Seventh Annual

Summer Research Symposium

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St. Thomas, U.S. Virgin Islands

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Acceleration of Logarithmic Convergence

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Our summer research was dedicated to the acceleration of the convergence of infinite series, $\sum_{n=1}^{\infty} a_n$, where $\lim_{n\to\infty} \frac{a_{n+1}}{a_n} = 1$. Such series are generally referred to as logarithmic series.

If $\{a_n\}_{n=1}^{\infty}$ and $\{b_n\}_{n=1}^{\infty}$ are sequences converging to A and B respectively and if $\lim_{n\to\infty} \left| \frac{a_n - A}{b_n - B} \right| = 0,$ then we say that $\{a_n\}_{n=1}^{\infty}$ converges more rapidly than $\{b_n\}_{n=1}^{\infty}$.

Throughout this paper, $\varphi(n)$ will denote a differentiable function on $[1,\infty)$ that satisfies $\varphi(n) > n$. Furthermore, we shall use ($S(\varphi(n))$) to denote the $\varphi(n)$ -th partial sum of the series $\sum_{n=1}^{\infty} a_n$.

First, we define T as a transformation on the partial sums of $\sum_{n=1}^{\infty} a_n$ that satisfies:

a. $T(S(\varphi(n))) \to S,$ and

b. $T(S(\varphi(n)) = S(\varphi(n)) + D(\varphi(n))$, where $D(\varphi(n)) = \dfrac{S(n) - S(\varphi(n))}{1 - \frac{1}{\rho}}$.

We then show that if $\lim_{n\to\infty} \dfrac{D(\varphi(n))}{S - S(\varphi(n))} = 0$, then $\lim_{n\to\infty} \left| \dfrac{T(S(\varphi(n))) - S}{S(\varphi(n)) - S} \right| = 0.$

This result leads naturally to the class of series accelerators $T_{\varphi,\rho}(S(n)) = \dfrac{S(n) - (1/\rho) S(\varphi(n))}{1 - (1/\rho)}$,

which are extensions of the T_m accelerators by Clark and Gray (see [3]).

It turns out that the quantity ρ in the formula for $D(\varphi(n))$ is not an arbitrary positive number, but rather one that is closely associated with the convergent series $\sum f(n)$ via: $\varphi'(x) f(\varphi(x)) = \rho f(x)$.

We conclude our research by showing how our accelerators can be used to accelerate the convergence of the series $\sum_{n=1}^{\infty} \frac{1}{n^2}$.

This research is funded by NSF HBCU-UP - Grant Number HRD 0506096

Lack of alarm responses in the long spined sea urchined *Diadema antillarum* and the reef urchin *Echinometra viridis*

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The ability to detect a predator before being consumed is a very advantageous trait. Alarm responses are a survival tactic initiated by the chemical detection of a predator or injured heterospecifics and conspecifics (Snyder and Snyder 1970). Many species of sea urchins (e.g. *D. antillarum* and *E. viridis*) demonstrate an alarm response to injured conspecifics, but their responses to predator's presence have been poorly documented (Snyder and Snyder 1970). My question was whether or not the presence of a predator, *Cassis tuberossa* (King helmet shell), can trigger an alarm response in both species. My null hypothesis stated: the predator's presence would not render an alarm response, so they would not move away from the predator. My hypothesis stated: the presence would trigger an alarm response, and I predict that the urchins would move away from the predator. I tested these hypotheses with a field experiment at Brewers Bay St. Thomas. I collected *D. antillarum* and placed them a sandy bottom. For the control group, I squirted fresh sea cucumber body fluids into the current towards the urchins because it was proven that these urchins aren't affected by these fluids (Snyder and Snyder 1970). I put the Helmet shell under a crate directly in the path of the current, and let the scent flow over the urchins, then I observed their behavior for 5 min. I replicated this experiment three times with *D. antillarum*, and then repeated with *E. viridis.* In both species, there was no movement observed at all. Therefore the presence of the predator did not affect the urchins which did not trigger an alarm response.

