hall and the creation of the Department of Applied and Computational Mathematics and Statistics.

Beyond the publication, the 2010-2011 academic year has been a time of significant growth for the journal. In the Fall, we instituted a new meeting format that combined discussions of journal business with presentations from undergraduate and faculty researchers. These public meetings were conceived as an opportunity for Notre Dame students to come together as a research community founded on dialogue and discussion. The meetings' informal atmosphere—as embodied by our poster slogan, which invites students to come to the meetings and “Talk Science!”—has been met with great enthusiasm. The speakers covered a diverse range of topics, as featured on page 39. We look forward to continuing these dynamic meetings in Fall 2011 with additional faculty and undergraduate speakers.

Also of note, this year we gained a new funding source for the journal. Since the creation of the journal, the College of the Science and several other donors have been very supportive of *Scientia*'s activities. However, finding a permanent donor was always a concern of the journal staff. In December 2010, thanks to the efforts of the Deans Office of the College of Science, the Charles Edison Fund agreed to provide *Scientia*'s publication costs each year. This generous grant will greatly ease our financial burdens, not only for next year, but the foreseeable future.

To close, we thank all of the people whose efforts have made *Scientia* possible. This includes especially Dr. Gregory Crawford, Dean of the College of Science; the Staff of the Dean's Office; Dr. Dominic Chaloner, our faculty advisor; and the tireless enthusiasm of our phenomenal editors, reviewers, and layout team.

In Notre Dame,



Nancy Paul



Paul Baranay



*Scientia* Co-Editors-in-Chief

# CONTENTS

## NEWS

- 4 Digital Visualization Theater  
*Elizabeth Huschke*
- 5 New Applied Math Department  
*Robert Burkett*
- 6 A Brighter Future: Novel Application of NIR Imaging Dyes in Fluorescence Guided Surgery - *Patrick Kramer, Ricky Hennessey, and Brooke Conti*
- 8 New Accelerator's Construction in Progress - *Henry Gens*
- 9 The Growth of Green Chemistry  
*Yuko Gruber*

## MATH

- 10 Random Knot Games  
*John Pardo, Eva Forneaus, and Alex Leaf*



## BIOLOGY

- 17 Differences Between Native and Non-Native Leaf Decomposition in Juday Creek - *Katherine Baglini, Adam Lamm, and Kevin Towle*
- 22 Inconsistency of Conferred Immunity in *P. Falciparum* Malaria Hotspots and Implications for Immunization Development - *Annette Marie Ruth*

## PHYSICS

- 30 A Compound Method for Finding a Pattern in the Progenitor Systems of Type 1a Supernovae - *Julie Cass*
- 36 An Examination of Possible Gravitational Perturbations in the Transit Timing Variations of Exoplanet WASP-3b  
*Colin Littlefield*

### ◀ ON THE COVER

An image taken with the Hubble Space Telescope of planetary nebula NGC 2818. The nebula is the outer remains of an exploded star, NGC 2818 is located in the open star cluster Messier 46. Credit: NASA, ESA, and the Hubble Heritage Team. Hubble-Site News Center image STScI-2009-05 .

### ON THE BACK COVER

Lensing Galaxy Cluster Abell 383. Credit: NASA, ESA, J.Richard and J.P. Kneib. Hubble-Site News Center Image STScI-2011-12

# DIGITAL VISUALIZATION THEATER

By: Elizabeth Huschke

For many students, Notre Dame's Philosophy of Cosmology class is the closest thing to time travel they will ever experience. They get the opportunity to step inside the minds of people from pre-Galilean times and literally see the cosmos in an entirely new perspective. Best of all, they can do it without leaving the comfort of the Notre Dame campus.

The "time machine" that makes this experience possible is the Digital Visualization Theater (the DVT for short), which director Keith Davis calls, "the most sophisticated classroom on campus." The DVT is a fifty-foot diameter dome housed in Jordan Hall of Science that seats 136 students. It is a descendant of planetarium technology, but its founders intentionally avoided the word "planetarium" because they saw how the facility could enhance learning across the disciplines and did not want its use to be limited to astronomy and astrophysics.

The Philosophy of Cosmology class uses the DVT to illustrate the pre-Galilean view of the universe and then to simulate Galileo's observations. Later, when the class moves on to studying Kepler, the DVT is used again to present an interactive 3-D version of Kepler's model of the cosmos.

As its founders wished, the DVT's use has not merely been limited to displaying the cosmos. Biology, chemistry, theology, music, and art are just some of the diverse disciplines that have begun incorporating the DVT into the learning process. Today, five years after its opening, classroom use remains the DVT's number one priority. This fact makes the DVT unique among similar facilities throughout the nation - and even the world - that often emphasize research above teaching.

The DVT's power as a learning tool, Davis says, comes from the immersive feeling that its 360 degree dome provides. "Rather than simply looking at some-



Source: Notre Dame College of Science

thing, you are inside of that thing," he says. The DVT also has specialized software that allows presenters to interact with 3-D objects in real time. This means that professors can adapt their presentation on the spot in response to student questions or reactions.

A DVT lesson usually begins when a professor comes to Davis with an idea. Davis works with the professor to adapt the idea to the DVT's capabilities, and then he and a group of undergraduates do most of the actual program-

ming. Depending on the complexity, a lecture can take anywhere from one week to two years to put together.

The DVT has a successful past, and Davis has even grander visions for its future. He is working with the Center for Research Computing to get a plug-in that will make it easier to get research into the DVT. This will allow professors to incorporate research data and images into the

classroom. Davis, who was heavily involved in the local planetarium during his college years, also sees the DVT as a source of innovation that can be shared with other planetariums. With all these exciting new plans, the future of the DVT looks almost as bright as the stars and galaxies it so dazzlingly displays.

## NEW APPLIED MATH DEPARTMENT

By: Robert Burkett

One of the most exciting developments in the College of Science this year was the opening of the Department of Applied and Computational Mathematics and Statistics to undergraduates. Whereas the current mathematics degrees offered in the College of Science and the College of Arts and Letters focus on pure math—that is, math done solely for the purpose of advancing mathematical knowledge—applied math takes a more holistic approach. Applied math seeks to integrate mathematical knowledge with other subject areas, ranging from business to the hard sciences and social sciences, in order to solve problems in the real world. It is for these practical reasons that the website *The Chronicle of Higher Education* has ranked computational science in its top five fastest growing majors.

Under the direction of Dr. Steven Buechler, the two fields were separated to allow for the development of a good statistics department. While there is some overlap between the mathematics and applied mathematics curriculums, the applied mathematics curriculum focuses more on the problem-solving aspect of math instead of writing formal proofs. Furthermore, the curriculum can be adjusted to better fit a student's interests; students can choose a concentration in biology, economics or sociology. A supplementary major is also offered, which is a beneficial choice for students majoring in accounting or finance due to the strong background that statistics provides for actuarial science and financial risk analysis. Applied mathematics and statistics also prepare students for a number of other jobs, including those in engineering firms and pharmaceutical and medical device companies.

Besides the varied and interdisciplinary career opportunities open to students who pursue a degree in applied mathematics and statistics, another important career path is applied mathematics research. One of Dr. Buechler's latest research projects involved the creation of a mathematical model to aid in the treatment of breast cancer. Patients diagnosed with breast cancer can choose from several treatments, yet current tests are unable to determine the necessity of chemotherapy. By examining gene expression in cancerous tumors with the help

of microrays, doctors can determine if chemotherapy is unnecessary or required. While chemotherapy kills cancerous cells, the heavy toll it takes on healthy cells causes many to choose to go without it, which is often a fatal decision. Dr. Buechler remedied this problem through the analysis of microray data of breast cancer patients over a ten year period, eventually creating an algorithm that connected gene expression with chemotherapy effectiveness, thereby making it possible to select the most critical genes causing metastasis. If the cancer metastasizes, or spreads to other parts of the body, the result is usually fatal.

In a recent interview, Dr. Buechler expressed his vision for the department and its current progress. The program offers both an undergraduate degree and a doctorate in Applied and Computational Mathematics and Statistics. Currently there are nine faculty in the department, but Buechler would like to see that number grow to somewhere between fifteen and twenty. He also hopes to see significant developments in the department connected to the fields of biology, medicine, social sciences and engineering. Finally, he hopes to enlarge the graduate program and all educational programs within the department. The department is already in the process of reaching these goals; while Notre Dame currently has no statisticians, three will soon be hired. Furthermore, the department is developing a concentration in statistics which will be available soon, possibly at the beginning of next year.



Source: Notre Dame College of Science

# A BRIGHTER FUTURE: NOVEL APPLICATION OF NIR IMAGING DYES IN FLUORESCENCE GUIDED SURGERY

By: Patrick Kramer, Ricky Hennessey, and Brooke Conti

## Introduction

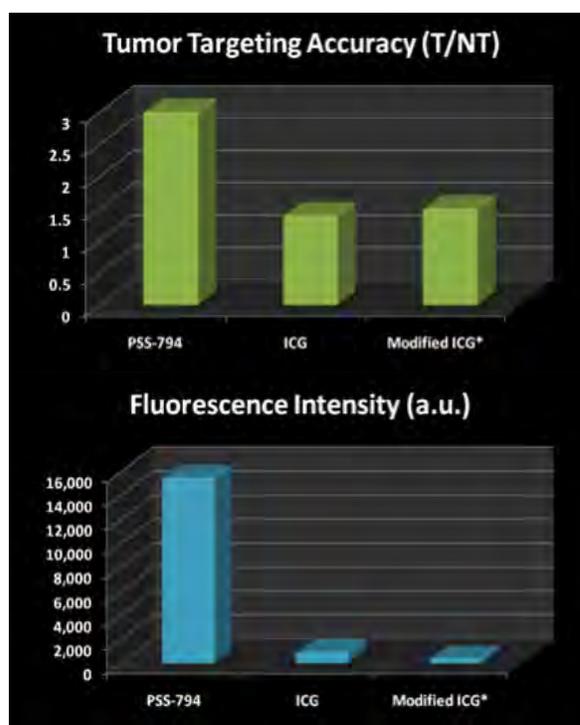
Cancer remains a central health risk in the 21st century, responsible for 13% of all deaths worldwide and affecting people of all ages, ethnicities, and genders [1]. Breast cancer, the third most common cancer, is generally unavoidable, as genetics play a larger role in the onset of the disease than personal life choices. According to the American Cancer Society, in 2010 over 200,000 women were diagnosed with breast cancer, affecting one in every eight American women [2].

Surgery is considered the first line of attack against breast cancer. Two current surgical procedures, mastectomies and lumpectomies, are readily available. Mastectomies involve the removal of the entire breast. It is a crude but usually successful option, although they are very extensive procedures and also require further surgeries to reconstruct the breast. The alternative surgery, a lumpectomy, preserves the appearance and sensation of the breast by only removing the tumor, but there remains a need for radiation therapy. In addition, there is a higher risk of developing a local recurrence of the cancer. Lumpectomies are less invasive, providing for a short recovery time, along with the ability to keep one's breast generally intact. A surgical technique known as fluorescence-guided surgery has the potential to greatly improve lumpectomies. The surgery uses dyes to target particular biomarkers in tumors, which glow when exposed to near-infrared light. In conjunction with a video display device, the tumors are illuminated on an LCD screen, allowing the surgeon to easily detect and extract malignant cells effectively and efficiently. Current products, such as methylene blue (MB) and indocyanine green (ICG), limit fluorescence-guided surgery because they are not effective at binding the cancerous cells, leaving the surgeon unsure as to whether the glowing regions seen on the monitor accurately represent the cancerous tissue [3]. This significantly increases the chances that the patient experiences a recurrent cancer, posing even more potential harm to the woman in question. Furthermore, these dyes reduce the effectiveness and the applications of fluorescence-guided surgery, keeping the "flashy" technology very impractical for large-scale implementation.

Dr. Bradley Smith, Professor of Chemistry and Biochemistry, is overcoming current imaging shortcomings of lumpectomies through the creation of brighter and more stable molecules that can be modified to be sited in specific surgical procedures [4]. One particular dye,

named PSS-794, has great potential, as it is sixteen-times more effective at binding to specific tissues than ICG (Figure 1).

Fluorescence-guided surgery using Dr. Smith's dyes has the opportunity to affect many different cancerous markets. The initial market, breast cancer, presents great opportunities for the use of this technique due to its large size and public awareness. Practical and effective fluorescent surgery for breast cancer will allow women to opt for lumpectomies instead of mastectomies more often. The worries of unnecessary breast removal, radiation, or chemotherapy will be drastically minimized, as surgeons will be absolutely sure of the location and presence of any stray tumor cells. Initial reports indicate that these near-infrared (NIR) dyes are also superior to existing products when used in imaging prostate tumors. [4]



**Figure 1.** Comparison of PSS-794 with popular dyes. PSS-794 is more than twice as accurate when attacking tumor cells. It also fluoresces at a much higher rate, nearly 16 times that of normal ICG.

## Image-guided Surgery

Imaging methods are crucial to optimizing surgical procedures, particularly oncological operations. However, the two most common techniques, basic ultrasound and x-ray fluoroscopy, are saddled with limitations. Ultra-

asound requires direct contact with body tissue, while x-rays expose the patient and doctors to radiation. A recent push in medicine to expand usage beyond these two techniques has led to a growing movement towards use of near-infrared (NIR) light techniques (wavelength range of 700 to 900 nm)

Currently, there are only two clinically available NIR fluorophores: ICG and MB. Attempts have been made to both improve and expand this field, as photobleaching (loss of fluorescence over time) and limited fluorescence excitation fluence rates (brightness) of these two dyes restrict full application of imaging techniques. The dye developed by Dr. Smith and his team at the University of Notre Dame has a distinctive ligand (secondary group) bonded to the base structure utilized in the indocyanine green probe that allows it to selectively target cells found in tumors better than the current options. They fluoresce in the near-infrared (NIR) spectrum (~775-2500 nm), which is advantageous because it allows for “minimal autofluorescence, less scatter, and high optical contrast” as opposed to regular fluorophores [4].

Anionic phospholipids, which are absent from the external leaflet of the plasma membrane of mammalian cells under normal conditions, become exposed on the outer surface of the cell in the event of cell death or damage. When the loss of asymmetry due to activation of the floppase enzyme occurs, the cell essentially flips. The probe, with the corresponding Zinc (II)-Dipicolylamine (Zn-DPA) ligand, targets these cells, which now contain exposed anionic phosphatidylserine (PS) molecules as the membrane no longer restricts the chemical from remaining in the interior, cytosolic part of the membrane. These dead and dying cells are found in most if not all tumor tissue. The two chemicals then associate, and, when the molecules are exposed to a near-infrared light (specifically at 794 nm), electrons are excited and fluorescence can be observed by appropriate equipment (i.e. cameras) at the source. This is known as PSS-794.

### Market

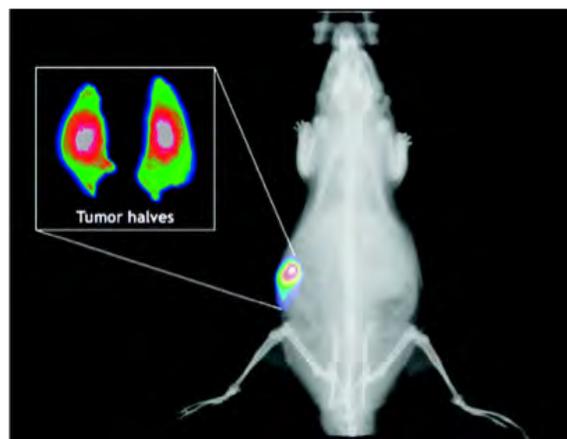
The 50,000 women who opt for lumpectomies annually are excellent candidates for fluorescence-guided surgery utilizing Dr. Smith's new and improved dyes. According to the National Institute of Health, “molecular imaging will become a powerful tool for biomedical research and will be synergistic component of research in molecular medicine that promises landmark improvements in clinical care” [5].

