SRI International – Summer REU Program 2017

Student Research Projects and Accomplishments:

Below is a summary of each student's project at SRI International during the summer of 2017 in their own words with some editing of the text as appropriate.

Photo Credit: Field trip- REU Students at Grabit™ headquarters in Sunnyvale, California. The company designs robotic platforms that harness electroadhesion to perform labor intensive tasks in industry.

[1] Student: Irene Jeong (Cornell University); Mentors: Drs. Roger Varney and Asti Bhatt

Project Title: Detecting Thin Layers in the Lower Ionosphere

My summer as an REU intern at the Center for Geospace Studies was focused on the development of an automated algorithm for detecting thin layers in the ionosphere. My project included the creation of a computer program to run through processed data from the Poker Flat Incoherent Scatter Radar (PFISR) and look for appearances of sporadic E layers (Es layers) and polar mesospheric summer echoes (PMSE).

PFISR is one of the three Advanced Modular Incoherent Scatter Radars (AMISRs) developed by SRI International. PFISR runs at high-latitude in Poker Flat, Alaska and has a phased array antenna that operates at 449-450 MHz. Using PFISR, I studied two kinds of thin layers in the lower ionosphere, sporadic E and PMSE. Sporadic E are descending, dense patches of ionization that appear sporadically in the E region of the ionosphere. They typically occur at 100-120 km, are thin in altitude, but can be horizontally expansive. PMSE are thin layers of coherent echoes from plasma turbulence; they are typically lower in altitude, 80-90 km, and are mostly seen during the summer months. PMSE are highly linked to the appearance of noctilucent clouds (NLCs), which are made up of ice crystals.

It is important to note that despite the brief appearances of these thin layers, they have considerable impact and meaning when they are present. Sporadic E are often called 'blanketing sporadic E' because they can hide objects above them by preventing ionsondes, high frequency (HF) radars used to analyze the ionosphere, from passing pulses through them. Moreover, sporadic E propagation, or 'E skip', is a phenomenon that permits the propagation of very high frequency (VHF) signals over great distances due to refraction by Es clouds. This can lead to issues of high interference when Es layers are present. PMSE, on the other hand, have a more hidden significance. Noctilucent clouds (NLCs), which are associated with PMSE, have greatly intensified and spread over the recent years. Now, NLCs can be viewed at earlier points in the year and closer to the equator at locations like Colorado or Utah. This intensification of NLCs and increase in PMSE is thought to be the result of human activity spawning a massive increase in methane in our atmosphere. Methane, a greenhouse gas, is oxidized to produce two water molecules, which then grow the ice crystals that make up NLCs. As a result, PMSE are a sign of our direct impact on climate change, which can have massive climatological consequences.

With the interest of studying these thin layers, my algorithm first sets out to be able to automatically detect these thin layers. Since these thin layers are visible as thin peaks in the electron density profiles, we can use wavelet analysis to compare these spikes with a wavelet. First, we take the processed data from PFISR and perform a continuous wavelet transform on the data, comparing the input signal with different shifts and scales of a Mexican Hat wavelet. This comparison produces a two-dimensional array of wavelet coefficients that represent the convolution of the signal and the wavelet of a specific shift and scale. We then select the largest wavelet coefficient and determine whether it is statistically significant or not. We do this by first, reconstructing the exact wavelet used to produce the largest coefficient. Then, if the amplitude of this wavelet is larger than the error associated with the electron density estimate, then the wavelet is statistically significant. Next, we check for whether this point is an Es layer or PMSE and record its timestamp, altitude, electron density, and scale width if it is indeed a thin layer. Otherwise, we simply take the reconstructed wavelet and subtract it from the data so that we can repeat this loop. Thus, the algorithm is picking out the first, second, third, etc. largest wavelet and checking for thin layers. A visualization of the algorithm can be seen in Figure 1. We then repeat this algorithm across all times for each beam in a given experiment.

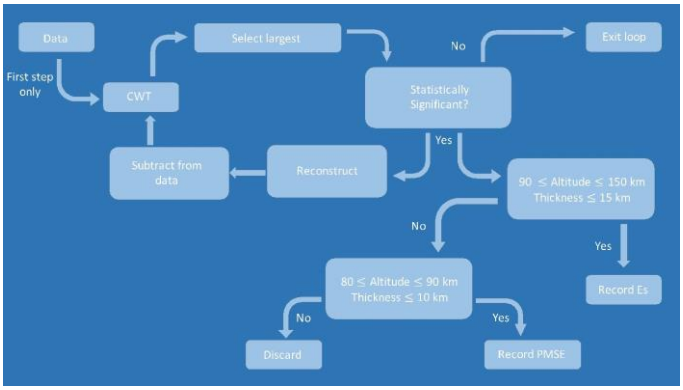


Figure 1: Algorithm Flowchart

The detection algorithm outputs the results in a text file and various plots that can be viewed through the AMISR_SCRATCH disks at the Center for Geospace. An example is shown in Figure 2, a plot tracing the algorithm's results in red asterisks on top of the actual data.