This work was supported by NSF HBCU-UP grant number HRD – 0506096

Bacterial Flora in the Reproductive Tract and Mammary Gland of the St. Croix White Hair Sheep

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Hair sheep farms in the Caribbean are exclusively for meat production. Between all sheep breeds in this region, the St. Croix White hair sheep is the most common, due to their superior adaptation to tropical conditions and other traits such good proliferation and resistance to parasites. The reproductive performance of livestock is negatively affected by uterine infections, which translates to a decline in profit potential for local farmers. In addition to uterine infections, mastitis is one of the more common health problems affecting sheep and goats. Moreover, reduced milk yield caused by mastitis leads to decreased growth of the lambs (Fthenakis and Jones, 1990). To date, studies using local ewes have been conducted to evaluate the effect of the type of feed on growth and carcass traits in lambs (Dodson et al., 2005; Godfrey and Weis, 2005), the effects of ram exposure on uterine involution and luteal function during the postpartum period (Godfrey et al., 1998), behavioral and endocrine responses of ewes exposed to different mating stimuli around estrus Godfrey et al., 2001), etc. However, there is no information about intramammary bacterial pathogens and normal flora of the reproductive tract of local hair sheep (e.g., St. Croix White hair sheep). This information will be of great significance to sheep producers confronting cases of mastitis or uterine infections. The uterine tract from cull ewes (n=4) were used to collect bacterial samples for classification and bacterial count. In previous pilot experiments, the method of collecting bacterial samples from the reproductive tract using the laparoscope was unsuccessful. A slightly different approach was used which was very time consuming and caused a delay in collection of data. Data collection is still ongoing.

This work was partially supported by NSF HBCU-UP grant number HRD – 0506096

Alpheid Shrimp Reduce Burial Time of Corkscrew Anemone

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The corkscrew anemone *Bartholomea annulata* resides at the sand-hard substrate interface and provides a home for many organisms including species of cleaner shrimp, which aid in coral health. This bottom-dwelling anemone is subject to sand burial by burrowing lugworm's mound, as well as by natural sand inundation. Snapping shrimp, *Alpheus* spp*.,* which reside at the base of *B. annulata,* have been observed using its pleopods to remove sand from buried anemones. Does this behavior significantly improve the ability and time of an anemone to be unburied? In field experiments, anemones were buried with and without alpheids. A day later observations were made of whether the anemones were buried or not. Lab experiments were conducted in shallow pools where anemones were subjected to the same treatments (with and without alpheids), and checked at fifteen minute intervals. Tests show that there is no difference for an alpheid to significantly improve the ability of an anemone to become unburied, in the field (p-value = 0.4924, T-test) and in the lab (p-value = .9058, T-test), although the alpheids did reduce the amount of time anemones were buried (p = 0.0439, T-test). The digging behavior of the alpheid shrimp may be used more to maintain an anemone's burrow than to rescue the anemone from burial.

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Tracking GABA-ergic Neurons in the nervous system of the Caribbean Spiny Lobster

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Gamma-aminobutric acid (GABA) is a neurotransmitter found in most invertebrates in vertebrates. GABA is generally inhibitory acting through receptors to increase chloride currents or to activate G protein cell inhibitos.

In this study, we are looking at the location and projections of GABA containing neurons found in the *Panulirus argus* stomatogastric nervous system (STNS). With this information we can then study how GABA influences small neural circuits such as those used for food sorting or chewing. Based on earlier studies with blue crabs we expect GABAergic neurons to be found primarily in the anterior STNS but not to project beyond motor circuits in the stomatogastric ganglion (STG).

GABA containing cells were located using rabbit anti-GABA and visualized with anti-rabbit antibodies labeled with Alexa 488. Alexa 488 epifluorescence was measured using Leica FLIII macroscope equipped with a sooled digital camera and analyzed in Photoshop™.

Unlike the blue crab, GABA was found in diffuse regions in the paired commissural ganglia (COG) and project through the inferior esophageal nerves (ion) to GABA-containing cells in the esophageal ganglion (EOG) where we see distinct cells, and axonal projections passing through the stomatogastric nerve (stn) to the STG. As in crab, no GABA-containing cell bodies were observed in the STG and no GABAergic axons projected beyond the STG. The neural sheaths in lobsters were of surprising thickness compared to those of the blue crab wthat made identification of axonal terminals difficult. More accurate localizations of GABAergic cell endings will require additional experiments where these sheaths are removed or rendered porous.

