SUMMER UNDERGRADUATE RESEARCH PROGRAM 2014

PROCEEDINGS

COLLEGE OF SCIENCE, ENGINEERING AND TECHNOLOGY TEXAS SOUTHERN UNIVERSITY







TABLE OF CONTENTS

GREETINGS FROM THE INTERIM ASSOCIATE PROVOST	1	Dr. Gregory H. Maddox
GREETINGS FROM THE DEAN	2	Dr. Lei Yu
SURP 2014: EXCELLENT ACHIEVEMENT	3	Dr. Hyun-Min Hwang Dr. Yunjiao Wang
TESTIMONIALS	4	
LIST OF PARTICIPANTS (STUDENTS)	5	
LIST OF PARTICIPANTS (FACULTY MENTORS)	6	
STUDENT ACTIVITIES	7	
MITOCHONDRIAL GENOME SEQUNCING Sequencing the complete mitochondrial genome of the malayan peacock-pheasant <i>polyplectron malacense</i> and estimating genetic distances with <i>p. Bicalcaratum</i> and <i>p.</i> <i>Napoleonis</i>	11	Benjamin Caballero* Hector C. Miranda Jr. [#]
DIFFERENCE EQUATION	16	FranChell Davidson*
On the solutions of the difference equation $x_{n+1} = \frac{f(x_n)}{x_{n-1}}$		Willie E. Talyor
GENE EXPRESSION IN BREAST CANCER Identifying gene expression in aggressive breast cancer vs. Less aggressive breast cancer	19	Brittani Davis* Audrey N. Prayer [#]
LONGITUDINAL ROAD CRACKING MODEL Longitudinal cracking model for farm-to-market (FM) roads over expansive subgrade	22	Aminata Dicko* Yachi Wanyan [#]
RADIATION FROM X-RAY THERAPY UNIT Modeling Stray Radiation Produced from an X-Ray Therapy Unit	29	Ugochukwu O. Ezenekwe* Mark C. Harvey [#]
NONLINEAR ORDINARY DIFFERENTIAL EQUATIONS Numerical solutions for a class of nonlinear ordinary differential equations	33	C. S. Ezeudu* J. L. Williams [#]
DIFFERENCE EQUATION On the solutions of $X_{N+1} = \frac{F(X_N)}{X_{N-1}}$, where f is piecewise linear	36	Marquesha Foreman* Roderick B. Holmes [#]

TABLE OF CONTENTS

DISEASES AND AVIATION

Disease and Aviation

MITOCHONDRIAL GENOME SEQUNCING

Genetic distance between two "allopatirc" island hawk-owls: *ninox philippensis* and *ninox spilocephala* based on nearly complete mitochondria genomes

TRICLOSAN IN URBAN SURFACE WATER

Triclosan (TCS) in White Oak Bayou, Houston

NETWORK SYSTEMS

Comparison of dynamics of boolean networks and networks of ordinary differential equations systems

GENE CLONING AND SEQUENCING

Cloning and sequencing of a plant glyceraldehyde 3phosphate dehydrogenase (GAPDH) gene

SMARTPHONE APPLICATION

Feasibility study of smartphone applications for traffic signal control

SMARTPHONE APPLICATION

Creating an application on google android platform

PHOTOVOLTAIC CELLS

Making more efficient photovoltaic cells using materials absorbing different colors of light

IDENTITY MANAGEMENT

A user centered approach to managing identities in online social network

NUCLEAR MAGNETIC RESONANCE

J-coupling and Imaging with Earth Field Nuclear Magnetic Resonance

APPENDIX

Complete mitochondrial genome of Palawan peacockpheasant Polyplectron napoleonis (*Galliformes, Phasianidae*)

- **39** Micah Harper* Vernon J. Baker[#]
- **41** Amanda Nicole Jackson* Hector C. Miranda Jr.[#]
- **45** Charese Jeffries* Hyun-Min Hwang[#]
- **48** Franklin Kigwe* Yunjiao Wang[#]
- 54 Ray Mbonu* Abigail Newsome Sodipe Ayodoton[#]
- 56 Ray Motte* Fengxiang Qiao[#]
- **61** Samuel Teferra* Moshen Javadian[#]
- 64 Fernando Valdez* Graham Thomas[#]
- **68** Terence Vaughn* Lila Ghemri[#]
- **70** Eric Wilson* Daniel Vrincianu[#]
- 77 Tommy Quatch* Daniel M. Brook Hector C. Miranda Jr[#]

*SURP Fellowship Recipient #Faculty Mentor

GREETINGS FROM THE INTERIM ASSOCIATE PROVOST



I am honored to take this opportunity to congratulate all the students who participated in this past summer's College of Science, Engineering, and Technology's Undergraduate Research Program as well as the faculty who mentored them. All universities have as core parts of their missions both education and the production new knowledge through research. COSET is committed to providing undergraduates an opportunity to participate in the research enterprise of our University.

Texas Southern University has a long tradition of training scientists and technical workers. It remains at the core of what we do today as much as when we took our current status as a university in 1957. COSET's well established program continues that tradition. With the addition of our new engineering programs, COSET and the University are well positioned to continue that tradition.

To all the students who participated – well done, we anticipate that you will use the skills and experiences you have gained to make a lasting contribution to our community. To all the faculty who mentored these outstanding students – your service will bring you repute and renown not just for now but for long after you have left the University.

Sincerely,

Gregory H. Maddox, Ph.D. Professor of History Interim Associate Provost/Interim Associate Vice President for Research

GREETINGS FROM THE DEAN



I am very pleased to have this opportunity to send my personal congratulations to all students who have participated and successfully completed the Summer Undergraduate Research Program (SURP) in the College of Science, Engineering and Technology (COSET). I also want to thank all faculty advisors who have dedicated their time and efforts to help students to learn and grow in their research endeavors. The publication of their research accomplishments in the Proceedings of SURP is undoubtedly a solid step for the SURP student participants to be truly successful in their future career pursuit!

In this SURP, we have had student participants from almost all programs in the COSET. We had more participants than the year before. We had more faculty members who expressed their willingness to supervise SURP students. All signs have shown that our SURP effort is moving in the direction towards the goal that was originally planned and becoming more and more successful in every year forward. It is our sincere hope that the SURP will help retain our top students and help them acquire the study skills needed to graduate on time.

The established scientific laboratories in the Leonard H.O. Spearman Technology Building and the TSU Science Center have continuously been upgraded with new equipment and technologies. We have strived to develop the necessary infrastructure to support any level state-of-the-art research endeavors. There are a number of significant on-going research programs supported by various federal and state agencies, which can support our students to be further involved in the advanced scientific research and inventions. Such opportunities of experiences for students are unique and invaluable.

I hope all of you will enjoy reading this research proceedings contributed by the SURP students of the COSET! Again, congratulations to those participants!

Sincerely,

Lei Yu, Ph.D., P.E. Professor of Transportation and Dean, College of Science, Engineering, and Technology

SUMMER UNDERGRADUATE RESEARCH PROGRAM 2014: EXCELLENT ACHIEVEMENT

We would like to thank all students and faculty mentors who participated in the second Summer Undergraduate Research Program (SURP). Thanks to their hard work and the financial support from the COSET, we successfully completed this program again. We are delighted to present the fruit of this program: "Proceedings of SURP 2014", which are the collection of research manuscripts written by student participants.

The COSET SURP sponsored 20 talented and motivated undergraduates from 9 departments, which is a significant increase compared to the last summer (16 students from 5 departments), with the primary intention to retain these students at TSU and increase their transition to graduate and professional programs in Science, Technology, Engineering, and Mathematics (STEM). The COSET invested substantial funding to students and faculty mentors (\$2,000 of fellowship to each student and \$1,000 to each mentor for research supplies) to promote their participation in various research projects in STEM fields.

All student participants worked very hard in laboratories with their mentors and earned hands-on research experience. They developed more efficient photovoltaic solar cells and low-cost NMR. They also investigated spread of disease through flight travel, impacts of the utilization of antimicrobial soaps on water quality, identifying biomarkers for aggressive breast cancers, toxicity of indoor dust to gut microbial system, and prediction of cracking on farm-to-market roads. They learned how to sequence mitochondrial genomes of birds and develop smart phone applications for traffic control around stop signs. They were exposed to research techniques such as polymerase chain reaction (PCR) and gel electrophoresis. They had opportunities to access many state-of-the-art instruments such as gas chromatograph-mass spectrometer, multimode inverted microscope, and virtual driving simulator. They also have a peak in the research world of mathematics.

Upon completion of this 9-week program, all students delivered excellent oral and poster presentations that were predominant among all TSU's summer research programs. Six SURP posters won the first, second, or third places that is more than 50% of the total awards. At the program closing ceremony, student participants mentioned that they would strongly encourage other student fellows to participate in this program next summer or later. They also expressed that the SURP facilitated their aspirations for and matriculations at STEM graduate programs. This feedback demonstrates that we will see more COSET students pursuing their graduate degrees that is another sign of success of the SURP. We believe that the SURP will significantly contribute to resolve underrepresentation of African American in STEM graduate programs and professional employment that is currently lower than 5%.

Although it was only the second year, there is no doubt that the SURP will be classed as another precious tradition of the COSET. We believe that the SURP is one of the vital step stones towards TSU's winning future. Again, we salute to all participants for your hard work, support, and remarkable accomplishment.