Although the algorithm successfully detects the overall Es layer, there are still ways to improve its accuracy and precision. Sometimes the algorithm either fails to pick out parts of the Es layer, or picks out false positives. After referencing some new literature, we found that high-latitude Es layers are much thinner than electron density enhancements due to auroral precipitation, which have scale widths of 5-10 km. With this stricter thickness condition, the

algorithm had improved accuracy, but still picked out some false positives. We are currently devising a post-processing method for comparing each output with its neighbors to determine whether it is an outlier or not. If a point has no nearby neighbors, then it is likely a false positive and the algorithm will discard it. We are also implementing the use of different integration times. To improve the detectability of the Es layer, we plan on averaging the data over different amounts of time, which will hopefully help to differentiate the Es layer from distractions like aurora, and fill in the gaps where the layer may become thin.

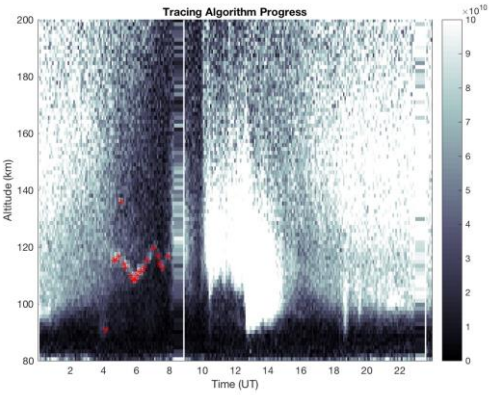


Figure 2: MSWinds23 ex. 20100725.001.done

I originally wrote my algorithm in MATLAB, but in order to perform mass statistical studies on all ten years of PFISR data, our next major checkpoint is to translate my code into Python. This way, we can run the algorithm on large amounts of data at faster speeds and be able to gather statistics on when such thin layers are typically visible, observe how detectable they are across beams, and possibly prove or improve current knowledge of the origins of these layers. I plan on continuing my studies throughout the fall and winter as well.

My time at SRI International has been absolutely inspiring and motivational. I not only gained experience in an entirely new field of physics and engineering, but also developed essential skills that apply across a variety of fields such as computing, data analysis, critical thinking, signal processing, and wavelet analysis. I would like to thank my mentors Dr. Roger Varney and Dr. Asti Bhatt, my REU directors Dr. Sanhita Dixit and Dr. Gregory Faris, everyone I came into contact with at SRI and the Center for Geospace Studies, as well as the National Science Foundation for providing me this wonderful opportunity.

[2] Student: Melany Vázquez Heredia (Boston University); Mentors: Drs. Gregory Faris and Yingdi Liu

Project Title: Hyperspectral Imaging

During my time at SRI, I worked on fast Hyperspectral Imaging. To save you a trip to the Google search bar, Hyperspectral Imaging's goal is to study samples using their spectra. What's special about this set-up is that we image many wavelengths to get this information as opposed to just using the three colors of a conventional camera. However, the time currently needed to run an analysis of the data is too long and too inaccurate which is where I came in.

Before starting this REU, I had some experience with coding, but I knew very little C++. So I had to start there as the code I was to optimize was written in C++. It took me some time to get used to it, but I finally learned enough to delve into the project fully. There is a MATLAB code that gets the job done accurately, but not efficiently so I could use that for comparison when I tried to get the C++ to run accurately.

In order to know where I needed to focus my attention for optimization, I needed to know where the run time was longer or where the calculations were off. I added some lines that would let me know how long each function in the code took to run and I wrote some save functions for both MATLAB and C++ that would save intermediate steps in the codes in order to compare the

outputs for MATLAB and C++. While I did that, I had to read through the C++ code which, if there were any minor mistakes in syntax, I would hopefully notice and fix them.