We now know where GABA is being created and stored and will next identify GABAergic targets. By doing this, we will better understand the path that GABA takes and how it affects certain small motor circuits like those in the STG. Studies will include the manipulation of neural signaling with GABA agonist and antagonists in temperature acclimated lobsters.

This project was sponsored by NIH MBRS-RISE Grant Award No. GM061325 and NSF HBCU-UP grant number HRD – 0506096

Differences in aggression may explain differences in numbers of *Periclimenes yucatanicus* and *P. pedersoni* inhabiting corkscrew anemones

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Several species of crustaceans reside on the corkscrew anemone, *Bartholomea annulata*, including the Spotted Cleaner Shrimp (*P. yucatanicus*) and the Pederson Cleaner Shrimp (*P. pedersoni*). Field surveys indicate that *P. yucatanicus* (Py) is often found solitarily while *P. pedersoni* (Pp) is found in groups. We wondered if this difference in sociality can be explained by a difference in aggression of the two species. We placed pairs of shrimp in a small container for 15 minutes and recorded various aggressive or non-aggressive actions. Three treatments were conducted (Pp vs. Py, Pp vs. Pp, and Py vs. Py) to test for differences in inter- and intraspecific aggression. We found a significant difference in the number of aggressive acts among the three trials (p = 0.011, ANOVA) where the aggression was significantly less in the Pp vs. Pp experiment in comparison to the Pp vs. Py and Py vs. Py trials. While there was no significant difference the aggression level between the two species in Pp vs. Py trials (p = 0.430, t-test), there is a higher level of aggression in the experiments containing the *P. yucatanicus*. These results may explain why the *P. yucatanicus* are more like to be found alone while the *P. pedersoni* are found in groups.

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Was the orange cup coral introduced to the Caribbean?

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The orange cup coral, *Tubastraea coccinea*, is an azooxanthellate stony coral that is indigenous to the Pacific. Besides *T. coccinea*, there are no other known coral species that are found in both the Pacific and Atlantic oceans. Its first documented reports on the coasts of Curacao and Puerto Rico were in 1943. *T. coccinea* is not reef building, but will grow on coral reefs and so may pose a threat to native coral species that do in fact build reefs. Corals are important in the protection of our coastlines and an asset to the economy. Although distributional studies have hypothesized that *T. coccinea* was introduced to the Caribbean from the Pacific, there are no genetic data to test this hypothesis. We are investigating whether there is genetic variation between Western Atlantic and Indo-Pacific *T. coccinea*. Pacific samples were previously extracted using a CTAB protocol. DNA was extracted from Caribbean samples using the DNeasy protocol. We then used the samples in PCR reactions with mitochondrial and nuclear primers. The primers we used targeted gene regions that have variation in other coral species. Once DNA sequences are obtained from these PCR products, comparison with each other and other sequences from Genbank will determine the amount of genetic variation between Caribbean and Pacific samples. If there is no variation, then this supports the hypothesis that the species was introduced and we fail to reject our null hypothesis that there is no difference between the genetic sequences of *T. coccinea* from both oceans. We can further this research by using a larger sample size with samples from more Caribbean localities.

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Effective Classification of Segments of *E. coli* DNA into Promoter and Non-Promoter Categories using Decision Tree Algorithm c4.5

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Promoters are the sections of DNA to which RNA polymerase first binds before starting transcription of each gene. Promoters are critically important, because they vary from gene to gene and influence the regulation of genes, that is, influence which genes will be turned on and which will be turned off at any given time. The most accurate method of identifying promoters is via biological experiments, but biological experiments can be prolonged and expensive. As a result, researchers would like to find a more efficient method to recognize promoters, for example, inductive machine learning classification. In general, this process follows three steps: feature extraction from a "training set" of data, classifier building using one of many possible algorithms, and classifier testing using a "testing set" of data. Rani et al. (2007) applied this approach to the classification of segments of *E. coli* DNA, previously known to be either promoters or not promoters, into promoter and none-promoter categories. The features they used for classification were the frequencies of occurrence of the 16 types of dinucleotides in each DNA segment. Using a neural network classification algorithm, 78% of the sequences were classified correctly. Our research improves on the results of Rani et al. (2007) by using the inductive machine learning C4.5 decision tree algorithm implemented in WEKA, instead of a neural network algorithm. Using this algorithm led to correct classification of 82% of the DNA segments. The preliminary results of this experiment slightly improve previous results and suggest inductive machine learning could effectively assist biologists to more rapidly identify previously unknown promoters in the future.

