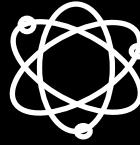


BREAKTHROUGH

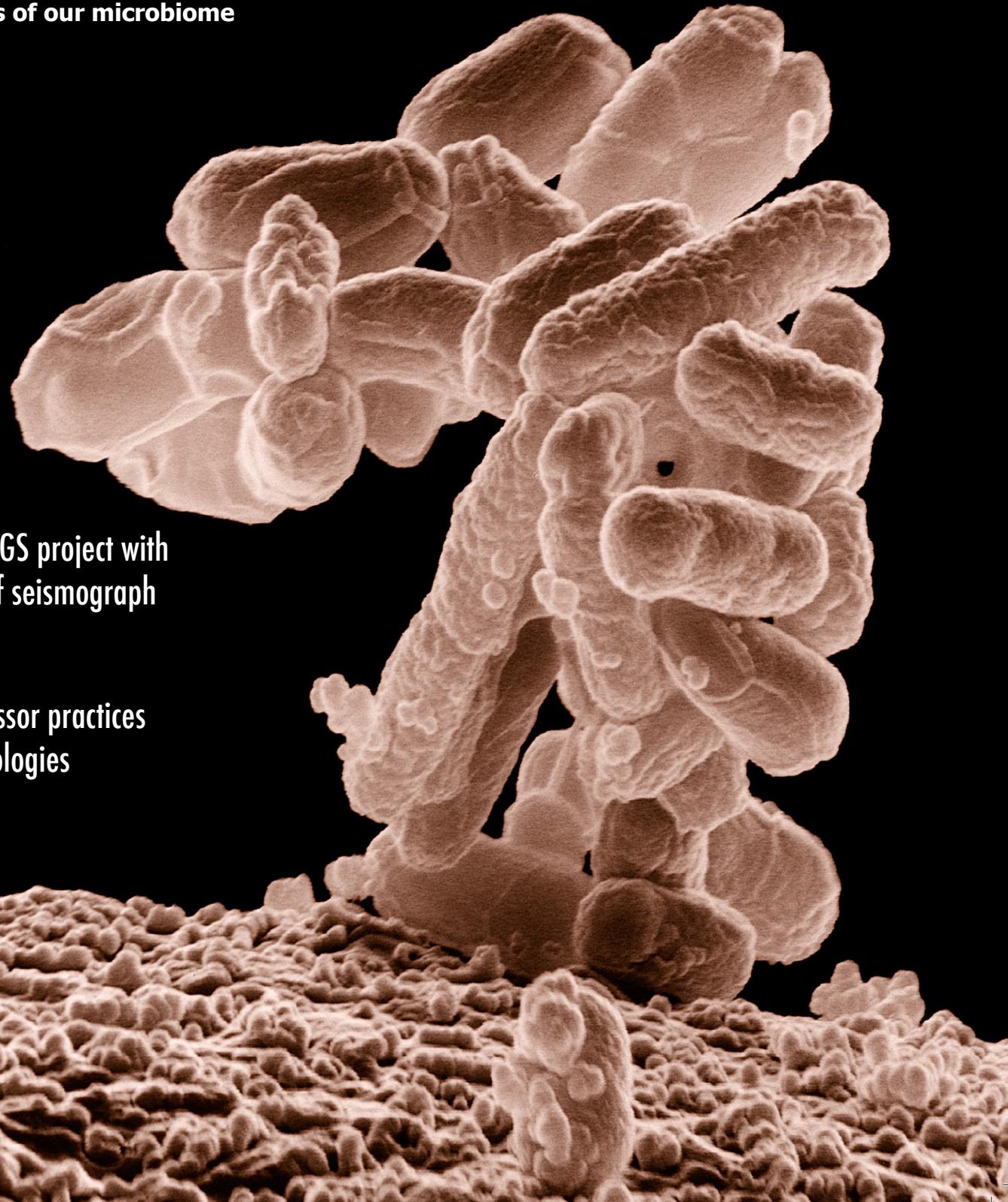


Fall 2013

Volume IV, Issue I

GO WITH YOUR GUT

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complexities of our microbiome
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Tufts joins USGS project with
installation of seismograph
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Physics professor practices
new epistemologies
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FROM THE EDITORS

Dear Readers,

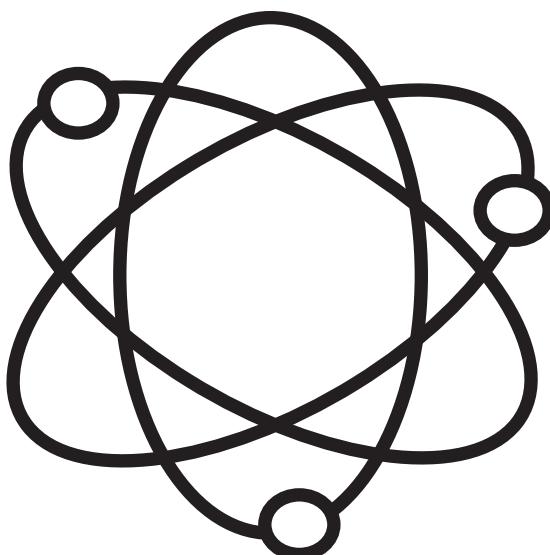
After a year-long hiatus, Breakthrough magazine is back in action and better than ever! We've taken this time away from producing our magazine to improve our publication process, from writing to editing to layout.

The articles in this issue span an entire year of exciting science events at Tufts and beyond. Inside, you'll find a semi-scathing book review, a sensational piece on slime molds, an interview about revolutionary physics epistemologies, and a series of investigative reports on alumni in the real world.

Through this issue, we hope to appeal to a wider audience of science and non-science majors alike. Ergo, we've designed this issue to cover topics from fields of science that have been under-represented in our previous publications. These topics include science education, geology, and computer science. Outside of our printed magazine, we have also expanded our reach through the creation of our online blog.

We'll let you get to reading this enthralling issue of Breakthrough, and hope this inspires your curiosity in science like never before. We thank you for your readership and enjoy this issue!

*Meg Berkowitz, Julia Hisey, and Stephen Walsh
Co-Editors-in-Chief*



*Cover image: Cluster of E. coli by Eric Erbe and Christopher Pooley (USDA)
Additional illustrations by Lucia Smith and Shoshanna Kahne*

The opinions expressed in each article are those of the author and do not necessarily reflect the opinions of the magazine or its staff.

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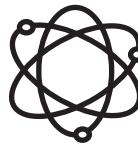
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BREAKTHROUGH



Tufts' Undergraduate Science Magazine

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Come to one of our meetings (Monday nights, 9:30p.m., Eaton 208), e-mail us at tuftresearch@gmail.com, or visit our blog tuftresearch.wordpress.com

Folding Biology into

Recent advances in the field

Soon, with some well-placed hydrogen bonds and twists of a protein's backbone, an anonymous figure on the internet could become the next Nobel prize winner. This is possible through Fold-it, a downloadable program that crowd-sources protein folding by turning it into a game.

Proteins are synthesized in a linear string of amino acids, but to become functional (and studyable) they have to fold into specific blobby shapes. Often scientists can find a protein's linear sequence but not its structure, so the University of Washington Center for Game Science and UW Dept. of Biochemistry's Baker lab designed Fold-it to help 'solve' these missing structures. After being given an unfolded graphic of a protein, players can add hydrogen bonds, twist the backbone, and minimize clashes (conflicts) for points.³ A player's score is directly related to the amount of energy required for the protein to hold the structure of their design: less energy is more points. The computer helps the player by 'shaking' the sidechains and 'wiggling' the backbone to further reduce clashes.

In the future, the creators of Fold-it plan to allow players to design brand-new proteins. The idea is to create useful proteins that could potentially bind to and stop viruses like HIV. An extremely useful solution to both serve humanity and fulfill all relevant criteria would win the player a Nobel prize.

Fold-it is just one of the more in-the-news examples of the up and coming area of computational biology. This intersection of computer science and biology is an exciting field encompassing bioinformatics, genomic analysis, molecular modeling, and more. Because of its wide range of opportunities, people from many different backgrounds go into computational biology: mathematicians, statisticians, chemists, biologists, physicists, and computer scientists have all entered this incredibly diverse field of research.

A good example of a variety of backgrounds producing diverse computational biology research can be seen right here at Tufts. Professors Ben Hescott and Donna Slonim and PhD candidate Noah Daniels are all currently doing computational biology research in our computer science department.

Daniels is a PhD candidate in the Department of Computer Science. His background is in computer science, and he started

working in computational biology while doing his masters at Tufts. Daniels particularly enjoys the combination of "problem-solving algorithms ... [and] real-world applications." He does research on protein structure, and his most recent project, MRFy (Markov Random Field), predicts protein structure through remote

homology detection. This compares the unknown protein to known proteins in a database and tries to find similar gene or amino acid sequences. If a similar sequence is found, the likelihood of the proteins having similar structures is much higher.

