



Research Scholars Program

2020 SPRING PRESENTATION

May 21, 2020 & May 28, 2020
Kingsborough Community College
Virtual Presentations via Zoom

SYMPOSIUM PROGRAM

May 21, 2020/May 28, 2020

- 3:00 PM** Registration
- 3:05 PM** Welcoming remarks
Christina Johnson, Administrator for CUNY Research Scholars Program
- 3:10 PM** Honors Program and Experiential Learning Opportunities
Dr. Homar Barcena, Director of the Honors Program
- 3:20 PM** Student Presentations
PowerPoint – May 21, 2020
Poster – May 28, 2020
- 4:45 PM** Closing Remarks
- 5:00 PM** Presentation concludes

PowerPoint Session

May 21, 2020

SCHOLAR

Jaweria Bakar
Levi Borevitz
Jun Ye Cai
Noel Castillo
Emily Morrissey
Natalie Mosseri
Jose Olivera
Jonathan Pinkasov

MENTOR

Laura Spinu
Dmitry Brogun
Kieren Howard
Homar Barcena
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Laura Spinu
John Mikalopas
Sarwar Jahangir

Teasing Apart Intonation and Segmental Information in the Perception of Foreign-Accented English by Native Speakers

J. Bakar and L. Spinu

Various studies [1] have found that people with a foreign accent are rated less favorably along subjective scales (e.g., intelligent vs. dull or kind vs. unkind) than speakers without a foreign accent [2, 5, 4]. Research suggests that foreign-accented speech causes a reduction in cognitive fluency, having a negative effect on credibility [3]. In a pilot study, we have found that out of five different accents in English, speakers with Russian and Arabic accents obtained consistently lower scores. While these findings may be partially explained by negative representations of the language in the media and pop culture [1], the question arises to what extent linguistic factors such as intonation or segmental properties also play a part. In other words, is Italian intonation universally perceived as beautiful [1], whereas Russian sounds are perceived as 'harsh' [5]? To address this question, we recorded English sentences spoken by native speakers of Russian and Italian (n=4). We created three sets, as follows:

(1) naturally pronounced

(2) Intonation only (sentences filtered such that only aspects pertaining to intonation were preserved without any linguistic content present)

(3) Segmental information (sentences preserved aspects of foreign pronunciation in terms of consonants and vowels, but the prosodic aspects (e.g., segmental length, intonation) resembled native English production).

Sentences spoken by English natives served as a baseline.

A perceptual experiment was set up using PsychoPy. Twenty-six native speakers of English listened to each sentence and rated the speaker in terms of pleasantness, honesty, self-confidence, and expressiveness on a 1-5 Likert scale. Mean scores for each variable were computed in order to determine the effect of language, sentence type, and gender. Our study thus adds to the body of work on foreign accent perception and the mechanisms underlying listeners' reactions.

We also wanted to expand our sample size (number of participants) to our experiment. Therefore, another step that we added is sharing our surveys with the internet community and compare the results.

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3D Homology Modeling of a Ribonuclease J1/J2 in the MRSA *Staphylococcus aureus* Sp.