Methods utilizing fluorescence-guided surgery are most advanced in procedures involving gliomas in the brain. When compared to regular operations, 65% patients in a study assigned with the fluorescing compound had their tumors completely resected, compared with 36% of pa-

tients operated on under white light. This significant 29% boost in success rate has the potential to advance surgery to new, unforeseen levels of accuracy and precision [6]

It should be noted that no fluorophores have been FDA-approved for use in either breast cancer removals or sentinel lymph node mapping. However, with recent studies producing positive results, as well as the success of fluorescence-guided surgery for other types of cancer, the stage seems to be set for a movement towards developing and employing these powerful NIR dyes [7].

If a dye such as PSS-794 were to be brought to market, a series of steps would have to take place over many years, perhaps decades. Initial research would have to be completed, as issues such as water solubility have yet to be completely resolved. Then, however, the dyes could begin pre-FDA trials through tumor imaging in animals. The human trials are both extensive and expensive, and the best way to achieve success in this area may be to license the technology to a larger pharmaceutical company with the resources and time to complete the many tests. After those are complete, full scale manufacturing and sales to hospitals could take place immediately.



**Figure 2.** Zn-DPA probes selectively image tumors in a rat. Figure adapted from reference 4.

### Conclusion

By reducing guesswork, fluorescence-guided surgery enhances procedures by making them more cost-effective for the hospital, more efficient for the patient, and more exact for the doctor. Improved NIR fluorophores such as PSS-794 are the keys to making this proposition a reality, as brighter and more precise dyes are desperately needed.

### Acknowledgements

Dr. Bradley Smith, Erin Cole, and the other members of his lab at Notre Dame were extremely helpful advising and directing our studies. In addition, special thanks to Dr. Norbert L. Wiech and Dean Greg Crawford for their invaluable insights on our project.

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## NEW ACCELERATOR CURRENTLY IN PROGRESS

By: Henry Gens

Every five minutes on the website of Notre Dame's Institute for Structure and Nuclear Astrophysics one can view the updated construction progress via webcam of the Institute's newest addition: a vertical nuclear accelerator. The first component of the accelerator, appropriately named St. GEORGE (Strong Gradient Electro-magnetic Online Recoil separator for capture Gamma ray Experiments), arrived on January 4th and will be assembled by the end of 2011. The new accelerator was purchased with funds obtained from a National Science Foundation Major Research Instrumentation grant given to Dr. Michael Wiescher of the Physics Department in 2009. In all, the cost of the accelerator and the construction on Nieuwland Science Hall to accommodate it will be roughly \$5 million.

St. GEORGE will replace the old horizontal nuclear accelerator that was given as a gift to the University in 1995, as the old accelerator was becoming problematically outdated. "A key replacement part, namely the charging belt, for the existing 4MV single-ended accelerator was becoming nearly impossible to find," said Dr. Ed Stech, Associate Professional Specialist of the Department of Physics. "Without a good belt, this accelerator could not reliably provide the proton and alpha beam intensity needed to continue the nuclear astrophysics research in the Nuclear Science Laboratory." The new accelerator also allows the implementation of an Electron Cyclotron Resonance (ECR) source, which enables the researchers to use highly-charged ions at low velocity.

St. GEORGE will play an integral role in the future research of the Institute. "The new accel-

erator will greatly enhance the ability of researchers...to study the nuclear reactions taking place in stars throughout our universe," said Dr. Stech. The reactions in stars take place at a very slow rate, making them difficult to study. Such reactions create heavier elements and provide the energy for these stars. St. GEORGE will facilitate the research of these processes with new methods that maintain the traditional measurement techniques in use by the Nuclear Structure Laboratory. With such a powerful new tool on its hands, it is easy to see why completion of its construction is so highly anticipated.



Source: Notre Dame College of Science

# THE GROWTH OF GREEN CHEMISTRY

By: Yuko Gruber

The push to “go green” is sweeping across Notre Dame’s campus, manifesting itself in the form of dorm energy competitions, Waste-Free Wednesdays in the dining halls, and the club GreeND. Recently, the trend has spread from residential life to the laboratory, where “green chemistry” has transformed from a buzzword into a multi-faceted initiative changing the way chemistry is conducted at Notre Dame.

At its core, green chemistry is an effort to replace wasteful, hazardous chemical practices with more sustainable ones. It allows for the creation of the same products and utilizes many of the same techniques as more traditional forms of chemistry while employing milder reagents and more efficient reactions to reduce waste products and minimize the handling of noxious chemicals.

Dr. John Warner and Dr. Paul Anastas coined the phrase “green chemistry” in their book *Green Chemistry: Theory and Practice*, which outlines twelve principles of green chemistry. The principles serve as guidelines for increasing safety and sustainability in all forms of chemistry, from those performed in industrial plants to elementary school science fairs. Dr. Warner was invited to campus last fall to participate in Energy Week, an event sponsored by the Colleges of Science and Engineering, where he lectured to over 175 students in his keynote address.

Dr. Kathleen Peterson is at the forefront of the drive to bring green chemistry from theory to practice in Notre Dame laboratories, and began her efforts with her own students. Dr. Peterson teaches between 450 and 550 organic chemistry students in labs each semester, where she emphasizes the importance of sustainability with every experiment. “In the organic laboratories students evaluate the experiments they conduct in terms of the twelve principles of green chemistry, looking at which aspects of their procedure align with the principles and which don’t,” Peterson says. “I also invite them to suggest improvements to make our labs more sustainable.”

Green chemistry has the potential to revolutionize the chemical field, simultaneously offering economic, environmental and health benefits. Reactions carried out in water rather than in hazardous solvents, for example, are cheaper to supply, generate less waste and can significantly reduce the need for expensive equipment like fume hoods. Most importantly, they present fewer risks for chemists and consumers.



Source: Notre Dame College of Science

A particularly green experiment currently being conducted by Notre Dame students in Dr. Peterson’s laboratory involves the extraction of the molecule limonene from citrus fruits using dry ice. The same process is used commercially to decaffeinate coffee. “Coffee used to be decaffeinated using methylene chloride, a chemical now suspected to be a carcinogen. This is just one of many examples of how the green initiative is transforming chemistry,” Peterson says.

In addition to the small improvements made by students to lab procedures, junior chemistry major Tricia Stepanek works with Dr. Peterson to specifically research ways to better align teaching labs with the principles of green chemistry. Eventually, Dr. Peterson hopes to build a whole team of students working to develop new green experiments. Regardless of their level of involvement, though, Dr. Peterson aims to raise awareness of the implications of sustainability among her students. “I want them to be ambassadors of green chemistry,” she says.

# Random Knot Games

John Pardo<sup>1</sup>, Eva Fornaeus<sup>2</sup>, and Alex Leaf<sup>3</sup>

Advisor: Allison Henrich<sup>4</sup>

<sup>1</sup>University of Notre Dame, Department of Mathematics; <sup>2</sup>Stanford University; <sup>3</sup>Princeton University; <sup>4</sup>Seattle University

## Abstract

Taking a previously developed game involving mathematical knots, we changed the player who normally has the winning strategy so that they now play “randomly”. Using previous results for the class of twist knot shadows, we calculated the probability that the “loser” will win. Specifically, we found that on a twist knot with  $n$  crossings, if  $n$  is odd the knoter has a:

$$1 - \frac{1}{2^{(n-1)/2}(n+1)}$$

chance to win when going first and a:

$$1 - \frac{2^{(n-1)/2} + n + 1}{2^{(n+1)/2}(n+2)}$$

chance to win when going second, and if “ $n$ ” is even the player going first has a chance to win if they are knotting and a chance to win if they are unknotting. We will explain some knot basics, the original game, and our own results.

## Introduction and Knot Basics

One of the most effective ways to solve problems in mathematics is to play with various mathematical objects and see what results from those careless antics. When we first learned about mathematical knots and what previous teams had done with them in [2], we immediately started to play around with knots to see what more we could learn about them. We ended up playing a variant of a knot game we had learned about, and came up with some interesting developments. First, we must explain what a knot is to a mathematician. Since it is often very important to have a rigorous and concise definition in mathematics, a knot is defined as follows:

**Definition 1.** A knot is any embedding of the circle into 3-dimensional space.

Although it is true that this definition is rigorous and concise, it lacks any sort of motivation - we will now provide a more intuitive construction. Take a piece of rope with the property that we may stretch and twist and pull this rope all we want without breaking it. Now, tangle and tie this rope up to your heart’s content, and then glue the two ends of the rope together. Then the resulting object is

a mathematical knot. Notice that this does in fact coincide with our more precise definition: the fact that we live in three dimensions matches the 3-dimensional space part, the fact that matter in our world cannot be ‘co-located’ with other matter (that is, two distinct objects cannot share the same spatial location) matches the embedding part, the fact that we twisted the rope in any way we wanted matches the any embedding part, and the fact that we glued the ends of the rope together at the end matches the circle part. Pictured below are some examples of knots; such pictures are called knot diagrams. Please take notice of the Unknot, the most basic and thus the most important knot considered.

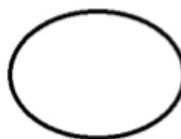


Figure 1a:  
The Unknot



Figure 1b:  
The Trefoil Knot



Figure 1c:  
A Celtic Knot

Now that we know what knots are, we can discuss some of the basic concepts needed for our game:

**Definition 2:** A knot shadow is a knot diagram without its crossings resolved. That is, in a knot shadow one does not know which strand is the over-strand and which strand is the under-strand. For this reason we call the crossings in a knot shadow precrossings.

The concept of a knot shadow is important because our game is played by turning a knot shadow into a knot diagram. Now we just need to answer one of the most fundamentally important questions in knot theory before we can move on to our game: how can we tell if two knots are the same knot? After all, if we were holding a knot in our hands and we decided to tangle and untangle the strands of the knot without ever breaking or cutting them, we would want to consider any resulting knot to be the same as the knot with which we started. But then if we are given two seemingly different knots, how can we tell that one can be contorted to match the other? To answer this question, let us introduce the concept of Reidemeister Moves, a set of three actions that can be performed on a knot that do not change the knot. The Type I Reidemeister Move allows one to remove (or introduce) a loop into the knot by crossing a strand over itself, the Type II Reidemeister Move allows one to pass one strand over or under another strand and the Type III Reidemeister Move allows one to pass a strand over or under a crossing (please notice that the strand must be either completely over or

completely under both strands involved in the crossing). These three maneuvers are pictured below:



**Figure 2a:**  
Type I

**Figure 2b:**  
Type 2

**Figure 2c:**  
Type 3

**Figure 2:** The Reidemeister Moves

It is obvious that the Reidemeister Moves do not appreciably alter the knot, but perhaps there are other ways we could alter a knot that are not encompassed in the Reidemeister Moves? In fact, it is a proven result of knot theory that two knots are the same if and only if each one can be made to match the other through a finite sequence of Reidemeister Moves. As a result, we can just focus on using Reidemeister Moves to determine the results of our game.

### The Game and How We Changed It

The basic knot game is quite simple. Given a knot shadow, two players take turns resolving precrossings on that shadow. That is, each player takes a turn picking one of the remaining unresolved crossings in the knot shadow and choosing which strand is the over-strand and which strand is the under-strand. The way the winner is determined is also simple - one player has the goal of ultimately making the unknot, and the other player wants the final result to be any other knot. In keeping with the Shakespearean theme of the original paper on this game and for ease of discussion, we will henceforth refer to the unknotter as Ursula and the knotter as King Lear.

It is a basic result of game theory that, given a game between two players such that the game must end after finitely many turns and such that the final configuration of the game must have a winner, one of the players in that game must have a winning strategy i.e. one player can be absolutely sure to win assuming that one player makes the best move at each stage of the game. Since each shadow has finitely many crossings and the final knot must either be the unknot or not the unknot, our game meets these conditions and so one of the players must have a winning strategy.

This knot game was originally developed by Henrich et al. in [2]. In their work, they determined the winning strategies for knot shadows of a special class of knots called twist knots. A twist knot is a knot that has two distinct “regions” of crossings, one of which has exactly 2 crossings, which we call the “clasp”, and the other of which has some positive number of crossings, which we

call the “twists.” The picture below provides examples of twist knots:



**Figure 3:** Some Examples of Twist Knots

And these are some examples of twist shadows:



**Figure 4:** Some Examples of Twist Shadows

Henrich et al. found that when the number of crossings in the twists is even the player who moves second has the winning strategy (regardless of whether they are knotting or unknotting), and that when the number of crossings in the twists is odd the unknotter has the winning strategy (regardless of whether they move first or second). We leave the proof of these results to the reader, as the coming discussion should make it clear how such proofs might work.

Given this knot game, we decided to make a slight alteration - we decided to change the way the “winner” (i.e. the player with the winning strategy) will play the game. Instead of making the best possible move at each stage, the winner will now make a random move, with each possible move having an equal probability. This brings us to the situation where there is a player who could be guaranteed to win but who does not necessarily win, thus giving the “loser” a non-trivial chance to win. Our work then became clear; we calculated the probability that the loser might win for the case of twist knots, and then attempted to expand our results to the more general  $m,n$ -twist knot (a twist knot where the clasp may have more than 2 crossings). We would like to emphasize that, although the probabilities calculated are important, it is the strategies themselves that are interesting. With that, let us take you through our thought process below.

### King Lear has a Winning Strategy

We will start with the case where the twist knot has an even number of twist precrossings and Ursula plays first. This is the only instance where King Lear has the winning strategy and is also the easiest case to work out. Before we consider this case however, let us clarify some of the

terms and techniques we will consider in our discussion. First, we introduce the concept of locking and unlocking the clasp. We call the clasp “locked” if it cannot be undone by a Type II Reidemeister Move, and we call it “unlocked” if it can be. These are both pictured below:



**Figure 5:**  
A Locked Clasp



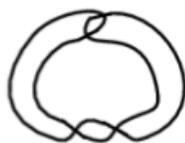
**Figure 6:** An Unlocked Clasp

This is a very important consideration because if the clasp is unlocked, the resulting shadow must be reducible to the unknot via a series of Type I Reidemeister Moves and so Ursula will always win in this situation. This is not the only way to make an unknot however.

It is also possible that two moves in the twists will be able to cancel each other using a Type II Reidemeister Move, as pictured below. Since only parity is important here, it does not actually matter that the moves be adjacent once the shadow is completely resolved. In the case of an even number of twists, it is possible to completely unknot the twists via Type II Reidemeister Moves and thereby turn the entire knot into the unknot via Type I Reidemeister Moves.



**Figure 7a:** Before



**Figure 7b:** After

**Figure 7:** A Partially Untwisted Twist via a Type II Reidemeister Move

Conversely, for a shadow having an odd number of twists, it is possible to reduce the twists to a single crossing, allowing the knot to be resolved in exactly one of the two ways pictured below.



**Figure 8a:** The Trefoil



**Figure 8b:** The Unknot

**Figure 8:** The Two Ways to Resolve a Twist Knot with One Twist

These are the means of creating the unknot from a knot shadow, and so the reader is encouraged to keep them in mind in reading this paper.