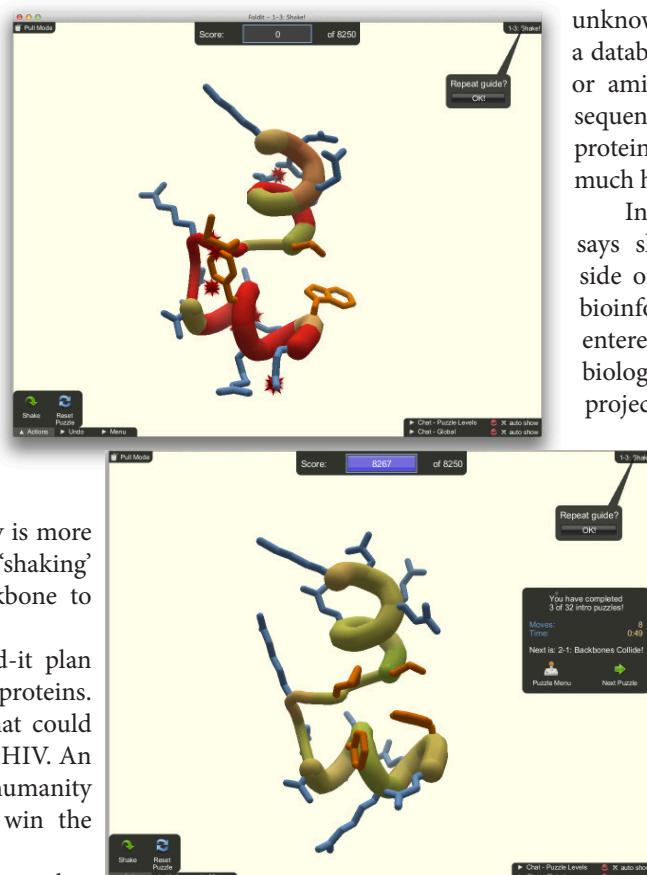
In contrast, Professor Slonim says she tends towards "the biology side of the spectrum" and does more bioinformatics-related research. She entered the field of computational biology through the Human Genome project, a race to sequence the entire

human genome that some say marked the beginning of computational biology. At Tufts, her research involves "genetics and genomics applied to human development," including the study of how diseases such as Down's Syndrome and autism develop. Professor Slonim teaches computational biology and bioinformatics courses, among others.

Professor Hescott works with the computational side of computational biology and

does a lot with algorithms. He has a PhD in computer science, and started doing computational biology research as well when he arrived at Tufts 6 years ago and found Professors Slonim and Cowen doing computational biology. Now, Hescott is creating a new model to predict protein function. It uses ideas from a combination of several other areas including computer science and network science, and so far, it "seems pretty promising." He teaches mainly computer science courses at Tufts.

Because the internet is less than twenty years old and the technology to create these kinds of programs is only just becoming available, computational biology is expanding exponentially. Computational biology is already well on the way to becoming one of the most interesting, exciting, and desired fields. For an example of this, we return to Fold-it.



Screenshots of fold-it: The same protein with and without clashes.

Computer Science

of computational biology

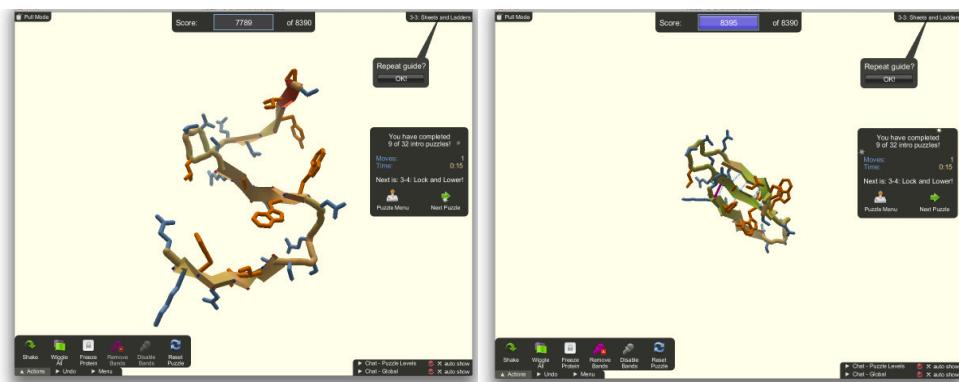
Fold-it's most famous success story so far took place last year, when players solved the structure of a retrovirus enzyme. Because retroviruses like HIV hijack a cell's own processes to recreate themselves and spread, they are hard to fight. Scientists 'assigned' the protein to different groups of gamers such as the "Void Crushers" and the "Contenders" and three weeks later, the gamers had produced a viable structure. The solution to an AIDS-like protein was a huge deal in the scientific world, especially because the structure showed likely deactivation sites on the enzyme, which could lead to a vaccine or even a cure in the future.¹ Scientists tweaked the solution a bit, gave the players huge kudos and congratulations, and continued to do research using the structure.

The reason Fold-it is so successful is because it combines a computer's algorithms with a human's ingenuity. "Rosetta@ home" was a screensaver created by the same group. Once installed, it ran when the computer was idle, trying to solve a protein's structure. People noticed that the computer was making mistakes that humans wouldn't, so the researchers added human input to the mix of algorithms and thus Fold-it was born. Daniels described this as "closing the loop – improv[ing] algorithms based on input from the user."

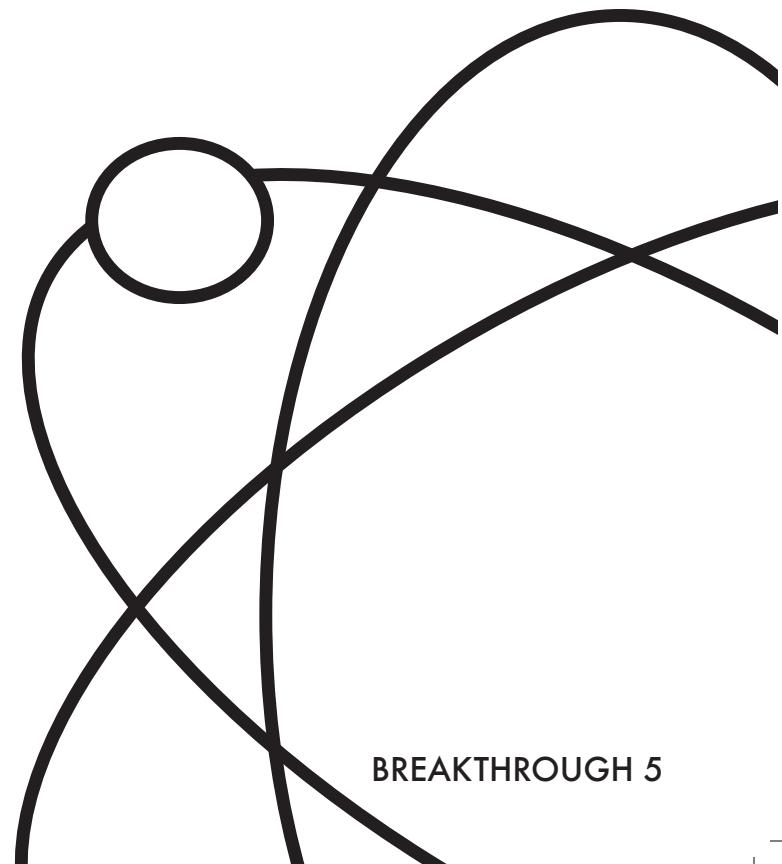
Daniels, Hescott, and Slonim all stressed that computational biology was an "incredibly exciting" and important field. Daniels added that it need be "no more about computers than astronomy is about telescopes;" it's more about problem solving and a certain way of thinking. The research can also be very rewarding. Hescott said that thinking of "applications you hadn't considered before" for your research is one of the most exciting parts.

The fact that "[the field] is moving in many different directions" makes it interesting, and also very worthwhile: with a background in computational biology, a person can focus his or her career on one of many options, says Hescott. The way that computational biology is becoming more prevalent is wonderful and holds great promise, but Slonim noted that we have to be sure to keep up in all fields: "Physicians ... [should] know what to do when a patient comes into their office and says 'I want this genetic test;' ... [including] whether they should get that test and how to interpret the results." Updating education practices throughout the sciences, especially for medical school, is

important so that computational biology can be accessible to everyone. And that is a worthwhile, if ambitious, goal: a world where the powers of computational biology were available to everyone would be revolutionary.



Story by Denali Rao, a sophomore majoring in Computer Science.



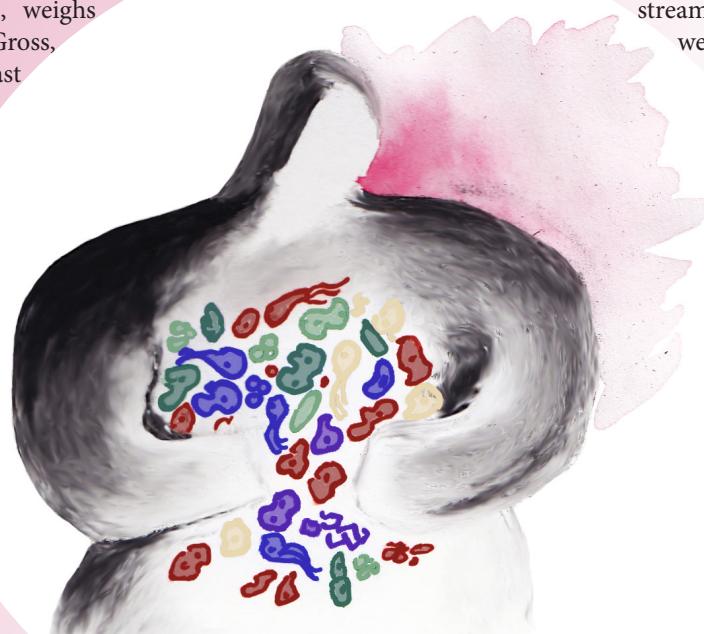
Microbe Magic

The underlying story of bacteria in our bodies

You are absolutely plastered with germs. Nearly every surface of your body, from the inside of your mouth to the inside of your ears, the lining of your digestive tract and every inch of your skin, is coated with bacteria.² They form a community of as many as ten thousand species. Numbering in the hundreds of trillions, their cells outnumber yours in a ratio of ten to one. All told, your microbiome, as this immense population is known, weighs about as much as your brain.² Gross, huh? But not to worry. The vast majority of the bacteria in your body are harmless, and many, in fact, are beneficial. Scientists have known for years that the bacteria in your gut help digest food and produce vitamins, while others may stimulate the immune system. Researchers are, however, still discovering the various advantages your microbiome may lend you. Believe it or not, some of them come from unexpected places.¹ *H. Pylori* infects the stomachs of half the people on the planet, causing ulcers that increase their risk of stomach cancer.² After the discovery of *H. Pylori* in the 80s, the medical community's stance on the bacterium was that it ought to be eradicated.² Luckily, this objective was never reached, for new research indicates that *H. Pylori* has some hefty benefits. Martin J. Blaser, chairman of the Department of Medicine and professor of microbiology at NYU, was interested in the correlation between rising levels of asthma and dropping numbers of children infected with *H. Pylori* after antibiotics became widely available in the late 40s.² His work, and that of other researchers, has produced convincing evidence that the bacterium has something to do with mediating allergic reactions and asthma.² But that's not all. It has also become clear that there