Writing the save functions for the C++ code took a long time due to the fact the outputs had different formats and I had to account for those. But once I finished them, I could compare the differences in the intermediate steps and I noticed where in the code did the C++ and MATLAB outputs diverged which of course was helpful to adjust the C++ code. While reading through the code I noticed some minor syntax mistakes which were inconsistent throughout the C++ code, like using a fixed value instead of a user-input variable, so I edited these so that the code would be self-consistent. By editing the code to fix the accuracy errors and editing the minor syntax errors, I managed to improve the running time from ~71 to ~58 seconds.

While I would love to write that everything went perfectly and that I perfected the code, that was not the case. Having to spend any time at all learning C++ code, while beneficial for me, did take away time that could have been spent working on the project. Additionally, writing the save functions and running them, on MATLAB especially due to how inefficient it is, took time that I would have liked to spend editing the code. However, I could not have started to edit the code without knowing where to work on, so while a little frustrating, it was necessary. It's also labor and time intensive to edit the code based on the saved outputs, because what you're doing is making educated guesses as to where something went off and for every educated guess, you have to run the code again. And, finally, one of the libraries we use, while pretty complete and highly documented, doesn't have that much support anymore so it took some extra effort to sort through the forums and the manual.

In all honesty, I could not be more grateful for the opportunity to work on this project. While at times frustrating, it was very rewarding. I learned C++ as it pertains to this project in a lot less time than I ever thought I would. I also managed to optimize the code. And I got to spend the summer at SRI with people who are beyond passionate about what they do and are willing to take time to teach you about it.

[3] Student: Nathan Dvorak (Coe College); Mentor: Dr. Thomas Shaler

Project Title: Identification Using Peptides and Mass Spectrometry

During the course of this summer, I was tasked to be able to quickly and effectively identify people by the mutations present in their peptide sequence by using a technique called mass spectrometry. The hypothesis behind my summer research project was to see whether protein sequences can be unique identifiers for people much like mainstream DNA technology. Many different samples and sample collection methods were investigated. These included discarded cherry pits, fingerprint oils left on microscope slides and skin collected by rubbing a subjects elbow and hand with sandpaper.

Results:

The cherry pit samples had enough saliva on them to be able to accurately assign samples to the subjects they were collected from. Since the pits were successful, we proved that a small volume residue sample (< 20 microlitres) can be used to associate samples with respective sources (here people).

Next steps:

We believe that the cherry pit samples can be improved more, and this comes down to concentrating the protein solution better. We also believe that the data analysis of the samples can be automatized so the data processing will be more efficient, faster and more accurate.

[4] Student: Yuzki Oey (Princeton University); Mentors: Drs. Sanhita Dixit and Gregory Faris

Project Title: Fast PCR

Background:

Polymerase chain reaction, or PCR, is a process in which certain parts of DNA are copied many times. This reaction is used to detect certain genes that may be known to cause disease, or be linked to a trait. It consists of many cycles of a lower temperature (60-72°C) annealing and extension step in which the DNA is copied, followed by a high (about 90°C) denaturation step to melt the DNA into two single strands. This process is usually done in a large machine in plastic well plates or PCR tubes. Once the DNA is amplified, it is run on an agarose gel and stained to detect the target DNA (the DNA is separated by size in the gel), and the complete process takes about 2-3 hours.

However, due to the diagnostic applications of PCR, there has been a demand for fast, easy, and small PCR machines. While progress has been significant, most machines still require the user to prep the sample and pipet it into PCR tubes or wells. This can be difficult for those who don't have a sterile environment to prep their samples and is also tedious. Development of a small footprint heater and a sample matrix that is more relevant to point-of-care settings would hugely benefit the diagnostics marketplace for this application.

Summary:

My goals this summer were to fine-tune the temperature control of our heater cell and the procedure for running matrix based PCR. For the temperature control, we used a proportional-integral-derivative (PID) system which considers the error between the current and desired temperature and accordingly adjusts the applied voltage across the heater. Once we found the right constants, it became a reliable method to hold the temperature constant. Getting PCR to work in a new matrix was trickier but worked after a lot of iterations.

Reflection:

I expected SRI to be much different than academia research. The big difference I noticed was how much everyone talked about money, since I haven't had to apply for funding at school yet. However, the general structure that I interacted with daily was similar, in that I had two "stages" of mentors—Sanhita, which I would compare to a grad student or postdoc, and Greg, who would compare to my PI. I'm not sure if I would want to work at a place like SRI, since writing grant proposals for a living sounds less than ideal, but it is nevertheless tempting because I won't be bound by my higher-ups to work on a project that I wouldn't want to, as I imagine real industry would be like.

