Volume 39 Spring 2020

MURJ

Massachusetts Institute of Technology
Undergraduate Research Journal

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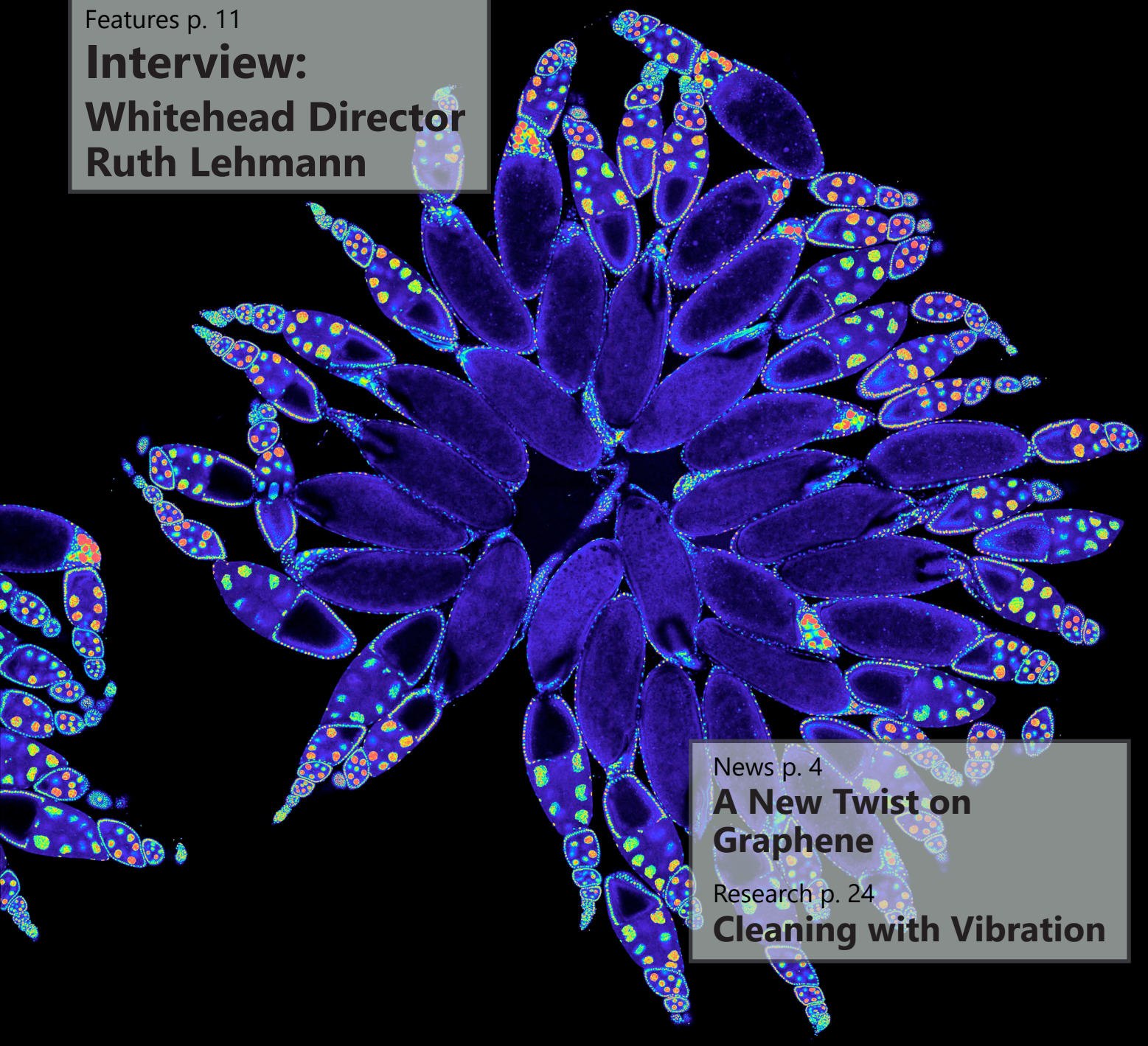
Whitehead Director Ruth Lehmann



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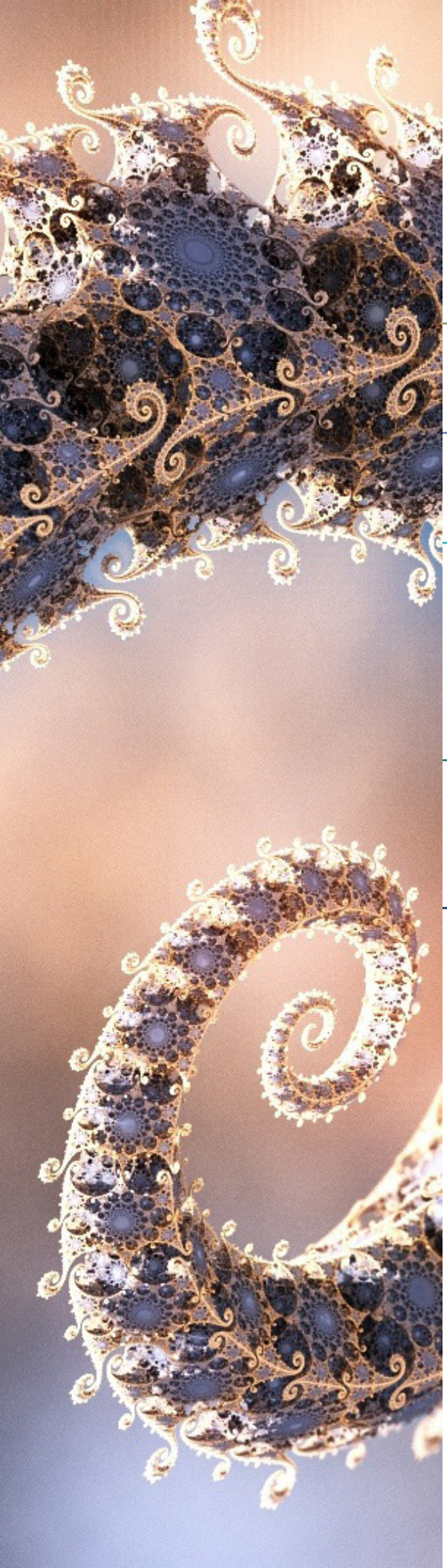

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Massachusetts Institute of Technology

UNDERGRADUATE RESEARCH JOURNAL
Volume 39, Spring 2020

May 2020

Dear MIT Community,

We are delighted to present the 39th issue of the MIT Undergraduate Research Journal. Over the past few months, the COVID-19 pandemic has scattered the MIT community, but our undergraduates continue their research. In this time of crisis, the ongoing efforts of scientists and the open sharing of research are absolutely necessary. We are proud to showcase the hard work and creativity of MIT students to the world.

In this issue, we feature original student work on the application of automated text summarization methods to medical literature, the characterization of small-scale interferometry for astronomical imaging, the use of vibration to clean the reverse osmosis membranes needed for desalinating water, and the deployment of nuclear magnetic resonance techniques to study the structure and motion of biomacromolecules.

In addition, this issue highlights current MIT research on the special properties of twisted graphene sheets, a computer vision model inspired by the way the human brain processes images, and a deep-learning approach to autonomous vehicles. Also featured is an interview with newly elected Whitehead Institute Director Ruth Lehmann about her career, research, and vision for the Whitehead.

Biannual publication of this journal is always a collaborative undertaking, but this semester especially we would like to thank our editorial board and contributors for their hard work and commitment in a time of great uncertainty. In addition, we would

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like to thank all the undergraduates who shared their research with us and the greater MIT community.

For previous issues of the MIT Undergraduate Research Journal, please visit our website at murj.mit.edu. If you are interested in contributing to future issues of the MIT Undergraduate Research Journal, we invite you to join our team of authors and editors or submit your research for our Fall 2020 issue. Please contact murj-officers@mit.edu if you have any questions or comments.

Best,

Allison Huske
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Massachusetts Institute of Technology

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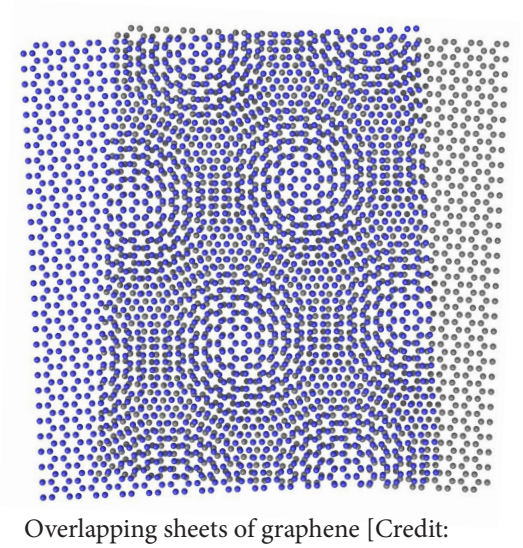

Overlapping sheets of graphene [Credit: National Intitute of Standards and Technology]

PHYSICS

Graphene sheets twisted at 'magic angle' electrify physics

The Jarillo-Herrero Group explores superconductivity and other exotic properties of twisted bilayer graphene

Graphene, touted as the wonder material of condensed matter physics, has generated much excitement since its discovery in 2004. Now, the Jarillo-Herrero Group at MIT launches a new wave of graphene enthusiasm by bringing a literal 'twist' into the material. They found that when two sheets of graphene are misaligned at a 'magic angle,' superconductivity and other strange behaviors emerge.

Graphene is the world's thinnest material, a single-atom thick lattice of carbon atoms arranged in a honeycomb pattern. Although the exceptional strength, thermal conductivity, and electrical conductivity of graphene are long established, its intrinsic superconductivity came as a surprise. This discovery could revolutionize the development of high-temperature superconductors, quantum computers, and low-cost energy solutions.

Jarillo-Herrero's team stacked two graphene sheets, twisted them at small angles between 0 and 3 degrees, and then cooled the device to a fraction of a degree above absolute zero. At the magic angle of 1.1 degrees, the material acted like an insulator, an unexpected behavior from the world's best conductor. When they applied voltage, the device transformed again into a superconductor–an even more shocking discovery.

Their crucial insight was that a single graphene-based device can be tuned to become an insulator, a superconductor, or anything in between. "We can explore all those physics in one device electrically, rather than having to make hundreds of devices. It couldn't get any simpler," says Pablo Jarillo-Herrero, the team's leader.

These properties cannot be observed in perfectly aligned graphene layers. But when they are rotated relative to each other, the graphene superlattice displays different moiré patterns. Precisely at the magic angle, the electrons in the sheets interact more strongly with each other, giving rise to curious physical effects.

"A single graphene-based device can be tuned to become an insulator, a superconductor, or anything in between"

In 2011, Allan MacDonald (UT Austin) and Rafi Bistritzer (Applied Materials-Israel) already predicted the connection between moiré patterns and electronic properties. But their idea was largely dismissed until Jarillo-Herrero pursued it experimentally in MIT's Building 13.

When the team finally published in *Nature* in spring of 2018, their results electrified the physics community. "I haven't seen this much excitement in the graphene field since its initial discovery," says physicist Chun-Ning Jeanie Lau in an interview with *Nature*.

This work birthed a new field dubbed "twistronics." Now, physicists around the world are exploring other twist angles and other 2D materials besides graphene. Earlier this year, Jarillo-Herrero, MacDonald, and Bistritzer received the prestigious 2020 Wolf Prize in Physics "for their pioneering theoretical and experimental work on twisted bilayer graphene."

When asked about his recognition, Jarillo-Herrero says "I see it as an acknowledgement…by the global physics community for the work of my fantastic group of graduate students and postdocs, as well as my collaborators here at MIT and around the world." He also hopes that more young physicists will explore the beautiful field of 2D materials.

— Hillary Diane Andales

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COMPUTER SCIENCE

A more human model of computer vision

Efficient inverse graphics computer vision uses artificial intelligence to approximate the way the human mind processes images

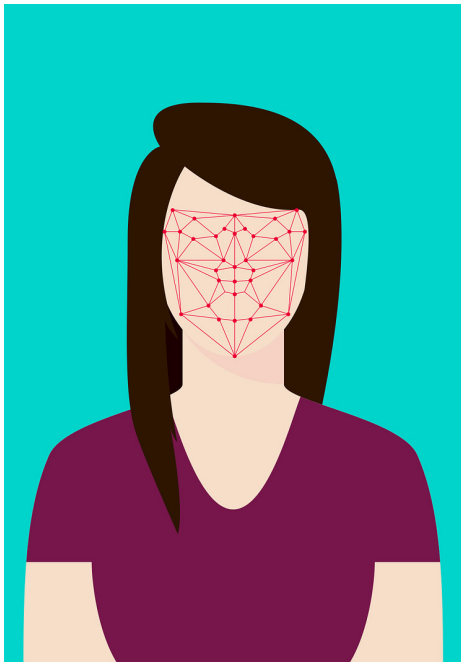
In the face of creative drought, when innovation calls and we seem to lack any good answers, humanity turns to a special, impunitive kind of plagiarism. We plagiarize from nature. Early airplane designs emulated avian wings; the noses of Japanese bullet trains were reshaped to mimic kingfisher beaks; gecko feet continue to influence climbing glove designs.

The human body is not exempt from this plagiarism. In fact, it is a prime candidate to plagiarize, mostly because of one organ: the brain. The human brain can carry out astounding processes at baffling speeds, all *without* leaving our head spinning.

One process worth special interest is vision, the plagiarism of which has helped birth the field of computer vision, a field that attempts to use artificial intelligence to train computers to interpret and understand the world through vision. Though we have a great understanding of how human vision functions on a basic level, the big colorful balls in our head that hook up to the brain enable us to do a number of things that we cannot explain but would like to emulate.

In a move toward advancing computer vision and improving our understanding of human vision, a team led by former MIT postdoc and Yale assistant professor of psychology Ilker Yildirim and containing MIT professor Josh Tenenbaum has created a computer model called efficient inverse graphics that better approximates the human faculty for quickly perceiving complex scenes in very rich detail.

Currently, high-end computer vision systems can be trained to recognize faces and objects by taking in image data that classifies the contents of the image. The model that Yildirim and his team designed uses a different approach. The AI is taught how to take a two-dimensional image and, from there, generate a three-dimensional representation.



[Credit: Teguhjati Pras via Pixabay]

First, the AI adds specific features to the two-dimensional image that are characteristic of three-dimensional perception such as texture, curvature, and lighting, among others. This produces what the group calls a "2.5-dimensional representation." These 2.5-dimensional representations correspond to how an object looks from a specific viewpoint. Then, the AI constructs a three-dimensional image that does not depend on viewpoint by combining 2.5-dimensional perspectives together. The AI can then run this process in reverse to identify three-dimensional objects.

This AI system has already seen impressive results. The research team compared the results of humans, typical high-end computer vision programs, and the new computer vision program for a task in which participants were asked to recognize faces. Results were recorded for instances in which tested faces had one of their properties — such as texture, curvature, or lighting — distorted. Humans perform predictably poorly when certain properties are removed. The noteworthy fact is that the researchers' new program performs more similarly to humans on the task than current computer vision programs do. This suggests that the new model may in fact be a better reflection of how vision is processed in the human mind.

It is important to note that this study used an image pool that only contains faces. The researchers plan to test the model on other non-face objects. Similar results for these tests would augur well for the future of computer vision. If, however, nothing comes of these new tests, we can still be sure of one thing. We will continue to do our best job of plagiarizing nature to push the boundaries of human knowledge and capabilities.

— Ryan Conti

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ARTIFICIAL INTELLIGENCE

A novel deep learning-based approach to autonomous vehicles

The Toyota-CSAIL Joint Research Center aims to reduce traffic casualties through the development of autonomous vehicle technologies

[Credit: Julien Tromeur via Pixabay]

The Self-Driving Vehicles project under the Toyota-CSAIL Joint Research Center, led by Director of CSAIL, Professor Daniela Rus, aims to further develop autonomous vehicle technologies geared toward the reduction of traffic casualties and accidents. It is focused on the development of precise and sophisticated decision-making algorithms, as well as systems that can operate reliably without human input, to perceive and safely navigate vehicles' surroundings.

The Distributed Robotics Laboratory's project on robust learning for autonomous vehicles aims to fill the gaps left by existing work in perception aspects of the autonomous driving task, which, despite the use of deep learning and end-to-end control, presents reactionary responses and produces output representations unsuitable for decision making or autonomous navigation. The researchers are hence developing a novel deep learning-based approach that accepts a single frame as input and outputs a control probability distribution for an autonomous vehicle. The approach is being tested on both simulations and real autonomous vehicles for a variety of driving conditions.