So now assume we are playing the game under the conditions above (there are an even number of twists and Ursula plays first) and that King Lear is playing “randomly.” Then we have the following result:

**Theorem 1.** *The probability for Ursula to win is*

$$P_n = 1 - \frac{1}{4(n+1)}$$

*This probability is the same regardless of whether Ursula starts in the clasp or in the twist.*

*Proof.* If Ursula starts by resolving one of the clasp pre-crossings, the probability that King Lear loses immediately by unlocking the clasp is:

$$\frac{1}{2(n+1)}$$

Moreover, if King Lear moves in the twist - an event which has probability:

$$\frac{n}{n+1}$$

Ursula can immediately win by unlocking the clasp on her second turn. So the only way King Lear can potentially win is by locking the clasp on his first turn, which has probability:

$$\frac{1}{2(n+1)}$$

So assume King Lear has locked the clasp. Now Ursula must be the first to move in the twists, which she does (it doesn’t matter what she does). King Lear must now move, and whatever he does will do one of two things; if his move matches Ursula’s, her next move must be to cancel his move in order to maximize her chances of winning they can win if they counter every move made by the unknotter with a move of the same sign, so that some pre-crossing, and if his move cancels out Ursula’s move with a Type II Reidemeister Move, it is as if Ursula is choosing a new first move for a shadow with 2 fewer twists. In fact, this will be the exact situation at every stage of play

until there is only one precrossing left in the twists, with King Lear having the final move. Because of Ursula's intelligent playing, all the resolved crossings will reduce to one crossing. Thus, King Lear can do one of two things: he can resolve the crossing so that a Type II Reidemeister Move will reduce the whole thing to the unknot, or he can resolve it so that it matches Ursula's final move and thus does not create the unknot. This second move is the only way King Lear will win, and he has a 1/2 chance of making each choice. Thus, King Lear has a total probability of winning of

$$\frac{1}{2(n+1)}(1/2) = \frac{1}{4(n+1)}$$

which accordingly gives Ursula a win probability of

$$P_n = 1 - \frac{1}{2(n+1)}(1/2) = 1 - \frac{1}{4(n+1)}$$

But now we must consider what could have happened if Ursula made her first move in the twists. So assume Ursula moves first in the twists. If King Lear ever plays in the clasp first, Ursula can then immediately unlock the clasp and guarantee a win. Thus, King Lear must keep making moves in the twists until Ursula is forced to move first in the clasp. The probability that he does this is

$$\frac{n-1}{n+1} \frac{n-3}{n-1} \cdots \frac{1}{3} = \frac{1}{n+1}$$

As before, King Lear must make his last move in the twists so that they do not all cancel out via Type II Reidemeister moves due to Ursula's clever playing, and he has exactly a 1/2 chance to do this. Then Ursula must move first in the clasp, and so King Lear will either lock or unlock the clasp with his final move. Since King Lear only wins if he locks the clasp at this time, his total chance of winning is

$$\frac{1}{n+1}(1/2)(1/2) = \frac{1}{4(n+1)}$$

which in turn gives Ursula a chance to win of

$$P_n = 1 - \frac{1}{4(n+1)}$$

Since this value matches our value above, we've shown that Ursula's first move does not affect his chance to win, completing the proof.

Again, this is the only case where King Lear had the winning strategy and so is also the easiest to consider, but

it should give the reader a taste of how the other, more difficult proofs will work.

### Ursula has a Winning Strategy

We will now look at the more complicated cases where Ursula has the winning strategy, starting with the other case for twist knots with an even number of crossings.

### The Number of Twists is Even and King Lear Goes First

Assume the number of twists is even and that King Lear plays first. Normally, Ursula has the winning strategy in this case, but since we are now assuming she plays randomly, King Lear has a chance to win. Thus, we have the following result in this situation:

**Theorem 2.** *The probability for King Lear to win is:*

$$P_n = 1 - \frac{2^{n/2} + 2n + 1}{2^{1+n/2}(n+1)}$$

*Moreover, it does not matter if King Lear makes his first move in the clasp or the twists.*

*Proof.* If King Lear makes his first move in the clasp, Ursula could immediately win by unlocking the clasp; since she is playing randomly, Ursula has a

$$\frac{1}{2(n+1)}$$

chance to do this. Conversely, Ursula has an equal chance of locking the clasp. In this case, King Lear and Ursula will take turns making moves in the twists, with King Lear playing first. Since the clasp is locked, the only way the knot could be the unknot is if the twist can be completely undone by Type II Reidemeister Moves. As a result, if Ursula ever makes a move that does not cancel out King Lear's last move with a Type II Reidemeister Move, King Lear can guarantee a win by also not cancelling out previous moves with a Type II Reidemeister Move. Thus, Ursula has a

$$\frac{1}{2} \frac{n}{2}$$

chance to win now, since she has a (1/2) probability of making the "right" move on each of her n/2 turns. If Ursula instead makes the most likely move to resolve one of the twist precrossings, King Lear can lock the clasp himself, once again ensuring that Ursula can win only if they every turn make a move with sign opposite to that of the last move in the twist. Thus, the total probability for victory for King Lear will be

$$P_n = \frac{1}{2(n+1)}\left(1 - \left(\frac{1}{2}\right)^{\frac{n}{2}}\right) + \frac{2n}{2(n+1)}\left(1 - \left(\frac{1}{2}\right)^{\frac{n}{2}}\right)$$

$$= \frac{2n+1}{2(n+1)}\left(1 - \left(\frac{1}{2}\right)^{\frac{n}{2}}\right) = 1 - \frac{2^{n/2} + 2n + 1}{2^{1+n/2}(n+1)}$$

Each precrossing in a shadow can be resolved to be either positive or negative. Of the possible Reidemeister Moves that can be made in a knot, the one most relevant to these probabilities is the Type II Reidemeister Move, through which two adjacent twists of opposite signs can be removed from a knot or a partially solved shadow. To simplify our notation, we will assume that the first move in any knot is positive. If, on the other hand, King Lear makes his first move in one of the twist precrossings in order to wait for Ursula to move in the clasp, his probability of winning can be calculated as follows:

If Ursula moves in the clasp, King Lear can also move there to lock it. Ursula can then only win if they resolve each precrossing in the twist in such a way that it can be removed by a Type II Reidemeister Move, meaning that for  $n/2$  turns she must make the opposite move to that of King Lear.

If Ursula makes the opposite move in the twist so that the resolved crossings can be removed by a Type II Reidemeister Move, the probability of victory for King Lear is reduced to the probability of victory in a twist knot with  $n - 2$  precrossings in the twist.

If Ursula makes a positive move in the twist, King Lear can resolve yet another precrossing to be positive, thus making it impossible for Ursula to unknot the twist. Then the only chance for Ursula to win is if they keep playing in the twist and thus force King Lear to move first in the clasp, as above. Even if Ursula does manage to force King Lear to make the first move in the clasp, she still only has a  $1/2$  chance to unknot the clasp. The chance of Ursula winning is thus

$$\frac{n-3}{n-1} \frac{n-5}{n-3} \frac{3}{5} \frac{1}{3} \frac{1}{3} \frac{2}{2}$$

since there are always two more possible crossings for her to act in than there are twist precrossings left. This simplifies to  $1/(2(n+1))$ , so the overall probability for King Lear to win is

$$P_n = \frac{2}{n+1}\left(1 - \left(\frac{1}{2}\right)^{\frac{n}{2}}\right) + \frac{n-1}{2(n+1)}P_{n-2} + \frac{n-1}{2(n+1)}\left(1 - \frac{1}{2(n-1)}\right)$$

$$= \frac{2}{n+1}\left(\frac{2^{n/2}-1}{2^{n/2}}\right) + \frac{n-1}{2(n+1)}P_{n-2} + \frac{n-1}{2(n+1)}\left(1 - \frac{1}{2(n-1)}\right)$$

$$= \frac{2^{n/2}-1}{2^{1+n/2}(n+1)} + \frac{n-1}{2(n+1)}P_{n-2} + \frac{2n-3}{4(n+1)}$$

Through a proof by induction we can show that it does not matter whether King Lear makes his first move in the twist or the clasp. For this we want to show that if the probability of winning when starting in the clasp in a  $(n - 2)$ -twist knot is plugged into the equation for the probability of winning when starting in the twist in a  $n$ -twist knot, the probability of winning when starting in the clasp in the same  $n$ -twist knot is obtained. This means that what we want to show is

$$P_n = 1 - \frac{2^{n/2} + 2n + 1}{2^{1+n/2}(n+1)} = \frac{2^{n/2}-1}{2^{n/2-1}(n+1)} + \frac{n-1}{2(n+1)}P_{n-2} + \frac{2n-3}{4(n+1)}$$

For the base case, we have calculated the probabilities for the knoter to win in the twist knot where there are 2 crossings in the twist, and found this to be  $7/12$ . The knot with no crossings in the twist is just the unknot, and such a shadow guarantees that the unknotter wins, and if this is used as a value for  $P_{n-2}$ , the above equation is correct for the  $P_2$ -case.

Suppose by the induction hypothesis that

$$P_{n-2} = 1 - \frac{2^{(n-2)/2} + 2(n-2) + 1}{2^{1+(n-2)/2}(n-2+1)}$$

(we are assuming our result for a twist knot with  $n - 2$  crossings in the twists in order to prove it for a twist knot with  $n$  crossings in the twists). Along with our work above, this gives us

$$P_n = \frac{2^{n/2}-1}{2^{n/2-1}(n+1)} + \frac{n-1}{2(n+1)}P_{n-2} + \frac{2n-3}{4(n+1)}$$

$$= \frac{2^{n/2}-1}{2^{n/2-1}(n+1)} + \frac{n-1}{2(n+1)}\left(1 - \frac{2^{(n-2)/2} + 2(n-2) + 1}{2^{1+(n-2)/2}(n-2+1)}\right) + \frac{2n-3}{4(n+1)}$$

$$= \frac{2^{n/2}-1}{2^{n/2-1}(n+1)} + \frac{n-1}{2(n+1)}\left(\frac{2^{n/2}(n-1) - 2^{n/2-1} - 2n + 3}{2^{n/2}(n-1)}\right) + \frac{2n-3}{4(n+1)}$$

$$= \frac{4(2^{n/2}-1)}{2^{1+n/2}(n+1)} + \frac{2^{n/2}(n-1) - 2^{n/2-1} - 2n + 3}{2^{1+n/2}(n+1)} + \frac{2^{n/2-1}(2n-3)}{2^{1+n/2}(n+1)}$$

$$= \frac{4(2^{n/2}) - 4 + 2^{n/2}n - 2^{n/2} - 2^{n/2-1} - 2n + 3 + 2^{n/2-1} * 2n - 3(2^{n/2-1})}{2^{1+n/2}(n+1)}$$

$$= \frac{3 * 2^{n/2} - 1 + 2 * 2^{n/2}n - 4 * 2^{n/2-1} - 2n}{2^{1+n/2}(n+1)} = \frac{3 * 2^{n/2} - 1 + 2^{1+n/2}n - 2 * 2^{n/2} - 2n}{2^{1+n/2}(n+1)}$$

$$= \frac{2^{1+n/2}(n+1) - 2^{n/2} - 2n - 1}{2^{1+n/2}(n+1)} = 1 - \frac{2^{n/2} + 2n + 1}{2^{1+n/2}(n+1)}$$

This means that the probability that King Lear wins is equal regardless of whether he first resolves a twist-precrossing or a clasp-precrossing for any number of crossings in the twist. This completes our proof.

**The Number of Twists is Odd and King Lear goes First**

For the case where there is an odd number of twist precrossings, King Lear never has a winning strategy, as shown by Henrich et al. [2]. Let us first consider the case where King Lear moves first against a random Ursula.

**Theorem 3.** *The probability for King Lear to win is*

$$P_n = 1 - \frac{1}{2^{(n-1)/2}(n+1)}$$

*The best strategy for King Lear is to move in the twist first.*

*Proof.* Let us first consider King Lear’s chances of winning if he starts in the clasp. If Ursula then unlocks the clasp, King Lear will certainly lose. However, since King Lear will make the last move of the game (because there are an odd number of total twists), he can always ensure that the shadow will knot if Ursula makes any other first move. Regardless of whether Ursula knots the clasp on her first turn or if King Lear does so himself on his second turn, King Lear will have the choice in his last turn to either make a trefoil knot if Ursula managed to make all earlier twists removable through Type II Reidemeister Moves, or to make sure that there are at least three crossings with the same sign in the twist in the final knot. Thus, King Lear’s chance of winning is

$$1 - \frac{1}{2^{(n+1)}}$$

his first move is in the clasp.

However, King Lear can do even better if he instead moves first in the twist. If Ursula should move in the clasp at any point before all twist precrossings are resolved, King Lear can win by knotting the clasp and then, through the same strategy as before, ensure that the final knot is either the trefoil or has at least three crossings of the same sign in the twist. Ursula can only win if she keeps making the opposite move in the clasp each turn for  $(n - 1)/2$  turns and then in the clasp resolves one crossing to have the opposite sign to the only remaining crossing in the twist. As we saw before, the probability that Ursula does not play in the clasp until the last turn is

$$\frac{n-1}{n+1} \frac{n-3}{n-1} \cdots \frac{3}{5} \frac{1}{3} = \frac{1}{n+1}$$

so the total probability that King Lear wins is

$$P_n = 1 - \frac{1}{n+1} \frac{1}{2^{(n-1)/2}} = 1 - \frac{1}{2^{(n-1)/2}(n+1)}$$

Since this probability is higher than the one calculated for when King Lear starts by moving in the clasp, the King Lear should make his first move in the twist to maximize his chance of winning.

**The Number of Twists is Odd and King Lear goes Second**

Now let us consider the case where King Lear goes second in a knot with an odd number of crossings in the twist, while playing against a random Ursula:

**Theorem 4.** *The probability for King Lear to win is*

$$P_n = 1 - \frac{2^{(n-1)/2} + n + 1}{2^{(n+1)/2}(n+2)}$$

*The best strategy for King Lear is to move in the clasp first regardless of Ursula’s first move.*

*Proof.* If Ursula’s first move is in the clasp, King Lear should move in the clasp to lock it. If after that Ursula makes even one positive move in a twist precrossing, King Lear has already won, since even if Ursula makes a negative move every turn from then on, strategic playing by King Lear will result in a knot with three positive crossings, which is the trefoil knot. Only if Ursula makes a negative move every turn after her first does she have a chance to win, and the probability of this is only  $1/2$  each turn for  $(n + 1)/2$  turns.

If, on the other hand, Ursula starts by making one of the twist precrossings positive, King Lear can move either in the clasp or in the twist. Let us treat these two cases separately, and call the probability that King Lear wins in this case  $P'_n$ .

1. If King Lear moves in the clasp, his optimal strategy is to resolve one of the clasp precrossings to be positive. Then Ursula has a  $1/2n$  possibility of winning immediately by making unlocking the clasp. However, Ursula is guaranteed to lose if she locks the clasp. By resolving yet another precrossing in the twist to be positive, King Lear can guarantee that the final knot will necessarily have at least three positive crossings - regardless of how many precrossings Ursula resolves to be negative - and thus make it so that the final knot cannot be the unknot.

The result is very similar if Ursula moves in the twist by resolving a precrossing to be positive.

Conversely, if Ursula makes a negative move in the

twist, she can still win if she continues resolving precrossings so that the previous move of King Lear can be cancelled out through a Type II Reidemeister Move. She would have to do this for  $(n - 1)/2$  turns, so the probability that King Lear wins is

$$P'_n = 1 - \left( \frac{1}{2n}(1) + \frac{1}{2n}(0) + \frac{n-1}{2n}(0) + \frac{n-1}{2n}(1/2)^{(n-1)/2} \right) = 1 - \frac{2^{(n-1)/2} + n - 1}{2^{(n+1)/2}n}$$

2. Had King Lear instead chosen to move in the twist, once again moving optimally so that the two crossings have the same sign, he is once again guaranteed victory if Ursula resolves a clasp precrossing to be positive, as he can then simply lock the clasp. If Ursula resolves the clasp so that one of the crossings is negative, King Lear should lock it by making the other clasp crossing negative too, although he might still lose if Ursula then makes negative crossings in the twist for their remaining  $(n - 1)/2$  turns. If Ursula instead makes a positive move in the twist, King Lear will lose only if Ursula keeps playing in the twist and thus force him to move first in the clasp - she must then counter his move. The probability of this occurring is

$$\frac{n-4}{n-2} \frac{n-6}{n-4} \cdots \frac{1}{3} \frac{1}{2} = \frac{1}{2(n-2)}$$

This probability is the same if Ursula makes a negative move in the twist, since King Lear can choose which way to resolve the clasp if he is forced to play first in the clasp. Thus, the probability that King Lear wins in this case is

$$P'_n = 1 - \left( \frac{1}{2n}(0) + \frac{1}{2n} \left( \frac{1}{2} \right)^{\frac{n-1}{2}} + \frac{n-2}{n} \frac{1}{2(n-2)} \right) = 1 - \left( \frac{1}{2n} \left( \frac{1}{2} \right)^{\frac{n-1}{2}} + \frac{1}{2n} \right)$$

## Conclusion

Once we considered all the relevant cases for twist knot shadows, we moved on to general  $m, n$ -twist knots i.e. knots with  $m$  crossings in the clasp. However, this class of knot shadows is significantly more complicated and so we've omitted that work here. Nevertheless, the reader should now have a sense of how to work with mathematical knots now. For those interested in learning more on knots in general, we suggest Colin Adams' book [1], and for those who want to better understand the knot game we've discussed, please see the work by Allison Henrich and her last REU team [2].