[5] Student: Brianna Zawacki (Kings College and University of Notre Dame); Mentors: Drs. Andrew Lowenthal and Peter Madrid

Project Title: Single Cell Detection of Secreted Proteins with Functionalized Polymers

Antibodies are y-shaped proteins that are comprised of a heavy and light chain which are held together by disulfide bonds. The tips of antibodies are called variable regions, which are unique to each type of antibody. Antibodies are secreted by B-cells when antigens, proteins that induce an immune response, are present in the system in order to bind to antigens and neutralize them. Antibodies will only bind with specific antigens that are compatible with their unique variable regions. Scientists take advantage of this antibody-antigen specificity to create

therapeutic antibodies which can target certain disease molecules. The goal of my project this summer at SRI was to develop a more efficient and low cost method for FAST cell scanning that will allow the detection of antibodies as part of a larger project that was working to develop human therapeutic antibodies.

The original method for this project involved taking advantage of the high affinity binding between the protein family avidin and the small molecule biotin. It begins by conjugating NeutrAvidin, a protein of the avidin family, to agarose and then separately conjugating biotin to a bait protein, the antigen. By then mixing the two together, an agarose bait conjugate is formed. The agarose will immobilize the cells, but the antibodies will be bound by the bait protein within the agarose matrix. The whole system is then run through the FASTcell rapid scanning system, in which cells are plated within the agarose and labeled with fluorescence tagged antibodies. FASTcell then identifies the locations of the antibody secreting cells (ASCs) using fluorescence. The goal of my project was to work on a new method of this project in which “click” chemistry is used to bind the antibodies to the agarose matrix.

Click chemicals took the place of the previously used NeutrAvidin and biotin. This click chemistry method is much lower in cost than the NeutrAvidin method; switching the methods would save costs 100-fold because the NeutrAvidin is much more expensive than what is initially conjugated to the agarose in the click chemistry method. The click chemistry reaction being used in the new method is the strain-promoted azide-alkyne (SPAAC) reaction. It is called strain-promoted because it is the strain between the cyclooctynes of the azide and alkyne groups that lowers the activation energy of the interaction and allow the molecules to ‘click’ into place. This forms a very strong covalent bond. The new process begins by conjugating an azide-amine to agarose and conjugating DBCO, an alkyne, to a bait protein. The two conjugations are then mixed together to create our new ‘CLICK’ gel. I made two CLICK gels with different concentrations of azide-amine conjugated to the agarose. One had the same concentration as the NeutrAvidin gel, 6.06E-06 M, and the second had a concentration at 5x’s that, 3.03E-05 M.

A serial dilution assay was then formed and run on the new CLICK gel to test its conjugation efficiency. For this assay 96-well plates, in which there are 8 rows and 12 columns, were used to run the tests. 50 µL of DBCO-Cy3 was placed in the first column and then another 50 µL of DBCO-Cy3 was serial diluted throughout the rest of the columns. 50 µL of unconjugated agarose was then placed in each column for the standard curve row. The other rows for comparison would be set up using the same procedure except using different agars. Cy3 is a fluorescent dye commonly used in biological essays. The whole plate had its fluorescence measured, and by using a standard curve, the conjugation efficiency of the azide-amine agars was calculated. The azide-amine agar with the 5X concentration of the original NeutrAvidin agarose had the highest conjugation efficiency. More trials were run using different batches of the azide-amine agarose at the 5x’s higher concentration and the conjugation efficiency was found to have an average of 32.7% with a standard deviation of 3.3%.

The CLICK gel was fully conjugated using a bait protein instead of a fluorescent dye; the bait protein we chose was bovine serum albumin arsenate (BSA-Ars). Using the amine agarose at the 5x’s higher concentration, the agarose was first brought to ~ 70℃ so that it could fully melt. It was then brought back down to ~ 39℃ before the bait protein was mixed into the system. The system was then left over night at ~ 39℃ before it was run through the FASTcell rapid cell scanning system. The CLICK gel proved not only successful, but it produced bigger and brighter fluorescent halos around the ASCs than the NeutrAvidin agarose. As long as the success of this new method continues, the goal is to fully shift the project from using the NeutrAvidin agarose technique to just using this click chemistry technique in order to save costs and increase efficiency. Before I finished my work on the project, I coupled a different bait

protein, ovalbumin (OVA), to both DBCO and biotin so that it could eventually be conjugated to the agars and run through the FASTcell system.