Rani, TS, SD Bhavani and RS Bapi. 2007. Analysis of *E. coli* promoter recognition problem in dinucleotide feature space. *Bioinformatics 23*: 582-588.

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Finding Weird Numbers of the Form $2^k pq$

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Weird Numbers: what are they and why are they important? Well, these numbers are defined as any number *n* whose sum of proper divisors are greater than *n* but no subset of which can be rearranged as a sum that exactly equals *n*. In more complex terms, a weird number is an integer that is abundant but not pseudoperfect. For example, the smallest weird number 70 has a set of proper divisors {1,2,5,7,10,14,35} that add up to greater than 70 itself, but if you were to add up any or all of its divisors, you would not obtain the sum of 70, the original number. The smallest such number 70 is not so closely followed by the second smallest weird number, 836. With their increasing complexity and rarity as they approach infinity, you can imagine why the mathematical world has not fulfilled the quest for finding them. However, the research completed by my mentors, my colleagues, and I, aimed to find weird numbers not yet found, focusing on those of the form $2^k pq$. We seek an algotithm where you would choose a *k* and input it into the algorithm to find a pair of primes, *p* and *q*. From there, you would run a test on the *p* and *q* to determine if $2^k pq$ actually is a weird number. Two group members worked on finding numbers with very large values of *k*, but my group member and I focused on finding numbers with all the smallest small values of *k*=1, 2, 3, etc., that we could handle. By hand, five numbers were found through tedious and time consuming equations, but by using a computer program, *Mathematica 3.0,* we were able to compute a program that would find weird numbers for us. Weird numbers can be used for encryptography; the study of encryption codes that are used to protect information passed over the internet. With the positive results discovered in our research, we plan to have these numbers published in some form so that they can be observed by the mathematical community.

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ISSR-PCR Protocols for *Zanthoxylum monophyllum*

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The plant that I am studying is the *Zanthoxylum monophyllum*, or the yellow prickle. *Zanthoxylum monophyllum* is a member of the citrus family, which are native to subtropical areas. *Z. monophyllum* is also one of the many understudied plants in the Virgin Islands. Experimenting with the *Z. monophyllum* will help us learn more about this plant in our ecosystem. The question that I am trying to answer is "What is the best ISSR protocol for *Z. monophyllum*?" I am doing ISSR experiments on this plant to find out more information about its DNA fingerprint and what ISSR- PCR protocol works to show the fingerprint. I am studying ten different primers, three of which are anchored. I am testing each primer with *Z. monophyllum* to see which one produces the best bands. Because I am looking for a protocol that bests works for the understudied plant, the hypothesis is that the protocol that uses anchored primers would be the best protocol. I predict the ISSR recipe that contains anchored primers would be effective and there will be distinct bands when viewed. The method that I used to develop an ISSR-PCR protocol was influenced by papers of similar experiments that I have read. I looked at the way the authors of the papers set up their experiments and I formed the experiment in the same way. As mentioned, ten different primers were used in this experiment and part of the creating a protocol process was to discover which of the primers worked best with the plant. So far, none of the primers have worked for *Z. monophyllum*. I also tried changing the temperatures of the thermocycling stage and trying out more taq DNA polymerase. None of those changes improved my plant's amplification.

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ISSR amplification of *Laguncularia racemosa* unsuccessful