One research article published under this project involves variational end-to-end navigation and localization, drawing inspiration from the core competencies of human drivers—being able to drive and navigate according to a map, localize within the environment, and reason when their visual perception does not match what the map says. The model thus learns steering control directly from raw sensing using three cameras and coarse state estimation from the GPS and IMU. This research article was also a best paper award finalist at the IEEE International Conference on Robotics and Automation (ICRA) 2019. Another paper presents a pipeline for the three-dimensional detection of vehicles by adopting a two-dimensional detection network and fusing it with a three-dimensional print cloud to generate three-dimensional information, alongside the help of a model fitting algorithm and a two-stage convolutional neural network. A variety of other projects, including a CAD tool for designing superintelligent human-computer groups, a data-driven parallel autonomy system, a safety interlock for self-driving cars, and all-terrain mobility and navigation systems, are racing to make the world of autonomous vehicles more safe, efficient, and convenient.

— Shinjini Ghosh

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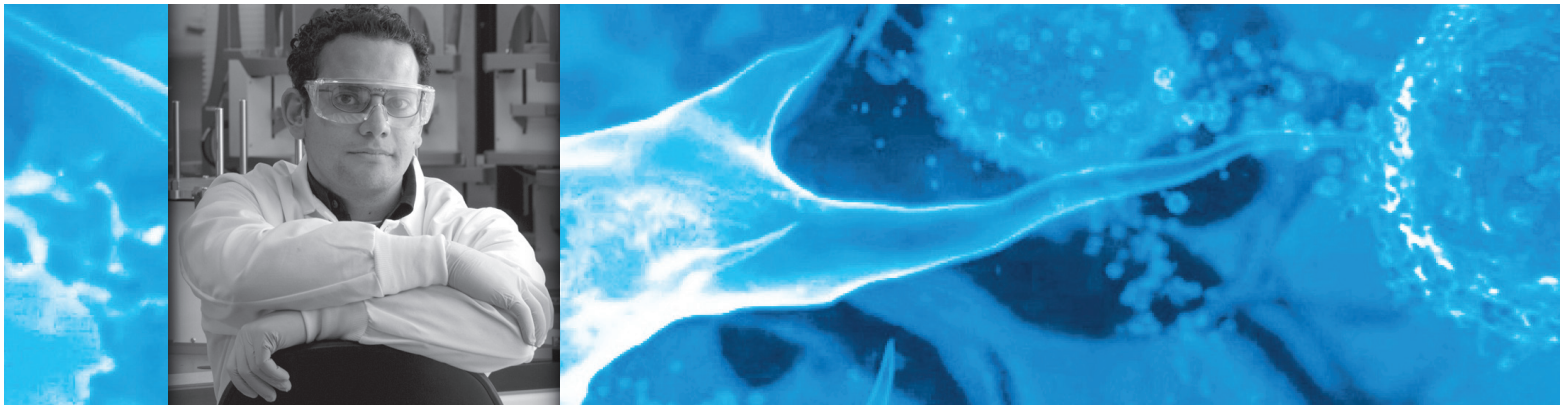

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MURJ Features

Whitehead Institute for Biomedical Research

MURJ Spotlight: Ruth Lehmann

This issue's spotlight features Ruth Lehmann, newly elected Director of the Whitehead Institute

By Rachel Rock

INTRODUCTION

Ruth Lehmann was announced as the second-ever female director of MIT's Whitehead Institute, effective July 1st of this year. With a relative dearth of female role models to guide her, Professor Lehmann forged her own path in biology. From a Fulbright in the United States to a faculty position and tenure at MIT, and leadership as Director of the Skirball Institute of Biomolecular Medicine and Chair of Cell Biology at NYU Medical School, Professor Lehmann has gone far. Her research on *Drosophila* development is remarkable, as is her ability to establish an environment that supports diversity and curiosity-driven research. This interview will cover Professor Lehmann's personal and scientific journey, as well as the priority values which will guide her in directing the Whitehead Institute.

INTERVIEW

When did you first become interested in science?

In high school, called gymnasium in Germany, I became interested in biology, as I had an engaging biology teacher, and I was always reasonably good in mathematics and quantitative areas. However, I was torn about what to do after high school. In Germany, you enter medical school directly from high school, and I was torn about medical school versus biology. Around that time, I was an intern at a doctor's office, and medicine didn't appeal to me, so, I was off to study biology.

Ruth Lehmann will begin her new role as Director of the Whitehead Institute on July 1, 2020

Did you have any early role models in pursuing science? You mentioned a high school teacher…?

Well, he was a very inspiring teacher, because he encouraged us to explore and learn about big open questions. Then, my first years as an undergrad were unfortunately quite boring. Funny, but the coursework at the university was less interesting than at high school, where we learned about memory, DNA replication, and so many interesting facets of biology to me. You're a biology major, right?

Yes, 100%!

So, I suspect you know what I'm talking about. Okay, good. The university's lectures were just basically professors reading their books, which I found really, really boring. Meanwhile, at the same time, I was editing a poetry journal with some friends, many of whom were from the US but had left because of the Vietnam War. With these friends, I learned to speak English better than my school English, and they encouraged me to consider studying in the US. At that time, I was becoming interested in ecology.

Oh, yes! You did a Fulbright in that! Could you tell me more?

Sure. It was a difficult time. I was very engaged in politics. You have to think about the time: this was '76, '77, and in Germany this was a time when we young people asked our parents and grandparents for answers about how a regime like Hitler could have come to power, what was their role then, and how could we prevent something like this from happening again. A take-home message was a strong distrust of baseless orders. This can get me into trouble with 'authorities' from time to time. At the same time, I was fascinated by a book by the Club of Rome called *The Limits of Growth*, which focused on the environmental consequences of economic growth, such as how food resources would become scarce if people continued to raise cattle for the consumption of large quantities of meat and failed to manage land use to feed an ever-growing world population. Sounds familiar? So, I thought that if I wanted to connect my political interests with my ambitions in biology, ecology would be a good field. However, you couldn't really study ecology in Germany, so I pursued a fellowship through the Fulbright program. The disappointment was that, when I started in the ecology program at the University of Washington in Seattle, specimen collection for the season was completed, and I was mostly responsible for data analysis; although I enjoyed working at the enormous computer center at the University of Washington, I had wished to learn experimental science: how to design and carry out experiments, how to test your own hypotheses, and how this information could lead to new insights and discoveries.

Drosophila limbs can regenerate even when some cells destined to develop into the limb are removed [Credit: André Karwath via Wikimedia Commons]

So, I sought and found a mentor, Gerold Schubiger, who gave me papers about *Drosophila* development to read. These papers described new discoveries of compartmental boundaries in the fly that restricted cell growth and about homeotic mutants that transformed one body part of the fly into another, and I was totally fascinated. Then, he took me into his fly lab, and that really shaped my career. I think this was such an amazing opportunity, going away from my family and being completely on my own (remember—there were only landline telephones and letters to communicate back home). Under Professor Schubiger, I began to understand what it means to be a scientist: to explore questions by doing experiments—experiments that mattered because they help distinguish between different hypotheses! Experiments were not like cooking and following a recipe book but testing and exploring ideas by experimentation. The Schubiger lab was studying limb development in the fruit fly, and they used classical genetics, as well as cell/tissue transplantation in the fly larvae to learn how, during development, a group of cells became distinct parts of the limb, and yet, how the entire limb could regenerate even when some cells, destined to become a certain part of the limb, were experimentally removed.

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At the end of this period, Professor Schubiger pressed me to attend a scientific conference and consider a career in biology. I attended a scientific conference, and what luck: I met Chritianne Nüsslein-Volhard, who, several years later, became my Doctor-mother (aka PhD supervisor). At that time, she was just a young scientist, who didn't have her own lab yet, but shared a lab with a male colleague, Eric Wieschaus. She talked about gradient formation and how gradients could influence the development of the top-to-bottom (dorsal/ventral) and head-to tail (rostral/caudal) axes of an embryo. These were questions that had captivated me for some time, as I was always interested in self-forming patterns. Several years later, I joined her lab, as a PhD student, at the Max Planck Institute in Tuebingen, a small student town in Germany. And so, she was the first professional woman role model who, to me, was astonishingly impressive. Yet, it was also clear that she had a difficult a time. Although she was doing very important work, recognized internationally at the time and for which she together with Wieschaus (and Ed Lewis, the person who defined the homeotic gene clusters) won the Nobel Prize in 1995, many did not take her as seriously as her male peers. Seeing her struggle to even obtain an independent position was discouraging.

"The importance of role models couldn't have been clearer"

As far as I remember, there were very few other female professors during these early years, and the few whom I remember weren't role models for me. Then there was my PhD advisor, but I was left with the feeling: "Oh my, she's really wonderful and making key discoveries, but it's so hard, even if you're brilliant, to succeed." During my PhD thesis work, my mentor was invited to a conference in the US; she didn't want to go, so she asked me, "Why don't you just go in my place?"

So, I went to this developmental biology conference. It was so amazing. It was a Gordon Conference. Have you heard of Gordon Conferences? They're small conferences that provide substantial time to intermingle with other attendees outside of the formal scientific sessions. So, it is a great conference to get to know people. To me it was thrilling that there were quite a few women attending. It was probably just a handful, but many of them were at early stages of their career. They were really interesting and inspiring people, and they also seemed to me, just 'normal people,' with whom I could identify. It was just so great. All of a sudden, I felt like there were other people like me, who were excited to share their work and enjoyed having intense discussions! The importance of role models couldn't have been clearer. This was a total eye-opener, and I realized that I would probably need to leave Germany. Barbara Meyer, then a professor at MIT, was at this conference, and we met. She somehow organized that I was invited for a seminar at MIT. I later learned this was an interview for a faculty position.

Oh, yeah, because you had a lab here for eight years.

Exactly. So, I was essentially hired while in graduate school, based on the work that I presented at that conference. I often feel that a lot of my life has been luck, although my advisor defines luck as 'being prepared for opportunities.'

And, people really can make their own luck, too! I mean, you've really persevered in spite of several things, like lacking key role models. How was the environment you encountered at MIT different?

Sadly, there were very few women faculty at MIT, and at the Whitehead Institute, they were initially all men. Do you know Terry Orr-Weaver? She and I were hired nearly at the same time. We were the first two women at Whitehead. In the entire Biology department, there were only a half dozen women. As a young professor, I felt very supported at MIT. Later, though, when I received tenure, I felt that the inclusiveness that I felt as a young faculty did not last and that it would be very hard to be accepted and integrated like my male colleagues.

Regarding MIT, how do you feel that the Institute has changed in terms of women's representation?

As to MIT, I think that I'll find out! I know that MIT has been working hard to increase the number of women faculty, and promote their integration into leadership positions, in particular after Nancy Hopkins spearheaded a report on equal opportunities for women faculty. This is a great step forward, but I don't yet know whether women are simply quantitatively treated equally to men, with regard to lab and office space and salary, or whether they actually feel empowered, which is the real measure of equality. It's not just numbers, and I will learn in time. At the Skirball Institute, where I am now director, I think we have done well not only in recruiting but also [in] empowering women. For a while, I was quite content that we had thirty percent women faculty, which reflected the job application pool, so I thought, that's a fair representation. And then I thought, how could I be content with that?

Whitehead Institute for Biomedical Research [Credit: Brian C. Keegan via Wikimedia Commons]

Fifty percent of our graduate students are women. After graduate school, however, the number of women who continue an academic career in biology begins to drop off. There are many possible factors and explanations for the fall-off. Some say, 'women need to decide between a demanding career as a scientist and having a family.' I don't have children, and at a point in time I felt that I needed to make such a decision. However, much has changed in attitudes, and I am convinced that now it is the time to look at how a change [can be made] in the workplace and the prejudices that still exist, even among women, to get to fifty-fifty. It's undoubtedly harder with children, so we need to ask how we are going to make it easier for people to [both have] an active career in research and [be] a parent. And of course that doesn't just affect women—it's also important for men. I strongly feel that to be competitive, we need to identify all talent irrespective of gender, race, or place of origin.

Now that we've discussed diversity, could we dive into the science and talk about what really gets you excited in the lab? You really do have a great corpus of work, and I am interested in learning more.

First, although I am sad to be leaving my colleagues at Skirball, I am really excited to be joining MIT, as when you are confronted with a new environment you are likely to develop new ideas, and new collaborations.

I have been working on germ cells, the primal cell type that ultimately develops into a complete embryo, and I will continue to work on germ cells in my new lab at the Whitehead. Germ cells are really fascinating and, in a way, an understudied cell type. What I find so interesting about germ cells is that they are 'immortal,' in a sense: they do not differentiate like somatic (body) cells, but instead must stay inert to signals that promote and drive somatic differentiation. Nonetheless, germ cells do differentiate into two highly specialized cells: egg cells and sperm cells. And then those cells have the potential to create a new organism. In a way, germ cells are also drivers of evolution, because evolution occurs from generation to generation. However, while germ cells facilitate evolutionary change, evolutionary material transmitted between generations must be as stable as possible. As such, an intricate balance must be met between evolutionary change and reproductive success, which is an exciting facet of germ cell biology on multiple levels.

Our approach to germline biology has been largely based on genetic analysis: we interfere with the fly genome by mutation or other means of disruption to identify genes that are important for normal germ cell development and fertility. Then by analyzing the critical gene products we begin to understand the cellular machinery and networks that control critical steps. These studies have led us to understand how germ cells are set aside during embryonic development and become distinct from all other cells that make up the body of the fly, and how the gonad develops into an organ with different specialized cell types that promote and nurture the stem cells for the next generation.

Perhaps the most surprising finding came from recognizing that the basic regulatory machinery for controlling the distribution and expression of RNA and protein is different in germ cells compared to somatic cells. Somatic cells rely mainly on transcription factors that regulate somatic cell fate programs (a really important concept for stem cell biology, where 'master regulator' transcription factors can drive pluripotent stem cells or reprogram differentiated cells toward specific somatic cell types or tissues). Initially, when I was still at MIT, we identified several genes that are important for germ cell specification.

"Germ cells are really fascinating and, in a way, an understudied cell type"

Studying the structure and function of these molecules brought several surprises: first, we found that some of the mRNA and proteins in the egg were not uniformly distributed in the egg but concentrated at one end, where germ cells would form. Second, these RNAs and proteins, which were critical for germ cell development, did not control transcription but acted post-transcriptionally and regulated the rate of mRNA translation. Once germ-cell specific genes were identified in other species, such as mice, worms, and amphibians, it became clear that post-transcriptional regulation is a conserved principle for germ cell development and that the same genes that we and other colleagues had identified in the fly were used in germ cells from other species. Starting with this initial discovery, we realized that the temporal and spatial regulation of RNAs deposited by the mother to the egg is not only important for the development of the embryo but also for the continuation of the species. Focusing on this post-transcriptional control, we are currently studying how mRNAs and other small RNAs are organized into cytoplasmic, membraneless granules that are only found in germ cells. We know most of the components of these granules and recently found that they assemble via a process called phase-transition, whereby seed components concentrate and recruit other components to initiate the formation of granules, thereby enabling molecular reactions to control RNA stability and translation in a subcompartment of the cell.

We also study how germ cells migrate from their site of origin to their ultimate destination in the gonad. We are interested in how the flow of genetic information encoded in the nucleus as well as cytoplasmic information embodied in RNA granules and cellular organelles passes only from mother to egg and ultimately the future embryo. Despite many years of study, fundamental questions regarding the fate and function of germ cells remain unanswered. In the past, such questions were largely addressed by studying one or a few genes, mRNA, or proteins at a time, but now we can take more systematic approaches and use clever labeling methods to follow and track multiple proteins and RNAs from the mother to the embryo. We are very excited about expanding this research and to explore new tools and technologies developed at MIT.