Best Regards,

Hyun-Min Hwang, Ph.D. Assistant Professor of Environmental & Interdisciplinary Sciences Yunjiao Wang, Ph.D. Assistant Professor of Mathematics

College of Science, Engineering, & Technology, Texas Southern University

TESTIMONIALS



Participating in the COSET Summer Undergraduate Research Program has been a great experience. I spent my summer researching a new possible prediction model for longitudinal cracking on low volume farm-to-market roads that are built over expansive subgrade. This research required extensive knowledge in the Geotechnical field, and I had only taken my first Geotechnical course in the spring. So, performing this research required me to learn a lot of material in a short amount of time. That was the part that I enjoyed the most during this experience. I enjoyed learning new ideas and concepts that I probably wouldn't have learned if I had not participated in this summer program.

Aminata Dicko (Junior), Civil Engineering

My experience with the SURP was filled with nothing but positivity and learning. Through the help of the SURP I have been able to gain research hours and lab experience while polishing my presentation skills. I would thoroughly recommend the SURP program to any TSU science student who is interested in expanding his/her knowledge and experience. *Ray Mbonu (Junior), Chemistry*



The SURP program was extremely instrumental in facilitating a stimulating learning environment by surrounding participants with mentors who are fully committed to the learning and success of each student. The SURP has helped me to develop and master valuable skills that have better prepared me for a career in science and technology. Over all, this experience was priceless!

Terence Vaughn (Senior), Computer Science

LIST OF PARTICIPANTS (STUDENTS)

BENJAMIN CABALLERO, Freshman Department of Biology Mentor: Dr. Hector C. Miranda Jr.

FRANCHELL DAVIDSON, Sophomore Department of Mathematics Mentor: Dr. Willie E. Taylor

BRITTANI DAVIS, Senior Department of Biology Mentor: Dr. Audrey N. Prayer

AMINATA DICKO, Junior Department of Engineering Mentor: Dr. Yachi Wanyan

JOHN EUNSON JR., Senior Department of Biology Mentor: Dr. Jason Rosenzweig

UGOCHUKWU O. EZENEKWE, Junior Department of Physics Mentor: Dr. Marc C, Harvey

CHIBUEZE S. EZEUDU, Junior Department of Chemistry Mentor: Dr. Jahmario L. Williams

MARQUESHA FOREMAN, Junior Department of Mathematics Mentor: Dr. Roderick B. Holmes

MICAH HARPER, Junior Department of Aviation Science & Technology Mentor: Dr. Vernon J. Baker

AMANDA NICOLE JACKSON, Junior Department of Biology Mentor: Dr. Hector C. Miranda Jr. **CHARESE JEFFRIES,** Freshman Department of Chemistry Mentor: Dr. Hyun-Min Hwang

FRANKLIN KIGWE, Junior Department of Engineering Mentor: Dr. Yunjiao Wang

RAY MBONU, Junior Department of Chemistry Mentor: Dr. Sodipe Ayodoton

RAY MOTTE, Sophomore Department of Transportation Studies Mentor: Dr. Fengxiang Qiao

MILES L. SEWELL-CORTEZ, Junior Department of Chemistry Mentor: Dr. Christopher J. Tymczak

SAMUEL TEFERRA, Sophomore Department of Computer Science Mentor: Dr. Moshen Javadian

FERNANDO VALDEZ, Senior Department of Engineering Mentor: Dr. Graham Thomas

TERENCE VAUGHN, Senior Department of Computer Science Mentor: Dr. Lila Ghemri

ERIC WILSON, Senior Department of Physics Mentor: Dr. Daniel Vrincianu

TEDRIC WILSON, Freshman Department of Biology Mentor: Dr. Erica Cassimere

LIST OF PARTICIPANTS (FACULTY MENTORS)

DR. VERNON J. BAKER Department of Aviation Science and Technology

DR. ERICA CASSIMERE Department of Biology

DR. LILA GHEMRI Department of Computer Science

DR. MARK C. HARVEY Department of Physics

DR. RODERICK B. HOLMES Department of Mathematics

DR. HYUN-MIN HWANG Department of Environmental and Interdisciplinary Sciences

DR. MOSHEN JAVADIAN Department of Computer Science

DR. HECTOR C. MIRANDA JR. Department of Biology

DR. AUDREY N. PLAYER Department of Biology

DR. FENGXIANG QIAO Department of Transportation Studies

DR. JASON ROSENZWEIG Department of Biology

DR. AYOTOTUN SODIPE Department of Biology

DR. WILLIE E. TAYLOR Department of Mathematics

DR. GRAHAM THOMAS Department of Engineering

DR. CHRISTOPHER J. TYMCZAK Department of Physics

DR. DANIEL VRINCIANU Department of Physics

DR. YUNJIAO WANG Department of Mathematics

DR. YACHI WANYAN Department of Engineering

DR. JAHMARIO L. WILLIAMS Department of Mathematics







College of Science, Engineering, & Technology, Texas Southern University



COSET SURP 2014

SEQUENCING THE COMPLETE MITOCHONDRIAL GENOME OF THE MALAYAN PEACOCK-PHEASANT POLYPLECTRON MALACENSE AND ESTIMATING GENETIC DISTANCES WITH P. BICALCARATUM AND P. NAPOLEONIS

Benjamin Caballero* and Hector C. Miranda Jr.*

Department of Biology College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

The evolutionary origin of the Polyplectron in Asia has been controversial. Some studies support the 'westward' colonization trajectory to main and Asia, while others suggest the opposite direction. To test these hypotheses, we are conducting a large-scale program of sequencing the whole mitochondrial genomes of about six species of Polyplectron, one of which is the Malayan Peacock –Pheasant (Polyplectron malacense). We designed primers using Primer3Plus, augmented by Geneious Pro and ClustalW programs. Both forward and reverse PCR reactions were sequenced and assembled. We have determined that the complete mitochondrial genome of Polyplectron malacense is 16,694 bp and contains 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes and one control-region. We measured the genetic distances of P. malacense with two other Polyplectron whose mitogenomes have been recetly published. We observed 93.3% resemblance of sequences between P. malacense and P. napoleonis, and 94.2 % between P. malacense and P. bicalcaratum. This values provide suggestion that P. malacense is more closely related to P. napoleonis relative to the mainland Asian P. bicalcaratum. The control region was determined to be 1165 bp, five bp shorter than that reported for P. bicalcaratum, and 15 bp shorter than P. napoleonis.

Key words: Malayan Peacock Pheasants, Migration, Mitochondrial genome sequencing, PCR

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

The peacock pheasants (genus Polyplectron) are some of the most spectacular pheasants of the world. There are about seven species belonging to the genus distributed in mainland Asia and Southeast Asia. There are two contrasting hypotheses on the origin and evolution of Polyplectron. One hypothesis based on three genes; two mitochondrial and one nuclear genes suggested that Polyplectron originated in Palawan and spread to Borneo then to mainland Asia including China (Westward speciation hypothesis). The other hypothesis, (Eastward speciation hypothesis) based on morphological studies, suggested that the clade originated in mainland Asia and terminating to Southeast Asian islands of Borneo and Palawan. Because of this conflict, we planned to use the whole mitochondrial genome of the six species as characters to test which phylogeographic hypotheses will be supported.

We have recently sequenced the mitochondrial genome of two species P. germaini (Omeire et al 2014) and P. napoleonis (Quach et al 2014). Our goal is focused on decoding the whole mitochondrial genome of Polyplectron malacense, the endemic found in the Malay Archipelago, and estimate its genetic distance with two other congeners."



Figure 1. Map of Southeast Asia showing the distribution of peacock pheasants, including *P. malacense* with *P. bicalcaratum* and P. napoleonis.

METHODS

Specific primers were designed using the published Polyplectron bicalcaratum (Genbank Accession No EU41782) as template. We used Primer3Plus (Untergasser et al 2012) as the primary tool for primer design. We avoided degenerate primers to minimize the incidence of PCR non-target amplification. " In cases when the primers did not work, we employed two strategies to cover the region, 1) we used the forward primer of the 5' upstream and the 3' downstream reverse primer of the nearest adjacent fragment. For longer fragments, PCR annealing and extension times were appropriately extended depending on the length of the target region. 2) We employed primer walking and designed new primers based on newly obtained sequences. "DNA extraction was performed using DNAeasy Tissue kit (Qiagen) following manufacturer instruction to obtain DNA from fresh tissue sample. We performed Polymerase Chain Reaction (PCR) with a total volume of 25uL containing 10-50 ng of template DNA, 4uL of deionized water, 4 uL of Amplitaq 360 Gold Polymerase Master Mix, and forward and reverse reactions of the primers. A total of 27 primers were used (Table 1).

The PCR cycles were: one cycle 10 minutes at 95°C, 35 cycles of 20 seconds at 95°C, 20 seconds at 60°C, and 50 seconds at 72°C." The PCR products were examined by gel electrophoresis in 1% agarose gel (Figure 2).