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The molecular diversity of many common, albeit understudied, plants in the Virgin Islands is unknown. Knowledge of molecular diversity may help protect many recognized products and services used by Virgin Islanders via the upkeep of their respective genetic diversities. One such plant, the white mangrove, *Laguncularia racemosa*, whose particular services include conservation of the shoreline and a nursery for juvenile fish, algae, and other aquatic organisms, was studied. It was the effort of our lab to determine a sound protocol, involving ISSRs (a molecular marker system that requires little information on the desired DNA fragment, but rather the short tandem repeats that encase them) as primers that would prove efficient and have visibly distinct and reproducible bands. We applied various published techniques to finding a suitable protocol for *L. racemosa.* Thus, I hypothesized that a procedure very similar to the ones that I read in four published papers would prove effective with *L. racemosa*, because of the similarity between the procedures and the wide range of plants that were studied. I also hypothesized that anchored primers (primers with an arbitrary nucleotide attached to the tandem repeat) would have greater reproducibility of bands. A total of ten randomly picked ISSR primers were used. None of the primers produced bands even when the quantity of taq DNA polymerase and DNA were altered positively and the annealing temperature was set to 50°C versus the initial 52°C. Thus, there was no difference between anchored and non anchored primers, as neither of them has produced bands thus far. This may mean that the ten ISSR primers are non complementary to any given loci on the genome of *L. racemosa* or that further alterations to the protocol must be made. It may also mean that the DNA was either not quantified correctly or that it was contaminated. The case may also be that ingredients used in the protocol, such as taq DNA polymerase are not fully functioning, as deviations from their ideal holding temperatures may cause them to degrade and hinder the reproducibility of bands.

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Bayesian Networks for Mining Census Data in Order to Develop Effective Marketing Strategies

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Millions of dollars are spent each year in order to develop cost-effective marketing strategies based on one or few key segments such as income, geographic or demographic segmentation. This research proposes Bayesian networks techniques in order to automatically determine the population income based on census data. Census data provide valuable information such as hours-per-week, race, age and can be exploited effectively through machine learning algorithms and decision support systems. Bayesian Networks can be viewed as graphical models that code probabilistic relationships among variables of interest. It can be used to learn causal relationships and also gain understanding about a problem domain and predict consequences of intervention. This research experiments with Bayesian algorithms implemented in *Weka 3.7.0* data mining software package. The model is trained with 32,561 training data sets obtain from census data sets (Ronny Kohavi and Barry Becker) The current esults thus far shows that 83.8% of the census training data have been correctly classified into two segments: greater than 50K and less than 50K. In the future, we would like to improve this percentage by looking at different algorithms and comparing them to see which algorithm is more efficient.

Reference: Ronny and Kohavi, Census data http://archive.ics.uci.edu/ml/datasets/Census+Income.

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Primers that work for a Caribbean Plant

Eliza Rampersad and Alice Stanford (mentor)

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*Coccoloba uvifera (*sea grape) is a Caribbean plant that is grown on the coastal regions. *Coccoloba uvifera* is vital because it is used for medicinal purpose such as diarrhea, and it has high content of vitamin A and vitamin C. This plant is also used as hedges around the costal areas. Before genetic diversity can be studied, molecular analysis techniques must be developed. One of the molecular anlaysis techniques is the ISSR technique, it is an inter simple sequence repeat. This technique functions by a marker system or better known as microsatelites that amplifies the section between the repeats, in addition it mostly targest the di- and trinucleotide repeats. The primary purpose is to find the proper protocol for *Coccoloba uvifera "*Sea grape" and also to test which primers work best. I used ten different primers and out of ten; some were anchored and non anchored primers. I created and used a protocal derived from different papers. So far there are five primers that work with the *Coccoloba uvifera*, which makes future studies of genetic diversity possible to learn and possible discoveries of different functions of this plant. The primers that worked for *Coccoloba uvifera* were AGAGAGAGAGAGAGAGC (anchored), GCCGCCGCCGCCGCC (non-anchored), ACCACCACCACCACCACC (non –anchored), CACACACACACACACAT *(anchored*), and AGAGAGAGAGAGAGAGT (anchored).Since these primers work, scientist can use this technique to learn more about the plant's population genetics.

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Snapping shrimp, *Alpheus* spp., instantaneously acclimate to the Caribbean corkscrew anemone *Bartholomea annulata*