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## About the Author

**Jake Pardo** is a senior Physics and Honors Mathematics double major from Rochester, New York. He has spent two summers doing math at Notre Dame and a third at the University of Washington, during which he helped with the research that led to his team's paper "Random Knot Games." After graduating, he intends to pursue a Ph.D in Mathematics.

# Differences Between Native and Non-Native Leaf Decomposition in Juday Creek

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## Abstract

*Differences in the rates of decomposition in native and non-native species are becoming increasingly important as invasive species create larger impacts on natural communities. These differences can disrupt natural nutrient cycles. Decomposition was compared among species found on the campus of the University of Notre Dame: white pine (*Pinus strobus*), sugar maple (*Acer saccharum*), Austrian pine (*Pinus nigra*), and Norway maple (*Acer platanoides*). Rates of decomposition were measured over a three week period after being placed in Juday Creek, a third order stream running through the campus of the University of Notre Dame. Decomposition occurred faster in the native than the non-native tree species, and deciduous trees decomposed faster than coniferous trees. Invertebrate abundances were measured after three weeks of decomposition in the stream, but among species were not statistically significant.*

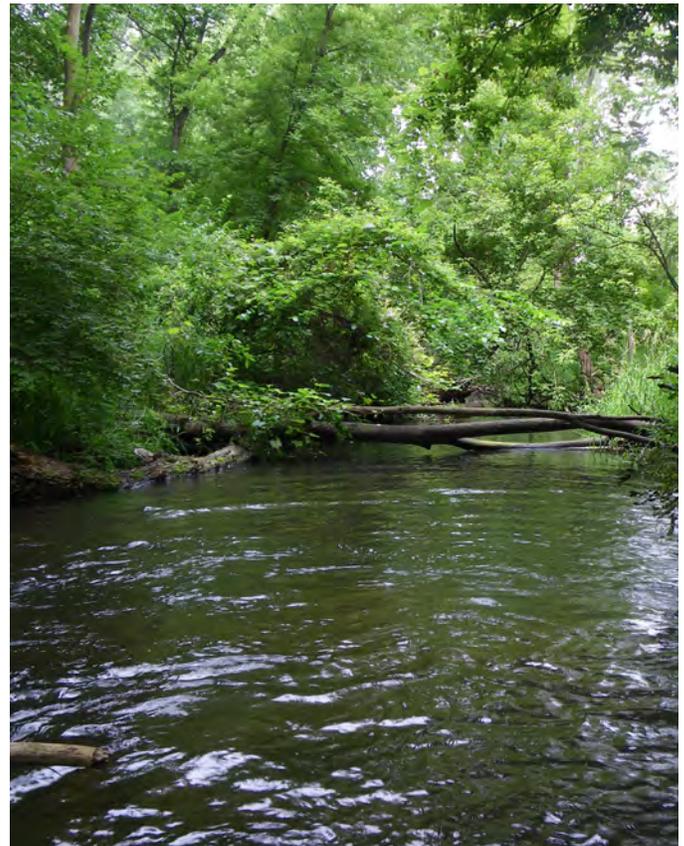
## Introduction

Leaf decomposition plays a key role in nutrient cycles and energy transfer in natural habitats. In addition, invasive and non-native species can seriously damage the health of a habitat, especially if the invasive species has a life cycle which has a different timing at key events than native species. Such differences can render leaf litter inaccessible to decomposers, keeping key nutrients from re-entering the habitat, and lowering the terrestrial carrying capacity. Decomposition rates are dependent on leaf lignin content, with higher lignin concentrations yielding slower rates of decomposition [1]. The same concept also applies to tannin content, which blocks bacterial colonization [2].

Previous studies comparing decomposition rates between native and non-native plants have yielded conflicting results. A previous study found that a non-native Japanese knotwood tree decomposed at a similar rate to native ash and cottonwood trees [3]. On the contrary, a study looking at decomposition of an invasive shrub

(*Lonicera maackii*) and two native species (*A. Saccharum* and *Quercus rubra*) found that leaf decomposition was 21 times faster with an invasive shrub than a native species [4]. Few studies have compared native to non-native trees of the same family. One that did compare decomposition in pairs of native and non-native species found a faster decomposition rate in native than non-native species [5].

This study aims to further the study of decomposition among native and non-native species. White pine (*Pinus strobus*), sugar maple (*Acer saccharum*), Austrian pine (*Pinus nigra*), and Norway maple (*Acer platanoides*) were used in the study, all of which were found on the campus of the University of Notre Dame. These species have been chosen for similar leaf structure in order to minimize extraneous variables (B. Hellenthal, personal communication). We hypothesized that the native species (white pine and sugar maple) will decompose faster than the non-native species (Austrian pine and Norway maple), because the invertebrate populations responsible for leaf decomposition have evolved to the native species, and will be better adapted for the timing of its life cycle. Invertebrate abundance was used to observe any invertebrate preference between native and non-native species.



Source: Patrick Shirey

**Figure 1.** Study site within the Warren Golf Course, Notre Dame, Indiana. Juday Creek is a modified stream which flows from Granger, Indiana, into the St. Joseph River.

## Methods

### Description of Study Site

Juday Creek is a third order stream that flows from Granger, Indiana into the St. Joseph River. The stream underwent restoration when the Warren Golf Course, which opened in 2000, was built on the campus of the University of Notre Dame (R. Hellenthal, personal communication). The portion of the creek that meanders through the golf course was re-routed by a stream restoration contractor, in order to minimize the environmental impact that the golf course's construction had on the trout population present in the stream (Figure 1).

### Leaf Bag Preparation and Processing

Nine 21cm by 39cm polypropylene leaf bags 3mm x 3mm mesh size were filled with 15.0 (+/- 0.1g) of dry leaf litter from each species: white pine, Austrian pine, Norway maple, and sugar maple. One bag from each species was attached to a piece of metal rebar secured in the streambed, with two sets of bags at each site. Bags were placed at three replicate sites, using a flow meter with depth gauge to ensure all three sampling sites had similar depth and water flow. Leaf bags were placed along the edge of the stream so that the slower river current would remove less leaf litter than faster currents, while maintaining ample current for abrasion. After one week in the stream, one piece of rebar and the attached bags was removed. After three weeks, the final replicate of leaf bags was removed. Three replicates of each species were removed and weighed to account for leaf loss during handling and processing.

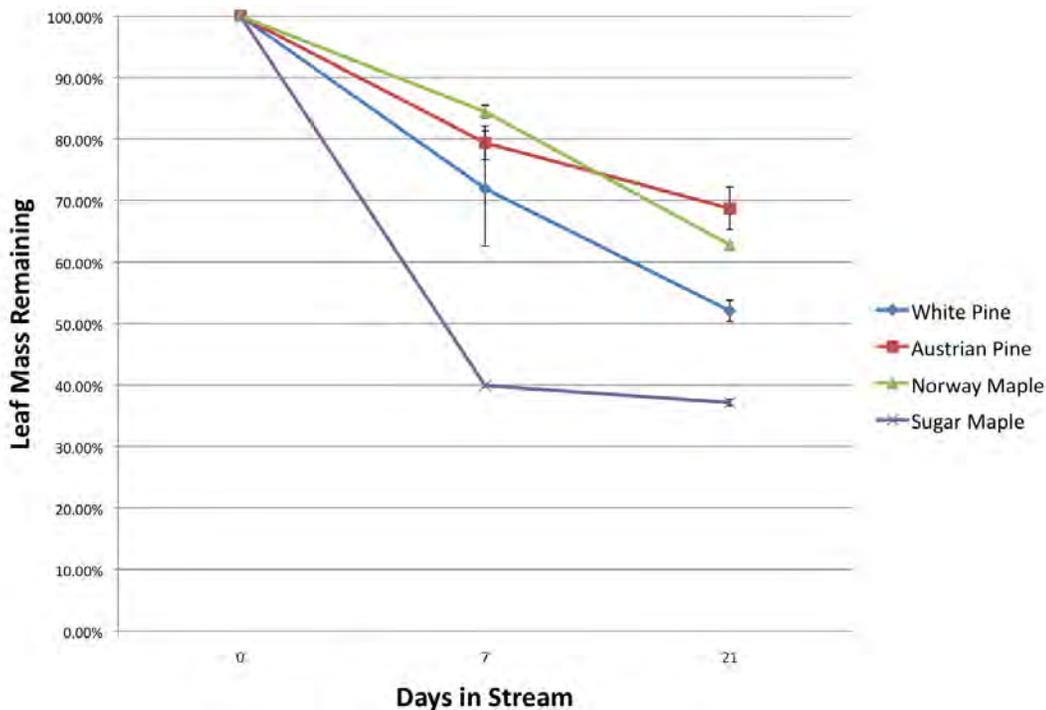
After the predetermined time in the stream, the leaf content was removed and washed to remove accumulated silt, and dried in an oven at 60°C for a minimum of 24 hours. After drying, leaves were again weighed. A two way ANOVA was used to compare leaf decomposition rates between native and non-native tree species, as well as between coniferous and deciduous tree species.

### Aquatic Invertebrate Abundance

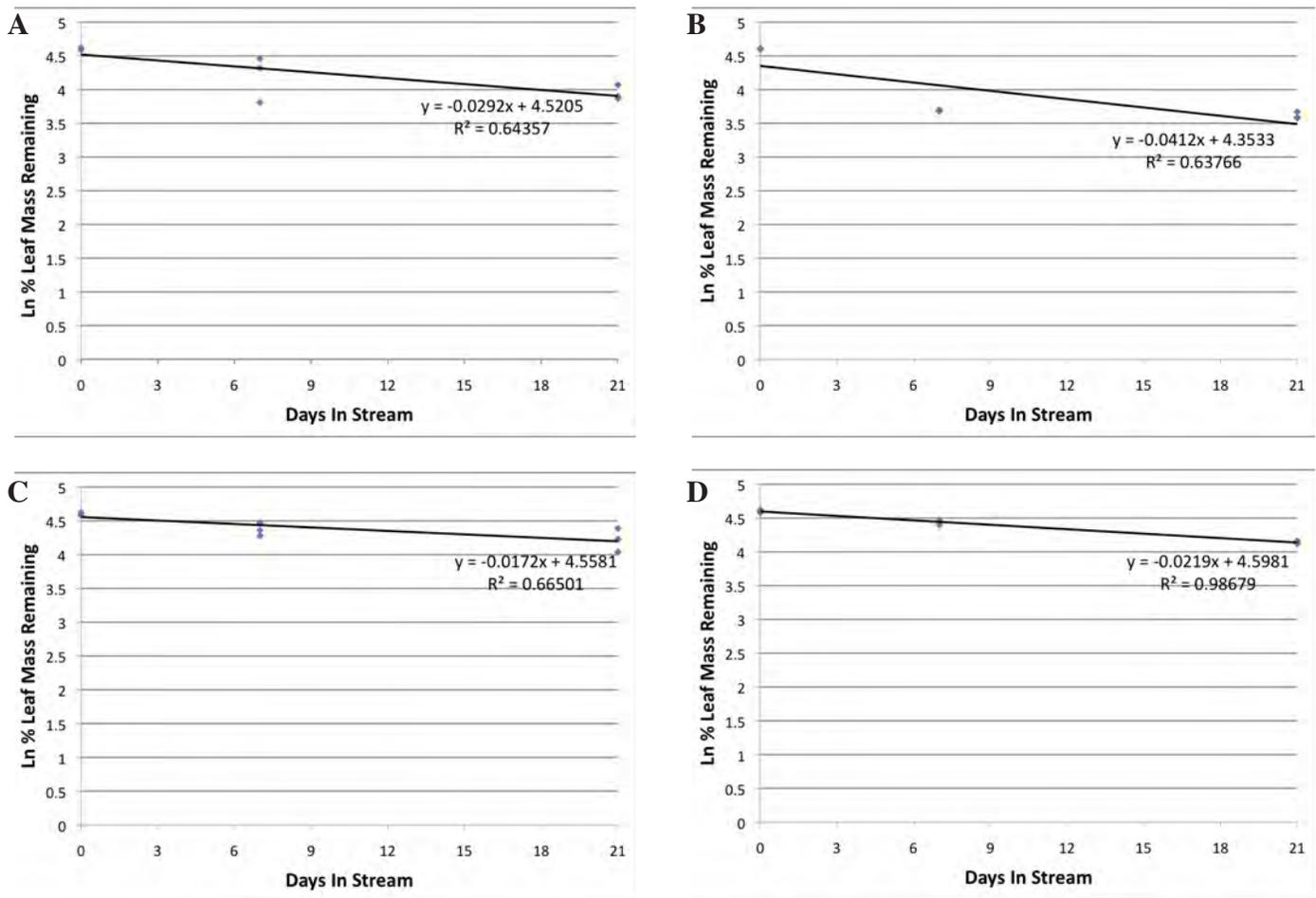
After 3 weeks in the creek, prior to drying at 60°C, the leaves in the samples were washed individually over a 250µm screen with distilled water to collect aquatic invertebrates. Aquatic invertebrates were washed from the screen and preserved in a vial filled with ethanol. After preservation, invertebrate abundance was determined for each replicate. A two way ANOVA compared invertebrate abundance between both native and non-native species, as well as between coniferous and deciduous tree species.

## Results

The rates of decomposition in deciduous species were significantly higher than in coniferous species ( $F_{1,11}(6.24)$ ,  $P=0.0371$ , Table 1, Figure 2). The rates of decomposition in native species was significantly higher than in non-native species ( $F_{1,11}(32.02)$ ,  $P=0.0005$ , Table 1, Figure 2). White pine decomposed at a rate of 0.0297 days<sup>-1</sup> (Figure 3), Austrian pine decomposed at a rate of 0.0173 days<sup>-1</sup> (Figure 3), sugar maple decomposed at a rate of 0.0412 days<sup>-1</sup> (Figure 3), and Norway maple decomposed at a rate of 0.022 days<sup>-1</sup> (Figure 3).



**Figure 2.** Percent leaf mass remaining. Leaf mass remaining measured after 1 week and 3 weeks in the stream.



**Figure 3.** Ln (% leaf mass remaining) for all four species tested. A=white pine, B=sugar maple, C=Austrian pine, D=Norway maple. Coefficients of decomposition are listed, in addition to the corresponding  $R^2$  value.

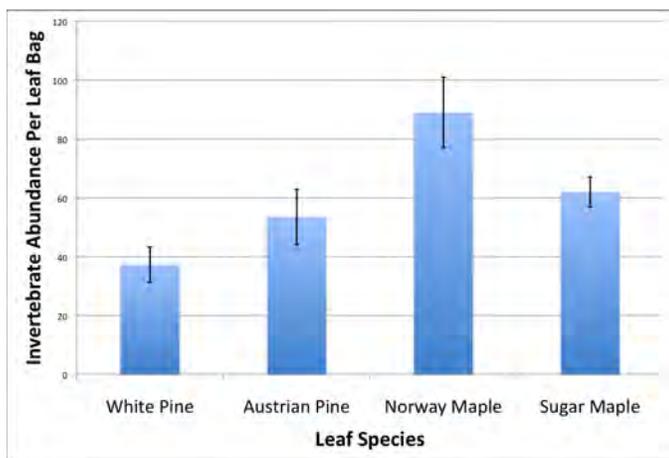
### Leaf Decomp

Source of Variation	Sum-of-Squares	df	Mean-Square	F-ratio	P-value
Type	5.45	1	5.45	6.24	0.0371
Location	27.98	1	27.98	32.02	0.0005
Type x Location	2.56	1	2.56	2.93	0.1253
Error	6.99	8	0.87		
Total	42.92	11			

### Inverts

Source of Variation	Sum-of-Squares	df	Mean-Square	F-ratio	P-value
Type	2730.08	1	2730.08	3.1	0.1163
Location	1386.75	1	1386.75	1.57	0.2456
Type x Location	90.76	1	90.76	0.1	0.7599
Error	7049.33	8	881.17		
Total	11256.92	11			

**Table 1.** Two-way ANOVA tests for both leaf decomposition (calculated using leaf mass remaining after 3 weeks in Juday Creek) and invertebrate abundance. Both deciduous versus coniferous and native versus non-native differences in decomposition were statistically significant. The interaction of the two was not statistically significant. No comparison was statistically significant for invertebrate abundance.