Products were sequenced bidirectionally on an ABI sequencer. The sequence were aligned and assembled, and aligned with other genomes using Clustal W and Genious Pro 5.5 (Figure 3). "Sequence contigs are subjected to BLAST (Basic Local Alignment Search Tool)

(http://blast.ncbi.nlm.nih.gov/Blast.cgi)." Sequenced fragments were assembled using ClustalW and GeneiousAlign option in Geneious Pro 5.5 program. "

Region	Forward Primer	Sequence 5' – 3'	Reverse Primer	Sequence 5' – 3'
D-loop	Po00080 F	TCGTGCATACATTTATATACCACA	Po00887 R	TGGTAAATCTCCTAGTTTTGTGGAG
D-loop-12S rRNA	Po00673 F	TCCTGCGTTGCGTCCTATTC	Po01519 R	TGGGTTTCTTGTGTGACCGC
12S rRNA	Po01302 F	CCAGTGAAAATGCCCCTAAA	Po02136 R	ATTTGTGCTGGTGGCTTTTG
12S rRNA-16S rRNA	Po01962 F	GGTGGAAGAAATGGGCTACA	Po02750 R	ACCCCCGTCGAGTTACTCTT
16S rRNA	Po02501 F	CAACCAAGCAAAGGGGACTA	Po03329 R	CGTTTTTGCACGAGGGTACT
16S rRNA-tRNA-Leu	Po03102 F	CAAACCAAAGACCCGACTGT	Po03942 R	AACCTCTGGGTAAAGGGCTTA
16S rRNA-nd1	Po03723 F	GCAATCCAGGTCGGTTTCTA	Po04541 R	ATTATTGCAAGGGGTCATGC
nd1-nd2	Po04354 F	GCCTCAAACTCCAAATACGC	Po05179 R	TTGCATGGGGGGTTCATTAGT
ndl-nd2	Po04892 F	GCCTCTGACACACCAGCATA	Po05728 R	AGCCTAGGTGGGAGATGGAT
nd2-tRNA-Ala	Po05575 F	CCAATCACCCTCCTTCTCCT	Po06339 R	AAAGCGTCTGGTTTGCATTC
nd2-cox1	Po06138 F	CGCCATTTTAACCGCACTAT	Po06953 R	AGTTCATCCTGTGCCAGCTC
coxl	Po06750 F	GCCCATGCTTTCGTCATAAT	Po07532 R	GACTTTAATGCCGGTTGGAA
cox1-tRNA-Ser(UCN)	Po07289 F	TCACCCCGAAGTCTACATCC	Po08137 R	TGAGGGTTCGATTCCTTCCT
cox1-cox2	Po07937 F	CATCGGCTCCCTAATTTCAA	Po08784 R	CAGGGATTGCGTCTGTTTTT
cox2-atp6	Po08474 F	AGTCCTACTCGCCCTTCCAT	Po09322 R	GGTGGACGAATCAGAGTTGAA
atp8-cox3	Po09113 F	AACAGCCCCACAGACAAAAC	Po09945 R	TGATTAGGCCAGAGGTGGTT
atp6-cox3	Po09736 F	GCCCTAACCGCTCTAATCCT	Po10550 R	TCCGAAGTGGTGACTTGATG
cox3-nd4L	Po10362 F	TACTTCACCGCCCTACAAGC	Po11206 R	GAAATGAGGTGGGTTCGATG
nd3-nd4	Po10963 F	AACCCTCACCTGAGCTACCA	Po11800 R	GGTGGGGATTAAGGTTGCTT
nd4-nd4	Po11610 F	TGGTCCTGTCCTCCTGATTC	Po12431 R	GGCTGTGTGTGTTCGTTCGTAG
nd4-nd5	Po12205 F	AGCCCTGTGAGGTGCTCTAA	Po13036 R	GTGGTACGAGGGTGTTGAGG
tRNA-Ser(AGY)-nd5	Po12868 F	GGCTCAAACCAGCAAGAACT	Po13655 R	GCTAGAATGAGGCCGAGAAG
nd5	Po13423 F	TTCGTAGGTTGGGAGGGAGT	Po14268 R	ACTGTAGGTTGCGGTGAAGG
nd5-cytb	Po14053 F	GGGGAACAAGACATCCGTAA	Po14857_R	TAAGAGGGGGGGGGGGATTTTC
nd5-cytb	Po14583_F	CTTCAACCCGCTCATACACC	Po15428 R	CGTGAAGGAATGTGAGGTGA
cytb-tRNA-Pro	Po15274_F	CTCAGCAATCCCCTACATCG	Po16073_R	GGAGCTGGAGAAGGAGGTTT
cyth-D-loop	Po15870 F	TCATTGGCCAAGTAGCATCC	Po00165 R	TGTCCGTCTACATATAATGGGTTT





Figure 2. Results showing polymerase Chain Reaction (PCR) product of about 800 bp. The marker to the left is phiX174-Hae III.



Figure 3. Map of a typical bird mitochondrial genome showing the position and sequence of the genes.

RESULTS AND DISCUSSION

The mitogenome of P. malacense contains 13 protein-coding genes, 2rRNA genes, and 22 tRNA genes with the general perspective of 16,694 bp total. Gene order and gene coding strand is consistent with those observed in galliformes and other birds, with tRNAGlu and nd6 found immediately adjacent to the control region The overall base composition is 23.9%T;29.5A,32.3%C, and 14.3%G with a total A+T content of 53.4%. Two reading frames overlaps occur on the same strand: atp8 and atp6 overlap by 8 nt, nd4L and nd4 by 5 nt. All of the protein-coding genes begin with the ATG start codon, except for cox1 which has a GTG start codon (Table 2).

	P malacense	P bicalcar	P napoleo
P malacense		94.2%	93.3%
P bicalcaratum	94.2%		93.3%
P napoleonis	93.3%	93.3%	

Table 2. Pairwise genetic sequence divergence of *P. malacense* with *P. bicalcaratum* and P. napoleonis.

The P. napoleonis contains the typical set of 22tRNA genes, which are interspersed between rRNAs and protein-coding genes. "There's 93.3% resemblance of sequences between P. malacense and P. napoleonis, and 94.2% between P. malacense and P. bicalcaratum. These values provide suggestion that P. malacense is more closely related to the mainland P. bicalcaratum. The control region was determined to be 1165 bp, five bp shorter than that reported for P. bicalcaratum, and 15 bp shorter than P. napoleonis. "Efforts to annotations, establishment of positions, identification of start and stop codons, cloverleaf secondary structures fo tRNAs are currently being undertaken by another student.

ACKNOWLEDGEMENTS

This study was supported by COSET Summer Undergraduate Research Program. Thanks to Dr. Dan Brooks of the Houston Museum of Natural Science for providing the tissue sample.

REFERENCES

BirdLife International 2005. Polyplectron germaini. 2006. IUCN Red List of Threatened Species. IUCN 2006.

- Desjardins P, Morais R. (1991) Nucleotide sequence and evolution of coding and noncoding regions of a quail mitochondrial genome. Journal of Molecular Evolution 32:153-161.
- Desjardins P, Morais R. (1990). Sequence and gene organization of the chicken mitochondrial genome. A novel gene order in higher vertebrates. Journal of Molecular Biology 12:599-634.
- Eo SH, Bininda-Emonds ORP, Carroll JP. (2009) A phylogenetic supertree of the fowls (Galloanserae, Aves). Zoologica Scripta 38:465-481.
- Harrison GL, McLenachan PA, Phillips MJ, Slack KE, Cooper A, Penny D. (2004) Four new avian mitochondrial genomes help get to basic evolutionary questions in the late Cretaceous. Molecular Biology and Evolution 21:974-983.
- Kimball RT, Braun EL. (2008) A multigene phylogeny of Galliforms supports a single origin of erectile ability in non-feathered facial traits. Journal of Avian Biology 39:438-445.

Kimball RT, Braun EL, Ligon JD, Lucchini V, Randi E. (2001) A molecular phylogeny of the peacock-pheasants (Galliformes:

- Polyplectron spp.) indicates loss and reduction of ornamental traits and display behaviours. Biological Journal of Linnean Society 73:187–198.
- Lowe TM, Eddy SR. (1997) tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Research 25:955-964.
- Pacheco M A, Battistuzzi FU, Lentino M, Aguilar RF, Kumar S, Escalante AA. (2011) Evolution of modern birds revealed by mitogenomics: timing the radiation and origin of major orders. Molecular Biology and Evolution 28:1927-1942.
- Paton T, Haddrath O, Baker AJ. (2002) Complete mitochondrial DNA genome sequences show that modern birds are not descended from transitional shorebirds. Proceedings of the Royal Society of London, Biological Sciences 269:839-846.
- Shen YY, Shi P, Sun YB, Zhang YP. (2009) Relaxation of selective constraints on avian mitochondrial DNA following the degeneration of flight ability. Genome Research 19:1760-1765.

15

ON THE SOLUTIONNS OF THE DIFFERENCE EQUATION $x_{n+1} = \frac{f(x_n)}{x_{n-1}}$

FranChell Davidson* and Willie E. Talyor[#]

Department of Mathematics College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004

ABSTRACT

In this paper we examine the solutions of the equation

(1)
$$x_{n+1} = \frac{f(x_n)}{x_{n-1}}$$

for various functions f. While equation (1) has been studied by several authors, no one has considered (1) for specific functions. This work will fill that void and focus on the qualitative behavior of solutions of (1) boundedness, periodicity, and oscillation of solutions are considered.

Keywords: boundedness, periodicity, oscillation

*SURP Fellowship Recipient #Faculty Mentor

INTRODCUTION

This research investigates the solutions of the nonlinear difference equation

(1)
$$x_{n+1} = \frac{f(x_n)}{x_{n-1}}$$

for various functions f. More specifically we consider the following forms of f:

(i) f(x) = 1(ii) f(x) = x(iii) $f(x) = max\{1, x\}$ (iv) $f(x) = x^2$ (v) $f(x) = x^3$

To begin our study of (1) we need the following definitions:

<u>Periodic</u>: A solution x_n of (1) is periodic with period p if $x_{n+p} = x_n$ for all $n \ge -1$. If there exist an integer k > -1 such that $x_{n+p} = x_n$ for all $\ge k$, then x_n is said to be eventually periodic with period p. <u>Bounded</u>: A solution x_n of (1) is bounded if there is a number M > 0 such that $|x_n| \le M$ for all $n \ge -1$.