L. Borevitz and D.Y. Brogun

The increasing use of antibiotics in medicine in the public domain, and the issue of drug-resistances is making serious bacterial infections more difficult to treat, as the genes involved in the bacteria are mutating rapidly and resulting in multiple drug-resistances. This is where the purpose of solving the mutated structure is significant and comes into place. The Beta-lactamase protein family cause certain antibiotic-resistance in various bacterial infections, some of which include Methicillin-Resistant *Staphylococcus aureus* (MRSA), penicillin-resistant *Streptococcus pneumoniae*, and vancomycin-resistant *Enterococcus*. Beta-lactamases are associated with the resistance to more than one class of beta-lactam antibiotics such as penicillin, cephalosporin, and cephamycin. Ribonuclease J1/J2 is a conserved enzyme in *Staphylococcus aureus* from the Beta-Lactam-metallo superfamily. The enzyme is composed of three domains. A b-lactamase core domain, a b-CASP domain, and a C-terminal domain that is unique to RNase J1/J2. The enzyme's function is to break down the RNA, and it has both endonuclease and exonuclease activity [1]. Previously we have identified the strain V605 of *Staphylococcus aureus* which originated from the human blood sample, containing a ribonuclease J1/J2 with a single nucleotide polymorphism (SNP). Thus, causing a mutation and the subsequent substitution of a Cysteine (C) instead of Arginine (R) at the 220th amino acid position within the protein sequence. To understand how this mutation changes the conformational structure of the enzyme, we performed homology modeling. We used BLAST to identify the solved crystal structure of ribonuclease J1/J2 from *Bacillus subtilis* with a 67% identity match. We used T-Coffee [2] to align the sequences, and SYMPRED [3] to predict the secondary structure conformation. Then, we used Modeller [4] to produce a structure of the ribonuclease J1/J2 enzyme for both *Staphylococcus aureus* strains USA300 and V605. We compared the two structures using the Fatcat algorithm, [5] to see how the mutation affects the folding and the tertiary structure of the ribonuclease J1/J2 enzyme. We found that the main differences are in the C-terminal domain. Knowing the 3D structure of the enzyme is the first step to the development of the potential medication so that we can counteract the drug-resistance in a timely manner.

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Carbonaceous Chondrite

J. Cai and K. Howard

In April 2019, a shower of carbonaceous chondrite meteorites fell on Earth into the Aguas Zarcas district of Costa Rica. The meteorite fragments come from a single asteroid in the carbonaceous chondrite (CM) class, being further classified in the Mighei group. The CM chondrites are predominately made up of clay like minerals called phyllosilicates and can be described as mud balls from space. The goal of this experiment is to test the hypothesis that plant growth is possible in regolith composed of the Aguas Zarcas CM chondrite and simulated CM material. If CM provides a fertile medium, then the implications for astrobiology are significant. Indigenous regolith on the moon and mars is known to lack organic and other critical compounds required for plant growth, such as reactive forms of nitrogen (Wamelink, et. al, 2014). Along with growing the plants, various chemical analysis techniques including X-ray Diffraction (XRD), Infrared Spectrometry (IR), Mass Spectrometry – Gas Chromatography (MS-GC) and litmus pH paper would be used to measure the trajectory of the plant growth in conjunction with the CM. The MS-GC involves demineralization with HF that called for proper safety protocol in the laboratory setting before the extraction step. Fragments of carbonaceous chondrites are likely to exist on surfaces of the Moon and Mars and by demonstrating the possibility of plant growth with CM can be precursor to human habitation in space. IR did not detect organic functional groups, so the MS-GC was needed. pH of CM was in the range of ideal amaranth growth pH. Findings indicate the ideal growth of amaranth would likely involve a mixture of CM soil with Martian or Lunar soil as the CM has a higher presence of sulfur which could potentially be toxic to the plant.

Qualitative Assessment of Pig's Blood Metabolites Using ^1H -NMR Spectroscopy

N. Castillo and H. Barcena

Metabolomics research ascertains the presence of key metabolites that can serve as indicators of biological processes within an organism and has far-reaching implications as a diagnostic tool in the medical field, forensics, drug testing, and so on. Here, we use proton Nuclear Magnetic Resonance (NMR) spectroscopy to distinguish between compounds found in the blood. The NMR takes advantage of the spin properties of protons within biological molecules and their interactions with radio waves to obtain spectroscopic data of the mixture.

A protein precipitation method was used to extract blood metabolites. It was found that water suppression methods were necessary to produce NMR spectra that are useful for metabolomic analysis. Multiple water suppression methods were performed in order to demonstrate consistency and confidence in the methodology. The possibility of ascertaining key metabolites was attempted through overlaying/superimposing of spectroscopic data. In the future, spiking methods could give more definitive results.

Re-emergent zoonotic diseases as well as new infectious diseases such as COVID-19, highlight the relevance of this research. Thus, testing animals and tracking the evolution or movement of diseases from their wildlife reservoirs, specifically those with infectious agents that have the potential to jump between animals to humans, could give understanding on how pandemics develop.