could be a relationship between the disappearance of *H. Pylori* and rising levels of obesity. People who lack the bacterium have elevated levels of ghrelin, the hormone that stimulates appetite.¹ Other bacteria in the digestive tract affect how we metabolize our food. For example, their destruction may lead to weight gain. This has been known since the advent of antibiotics, when scientists realized that feeding livestock a steady stream of antibiotics helped them gain weight at a vast rate.¹ The implications are particularly alarming in the face of the growing obesity epidemic in America and culture-level germophobia.

Luckily, we won't be in the dark about our relationship with our microbiome forever. In 2007, the National Institutes of Health launched the Human Microbiome Project (HMP) as a logical extension of the Human Genome Project, with the intention of mapping out the genomes of every bacterium occupying the human body.³ Various scientists working on the project are hoping to learn about the genetic diversity of our microbiomes and how, like *H. Pylori*, certain bacteria can have positive and negative effects on our health, and how these effects could be regulated. Many hope that cures for diseases such as sinusitis, inflammatory-bowel diseases, allergies, and those associated with our metabolism can be found within our own microbial communities, and early results are promising.³ So the next time you reach for a bottle of hand sanitizer, take a moment to consider the part of your body's vibrant ecosystem you are about to destroy. Then do it anyway, because it's flu season.



Story by Molly Barth, a sophomore majoring in Biology and Dance.

The Solution: Slime Mold

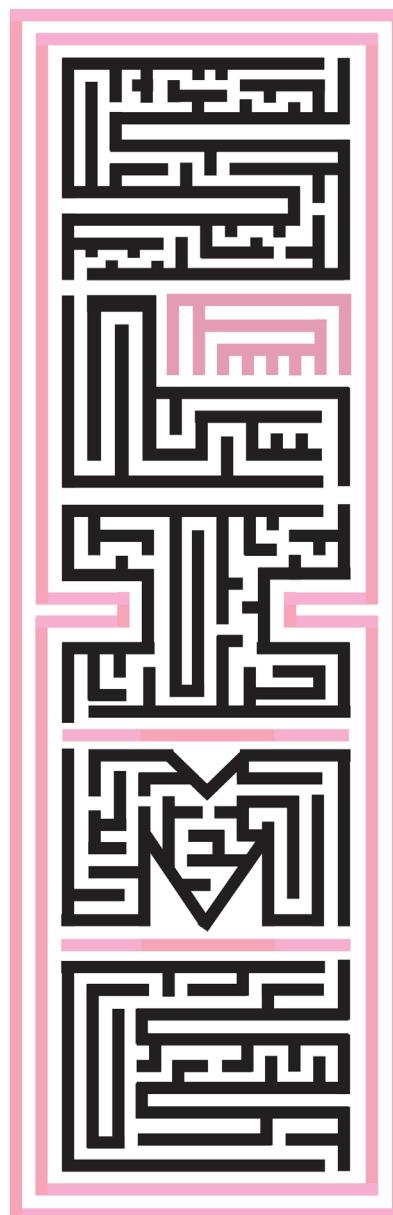
Without a brain, Physarum polycephalum outwits engineers with external memory

It's been known for slightly more than a decade that *Physarum polycephalum*, more commonly called slime mold, is able to do the same work as a team of engineers in a fraction of the time. Despite being single-celled and having no brain or nervous system, it can solve complex optimization problems and even mazes. It works on the basic principle that the slime mold likes oatmeal and darkness and dislikes salt and light.

In 2010 scientists from Kokkaido University in Japan placed a sample of slime mold on a map of Tokyo and the surrounding area. The mold started on Tokyo and oatmeal was placed on each of the cities. Within 26 hours, it formed optimized paths between all of the cities, a near replica of the current rail system.¹

“Whereas we store memories in our brain, the slime mold has no brain, so it stores its ‘memories’ outside of itself.”

The slime mold works by spreading out tendrils in every direction until it has covered the surrounding area. If the slime mold encounters something good, like food, the tendril remains. If the slime mold finds something it dislikes like bright light, the tendrils move on. Once it has explored its surrounding area (in the lab this is usually a petri dish), it retracts all of the excess tendrils. What remains are optimized paths between all of the locations of food.



But without a brain, or memory, how does it remember which areas have food and which don't? In 2012, scientists from the University of Arizona determined that the slime mold uses “externalized spatial ‘memory’ to navigate in complex environments”^[2]. Whereas we store memories in our brain, the slime mold has no brain, so it stores its ‘memories’ outside of itself. The concept of externalized memory is not unique. Most species of ants use pheromones as an external group memory, so any ant can know where food or a colony is. The difference is that the slime mold isn't many entities working together; it is a single celled organism.

To ‘remember’ where it has been, the slime mold leaves behind a trail of “thick mat of nonliving, translucent, extracellular slime.”² When there are still uninvestigated areas, it avoids going over the slime; this way, it doesn't search areas more than once. However, when the slime mold runs out of new areas to investigate, it will travel over the slime.

Physarum polycephalum isn't the only slime mold, but it's one of the two lab-friendly species. Don't try using the mold that grows on your food because you won't get the same results. But you can order *Physarum polycephalum* if you want to try your own experiments!

Story by Amelia Downs, a senior majoring in Physics.

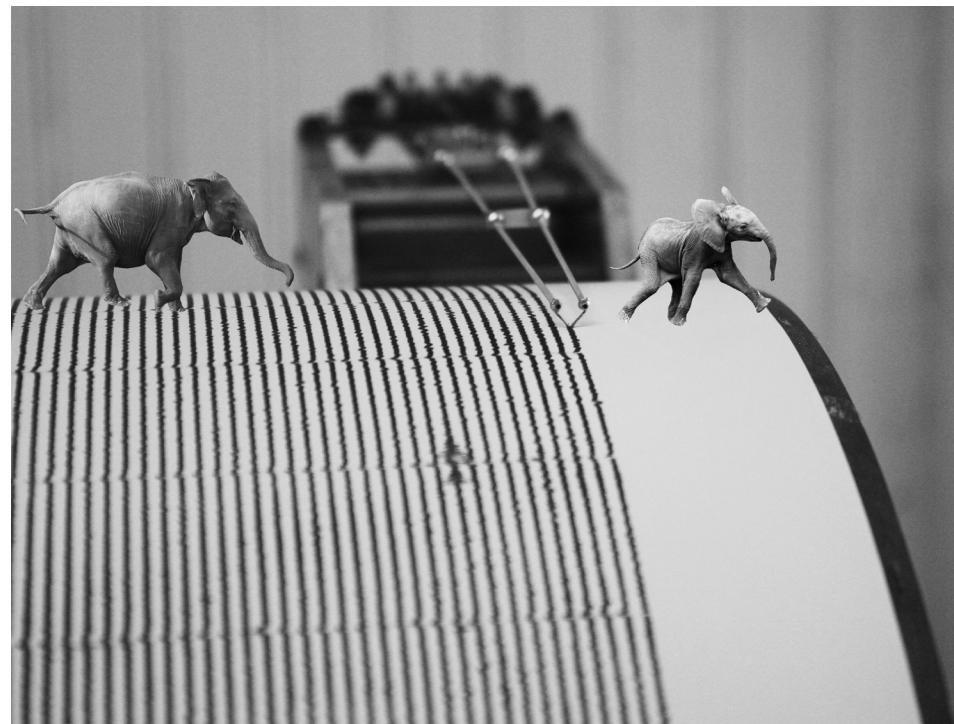
Tufts Installs Seismograph

Professor awaits massive earthquake to test equipment

As part of the United States Geological Society's (USGS) National Strong-Motion Project (NSMP), Tufts University has recently installed a strong-motion seismograph to record ground movements beneath campus. This seismograph installation is part of an East Coast expansion of the NSMP, which, as of Oct 2nd, operated 1078 seismographs at over 700 sites. Since 1932, the mission of the NSMP has been to record "each damaging earthquake in the United States on the ground and in man-made structures in densely urbanized areas to improve public earthquake safety."¹ By recording ground motions over the past 80 years, the USGS has been able to produce national seismic hazard maps and make informed recommendations to change national building codes, leading to a reduction in structural damages, and a critical reduction in fatalities during more recent earthquakes in the US.

As one may suspect, the network of strong motion stations run by the USGS is primarily focused in the West Coast where active plate tectonics yield an incredible amount of earthquakes in the region. Recent earthquakes on the East Coast, e.g. a M4.0 in Waterboro, ME on Oct. 15, 2012 and a M5.8 in Mineral, VA on Aug. 23, 2011 serve as reminders that we do feel potentially damaging ground motions on the East Coast, and should anything hit close to Boston, severe structural damages could result.