<u>Oscillation</u>: A solution x_n of (1) is oscillatory if it is not eventually positive or eventually negative.

Properties such as boundedness, periodicity, and oscillation will be studied for the solutions of (1). Moreover, the relationship between initial conditions and these properties will be examined. This paper can also be viewed as an introduction to the study of difference equations and the qualitative behavior of their solutions. This is done as an introduction to being able to study dynamics. If we don't have a concept of these properties it would be difficult to do further research into dynamics because the other properties would be too complex to comprehend.

COSET SURP 2014

RESULTS AND DISCUSSION

Results for f(x) = 1

In this section our equation becomes

(*E_o*) $x_{n+1} = \frac{1}{x_{n-1}}$, where $x_{-1} = a \ x_0 = b, ab \neq 0$

Theorem Equation (E_0) is a 4-cycle, i.e., a solution x_n of (E_0) has the form $a, b, \frac{1}{a}, \frac{1}{b}, a, b, \frac{1}{a}, \frac{1}{b}, a, b, \dots$ Proof: Note that $x_1 = \frac{1}{a}$ and $x_2 = \frac{1}{b}$, so $x_3 = a$ and x_4 and since $x_{n+4} = x_n$ for every n it follows that (E_0) is a 4-cycle. More specifically $x_{k-1} = a$, $x_k = b$, $x_{k+1} = \frac{1}{a}$, $x_{k+2} = \frac{1}{b}$ for ≥ 0 . Q.E.D.

Remark Choosing a = 1 and b = -1 yields a period 2, oscillatory solution. Choosing a = b = 1 yields a constant solution. Consequently, every solution of (E_0) is either constant, has a period of 2 or has period of 4.

Results for f(x) = x

In this section we study

(E₁) $x_{n+1} = \frac{x_n}{x_{n-1}}$, where $x_{-1} = a$, $x_0 = b$, $ab \neq 0$ **Theorem** Equation (E₁) is a 6-cycle, i.e., a solution x_n of (E₁) has the form $a, b, \frac{b}{a}, \frac{1}{a}, \frac{1}{b}, \frac{a}{b}, a, b, \frac{b}{a}, \frac{1}{a}, \frac{1}{b}, \frac{a}{b}, a, b, ...$ Proof: It is easy to show that $x_1 = \frac{b}{a}, x_2 = \frac{1}{a}, x_3 = \frac{1}{b}, x_4 = \frac{a}{b}, x_5 = a, x_6 = b$ and since $x_{n+6} = x_n$ for every n it follows that (E₁) is a 6-cycle. More specifically $x_{6k-1} = a, x_{6k} = b, x_{6k+1} = \frac{b}{a}, x_{6k+2} = \frac{1}{a}, x_{6k+3} = \frac{1}{b}, x_{6k+4} = \frac{a}{b}$ for $k \ge 0$. Q.E.D.

Remark Choosing a = 1 and b = -1 yields a period-3, oscillatory solution, 1,-1,-1,1,-1,-1,-1,...

Choosing a = b = 1 yields a constant solution

1,1,1,1,1,...

Indeed, every solution of (E_1) is either constant, has a period of 3, or has a period of 6.

Results for $f(x) = max\{1, x\}$

In this section our equation is a hybrid of (E_0) and (E_1) , (E_m) $x_{n+1} = \frac{max\{1, x_n\}}{x_{n-1}}$, where $x_{-1} = a, x_0 = b, ab \neq 0$

Theorem Equation (E_m) is a 5-cycle, i.e., a solution x_n of (E_m) has the form a, b, $\frac{b}{a}, \frac{1}{a}, \frac{1}{b}$, a, b, $\frac{b}{a}, \frac{1}{a}, \frac{1}{b}$, a, b, $\frac{b}{a}, \frac{1}{a}, \frac{1}{b}$, a, b, ...

Proof: Observe that (E_m) is related to both (E_0) and (E_1) . Assuming $a \le 1 \le b$ yields, $x_1 = \frac{b}{a}$, $x_2 = \frac{1}{a}$, $x_3 = \frac{1}{b}$, $x_4 = a$, $x_5 = b$ and since $x_{n+5} = x_n$ for every n it follows that (E_m) is a 5-cycle. More specifically $x_{5k-1} = a$, $x_{5k} = b$, $x_{5k+1} = \frac{b}{a}$, $x_{5k+2} = \frac{1}{a}$, $x_{5k+3} = \frac{1}{b}$, for $k \ge 0$. Q.E.D. Remark Choosing a = 1 and b = -1 yields a period-2, oscillatory solution. Choose a = b = 1 yields a constant solution. Consequently, every solution of (E_m) is either constant, has a period of 2 or has a period of 5. Making the following assumptions, $a \ge b \ge 1$ and $a \ge 1 \ge b$ will also generate period 5 solutions.

Results for $f(x) = x^2$

In this section we consider

(E₂)
$$x_{n+1} = \frac{x_n^2}{x_{n-1}}$$
, where $x_{-1} = a, x_0 = b, ab \neq 0$

Theorem Equation (E_2) possesses a period-2, oscillatory solution, an unbounded solution, a solution that converges to 0, and an oscillatory, non-periodic solution.

Proof: Notice that $x_1 = \frac{b^2}{a}$, $x_2 = \frac{b^3}{a^2}$, $x_3 = \frac{b^4}{a^3}$, $x_4 = \frac{b^5}{a^4}$, and $x_5 = \frac{b^6}{a^5}$. So the general solution for the difference equation is $x_n = \frac{b^{n+1}}{a^n}$. **Q.E.D.**

Remark Choosing a = 1 and b = -1 will produce a period-2, oscillatory solution. Letting a = 1 and b = 2 produces an unbounded solution,

Taking a = 2 and b = 1 yields a solution that converges to 0,

$$2,1,\frac{1}{2},\frac{1}{4},\frac{1}{8},...$$

Choosing a = 1 and b = -2 gives an oscillatory, unbounded non-periodic solution.

Results for $f(x) = x^3$

In this section our equation becomes

(E₃)
$$x_{n+1} = \frac{x_n^3}{x_{n-1}}, x_{-1} = a x_0 = b$$

Theorem Equation (E_3) is possesses a period-3, oscillatory solution, an unbounded solution, a solution that converges to 0, and an oscillatory, non-periodic solution.

Proof: Note $x_1 = \frac{b^3}{a}$, $x_2 = \frac{b^8}{a^3}$, $x_3 = \frac{b^{21}}{a^8}$, etc. Generally for $n \ge 0$, $x_n = \frac{b^{P_{n+1}}}{a^{P_n}}$, where P_n is a solution to the difference equation

$$P_{n+1} = 3P_n - P_{n-1}$$

subject to the conditions $P_0 = 0$ and $P_1 = 1$. Even more interesting is that $P_n = \frac{1}{\sqrt{5}} \left[\left(\frac{3+\sqrt{5}}{2} \right)^n - \frac{1}{\sqrt{5}} \right]$

$$\left(\frac{3-\sqrt{5}}{2}\right)^n$$
]. **Q.E.D**.

Remark Choosing a = 1 and b = -1 results in the period-3 solution -1,-1,1,-1,-1,... Also a = 1 and b = 2 yields an unbounded solution, while choosing a = -2 and b = 1 generates an oscillatory solution that converges to 0.

ACKNOWLEDGEMENTS

This study was supported by Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

Abu-Sarris, R.M, Characterization of rational periodic sequences, Journal of Difference Equations and Applications 2000, Vol.6, pp.233-242.

Mestel, B. D., On globally periodic solutions of the difference equation $x_n = \frac{f(x_n)}{x_{n-1}}$, Journal of Difference Equations and Applications 2003, Vol. 9(2), pp. 201-209.

IDENTIFYING GENE EXPRESSION IN AGGRESSIVE BREAST CANCER VS. LESS AGGRESSIVE BREAST CANCER

Brittani Davis* and Audrey N. Prayer[#]

Department of Biology College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

The objectives of this study were to identify biomarkers related to TN cancers and validate their reliability. A total of six genes were put through a screening process to determine candidacy for further study. IL32 was one of several genes identified. It was examined to determine if it would be a potential biomarker for TN cancers. The thousands of genes were first grouped and then analyzed using T test to compare the two groups of genes (aggressive and less aggressive). From this, six genes were screened and examined using MDA MB231 RNA to represent TN and MCF7 cell line RNA to represent less aggressive breast cancer types. RNA levels were analyzed by performing Polymerase Chain Reaction (PCR). The six genes were screened and compared. The PCR and gel results showed that the IL32 gene showed the biggest difference in expression in the 231 versus the MCF7. From this IL32 was chosen for further study. For future experimentation, IL32 is a great candidate to help identify and understand aggressive breast cancer.

Key words: Breast Cancer, Interleukin 32, PCR, Biomarker

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

According to recent statistics about 1 in 8 U.S. women will develop aggressive breast cancer over the course of her lifetime. In the last year an estimated 232,340 new cases of aggressive breast cancer are expected to be diagnosed in women in the U.S. Aggressive breast cancer is characterized by the Triple Negative (TN) combination of the estrogen receptor, progesterone receptor and ERRB2 genes. TN behavior causes metastasis or the unwanted spread of the cancer into unsolicited places in the body which in most cases results in the death of patients. The goal of this study is to not only better understand genes that may be related to aggressive and/or fatal breast cancer, but to also try to find genes that one day might be used to diagnose patients and ultimately increase patient survival. After undergoing a particular

screening process and being compared to hundreds of other genes, we identified IL32. Interleukin 32 (IL 32) is a cytokine which is responsible for mediation of immune responses within our body's immune system. IL 32 is a good candidate because it has a higher expression in aggressive cancer (MDA MB231) than in less aggressive cancer (MCF 7).