[6] Student: Joseph Bales (Colorado School of Mines); Mentors: Drs. Sanhita Dixit and Gregory Faris

Project Title: Putting Things Only a Little Bit Together: Artificial Lipid Bilayers and the Methods of Forming Them

During this summer (2017), the Artificial Lipid Bilayer project was essentially resurrected, brought back from a shallow grave where it had been languishing so that this humble student could start the ball rolling again.

Here's the basis: so there are these things called lipids which form a single, continuous layer (monolayer) on the interface between water and oil. Taking advantage of that, I've been forming extremely tiny droplets of lipids dissolved in water inside a puddle of oil. Then I've been pushing the droplets together to form lipid bilayers, which are what cell membranes are made of.

All of this has been done using a proprietary technique, and a fairly powerful microscope. This is all in an effort to create a cell-membrane-like environment which is mass-producible and where we can isolate specific elements of those membranes for further study. This could have implications for how we test drugs and how we study transport properties of cell membranes.

Right, so, what have I been up to?

Well, at the beginning of the summer, we didn't have much information on the specific settings of the instrument that was used to form droplets under oil, lipid concentrations, and the mechanical parameters required for this process. My job was to fine-tune the process as much as possible and move us in the direction of running complete experiments.

The most interesting part of the whole experience was developing my own method for forming droplet bilayers. At the beginning of the summer, I was given a procedure and told it had worked in the past. The idea was to create drops on the bottom of the oil puddle and then create the said instrument. Well, I tried that procedure several times and could never get it to work correctly. So I bravely gave up and tried something a bit different. This decision was followed by immediate results. It was very satisfying to solve this particular issue.

There were also some issues with such things as lipid concentration in the aqueous solution, extrusion methods, and doping the solution with fluorescent dye as well as myriad other challenges. You might be able to tell from that particular word choice, but I'll make it blatantly obvious: I loved it. All the problems to solve are what makes science, science.

Now, we also had to prove that this method was useable for testing drugs. I spent the last few weeks of the summer inserting P-glycoprotein (a protein important in drug-transport tests) into the bilayers I was forming and seeing what happened when we tried to make transport happen. This, of course, carried its own list of technical issues. And this, sadly, was not a part of the process I was able to finish. But hey, I managed to get it started, and I left the project in good hands. May not be entirely satisfying, but there it is.

Now, I must say that this project by itself was just not enough to occupy me for the whole summer. After indicating that I had some free time on my hands, my mentors assigned me to - building a microscope apparatus for another project. More specifically, I did a bunch of soldering, building such electronics as voltage dividers, special LED circuits, and even full-on cables. I also helped set up a filter cube to regulate the fluorescent behavior of the tracer dye being used in the other experiment.

Through this summer, I learned a fair amount of biophysics, optics, liquid dynamics, microscale physics, and even some circuitry and programming. I also gained some more experience with such things as soldering, microscopes, lasers, and wet chemistry. And of course, I learned more about the behavior of tiny water droplets than I could ever want to know.

[7] Student: Chayse Jones, Western Washington University; Mentors: Drs. Zheng Ao and Lidia Sambucetti

Project Title: Identification of antibody secreting plasma cells using high throughput optical scanning technology (FAST)