Lunar Ecology: Plant growth in Lunar and Aguas Zarcas meteorite soil

E. Morrissey and K. Howard

This paper reviews the process and product of planting seeds in a simulated Lunar regolith-carbonaceous chondrite meteorite mix. Due to the increasing threat of climate change, many people have begun to speculate on whether colonizing other celestial bodies would be a sustainable course of action. One complication is the capacity for crop growth in extra-terrestrial soil [1]. This experiment was performed to investigate if carbonaceous chondrites can be added as a fertilizer into lunar regolith to improve its fertility. This experiment will also explore if as generations pass, if the regolith will become more nutrient rich. To answer these questions, we compared Amaranth seed growth in 3 types of soil. These seeds were grown under a 2000W Full Spectrum LED light with LMS-1 Lunar Mare simulate was mixed with inert perlite, at a 1:1 ratio by volume, was used as the initial soil. The Aquas Zarcas meteorite was dissolved in distilled water and used as a fertilizer. The experiment produced 80 percent successful growth, with successful being defined as a sprouted seed that produces a secondary set of leaves. We also examined the mineralogy of the soil using X-ray diffraction [2]. Atmosphere and gravity are not accounted for in our experiment. Due to the Novel Corona Virus, this experiment was not completed. However, using the information from X-ray Diffraction, models were produced that indicated favorable growing conditions for the Amaranth plants. However, the experiment would have to be performed in full to gain a higher level of certainty.

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Teaching stress to L1 speakers of tone languages: a gamified approach

N. Mosseri and L. Spinu

Languages differ in their prosodic properties. For example, in English words bear primary stress, which is signaled by an excursion (often an increase) in pitch, intensity, and/or duration. In some cases, the meaning of a word can be changed by shifting the stress, e.g. *a record* (first syllable stressed, noun) vs. *to record* (second syllable stressed, verb). Such languages are called stress languages. By contrast, languages such as Mandarin Chinese or Vietnamese do not employ stress but tonal melodies (that is, specific intonation patterns such as mid, high, low tone or a combination of these) for each spoken syllable. In such a language, also called a tone language, a single syllable can have multiple meanings depending on the specific melody employed, e.g. in Chinese *ma* can be pronounced in four different ways, meaning *horse*, *mother*, *hemp*, or a *question particle*. Because of this substantial difference, it is often difficult for adult learners of a stress language to learn a tone language or vice versa. ESL learners who speak tone languages natively have difficulties processing spoken English in a classroom context, such as the one at KBCC, which hinders their academic development. These difficulties in perception have often been ascribed to intonation. In this study, we propose to test out a new approach for teaching English intonation to native speakers of tone languages such as Chinese, Thai and/or Vietnamese speakers, by using a professionally trained voice to produce exaggerated intonation patterns (i.e. sad, happy, and angry) in sentences that are context-appropriate (e.g. the sentence "I won the lottery" coupled with a happy rendition) or context-neutral (e.g. "I just saw your friend" coupled with a happy rendition). The subjects are ten ESL students who speak a tone language natively. They will be trained by first listening and then imitating each sentence. Another group of ten ESL students will be trained with sentences bearing natural, non-exaggerated intonation in order to serve as a control group.

Furthermore, we will utilize a gamified approach in which the sentences are accompanied by appropriate smiley faces. In conclusion, our method combines some of the latest trends reported in the literature with the goal of improving the subjects' production and comprehension of spoken English. Participants will be tested right after the initial training as well and a week later, following daily practice, and compared to a control group of speakers with the same background who will not have received any training. Identifying effective language learning strategies will have important implications in language teaching for the future.

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Electronic Equivalent to Natural Neural Networks

J. Olivera and J. Mikalopas

The memristor is the most recently proposed (1971) and produced (2010) of the four basic two-terminal independent circuit elements (resistor, capacitor, inductor, and memristor). It is a nonlinear electrical component where the magnetic flux is related to the amount of electric charge passed through the device.

Memristors can be programmed to have different resistant states which allow storing information as resistance scales. Memristors enable memory and processing in the same device and can be used to construct novel and innovative memory circuits. These memristor memory circuits can produce the results associated with traditional logic circuits and can also mimic results associate with bio-neuro-memory. The main purpose of this project is to find novel ways to use memristors. We will simulate memristor memory circuits with already-established designs, as well as propose new ones.