METHODS

Seven cell lines were initially used to generate data for this study. Each was previously characterized for ER/PR/ERBB2 receptor status, subtype and aggressive behavior (Atcc.org and Asterand.com). Affymetrix U133 plus 2 gene expression hybridizations were performed previously following suggestions of the manufacturer (Affymetrix.com) using seven different cell lines and 15 total hybridizations (AP). Each Affymetrix microarray contained 54, 675 genes and Expressed Sequence Tags (EST) corresponding to all known and purported genes. Affymetrix hybridization datasets were deposited on National Cancer Institute's mAdb website (https://madb.nci.nih.gov/) and grouped consistent with groupings above (i.e., Group A and Group B, representing aggressive and less aggressive.)

Grouped samples were normalized using Robust Multiarray analysis (RMA), and group comparisons performed using t-test. T-test group comparisons allowed detection of gene levels that differed between Group A compared to Group B. Hierarchical clustering (HC) analysis was performed using programs available on mAdb. All data analyses were performed by AP and RN.

IL32, PCDH A9, PDE 10A, SLC 9A3R1, GOS2, BAG 2 (and MRLP 19 as the control) primers were generated using Primer 3 program (http://biotools.umassmed.edu/bioapps/primer3_www.cgi). Primers were synthesized by IDTDNA. PCR was performed using melting temperature of 56deg for 29cycles. PCR products (for analysis of gene expression levels) were analyzed using 1% agarose gel electrophoresis.

RESULTS AND DISCUSSION

The six candidate genes in the previous figures were chosen based on a screening process and further investigated through PCR and gel electrophoresis. Based on observations made on the gel as well as the results from the T test, IL32 showed the biggest difference in expression in the aggressive MDA MB231 in contrast to the less aggressive MCF 7. IL32 has proven to be a credible candidate for further studies.



Figure 1. IL32 RNA levels are highest among the TN samples (red compared to black and green).

COSET SURP 2014

Α	Α	Α	Α	Α	Α	Α
#1	#2	#3	#4	#5	#6	#7
327.4	263.6	267.9	339.8	298.3	329.7	289.8
57.2	134.0	86.5	72.2	240.0	190.2	262.4
494.7	413.8	555.8	633.9	149.4	151.2	150.5
420.6	272.6	1034.4	388.0	3370.2	3790.7	2294.9
1070.5	1109.2	905.4	1066.4	1414.5	1789.5	1724.3
18.1	12.7	18.6	10.7	9.2	7.6	8.1

 Table 1. Number of transcripts per aggressive breast cancer cell.

 Table 2. Number of transcripts per less aggressive breast cancer cell.

В	В	В	В	В	В	В	В
#8	#9	#10	#11	#12	#13	#14	#15
3006.2	2556.5	3227.7	3005.5	2859.8	2799.9	2014.7	2054.6
6.8	11.8	24.9	5.9	6.8	6.7	6.8	7.0
33.6	25.2	29.7	43.4	61.7	41.7	43.4	30.4
17.3	23.1	20.5	23.4	27.5	25.1	20.4	21.1
194.9	74.7	167.2	8.3	8.0	7.4	44.5	46.6
716.3	536.6	859.3	354.4	318.8	307.6	21.5	18.0

Table 3.	Sequence	of breast	cancer	genes	
----------	----------	-----------	--------	-------	--

Gene	Product Size	Left Sequence (Backward)	Right Sequence (Forward)
IL32	207 BP	AGCTGGAGGACGACTTCAAA	CCTGGAACCATCTCATGACC
PCDH A9	305 BP	GGCTGCCTCTTGCATGTATT	TGGGAGATTGATTTCAGGTAAC A
PDE 10A	263 BP	TGC CCA ACA CAC TGT GAA AT	TTC TGG ACA CAG GTT CAT TGA C
SLC 9A3R1	234 BP	GTCCAGGGCTGATCAAAGAA	TGAGGGTGGGAGTAGGAACA
G0S 2	265BP	ACAGGCTCTCCAGAAGCAAG	TGTCAGCGGTTTCTCTGAAGT
BAG 2	167 BP	ATG GGC CAG TTG ATC AGA AG	TTG CAG AGT TTT GGA ACC AG
MRLP	306 BP	AAGCGTCGAAAAGGTCTTGA	GCTCAGGTTCCATGCTCATT

LONGITUDINAL CRACKING MODEL FOR FARM-TO-MARKET (FM) ROADS OVER EXPANSIVE SUBGRADE

Aminata Dicko* and Yachi Wanyan[#]

Department of Engineering College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

Low-volume roads that are built over expansive soils experience frequent premature damage due to its light weight. Longitudinal cracking was reported by a district survey throughout Texas to be one of the most dominant types of distress (Wanyan et al., 2008). This is a critical issue in regions with expansive clays therefore it is imperative to have efficient prediction models that can aid engineers in improving structure performance. This report focuses on the findings from literature reviews regarding expansive soil behaviors, laboratory testing and longitudinal shrinkage cracking simulation. It also covers basic data analysis methods and preliminary results from different regions in Texas. The results are examined and compared in order to find trends and/or discrepancies. This analysis will be used in developing a flexible longitudinal cracking prediction model. Through previous research, it has been determined that certain parameters of expansive soil are related to one another. Moisture content was determined to be a parameter that had a strong relationship to a soil's expansiveness. The degree of change in moisture content is what causes the soil to undergo volumetric changes.

Key words: longitudinal cracking, Farm-to-market roads, Moisture content, Soil expansion

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Expansive soils are those that undergo large volume changes when the natural environmental conditions of the soil are altered (Dakshanamurthy et al., 1973). This accounts for weather changes and other environmental factors. Expansive soil absorbs surrounding moisture and easily dries out under certain circumstances. This change in moisture content causes the soil to swell and shrink. Soil particles change in size, which eventually lead to the superficial cracking on overlaying pavements. Expansive soils cause more damage and financial loss to infrastructures than earthquakes, floods, hurricanes, and tornadoes combined in a typical year (Kerrane).

Low volume farm to market roads are mainly affected by the volumetric changes in the subgrade because its infrastructure is lightweight and its self load does not exert enough force on the underlying subgrade to keep it compacted and free of voids. This allows the soil to move more freely, shrinking and expanding as possible. Heavier infrastructures in the same region will not experience this type of problem because of its weight. Heavier infrastructures apply more force on the subgrade which will keep it compacted and will not allow any voids for particle movement and volumetric changes.

The purpose of this research project is to develop a moisture-content based model that will help civil engineers better predict premature failure of low volume farm to market roads, in the form of longitudinal cracking, due to the volumetric changes that occur in expansive soils. This model will use different easy-to-acquire properties of expansive soils, such as moisture content, Atterberg limits, dry unit weight, etc. to predict longitudinal cracking of roads that are built over expansive soils. Longitudinal cracking was reported by a district survey throughout Texas to be one of the most dominant types of distress (Wanyan et. al., 2008). Damage caused by expansive soils requires constant repairs that are generally temporary and are subjected to further repairs. Damage that goes unnoticed will propagate, thus leading to more substantial damage requiring extensive repairs. The predictions yielded by this moisture-content based model will improve design efficiency because it will diminish the need to over design pavements, which will save time and money that would have otherwise been used for unnecessary excess material and labor.

METHODS

Successful accomplishment of this project requires good understanding and backgrounds in expansive soil behavior, field and laboratory soil testing, and analysis (Wanyan & Abdallah, 2013). An intensive research and review of literature was performed to gather information on previous findings in regards to the behavior and characteristics of expansive soil and its effects on overlaying structures. Laboratory tests were conducted on soil samples from different regions in Texas to characterize their expansive behavior according to its plastic limit (PL), liquid limit (LL), plasticity index (PI), dry unit weight, and optimal moisture content. The soil samples were all tested at different moisture content to observe changes in strength. After the raw data was compiled, data analysis was executed er to develop a prediction model.

The soil samples were collected from San Antonio, Houston, Paris, Fort Worth, and El Paso. An unconfined compressive strength (UCS) test was performed on all samples at different moisture contents (dry, optimum moisture content, and saturated). This test determines the unconfined compressive strength of the soil and the results are plotted on stress/strain graphs. The main objective of the UCS test was to examine the relationship between the moisture content and its impact on the soil.



Figure 1. Longitudinal cracking on FM 911 in Paris, Texas in June 2008 (Wanyan et al. 2008).

It is also important to consider climate while analyzing soil behavior. According to a research previously conducted, sensors were used to measure moisture fluctuations in soils. This information,

along with physical observation of the sites, was compiled to prove that high moisture variances ultimately led to the initiation and propagation of longitudinal cracks in pavements of low volume FM roads (Puppala et. al., 2011).

RESULTS AND DISCUSSION

According to the Unified Soil Classification System (USCS), samples from first four aforementioned locations are classified as 'CH' and samples from El Paso are classified as 'CL'. Soils classified as 'CH' are described as fatty clay; inorganic clays of high plasticity and 'CL' are described as sandy, gravelly, silty, lean clay; also inorganic but of low to medium plasticity (TxDOT). Samples from all locations except El Paso were considered to have high swelling potentials while samples from El Paso were considered to have low swelling potentials (Puppala et al., 2013). Due to the parallel characteristics of some of the samples, only results from Houston and El Paso will be analyzed in this report. The graphs are included in the appendix A. Table 1 shows a summary of important data gathered from the UCS test.