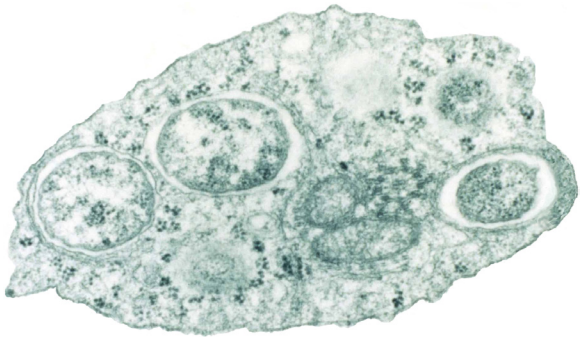
Recently, returning to the transgenerational conflict of stability versus change, we have investigated transmission of mitochondria, which are passed on to the next generation exclusively through the female germ-line. Mitochondria possess their own DNA which replicates independently of nuclear DNA through a process that is inefficient and leads to many errors or mutations. It has long been known that some sort of selection mechanism

must be engaged to ensure that the mitochondria that are passed on to the next generation remain functional. For nuclear DNA, each parent contributes one of each paired chromosome to the next generation. A single mitochondrion contains multiple genomes, some good and some faulty, and several hundreds of thousands of mitochondria are passed from the egg cell to the embryo. Recombination of nuclear DNA, which occurs during meiosis, plays an important role in eliminating chromosomes with severely deleterious mutations. Mitochondrial DNA, however, does not undergo recombination, so the mechanisms for sifting through and selecting undamaged mitochondrial chromosomes must be distinct from that used to extinguish defective nuclear chromosomes. This is an important step, however, as without such selection, mutations would continue to accumulate in mitochondria of the following generation and eventually lead to the extinction of the entire species.

That is super cool!

Yes, this is a very interesting, important problem and one shared with cells in other contexts. For example, there is an extensive literature describing how defective mitochondria behave in cancer cells, and how compromised mitochondria may be involved in neurodegeneration. As such, there is much interest in manipulating mitochondria to selectively remove damaged mitochondria. There is likely a lesson to be learned from germ cells, as they have clearly established a process to distinguish and select good from bad mitochondria. We found that during a window of time, early during the development of the oocyte, the gene that normally maintains large mitochondria with many genomes is downregulated, and mitochondria break up into small mini mitochondria, each with one genome on average. Now, the 'bad' mitochondria can be functionally selected, as defects in one genome are no longer covered up (complemented, in genetic terms) by another 'good' genome in the same mitochondrion. Obviously, we are curious to learn whether a similar process occurs in the germ cells of other organisms, like mice or humans, as they face the same problem of selection. Of course, it is possible that manipulation of this pathway and process would allow damaged mitochondria to be removed in other circumstances.

Mitochondria are fascinating, and a favored hypothesis suggests that at the beginning of eukaryotic life bacteria were taken up into the ancestor of a eukaryotic cell in a process termed endosymbiosis and the engulfed bacteria were the origin of mitochondria. How may this have happened? How could such a symbiosis occur? There are a number of examples of intracellular bacteria which exist now and could provide clues to how such a symbiosis may have evolved. Most intracellular bacteria are harmful to the survival of the cell or organism, but some provide a benefit. In this regard, we have become interested in studying a particular class of intracellular bacteria which, like mitochondria, are passed from one generation to the next through the fly egg and provide benefit to the host. These bacteria, called *Wolbachia*, are part of the same family, the *Rickettsia* family, that are thought to have been engulfed by the ancestors to eukaryotic cells and contributed to the origin of mitochondria in eukaryotic cells.



Wolbachia are among the most successful intracellular bacteria [Credit: Scott O'Neall via Wikimedia Commons]

Oh my gosh, yeah! I've heard of *Wolbachia* before with regard to Zika virus, but tell me more.

Yes, exactly! So, *Wolbachia* are among the most successful intracellular bacteria. And insects are some of the most successful animals, and most insects can be infected by *Wolbachia*.When insects carry *Wolbachia*, the bacteria have numerous effects. For example, they can change the sex ratio. There is also this interesting phenomenon called

cytoplasmic incompatibility: *Wolbachia*, like mitochondria, are only transmitted through the mother. But crosses between *Wolbachia*-infected males and uninfected females result in early embryonic lethality, while the reciprocal cross produces viable offspring. This incompatibility, which seems associated with defective chromatin reorganization of the sperm DNA upon fertilization, guarantees quick spreading of *Wolbachia* though an insect species. So much cool biology! The major excitement, however, which you have heard about with the Zika virus, is that *Wolbachia*-infected insects are less likely to transmit viruses. This effect is not specific to the Zika virus but includes other viruses and even other pathogens, such as malaria. We do not know how this works. We do know that a higher density of *Wolbachia* within cells correlates with a higher antiviral effect, and our recent results suggest that *Wolbachia* may reduce the rate of mRNA translation in the host cell, but that is still speculative at this point. I think understanding how *Wolbachia* are transferred from cell to cell and how *Wolbachia* and the host cell co-exist will provide insight into the adoption of bacteria into eukaryotic cell ancestors and perhaps the origin of mitochondria in eukaryotic cells.

That's really interesting, considering the endosymbiotic theory. Wow, that's so cool.

Yes, I am glad I could tell you why I think germline biology is so exciting.

To close, what is your vision for the Whitehead Institute? What are some of the things that you're excited to do, and how do you imagine your role as director?

I left MIT and the Whitehead when I was a young professor, and now I'm coming back with some experience and ambitions beyond my own research. When I left MIT and moved to NYU I joined a research center within a hospital, where research is focused on translational biology with an immediate goal to treat diseases. However, major insights into understanding and ultimately treating diseases do not commonly arise from studying a specific disease but rather from key discoveries which lead to an in-depth understanding of a biological process. And that is the type of science that has attracted me back.

"I want to be the champion for scientists at the Institute"

The Whitehead has always stood for curiosity-driven science. Indeed, the many discoveries and accomplishments made here are probably among the best arguments for supporting bold and creative approaches to science, which ultimately serve the interest of better human health. So, if Whitehead is already so wonderful, what can I do? I am excited to explore, together with my colleagues, how to build an environment that encourages inquiries of fundamental importance [that] are driven not by a particular fad of the moment nor constrained by a favored method but rather by the excitement and interest of the question and the likelihood for discovery. As you know, you can't plan for a discovery but you can increase its likelihood, and I believe that is achieved first and foremost by empowering the individual scientist. First, I want to be the champion for scientists at the Institute. Irrespective of whether they are seasoned professors or beginning graduate students, I want to encourage them to be fearless, think big, and explore new frontiers. Next, I want to explore how our science can benefit from connections with other departments at MIT. At MIT, there's engineering, computational biology, artificial intelligence, physics, and chemistry (surely, I'm leaving out a field of importance), and we are just a small part of this enormous research universe. Importantly, we will have the opportunity to recruit new faculty and fellows, who can bring diversity in personality as well as study area. Finally, the question that probably inspires me the most is how to optimize not just the research conditions but the workplace itself to foster discoveries that are at the heart of science and medicine. ▪

MURJ UROP Summaries

^{13}C-^{2}H REDOR Magic-Angle-Spinning Solid-State NMR for Characterizing Biomacromolecular Conformational Dynamics

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1. Summary

Nuclear magnetic resonance (NMR) spectroscopy provides detailed information on the structure and dynamics (i.e., motion) of molecules. It has emerged as a powerful tool for studying proteins and other biomacromolecules, whose structure and dynamics are integral to their functions and mechanisms of action (Marion, 2013). Broadly speaking, NMR measures the behavior and interactions of nuclear spins in a sample: any nucleus with nonzero spin possesses a spin magnetic moment (which may be thought of as a vector) and is therefore NMR-active.

In the absence of an external magnetic field, the orientations of the spin magnetic moments are uniformly distributed, so there is no net magnetic moment; the addition of a magnetic field induces a net polarization of the spin magnetic moments along the magnetic field axis and causes each individual spin to precess about the field axis at some resonance frequency. In the simplest possible NMR experiment, the sample is placed in an external magnetic field and then excited with a single radio-frequency (rf) pulse, which temporarily rotates the spin magnetic moments out of alignment with the magnetic field so that the net magnetic moment precesses. The NMR spectrometer detects this net precession as a decaying time-domain signal and Fourier-transforms it to yield the frequency-domain NMR spectrum, which contains peaks at the resonance frequency of each nucleus. Each NMR-active isotope has a characteristic frequency that is slightly perturbed by the local electronic environment of the nucleus, a phenomenon known as the chemical shift that distinguishes nuclei in different electronic environments (Levitt, 2008).

Solid-state NMR is useful for samples that cannot be solubilized, including many biomacromolecules, and involves large anisotropic (i.e. orientation-dependent) nuclear spin interactions which provide additional information but complicate the NMR spectra. Magic-angle-spinning (MAS) is used to average out some of these interactions (Polenova et al., 2015). We focus specifically on frequency-selective ^{13}C-^{2}H Rotational-Echo DOuble-Resonance (REDOR) experiments. REDOR is a well-known technique that determines the distance between two NMR-active nuclei by measuring the strength of the (distance-dependent) dipolar coupling interaction between them (Gullion, 1998).

^{2}H and ^{13}C nuclei are particularly suitable for studying biomacromolecular conformational dynamics (Gullion, 2008): ^{2}H exhibits quadrupolar coupling, an anisotropic interaction that can be averaged out by conformational dynamics; thus one can determine the amplitude of the conformational dynamics by comparing the motionally-averaged quadrupolar coupling to the known rigid-limit quadrupolar coupling. Unfortunately, in systems containing multiple magnetically inequivalent ^{2}H, the quadrupolar coupling interaction is typically several orders of magnitude larger than the ^{2}H chemical shift dispersion, making the resulting spectra too overlapped to determine individual quadrupolar couplings (Palmer, 2001). ^{13}C, on the other hand, does not exhibit quadrupolar coupling but can provide site-specific resolution via the chemical shift. The ^{2}H quadrupolar coupling and ^{13}C chemical shift can be correlated to provide site-specific dynamics information.

The rf pulse sequence used in this project is shown in Figure 1. This is a common pulse sequence for a ^{13}C-^{2}H REDOR experiment. It begins with a ^{1}H-^{13}C cross-polarization (CP) step to enhance the ^{13}C NMR signal (Pines et al., 1973). The pulse sequence then contains a string of pulses on ^{2}H, followed by a single pulse on ^{13}C and then another string of pulses on ^{2}H to reintroduce the ^{13}C-^{2}H dipolar coupling. The frequency domain excitation profile of a pulse depends on its shape, power, and

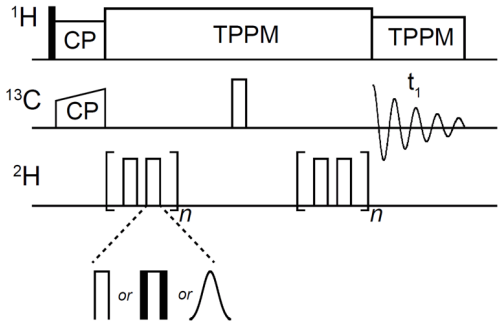

Figure 1. The REDOR pulse sequence used in our experiments and simulations. Pulses are represented by rectangles and signal detection by a decaying sinusoid; simulations were run for all values of *n* from 1 to 100. Note that the CP and two-pulse phase-modulated (TPPM) decoupling sequences are necessary for experimental data collection but are omitted in our two-spin simulations because their effects can be accounted for in the SpinEvolution options.

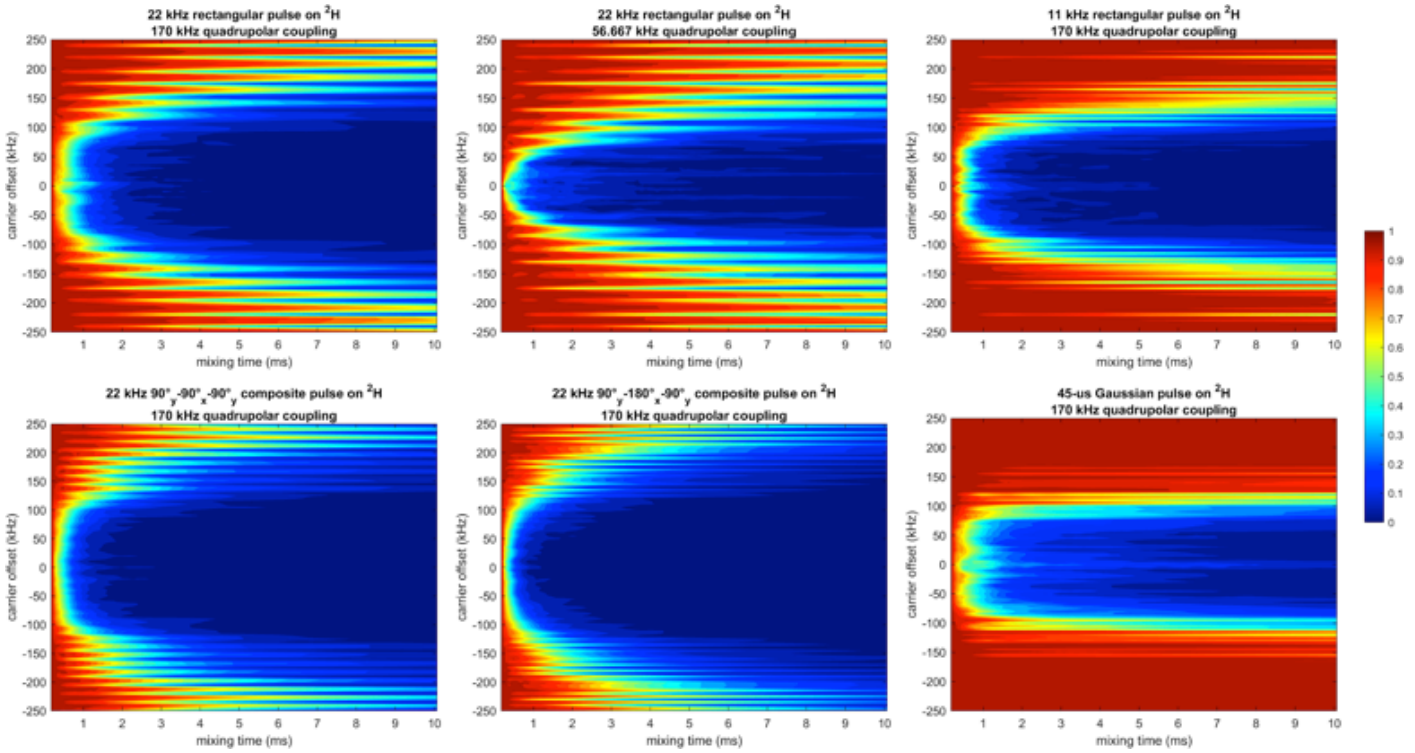

Figure 2. REDOR simulation data showing the NMR signal decay S/S_0 as a function of mixing time and carrier offset frequency. All simulations were run with a static magnetic field strength of 600 MHz, an MAS frequency of 10 kHz, and a 50 kHz rectangular pulse on ^{13}C. Quadrupolar couplings of 170 kHz and 56.667 kHz were chosen because they correspond to a completely rigid aliphatic ^{2}H and a methyl ^{2}H, respectively.