**Figure 4.** Average invertebrate abundance for the four species sampled after 3 weeks in Juday Creek. Standard error bars are shown.

The relationship between species type and origin for rate of decomposition was not significant ( $F_{1,11}(2.93)$ ,  $P=0.1253$ , Table 1). The invertebrate abundance showed no significant difference between species type ( $F_{1,11}(3.1)$ ,  $P=0.1163$ , Table 1). The invertebrate abundance showed no significant difference between differing origins ( $F_{1,11}(1.57)$ ,  $P=0.2456$ , Table 1). The relationship between species type and origin for invertebrate abundance showed no significant difference ( $F_{1,11}(0.1)$ ,  $P=0.7599$ , Table 2). Invertebrate abundance showed the general trend that non-native species had greater abundance than native species (Figure 4).

## Discussion

Previous studies comparing decomposition rates between native and non-native tree species have yielded conflicting and confusing results. Braatne et al. (2010) found similar rates of decomposition between a Japanese knotwood tree and a native cottonwood tree, while Blair et al. (2009) found that decomposition occurred 21 times faster in a non-native shrub species than it did in a native shrub. Godoy et al. (2010) compared native and non-native pairs and found that decomposition occurred faster in the native species than in its non-native pair. With such conflicting and confusing results, it is hard to draw any concrete conclusions, especially with so many sources of variation unaccounted for in previous studies.

This experiment sought to eliminate extraneous variables, by testing two pairs of species, one coniferous and one deciduous, which were chosen because of similar leaf morphology. By controlling for leaf morphology, we could eliminate a source of variation in the study (B. Hellenenthal, personal communication). In previous studies, if invertebrates more easily decompose one leaf structure than another, it would decompose faster than the other species studied, regardless of whether it was native or

non-native. Godoy et al. (2010) had the one study that looked at decomposition in pairs of similar species, and our research supports their conclusion; native species decomposed faster than non-native species. Similarly, to ensure that our leaves decomposed at rates that we expected, we measured decomposition between deciduous and coniferous trees, and found that the deciduous trees did decompose faster than coniferous as expected (B. Hellenenthal, personal communication). This is likely due to an interaction of factors such as higher tannin and lignin contents, and these differences have been noted throughout the primary literature<sup>1,2</sup>.

This study also expands on exploring possible sources for variation in decomposition rate between native and non-native species, something that has been largely absent from the literature. Many studies simply measured decomposition rates without measuring invertebrate abundance to help determine what makes a species decompose faster. This study found that differences in invertebrate abundance were not statistically significant, the same result that Braatne et al. (2007) found. There were problems with collecting invertebrates, which stem from leaf morphology, because deciduous trees have a greater leaf surface area for invertebrates to graze upon than coniferous trees. The streamlined nature of pine needles likely made it difficult for invertebrate decomposers to remain in the sample without being forced downstream by the current. This may explain why maple species had more invertebrates on its leaves than pine species, albeit not statistically significant.

A future modification to this experiment would include the use of tighter mesh bags to reduce the potential of extraneous loss of white pine needles due to water current. Decomposition bags would be designed with smaller holes to retain the needles, but large enough to allow for the colonization of the litter by invertebrates. Time constraints forced this experiment to take place in an aquatic environment to take advantage of higher rates of decomposition than those of terrestrial habitats, but future studies should examine the difference in invertebrate abundance between native and non-native trees in terrestrial habitats. Invertebrates should also be classified (not done in this experiment due to time constraints), because there may be a difference in key decomposers that makes a difference in decomposition rate, and not sheer invertebrate abundance. One possible source of variation in decomposition rate would be differing proportions of grazers, collectors, shredders, and predators (R. Hellenenthal, personal communication). Similarly, it is difficult to apply the findings of two pairs of leaf species to all species: native and non-native, deciduous and coniferous. Therefore this experiment should be expanded upon, just like the work of Godoy et al. (2010), and find more relat-

ed native and non-native species to test, perhaps even expanding into taxa such as shrubs, grasses, and agricultural vegetation. Results from this increased research protocol could inform management efforts on the implications of non-native plant invasion on ecosystem health

### Acknowledgements

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# Inconsistency of Conferred Immunity in *Plasmodium falciparum* Malaria Hotspots and Implications for Immu- nization Development

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## Abstract

Newborn infants in malaria-endemic regions are markedly resistant to *Plasmodium falciparum* malaria. Such protection is related principally to the transplacental transfer of maternal variant surface antigen (VSA)-specific immunoglobulin G antibodies, which confer immune resistance for approximately the first six months of life. During this period, infections tend to be low-density and relatively asymptomatic, as in adults who have naturally acquired immunity (NAI). After this passive immunity diminishes, children have increased susceptibility to severe infection for one to two years before they acquire active immunity, the maintenance of which requires repeated parasite exposure. Genetic variability of the human parasite, parasite-induced immunosuppression, and transmission heterogeneity largely account for this discontinuity. These factors also have been shown to inhibit NAI in areas of high endemicity, or hotspots, widening the susceptibility period and increasing the risk of acute infection among children. The resulting inconsistency of timing and duration of childhood susceptibility poses an epidemiological challenge in determining immunization strategies suitable for large populations, prompting the necessity to consider region-specific factors in vaccine development. The complexity of the *Plasmodia* parasites and their life cycles dictate the need for novel approaches to vaccine design, the most promising of which are recombinant DNA strategies that target the most stable components of parasitic genomes.

## Introduction

Although children under five years of age typically face a high risk of malaria-related morbidity and mortality in malaria-endemic regions, infants enjoy relative im-

munity from infection [1]. The greatest protection from *Plasmodium falciparum* malaria infection occurs during the first few months of life, and infants often are fully protected until the age of 12 months [2],[3],[4]. However, not until the age of five years do most children develop sufficient active immunity to reduce the risk of death from *P. falciparum* malaria over the long term. This active immunity provides protection against severe disease and reduces the frequency of clinical malaria episodes. Low levels of susceptibility in infancy result from the passive transfer of maternal anti-*Plasmodium* antibodies that are specific for clonally variant surface antigens (VSAs) encoded by the parasite [4]. Recognition of these viral antigens is essential to antimalarial immunity in general.

The *P. falciparum*-specific immunoglobulin G (IgG) antibodies that recognize these antigenic variants, including IgG1 to IgG4 subclasses, have been found in the serum of immune populations in malaria-endemic regions, including pregnant women [5],[6]. Pregnant women are especially attractive to female *Anopheles* mosquitoes [7], and malaria in pregnant women is an important cause of stillbirths, infant mortality and low birth weight [8] This is particularly true of *P. falciparum* infections and also applies to infections caused by other species such as *P. vivax* [9]. IgG antibodies are the only immunoglobulins that cross the placental barrier and thus factor into fetal immunity [10]. Concentrations of fetal IgG may vary, depending upon the level of maternal IgG [11]. Thus, it is suggested not only that the immune resistance of pregnant women with naturally acquired immunity (NAI) to *P. falciparum* malaria in hyperendemic regions is transferred to their infants, but also that women with higher *P. falciparum*-specific IgG antibody levels confer greater protective immunity to their offspring than do women residing in areas of intermediate to mild endemicity who may have lower maternal antibody levels.

Variations in rates of transmission and in children's ages at acquisition of active immunity among areas where malaria is hyperendemic pose a considerable challenge to treatment and control strategies. The unpredictable temporal gap between the waning of passive immunity and the acquisition of active immunity leaves children under the age of 5 in unknown states of vulnerability to acute infection and resulting death. The *P. falciparum*'s rapid mutation rate, which continually modifies the structure of its VSAs, further complicates the situation and renders many drug therapies ineffective. A better understanding of malarial pathogenesis and the relationships among endemicity, local VSA variability, and infant immunity can be used to develop more effective immunization strategies.

### Pathogenesis Overview

Malaria in humans develops in two phases, known as the exoerythrocytic phase (hepatocyte infection) and the erythrocytic phase (red blood cell, or RBC infection). Sporozoites from a mosquito's salivary glands enter the bloodstream and migrate to the liver, where they infect hepatocytes within a few minutes of injection. Inside the hepatocytes, all *Plasmodium* species multiply asexually and asymptotically for a period of 8–30 days [12]. This period of differentiation yields thousands of merozoites that, upon the rupture of their host cells, disperse throughout the bloodstream and infect erythrocytes, thus beginning the symptomatic erythrocytic stage. Several asexual multiplication cycles occur within the RBCs over a period of two or three days, after which they rupture, releasing increasing numbers of merozoites into the bloodstream [12]. Thus begin the waves of fever characteristic of the symptomatic stage of infection.

The parasite is relatively protected from the immune system because it spends much of its life cycle residing within hepatocytes and erythrocytes, effectively evading immune surveillance [13]. *Plasmodium falciparum* induces the production of binding proteins on RBC membrane surfaces, thus encouraging the infected erythrocytes to stick to the walls of small blood vessels. This strategy sequesters the parasite from passage through the spleen [14] and can cause hemorrhagic complications when the infected erythrocytes occlude venules. In cerebral malaria the sequestered RBCs can breach the blood-brain barrier, potentially invoking a comatose state [15].

Although the RBCs' surface binding proteins are exposed to the immune system, they do not serve as effective immune targets due to their extreme diversity. At least 60 variations occur within a single parasitic specimen, and effectively limitless variations are found within parasite populations. With each generation, at least 2% of the parasites produce novel RBC surface proteins [14] – the VSAs mentioned previously – thus staying one step ahead of the pursuing immune system.

In response to an unknown triggering mechanism [12], some of the merozoites differentiate into male and female gametocytes soon after infecting RBCs, thus making the human the definitive host of the disease. When a mosquito ingests parasitic gametocytes, they pair up and burrow into the insect's stomach lining [12], where fertilization and sexual recombination occur, forming ookinetes that mature into oocysts in which new sporozoites develop. Eventually the oocysts rupture and release the new sporozoites, which travel to the mosquito's salivary gland and are ready for injection into a new host, thus completing the cycle.

### Early Immunity and Passively Acquired IgG

During infancy, malarial infections produce only mild

symptoms with few parasitemias [2],[6],[17]. The first few months of protection have been attributed to the passive transfer of IgG, as evidenced by the similar levels of maternal and infant IgG at birth [18] and by the rough correspondence between the initial period of protection and the estimated dissipation time for maternal IgG [19],[20]. Paradoxically, recent studies have failed to provide direct evidence of this correlation despite having been designed with that goal in mind [21]. This dearth of evidence may result from excessive specificity in the investigation of IgG patterns thus far.

The highly variable nature of VSAs distinguishes them from other parasitic antigens that immunologists have targeted. Infected erythrocytes obtained from malaria patients consistently express VSAs for which the specific IgG levels have not yet developed but rapidly rise shortly thereafter [22],[23]. The variation of VSA expression with host age and disease severity implies that acquired immunity suppresses the parasite's expression of VSAs characteristic of severe malaria and drives them toward forms associated with uncomplicated malaria and asymptomatic parasitemia [23],[24]. These findings strongly suggest that VSAs represent major targets of protective immunity. They also suggest that successful immune responses target the VSAs that most effectively enable the infected erythrocytes to evade filtration – the “stickiest” VSAs.

In 2003, Cot et al. [25] published the only longitudinal study to date that has investigated the relationship between VSA-specific IgG and clinical protection from malaria during the first two years of life. The levels of any VSA-specific IgG correlate with transmission intensity; however, the placental form of the parasite cannot survive in the absence of a placenta, so placental VSA-specific IgG is not expected to benefit the newborn infant. In consideration of passively transferred, non-placental VSA-specific antibodies' presence in infants, one would expect to find a positive correlation of such IgG levels with time to first infection and a negative correlation with parasite load. Indeed, such correlations were found within the first six months [26],[27]; however, when considering the first two full years, Cot's team found that natal levels of IgG specific to placental malarial VSAs negatively correlated with time to first infection and positively correlated with mean parasite density [25]. More studies of this nature are desirable to substantiate these findings.

### Infant Immunity and the NAI Interface

Infants in highly endemic areas benefit from passively transferred VSA-specific IgG during their first few months of life [28]. The theories that explain this phenomenon may also help to explain why rates of severe disease and mortality from *P. falciparum* malaria are relatively low

in areas having the highest rates of parasite transmission, despite (or perhaps due to) the intense exposure to parasites [29]. Some studies suggest that the cumulative risk of malarial infection increases with decreasing endemicity a seemingly counterintuitive hypothesis [30]. Immunity may be acquired without serious clinical consequences if sufficiently intense exposure occurs during the period of passively transferred immunity [31]. Individuals who possess notable protective immunity typically exhibit high levels of IgG specific for VSA variants that are associated with severe malaria [23],[24],[32]. Thus, the infant's levels of passively transferred IgG specific to severe malarial VSAs remain at protective levels for several months, during which the exposure gained in highly endemic areas may be sufficient to boost active immunity to at least partially protective levels. Higher transmission intensity can be expected not only to confer higher levels of passively transferred IgG specific to severe malarial VSAs, but also to speed the development of active immunity through exposure to parasites expressing such VSAs before the passively acquired IgG becomes fully catabolized, thus minimizing or even eliminating the window of opportunity for the parasites to cause severe illness. This window is expected to become shorter with increasing endemicity [28]. The relationships among intensity of exposure, conferral of passive immunity, and development of active immunity likely are much more complex than this simplified analysis suggests. Clues to this complexity can be seen in studies of the impact of maternal antibodies on the outcome of vaccination in infants [35].

A similar line of thought may explain why the relatively few infections occurring in infants born to clinically immune mothers typically follow asymptomatic pathologies characterized by very low parasitemias. The infant's IgG levels for severe malarial VSAs may be sufficient to effectively suppress parasites that express such VSAs for up to a year, while lower levels of IgG specific to uncomplicated malarial VSAs decay to non-protective levels early enough to permit some early-life infections producing few symptoms [30]. During this critical period, any parasites employing VSAs associated with severe symptoms may be suppressed through passive immunity while still helping the infant's immune system to learn how to recognize future threats of this nature. Eventually the protective VSA-specific IgG decays to non-protective levels, allowing the parasites to express VSAs associated with severe illness while active immunity continues to develop, finally restricting the parasites' expression of VSAs to those associated with uncomplicated malaria and thus elevating the child to the status of clinical immunity [28]. This hypothesis can be tested through additional studies.

One study has demonstrated that IgG from protected subjects cooperates efficiently with blood monocytes,

whereas IgG from non-protected groups does not [34]. Furthermore, non-protected subjects have antibodies to epitopes critical for protection, but these antibodies are nonfunctional. These results shed some light upon the long delay in reaching clinical immunity, clearly stressing the need to investigate immune responses in both qualitative and quantitative terms.

The selective transfer of immunoglobulin isotypes may limit the protective effect of maternally derived antibodies, which may prevent the priming of specific cells in infants. Maternal antibodies may inhibit the child's antibody production by interacting with B-cell receptors or with the idiotypic repertoire [35]. The complex relationships between endemicity and the vulnerability gap are believed to manifest themselves in widely varying patterns of disease outbreak.

### **Transmission Heterogeneity and Unstable Hotspots**

Researchers in the field have found marked heterogeneity of transmission [36], which is expected to reduce the efficacy of disease control strategies [37]. To reduce overall transmission, researchers recommend that control measures be focused upon the "hotspots", defined as localities ranging in size from a single household (in sparsely populated areas) to a kilometer or so (in more populous areas) in which the highest transmission rates are found to occur at any given time [36]. Malaria transmission has been found to exhibit such spatial heterogeneity on the household level [38]-[44], with implications of both genetic and environmental factors [38],[45].

Environmental factors affecting malaria risk [46] include altitude [47], urbanization [48], cultivation practices [49], and distance from water [50]. Efforts to guide malaria control through ecological analysis have encountered difficulty with model complexity [51] and inconsistent effects of various ecological features among settings [52] as well as significant residual risk variation independent of the ecological data [53]. Additionally, remote sensing satellite data rarely provide resolution finer than 0.5–1 km [54], similar to the distances over which vector dispersion typically occurs as determined through studies of mosquito behavior [55]-[58]. High-resolution geospatial analyses conducted in Uganda [42], Mali [41], Ethiopia [59], and Kenya [60],[61] have found malaria hotspots at this same scale.