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Developed a successful novel protocol to induce spawning of American eel (*Anguilla rostrata*) for meeting market demand as well as conservation

J. Pinkhasov and S. Jahangir

American eel (*Anguilla rostrata*) is a catadromous fish. Their spawning cycle occurs at the Sargasso Sea. From eggs, they develop as leptocephalus in the sea, moving along the Gulf Stream, till they reach the West Atlantic coasts as elvers. They continue to migrate into freshwaters where they become sexually mature until they eventually migrate back to the Sargasso Sea to spawn and die. Due to destruction of its natural habitats by dams, hydroelectric projects and barriers, its migration to freshwater has been affected drastically over many years. In addition, decline in European eel and Japanese eel populations increased the demand for American eel dramatically leading to overfishing and thus decline in its population. Its landings in USA declined at 2,900 fish per day during 1984-86 to approximately 50 fish per day, today. Its spawning escapement decreased recently by 65% over a period of 14 years. In the meantime, the global demand for baby American eels continues to grow sky-rocketing its price to as high as \$2800 per pound in 2017. Today, the American eel is an endangered species by U.S. Fish & Wildlife, since 2014, and IUCN today. Much about the biology of the American eel is still unknown, yielding questions that need to be answered in order to meet market demand and support conservation efforts.

Spawning and raising American eel in vitro will help the US aquaculture industry produce American eel in captivity. This will help meeting market demand, increase employment and reduce pressure on its wild population and sustain them. While Japanese eel, *Anguilla japonica*, was spawned and raised in vitro up to second generation, American eel needs to be spawned and raised in captivity. This will make American eel available in the market and restore its population in the wild like restoring wild turkey (*Meleagris gallopavo*) with successful indoor farming in USA.

Our project aims to test and analyze three scenarios to enhance our understanding of eel biology. The first is to reaffirm successful induced spawning American eel in-vitro using a novel combination of gonadotropin hormone, dopamine antagonist, metoclopramide, oestradiol-17 β , and pheromone. The second will induce spermatogenesis using testosterone in sexually immature eels to yield males. This scenario will also be modified to experiment on females to test the theory of "Gender Bending", converting a known female into a male. The third scenario is to karyotype the American eel chromosomes, and sequence them to locate potential SRY gene.

Poster Session

May 28, 2020

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Soil Nematode Project

V. Halabani, M. McGovern and D. Michaelson

Nematode refers to, a worm of the large phylum *Nematoda*, such as a roundworm or threadworm. There are many species of nematodes. An example of this is, the golden nematode, which is also known as a species of potato cyst. This nematode is one of the world's most damaging potato pests. An effective Federal and state quarantine program were able to confine this nematode to nine counties in New York. It's true that nematodes are parasitic and bad for the environment. However, there are some species of nematodes which benefit the environment. Some species eat both bacteria and fungi which is detrimental to plants growth. Some help to aerate soil. We've discovered that a diverse population of nematodes in soil or compost are comorbid with healthy plants.

Nematodes are amongst the most abundant creatures on earth. They occur as parasites in animals, plants, soil, fresh water, and many other places. In fact, there are over 400 quintillion nematodes which inhabit the earth. Many people mistake nematodes for segmented worms or annelids. But they are not closely related to worms. Nematodes are about 0.1 – 2.5 mm long. That's extremely small!

There are multiple ways to isolate nematodes from soil. We received samples from the Brooklyn botanical gardens and KCC urban farm. We isolated individual worms from these samples. The worms were treated to release their DNA. The ribosomal DNA was amplified using PCR. A gel was used to confirm DNA was amplified. The amplified DNA samples were sent out to be sequenced. The sequences were analyzed to determine the genus and possible species of worms present in 15 grams of each sample.

Most recently we are having problems with determining the types of worms present. Although the primer used in the PCR reaction have been optimized to recognize nematodes, we keep on getting fungi sequences. We are troubleshooting this now to determine the cause.