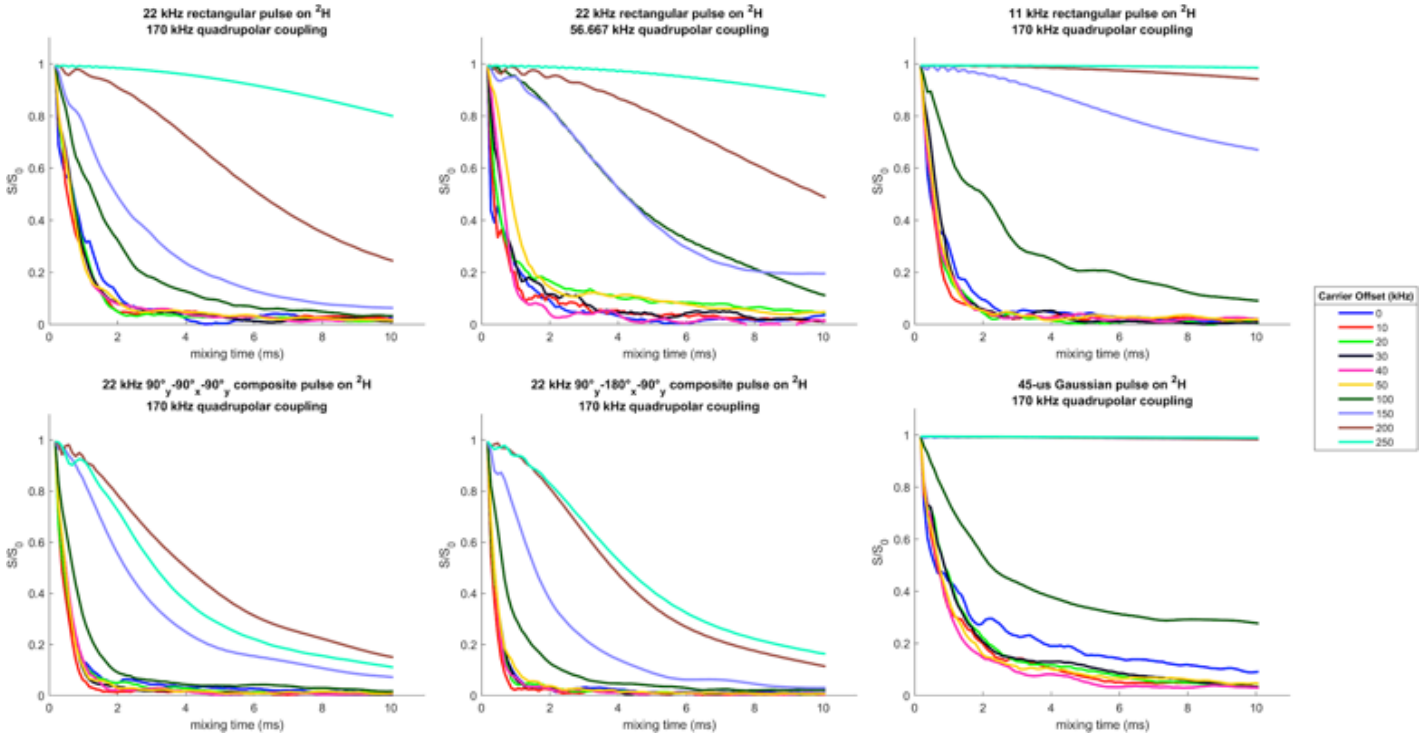

Figure 3. REDOR decay curves at a selection of carrier offset frequencies (i.e., horizontal cross-sections of the data in Figure 1).

length (Atta-ur-Rahman et al., 1996); specific regions of the NMR spectrum may be selectively excited by designing a suitable pulse. We use rectangular, composite, and Gaussian pulses of different powers and lengths to study the experimental effects of frequency selectivity.

We focus on a novel implementation of REDOR that combines frequency-selective ^{2}H pulses with varying ^{2}H carrier offset frequencies. (The carrier frequency is the center frequency of the rf pulse applied to the sample, which most effectively excites nuclei with similar resonance frequencies; thus the larger the carrier offset, the smaller the excitation.) This allows us to determine ^{2}H quadrupolar couplings in addition to ^{13}C-^{2}H internuclear distances. We use the software package SpinEvolution to simulate NMR experiments on a coupled two-spin ^{2}H and ^{13}C system with

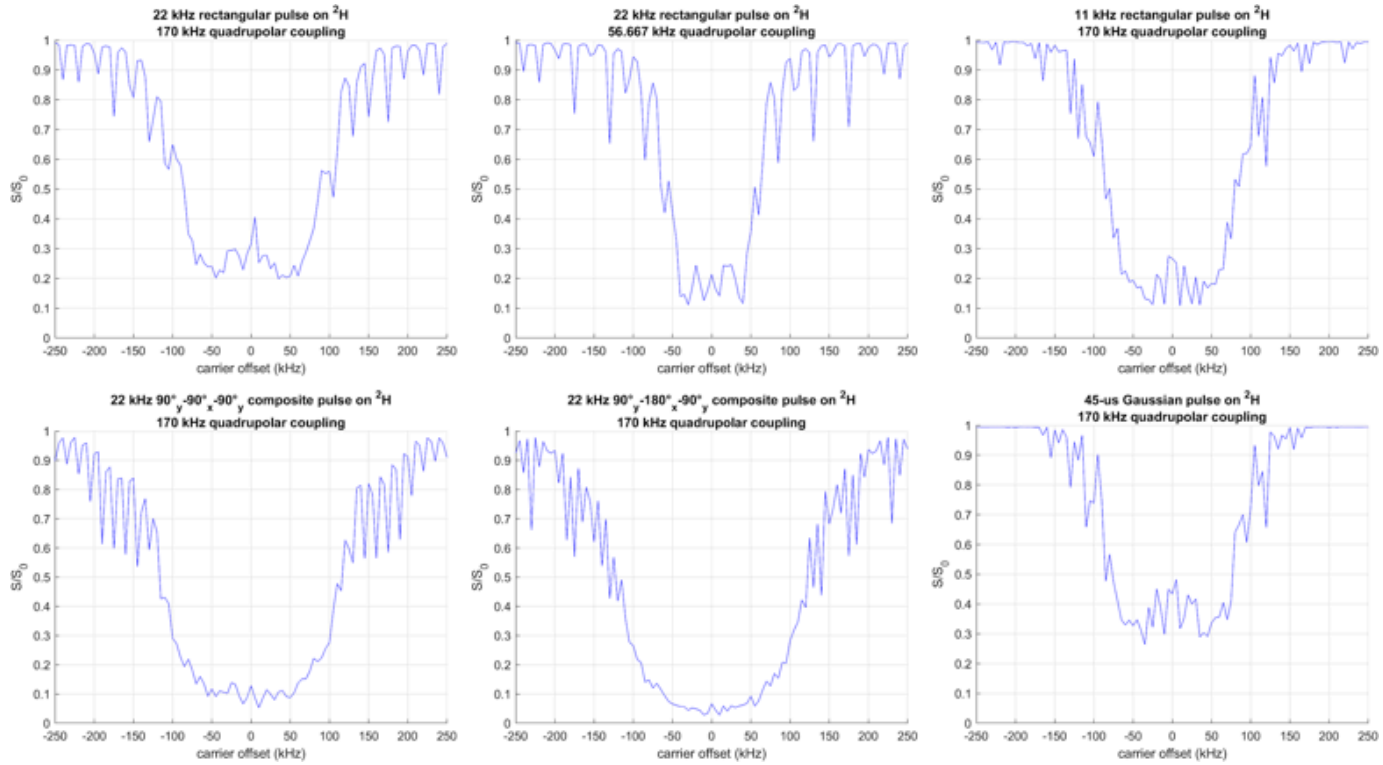

Figure 4. Carrier offset dependence of S/S_0 at a mixing time of 1.075 ms (i.e., vertical cross-sections of the data in Figure 1).

different experimental parameters and quadrupolar couplings. We have already collected experimental NMR data for bacterial cellulose, whose conformational dynamics and quadrupolar couplings are well understood. By comparing simulation and experiment, we can better understand the effects of the REDOR mixing time (determined by the parameter *n* in Figure 1), ^{2}H carrier offset, ^{2}H quadrupolar coupling, and ^{2}H pulse shape on the REDOR dephasing of ^{13}C nuclei coupled to nearby ^{2}H nuclei. Eventually, we will be able to determine unknown quadrupolar couplings with site-specific resolution in other biomacromolecules.

Above are data from six REDOR experiment simulations with various types of ^{2}H pulses and quadrupolar couplings. Figure 4 is particularly useful for our purposes and qualitatively reflects experimental results: for the 170 kHz quadrupolar coupling simulations, both composite pulses are less selective than the 22 kHz rectangular pulse and therefore produce a more rapid NMR signal decay across a wider range of carrier offset frequencies; conversely, the 11 kHz rectangular pulse and the Gaussian pulse are more selective and produce a slower signal decay. Additionally, for the two 22 kHz rectangular pulse simulations, the smaller 56.667 kHz quadrupolar coupling produces a faster signal decay, but across a narrower range of carrier offset frequencies.

Our next step is to fit our simulations to the experimental data. This will guide us in refining our simulations to remove the spikes and slight asymmetry in the current data, which are not observed experimentally. Our goal is to be able to determine upper and lower bounds for the quadrupolar coupling.

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MURJ Reports

Vibration-Induced Anti-Biofouling of Reverse Osmosis Membranes

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Reverse osmosis (RO) currently stands as one of the most efficient desalination technologies. Biofilm formation on the surface of the membrane by microorganisms is a major source of fouling, reducing filtration efficiency and requiring frequent cleaning. However, the current state-of-the-art methods for cleaning RO membranes involve the use of harsh chemicals, are expensive, and not adequately efficient. Here, we investigate a method to clean RO membranes using vibration to promote detachment of the biofilms from the membrane surface and potentially reduce the costs and frequency of cleaning and show that vibration can potentially reduce the extent of biofilm growth on RO membranes.

1. Overview

Over a billion people around the world suffer from water scarcity today, and with a growing global population, this issue will only worsen (Mekonnen & Hoekstra, n.d.). Many regions of the world lack sufficient access to sources of freshwater and rely on purification of wastewater to meet demands for both domestic and industrial purposes. Reverse osmosis (RO) is currently one of the most prevalent methods of desalination. High pressure is applied to the feed water, and the RO membrane acts as a barrier to highly soluble salts and bacteria, allowing only water molecules to pass through (Fritzmann, Löwenberg, Wintgens, and Melin, 2007).

Although effective, this method is often assocatied with the fouling of RO membranes, i.e., the accumulation of various impurities on its surface. To maintain the efficiency of desalination, these impurities must be removed by cleaning the membranes frequently and with chemicals (Flemming, 1997). This is not only costly, but also counterproductive. Studies have shown that use of chlorine (a commonly used microbiocide) can worsen biofouling: while chlorine is effective at eliminating bacteria at first, it can later result in faster regrowth of bacteria by inducing bacterial resistance (Baker and Dudley, 1999). Chemical cleaning also involves long shutdown periods. Alternative chemical-free cleaning methods such as UV irradiation are expensive and not suitable for large RO membrane systems (Saad, 1992).

Biofilm formation involves several stages. The first stage involves transport of organic materials and bacterial cells in the wastewater to the surface of the RO membrane. This is followed by adsorption of the organic material to the membrane, and then the attachment of the bacteria to this 'conditioned" surface (Characklis, 1981). Once attached, bacteria then produce extra polymeric substances (EPS) which aid in attachment to the membrane (Sutherland, 1982). EPS plays a major role in biofouling as it provides the bacteria mechanical stability to resist the shear forces of the water flow (Mayer, 1999).

Biofouling causes a number of issues. It increases the overall membrane resistance, resulting in a need to apply greater pressure to maintain the same production. This results in higher energy consumption and therefore greater costs to continue operation. Furthermore, acidic byproducts released from the bacteria can also degrade the membrane surface (Nguyen, Roddick, & Fan, 2012). Efficiency of desalination declines as the membrane becomes more permeable to salts. In response to biocides such as chlorine, bacteria are induced to produce tougher EPS which protects them from future biocide treatments, and therefore obtain a degree of resistance (Al Ashhab, Sweity, Bayramoglu, Herzberg, and Gillor, 2017).

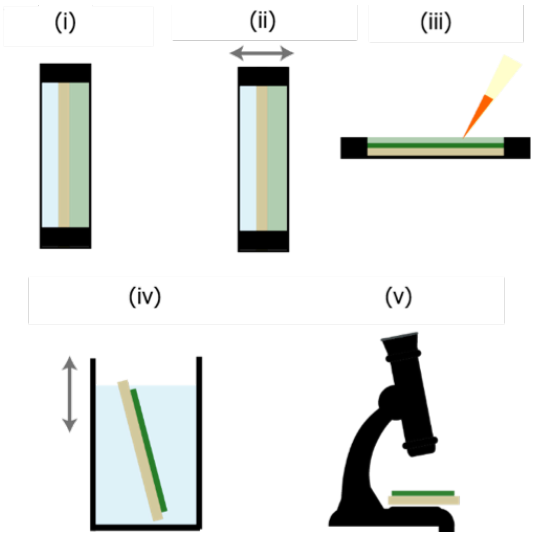

Figure 1. Methodology for vibration tests and observing biofilm removal on RO membranes. (i) Set up membrane and bacteria culture. (ii) Vibrate or soak as needed. Test over a total of 3 hours. (iii) Add SYTO (a fluorescent nucleic acid dye) to stain living bacteria cells. Soak for 15 minutes. (iv) Dip membrane in water to remove unattached cells. (v) Observe under microscope.

Reducing the initial adhesion of the bacteria to the membrane can potentially slow down subsequent biofilm growth. We hypothesize that one such method may be agitation of the membrane with vibration, causing any adherent cells to dislodge from the surface. Potential benefits of this new cleaning method are lower costs, shorter shutdown times for RO facilities, and reduced chemical wastes.

In this study, we aim to investigate the changes in biofilm density in response to vibration of the fouled RO membrane. An apparatus was designed for vibrating RO membranes that were in contact with bacterial culture solution. Membranes were treated using different vibration regimes, and then the area of adherent biofilm was determined using confocal microscopy (Figure 1). Additionally, bubble contact angle tests were used to assess change in the RO membrane properties in response to biofouling, particularly the hydrophobicity of the membranes.

2. Methods

2.1 Microbiology/Membrane fouling

Cobetia marina was stored in frozen stock aliquots at -80°C. Initial culture was produced by inoculating in sterilized marine broth (MB) (37.4 g/L)(BD Difco) and agitating overnight. From this liquid culture, bacteria were transferred to an agar plate, which was agitated at room temperature for 24 hours. The plates were stored at 4°C in the fridge for up to 6 weeks. Liquid cultures used in the experiments were inoculated with one colony per 15 ml MB followed by agitation for 12–15 hours at 25°C. The target OD of the culture was 0.5-0.75.

Artificial seawater (Sigma-Aldrich) of concentration 35 g/L was prepared using sterilized DI water and stored at 4°C. Liquid cultures and artificial seawater were allowed to approach room temperature before use.

2.2 Membrane preparation

The RO Membrane coupons (DOW SW30HR Sterlitech) of dimensions 10 cm x 5 cm were activated by soaking in distilled water for at least 24 hours prior to first use. Before each test, membranes were sterilized by rinsing with 70% ethanol followed by rinsing with DI water. At the end of each experiment, membranes were gently scrubbed to remove the biofilm and reused for 7–8 more tests.

2.3 Vibration tests

All apparatus was sterilized using 70% ethanol followed by rinsing with sterilized DI water. The sterilized membrane was secured between the two halves of an acrylic cell, which were fastened together with screws and O rings to form a watertight seal. The front half of the cell was filled with bacterial culture and the back half of the cell was filled with artificial seawater to ensure that the osmotic pressure difference was zero. The cell was stood upright and bolted down to the linear stage. A sinusoidal signal from an arbitrary function generator was amplified by a 20:1 voltage amplifier, resulting in a +80 V signal. The signal was used to generate vibration of the cell via a piezoelectric actuator. In each experiment, the cell was vibrated at a fixed frequency. The experiment was repeated over a frequency range from 20 Hz to 100 Hz in 10 Hz increments.

For each frequency, there was a no-vibration control. There were also 6 different vibration regimes that lasted 3 hours in total. The cell was vibrated for 5-minute intervals every 10, 30, 60, and 90 minutes as well as two sets of experiments where the cell was vibrated for 5 minutes at the beginning and at the end (Figure 2).

2.4 Membrane characterization

After each 3-hour experiment, the fouled membrane was removed from the cell onto a customized acrylic dish. The biofilm was stained with 3 µl of SYTO 13 Green Fluorescent Nucleic Acid Stain (Thermofisher) for 15 minutes before observation under the confocal microscope. SYTO 13 only stained the bacteria that were alive, and images taken were analyzed by calculating the average area covered by the living bacteria.

2.5 Bubble contact angle determination

Bacterial culture of OD 0.5-0.6 was used as a stock to make 6 dilutions (0%, 10%, 20%, 50%, 80%, 100%), where 0% is distilled water and 100% is the original bacterial solution. Membrane pieces (1.5 cm x 1.7 cm) were soaked in each dilution in a 6-well plate for different fouling times: 1 hour, 3 hours, 6 hours, 18 hours, and 24 hours. After fouling, each membrane was rinsed by dipping in distilled water, attached to an acrylic support, and submerged (inverted) in distilled water. A syringe was used to release air bubbles onto the surface of the membrane. Photographs of the bubbles were taken using a DinoLite Edge Digital Microscope. The membrane was gently scrubbed with 70% ethanol, rinsed with DI water, and immediately imaged again. Thus, two batches of images were obtained: "fouled" and "fouled and cleaned." The experiment was done with both old membranes that had been used for the vibration tests and new, unused membranes. The contact angle tests were repeated with dilutions of polystyrene colloid with new membranes for 1 hour, 6 hours, and 24 hours as controls.

2.6 Data processing

Using the image editing software Inkscape, the angle between the bubble and the membrane surface was determined for each photograph.