One study identified stable hotspots of asymptomatic parasitemia characterized by insignificantly higher mean antibody titers, a significantly lower mean age at febrile episodes, and significantly lower overall incidences of febrile disease [62]. The incidence of febrile malaria increases significantly in the areas surrounding the hotspots of asymptomatic parasitemia, which remained stable over a full 7-year monitoring period. In contrast, hotspots of

febrile malaria were found to be unstable, not surviving past 3 years of monitoring. These observations suggest that a rapid acquisition of immunity in stable high transmission hotspots offsets the high rates of febrile malaria that would otherwise result. Instead, a high prevalence of asymptomatic parasitemia is seen [30]. Unstable hotspots are associated with no prior exposure, and hence relatively low levels of immunity, and therefore exhibit higher incidences of febrile disease.

Although the unstable hotspots are directly associated with more febrile disease, stable hotspots of asymptomatic parasitemia may be critical in maintaining transmission because they maintain reservoirs of infected but asymptomatic individuals from whom the mosquitoes continually acquire gametocytes [63]. Both types of hotspots lend an essential balance necessary for disease persistence through transmission. The goal of vaccination strategies is to end this cycle by inoculating otherwise susceptible individuals who perpetuate the spread of infection.

### Immunization Challenges

Global levels of *P. falciparum* malaria increased during the first decade of the 21st century due to a combination of drug-resistant parasites and insecticide-resistant mosquitoes. The disease has re-emerged in areas that previously had been malaria-free [64]. However, this same time period has seen reductions in mortality in many localities. Likely contributors to this trend include improving socioeconomic conditions, combination drug therapies, and insecticide-treated bed netting. Early evidence of resistance to artemisinin drug therapy has manifested itself through delayed parasite clearance times in western Cambodia. This is the same area where resistance to earlier antimalarial drugs such as chloroquine first appeared. Due to these concerns, the anti-malaria community is shifting its focus from sustained control toward eradication. This goal is unachievable with current materials and techniques; research and development of new diagnostic methods, drugs, and deployment strategies are needed, and more effective insecticides also would help to facilitate this goal.

The task of developing an effective vaccine for malaria is daunting. The numerous factors to consider include parasite diversity, VSA variability and switching, and the complex interplay between endemicity and the natural immune response. The *Plasmodium* genus replicates rapidly, thereby increasing the probabilities of both transmission and immune system evasion. Treatments that reduce the parasite's reproduction rate without full suppression have been found to exert a selective pressure favoring the development of drug resistance [63]. An ideal vaccine candidate would stimulate a more substantial immune response to the VSAs associated with the most severe ma-

larial symptoms. This would increase the rate of parasite clearance, thus reducing the duration of symptoms and elevating immunity against future attacks.

The multicellular nature of a parasite introduces complexities of pathology beyond those of bacteria and viruses. The parasite's complicated structure and life cycle pose challenges to vaccine development; however, *Plasmodium*'s distinct developmental stages offer various opportunities for targeting antigens, thus potentially inducing immune responses at multiple levels [14]. A vaccine component targeting the hepatic phase would attack the invading sporozoites and could inhibit the development of merozoites in the hepatocytes through cytotoxic T-lymphocytic destruction of infected hepatic cells. A second vaccine component, targeting the erythrocytic phase, could prevent merozoitic multiplication or their invasion of erythrocytes. This component could target a multitude of symptomatic malarial VSAs, or it could block the process of erythrocyte adherence to blood vessel walls, which is believed to account for much of the clinical syndrome associated with malarial infection. Such a vaccine component would be expected to have prompt therapeutic benefits. Finally, a third vaccine component could target the parasite's gametes, thus blocking the parasite's sexual reproduction in the mosquito's gut. This feature would help to eradicate the parasite from areas of low endemicity and could prevent the development and spread of drug-resistant parasites. Such transmission-blocking behavior could become a key component of the eradication strategy. Resistance evolves very quickly in *Plasmodium*, potentially rendering any vaccine ineffective within a few generations. Therefore, it is essential that such transmission blockage be included with any new vaccine targeting the parasite's other stages of development. The most effective strategy against *Plasmodia* may have to target multiple phases of its life cycle.

A promising vaccine candidate currently undergoing clinical trials targets a circumsporozoite protein. The vaccine is genetically engineered to include the carboxyl terminus of the *P. falciparum* circumsporozoite antigen, a highly stable structure [65]. Known as RTS,S, the vaccine has demonstrated clinical effectiveness in terms of both infection and clinical malaria in both adults and children, a success that has been replicated multiple times [66]-[68]. Subsequent phase III trials have successfully tested the vaccine's effectiveness in various geographic regions employing various transmission scenarios and may result in its general availability as early as 2012 [69].

### Future Perspectives

To develop a vaccine of therapeutic and protective benefit against a parasite requires a novel approach, and to date there are no implemented vaccines that effectively

target a parasitic infection, although as noted above, some progress has been made toward that goal. The predominant focus so far has been on the use of sub-unit vaccines. The use of live, inactivated, or attenuated whole parasites is not feasible; therefore, antigenic particles, or subunits, are isolated from the parasite and tested for immunogenicity, i.e., the ability to elicit an immune response [65].

Recent advances in the field of sub-unit vaccine development include the use of DNA vaccination. This approach involves removing sections of DNA from the parasitic genome and inserting those sequences into a vector such as a plasmid genome, attenuated DNA viral genomes, liposomes or proteoliposomes, and other carrier complex molecules [68]. After inoculation the plasmid or attenuated virus is endocytosed into a parasitic cell, where the DNA sequence is incorporated into the parasite's DNA and replicated by protein synthesis [65]. The resulting proteins are expressed on the cell surface membranes of the affected parasitic cell. By binding to the HLA molecules, these proteins prime the host's T cells and create a population of memory T cells specific to the inoculated DNA subunit. This technique has produced a high rate of T cell response but low levels of antibody production.

DNA vaccines offer several advantages over classical attenuated vaccines, including the ability to mimic MHC class I CD8+ T cell specific responses, which may reduce the safety concerns surrounding vaccine therapy. DNA vaccines also benefit from reduced production costs and increased ease of storage.

In Gambian field trials of the previously mentioned RTS,S recombinant vaccine, researchers administered three repeat doses to each of 250 male volunteers during the six months prior to the time of greatest malaria transmission rates. During the first two months of follow-up, the vaccine was found to be effective at a level of approximately 71%; the 95% confidence interval spanned from 46% to 85%. However, during the final six weeks of the study, the effectiveness dropped to zero [67]. Subsequent analysis revealed that most of the control subjects had become infected during the latter weeks of the follow-up period; thus only the uninfected, and presumably more immune, control subjects were included in the comparison to inoculated test subjects [62]. Therefore, the vaccine's apparent decrease in effectiveness was an artifact of its having been tested against an increasingly immune subset of control subjects and does not necessarily reflect an actual reduction. Another complicating factor was the expected increase in the rate of malaria transmission toward the end of the follow-up period as the time of peak transmission approached.

The RTS,S vaccine shows promise as a means of bridging the gap between passive and active immunity in very young children [69]. Even if it does not prove effective

over the long term, RTS,S may become an important component of more advanced vaccination strategies that target multiple stages of the *Plasmodia* life cycle. Such a complex and rapidly evolving organism needs a multiple-pronged approach if we are to succeed in eradicating it from the global human population.

## Conclusion

This summary of the current state of the antimalarial art provides a broad-brush overview of current field research findings, the theories that have been developed to explain those findings, and progress toward the development of effective vaccines. Considerably greater detail may be found in the cited papers. The knowledge gained through research continues to enhance our understanding of the *Plasmodium* genus and the challenges it poses to the human immune system. Vaccines based upon recombinant DNA currently show the greatest potential for success, but the goal of malaria eradication may require a multi-pronged strategy that attacks the parasite at multiple stages of its life cycle. This goal, which has proven elusive for many decades, now appears to be attainable in the 21st century. Although much work remains to be done, the progress made during the first decade of this century suggests that malaria research is on the right track.

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## About the Author

A member of the Class of 2011, **Annette Marie Ruth** is a dual-degree candidate, graduating this spring with a B.S. in Biological Sciences and a B.A. in Psychology. With regard to research, she is primarily interested in disease transmission models and their implications for developing effective vaccination strategies, especially with respect to pathogenic mutagenesis and serotype conversion. She also looks at the development and dynamics of naturally acquired immunity to various diseases among populations in areas of high endemicity and the protective role of maternal antibodies upon primary infection in infants. Annette plans to pursue graduate studies in global public health and to continue epidemiological research through to professional school. She wishes to combine her research with work in the arena of public policy to help bridge the communication gap between scientists and policy makers, especially in developing nations.

# A Computational Method for Finding a Pattern in the Progenitor Systems of Type Ia Supernovae

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## Abstract

*Supernovae are highly energetic stellar explosions that may be used as standard candles to measure distances in space (Phillips 1993). We present an analysis of a set of over 30 Type Ia supernovae (SNe Ia) from the Sloan Digital Sky Survey to find a pattern in their locations within their host galaxies. This analysis takes images of the supernovae from the Hubble Space Telescope (HST) and calculates the relative flux at the supernova position with respect to light from their host galaxies. Applying this method to the complete set of supernovae allows for an analysis of the regions that produce SNe Ia, indicating trends in the formation environments and leading to a deeper understanding of the nature of their progenitor systems. The goal of this project is to find a trend in either of these parameters, as this may offer insight into the nature of the progenitor systems of SNe Ia.*

## Introduction to SNe Ia

SNe Ia are produced when a white dwarf star accretes enough mass, usually from a secondary star in a close binary system (or system of two nearby stars orbiting about their common center of mass) to produce a runaway nuclear reaction in its core. Each reaction rapidly sets off a cascade of further reactions, resulting in a violent nuclear explosion [1]. As the star approaches the Chandrasekhar limit of approximately 1.4 Solar Masses the dwarf star shrinks, raising the temperature and density in the core, reigniting it in nuclear fusion. This causes a runaway nuclear reaction that releases enough nuclear energy to unbind the star in an explosion, called a Type Ia supernova.

In general, supernovae are classified by the characteristics of their spectra. Those whose spectra lack hydrogen are classified as Type I Supernovae. SNe Ia are distinguished from other Type I SNe by their abundance of silicon. These spectral differences are indicative of a

physical difference in the development of these exploding stars, evident also in their differences in progenitor systems. While Type Ib and Ic supernovae tend to occur in star-forming regions of spiral galaxies [2] and are thus associated with massive but short-lived stars, no trend in location for SNe Ia has been established.

SNe Ia are important to astrophysics because they produce very consistent peak luminosities giving them characteristic light curves. Their exceptional brightness, along with these consistent light curves and common elemental abundances make them excellent candidates for standard candles used to measure the distances to their host galaxies [3]. The distance modulus relates the difference in apparent and true magnitude of a star to its distance by the following equation:

$$m - M = 5 \log (d) - 5 \quad (\text{Eq. 1})$$

where  $m$  is the apparent magnitude,  $M$  is the true magnitude and  $d$  is the distance to the star in parsecs. Thus by using these bright and easily distinguishable stars, we have a standard candle for measuring the distance to the supernovae and therefore an estimate of the distance to its host galaxy.

## Project Motivation

While SNe Ia are used as standard candles in many major astrophysical projects, such as the study of the expansion of the universe, there is a still uncertainty in the development process of these stars. While we know they often accrete mass from their binary partners, the exact mechanism for this process remains unclear and a pattern in their formation locations remains to be found. Searching for a pattern in the brightness of the SNe locations within their hosts may help us to establish a greater understanding of the progenitor systems for these supernovae.

The brightness of the SNe locations relative to their hosts allows us to determine if they tend to occur in areas containing stars of large or small luminosities. From the bright blue glow of young stars we can determine if the supernova is in a star-forming area within the galaxy by considering the relative brightness and color at the position of the SN. This will allow us to constrain the range of masses of white dwarfs that develop into SNe Ia.

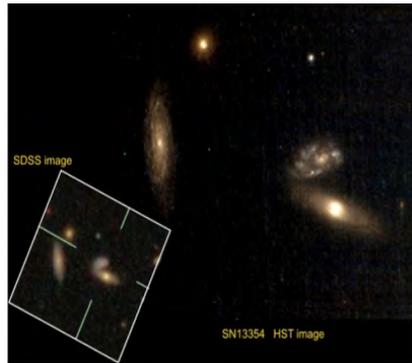
## The SNe Targets

The SNe targets used in this analysis were discovered by the Sloan Digital Sky Survey (SDSS). SDSS data was supplemented with higher resolution images from Hubble Space Telescope (HST). A compilation of the images from SDSS is shown in Figure 1. Figure 2 shows both the HST (larger image) and SDSS images of the same host SN host galaxy, displaying the significant difference in resolution between the resolution of the image from the SDSS ground-based telescope and HST.



◀ **Figure 1.**  
Compilation of SDSS SNe Ia (Image by Ben Dilday).

**Figure 2.** ▶  
SDSS and HST images of SN13354 host galaxy.



Before the images were used for computational analysis, the cosmic ray hits had to be removed. When pixels are hit by cosmic rays in the detector they create areas ranging from one to several pixels of extremely high counts, making them appear extremely bright. These random high values are not actual light from the galaxies and were eliminated by filtering through use of two images of the galaxy. The remaining small portions of cosmic rays were removed using the “imedit” function of IRAF, replacing the inaccurate high pixel values at the cosmic ray hit locations with an average of the sky pixel values surrounding them.

### The Method: Fractional Flux Program

An IDL program was written to determine the fractional flux of each SN relative to its host galaxy, using HST images of SDSS SNe Ia host galaxies. The fractional flux for each galaxy is calculated as follows:

$$\text{Fractional Flux} = \frac{\sum_{\text{counts in pixel} < \text{counts at SN}} \text{counts in pixel}}{\sum_{\text{all galaxy pixels}} \text{counts in pixel}}$$

This method was used by [2], a study of long gamma ray bursts and SNe Ia. An outline of the program we developed will now be presented and the fractional flux method will be explained in greater detail.

### Smoothing

In order to fully understand the results of our project,

we needed to determine how the resolution of the host galaxy image affects the trend in SNe Ia fractional flux. We introduced a smoothing function to lower the resolution to one similar to the resolution of the images used in Kelly’s paper [2] in order to compare our results. First, a kernel is generated by creating a square 11x11 matrix of float values. A FOR loop was then used to fill the elements of the matrix so that the greatest value was at the center of the matrix and the values fall off exponentially outwards.

When the kernel was applied to the fits image, it adjusted each pixel to be a combination of its own value and the value of those pixels nearby, thus smoothing over the image. As the image was convolved, the center of the kernel scanned over the image, adjusting each pixel value. The pixel values were weighted mostly heavily by the initial value and the values of those pixels nearest it, with the farthest pixels contributing exponentially less. The sigma of this Gaussian kernel was set to one so that the center value and the values of those elements directly next to it would be weighted much more heavily than the rest.

### Displaying the Image for the User

An important aspect of this program is ability of the user to interact directly with the image of each galaxy. The user can individually select the portion of each HST image to be used for the computation of the fractional flux to compare each individual SN location to the rest of its host galaxy.

The image is scaled to make the galaxy more visible. First a value of 0.1 is added to a copy of the image to avoid having negative values (the display ranges from values of 0 to 255). The number of sky pixels and mean and median values of the image, and the values of all pixels with values less than ten times the median sky value are determined. These are used to calculate sigma for the sky as follows:

$$\sigma = \frac{\sqrt{(\text{total}(\text{sky2} - \text{sky}))^2}}{n\_elements(\text{sky2})}$$

where sky is the median image value and sky 2 contains all the locations where the pixel value is less than ten times the median sky value. The copy of the image to be displayed is then scaled by a factor containing this sigma and the median sky value to bring out the galaxy and make it more visible.

The host galaxies for the supernovae are dim, so the display is set to invert the scaling of the images so that those pixels that are darkest or have the least counts (the sky) are displayed as white and brighter pixels (those of the galaxy) appear in the gray to black range. This scaled and inverted image is then displayed to the user using the tv function of IDL. It is important to note that all adjustments described in this section regarding the size and

scaling of the image are made to a copy of the image and not the image itself, so that the variable for the smoothed HST image is preserved.