This discrepancy in seismographs has led to a divide between the two halves of the country for how seismic hazards can be reliably predicted. In California and the surrounding area, a series of models were developed in 2008 based on recorded data that are now used in hazard potential mapping.² These models, while useful in West Coast applications, may not be truly global in their applicability. One example of why these models break down on the East Coast is that the rock here is much harder and leads to less



Courtesy of Ray Bouknight

attenuation (energy loss) of seismic waves. Thus, for an earthquake along the San Andreas Fault that is felt 200 km away, that same earthquake in NYC could produce ground motions felt from Montreal to the Carolinas.

Since the East Coast lacks the density of instrumentation that California has, most of the East Coast ground motion information currently comes from the "Did You Feel It?" (DYFI) survey put out by the USGS. DYFI data is based on the Modified Mercalli scale, a qualitative measure of perceived shaking and noticeable damage to structures which is rated numerically 1-12 (12 being catastrophic failure). The strength of the DYFI model comes from the volume of individual responses generated. In the recent Waterboro, ME earthquake (M4.0) local feedback poured in, with over 18,000 survey responses within 24 hours of the event.

In large sample sizes the distribution of response will approach normal, at which point the USGS can take the median response for some geographic area (typically zip codes)

and assume that to be the true ground shaking intensity at that location. While this method for data collection is very cheap, it isn't a perfect model since human factors, such as many of us on the East Coast have never felt an earthquake and will tend to overstate the shaking or the improvement of building codes which reduce damage during shaking are not necessarily taken into account for the current Modified Mercalli scale. One improvement the East Coast can make over our current reliance on DYFI data is to increase the amount of seismographs in the region, which will provide numerical data for ground motions in locations where qualitative reports and historic journal entries have been our only source of information.

Civil Engineering Professor of Practice Eric Hines asked in a TuftsNow article "How do we decide what to believe about an event for which we have almost no data, but which could destroy our city if it actually occurred? We must insist that the scientific and philosophical bases for our practice are the best they can be." This has

become the driving thought behind the NSMP's expansion on the East Coast, to provide the best scientific basis possible to build our predictive models on. With the increase in strong motion stations on the East Coast, new models for predicting ground motions will be able to be developed based on geospatially linked quantitative data, ideally leading to more accurate hazard maps. These hazard maps are important because the cost and safety of new buildings, as well as retrofitting existing sites, is highly dependent on the maximum expected ground motion for a given time period. Retrofitting of old buildings is particularly relevant in Boston where "our structures are less ductile-they are less able to yield during an earthquake without breaking."³ Additionally, we only have to consider a couple of types of critical structures, such as hospitals and power plants, to see the importance of accurate hazard mapping. Buildings where the cost of failure is high to

society are built to very rigorous hazard potential standards, but if the maximum potential earthquake is underestimated then catastrophic failure of these structures is possible resulting in loss of life or disruption of essential social commodities.

Prof. Laurie Gaskins Baise, Associate Professor in Civil Engineering, has spent the past few years developing a digital model of the Boston basin used for ground motion predictions. With the addition of the Tufts seismograph and any ground motion records it may capture, she will be able to assess the validity of her model and make improvements on how we expect earthquakes to affect Boston. While the probability of a large earthquake hitting Boston is relatively small, the weak sediments under much of the city and age of buildings could lead to significant damage to structures in even in a moderate earthquake. Therefore, accurate predictions of shaking are

needed for Boston so that engineers can structurally retrofit Boston's existing infrastructure, and design for appropriate earthquakes for all future buildings. Additionally, it is her goal that a live feed of the data collected by the seismograph be available in Anderson hall for educational purposes. While earthquakes are very rare occurrences, there is a constant amount of motion in the ground that students of Prof. Gaskins Baise will be able to analyze and gain insight on what is occurring beneath us. During our observation of the installation of the seismograph, Prof. Gaskins Baise remarked on the catch-22 she now finds herself in, because her research will now benefit from all future moderate to large earthquakes in Boston. It's a funny thing to hope for.

Story by Alex Grant, alumnus of 2013, who majored in Civil Engineering and minored in Geology.

World's Fastest Supercomputer

*The United States
Department of Energy
beats its own record*

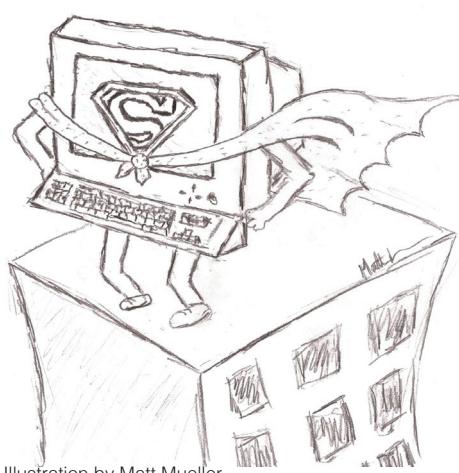


Illustration by Matt Mueller

In October 2012, the Oak Ridge National Laboratory in Tennessee (affiliated with the United States Department of Energy) introduced Titan, its new supercomputer.¹ Considered the most powerful supercomputer in the world, it is capable of computing at a rate of 17.59 petaflops, or over seventeen trillion floating point operations per second.²

The increase in computing power from its predecessors was not a result of additional central processing units (CPUs) like the ones you might find in your laptop; instead, the graphics processing units (GPUs) present in many video

game systems were used.¹ GPUs can perform many more calculations at one time than CPUs, and they consume only moderately more electricity. These processors are responsible for the tenfold increase in computing power over Titan's predecessor, Jaguar.

Titan currently supports six research projects in a variety of energy-related fields: S3D models how fuels combust to improve the efficiency of future biofuels and diesels; WS-LSMS investigates the relationships between electrons and atoms in magnetic objects; the Non-Equilibrium Radiation Diffusion project describes how uncharged

particles travel through space and time; CAM-SE models global atmospheric conditions and tests various climate change mitigation scenarios; LAMMPS is a general-purpose atomic-scale model.³ Denovo simulates nuclear reactions.

This last project, originally implemented on Jaguar, has benefited greatly from the introduction of Titan: simulations of an entire reactor core, which used to take two and a half days on Jaguar, can now be completed in thirteen hours.¹

Story by Ashley Hedberg, a junior majoring in Computer Science.

Useful Junk

The ENCODE PROJECT

At the most basic level of understanding biology, our genes encode for proteins. Expression of different genes leads to production of various proteins in a cell, which then alters cellular function. Understanding of gene regulation in the scientific community has risen exorbitantly since the introduction of this central dogma of biology. ENCODE, or the Encyclopedia of DNA Elements, is a massive research consortium of over four hundred

researchers and \$228 million dollars in funding from the US National Genome Research Institute. ENCODE shows the beauty of the central dogma model as a basis for understanding biological processes, yet expands our knowledge of how non-coding DNA, seemingly useless sequences, play into the central dogma.

Researchers have been exploring the function of non-coding sequences since they were discovered. Dr. Philip Sharp's Nobel Prize winning work discovering intron splicing, the removal of non-coding DNA from transcribed messenger RNA, was groundbreaking in that it offered new ideas about the function of this supposed "junk" DNA. Sharp's research shows how alternative splicing creates an array of different proteins. Splicing is only one of a multitude of epigenetic regulatory processes that regulate the transcribed gene, which ultimately yields a specific phenotype. In 30 publications, all published within a week, in journals including *Nature* and *Science*, the findings of ENCODE indicate that 80% of the sequence in the human genome serves a metabolic function in gene regulation or expression, questioning the idea of "junk" DNA.

Much of the research on non-coding regions shows that, although they do not code for proteins, their role in encoding small RNA regulators, such as microRNA, is immense. Some functions of these regulators include DNA methylation, chromatin interactions, histone modification, and transcription factors and their binding sites. This secondary level of epigenetic

regulation represents a new dimension in understanding the processes governing genetics, beyond just defining sequences as coding and non-coding.

Another facet of the non-coding DNA the ENCODE project studied is its effect on single nucleotide polymorphisms (SNPs). SNPs are genetic mutations in which one nucleotide is different from the normally transcribed gene, often leading to polar mutations in the gene being transcribed. ENCODE data shows SNPs associated with disease are complimented with non-coding DNA elements and many SNPs occur outside the open reading frame, further supporting the idea that non-coding DNA has a larger function.

ENCODE data also indicates regions of the non-coding genome as having other important epigenetic properties. A transcriptional enhancer is a region of non-coding DNA that increases the amount of a particular gene's transcription into RNA. Past data has shown that enhancers do not need to be near the gene that they modify. ENCODE data supports this, as it has discovered 399,124 regions of non-coding DNA with these properties. Furthermore, the data indicate over 70,000 regions of DNA with features of a promoter, a site to which the RNA polymerase recognizes and binds to, starting the transcription of a gene. Additionally, hundreds of thousands of sequences involved in processes slowing the rate of gene expression or gene silencing have been discovered or confirmed by ENCODE data. More specific data sets have defined



Courtesy of National Human Genome Research Institute

Over 80% of the human genome (karyotype shown above) serves a metabolic function in gene regulation or expression.

AGTTTCGAAC~~T~~CTGGCACCTT
AGTTTCGAAC~~T~~CTGGCACCTT
AGTTTCGAAC~~C~~CTGGCACCTT
AGTTTCGAAC~~A~~CTGGCACCTT

ENCODE researchers analyzed the relationships between Single Nucleotide Polymorphism (SNPs) and diseases. SNPs are genetic mutations in which one nucleotide is different from the normally transcribed gene.

specific non-coding regions with specific metabolic activity for particular genes.