Table 1 contains the modulus, peak strength, and strain at peak strength at dry (low), optimum, and saturated (high) moisture contents for the soil samples collected from Houston and El Paso. A soil's modulus is an elastic parameter and is a measure of stiffness (Geotechdata). The peak strength represents the ultimate strength of the sample and the strain at peak strength represents the sample's volumetric deformation at its highest strength.

Moisture Conte	ent	HOUSTON	EL PASO
	Modulus, psi	58177	28770
DRY	Peak Strength, psi	267	157
	Strain at Peak Strength, %	0.7	0.8
OPTIMUM	Modulus, psi	3719	1722
	Peak Strength, psi	42	28
	Strain at Peak Strength, %	1.9	3.8
	Modulus, psi	479	193
SATURATED	Peak Strength, psi	3	3
	Strain at Peak Strength, %	10.0	10.0

 Table 1. Characteristics of soils having different moisture content.

The data provided shows that the modulus for the Houston sample is consistently higher than the El Paso sample throughout the varied moisture contents. This indicates that the soil in Houston is much stiffer than the soil in El Paso. It is also important to note that the strain at peak strength is higher in El Paso for two of the three moisture contents.

With the results from the UCS test and literature review, it is safe to conclude that a model that utilizes moisture content as a main parameter along with other easy to acquire parameters, such as, plastic and liquid limits, plastic index, etc., can be used to describe and predict the behavior of expansive soil under different conditions. With further studies, an empirical equation can be developed to predict the location of longitudinal cracking as a function of moisture variation and environmental factors from the analysis made from this research.



Houston-Dry

Houston-Optimum



Houston-Saturated



El Paso-Dry



El Paso-Optimum



El Paso-Saturated



Figure 2. Unconfined compressive strength test results

ACKNOWLEDGEMENTS

This study was supported by the Summer Undergraduate Research Program (SURP) of the College of Science, Engineering and Technology at Texas Southern University. The undergraduate researcher would like to express appreciation to the project's faculty advisor, Dr. Yaqi "Yachi" Wanyan, for the provided mentorship and guidance and also to Dr. Hyun-Min Hwang for his time and dedication to the success of all the students who participated in this program.

REFERENCES

Briaud, J-L. "Introduction to Soil Moduli." INTRODUCTION TO SOIL MODULI (2001): BiTech Publishers Ltd. Web. https://ceprofs.civil.tamu.edu/briaud/Intro%20to%20Moduli/Intro%20to%20Moduli.pdf

Dakshanamurthy, V., and V. Raman. "A Simple Method Of Identifying An Expansive Soil." Soils And Foundations 13.1 (1973): 97-104. Web.

Geotechdata.info, Soil Young's modulus, http://geotechdata.info/parameter/soil-elastic-young-modulus.html

Kerrane, Jeffrey P. Esq., http://www.bensonpc.com/downloads/public/What_Are_Expansive_Soils.pdf.

- Puppala, Anand J., Thammanoon Manosuthikij, and Bhaskar C.S. Chittoori. "Swell and Shrinkage Characterizations of Unsaturated Expansive Clays from Texas." Engineering Geology 164 (2013): 187-94. Web.
- Puppala, Anand J., Thammanoon Manosuthkij, Soheil Nazarian, and Laureano R. Hoyos. "Threshold Moisture Content and Matric Suction Potentials in Expansive Clays Prior to Initiation of Cracking in Pavements." Canadian Geotechnical Journal Can. Geotech. J. 48.4 (2011): 519-31. Print.

"Texas Department of Transportation (TxDOT)." Unified Soil Classification System. Print.

- Wanyan, Y., & Abdallah, I. "Moisture Content-Based Longitudinal Cracking Prediction and Evaluation Model for Low-Volume Roads over Expansive Soils." (2013). Research Proposal.
- Wanyan, Y., T. Manosuthkij, I. Nazarian, and A. J. Puppala. "Expert System Design Guide for Lower Classification Roads over High PI Clays." ETD Collection. Texas Department of Transportation, Oct. 2008. Web. <http://digitalcommons.utep.edu/dissertations/AAI3341656/>.

MODELING STRAY RADIATION PRODUCED FROM AN X-RAY THERAPY UNIT

Ugochukwu O. Ezenekwe* and Mark C. Harvey[#]

Department of Physics College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

Over the years, conventional shield designs of radiation therapy rooms have varied in layout and structure. Therapy room designs were generally based on circular accelerator movement about the patient. To that end, primary radiation has been limited to the direction of the accelerator; whereas, produced secondary radiations freely scattered about the treatment room surfaces (e.g., floors, walls, ceiling). The purpose of this study was to calculate the energy and magnitude of scattered radiation produced external to a standard radiation therapy room. The Geant4 Monte Carlo Toolkit (version 10.00) was used to (1) design the walls of a computer-generated radiotherapy room and (2) simulate a source of photons consistent in energy with those produced from a conventional x-ray therapy unit. The photon source was positioned at a stationary point (i.e., isocenter) within the room and aimed directly at one of the walls. A detector consisting of Cesium Iodine (CsI) was placed just outside the room to detect the photons attenuated by the wall. For this extreme case, calculations were performed to assess the energy and magnitude of stray radiation penetrating the walls of the radiotherapy room layout. Our preliminary results suggest that leakage radiation (e.g., photons) is created external to the radiotherapy room.

Key words: Stray radiation, X-ray therapy, Grant4 Monte Carlo Toolkit, Cesium iodine

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Conventional design of radiotherapy rooms have varied over the years. Radiotherapy rooms mainly consist of concrete interspersed with thin sheets of lead to prevent radiation leakage outside of the treatment room. Radiotherapy rooms are designed to protect personnel and also patients in the waiting area from highly penetrating scatter radiation. The layout of typical a radiotherapy room accounts for primary x-ray radiation generated from linear accelerator/target combination within the gantry treatment unit. Scatter radiation produced inside the rooms is also factored into the design of a radiotherapy room. Secondary neutrons are produced from high energy photon interactions within the treatment unit or

concrete walls of the radiotherapy room arise (Masbahi et al., 2012). The purpose of this project was to calculate the energy and magnitude of scattered radiation produced external to room.

METHODS

The Geant4 Monte Carlo Toolkit (version 10.00) was used to a computer-generated radiotherapy room. The walls of the room consist of concrete and are 0.5 m thick (McGrinley, 2002). Geant4 was used also to simulate a source of photons consistent in energy with a typical x-ray therapy unit. The photon source was positioned about 1.5 m away from the wall. For an extreme case, a beam of photons was directed at one of the walls for energies of 10, 15 and 18 MeV, respectively. A CsI radiation detector was positioned about 0.1 m external to the wall to count highly penetrating photons and their associated energy



Figure 1. The x-ray therapy gantry is shown with a radiation detector positioned on the couch in a treatment room at the M. D. Anderson Cancer Center.

RESULTS AND DISCUSSION

A source of 100 photons (i.e., beam) was directly aimed at a wall of the radiotherapy room. The results qualitatively suggest that very little radiation penetrates the concrete wall barriers of the room for all incident beam energies considered in this study. A minimal number of highly energetic photons and/or other radiations (e.g., secondary neutrons) penetrate the concrete wall barrier for the photon source and associated energies considered in this study. Further study is currently underway in our computational laboratory to perform detailed calculations for highly penetrating scattered radiations produced within a radiotherapy room (Polaczek-Grelik et al., 2013)

Element	Atomic Number	Fraction by Mass
Hydrogen	1	0.010000
Carbon	6	0.001000
Oxygen	8	0.529107
Sodium	11	0.016000
Magnesium	12	0.002000
Aluminum	13	0.033872
Silicon	14	0.337021
Potassium	19	0.013000
Calcium	20	0.044000
Iron	26	0.014000

Table 1. Dimensions of the radiotherapy room and elemental composition of concrete wall material (http://physics.nist.gov/cgi-bin/Star/compos.pl?matno=144).

Table 2. Incident beam energy of the photon source along with the energy deposited by highly penetrating photons.

Beam Energy (MeV)	Detected Radiation	Mean Energy Deposition (keV)	Number of counts in CsI detector
10	Photons	116	1
15	Photons	9.83	3
18	Photons	491	5



Figure 2. Computer generated illustration of a conventional radiation therapy room design.



Figure 3. Top-view of a computer generated illustration of a photon beam (in magenta) interacting with the walls of the radiation therapy room (in gray) using the Geant4 Monte Carlo toolkit. The CsI detector is shown in yellow.

ACKNOWLEDGEMENTS

This project was supported by COSET Summer Undergraduate Research Program. The authors acknowledge Dr. Laurence Court of The University of Texas MD Anderson Cancer Center for useful discussions about this work.

REFERENCES

Masbahi, A., Alizadeh, G., Seyed-Oskoee, G., Azarpeyv, 2012. A new barite-colemanite concrete with lower neutron production in radiation therapy bunkers. Ann. Nucl. Energy, 15, 107-111.

McGinley, H., 2002. Shielding Techniques for Radiation Oncology Facilities. Medical Phys. 9-26.

Polaczek-Grelik, K., et al. 2013. Assessment of radiation exposure outside the radiatherapeutic room during medical accelerator beam emission with the use of TL detectors. Radiation Protection Dosimetry, 156, 268-276.