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The Caribbean corkscrew anemone *Bartholomea annulata* houses many shrimp symbionts, which live on and near the anemone's tentacles, including snapping shrimps, *Alpheus* spp., which reside by the anemone's column. The ability of the shrimp to maintain this commensalism with the anemone without being stung or consumed is poorly understood. Studies have shown that some anemonefishes and some shrimp of the genus *Periclimenes* acquire protection from the stinging tentacles of other species of sea anemones after a lengthy acclimation period, wherein individuals display specific behaviors after initial contact with an anemone until they no longer trigger a detectable stinging response. The purpose of this investigation was to determine the acclimation behavior and time of *Alpheus* spp. to *B. annulata.* Shrimp were collected and isolated from sea anemones for 4 plus days. Shrimp were then randomly selected and placed haphazardly near a sea anemone. The time and the behavior of both shrimp and sea anemones were monitored and recorded until the shrimp was settled underneath the anemone. After one hour, the acclimated shrimp was removed and immediately placed near a second sea anemone, where behavior and time was again monitored. No statistically significant difference in acclimation time between isolated and previously acclimated shrimp was present ($p = 0.589$, T-test). Shrimp were consistently observed moving immediately into the anemone without triggering any detectable stinging response. This instantaneous acclimation is considerably less then that seen by other researchers for anemonefishes and *Periclimenes* spp., which took at least 2 h and 40 min to become acclimated. *Alpheus* spp. may have an innate protection from corkscrew anemone stings.

This research was supported by NSF HBCU-UP grant number HRD – 0506096

ISSR-Protocol Established for Local Plant Killer

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A well known plant introduced to the United States Virgin Islands (USVI) is killing local plants. In the USVI, *Melicoccus bijugatus* better known as "Genip" is a naturalized plant that is very invasive. As a result, *M. bijugatus* is presently changing the structure of the USVI's forests and is endangering local plants. To gain more understanding and knowledge of *M. bijugatus*, the inter-simple sequence repeat (ISSR) technique will eventually be used to study the population genetics of the plant species. My research asks, what is the most effective ISSR-protocol specific to *M. bijugatus*? Based on similar research, I predict that anchored primers (primers with a base pair not part of the repeat sequence that forces the primer to anneal/stick at the end of the DNA repeat) will work best in procuring an effective protocol. In order to develop a protocol, a DNA extraction from *M. bijugatus* leaves was taken. That was followed by creating a Polymerase Chain Reaction (PCR) master mix and thermo cycling the mix with DNA and primer to amplify the DNA. Lastly an electrophoresis gel containing the mix was run and the results were recorded. Out of the ten primers used, two anchored primers as well as two non-anchored primers showed positive results for creating an ISSR-protocol for *M. bijugatus*. As a result, it can be concluded that both anchored and non-anchored primers work for *M. bijugatus*. Future studies can focus on which *M. bijugatus* population has the highest diversity and require more studies as well as how to eradicate those populations to preserve local plants.

This work was funded by NSF HBCU-UP grant number HRD-0506096

Cleaner shrimp *Stenopus hispidus* affects the mean size but not load of the flatworm parasite *Neobenedenia mellini* on a Caribbean reef fish

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Monogenean trematodes are harmful to reef fish because they damage the fishes' skin and make them more susceptible to disease (Thoney and Hargis 1991). Fish may be cleaned of parasites and other debris by cleaner fishes or shrimps at cleaning stations. The effectiveness of cleaner fish is well documented, but the role of different cleaner shrimp species is not well studied (Becker and Grutter 2004). The ability of cleaner shrimps to remove parasites should have a positive impact on fish health by reducing damage to the host's skin. In addition, reduced parasite size could reduce overall parasite populations on the reef by removing the parasites with the greatest reproductive output. The number and mean length of parasites from fish that did or did not have access to cleaning shrimp was quantified *to test the hypothesis that the banded coral shrimp (Stenopus hispidus) affect the monogenean loads and the average size of monogenean parasites on the blue tang fish (Acanthurus coeruleus)*. Blue tang were housed in a semi-natural aquarium where they were constantly exposed to the infective stages of the parasite. The control treatment contained 14 blue tang and the experimental treatment contained 14 blue tang and 25 banded coral shrimps. Observations were made to see if there were any interactions between fish and shrimps. After two weeks, each fish were given freshwater baths for three minutes to remove their parasites. The parasites were preserved in ethanol and counted. The banded coral shrimp did not affect the parasite loads between the two treatment groups (p=0.696, t-test). This is in contrast to our results from last year's experiment with the Pederson cleaner shrimp (*Periclimenes pedersoni*), where the Pederson shrimp was found to reduce the monogenean loads on the blue tang. The parasites were photographed under a microscope and their lengths measured using computer software NIH Image J. The average parasite length was significantly smaller on fish that had access to the banded coral shrimp (p=0.0005, t-test). During our observations, no cleaning behavior was witnessed which makes us question whether the banded coral shrimps actually clean. Our results conclude that the banded coral shrimp is not an effective cleaner of the monogenean trematode and more research on what exactly it cleans needs to be done.