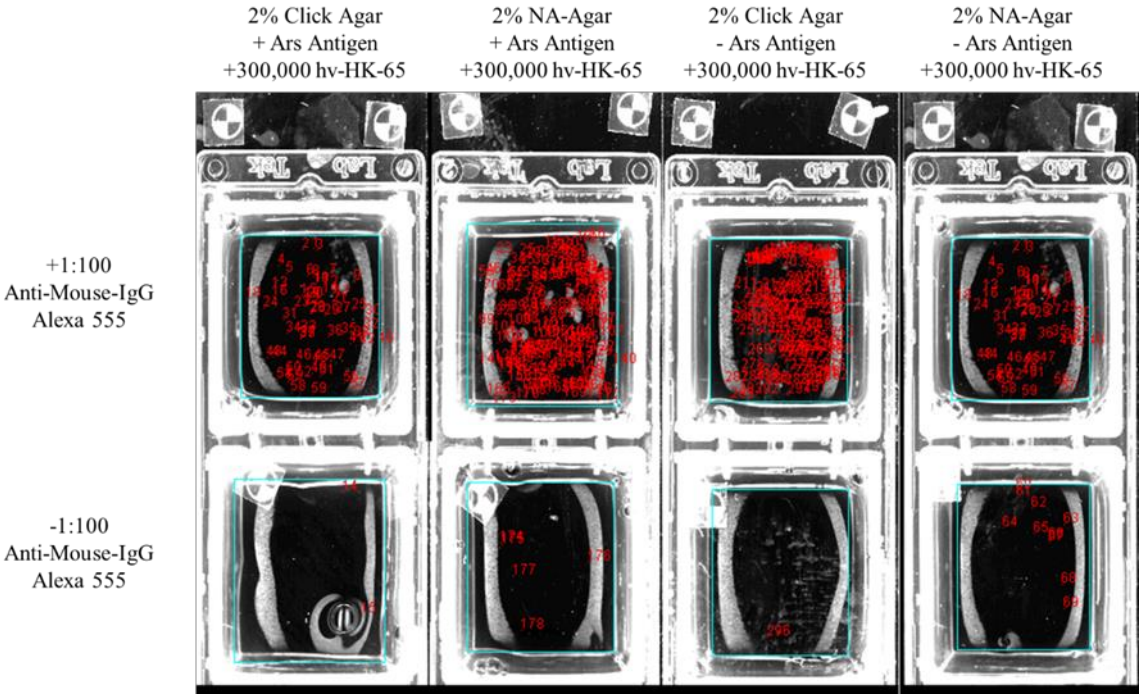
This summer at SRI International, I have been given the opportunity to participate in a fairly new research project, FASTclone. This project focuses on developing an antibody discovery platform that allows for high-throughput screening of antibody secreting plasma cells. The applications allows us to generate humanized antibody from human peripheral blood mononuclear cells (PBMCs), which can then be applied for downstream applications such as radio-immunotherapy, antibody-drug conjugate therapy, and tumor-specific IgG just to name a few! Currently, monoclonal antibodies are harvested from animals. This poses a problem because animal antibodies will generate an immune response if introduced into the human bloodstream. Further humanization is required, but is expensive and labor intensive. Our approach is fast, cost effective, versatile, and does not need further humanization.

Once the protocol is optimized (my project) we will be able to harvest human monoclonal antibodies. The first step to this process is obtaining a blood sample from a person challenged with an antigen. Using Ficoll, we will isolate the PBMCs from the blood and resuspend them in our antigen-infused gel. Specific antibodies will bind to the antigen cemented in the gel. Three thorough washes will be conducted to clean the gel of any unspecific antibodies. We will then stain with an anti-human IgG fluorescent antibody. The fluorescent antibodies will form a halo around our target B cells. Using FASTcell we will be able to detect hits (spikes in fluorescence) and transfer their coordinates to Cell Celector™ to be imaged and picked. With the picked B cells we can perform reverse transcription polymerase chain reaction (RT-PCR) to clone the cDNA. We will then amplify the synthesized cDNA using traditional PCR, giving us genes encoding monoclonal antibodies specific to our antigen! Before all of this is possible, many experiments will be conducted to test efficiency and accuracy.

In my first two weeks working in the lab, we have conducted some preliminary experiments in order to fine-tune our procedure and identify parameters that will keep our target cells healthy. So far, in our experiments we have used mouse hybridomas to mimic the antibody secreting plasma cells. Eventually, we will apply this platform to discover and isolate single human plasma cells. Our first experiment was to determine the percentage agar that would be

easily plated, adhere to slide during washes, and allow for the clean retrieval of cells. After testing five different options, 2% agar proved to be the best in all three categories. Next, we tested two different types of agar to see which would best retain the antibody secreted by the hybridomas.

A total of eight samples were made, four of 2% click agar and four of 2% NeutrAvidin agar. Our controls for this experiment were created by either withholding the Ars Antigen or the Anti-Mouse-IgG from two samples in either type of agar. We then pipetted the samples into their own well, allowed them to solidify during incubation, washed all wells with hybridoma media, and incubated them again overnight to allow the cells time to secrete antibodies. The next day, we washed with 1xPBS and used FASTcell to locate hits, the presence of fluorescence. The image below depicts the hits that FASTcell was not only able to identify, but also determined whether or not those hits were true positives using the imaging and analysis features offered by Cell Celector™.



Cell Celector™ allowed us to visualize whether the hits were true positives with halo staining (antibodies were captured around cells), false positives with the antibodies inside the cytoplasm, debris, or nothing at all. We found extremely bright halos in the plates that included antigen and small, dim halos around cells in plates without antigen. The dim halos should not have appeared and may have been the result of formalin fixation. Although the difference between the bright, correct halo and dim halo is recognizable, this is a key element we aimed to tweak in later trials. Our results also showed that fluorescence was much greater in click agar gel than in the NeutrAvidin gel. Before jumping to the next step, we conducted a small experiment in order to save expensive reagents.