NUMERICAL SOLUTIONS FOR A CLASS OF NONLINEAR ORDINARY DIFFERENTIAL EQUATIONS

Chibueze S. Ezeudu* and Jahmario L. Williams[#]

Department of Mathematics College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004

ABSTRACT

Consider the following initial value problem,

$$\begin{cases} y'(t) = f(t, y(t)) & \text{ in } (a, b), \\ y(t_0) = y_0, \end{cases}$$
(*)

where $f: (a, b) \times \mathbb{R} \to \mathbb{R}$ is continuously differentiable and satisfies a Lipschitz condition with respect to the second variable, that is, *there exists* L > 0 such that $|f(t,y_1) - f(t,y_2)| \le L|y_1 - y_2|$ for any $(t,y_1), (t,y_2)$ in $[a,b] \times \mathbb{R}$. We shall use the well-know Euler's, Runge-Kutta, and Adam Bashforth methods to approximate the solutions of (*) and compare each method to the true solution. We will analyze the global error, that is,

$$\max_{a \le t \le b} |y(t_n) - y_n| \le ch^p$$

where $y(t_n)$ is the exact solution, y_n is the approximate solution, and $p \ge 1$ is the order of the method. Existence of a unique solution in the neighborhood of $t = t_0$ of (*) is obtain using Picard theorem and in particular we will use Gronwall's inequality to obtain a uniqueness result.

Keywords: Lipschitz, existence, uniqueness, Gronwall Inequality, numeri- cal solution, & nonlinear

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Consider the following initial value problem,

$$\begin{cases} y'(t) = 1 + \sin(y/3) & \text{ in } (0,6), \\ y(0) = 0, \end{cases}$$
(1.1)

where $f(t; y(t)) = 1 + \sin(y/3)$ is nonlinear in y and does not satisfy a superposition principle, that is, the solution can not be written as a linear combination of functions, namely, yc + yp where yc satisfies the
homogeneous equation and yp is a particular solution of (1.1). Existence and uniqueness results of (1.1) is shown using Picard's Theorem and a proof of Picard's Theorem can be found in [1]. Equation (1.1) have been examined by many authors. In particular, we shall use Gronwall's inequality to obtain a uniqueness result for (1.1). A detailed proof of Gronwall's inequality can be found in [2].

RESULTS AND DISCUSSION

Theorem 2.1 (Picard Theorem). Consider the following initial value problem,

$$\begin{cases} y'(t) = f(t, y(t)) & \text{in } (a,b), \\ y(t_0) = \alpha \end{cases}$$
(2.1)

where $f: (a, b) \times R \rightarrow R$ is continuously differentiable on (a, b) and satisfies a Lipschitz condition with respect to the second variable, that is, $\exists L > 0$ such that Then (2.1) has a unique solution in the neighborhood of $t = t_0$.

Remark 2.1 The Lipschitz constant L is given by

. .

$$L = \max_{(t,y) \in [a,b] \times R} \left| \frac{\partial f}{\partial y} \right|$$

Next we shall show that $f(t, y(t)) = 1 + \sin(y/3)$ satisfies a Lipschitz condition with respect to the second variable y. Observe,

$$|f(t, y_1) - f(t, y_2)| = |1 + \sin(y_2 / 3) - (1 + \sin(y_1 / 3))|$$
$$= |\sin(y_2 / 3) - \sin(y_1 / 3)|$$

Let $u = y_2/3$ and $v = y_1/3$. Then by the Mean Value Theorem $\exists c$ between u and v such that

$$\begin{cases} y'(t) = 1 + \sin(y/3) & \text{in } (0,6), \\ y(0) = 0, \end{cases}$$
(1.1)

Therefore,

$$|f(t, y_1) - f(t, y_2)| = |1 + \sin(y_2 / 3) - (1 + \sin(y_1 / 3))|$$

= $|\sin(y_2 / 3) - \sin(y_1 / 3)|$
 $\leq |y_2 / 3 - y_1 / 3|$
= $\frac{1}{3}|y_2 - y_1|$

where L = 1/3 is the Lipschitz constant. Hence (1.1) satisfies a Lipschitz condition and therefore has a unique solution in the neighborhood of $t_0 = 0$.

Lemma 2.1 (Gronwall's Inequality). Let $A, B \ge 0$ and

$$f(t) \le A + B \int_{\alpha}^{t} f(s) ds$$

Then,

 $f(t) \leq A e^{B(t-\alpha)}$

We know that equation (1.1) has a unique solution in the neighborhood of t0 = 0 since f (t, y(t)) = 1 + sin(y/3) satisfies a Lipschitz condition with respect to the second variable y. Next we shall obtain a uniqueness result of (1.1) as an application of Gronwall's Inequality.

Indeed, suppose that (1.1) has two solutions, namely, u and v. Let w = u - v.

Then

$$\begin{cases} w'(t) = \sin(u/3) - \sin(v/3) & \text{in } (0,6) \\ w(0) = 0, \end{cases}$$
(2.3)

Integrating (2.3) from 0 to t and using the fact that the right-hand sides satisfies a Lipschiptz condition implies

$$\left|w(t)\right| = \left|0 + \frac{1}{3}\int_{0}^{t} \left|w(s)\right|\right| ds$$

We shall proceed by approximating the solutions of (1.1) for i = 1, ..., n by Euler's, Runga-Kutta, and Adam-Bashforth methods respectively:

$$(M1) y_{i+1=}y_i + hf(t_i, y_i)$$

$$(M2)y_{i+1} = y_i + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4); \text{ where}$$

$$k_1 = hf(t_i, y_i)$$

$$k_2 = hf(t_i + \frac{1}{2}h, y_i + \frac{1}{2}k_1)$$

$$k_3 = hf(t_i + \frac{1}{2}h, y_i + \frac{1}{2}k_2)$$

$$k_4 = hf(t_i + \frac{1}{2}h, y_i + k_3)$$

$$(M3) y_{i+1} = y_i + (\frac{1}{24})(55f(t_i, y_i) - 59f(t_{i-1}, y_{i-1}) + 37f(t_{i-2}, y_{i-2}) - 9f(t_{i-3}, y_{i-3})$$

The true solution of (1.1) is given by

 $y(t) = -6\tan^{-1}\left(\frac{t}{t-6}\right)$

ACKNOWLEDGEMENTS

This study was supported by Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

 Pablo Are's-Gastesi and T. N. Venkataramana. The big Picard theorem and other results on Riemann surfaces. *Enseign. Math.* (2), 55(1-2):127–137, 2009.

[2] Xueru Lin. A Note on Gronwall's Inequality on Time Scales. Abstr. Appl. Anal., pages Art. ID 623726, 4, 2014.

ON THE SOLUTIONS OF $x_{n+1} = \frac{f(x_n)}{x_{n-1}}$, where f is piecewise linear

Marquesha Foreman* and Roderick B. Holmes[#]

Department of Mathematics College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004

ABSTRACT

Our goal in this paper is to examine the long-term behavior of solutions of the following difference equation $x_{n+1} = \frac{f(x_n)}{x_{n-1}}$, where *f* is piecewise linear, and the initial values x_{-1} and x_0 are non-zero real numbers. We examine the boundedness, periodicity, and the existence of oscillatory solutions.

Key words: boundedness, periodicity, oscillatory

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

In this paper, we are concerned with solutions of the difference equation

$$x_{n+1} = \frac{f(x_n)}{x_{n-1}}$$
(1)

Equation (1) has been studied in several works including papers by R. M. Abu-Saris, Saris and AI-Jubouri, B.D. Mestel and the book by Kulenovic and Ladas. In these works it was required that f be positive and continuous on $(0, \infty)$. Generally these restrictions will not be necessary in this work. We do however require that f be piecewise linear. One of our main concerns will be in determining how initial conditions effect periodicity as well as possible periods of solutions. There are cases where formulas for general solutions are obtained and solutions may not be periodic but have other interesting behavior.

The initial conditions to be considered are as follows

$$(c_1): 0 < x_{-1}, x_0$$
$$(c_2): x_{-1} < 0 < x_0$$
$$(c_3): x_{-1}, x_0 < 0$$

 $(c_4): x_0 < 0 < x_{-1}$

Additionally, certain conditions on the function f will be used. These are

$$(H_1): f(x) = \begin{cases} A, \ x > 0 \\ B, \ x < 0 \end{cases} \text{ where } A > 0, B < 0$$
$$(\overline{H_1}): f(x) = \begin{cases} A, \ x > 0 \\ B, \ x < 0 \end{cases} \text{ where } A < 0, B > 0$$

COSET SURP 2014

$$(H_{2}): f(x) = \begin{cases} Ax, & x > 0 \\ B, & x < 0 \end{cases} \text{ where } A > 0, B < 0$$
$$(\overline{H_{2}}): f(x) = \begin{cases} Ax, & x > 0 \\ B, & x < 0 \end{cases} \text{ where } A < 0, B > 0$$
$$(H_{3}): f(x) = \begin{cases} Ax, & x > 0 \\ Bx, & x < 0 \end{cases} \text{ where } A > 0, B < 0$$
$$(\overline{H_{3}}): f(x) = \begin{cases} Ax, & x > 0 \\ Bx, & x < 0 \end{cases} \text{ where } A > 0, B < 0$$
$$(H_{4}): f(x) = \begin{cases} 1 + x, & x > 0 \\ 1, & x < 0 \end{cases}$$

Remark: The cases $f(x) = \begin{cases} Ax, x > 0 \\ Bx, x < 0 \end{cases}$ where A, B have the same sign are omitted.