Annotation of the Multi-Drug Resistance Genes in *Staphylococcus aureus* species

B. Hananiyaev, S. Piller and D. Y. Brogun

Staphylococcus aureus is a gram-positive bacterium resistant to antibiotics [1]. It is the most common bacteria found in hospitals worldwide [2]. The bacteria are prone to a rapid rate of the mutations on the DNA level; thus, it acquires the resistance to the new antibiotics. Once it infects a human host, it can cause problems such as skin infections, pneumonia, meningitis, and it can be lethal to humans [2]. Health professionals need to take a quick decision to administer proper antibiotics to a patient, however because of the adaptable nature of the infection, the doctors are unable to treat their patients, unless they have enough information about the strain. It is necessary to annotate the Methicillin-Resistant *Staphylococcus aureus* (MRSA) genomes and other pathogens to develop proper and effective treatments against infections from the strains. Currently, we are manually annotating and identifying orthologous genes in 161 *Staphylococcus aureus* genomes. We use the genome of *Staphylococcus aureus* strain, USA300, a strain of community-associated methicillin-resistant *Staphylococcus aureus*, as our reference [2]. However, Manual Gene Annotation (MGA) is a very long, laborious, exhaustive, tedious process that is prone to human error. In order, to automate gene annotation and to cut down on the time needed to retrieve crucial information, our research team has written the Blast-off algorithm, using Python, Linux/Unix computer languages. Further development is required on the Blast-off algorithm. The prototype requires that the user perform a combination of sorting the datasets, then copy and pasting into a web browser to upload annotation files. We rewrote the file manipulation and data preparation part of the program into bash programming language in a Unix environment. Thus, we initiated the improvement of the annotation workflow and were able to eliminate human interaction. Currently we are continuing to improve the Blast-OFF algorithm by combining the data preparation bash scripts with container technology to further streamline the workflow. Finally, a comparative analysis of the results from the manual gene annotation versus the Blast-off algorithm results for accuracy is on the way.

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First Language Attrition Across Three Different Generations

R. Hanini and L. Spinu

This study explores the phenomenon of language attrition. Specifically, we investigate the phonetic properties of consonant gemination across three groups of speakers of Palestinian Arabic: monolinguals (i.e. native speakers born in Palestine who have lived there their entire life, n=5), late bilinguals (i.e. speakers born in Palestine who emigrated to the US during their teens, n=6), and heritage speakers (i.e. speakers of Palestinian descent, born in the US and who speak both English and Arabic in their daily lives, n=7). All speakers were in their mid-20s. The participants were tested using a delayed word repetition task. The stimuli comprised 60 bi-syllabic Arabic minimal and near-minimal pairs (e.g., /sadaq/ 'he said the truth' vs. /sad:aq/ 'approved') including long and short stops. We controlled for stress and syllabic position. Distractors were also included. The acoustic analysis is underway, and consists of manually aligning the target consonants, extracting the mean consonant duration and comparing it across groups. Additional measures include voicing, aspiration, and formant transitions. The findings will enable us to address the question whether universal phonetic factors (from the perspective of Markedness Theory) influence degree of attrition by specifically comparing consonants from different voicing categories and manners of articulation.

Plant Growth on Mars

I. Ivanyuk and K. Howard

We will study the Aguas Zarcas meteorite, which belongs to the Mighei type (CM) group of carbonaceous chondrites. These meteorites are composed of clay like minerals and contain organic components [1,2]. We seek to test the hypothesis that addition of carbonaceous chondrite material can fertilize sterile simulated Mars regolith. Our experiments will attempt to grow seeds in soil which is a mixture of carbonaceous chondrite, simulated Mars 'soil' and inert perlite (to reduce the volume of meteorite and regolith used). Growth experiments will be performed under a full spectrum LED grow light. The mineralogy of the meteorite and stimulant will be characterized by X-ray diffraction (XRD). It will be significant if our results show the successful growth of a plant. It will provide a potential future means to grow plants or even grow food the surface of Mars, because clay meteorites (fertilizer) can be found on the surface of Mars or delivered to its surface by space missions. This could be an important step towards Martian colonization.

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Extraction of DNA from Diverse Plant Taxa: A Comparison of the CTAB and Edward's Buffer

A. Movsisyan and F. Tamari, Ph.D.

A comparison of two methods used to extract DNA from the angiosperm species *Petunia hybrida* has shown that DNA yields differ between tissues, with reproductive tissues possessing the most DNA [1,2]. It has also been shown that, at least in this species, the Doyle and Doyle [3] method which uses organic compounds for extraction yields lower quantity and quality DNA compared to the Edward's [4] buffer method which does not use organic compounds [1].