Tufts Developmental Biology Professor Susan Ernst commented on the vast data set saying, "The wealth of data produced by the ENCODE project is staggering. This holistic approach to annotating the human genome has revealed that 80% of the human genome is composed of functional elements. The simplicity of this statement belies its significance. For decades, biologists have known that there is more information in the human genome than is found in the small percentage of the DNA coding for 20-30 thousand genes. There are regulators of the genes, regulators of the regulators, and complex gene regulatory networks further influenced by epigenetic factors contained within that 80% of the DNA. It is that information hardwired into the DNA that enables the fertilized egg to develop and differentiate into a fully formed and functional individual."

One important takeaway from this data is the fact that often, disease is a function of a genetic modification. Disease often occurs when a certain protein is either deficient or produced in excess. The multitude of

evidence the ENCODE project provides for epigenetic regulation as a basis for disease and genetic disorders justifies funding of this hot spot in research.

The significance of ENCODE data lies not only in our understanding of human disease, but also our understanding of how we define the genetic basis of life.

Some researchers involved in ENCODE, including principal investigator John Stamatoyannopoulos, believe the data indicates a turning point in the way we define the unit of heredity. He poses the idea that this unit should be defined as the RNA transcript, the end result of the genetic and epigenetic processes, rather than the classical genetic or Mendelian notion of one gene coding for one product. For years, molecular biology has been leading researchers to the conclusion that molecular genetics will ultimately replace Mendelian genetics. "The project has played an important role in changing our concept of the gene," Stamatoyannopoulos says.

Dr. Patrick Forber (M.S. Biological Sciences Ph.D. Philosophy Stanford University), Professor of the Philosophy of Biology at Tufts University agrees and adds

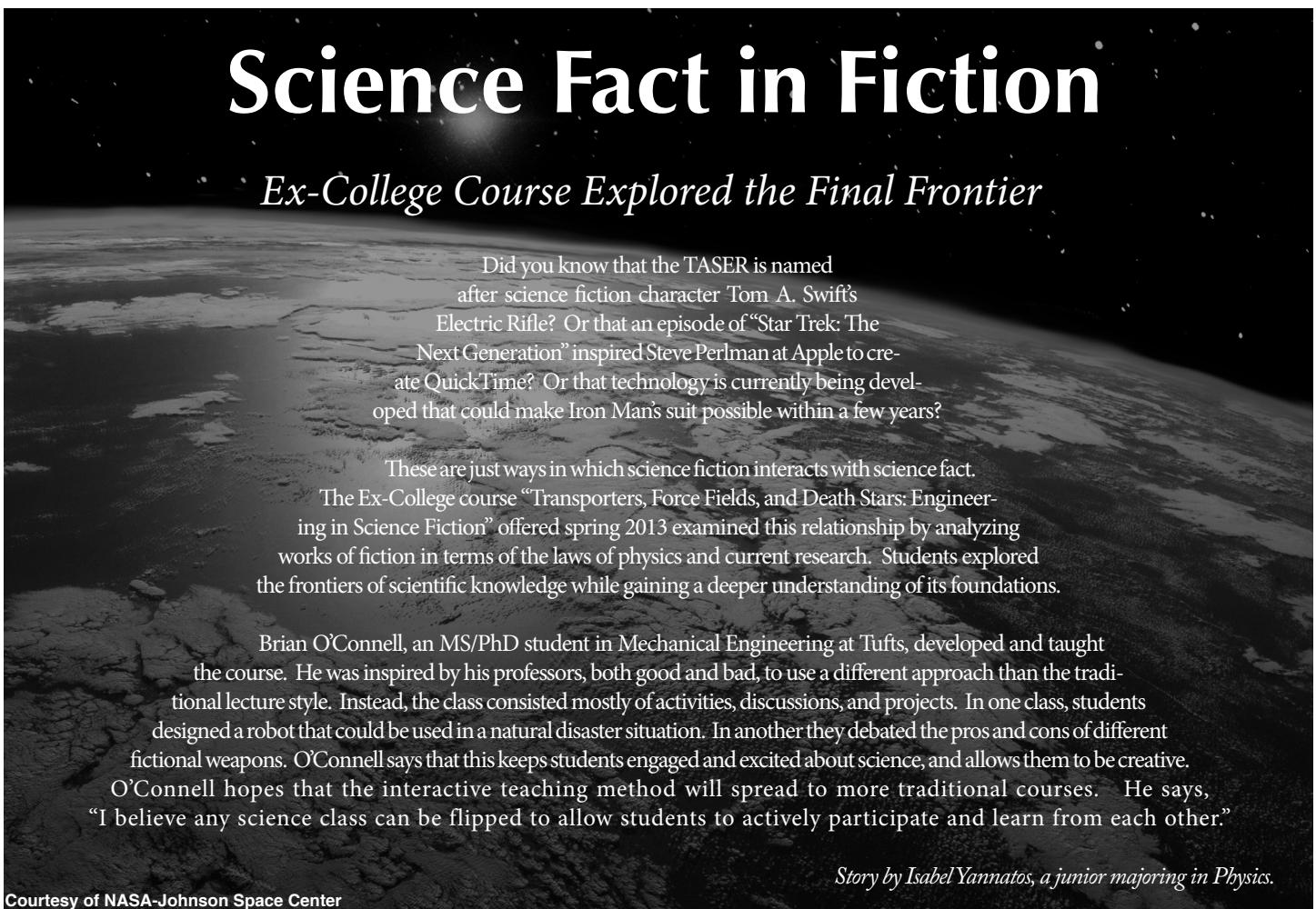
to Stamatoyannopoulos' claim, describing ENCODE's findings as "Part of a wave of research in molecular biology that reveals how just how incredibly complex the causal pathways are from genes to phenotype." Forber continued in stating that he agrees with Stamatoyannopoulos: "I would say that this research eliminates one standard gene concept: we can no longer make claims about particular genes for particular traits. At best we can identify gene complexes for particular traits. So there is a conceptual shift: from 'gene for' to 'gene complex for' or 'genetic regulatory network for'."

The immense significance of ENCODE's will be felt throughout the scientific community as we continue to learn about the significance of epigenetic regulatory processes and General Biology textbooks rewrite their section on "junk" DNA.

Story by Matthew Mule, a senior majoring in Biology.

Science Fact in Fiction

Ex-College Course Explored the Final Frontier



Did you know that the TASER is named after science fiction character Tom A. Swift's Electric Rifle? Or that an episode of "Star Trek: The Next Generation" inspired Steve Perlman at Apple to create QuickTime? Or that technology is currently being developed that could make Iron Man's suit possible within a few years?

These are just ways in which science fiction interacts with science fact.

The Ex-College course "Transporters, Force Fields, and Death Stars: Engineering in Science Fiction" offered spring 2013 examined this relationship by analyzing works of fiction in terms of the laws of physics and current research. Students explored the frontiers of scientific knowledge while gaining a deeper understanding of its foundations.

Brian O'Connell, an MS/PhD student in Mechanical Engineering at Tufts, developed and taught the course. He was inspired by his professors, both good and bad, to use a different approach than the traditional lecture style. Instead, the class consisted mostly of activities, discussions, and projects. In one class, students designed a robot that could be used in a natural disaster situation. In another they debated the pros and cons of different fictional weapons. O'Connell says that this keeps students engaged and excited about science, and allows them to be creative. O'Connell hopes that the interactive teaching method will spread to more traditional courses. He says, "I believe any science class can be flipped to allow students to actively participate and learn from each other."

Story by Isabel Yannatos, a junior majoring in Physics.

An Investigation into Science Learning

While you're sitting in a science lecture of hundreds of students, have you ever wondered if the class could be taught in a more effective way? Though instruction is nuanced, most of the introductory science classes at Tufts are taught in a relatively similar fashion: students sit in a large lecture, rarely ask questions, and are expected to memorize a large breadth of material and successfully demonstrate this knowledge on an exam.

Using Professor David Hammer's Spring Physics 11 classes as a vehicle for studying science learning, alumnae Mary Sypek wrote her senior honors thesis to address just that question – are traditional methods of science teaching in college the most effective?

Sypek, who double majored in Biology and Child Development and intends to eventually teach science to middle or high school students, started thinking about how science classes are taught while taking Biology 13. Even though she felt like a large amount of material was covered, she said she did not feel like she retained much of it after the course. Part of this could be attributed to how the class was run: the lectures were huge, students couldn't ask a lot of questions, and the tests were twenty multiple-choice questions.

Frustrated and intrigued, Sypek started thinking about introductory science courses in general and how they could be taught to best serve the students in them. While taking Development of Knowledge and Reasoning in the Science Curriculum, an Education class taught by Hammer to both undergraduate and graduate students, she investigated this question further through a final project on the Biology 13 class and how it is taught. Sypek conducted this project through interviewing students who had taken Biology 13. Finding success with this strategy, she wanted to continue her research into science learning with a class that is taught in a different way than most other introductory science classes.

Sypek began by interviewing 15 students who had taken Physics 11 with David Hammer in the spring of 2011 or 2012 and asked them questions pertaining to how the course practices affected their learning, how much information they retained, and whether or not they liked the course. Using the information from the interviews, she tried to synthesize the students' answers and

determine how the teaching affected students' learning and their enjoyment of the course.