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Thoney, D.A. and Hargis, W.J. Jr. 1991. Monogenea (Platyhelminthes) as hazards for fish in confinement. Annual Review of Fish Diseases 1: 133-155.

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ISSR protocol has been established to aid in conservation of endangered native plant, *Erythrina eggersii*

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Erythrina eggersii (Cock's-spur) is a native plant of Puerto Rico and the Virgin Islands that is currently classified as threatened and endangered. Habitat destruction such as quarrying has majorly contributed to the plant's future extinction. No research was reported on this plant species. As a result, there is only a little amount of information about the potential uses of the plant. In order to prevent local extinction, the main goal is to obtain knowledge about *E. eggersi.* Therefore, I conducted a study to determine an effective inter-simple sequence repeat (ISSR) protocol specific to *E. eggersii* that will yield visible DNA bands. After reading four similar studies, a temporary protocol was created using the protocols obtained from the studies. Ten randomly selected primers (anchored and non-anchored primers engaged in the Polymerase Chain Reaction (PCR) process. I placed the amplified DNA in an electrophoresis gel and then observed and recorded the results. The results from six PCR reactions showed that two primers, one anchored (CA8T1) and the other non-anchored (GCC5), showed visible bands for the various ISSR protocols that were performed for *E. eggersii*. However, the inconsistency of the results led to the manipulation of the created protocol; such as lowering the annealing temperature and increasing the concentration of taq polymerase. Yet, these results illustrate primary knowledge of *E. eggersii* that may be useful in the future for its conservation. Further studies can be conducted to determine whether this species is diverse. Diversity is crucial for survival and in this situation survival is the major issue for *E. eggersii*. In addition, other studies can be conducted to determine whether medicinal properties exist within this species or whether there is any biological use for this native plant.

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Mathematical Models of Digital Sounds to reproduce Human voices?

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Suppose that someone that you cared for deeply lost his or her voice to a severe bout of laryngitis. Suffering from this debilitating complication of the disease can cause severe emotional and psychological problems and can even lead to a chronic case of depression. Fortunately, mathematical modeling shows the capacity to be able to recreate and mimic various natural and unnatural sounds. In our fieldwork, various raw sound data were recorded from different people using sound processing software. Once stored on the computer it was placed into "fully integrated technical computing software"(Wolfram Research) where we fragmented the samples in order to seek out specific cycles in the characteristics of the waves. Once broken down, we had the software apply a Fourier analysis in order to determine an accurate mathematical model for the raw sound data. A **Fourier series** is an expansion of any periodic function *f(x)* in terms of an infinite sum of sines and cosines. Since vibrations that create waves in air molecules produce sound and since waves are cyclical, Fourier analysis is ideal for examining their respective characteristics. After the models were generated we searched for numerical patterns in the coefficients of the sines and cosines and compared the coefficients generated by male and female voices to one another. We expect further research in the application of Fourier analysis to sound data to lead to improvements in sound processing and the synthesis of musical instruments.

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Implementing the Tabu Search Algorithm for solving Airport Gate Assignment Problems

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With more and more passengers flying around the world, the increase in airport activity and expansion of these airports, and the demand for faster accommodation of arriving, and incoming, aircrafts, airport managers, with the help of researchers, have searched algorithm or mathematical model for large and small airports. This research studies the Airport Gate Assignment Problem and proposes a solution based on the popular Tabu Search Algorithm. The solution has been implemented in C++ for the Cyril E. King Airport with two specific constraints (rules): 1) the aircraft must be gated at its general boarding gate and 2) the aircraft must be gated at the first available gate while still complying with constraint #1. These constraints were obtained after interviewing an air traffic controller and the airport manager at the Cyril E. King Airport. Presently, the algorithm has been tested with four scenarios in which in each case it has found the optimal gate assignment with the least waiting time; additional scenarios are currently being added and tested. This algorithm will be expanded and adapted to problems presenting additional constraints and larger number of gates and traffic.

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