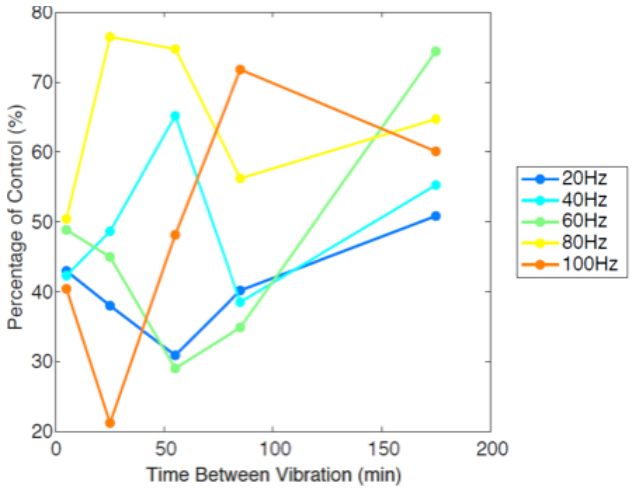

Figure 2. Vibration at various frequencies shows overall decrease in the number of bacteria on the surface of RO membrane.

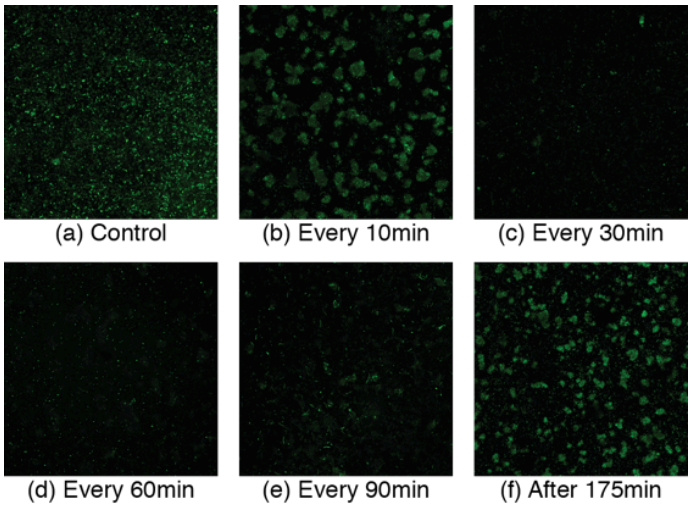

Figure 3. Vibration at 60 Hz shows overall decrease in bacterial numbers on RO membrane surface. Living bacteria are stained green.

3. Results

The biofilm coverage of the membrane is as shown in Figure 2. In general, vibration decreased the area covered by the biofilm relative to the control. However, there does not seem to be an obvious trend in biofilm reduction as we vary the optimal frequency or time between vibrations. Nevertheless, there are combinations of frequency and time between vibrations that appear effective at mitigating biofilm growth, exhibiting at least 20% reduction in biofilm area, while there are other combinations that show very little impact on the biofilm. Figure 3 shows examples of these effective combinations for vibrations experiments at 60 Hz. Vibrating every 30 and 60 minutes (25-minute and 55-minute intervals between vibrations) appears most effective at this frequency. In some cases, bacterial aggregates are observed on the membrane surface (Figures 3b and 3f) in contrast to more uniformly spread biofilm (Figure 3a).

The Bubble Contact Angle test was designed to track any changes in the hydrophobicity or hydrophilicity of the membrane surface caused by biofilm growth. Polystyrene colloid was used as a control in place of bacteria (Figure 4). However, there was no observed trend in the results.

4. Discussion

The vibration tests show that exposure to vibration causes an overall decrease in biofilm on the membrane surface. However, the effectiveness of membrane vibration is inconsistent and changing the time interval between vibrations does not seem to correlate with the area of adherent biofilm. The bacteria sometimes form aggregates and sometimes spread evenly across the surface (Figure 3), but it is unclear what differential factors determine these behaviors. Generally, movement of bacteria in the feed water is likely random and based on Brownian diffusion, which may explain a more uniform biofilm coverage. Alternatively, bacteria may actively migrate towards proteins seeded on the surface during initial conditioning of the membrane, whose distribution is also determined by Brownian diffusion. On the other hand, the membrane surface may not be uniform, resulting in preferential attachment to some sites over others and producing bacterial clusters (Characklis, 1981).

Furthermore, while a number of studies support that vibration may be effective under specific conditions (Paces et al., 2014; Shivapooja et al., 2013), other research indicates that it is ineffective in some cases. Indeed, this is a complex problem that is dependent on a range of factors, including the concentration of impurities in the waste water, pore size of the membrane, and the direction of vibration (Kola, Ye, Ho, Le-Clech, and Chen, 2012). A more comprehensive investigation would be necessary to ascertain which parameters would allow the vibration method to be a worthwhile and reliable way to reduce biofouling.

Regarding the mechanism of biofilm removal, we think that bacterial adhesion is reduced via physical agitation of the membrane surface, inducing shear stresses that cause detachment. Other factors may play a role; for instance, clustering behavior of bacteria may occur in response to vibration, possibly as a survival mechanism. Moreover, vibration can cause constant mixing of nutrients in the feedwater as opposed to settling onto the membrane surface. Mitigating this seeding stage therefore decreases the chances that bacteria will attach to the membrane surface and develop into a biofilm. Conversely, the same physical agitation may increase the chances of bacteria in the waste water coming in contact with the membrane, hence promoting biofilm growth. Ultimately, the competition between seeding and shearing

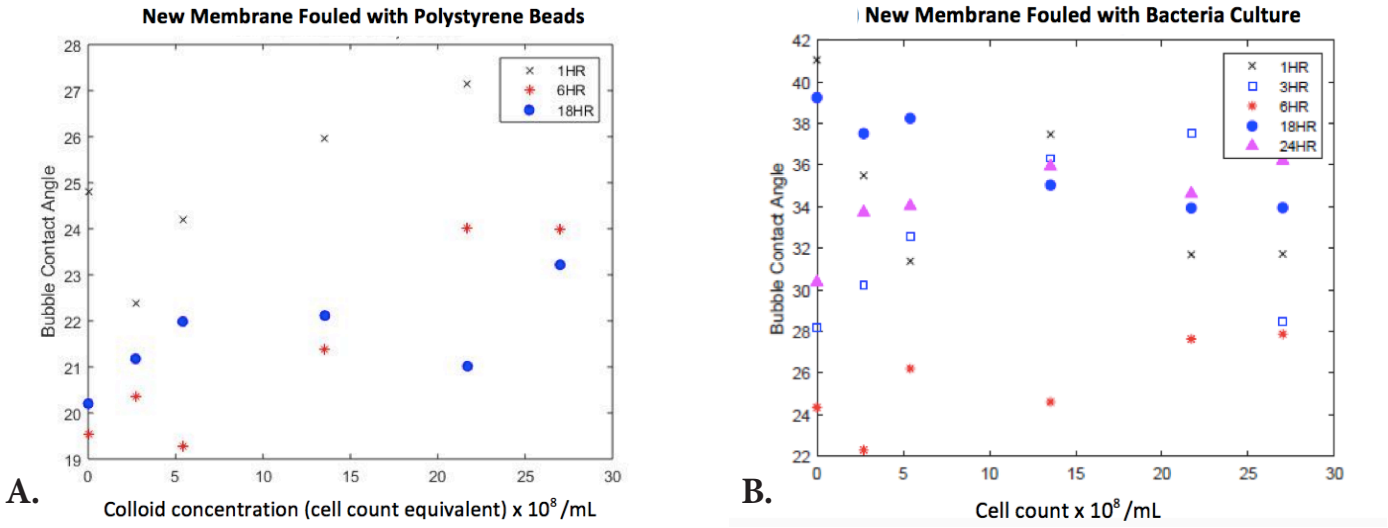

Figure 4. (a) The contact angle of air bubbles on a piece of new membrane exposed to polystyrene colloid solution over 1-hour, 6-hour, and 24-hour durations are plotted against colloid concentrations, expressed as an equivalent to bacterial cell count. (b) Contact angles of new membrane fouled with bacteria shown for comparison.

of the biofilm on the membrane surface favors biofilm reduction (Characklis, 1981).

Previous studies have shown that physical agitation or topographical changes are effective in biofilm removal. For instance, a 2014 study found that sub-micrometer vibrations can be used to reduce bacterial adhesion on magnetoelastic materials (Paces et al., 2014). Another study found that deformation of a silicone elastomer surface by electric fields also results in biofilm detachment (Shivapooja et al., 2013). In both cases, changes in topology of the surfaces resulted in significant loss of bacterial adhesion. Our results suggest that a similar effect can be achieved not only on these specific magnetoelastomers and silicone elastomers, but directly on the RO membranes which do not have those electromagnetic properties.

To ascertain whether the biofilm had any effect on the physical characteristics of the membrane surface, we conducted a bubble contact angle test. Changes in bubble contact angles of polystyrene surfaces are indicative of changes in hydrophobicity. It has been shown that when bacteria culture supernatant was adsorbed onto the surface, an increase in hydrophilicity was seen (Fletcher and Marshall, 1982). We designed a bubble contact angle study to investigate the effects of the *C. marina* biofilms on the membrane surface, expecting that exposure to higher concentrations of bacteria would make the membrane more hydrophilic, reducing observed contact angle. However, we could not make this observation from our data. Polystyrene colloid solution was used as a control and the results exhibit high variability with no clear trend (Figure 4). Again, this may be attributed to variations in the membrane samples.

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Characterizing Aperture Masking Interferometry in the Near-Infrared as an Effective Technique for Astronomical Imaging

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Radio interferometry is the current method of choice for deep space astronomy, but in the past few decades optical techniques have become increasingly common. This research seeks to characterize the performance of aperture masking interferometry in the near-infrared at small scales. A mask containing six pairs of apertures at varying diameters and separations was constructed for use with a 24-inch telescope at the MIT Wallace Astrophysical Observatory. Test images of Spica and Jupiter were captured for 28 different telescope configurations, varying aperture separation, aperture diameter, collection wavelength, and exposure time. Lucky imaging was used to account for atmospheric perturbations. Each image was reduced via bias and dark frames to account for sensor noise, and then the full width at half maximum for each image was computed and used as a proxy for maximum angular resolution. The data imply that at small scales aperture size primarily controls the observed maximum angular resolution, but further data are required to substantiate the claim.

1. Introduction

Stellar interferometry uses the interference pattern between light collected between two or more apertures to produce a high-resolution image of astronomical phenomena (Born & Wolf, 1959). Interferometric techniques have become increasingly common in the astrophysics and planetary science communities primarily due to their ability to resolve deep-space objects with higher angular resolutions at lower cost than traditional optical methods (Tuthill, 1994). This growing popularity is due to the effective angular resolution of interferometric systems, which is proportional to the diameter between receptors. As a result, receptors spaced far apart and interfered can achieve resolutions far higher than traditional methods could feasibly produce (Hariharan, 2003). Even short baseline systems experience a resolution gain greater than the angular resolution possible with an equally-sized traditional system, making them more efficient at performing the same tasks.

Because of the resolution gains possible using large systems and the ease of interfering long wavelengths to produce high fidelity results, most research regarding stellar interferometry has focused on very large radio telescope arrays, such as the Very Large Array (VLA). As a result, very little work has been done regarding the dynamics of small-scale stellar interferometers. Due to their ability to image higher energy thermal sources such as stars, optical stellar interferometers have become more common in the last twenty years (Tuthill, 1994), but longer wave infrared applications at small scales have remained less well understood, even though they may provide additionally valuable thermal profiles.

Beyond deep space astronomical imaging, stellar interferometry at small scales has potential to be effectively applied to a variety of other applications as well. Amateur astronomers may find stellar interferometry to be significantly more cost effective, as the price for larger equipment grows exponentially. Small subsystems acting as an interferometer may be able to achieve similar results to larger systems at a fraction of the cost. Similarly, the proliferation of small satellites has produced growing interest in portable, inexpensive passive tracking systems for both military and commercial applications. Small-scale stellar interferometry may be effective in both cases, but the optics and the relationship between frequency and performance are not well documented in literature, limiting the development of such systems.

This research proposes to tackle both problems: characterizing the dynamics of small-scale stellar interferometry and understanding the spectral dependence of their performance. To that end, a variable sweep will be performed in simulation to derive a reasonable test matrix of telescope configurations to test. In order to ensure ample light is available to construct high resolution images even at short exposure times, this work will use Spica and Jupiter as the primary targets. Spica is a bright binary star which can be viewed as a point source, while Jupiter is the second brightest object in the night sky after the moon.

2. Methods

2.1 Experimental Setup

All data was collected at the MIT Wallace Astrophysical Observatory in Westford, Massachusetts. The basis of the

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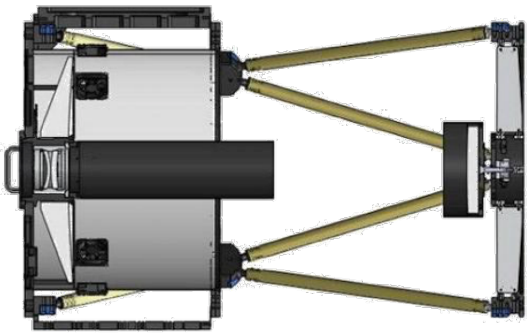

Figure 1. PlaneWave CDK24 Telescope CAD Model. Light enters from the right, is reflected off the primary mirror at the rear, and then bounces off the interior secondary mirror into the CMOS camera.

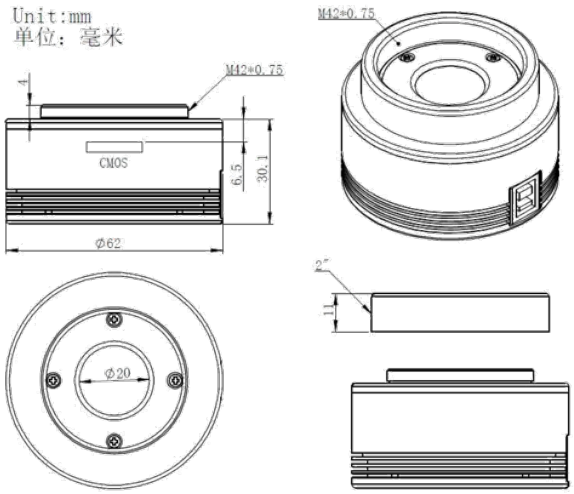

Figure 2. ZWO174 CMOS Schematics. This CMOS is fixed to the back of the telescope (the center on the left in Figure 1).

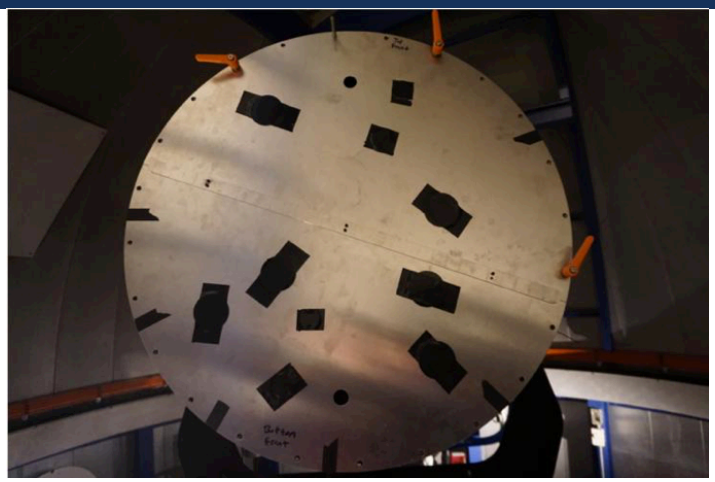

Figure 3. Finished mask bolted to the 24in telescope at the MIT Wallace Observatory. The mask is larger than the 24-inch telescope diameter in order to bolt the mask to the outside casing, as shown in Figure 1. The mask contains 6 pairs of subapertures. There are four centered axial pairs (1L, 1S750, 1S850, 2L) and two off-axial pairs (2S750, 2S850). At the time of imaging the pair of interest is uncovered, while the remaining subaperture array remains covered.