We intend to determine whether the Edward's method would yield higher quantities and better-quality DNA in unrelated taxa. To do so, we will purchase plants from phylogenetically distantly related taxa (avascular, seedless vascular and seed plants including gymnosperms and other angiosperms). We will use the plants for DNA extraction using the methods mentioned above. The DNA will be quantified by another member of the lab. The quality of the DNA will also be assessed using PCR by yet a third member of the lab.

References:

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Competition of PARN and HuR for p53 mRNA regulation during DNA damage

E. Oprea and E. Devany

The *TP53* gene provides instructions for making a protein called tumor protein p53. The p53 stops the formation of tumors and plays a crucial role in inhibition of tumor growth and retention of genetic stability. Abnormal p53 could allow damaged cells to proliferate resulting in cancer. Hence, it is essential to understand the major steps of p53 expression, and methods of regulation. Gene expression is a process by which the instructions in our DNA are converted into a functional product, such as proteins. There are two key steps involved in making a protein, transcription and translation. Transcription is when the DNA in a gene is copied to produce an RNA transcript called messenger RNA. In eukaryotes translation mRNA undergoes several modifications like splicing, addition of 5' G cap and Poly A tail to 3' end. After the modification it is transferred to the cytoplasm for translation. In cytoplasm the message from mRNA is read and decoded by the ribosomal complex. A new polypeptide of amino acids is synthesized and a protein is formed. Exist many ways in which gene expression is regulated in the cell, this project will focus particularly on regulation of p53 expression at mRNA processing step, specifically by two mRNA binding proteins: *Poly(A)-specific ribonuclease* (PARN) and *Human antigen R* (HuR). PARN is a key deadenylase involved in regulating gene expression in mammals. Deadenylation plays a crucial role in the control of mRNA steady state levels and therefore gene expression in various cellular conditions. HuR is an RNA-binding protein too, associated with numerous transcripts, coding and noncoding, stability, and translation. HuR has an effect on mRNA stability, it has been implicated in cellular events including proliferation, senescence, differentiation, apoptosis, and the stress and immune responses. HuR influences processes such as cancer and inflammation. Both PARN and Hur bind within 3' end of mRNA. The effects of HuR and PARN are opposite. PARN wants to destroy the mRNA and HuR stabilizes it. This research will explore the relationship between HuR and PARN in regulation of p53 mRNA. Finding the competition between HuR and PARN could be used for advantage of cancer treatment.

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Annotation of the Multi-Drug Resistance Genes in *Staphylococcus aureus* species

S. Pillar, B. Hananiyaev and D. Y. Brogun

Staphylococcus aureus is a gram-positive bacterium resistant to antibiotics [1]. It is the most common bacteria found in hospitals worldwide [2]. The bacteria are prone to a rapid rate of the mutations on the DNA level; thus, it acquires the resistance to the new antibiotics. Once it infects a human host, it can cause problems such as skin infections, pneumonia, meningitis, and it can be lethal to humans [2]. Health professionals need to take a quick decision to administer proper antibiotics to a patient, however because of the adaptable nature of the infection, the doctors are unable to treat their patients, unless they have enough information about the strain. It is necessary to annotate the Methicillin-Resistant *Staphylococcus aureus* (MRSA) genomes and other pathogens to develop proper and effective treatments against infections from the strains. Currently, we are manually annotating and identifying orthologous genes in 161 *Staphylococcus aureus* genomes. We use the genome of *Staphylococcus aureus* strain, USA300, a strain of community-associated methicillin-resistant *Staphylococcus aureus*, as our reference [2]. However, Manual Gene Annotation (MGA) is a very long, laborious, exhaustive, tedious process that is prone to human error. In order, to automate gene annotation and to cut down on the time needed to retrieve crucial information, our research team has written the Blast-off algorithm, using Python, Linux/Unix computer languages. Further development is required on the Blast-off algorithm. The prototype requires that the user perform a combination of sorting the datasets, then copy and pasting into a web browser to upload annotation files. We rewrote the file manipulation and data preparation part of the program into bash programming language in a Unix environment. Thus, we initiated the improvement of the annotation workflow and were able to eliminate human interaction. Currently we are continuing to improve the Blast-OFF algorithm by combining the data preparation bash scripts with container technology to further streamline the workflow. Finally, a comparative analysis of the results from the manual gene annotation versus the Blast-off algorithm results for accuracy is on the way.