A dilution test was done to pinpoint the minimum amount of reagents needed for the experiment to work. We pipetted the original concentration gel into two separate wells, one with antigen and one without to serve as our controls. This step was repeated with 1:1 and 1:3 dilutions. The dilutions were made by mixing the antigen infused gel with the correct proportions of regular 2.5% agar. Our results from this experiment were not at all what we expected to see. FASTcell recorded hundreds of hits on every well. We knew something went wrong because the antigen deprived wells should have had zero hits. If there is no antigen cemented in the gel, the secreted antibodies from our target B cells are not captured and are washed away leaving nothing for our fluorescent antibodies to attach to. We assumed that the samples were mixed up during the experiment. Nevertheless, we took a look at the wells using Cell Celector to see if there was anything we could take away from this experiment. We found that the number of cells (300K) in each well was too dense and resulted in a cloudy image. To achieve a picture with well-defined halos, we decided to lower the cell density to 50K cells per well.

Along with the lower cell density, we included some extra factors in our next experiment. Our goal was to assess cell viability over time using the LIVE/DEAD staining assay. We put together six different wells. Two wells were stained right after plating, three hours after plating, and the next day. One well from each time point was washed with 1x complete RPMI while the other well was washed with 1x complete RPMI with factors. The factors added were HEPES, BAFF, IL-4, and sCD40. To ensure we were only seeing the effect of the factors, the cells were plated in 2% agar-1x RPMI mixture instead of click agar. The results from this experiment brought another wave of frustration. There seemed to be no consistent trend, high death count, and we became unsure if the microscope was compatible with the staining.

From the disappointing results in the previous experiment sprung a new opportunity to do a LIVE/DEAD staining and microscope check. Our plan was to suspend the cells in PBS and pellet into two separate wells, stain one well with the LIVE/DEAD original staining concentrations, stain the other well with the LIVE/DEAD 1:3 diluted dye, and image/analyze using a EVOS FL Auto. Our results from this experiment were a small victory given the recent failures. There was little cell death, clear staining for both concentrations, and no overlapping staining (one cell stains for live and dead). This told us that our microscope and staining method were working great and that something must be wrong with the plating method or gel concentration. A high percentage click agar could be toxic to the cells.

Unfortunately, this is where my time at SRI International has come to an end. The next steps carried out by my mentor will be determining what is killing the cells and tweaking the protocol accordingly. I am ending my time here encouraged and full of wonder. I am excited for the future of this project and having had the chance to be involved. Thank you to SRI International for giving me this opportunity to pursue my love and curiosity for drug discovery

SRI REU Program Activities:

Regular meetings with the REU students were scheduled to gauge student progress and address any concerns. In addition, several activities were included in the 12-week program to provide a well-rounded and fun-filled REU experience. These are described below.

1. Field Trips:

- 07-25-2017: Stanford University - The REU students accompanied by the program PI's Drs. Dixit and Faris visited Prof. W.E. Moerner's labs at Stanford University. The students were really excited to meet with a Nobel Laureate. Prof. Moerner was phenomenal with the students. He gave an engaging presentation on his scientific journey and had organized a lab tour for the group. The REU students could speak with graduate students and postdocs in his lab and also saw some experiments in action! All in all, the students, and the program PI's enjoyed every minute of the field trip.
- 08-03-2017: Grabit Inc - The REU students accompanied by the program PI's Drs. Dixit and Faris, visited the headquarters of Grabit Inc., an SRI international spin-off that harnesses the power of electroadhesion technology to build robots that can perform labor intensive tasks in industry. Dr. Harsha Prahlad was our host and gave a wonderful presentation of the company's mission to the students. The students were also able to see some of the robots and it was a very informative tour!
- 08-15-2017: NASA Ames- The REU students accompanied by the program PI's Drs. Dixit and Faris visited the NASA Ames Research Center in Mountain View, CA. Dr. Christopher Dateo, Chief of the Exobiology Branch in the Space Science & Astrobiology Division hosted the group. Dr. Dateo gave an overview of NASA to the students via a presentation and staff from the exobiology branch spoke to the students about their research efforts, followed by a lab tour. The students enjoyed the field trip.

2. Seminars at SRI International:

This seminar series is hosted by the Biosciences Division at SRI International, and the REU students had the opportunity to attend these seminars.