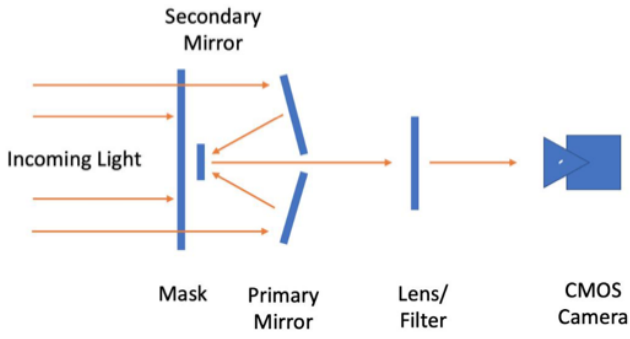

Figure 4. Cross-section of stellar interferometer configuration. Mask configuration and filter are configurable.

interferometer was the 24-inch PlaneWave Instruments CDK24 telescope. See Figure 1 for CAD drawings. Data was collected by a ZWO174 Complementary metal–oxide–semiconductor (CMOS) Imager at the rear of the telescope, cooled to 20°C below ambient. See Figure 2 for schematics. A single mask made of an aluminum sheet containing each pair of apertures, depicted in Figure 3. Six geometries were tested: two apertures at 20.4 inches separation for maximum resolution, two apertures at 3.3 inches separation and two apertures at 3.7 inches separation for the zero-fringe condition, as given by D_i at 750 nm and 850 nm, respectively. The same set is produced for both 1-inch and 2-inch diameter apertures yielding six unique masks, each containing a pair of apertures. Only one pair of apertures are open at a time, with the other five pairs blocked. A cross-section of the apparatus can be seen in Figure 4. Data was also taken with all apertures covered for the generation of dark and bias frames. See Photometry Section for further discussion on dark and bias frames.

The optimal aperture diameter was found by running over 10,000 simulations sweeping over the variables of collection wavelength, aperture spacing, and aperture diameter. The simulation provided an ideal aperture width of 1 mm. This is to be expected, as the peak of the intensity pattern grows inversely with aperture width for small apertures. To ensure sufficient light is collected to resolve Jupiter and Spica, the minimum aperture diameter is set larger than the optimal value. Beyond 25 mm the intensity peak falls off quickly, but 80% to 90% of the intensity in the diffraction patterns for the 1 mm configuration can be preserved with aperture widths up to that width.

For this simulation, the diffraction pattern of the interferometer was approximated as a double slit with Fraunhofer diffraction. Fraunhofer diffraction assumes parallel wavefronts in the far-field and is valid for F<<1, where F is the Fresnel Number. At larger values of F the wavefronts cannot be assumed to be parallel and are instead represented as parabolic. This regime with parabolic wavefronts in the near-field is called Fresnel diffraction. The Fresnel number is a measure of length-scale and determines what approximations are appropriate for different distances between the double slit and observation point. Because we care about the relative intensity of the diffraction pattern only at the midway point between the two apertures where light is being collected by the CMOS – which is the same whether in the parallel or parabolic wavefront regimes – we can consider this approximation good enough for first pass analysis to determine mask geometries, even though the Fresnel Number of the actual telescope is ~12.5. The expected error given this assumption is not significant enough to alter the outcome of the simulations.

2.2 Data Collection

Data collection occurred during April of 2019. Spica and Jupiter were chosen as the primary targets. Each mask was bolted to the telescope and the telescope was set to track the target object. With each mask a series of images were taken at two different exposure times for each aperture with each corresponding filter. In total 30,000 images were taken representing 28 different configurations of aperture diameter, aperture separation, wavelength filtering,

Aperture Diameter	Aperture Separation	Filter	Exposure Time
1 in	20.4 in	Clear	100 ms
1 in	20.4 in	Clear	5s
1 in	20.4 in	i' 750 nm	500 ms
1 in	20.4 in	i' 750 nm	5s
1 in	20.4 in	z' 850 nm	1250 ms
1 in	20.4 in	z' 850 nm	5s
1 in	3.7 in	Clear	100 ms
1 in	3.7 in	Clear	5s
1 in	3.7 in	i' 750 nm	500 ms
1 in	3.7 in	i' 750 nm	5s
1 in	3.3 in	Clear	100 ms
1 in	3.3 in	Clear	5s
1 in	3.3 in	z' 850 nm	1250 ms
1 in	3.3 in	z' 850 nm	5s
2 in	20.4 in	Clear	25 ms
2 in	20.4 in	Clear	1250 ms
2 in	20.4 in	i' 750 nm	125 ms
2 in	20.4 in	i' 750 nm	1250 ms
2 in	20.4 in	z' 850 nm	312 ms
2 in	20.4 in	z' 850 nm	1250 ms
2 in	3.7 in	Clear	25 ms
2 in	3.7 in	Clear	1250 ms
2 in	3.7 in	i' 750 nm	125 ms
2 in	3.7 in	i' 750 nm	1250 ms
2 in	3.3 in	Clear	25 ms
2 in	3.3 in	Clear	1250 ms
2 in	3.3 in	z' 850 nm	312 ms
2 in	3.3 in	z' 850 nm	1250 ms

Table 1. Test Matrix.

and exposure time for each target. The full test matrix is listed in Table 1.

2.3 Photometry and Data Post-Processing

The main goal of post-processing is to reduce blur and atmospheric effects from the data, as well as any other perturbations causing the signal to lose fidelity. It is important to keep in mind physical limitations that cannot be overcome. There are broadly two sources of distortion: atmospheric and telescopic. The atmosphere is a strong absorber in certain bands of the infrared, but there exist "windows" in which transmission is high. The 600 nm to 800 nm band is a prime example of one such window (Sterken and Manfroid, 1992). Taking short exposure images mitigates variable path length and resulting phase shifts due to atmospheric distortions. An additional method of dealing with atmospheric aberrations is knows as chopping. Chopping is the process by which consecutive images are taken of the area of the sky of interest and an immediately adjacent area and then the second image is subtracted from the first (Sterken and Manfroid, 1992). This method only works over very short time and spatial scales, however, as atmospheric cells cannot

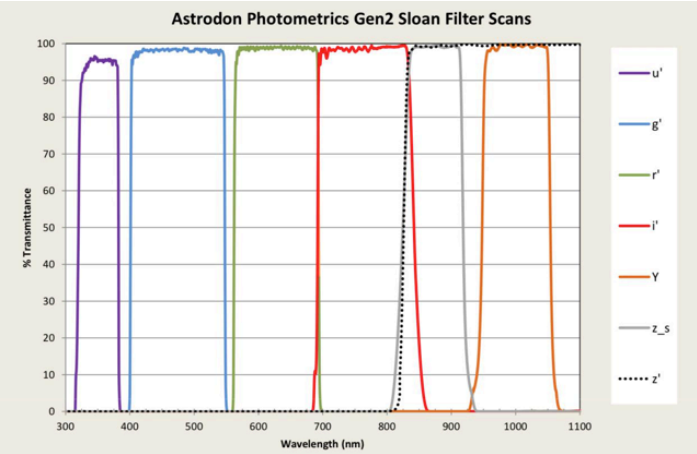

Figure 5. Transmissivity of the ZWO174 CMOS Imager. The bottom axis is wavelength in nm and the right axis is percent transmission. Transmission stays above 98% for the i' and z' filters, which lie in the near-infrared.

be assumed to be congruent at distances greater than 300 mm (Tuthill, 1994). Factors that influence the noise from the telescope itself include the telescope's black-body radiating temperature and the transmissivity of the CMOS. The transmissivity curve for the filters used on the ZWO174 CMOS can be seen in Figure 5. The i' and z' filters will be used for this experiment, as they provide near complete coverage of the aforementioned 600 nm to 800 nm band (Sterken and Manfroid, 1992). The two filters are centered on 750 nm and 850 nm, respectively, which are the wavelengths used for the final simulations. Each filter approximately covers a 100 nm band.

A photometric pipeline is required to reduce raw photo data into a usable image. First, dark, bias, and flat frames must be acquired. A bias frame is the result of taking the fastest possible image with the shutter closed/telescope covered. Doing so eliminates any integration time and measures intrinsic CMOS noise. A dark frame is similar but requires integration times on par with those used to capture the data. Because the CMOS is cooled and the exposure time so short, the dark frame and bias frame can be expected to be very similar for this experiment. In order to construct a master dark and master bias frame, a few hundred of each bias frames and dark frames are captured, and their values averaged pixel-by-pixel to produce a *master bias* and *master dark* frame for that observation session. The flat frame is acquired by imaging a source of uniform illumination to estimate the pixel efficiency of the CMOS. The photometric pipeline is then as follows, as sourced from Poggiani, 2017:

1. The bias frame is subtracted off from the object raw frame.
2. The bias frame is then subtracted from the flat frame, and then that quantity is normalized to its mean value.
3. The first result is then divided by the second to produce a reduced image from the raw photo data.

$$\text{Reduced Pixel} = \frac{\text{Raw - Bias}}{(\text{Flat- Bias})_{\mu}}$$

which can be summarized mathematically as:

For this experiment, a flat frame was not used and a uniform matrix of 12-bit pixels was used instead. Flat frames primarily correct for variations in the chip, but because the chip is small, has a fairly consistent response, and the angle subtended was small, it was determined that flat frames would not enhance the reduced image quality significantly. Beyond noise from the CMOS, cosmic rays also cause distortions in the form of "hot pixels," or

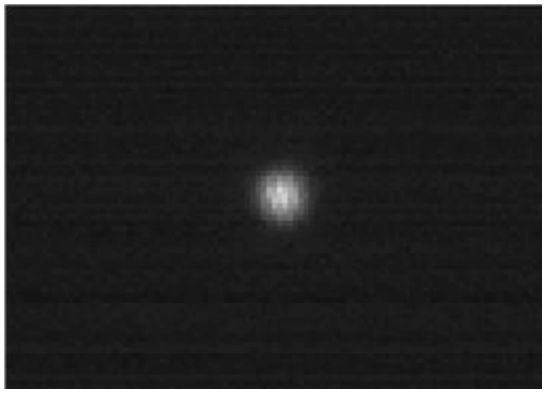

Figure 6. Raw Image of Spica.

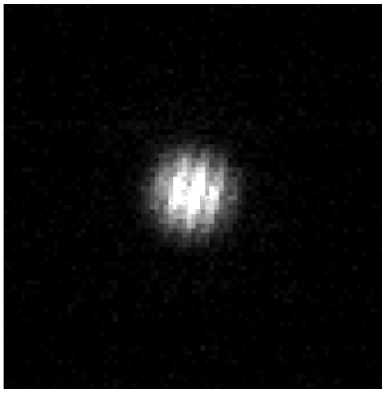

Figure 7. Reduced Image of Spica with clearly exposed fringes.

Figure 8. Overexposed raw image of Jupiter and two of its moons.

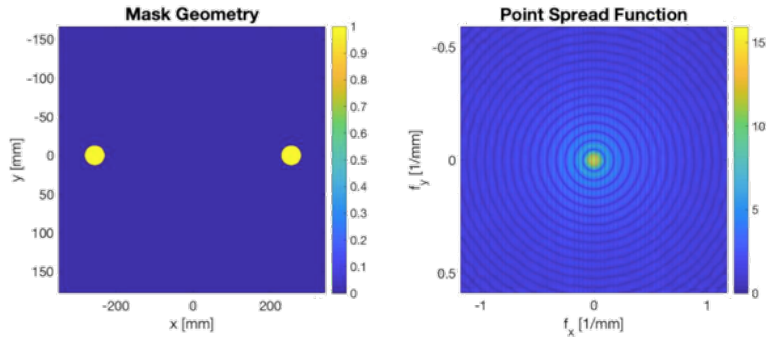

Figure 9. Point spread function (Right) generated from an example mask configuration (Left).

Aperture Diameter	Configuration	FWHM
1 in	Single Aperture	0.002 rad
2 in	Single Aperture	0.0005 rad
20.4 in	Single Aperture	0.0005 rad
24 in	Single Aperture	0.000003 rad
1 in	20.4 in Separation	0.00009 rad
1 in	3.7 in Separation	0.0005 rad
1 in	3.3 in Separation	0.0005 rad
2 in	20.4 in Separation	0.00004 rad
2 in	3.7 in Separation	0.0002 rad
2 in	3.3 in Separation	0.0003 rad

Table 2. Theoretical Minimum Full Width at Halm Maximum.

pixel values erroneously high when compared to its surrounding neighbors. These pixels can be averaged with their neighboring pixels to mitigate this effect. This process can be done with a simple filter. The result from this entire process is a reduced image that can be used to make measurements about the relative angular size of targets. An example of a raw image and a reduced image can be found in Figure 6 and Figure 7, respectively.

The final step in the data post-processing pipeline is down sampling. Due to rapidly changing atmospheric conditions, "Lucky Imaging" was used whereby many hundreds of images are taken for a given configuration, and then down sampled for each configuration such that only a small percent of the images are selected for the final dataset. The remaining images represent the best atmospheric conditions for a given night, which mitigates a large proportion of atmospheric noise. The images were selected via a two-step process. First, the maximum valued pixel for each reduced image was found. If that pixel value was greater than 80% of the maximum possible intensity (2^{12}=4096 for a 12-bit sensor), then the image was discarded, as pixel values nearing the saturation point of the sensor cause distortions in image quality. Second, the Full Width at Half Maximum (FWHM) is calculated for each of the remaining images. FWHM is twice the distance between the maximum value point and the nearest half maximum point for a data series, and is a measure of how well resolved the data are. Smaller FWHM scores correlate with higher maximum angular resolutions. Because many of the images of Jupiter were overexposed and because Jupiter was too large to constitute a point source, the decision was made to at this time only use data points collected of Spica to characterize the performance of the telescope. An example of one of the overexposed images of Jupiter can be found in Figure 8.

3. Results

3.1 Baseline Calculations

In order to measure the performance of the interferometer, baseline measurements are first required. Taking the 2D Fourier Transform of a given mask configuration yields a point spread function (PSF), which is a reconstruction of the image that would be generated by that mask, as shown in Figure 9. The key difference between a single aperture configuration versus the two-aperture configuration shown is the existence of vertical fringes. These fringes result from the time delay between the signals at each aperture when interfered (Hariharan, 2003). Given the close proximity of the apertures, we expect the fringes to be narrow. Taking the FWHM of the PSF gives the maximum angular resolution of that mask configuration, assuming no atmospheric effects. To demonstrate the resolution gain described previously, the theoretical minimum FWHM for various telescope configurations is provided in Table 2. From the table it is clear to see the resolution gained by the interferometer over the single aperture configuration. Lower values are better because they imply that the system could detect a fainter object.

3.2 Data Analysis

To determine the effect of the tested parameters on the angular FWHM, each pair of variables was separated and plotted against the demonstrated FWHM. While four variables were varied throughout the experiment, they are not all independent. The aperture separation determines the collection wavelength by setting the zero-fringe condition. The aperture diameter sets the exposure time to prevent oversaturation at larger diameters. Thus,

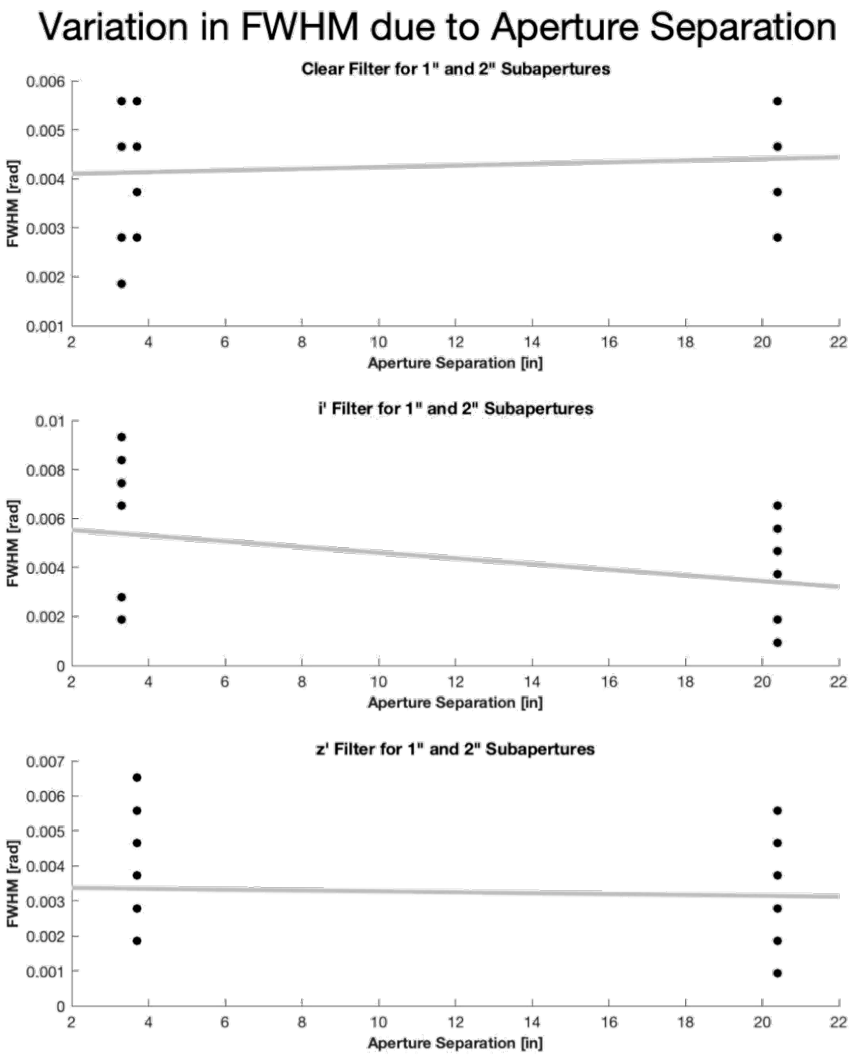

Figure 10. Variation in aperture separation is poorly correlated with FWHM.

by varying the aperture diameter and separation – the two physical qualities set by the mask – with respect to the achieved FWHM, the full variable space is accounted for. Figure 10 and Figure 11 show these isolated variables. While aperture separation did not appear to be significantly correlated with the demonstrated full width at half maximum, aperture diameter shows strong negative correlation.