Hammer, a professor in both the Education Department and the Physics and Astronomy department, conducts research about student learning and has applied what he has learned to how he educates his students. When asked about his teaching style, Professor Hammer mentioned a "change in objectives—in particular toward helping students learn how to learn."

Course practices in Hammer's Physics 11 class differ from traditional large lectures: there are many opportunities for class discussion through clicker questions, students design their own labs, and problem sets are focused on the process of reaching an answer rather than obtaining the correct answer.

“Are traditional methods of science teaching in college the most effective?”

Hammer asks questions in his lectures that are not necessarily based on concrete mathematical equations but instead questions that encourage students to think and discuss with their classmates, Sypek said. For example, "If you pull a string on a spool, does the spool come towards you or move away from you?" In addition, Hammer focuses on being able to derive the formulas instead of memorizing them or reasoning through a problem. As a result, Hammer says that students who can memorize effectively usually earn good grades on traditional exams but can have a hard time in his class.

In her study, Sypek asked questions about the students' description of the class, tests, and labs, how involved they were in attending lecture, recitation or office hours, and how the students felt about the aforementioned subjects. From her investigation, Sypek makes three claims in her thesis. Her first assertion is that the students' enjoyment of the class largely hinges on whether or not they understand what the class was about and further explains that the point of the class is "to think about things that are confusing, to ask new questions, to come up with new ideas, to reason everything down to a very simple level" and in fourteen out of fifteen cases, if the students understood this, they enjoyed the class.

Are we effectively teaching science to students?

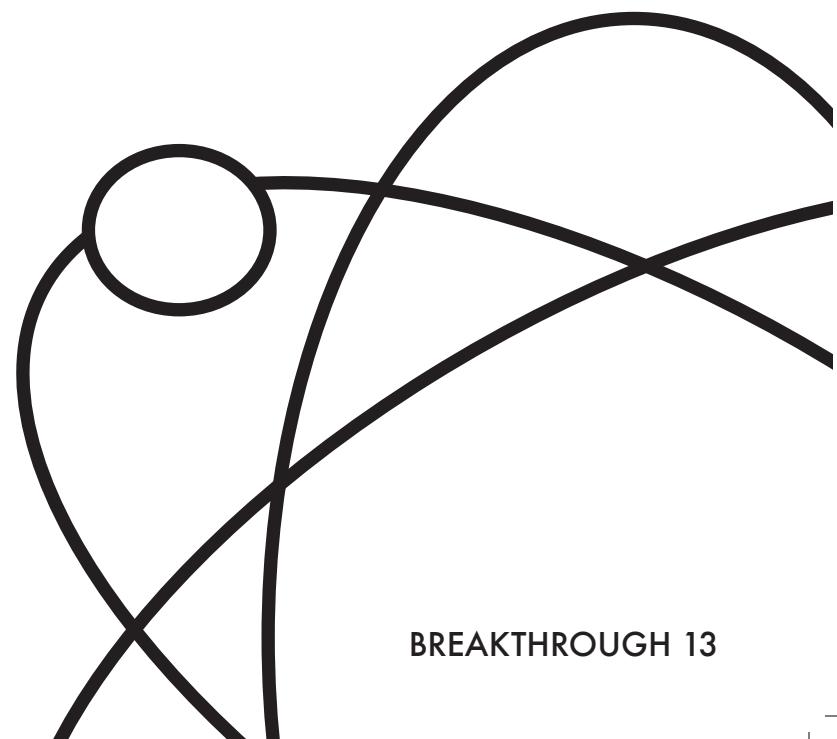
Her second claim is that there are varying degrees of understanding the class. Understanding and liking one part of the class didn't necessarily mean that a student understood and liked all aspects, and vice versa. Sypek's last conclusions involve why these inconsistencies happen: her hypothesized variables include student epistemologies, the amount of support they have to work through a question, and a student's concern for their grades. She explains that it's harder to "dive in and enjoy it" on a graded test like they can in lecture.

Sypek acknowledges that her study was small and did not bear conclusive data, but believes that her work could help to inform future studies about collegiate science learning. It would serve future studies to have a control to compare with this type of learning and to have more quantitative data, she says. She also believes it would be interesting to be able to follow students through the course of a class, have students live blog about their experience in a class, or to develop a survey to enable future studies to have more representative data.

Story by Julia Hisey, a senior majoring in Biology.



Courtesy of Tufts Physics Department



BREAKTHROUGH 13

Derek Mess Bridges Research, Classroom

The Projects Laboratory course, designated CHBE 0052, is required of all chemical engineers at Tufts; students are sorted into teams to tackle unique semester-long research assignments in disciplines from electrochemistry to advanced fluid dynamics. As the coordinator of this course, Professor Mess draws upon his experience in the industry and upon the work of his colleagues in the department to devise new topics to challenge students in their final semester of study.

Mess earned his PhD in Chemical Engineering from MIT. With a deep appreciation for the scientific literature he devoured as a graduate student, and looking to avoid the high-stakes game of publishing papers, he found himself drawn to commercial research and development. He got his start as a group leader for Alcan Aluminum Corporation, which had a small ceramics lab in Cambridge.

"It's just great to be in a commercial environment," Mess says. "You have exposure to a much broader spectrum of people and career types." His time at Alcan fed a growing interest in the business and economics of the industry, where he felt his skills as an engineer could be applied as readily as in the lab. When business slowed down at Alcan, Mess struck out on his own and founded Cambridge Microtech Inc., where he focused on developing novel materials and scaling up production processes. The work he began at Cambridge Microtech lives on in CHBE 0052, where one team of class of 2013 graduates developed hollow ceramic microspheres reminiscent of the thermal barrier coatings Mess once produced for NASA.

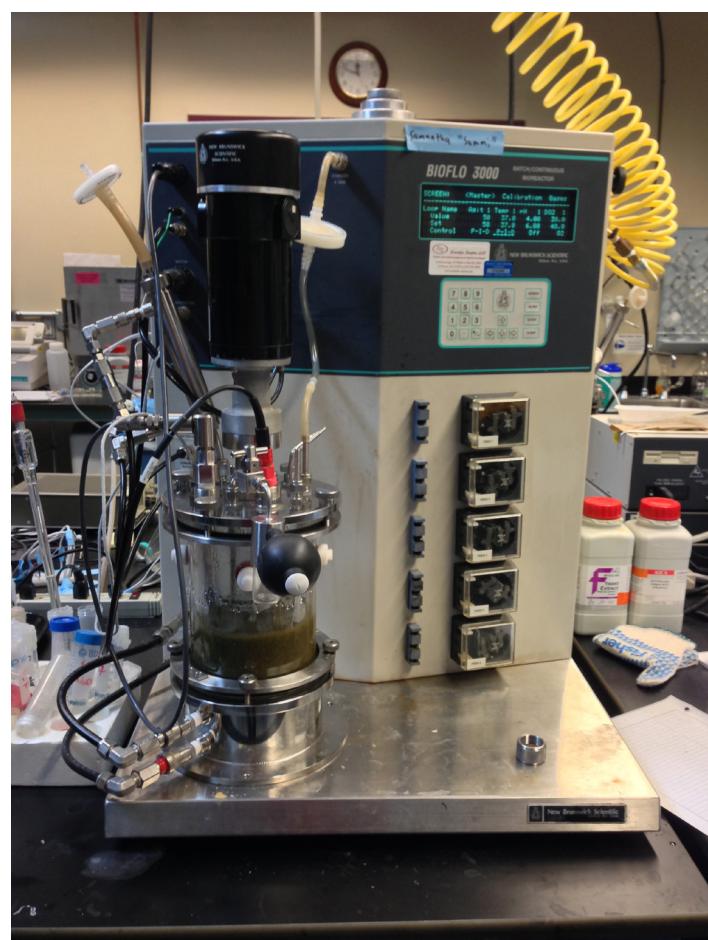
Other projects in the capstone course have stemmed from Mess's other research interests, such as advanced energy technologies. Some students, for example, investigated the production of ethanol from duckweed. Another group, featuring seniors Christopher Beltis, Anthony Burzesi, and Christopher Lowe, saw an opportunity to showcase their research at this year's Tufts Energy Conference. The three were named finalists and received second prize for their work on a zinc-cerium flow battery.

"I want to see us do more of that," said Mess of their achievement. "I don't know that our profile is as high as it should be." He envisions a closer relationship between the University's researchers and The Fletcher School as a means to enrich discussions of energy and environmental policies. Mess has also been reaching out to local tech companies to develop and sponsor new capstone research projects. This year, one group of Tufts seniors is working with Cambridge Polymer Group to develop soft gel-matrix biomedical materials for use in knee joints, and another is collaborating with Millipore to investigate a novel method for clarifying *E. coli*-derived products. These projects in particular

neatly encapsulate Mess's philosophy of preparing seniors for life after graduation.

"A lot of times in school you're asked to calculate the answer," Mess notes, "but there isn't one answer... I'm trying to bring in the idea of practical problem solving, addressed by the fundamentals that underlie the discipline." By emulating the open-ended nature of commercial projects, Mess strives to deliver an enlightening experience for his students that stretches the boundaries of an ordinary chemical engineering curriculum.

"If you don't take [a course], you'll never need it," he says, quoting a lecture by a Harvard applied mathematician he once attended. It is an idea that has stuck with him as he has reentered



Courtesy of Dan McNeely

Long Bin Pan, Ryan Pandya, and Anh Phong Tran are using this bioreactor to investigate the fermentation of duckweed for biofuel production. In another project, the reaction is being monitored with equipment designed by John Abel, Earl St. Sauver, Kim Stachenfeld, and Jay Stotsky in order to produce a neural network model of the batch fermentation process.