- 06/02/2017: Speaker - Patrick J. Paddison, Ph.D., Associate Member, Human Biology Division, Fred Hutchinson Cancer Research Center; 'Where the rubber hits the road for precision oncology: using functional genomic screens to reveal molecular vulnerabilities in patient-derived tumor stem-like cells'.
- 06/16/2017: Speaker - Antoine Snijders, Ph.D., Research Scientist and Department Head, Division of Biological Sciences and Engineering, Lawrence Berkeley National Laboratory; 'Impact of host microbiome on disease susceptibility'.
- 06/30/2017: Speaker - Zheng AO, Ph.D., Postdoctoral Fellow, SRI International; 'Multi-component Liquid Biopsy Enabled by High-throughput Optical Scanning Technologies'.
- 06/30/2017: Speaker - Kalyani Jambunathan , Ph.D., Research Scientist, Molecular Toxicology, SRI International; 'An In vitro assay panel to predict drug induced mitochondrial toxicity'.

- 07/21/2017: Speaker –Sanhita Dixit, Ph.D. and Gregory Faris, Ph.D., Research Scientists, SRI International; 'Droplet Platforms for Membrane Based Assays and Biological Reactions'.
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4. REU Student Presentation:

Around the 11th week of the program, each REU student gives a presentation outlining the research they conducted over the summer. Staff members attend these seminars schedules permitting. Presentations last approximately 20 minutes with an additional 10 minutes reserved for questions and discussion. Prior to these presentations, each student hosts the remaining group for a tour of their lab and experimental set up.

5. Graduate School Application information:

The program coordinators encouraged our REU students to attend webinars on the website hosted by the Institute of Broadening Participation (http://www.pathwaystoscience.org/) and to navigate the IBP's website for information on fellowships and graduate school applications.

6. Ethics Training

A formal mechanism to train the students in the ethics of scientific research was put in place in the summer of 2010. As part of this training, the students were required to take an online course to educate themselves about ethics in a research environment. The online course is available freely at: http://ori.dhhs.gov/education/products/montana_round1/issues.html#intro. The study of the following three sections was mandatory; Section One: Ethical issues in Research, Section Two: Interpersonal Responsibility, and Section Four: Professional Responsibility. At the end of their study of each section, this website provided a test. The students were asked to take the test and furnish copies of their scores to Dr. Sanhita Dixit.

7. Social Events

Students were invited to attend SRI events during the course of the REU program.

- A welcome party for the REU students was organized at the start of the summer. An end of program party was organized to declare the Peterson Award Winner and to celebrate the successes of the REU students!
- Breakfast with the CEO Dr. Bill Jeffery: The students participated in a breakfast event with the CEO along with other campus interns.
- Division All Hand meeting: The students attended the All Hands Meeting for the Biosciences Division during the summer.
- Summer Concert Series: The students enjoyed lots of good music and California sunshine during the summer concert series on campus which featured a great band line up and each act features at least one SRI employee or alumnus.
- SRI's robotics team hosted the Silicon Valley Bots & Beer Meetup on June 7th 2017. This monthly get-together of Bay Area roboticists provides a great opportunity for SRI to showcase some of its cutting-edge advances in robotics, while taking an active role in the community.
- SRI's studio on Aging hosted an on campus open house on August 3rd 2017.

8. James R. Peterson Award for Excellence in Undergraduate Research

During its 50th anniversary reunion in 2006, the former Molecular Physics Program at SRI International, announced the creation of the James R. Peterson Award for Excellence in Undergraduate Research. This award is given to the summer undergraduate student participating in SRI's NSF-supported Research Experiences for Undergraduates (REU) program that best combines Jim Peterson's technical excellence and spirit of friendliness and cooperation.

REU student nominations determine the winner of the Peterson Award. The 2017 winner was Brianna Zawacki of Kings College, Wilkes-Barre, PA. To date, winners include Anand Oza, Princeton University (2006), Zachary Geballe, University of Michigan (2007), Brad Hartl, University of Wisconsin, LaCrosse, (2008), Aya Eid, Illinois Institute of Technology (2009), Alejandro Ceballos, Northern Arizona University (2010), Michael Rodriguez, California Lutheran University (2011), Stefan Mellem, St. Olaf College (2012), Timothy Weber, Columbia University (2013), Collen Werkheiser, Reed College (2014), Brendan Marsh, University of Missouri-Columbia (2015), Gabriel Barajas, Stanford University (2016) and Brianna Zawacki, Kings College (2017).