### Computation of the Fractional Flux

The smoothed Hubble image was converted to a subimage containing only the pixels that fell within the region specified by the user in the previous section. The minimum value of the remaining image was then subtracted from all pixels within the subimage to subtract off (approximately) the contribution to the pixel values from the sky while keeping a positive value for all pixels.

We are now ready to perform the calculation of the fractional flux. Equation 2 produces a weighted rank for the SN pixel, describing the brightness of the SN pixel relative to the rest of the galaxy weighing the relevance of each pixel by its brightness, to avoid driving the rank upward due to the large number of sky pixels. This rank will thus be a number ranging between 0 and 1 with lower values corresponding to lower relative fluxes of the SN, indicating that the SN occurred in a region of lower brightness, or possibly an region containing older stars. A high rank indicates the SN may have occurred in a bright area of the galaxy, possibly indicating that it formed in a star-forming region.

To calculate the fractional flux we calculated the denominator by finding the total of all pixel values in the subimage. A FOR loop was then used to find the numerator, summing the values of all pixels with values than the value of the SN pixel. Finally the numerator is divided by the denominator to find the fractional flux for this SN and its host galaxy. The program is now complete.

### Finding A Trend

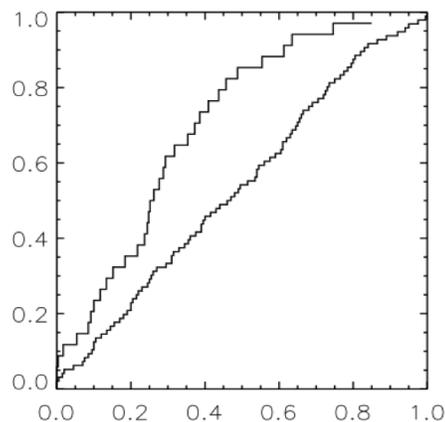
In order to determine a trend in the progenitor regions of these SNe the program was run for each of the SNe, generating a list of the fractional flux for each supernova and its host galaxy. A cumulative histogram of these fluxes was then plotted, with the fractional flux for the galaxy along the x-axis and the cumulative fraction of SNe with each flux running along the y-axis. We then plotted a cumulative histogram of the SNe Ia data from Kelly's paper [2] along with our plot for comparison.

### Results and Discussion

The cumulative plot of both these data sets is given below in Figure 3. The steeper line plotted below represents our data including a set of 34 supernovae with a smoothing sigma of 1. The Kelly dataset [2] includes 96 SNe Ia.

It is apparent that the trends in our results differ greatly from that of Kelly et. al [2]. The greater slope of our line for lower fluxes indicates that we expect SNe Ia to avoid bright parts of the galaxy. The near-linearity of the

fractional flux to cumulative fraction of supernovae from Kelly's results [2] would indicate that there is an even distribution of SNe Ia developing in environment of various brightness/age. In other words, it would seem as though SNe Ia do not tend to occur in any particular region of a galaxy, their development is equally probable regardless of the location within the galaxy. Our results, however, seem to disagree. The much greater slope of the cumulative histogram for lower fractional flux values indicates that much more of our SNe fell in the range of having lower fractional fluxes. Our results indicate that SNe Ia are more likely to develop in progenitor system of low luminosity or regions of older stars, avoiding bright regions. If the stars take longer to develop into supernovae, this might indicate that supernovae develop from low mass stars that burn their fuel more slowly and have longer lifetimes than high mass stars.



**Figure 3.** Cumulative Histogram of fractional flux in SNe Ia

It is important to note that the value of sigma used in the smoothing made a noticeable difference in the numbers generated for our data. The fluxes would vary depending on sigma but not consistently; some fractional fluxes would increase while others would decrease. While the fluxes did not vary dramatically between sigmas of 2, 3, and 4, the results for these numbers differed dramatically from the results using a sigma of 0.5. In the most extreme case, the flux of one supernova differed by over 250%. Since the fractional fluxes did not always increase or always decrease with sigma, but merely changed dramatically between sigma of 0.5 and sigma of 2, we chose to plot our data vs. the Kelly data using a sigma of 1.

One of the major differences between our study and the Kelly study [2] was the difference in resolution and the amount of smoothing, which seemed to have a noticeable difference in our results. Thus, we then investigate the affect of noise on the trend in fractional flux.

### Program for Study of Noise Dependence

To study the true dependence of our fractional flux

method on noise level we created a simulation by sampling a very well-resolved galaxy. The points were selected at random to see the effect of adding noise to the trend at point of varying fractional fluxes. To study this noise dependence, varying amounts of random noise were added to the image, with the fractional flux trend (cumulative histogram) analyzed for each degree of noise.

#### *The Simulation Host Galaxy*

The image we used for this simulation was an SDSS image of the galaxy NGC 2532, a nearby galaxy (redshift 0.017) pictured in Figure 4.



**Figure 4.** SDSS image of Galaxy NGC 2532. The above image depicts the galaxy selected for our simulation of fractional flux calculation with varying amounts of noise.

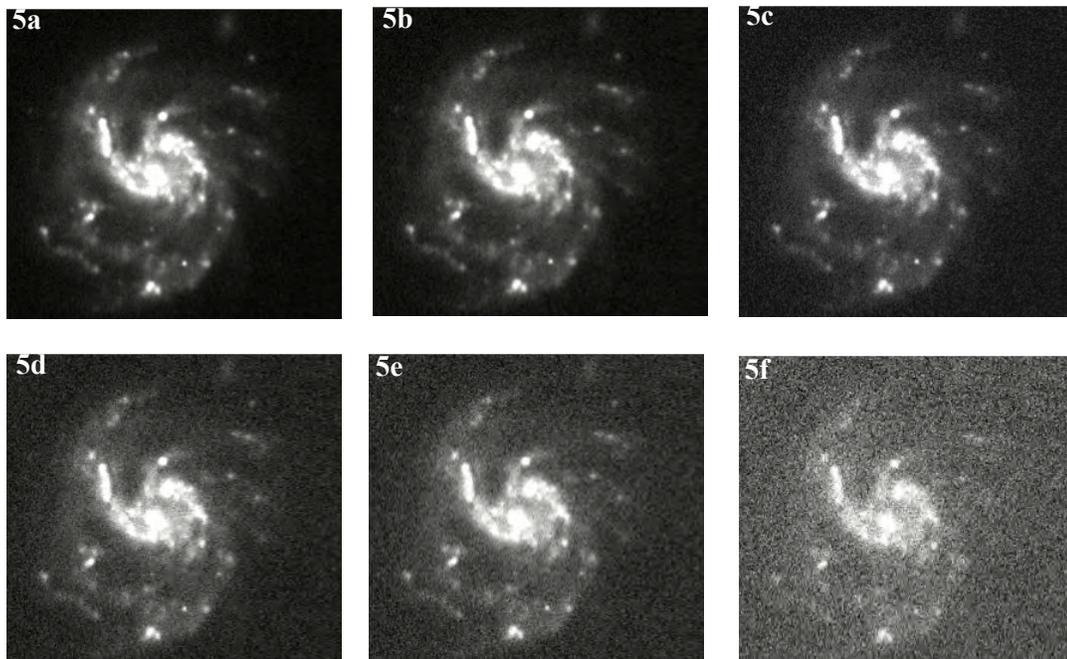
This galaxy was chosen merely for the fact that its closeness allowed us to easily find a well-resolved and

bright image of the galaxy. We controlled the amount of the noise in the image by starting with an image of very low noise and adding our own simulated noise. The image was trimmed using the “imedit” function of IRAF so that, similarly to the user-designated regions of the HST galaxy images, we could calculate the fractional flux at various points using a region of the image containing as little extraneous sky pixels as possible.

#### *The Program Outline*

This program begins with the user inputting the test galaxy image. The x and y dimensions of the image are then obtained. The IDL function RANDOMU and these dimensions were then used to create a set of random x and y locations. Paired together, these random locations were used as the coordinates for the random pixels in the image whose fractional fluxes would be tested. We chose to analyze 100 such locations in order to ensure we were including a broad range of pixels (and therefore brightness) in our study.

The program is then written to create a matrix of random noise to be added to the image. This was done by creating a 2D array of the same dimensions as the image of random numbers using the IDL function RANDOMN. We could choose and adjust the amplitude of the noise added by multiplying the output of this random function by varying factors. This matrix is then added to the original image, adding a random amount to each pixel value and thus creating noise of a controllable amount. Images of the galaxy image with various magnitudes of simu-



**FIGURE 5.** Galaxy NGC 5235. The pictures above show the galaxy image used for our fractional flux simulations with varying amounts of noise added. The magnitudes of added noise for these images are 1, 5, 10, 15, 20 and 50 respectively.

lated noise are given in Figures 5a-e.

A 100-element array is then created to hold the calculated fractional fluxes for each of the random points. This is done in a FOR loop, calculating the flux at each point in the same way as in the previous program. The pixel values with values less than the pixel value of the random pixel or simulated SN location in question are summed and divided by the sum of the values of all pixels in the image. Once this has been done for each of the fake SN locations the array containing the fractional fluxes is used to generate a cumulative histogram of the fractional fluxes, just as for the real supernovae of various location brightness.

The program was then run for various amplitudes of noise, each with a fake SN sample size of 100. The same program was also run for these different cases but with an additional adjustment. The previous program description does not take into account the sky value as the other program did. Thus the program was run again but with first subtracting off the minimum pixel value from the entire image to account sky value.

### Simulation Results and Discussion

The analysis of several different noise amplitudes without subtracting off the sky is shown in the histograms (Figure 6a-6f).

All of these cases produce plots that show a more heavy distribution of SNe or pixel locations with low fractional fluxes, indicating a bias towards the dimmer areas of the galaxy or galaxies. However there is an interesting progression in these plots. While they are all nonlinear, they seem to approach linearity as the amount of noise is increased.

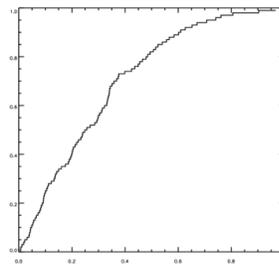
The first curve, with noise amplitude of 1, is much more curved than the final plot with the drastic noise amplitude of 50. This would seem to indicate that when more noise is added our results change from indicating a bias towards dimmer locations within galaxies to no indication of any bias.

This result is fitting with what we see in Figure 5. As more noise is added, the pixels tend to approach a similar value, with the image losing contrast as noise is increased. We can see this as the images in Figure 5 progress. The first image with almost no noise added has deep contrast between the galaxy and the surrounding sky values. In contrast the final image with an enormous amount of noise (magnitude 50) has very little contrast with most of the image appearing gray. This result is reflected in the fractional flux. As noise is added the magnitude of the noise becomes increasingly more relevant. As this magnitude grows large, the values of the pixels converge and thus the fractional fluxes do the same. The skewing of our results based on the amount of noise added is consistent with the fact that the amount of smoothing in the study

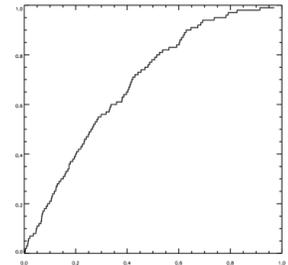
with real supernovae seemed to shift our fractional flux results.

But before we begin to draw conclusions, it is interesting to also consider the plots from when we subtracted off the minimum pixel value from the image and found the trends again. These plots are given in plots 7a-f.

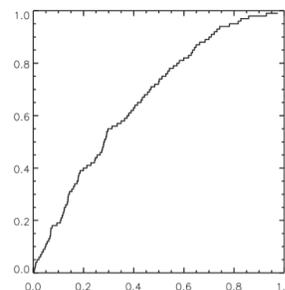
With the sky subtracted, we see that all noise amplitudes produce similar trends. They follow the same trend as the results from [2] showing a linear dependence or an unbiased distribution of fractional fluxes, regardless of the amount of noise added to the image. Thus it seems that both the inclusion of the sky value and, in the case of no sky subtraction, the degree of noise added both seem to affect the results of our study.



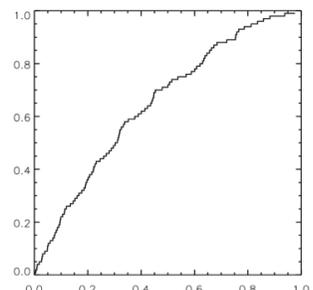
**Figure 6a.** Noise Amplitude of 1, sky included



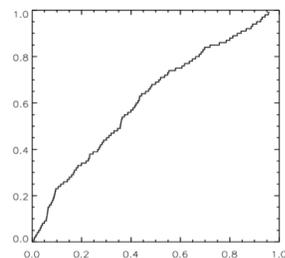
**Figure 6b.** Noise Amplitude of 5, sky included



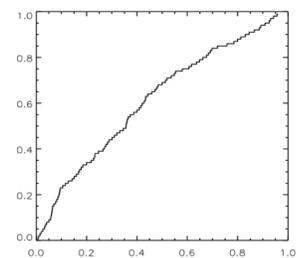
**Figure 6c.** Noise Amplitude of 10, sky included



**Figure 6d.** Noise Amplitude of 15, sky included

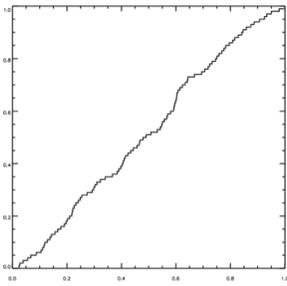


**Figure 6e.** Noise Amplitude of 20, sky included

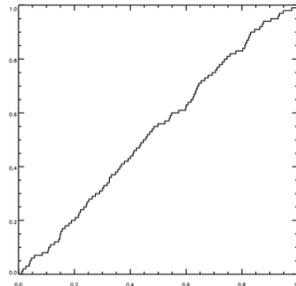


**Figure 6f.** Noise Amplitude of 50, sky included

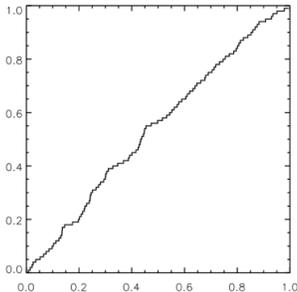
**Figures 6a-f.** The above plots are cumulative histograms for the fractional flux at various random pixels with noise added. For these plots, the minimum pixel value was not removed from the image, so flux from the sky has been included in this data. The magnitude of added noise for each histogram is indicated beneath the individual plot.



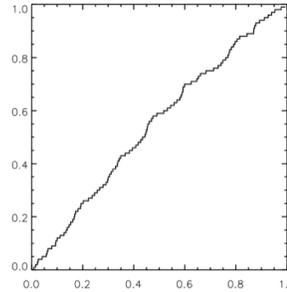
**Figure 7a.** Noise Amplitude of 1, sky included



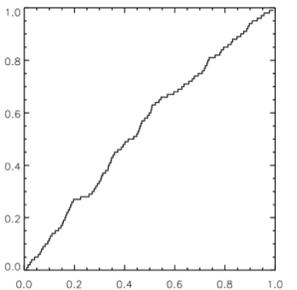
**Figure 7b.** Noise Amplitude of 5, sky included



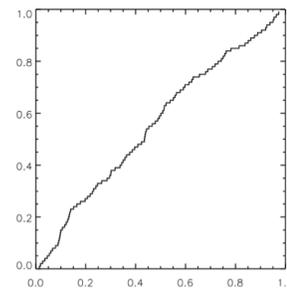
**Figure 7c.** Noise Amplitude of 10, sky included



**Figure 7d.** Noise Amplitude of 15, sky included



**Figure 7e.** Noise Amplitude of 20, sky included



**Figure 7f.** Noise Amplitude of 50, sky included

**Figures 7a-f.** The following plots are cumulative histograms for the fractional flux at various random pixels with noise added. For these plots, the minimum pixel value has been subtracted off the image. The magnitude of added noise for each histogram is indicated beneath the individual plot.

### Conclusion and Plans for Further Study

The results of analysis of the fractional fluxes of SNe Ia seem to indicate that these SNe avoid bright regions of galaxies, developing in dim progenitor systems, probably containing mostly older stars. This contrasts with the results found in the work of Peter Kelly [2], which indicates that SNe Ia are more evenly distributed, showing no preference for any particular area within a galaxy. We developed the simulation program to determine whether our subtraction of the sky or the amount of noise in our HST images was causing the difference in our results. The simulations seem to both indicate that adding noise and subtracting the sky off of a random distribution of locations within a galaxy should produce a linear cumulative

histogram of fractional fluxes.