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Identifying nematode population and demography to determine their importance in soil to predict floral health

J. Pinkhasov, M. McGovern, and D. Michaelson

Historically, agriculture always placed an emphasis on the physical and chemical aspects of plant growth while the biological aspects were neglected. Soil, much like the human body depends on a symbiotic relationship with all the organisms it houses. The human gut relies on a balance of specific bacteria and microorganisms to maintain homeostasis, of which disruption of that balance can lead to negative effects. With technology, the world understands the importance of that neglected aspect to ensuring efficient agriculture. From utilizing *Bacillus thuringiensis* found in soil to kill pests, to discovering the importance of annelids such as earthworms for floral health and composting. Scientists and farmers alike are realizing how important it is to understand these biological interactions between crops climate soil and living organisms in sustaining agriculture.

Nematodes are classified within the diverse animal phylum Nematoda. They inhabit a broad range of soil and aquatic environments. More than 15,000 species and 2,200 genera of nematodes have been described. Many nematodes are specialized parasites affecting vertebrates such as humans and insects causing disease, while others affect plants causing economic and environmental damage. Various authorities distinguish among 16 to 20 different orders within this phylum. Only about 10 of these orders regularly occur in soil, and four orders (*Rhabditida*, *Tylenchida*, *Aphelenchida*, and *Dorylaimida*) are particularly common in soil.

Plant-parasitic nematodes are well known and studied. However, many free-living nematodes have not been studied. Therefore, there is a high probability that most soil habitats will contain undescribed species of free-living nematodes that are necessary to floral health. Identification of these groups is difficult, due to high morphological variability that can lead to considerable overlap of many characteristics. To address this issue, DNA Barcoding will be performed using ribosomal markers as they are highly conserved sequences to identify nematode species found within soil samples collected from the Brooklyn Botanical Garden, Kingsborough Community College Urban Farm, and from a laboratory established Vermiculture. Our study seeks to underline that soil containing a variety of identified nematodes will yield efficient floral health and growth. This study will also analyze soil samples modified to have a higher concentration of specific species of nematode to compare floral health and growth rates.

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Determination of DNA quality following DNA extraction using PCR amplification of the *Tubulin* gene from *Saintpaulia ionantha*

D. Ramirez and F. Tamari

There are numerous ways to identify a plant species. One commonly used by scientists is DNA extraction via two methods: Doyle and Doyle (1990) and Edward's method. Doyle and Doyle use organic compounds for extraction while Edward's method used non-organic compounds. With regards to the Doyle and Doyle method, the presence of phenols in the final eluate can be an issue for the downstream application. In the past, Dr. Farshad Tamari concluded that the Edwards method of DNA extraction has yielded greater quantities of DNA in the plant species *Petunia hybrida*. It was with this knowledge that we can hypothesize that the Edwards method will also yield greater quantities of DNA in a different plant species, *Saintpaulia ionantha*, commonly known as an African Violet. African Violets are perennial, horticultural flowering plants. Often appearing in a variety of shades of violet, these angiosperms have five petals that are bilaterally symmetric and are soft to the touch. They are native to Eastern Africa and can thrive in low light conditions. Following the extraction of DNA from the African Violet, the downstream application Polymerase Chain Reaction (PCR) will be utilized; specifically, the PCR amplification of the plant gene α -*Tubulin*. PCR is essentially making multiple copies of your DNA through a series of steps: Denaturation, Annealing, and Extension. Each step is performed best at a specific temperature and for a specific amount of time: Denaturation is best anywhere between 94-95 degrees Celsius, Annealing is best around 55-62 degrees Celsius, and Extension is best at 72 degrees Celsius. Each step is about 30 seconds long (the whole process takes about 2.5-3 hours to complete) however they must be repeated 30-35 times to get the end-product of multiple copies of the desired DNA.