4. Conclusions

The argument best supported by the data is that variation in full width at half maximum is primarily controlled by the diameter of the aperture. This is intuitive – a larger aperture allows more light to be captured and so allows for the system to more precisely discriminate between targets. However, this result also stands in contrast to the primary justification for using stellar interferometry. Stellar interferometry dominates earth-based deep space imaging primarily because its performance is characterized by the separation of the apertures, not the size of the aperture. The data imply that at small scales, aperture size is of greater importance to the system's resolving power than the separation of the apertures. Therefore, the data suggest that there is a fundamental tradeoff between resolving power and scalability for stellar interferometers. At sufficiently large scales, the separation between the apertures dominates the observed resolution, while at small scales this relationship reverses.

This conclusion has three primary implications. First, there is a hard cutoff to the achievable resolving power of optical stellar interferometers for amateur astronomical use. Given the wavelengths involved, the complexity of interfering optical wavefronts grows exponentially with the baseline, and for the amateur astronomer this growth in complexity will not be worth the marginal gain in resolution, assuming the maximum aperture size is fixed by price limitations. Second, military applications are still viable but remain impractical until a greater understanding of the tradeoff suggested is achieved. Third, commercial applications also remain viable but will be driven primarily by the ability of companies to find profitable uses of the data. The technology alone is not sufficient to commercial adoption.

There exist two primary areas of future work. First, more data are needed to conclusively argue that aperture size controls the observed variation in FWHM. Because so many different configurations were tested, there are not sufficient data points to confirm this trend, especially given its departure from theory. Additionally, more data are required to conclude that aperture separation is as uninfluential in the observed variation in FWHM

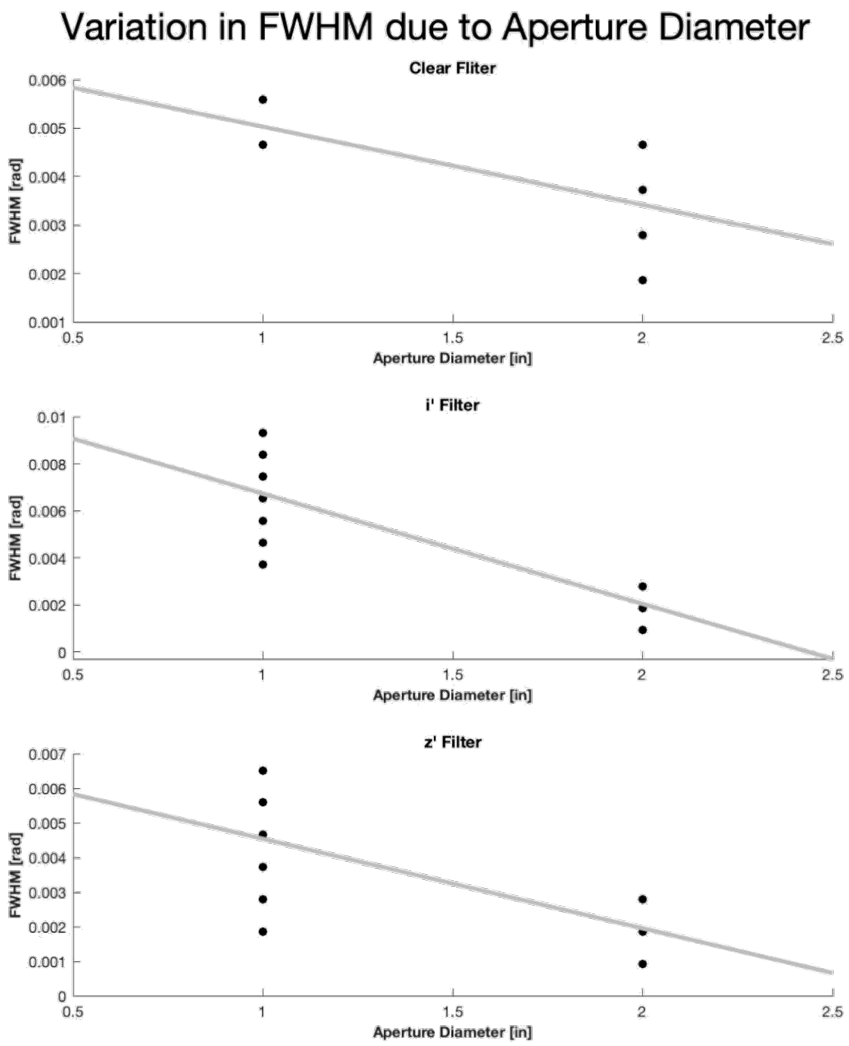

Figure 11. Variation in aperture diameter is negatively correlated with minimizing FWHM.

as the current data suggest. The second area of future work relates to the reversal in trends that the data suggest. If it is the case that at small scales aperture size determines the observed angular resolution, then finding the crossover point, both in terms of minimum aperture size and minimum aperture separation, will be integral to the future design of stellar interferometric systems.

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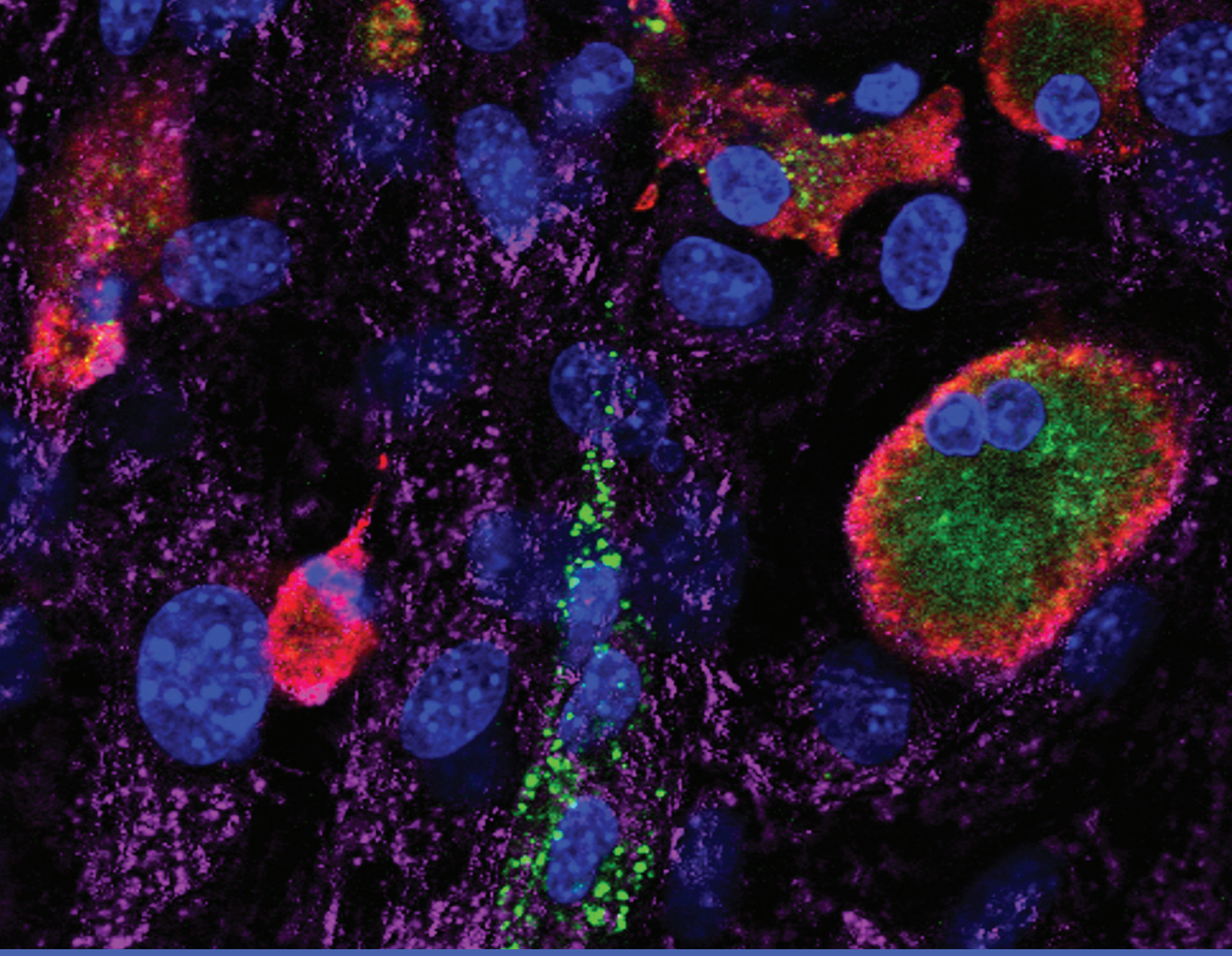

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Adapting TextRank for Medical Text Summarization

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In this study, we compare the quality of two extractive summarization methods using TextRank on summarizing medical journals. The first approach uses general word embeddings not specific to medical settings (GloVe), while the second approach uses entity extraction in conjunction with TextRank. In particular, we extract medical entities using ScispaCy, then apply word vectors specific to medical CUI (Context Unique Identifier) codes. We discover that both methods perform comparably well with ROUGE-F scores around 0.8, suggesting that even using a general, non-medical word embedding like GloVe will significantly simplify medical journals. We conclude that it is worthwhile to apply common summarization approaches like GloVe to the medical setting to facilitate medical research; we might also consider more specialized methods of entity extraction, if we want to obtain an even more significant improvement with TextRank.

1. Introduction

Text summarization aims to obtain a quick summary while still preserving the important ideas. Because of the abundance of medical texts, applying summarization to the medical field has the potential to reap great benefits for society. In medical research, it can help researchers quickly browse through existing research papers, speeding up the pace of discovery. As more and more papers are published over time, and various subfields are being explored, a summarization tool could be the key to quickly extracting what is essential to a researcher's work. This could even be beneficial in times of emergency, when society is demanding results.

In addition to helping the research process, text summarization can also be applied in the hospital setting. One major application is in providing discharge summaries. Doctors provide discharge summaries containing crucial information about a patient's history; but these are often confusing for patients, and this confusion could have adverse impacts (Samuels-Kalow et al., 2012). If a summarization tool could quickly grasp the essentials, it would not only save the doctor's time and help them provide better care for the patient, but also provide the patient a better understanding of their condition.

Given the numerous applications, we might question whether existing general-purpose summarization algorithms are suitable for the medical field. Medical texts contain technical terms, many of which are not found in a general setting. Furthermore, standard approaches may not address the complexities of medical acronyms, or words that have different meaning in the medical setting. For example, a "positive" test result does not have positive connotations; rather, it is often indicative of disease.

In order to apply text summarization to the medical field, we may need to modify existing general-purpose algorithms. Various approaches exist (Moradi, 2019); some existing approaches use topic modelling (Arnold et al., 2015). One study (Pivovarov, 2016) uses LDA (Latent Dirichlet Allocation), which clusters sentences and extracts a topic from each clustering. However, many medical texts (such as journal articles) already include tags for important ideas when they were written.

Other approaches produce more readable results, such as extractive summarization. One example is *TextRank* (Mihalcea et. al., 2004), an algorithm similar to PageRank that evaluates sentence importance based on how it relates to other sentences. *Extractive summarization* produces a summary composed of the most important sentences in the existing text. Note that while extractive summarization does not generate any new sentences, this is particularly useful if the reader would like to glimpse the tone of the original text, or quote certain sentences directly from the summary.

Still other techniques aim to compose summaries from interpreting text. However these techniques are less reliable as it requires not only being able to extract meaning from the text, but also being able to generate human-readable, grammatically correct results. These summaries are not guaranteed to preserve the original wording or tone, which might be of interest to the reader. Furthermore, for these models to perform well, substantial data is required with labels specific to the setting. In one study (Alsentzer et. al., 2018), the labels were the ten HPI (History of Present Illness) categories, and they were applied to every word in each sentence that was under a certain category. But this also means the pre-trained model is limited to its setting, and is also subject to bias depending on training data. A more useful tool does not need to be pre-trained, and can apply to any medical subfield.

In this study, we focus on extractive summarization because it provides readable text in the writer's own words, making it productive and immediately usable. We explore various modifications and evaluate their performance, namely an approach that uses GloVe embeddings, and an adapted approach using cui2vec embeddings and ScispaCy entity detection. The summaries are evaluated against the corresponding abstracts. We find that both the general and the modified approaches perform

similarly well on medical papers, suggesting that either the entity detection step is not necessary, or a deeper detection method is needed to significantly improve summarization.

2. Methods

We compare two different methods of summarization: a baseline using general *GloVe* vectors, and an alternative that considers entities and vectorized *CUI* concepts (defined below). Both methods share the same text samples, preprocessing, and TextRank steps, which are described below.

2.1 Text Samples

Four medical papers with abstracts were selected for our text samples. Because many medical journals require memberships, samples were taken from NCBI Pubmed texts with free access. The summary is compared against the abstract, which serves as a reference summary. The abstract is chosen because

1. The abstract preserves the original authors' tone;
2. The abstract is a human created summary, and therefore represents what human experts deem most important in the article;
3. Asking a third party expert to summarize articles could introduce bias; and generally, a third person may not capture the original paper's ideas as accurately as the original authors themselves.

2.2 Preprocessing

The following preprocessing steps were applied to all approaches.

1. Text is split into sentences;
2. Text is converted to lowercase;
3. Non alpha-numeric characters are replaced with whitespace for later removal;
4. Stop words are removed. Stop words are determined from the nltk corpus;
5. After the above steps, sentences with few remaining words (below a threshold *sentence_length_cutoff*) are removed.

By experimentation, we find that removing short sentences (step 5) generates more useful results. After preprocessing, each method has distinct steps for vectorizing words.

2.3 Method 1: GloVe vectorization

GloVe (Global Vectors for word representation) contains pre-trained vector representations of words (Pennington et. al., 2014). These vector representations are global because the difference between vectors represents their relationship. For example, the vector from king to queen should be similar to the vector from man to woman, as both represent a similar relationship.

In the baseline approach, all words in the given sentences are converted to the corresponding GloVe representation. The vector for each sentence was then the mean of all word vectors in the sentence. Note that because we have preprocessed the text to remove all stop words, the remaining word vectors should hold more importance.

2.4 Method 2: Cui2vec vectorization

To cater our approach to medical papers rather than general words, we first extract important words, and then apply cui2vec word embeddings.

Before we discuss methods, we first define CUIs and entities. *Entities* are words or phrases with medical importance. *CUIs (Concept Unique Identifiers)* are codes that represent medical concepts. These are standardized with UMLS (Unified Medical Language System), a glossary of standard medical terms. CUIs ensure that different terms referring to the same concept share the same code, thus helping preserve meaning.

The first step in our method is entity extraction. ScispaCy is a Python package that processes medical texts, and extracts entities (Neumann et. al., 2019). (It is similar to SpaCy but adapted to various scientific contexts). This package was chosen because it can find the corresponding CUI to each entity, and it also has the benefit of recognizing abbreviations. This ensures that only the medically relevant words from each sentence are incorporated into our vectorization.