Since the HST images are very noisy and the sky was subtracted off of the images before completing our analysis, one would expect the fractional flux distribution to be pushed towards having this linearity in the cumulative histogram. Yet, looking at Figure 3 it is clear that this is not the case. It appears that our unexpected results were not merely the results of a faulty choice in the method of determining the fractional flux trend. They may, in fact, be indicating the true progenitor systems of SNe Ia. We thus predict, based on this model, that SNe Ia may in fact prefer dimmer locations within galaxies. It remains that these predictions would disagree with the predictions from Kelly [2]. Thus, we may further strengthen our results and understanding of the trend in SNe Ia progenitor system brightness by continuing to run simulations in an effort to determine why our results differ.

The results of this project seem to indicate that Type Ia Supernovae tend to develop in older or more dim progenitor systems, in contrast with the conclusions of a similar study that predicts them to develop in bright, young systems. Investigating the reasons for the difference in our results to determine which model is more accurate will help us to understand more fully the progenitor systems of these stellar objects so important in current astrophysical studies.

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### About the Author

**Julie Cass** is a junior at the University of Notre Dame majoring in Physics with a concentration in Advanced Physics. Julie first became involved in physics research in her sophomore year, working with Professor Peter Garnavich on the study of Type Ia Supernovae described in this paper. In the following summer, Julie participated in the 2010 University of Washington Physics REU, working with the Professor Markus Raschke group in nano-optics research. Julie is currently working in the campus Nuclear Structure Laboratory with Professor Ani Aprahamian, helping to design and implement a cooling system for detectors in the new St. George recoil mass separator. In the summer of 2011 Julie will be participating in the SULI undergraduate research program at the Stanford Linear Accelerator Center (SLAC) at Stanford University. Following her graduation from Notre Dame in 2012, Julie plans to attend graduate school to pursue her Ph.D. in physics.

# An Examination of Possible Gravitational Perturbations in the Transit Timing Variations of Exoplanet WASP-3b

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Advisor: Peter Garnavich

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## Abstract

*In a 2010 paper, Maciejewski et al. claimed to have detected a possible sinusoidal variation in the transit timing variations of exoplanet WASP-3b [1], which is currently the only known planet orbiting the star WASP-3. According to Maciejewski's analysis, this signal might be the consequence of gravitational perturbations caused by a hypothetical second exoplanet in the WASP-3 system. I report five transit timing variation measurements from the summer of 2010 which provide modest support for Maciejewski's proposed sinusoidal signal.*

## Introduction

Exoplanet transits are eclipses which occur when a planet orbiting another star passes directly between that star and the Earth. Although no current telescope can actually resolve the miniscule silhouette of the planet against its star, it is possible to detect the small fade produced as the planet blocks some of the light of its star from reaching Earth. Transits for a particular exoplanet occur at very regular intervals, and by examining a planet's transit timing variations (TTVs)—i.e., how early or late each transit occurs—it is theoretically possible to detect the effects of gravitational perturbations from other exoplanets in the same system.

Maciejewski's group observed six transits of exoplanet WASP-3b and combined them with eight others from previous publications. They found a statistically significant sinusoidal signal in the fourteen TTVs, which spanned a period over three years. Maciejewski found that the data are consistent with gravitational perturbations caused by a hypothetical second planet, WASP-3c, with about 15 Earth masses in a 2.02:1 orbital resonance with respect to WASP-3b—very close to a stable 2:1 resonance. They predict that such a planet would be difficult to detect via

radial velocity measurements because WASP-3's minute oscillations would obfuscate WASP-3c's weak radial velocity signature.

To test Maciejewski's claim, retired professional astronomer Bruce Gary calculated WASP-3 TTVs from dozens of amateur observations in the Amateur Exoplanet Archive, his database of amateur exoplanet transit observations [2]. He concluded that there was little evidence of sinusoidal variation in the amateur TTVs, many of which had relatively high uncertainties. Gary's procedure required each observer to perform basic data analysis, such as rejection of outlier data and reference star selection, potentially injecting some measure of subjectivity into the process. Consequently, even though Gary performed the final analysis, it might not be appropriate to compare observations between different amateur observers, and his analysis of amateur WASP-3 observations is not necessarily conclusive.

## Materials and Methods

I observed five WASP-3b transits using an 11-inch Schmidt-Cassegrain telescope and a CCD camera at the observatory at the Jordan Hall of Science. Before each observing session, I synchronized the computer's time with Microsoft's Internet time server. I then took a continuous series of unfiltered images of WASP-3, spanning the length of the eclipse. When possible, I also obtained several hours of data before and after the transit in order to better characterize systematic errors. For example, the star's magnitude should theoretically remain constant outside of transit, but in practice, it will usually vary slightly as a function of the star's changing airmass if the target and reference stars are different colors. After each observing session, I reduced the data by applying flat fields and dark frames before performing aperture photometry to measure the fluxes of WASP-3 and twenty nearby reference stars. To account for night-to-night differences in the point-spread function of the stars, I used different aperture sizes for each session in an effort to maximize the quality of the photometry.

In order to derive estimates of important transit parameters, especially the time of midtransit, I used an advanced spreadsheet designed by Gary for analyzing photometry of exoplanet transits [3]. Caltech's NASA Star and Exoplanet Database, which subsumed Gary's database in 2010, has specifically endorsed Gary's procedure, which determines the best-fit model for each transit through chi-square minimization [4]. This process produced estimates of a variety of important transit parameters, including midtransit time, along with the corresponding uncertainties. To determine the expected time of midtransit, I adopted Maciejewski's ephemeris of

$$TC(E) = 2454605.56000 \text{ [BJD]} + E \times (1.8468355 \text{ days}).$$

The TTV is simply the difference between the predicted and observed times of midtransit. Table 1 lists my individual TTV estimates.

Date (UT)	TTV (min)	Midtransit Time (TBD)
June 4, 2010	2.4 ± 1.6	2455351.6832 ± 0.0011
July 22, 2010	0.9 ± 2.2	2455399.6999 ± 0.0015
August 2, 2010	-0.2 ± 1.8	2455410.7802 ± 0.0013
August 28, 2010	-0.1 ± 1.2	2455436.6359 ± 0.0008
September 8, 2010	-2.1 ± 1.1	2455447.7155 ± 0.0008

**Table 1.** Individual TTV Estimates

Since Maciejewski’s ephemeris and subsequent TTV measurements relied upon the Barycentric Julian Date (BJD) reference frame and terrestrial time (TT) time standard, it was necessary to convert my data into a comparable time stamp. To accomplish this, I found the midtransit time in Julian Date and converted it to the BJD frame of reference using the barycentric dynamical time standard (TBD) with the assistance of an online conversion utility [5]. BJD\_TT and BJD\_TBD adopt the solar system’s barycenter as their frame of reference, and according to Eastman, they vary from each other by no more than 50 milliseconds, an insignificant difference for TTV analysis [6]. These extremely accurate time stamps compensate for a variety of factors, such as Earth’s orbital motion and gravitational perturbations from other planets in the solar system, which would otherwise taint TTV data due to the finite speed of light.

## Results

I combined my data with Maciejewski’s and fitted it with several different chi-square models. A purely linear fit was quite poor, producing statistically insignificant coefficients and a  $\chi^2$  of 64.3 with 17 degrees of freedom. The resulting p-value of  $2.0 \times 10^{-7}$  suggests an unacceptable fit to the data. I then fit a three-parameter sinusoid to the data, retaining the linear term because an inaccurate ephemeris would manifest itself as a linear variation in the TTV plot. I found that the combined data exhibited a sinusoidal variation with a period of  $125.9 \pm 0.4$  days with a full amplitude of  $3.4 \pm 0.6$  minutes. Furthermore, my analysis calls for a slightly refined ephemeris for WASP-3b, including a longer orbital period. Table 2 summarizes the parameters of my best-fit model, including my proposed ephemeris.

Maciejewski proposes both short- and long-term sinusoidal variation in the TTV data, so I performed the analysis again, allowing for two independent sinusoids. With-

Full Amplitude (min)	3.7 ± 0.6
Sinusoid Period (days)	125.9 ± 0.4
Orbital Period (days)	1.8468372 ± 0.0000006
T <sub>0</sub> (BJD)	2454605.55978 ± 0.00010
$\chi^2$	18.21
df	14
p-value	0.20

**Table 2.** Best-Fit Model

out a linear term, the double sinusoid model produced a strong fit; however, once I included the requisite linear function to account for possible errors in the ephemeris,  $\chi^2_{red}$  plummeted from a nearly ideal 1.05 ( $\chi^2 = 13.62$ , 13 df) to just 0.5 ( $\chi^2 = 5.5$ , 11 df), indicating a serious overfit of the data. The extremely low  $\chi^2_{red}$  reflects that the total number of parameters in that model ballooned to eight, an ungainly number for just nineteen observations. Thus, I rejected this model, though I was reluctant to do so because Maciejewski’s computational models predicted that WASP-3c would cause two separate periodicities in WASP-3b’s TTVs.

## Discussion

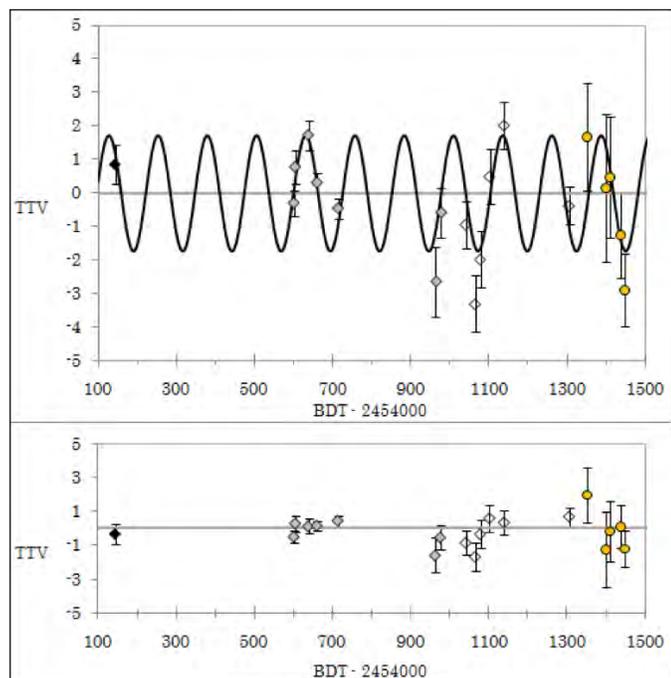
My observations provide equivocal support for Maciejewski’s hypothesis. However, five closely-spaced observations with a small-aperture telescope are insufficient to provide convincing support for Maciejewski’s sinusoidal model, which includes high-quality data obtained over a span of over three years. Additional observations would permit a more rigorous characterization of the TTV of WASP-3b, including an examination of whether there is a second periodicity in the TTV plot.

One concern is that several of Maciejewski’s TTV estimates between BJD 2454900 and 2455100 are somewhat inconsistent with my fit. The residuals for these observations were much smaller for the double sinusoid model, but for reasons already discussed, I decided that a single periodicity best represented the data. Additionally, Maciejewski’s published TTV estimate for BJD 2455102 is apparently incorrect. I used Maciejewski’s ephemeris and estimated midtransit times to verify the published TTV estimates, and the BJD 2455102 datum showed the only discrepancy. The most likely explanation is a misprint of that one TTV estimate, and I was able to calculate the correct TTV using other data in Maciejewski’s paper.

The data quality for my June 4 observations left much to be desired, potentially making that TTV estimate unreliable. Jordan Hall is a notoriously vibration-prone building, and that night, high-frequency vibrations distorted the star images into elongated streaks. In some of the worst images, star images were over 13 arcseconds long. To put this into perspective, star images at Jordan Hall are normally circular and no larger than 5 arcseconds in

diameter, even on a night of poor seeing. In light of this problem, it is prudent to be somewhat skeptical of the accuracy of this particular TTV measurement.

On a final note, Maciejewski predicts that the hypothetical second planet would produce a transit depth of up to 0.35% if it undergoes transits. Although I did detect a barely significant, 0.3% fade in the flux of WASP-3 on August 1, 2010, my own follow-up observations strongly suggest that this feature was spurious, a product of a common systematic error, such as an imperfect flat-field. My experience suggests that while the equipment at Jordan Hall is just capable of detecting a transit depth of 0.3% under ideal conditions, it is extremely easy for any number of errors to produce false “transits” of that depth.



**Figure 1.** The best-fit, two-periodicity sinusoidal model, with TTV estimates superimposed. The TTV is represented in minutes. The yellow symbols represent my data, while the rest are the mix of observations—both original and previously published—used by Maciejewski. The six clear symbols are Maciejewski’s original observations, whereas the seven gray symbols and the lone black diamond represent data from various publications cited by Maciejewski. Below are residuals from the fit. The revised ephemeris used for these plots is provided in Table 2.

On a final note, Maciejewski and his team predict that the hypothetical second planet would produce a transit depth of up to 0.35% if it transits WASP-3. Although I did detect a barely significant, 0.3% fade in the flux of WASP-3 on August 1, 2010, my own follow-up observations strongly suggest that this feature was spurious, a product of a common systematic error, such as an imperfect flat-field. My experience suggests that while the equipment at Jordan Hall is just capable of detecting a transit depth of

0.3% under ideal conditions, it is extremely easy for any number of errors to produce false “transits” of that depth.

## Conclusion

Between June and September in 2010, I observed five transits of WASP-3b, and my data, when analyzed in conjunction with previously published observations, suggests that there is indeed significant sinusoidal variation in WASP-3b’s TTVs. Plainly, nineteen combined observations do not provide a very large sample size, and more observations are necessary to explore this possibility. Nevertheless, there appears to be considerable, albeit inconclusive, evidence that a second, undiscovered exoplanet is perturbing WASP-3b.

## Acknowledgements

I wish to thank Professor Peter Garnavich for his guidance with this project. Additionally, my research was subsidized in part by an AL/SCI UROP grant from Notre Dame’s Institute for Scholarship in the Liberal Arts

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- [6] Jason Eastman, Robert Siverd, and B. Scott Gaudi, “Achieving Better Than 1 Minute Accuracy in the Heliocentric and Barycentric Julian Dates,” *Publications of the Astronomical Society of the Pacific* 122, No. 894 (2010): 935-946, <http://arxiv.org/abs/1005.4415>.
- [7] The parameters were amplitude, period, and phase.

## About the Author

A senior majoring in political science and minoring in peace studies, **Colin Littlefield** has been an avid amateur astronomer for over ten years. Due in large part to the generosity of Notre Dame’s astrophysics faculty—especially Professors Garnavich and Rettig—he has taken advantage of the opportunity to move beyond visual astronomy and engage in research projects while at Notre Dame.

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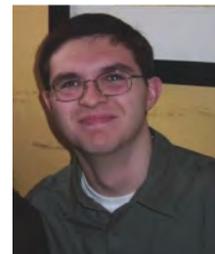


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*If the doors of perception were cleansed everything  
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–William Blake

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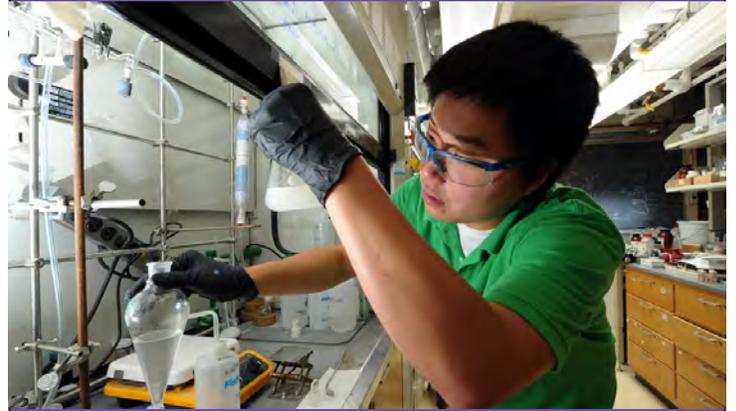
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