Comparing Beer Yeast Strains Using Polymerase Chain Reaction and Restriction Digest

S. Small and E. Mulligan

Saccharomyces cerevisiae is the microorganism responsible for fermenting wine and ale style beers while *Saccharomyces pastorianus* is responsible for fermenting lager style beers. Brewers found that different yeast strains are key to the development of certain distinctive scent and flavor compounds. This led to selection of yeast for certain flavor profiles and created different yeast strains. In this study, we will look at the genetic expressions of different yeast strains using Polymerase Chain Reaction (PCR) to amplify the Internal Transcribed Spacer (ITS) region and the 5.8S rRNA gene followed by restriction digest by CfoI, HaeIII, and HinfI to differentiate strains of commercial brewing yeasts. We hypothesize that the different strains will have different patterns of cutting after restriction digest. We will analyze yeast from the WYeast catalog. If successful we will also look at some yeast samples from bottle conditioned (still containing live yeast) commercially available beers to see if we can identify the strain.

There's a Storm Coming: Could Superstorm Sandy Serve as an Indicator of Future Storms & Climate Trends?

A. Sobolewska & S. Benincasa

While Hurricane Sandy happened in 2012, it is still evident across the east coast, especially the tri-state area. This is due to the fact that we've never truly experienced a storm so prevalent before. However, in recent years it has become more and more apparent, that the Hurricane turned Superstorm Sandy (Due to its force), will eventually become a more common place. Places such as Florida, have been dealt the brunt of this. There appears to be a correlation between our current climate trends and the increase in natural disasters. Using Geographic Information Systems (GIS) data and imagery that was collected from NOAA as well as recent climate data, this study will prove that there is a correlation between the two as well as provide predictions for what the future holds.

Shirley Chisholm State Park as an example of economic sustainability

H. Stojku and L. Martin Del Campo

¹Shirley Chisholm State Park is a unique 407-acre park that opened to the public in July 2, 2019 under Governor Andrew Cuomo's \$1.4 billion "Vital Brooklyn" initiative. ²Built on top of the Pennsylvania Avenue and Fountain Avenue landfills in Jamaica Bay, Brooklyn, the park holds environmental and economic significance because of its transformation from decades (1956 to 1983) of toxic land-use, to a park that serves the community as well as the environment. The new state park includes 10 miles of trails for hiking and biking, kayaking, picnic areas, educational facilities, an amphitheater and more.

The purpose of my research is the study of the environmental and economic benefits of the Shirley Chisholm State Park utilizing the National Park Service (NPS) economic output measurement and by studying and comparing different stages of the land-use affecting water, flora and fauna. This research will first demonstrate how land-use holds hidden economic values and environmental sustainability importance. Second, it will illustrate how transforming landfills to community state parks are economic and environmentally sustainable. Third, it will aim to evaluate the social impact such initiatives have in areas of marginalized communities.

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Strategies in Second Dialect Learning: A Study of how Monolinguals and Bilinguals learn Epenthesis in S-clusters

M.Vasilita and L. Spinu

Bilingualism has been linked with improved function regarding certain aspects of linguistic processing, e.g. manipulating language in terms of discrete units, novel word acquisition, and learning unfamiliar sound patterns in novel accents. Recent experimental work with non-native contrasts suggests that bilinguals have enhanced phonetic learning and speech perception abilities compared to monolinguals. We investigate phonetic learning skills in monolinguals (n=20) and early, simultaneous bilinguals (n=20). The subjects were trained and tested on an artificial accent of English. One of the features distinguishing the novel accent from the standard variety was the presence of vocalic epenthesis in the voiceless s-clusters [sp, st, sk]. For example, words such as 'spy' or 'school' were pronounced as 'suh-py' [səpaj] and 'suh-cool' [səkul]. A total of 760 target items were evaluated manually. A score of 1 was assigned for each token produced with an epenthetic vowel between s and the following consonant, otherwise the score was 0. Early bilinguals outperformed the monolinguals on the acquisition of this pattern. Acoustic analyses are underway to assess the differences between the two groups' productions, such as quality, duration, and placement of the epenthetic vowel, as preliminary observations revealed a high number of long-distance phenomena such as [spəhaj] or [spəʔaj].

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