In particular, cui2vec contains pre-trained embeddings for CUIs (Beam et. al., 2018). This means that each CUI can be transformed into a corresponding vector, where the vector represents word importance in a medical setting. It is in principle similar to GloVe vectors, except they were pre-trained on medical CUIs rather than general text.

All entities are then converted to word embeddings. Using the CUIs found by ScispaCy, these CUIs are converted to corresponding vectors using cui2vec embeddings.

2.5 TextRank

TextRank is an algorithm based on PageRank which evaluates sentence importance based on other sentences' relationship with each specific sentence (Mihalcea et. al., 2004). Much like how an important webpage in PageRank would have many incoming and outgoing links to other important pages, TextRank considers a sentence important if it is similar to many other important sentences.

To perform TextRank, vectorized sentences are compared pairwise with cosine similarity, and these comparisons are placed into a matrix. Many similarity metrics are possible; cosine similarity - one of the better performing metrics in the study (Barrios, 2016) - factors in the angle between vector pairs. This means similar vectors are parallel, and different vectors are perpendicular. TextRank then iterates over the matrix to obtain importance scores for each sentence.

Performing TextRank on the GloVe or cui2vec vectorized sentences helps extract the most important sentences. All summaries were composed of the top five highest-scoring sentences.

3. Results

Several evaluation metrics are considered below. Note that figures were generated with Article 1 for discussion purposes, but are representative across all four articles. Full code and figures can be found at https://github.com/gloriafang123/med_text_summarization.

Article	Metric	Method: GloVe vectors	Adapted method: entity and cui2vec vectors
1	ROUGE R	0.763	0.665
	ROUGE P	0.985	0.982
	ROUGE F	0.860	0.793
2	ROUGE R	0.956	0.906
	ROUGE P	0.914	0.978
	ROUGE F	0.935	0.935
3	ROUGE R	0.740	0.728
	ROUGE P	0.982	0.969
	ROUGE F	0.844	0.831
4	ROUGE R	0.822	0.773
	ROUGE P	0.963	0.963
	ROUGE F	0.887	0.857

Table 1. ROUGE metrics for quality of summarization between the GloVe method, and adapted cui2vec method. ROUGE R is the measurement for recall, ROUGE P is for precision, and ROUGE F is the F-metric which captures both precision and recall.

3.1 ROUGE

ROUGE (Lin, 2004) is a well known metric for evaluating the quality of a summarization. In particular, there are three aspects - precision, recall, and the overall F-score (which depends on both precision and recall).

Although there are various n-gram forms of ROUGE, we only use the unigram version to evaluate our summaries, and we remove stop words during the evaluation. This is because doing so emphasizes how well it captures the important terminology, rather than putting unnecessary focus on stop words and their phrasing.

For example, in Table 1 for Article 1, the ROUGE-F score for GloVe method is 0.860, which is slightly better than 0.793 for the adapted cui2vec method. The slight difference between the two methods is also visible across the other articles.

3.2 Histogram of Importance Scores

Although this isn't a direct or formalized metric for the quality of the summary, it helps visualize whether the embeddings are effective.

For example, with the GloVe embedding of Article 1, the histogram in Figure 1 is tall and narrow for higher importance (TextRank) scores. This means there are many sentences ranked with high importance, and few ranked with medium or low importance. This isn't consistent with our intuition, as we'd expect an article to have a few important sentences and many medium or low importance ones.

In contrast, the adapted cui2vec histogram in Figure 2 is wide and bell-shaped. This suggests that there are fewer sentences ranked with high importance, and most sentences are ranked with medium importance. This is consistent with our intuition that an article would have a few important sentences scattered among a sea of less important ones.

Both histograms have a tall bar of very low importance sentences, which is expected - among these are sentences consisting of stop words, short sentences that were filtered out in preprocessing, or sentences that simply had very low correlation with other sentences.

3.3 Sentence Importance and Length

In many summarization algorithms, longer sentences tend to rank higher importance. This could result in a summary that only captures the longest sentences. Although we could penalize sentence length, this isn't an intuitively correct approach: long sentences do have more words, and thus are more likely to capture several key ideas. Thus, we do not penalize sentence length, but visually check the correlation between length and importance.

Both Figure 3 and Figure 4 demonstrate a positive correlation between importance and sentence length overall. The GloVe method results in a stronger correlation between importance and sentence length, as noticed in the denser scatter plot of Figure 3. This suggests that the GloVe method may be more strongly influenced by sentence length.

The cui2vec method results in a more dispersed scatter in Figure 4, suggesting that length is not as influential in importance score. This agrees with the intuition that while long sentences overall tend to be important, many exceptions also exist. The result is also consistent with our methods, as the additional entity detection step eliminates long sentences with few entities (and thus low importance).

4. Discussion

From our results and ROUGE-F scores, we see that GloVe and cui2vec perform comparably well. However, the modified cui2vec method is more consistent with intuition, based on histogram visualizations.

If both methods are comparable, this suggests that perhaps the entity detection step is not necessary in summarization; or, perhaps a deeper entity detection method is needed to improve the result more significantly from the GloVe baseline.

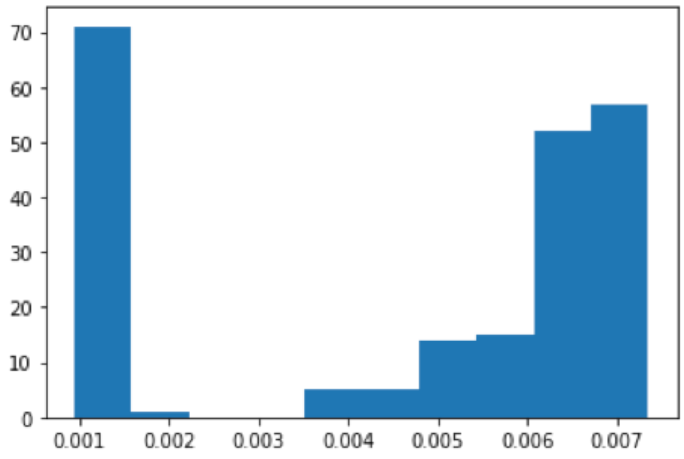

Figure 1. Histogram of importance scores using GloVe method. x-axis is the importance score, y-axis is the sentence count.

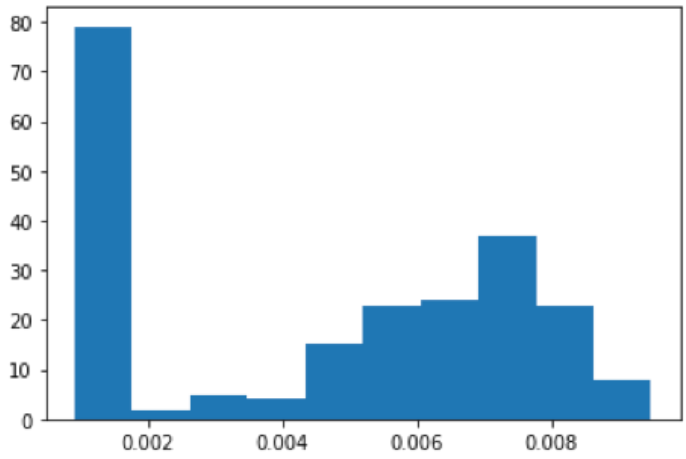

Figure 2. Histogram of importance scores using adapted cui2vec method. x-axis is the importance score, y-axis is the sentence count.

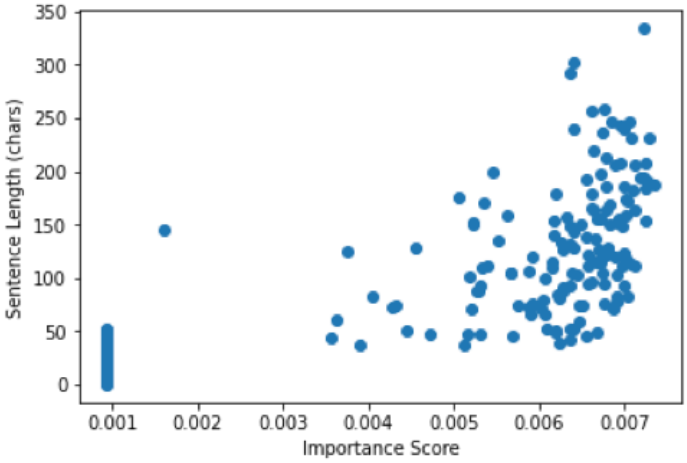

Figure 3. Sentence length versus scores, using GloVe method.

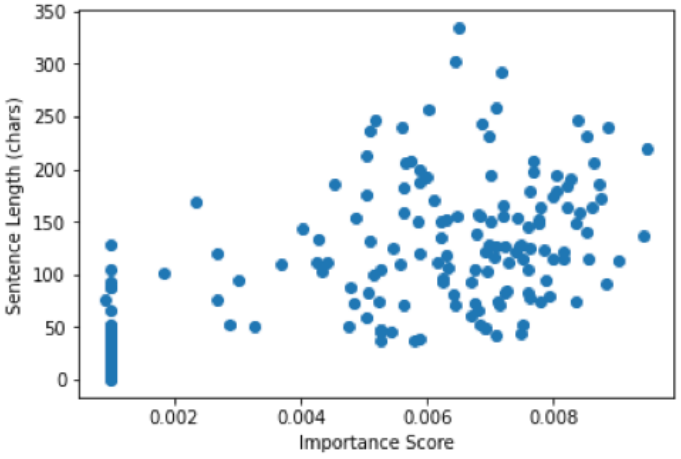

Figure 4. Sentence length versus scores, using adapted cui2vec method.

Nevertheless, a summarization method like the ones explored have significant practical value, whether it is for generating medical journal summaries, or summarizing discharge summaries for a quick screening.

Several areas are worth exploring in future research. One key step in the adapted cui2vec method was entity detection. Only after determining the important entities in a sentence were we able to filter out the important words, obtain their vectors, and perform TextRank. However, ScispaCy is one among many existing entity detection tools. An alternative, perhaps more well known method, uses metamap, which is also able to extract UMLS entities. It would be interesting to compare how effective other entity detection methods perform.

An additional constraint in this study was summary length. All summaries were chosen to be five sentences long, as a length of five sentences is long enough to capture a reasonable amount of information, while still short enough to be a readable summary. However, a more comprehensive study might consider ensuring that the number of sentences or the number of words in the generated summary matches that of the abstract, or more formally exploring various sentence lengths.

Finally, it would be interesting to delve deeper into the metric of using histograms of sentence importance. For some summaries, the GloVe method had less intuitively correct histograms compared to the adapted cui2vec method, but still produced a higher ROUGE-F score. Thus, it would be ideal to find a way to visualize sentence importance, while maintaining consistency with ROUGE.

5. Acknowledgements

This project was inspired while taking the course HST.956 taught in Spring 2020 by Professor David Sontag and Professor Peter Szolovits, TA'd by Monica Agrawal and Matthew McDermott. Using TextRank for summarizing discharge summaries was an idea I proposed for a group project, and had assigned myself this section in our division of tasks. Since we ended up changing our proposal, I decided to keep exploring on my own as I'd already begun coding and research. So, I'd like to acknowledge the class, and project members Eric Yamga and Xiaoyi Wang, for introducing me to the resources and concepts.

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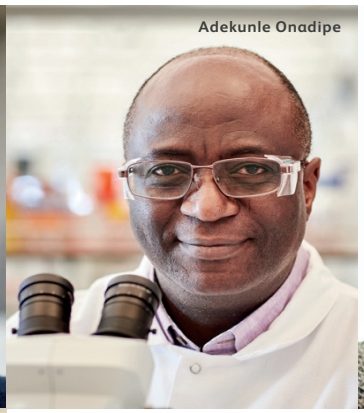

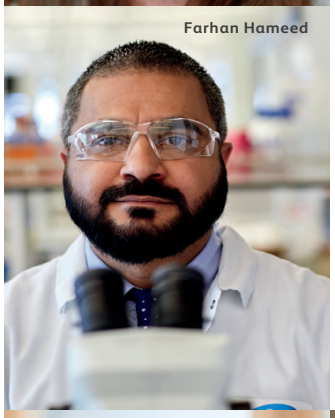

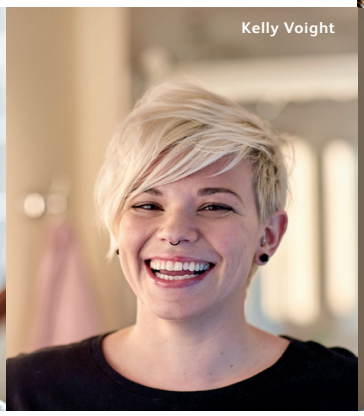

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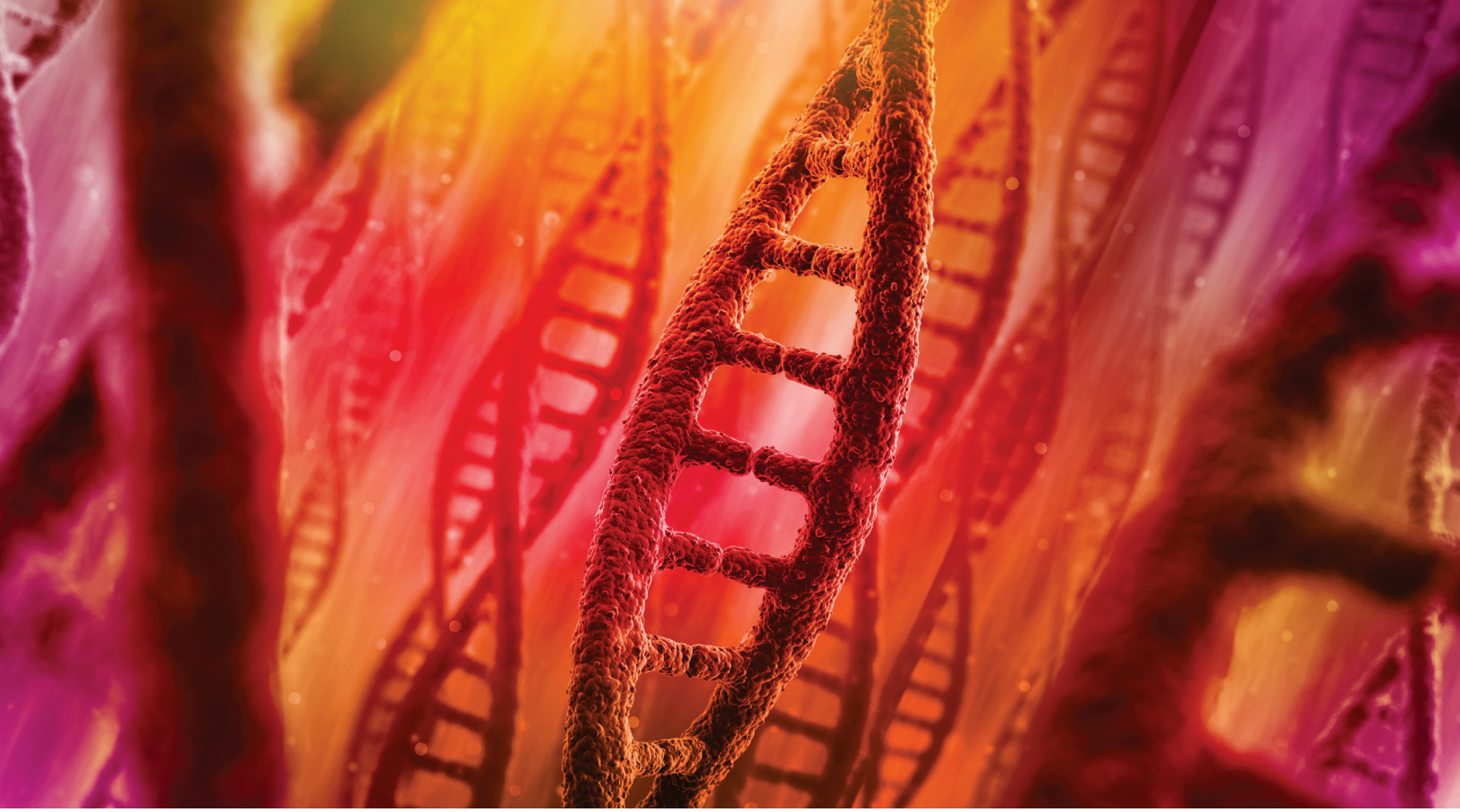

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