CHBE Professor has worked to expand the role of research in curriculum.



Courtesy of Dan McNeely

the world of academia. "It's a good reminder to follow our passions and explore things that aren't in the curriculum," Mess explains, "and of course the projects course is a good example of that. It's open-ended, and there are groups that are going to find a lot of excitement about pursuing things off the trail. It's a good way to get a taste of the real world."

"...I'm trying to bring in the idea of practical problem solving..."

In the future, Professor Mess hopes to incorporate more projects in disciplines such as bioengineering and energy materials, which he feels are two emerging research strengths in the department. He is investigating solid oxide fuel cells as a possible research target for their applicability in large-scale high-temperature energy production, and is always reaching out to his colleagues within the department for new ideas. His advice?

"Make it something you'd want to do."

The results are challenging projects that give students a long leash to be creative, make mistakes, and develop focus. Those tackling recurring research topics also have the opportunity to build upon the work done and the knowledge gained by students in previous years. Mess enjoys the continuity that this creates in the department.

"It shouldn't feel like a chemistry lab you did in your first or second year," he says. "What we do really does make a difference."

Story by Dan McNeely, alumnus of 2013, who majored in Chemical Engineering.

Tufts Idea Exchange



Courtesy of Sujata Bhatia

Last April, Tufts hosted the fourth annual Tufts Idea Exchange in Cabot Auditorium. The event featured student, faculty, and alumni speakers, giving lectures in a format modeled after the TED conference. This year's TEX speakers focused on topics ranging from musical appreciation to mental health, presented in eight to ten minute talks.

Sujata Bhatia, MD, PhD, PE, a professor of Chemical and Biological engineering at Tufts, gave one of the more scientifically focused talks of the night. Dr. Bhatia spoke about her research on sustainably-produced medical devices made from bio-materials. She claims that these materials, derived from environmental products such as fruits and vegetables, can be used in a clinical setting as implantable medical devices due to their molecular compatibility with the human body. This compatibility is established by the fact that these materials are comprised of "bio-polymers", large biomolecules made of smaller, monomeric subunits. Natural bio-polymers in our bodies include nucleic acids, proteins, and carbohydrates.

Since these devices would require agricultural growth, Dr. Bhatia claims that focusing on this new class of medical materials would allow developing nations with broad agricultural resources to take part in biomedical research. In addition, this would allow engagement of both developing and developed countries in advancing medical treatments around the world.

Dr. Bhatia has said that she was "thrilled" to be chosen as the faculty speaker for this year's TEX event. " I want students to believe in their ability to change the world. Even if a student chooses not to study science or engineering, issues regarding healthcare, sustainability, and innovation affect all of us."

Story by Stephen Walsh, a senior majoring in Biology.

Life After Tufts:

Alumni who majored in science offer advice to



Avigya Shrestha
Biopsychology, A'12

Looking to go to dental school, Avigya currently works at BU as a research assistant studying ways to prevent cavities in young kids that live in public housing. At Tufts, Avigya was involved with TASA, Tufts Literacy Corps, Jumpstart, and TuftScope.



Marissa Fruchter
Clinical Psychology, A'12

Marissa is currently pursuing her PsyD at Widener University, and also has a practicum placement at a community mental health center in Wilmington, Delaware. At Tufts, she was a member of AOII, the Tap Ensemble, and TDC.



Dan Rizzo
Engineering Physics, E'12

Heading to a PhD program at "either Penn, Chicago, or Berkeley" next year, Dan currently works in Professor Cristian Staii's biophysics lab, which he has been a part of since an undergraduate. Outside of classes, Dan was involved in the Society of Physics Students, the Observer, and a classical sax quartet.



Natalie Perry
Engineering Physics, E'12

Currently taking a year off abroad, Natalie lives in Spain and works as an English teacher. At Tufts, she was Vice President of the Society of Physics Students, a member of the Women's rugby team, volunteered with the Science Club for Girls, Boston, and minored in Geology.



Arielle Carpenter
Psychology & Community Health, A'10

In addition to doing research in the Nutrition and Behavior lab in the Psychology department, Arielle was involved in the Tufts Tap Ensemble, the Culinary Society, and Tufts Hillel. She has completed her BA/MPH at the Tufts School of Medicine and obtained her MBA from the Collège des Ingénieurs in Paris. She currently works as the Project Manager of the Global Employee Wellness Program at Sanofi.



Lucas Schlager
Biology, A'11

A member of Dr. Catherine Freudenreich's lab since his freshmen year, Lucas continues a focus on research today while working for ReadCube, a software that "makes working with scholarly literature easier, faster, and more efficient". At Tufts, he was also involved with the FieldEx program.



Jackson Dolan
Mechanical Engineering, E'11
Masters in Mechanical Engineering, Tufts School of Engineering, 2012

Jackson is working for HART Technologies, a defense contractor in Manassas, Virginia, and "[tinkers] incessantly on various projects at home". At Tufts, he was a part of the Frisbee team, ASME, Breakthrough, and had tutoring, music, and restaurant jobs.

What was your favorite class at Tufts?

AS: I really liked all of the Ex-college classes I took and Endocrinology with Romero

DR: Intro to Quantum Mechanics II

AC: Community Health 1, Dance Movement & Creative Process, West African Dance, Kathak Dance, Sephardic Tradition, Introduction to Yiddish Culture, and Education for Active Citizenship.

LS: Tough call. I know this is a bit of a non-answer, but I'd say a tie between Counterinsurgency Seminar and Seminar in Darwinian Medicine.

JD: Inventive Design and Mechatronics

MF: It's a tie between Flowers of the Alps, which I took at Tufts in Talloires, and Food, Nutrition, & Culture.

NP: Phy61 Quantum Theory!

Did you participate in research at Tufts?

DR: I worked in Prof. Cristian Staii's biophysics lab. Experimental work centers around experiments that can be performed with the Atomic Force Microscope. My personal research has involved some nanopatterning with the AFM, though the majority of my time has been spent developing a theoretical model for neuron (brain cell) growth.

LS: My research in Dr. Freudenreich's lab investigated the role that non-triplet, AT-rich repetitive DNA plays in chromosome fragility. The classic model here is that trinucleotide repeats form stable secondary structures which physically impede the normal DNA replication, recombination, and repair processes, causing [expansions or contractions] of the repetitive section, or [chromosomal breakage]. I studied a pentanucleotide repeat which does not form stable secondary structures, but does increase chromosome fragility the way its trinucleotide brethren do.

JD: I tried to use a Lego NXT and LabVIEW to control a robot so

Alumni of Science

current Jumbos and tell us where they are now

it could balance on a ball. My Masters thesis involved looking at the solidification process of undercooled iron-cobalt alloys.

NP: I did research with Professor Marchesini in Astronomy. In my project, I studied the evolution of supermassive blackholes as a function of the host galaxy properties- how they changed with redshift and luminosity.

How has a science degree at Tufts prepared you for what you are doing now?

AS: I don't get overwhelmed with everything I have to do and I am always one of the first people in my office to offer to take on more.

DR: It has prepared me to solve large-scale problems by thinking of them in terms of a series of concrete, well-defined and testable questions.

AC: Graduating from Tufts with a B.S. in Psychology, being highly involved in academic research throughout my university studies, and having some published journal papers to my name makes me feel confident that I can succeed in a scientific setting.

LS: I'm of the opinion that the cognitive skills taught by academic science are applicable to nearly any job. On the other side, having spent time doing research is very helpful in terms of understanding our customers. Whether I'm visiting a lab to help a user out with a technical issue or collaborating with our developers on a new feature, drawing upon past experience in the lab is often essential.

JD: The biggest thing engineering did for me was give me the confidence to know I am capable of figuring anything out. The key is to not get intimidated by the task and just start working. However, with regards to the fields I'm working in now, I'm glad I went with mechanical since it seems to me the most difficult to teach yourself the basics using only the internet.

MF: It is rare for universities to offer undergraduate degrees in clinical psychology, as opposed to general psychology. This allowed me to take more specialized courses. I was able to learn specific techniques from different models of psychotherapy and practice skills for building therapeutic relationships with patients.

NP: Clearly, my science degree has very little to do with my current job, but I would argue that studying science, especially physics, gives you life skills that are applicable no matter what you do. The ability to reason and problem solve and make connections!

If you could offer one piece of advice to a science major, what would it be?

AS: Don't forget to make time for yourself. Watch that crappy TV show religiously with your roommate, get lost in Boston and have 3 hour brunches with your friends in Dewick. Your memories are just as important and valuable as your grade in that one class.

DR: Keep it up. The subject you are studying is much more interesting than what you'll find in other fields.

AC: For me, finding a way to bring pure research data into mainstream media, which can be understood by the public, is the most

challenging and most essential part of our work in science.

LS: Do research! Beyond just helping you get into grad school or med school or whatever, you'll make great friends in the lab, you'll be enriched by discussing what you're doing with people who know way more about it than you, and it puts you in a position to be asked tough questions you might not be able to answer.

JD: Take courses outside of your major. The more experiences you have, the easier it'll be to learn things in the future, and the more confident you'll be approaching life.

MF: Take advantage of any opportunities that Tufts offers to get experience in your field and explore your interests. Do an internship, participate in research, or talk to your professors about their interests and their careers.

NP: Love your field and what you do, but never limit yourself! Don't hesitate to take a class in another branch of science, or even something totally unrelated. Tufts has so many opportunities, take advantage of anything and everything.

What's next for you in science?

AS: Dental school, fingers crossed!

AC: Besides being employed for a pharmaceutical company, I currently work very closely with the Institute of Cardiometabolism & Nutrition at one of Europe's most renowned academic hospitals, Hopital Pitie-Salpetriere in Paris. This experience has given me the perfect opportunity to combine working in industry but also staying close to my roots in academia.

LS: Not sure!

JD: It'd be great if one of my side projects suddenly made me a millionaire, but until then, I'm going to keep learning and making stuff and try to get a job at a product design firm.

MF: I hope to be a psychologist for the more severe and chronic populations, like people with schizophrenia and other psychotic disorders. However, I plan on using the rest of my time in grad school to explore as many areas of psychology as I can.

NP: When I come back to the US, I will be looking for work somewhere in the environmental field. Last summer I interned with the Mystic River Watershed Association, and I really enjoyed water quality science and being in the field.

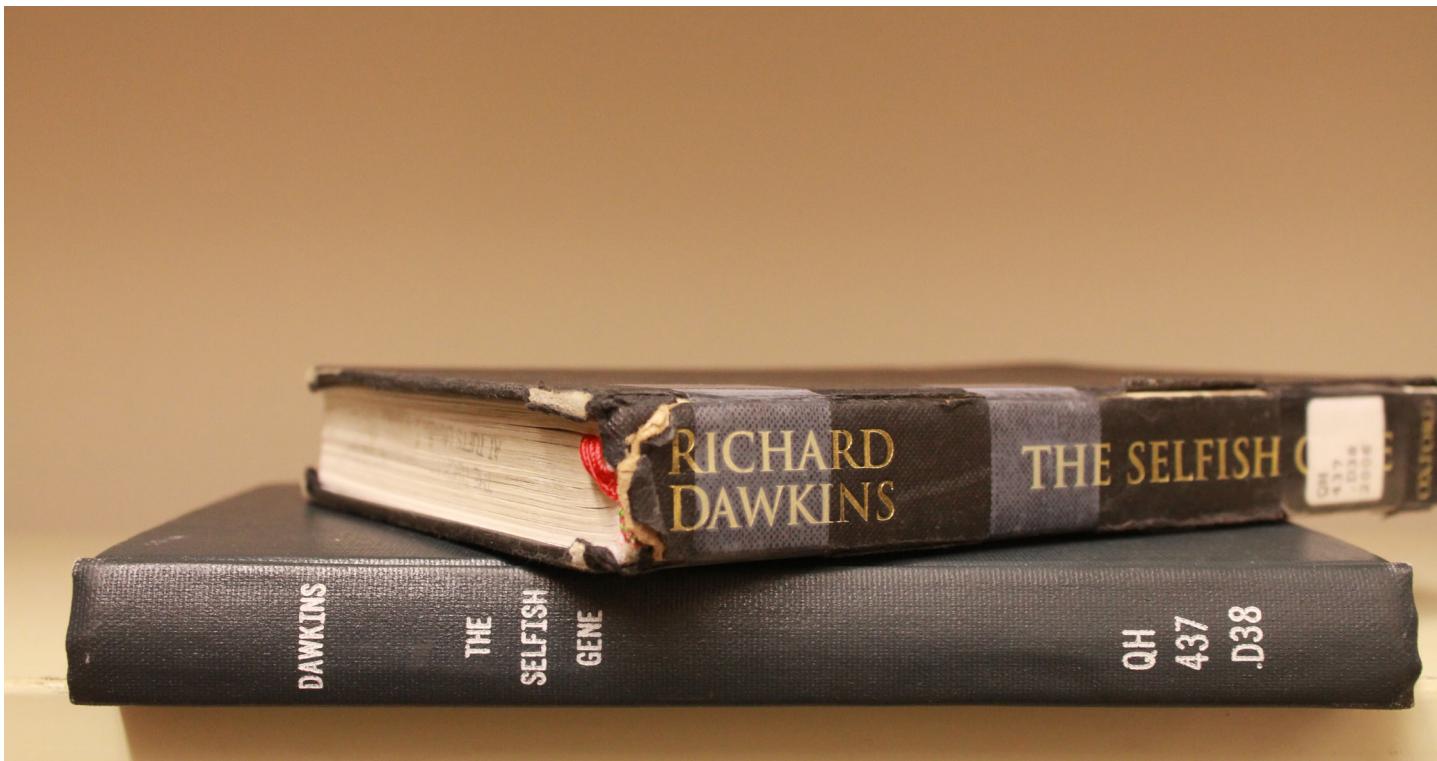
Nerdiest thing you did at Tufts?

DR: Dress up as various organelles with my friends and collectively form a cell for Halloween. I was the nucleus.

LS: Well...there might be a vial of my whole genomic DNA in the -80 freezer of Dr. Freudenreich's lab.

JD: I was responsible for the Tufts mp3 Experiment and was a cofounder of Cardibo (the laundryview for the gym site that is currently being upgraded). I may have assumed nerdy was synonymous with awesome in that question.

NP: I got a noise violation for discussing physics and anthropic reasoning too loudly!



Courtesy of Alex Azan

Richard Dawkins's *The Selfish Gene*

In his book *The Selfish Gene*, Richard Dawkins defines the term “gene” as a fundamental replicator for biological systems. A biological replicator is considered to be an entity that is able to undergo asexual reproduction. Biologists and chemists believe that during the time period in which life evolved, “the primordial soup,” there existed molecules with certain properties that allowed for self replication.¹ However, Dawkins believes that the copying mechanisms of these replicators was not perfect, and therefore may have been led to amplified reproductive and gene mutations. Despite these imperfections, Dawkins also suggests the possibility that some of these errors maximized inclusive fitness. Over time, the amplification of “good” errors eventually led to more complex relationships between replicators. According to Dawkins, these replicators gradually evolved into frequently successful genes and were passed on from one generation to the next.

Many evolutionary theories in the past focussed on individuals as the concrete basis of evolution. It was perceived that individual organisms evolve based on their success within their surroundings. On the other hand, Dawkins uses multiple examples in his book to emphasize the importance of genes being selected for “future generations,” despite what might be best for the “individual.” As a result, Dawkins claims that the gene is the fundamental replicator that helps us analyze family relationships, altruism, and other similar topics in light of his theory. Throughout his book, Dawkins is able to largely shift the modern biology mindset towards one that is evolutionarily geared.

Although *The Selfish Gene* was written well over thirty years ago, misconceptions of the theory are still prevalent today. One of the main criticisms of Dawkins’s main theory is that the idea of a gene “wanting” a particular outcome or “being selfish” is absurd. Many would agree that a portion of a chromosome is not complex enough to have desires or any other form of human emotion. Yet it seems that even authors who understand this theory have a tendency to tell readers about the “will” of a gene. In the introduction to the 30th anniversary edition, Dawkins himself highlights the ways in which the implications of his statements about replicators could be misleading. Moreover, he believes that he should have listened to a colleague’s recommendation that the book be named *The Immortal Gene*. However, he does give a justification for his chosen title and for using such human-like qualities when describing the genes.

By taking his readers through the journey of *The Selfish Gene*, Dawkins leaves them with a theory that attempts to explain one of the most unusual phenomena of nature. By delving into themes ranging from gender differences to the evolution of culture, Dawkins has not only written a truly comprehensive book, but has also crafted a scientific work of art.

Story by Zach Tripp, a sophomore majoring in Computer Science.

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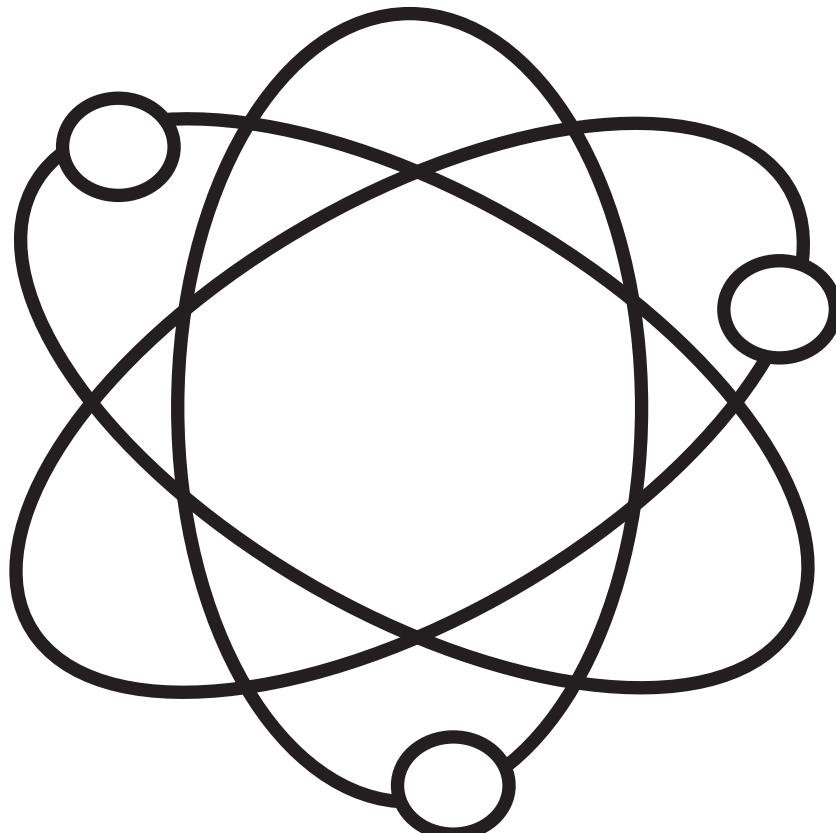
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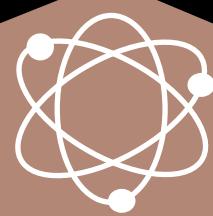
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