Recall that a solution of (1) is periodic of period p if $x_{n+p} = x_n$ for all $n \ge -1$ and eventually periodic if there exists an integer k such that $x_{n+p} = x_n$ for all $n \ge k$. Since the range of a periodic sequence is finite it follows that periodic sequences are always bounded. On the other hand, there are bounded sequences that are not periodic. Convergent sequences with an infinite range are bounded but not periodic.

RESULTS

THEOREM 1 Assume (H_1) holds

- a) Let $\{x_n\}$ be a solution of (1) such that (c_1) holds, then $\{x_n\}$ is periodic with period 4.
- b) Let $\{x_n\}$ be a solution of (1) such that (c_2) , (c_3) , or (c_4) holds, then $\{x_n\}$ is periodic with period 12.

THEOREM 2 Assume $(\overline{H_1})$ holds

- a) Let $\{x_n\}$ be a solution of (1) such that (c_3) holds, then $\{x_n\}$ is periodic with period 4.
- b) Let $\{x_n\}$ be a solution of (1) such that (c₁), (c₂), or (c₄) holds, then $\{x_n\}$ is periodic with period 12.

THEOREM 3 Assume (H_2) holds

- a) Let $\{x_n\}$ be a solution of (1) such that (c_1) holds, then $\{x_n\}$ is periodic with period 6.
- b) Let $\{x_n\}$ be a solution of (1) such that (c_2) , (c_3) , or (c_4) holds, then $\{x_n\}$ is periodic with period 9.

THEOREM 4 Assume $(\overline{H_2})$ holds

a) Let $\{x_n\}$ be a solution of (1) such that (c₁) holds. Let $r = \frac{x_0}{x_{-1}}$. The general solution of (1) is given by $x_n = r^{2k-1}x_n + r^{2k}x_n + r^$

$$by x_{6k-1} = r^{2k-1}x_0, x_6 = r^{2k}x_0, x_{6k+2} = \frac{2}{r^{2k}x_0}, x_{6k+3} = \frac{2}{r^{2k+1}x_0}, x_{6k+4} = \frac{2}{r^{2k+1}x_0}$$

b) Let $\{x_n\}$ be a solution of (1) such that (c_2) holds. Let $= \frac{A}{x_{-1}}$. The general solution of (1) is given by $x_{6k-1} = \frac{A}{t}$, $x_{6k} = t^{2k}x_0$, $x_{6k+1} = t^{2k+1}x_0$, $x_{6k+2} = At$, $x_{6k+3} = \frac{B}{t^{2k+1}x_0}$, $x_{6k+4} = \frac{B}{t^{2k+2}x_0}$.

Moreover, these solutions are oscillatory.

c) Let $\{x_n\}$ be a solution of (1) such that (c_3) holds, then $\{x_n\}$ is periodic with period 4.

d) Let $\{x_n\}$ be a solution of (1) such that (c_4) holds. Let $=\frac{A}{x_0}$. The general solution of (1) is given

$$by \ x_{6k} = \frac{A}{u}, \ x_{6k+1} = \frac{Bu^{2k}}{x_{-1}}, \ x_{6k+2} = \frac{Bu^{2k+1}}{x_{-1}}, \ x_{6k+3} = Au, \ x_{6k+4} = \frac{x_{-1}}{u^{2k+1}}, \ x_{6k+5} = \frac{x_{-1}}{u^{2k+2}}.$$

Remark: To show that the formulas in the above theorem part *d*) are correct we use the following illustration

$$x_{6k+2} = \frac{f(x_{6k+1})}{x_{6k}} = \frac{\frac{ABu^{2k}}{x_{-1}}}{\frac{ABu^{2k}}{u}} = \frac{Bu^{2k+1}}{x_{-1}}$$

THEOREM 5 *Assume* (*H*₃) *holds*

Let $\{x_n\}$ be a solution of (1) such that (c_1) , (c_2) , (c_3) , (c_4) holds, then $\{x_n\}$ is periodic with period 6.

THEOREM 6 Assume $(\overline{H_3})$ holds

Let $\{x_n\}$ be a solution of (1) such that (c_1) , (c_2) , (c_3) , (c_4) holds, then $\{x_n\}$ is periodic with period 12.

THEOREM 7 Assume (H_4) holds

a) Let $\{x_n\}$ be a solution of (1) such that (c_1) holds, then $\{x_n\}$ is periodic with period 5.

b) Let $\{x_n\}$ be a solution of (1) such that (c₂) holds. Let $v = \frac{x_0}{x_{-1}}$. The general solution of (1) is given

$$by x_{4k-3} = v x_0^{k-2} (1+x_0), \ x_{4k-2} = \frac{1}{v x_{-1}}, \ x_{4k-1} = \frac{1}{v x_0^{k-1}}, \ x_{4k} = v x_{-1}.$$

c) Let $\{x_n\}$ be a solution of (1) such that (c_3) holds, then $\{x_n\}$ is periodic with period 4.

d) Let $\{x_n\}$ be a solution of (1) such that (c_4) holds. Let $= x_{-1}x_0$. The general solution of (1) is given by $x_{4k-3} = \frac{x_0}{z}$, $x_{4k-2} = \frac{1+x_{-1}}{zx_{-1}^{k-1}}$, $x_{4k-1} = \frac{z}{x_0}$, $x_{4k} = zx_{-1}^{k-1}$.

ACKNOWLEDGEMENTS

This study was supported by TSU College of Science, Engineering, and Technology (COSET) Summer Undergraduate Research Program (SURP) and Professor W. E. Taylor, Department of Mathematics

REFERENCES

Abu-Saris, R.M., Characterization of rational periodic sequences, Journal of Difference Equations and Applications 2000, Vol. 6, pp. 233-242.

Mestel, B.D., On globally Periodic Solutions of the difference equation $x_{n+1} = \frac{f(x_n)}{x_{n-1}}$, Journal of Difference Equations and Applications 2003, Vol. 9(2), pp.201-209.

DISEASES AND AVIATION

Micah Harper* and Vernon J. Baker*

Department of Aviation Science and Technology College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004

ABSTRACT

One place you should stay away from when sick is an airport. Why, because a viral pandemic could arise if you didn't. When you enter an airport sick, it's possible to leave traces of bacteria: on your luggage entering security clearance, the boarding pass given to the attendant before catching a flight, and even the aircraft you're boarding! When you inhale/exhale on an airplane, your germs are being recirculated through the air conditioning system in the fuselage, this may infect many passengers on the plane with you. A sars patient on an international flight in 2002 affected 20 passengers before the plane reached its destination. During the influenza pandemic in 2009, the heath protection agency prescreened passengers prior to them boarding aircraft to the United Kingdom and found that 1 out of 6 passengers were infected with diseases. Given the effects aviation has on disease spread, the health protection agency established two primary solutions to prevent airport induced outbreaks; the first is to cancel a proportion of flights from a country reported with a specific amount of pandemic cases. The second is to identify sick patients before they board commercial aircraft, if there are sick patient(s) on board, public health authorities should obtain contact information of exposed travelers from the respective airline so they may be contacted and offered intervention. This article will talk about possible infections people are exposed to during flight, major pandemics involving aviation, and good preventative methods for combating these pandemics along with success rates.

Key words: Infection in aircraft, Disease spread

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Hypothesis: when you are sick, it is best to always stay home because viral pandemics arise when you don't. The reason for this is because germs are quite fast at spreading, but just how fast? According to centers for disease control and prevention, healthy adults may be able to infect other people beginning one day before symptoms develop and up to 5 to 7 days after becoming sick. Children may pass the virus for longer than 7 days.

Viruses spread mainly by droplets made when people with a flu cough, sneeze or talk; these drops can enter another person's mouth or nose, and begin to replicate new viral cells immediately. Finally viruses can live on objects between one to two days on nonporous surfaces, and 8 to 12 hours on porous surfaces. That means that it's possible to pick up a flu just by touching a doorknob, shopping cart, keyboard, or eating a meal prepared by an infected person

FACTS

Each day, approximately 4.5 million iata members travel on airplanes daily and 1.65 billion iata + non-iata members fly daily. During the influenza pandemic in 2009, the heath protection agency prescreened passengers prior to them boarding aircraft to the united kingdom and found that 1 out of 6

39

passengers were infected with diseases. Given how viruses spread through small droplets and their long survival duration on objects, it's possible to leave traces of bacteria: on your luggage entering security clearance, the boarding pass that you handed to the attendant before catching your flight, and even the aircraft you're boarding!

PRECONDITIONS FOR VIRAL TRANSMISSION ON AIRPLANES

- 1) When you inhale/exhale on an airplane, your germs are being recirculated through the air conditioning system in the fuselage, the air conditioner operates this way because hypoxia and other decompression sicknesses rule out possibilities of airplanes having functional windows, so the recirculated air that's now carrying your germs may infect many passengers on the plane with you.
- 2) The second culprit that makes disease transmission rapid on airplanes is the low cabin humidity followed by the low humidity of ambient air due to the high elevations that airplanes operate. At elevation ranges of 30,000 to 35,000 feet, humidity drops by 10% and so does the mucus membranes in our throats and noses which is our first line of defense against sicknesses
 - Airborne infectious diseases transmitted during commercial air travel are of concern to public health officials; in 2002, 20 people on an international flight were infected by a single sars patient,

INDUSTRY REMEDIES

- New jet engines can now draw fresh air from outside the plane and compress cold and extremely thin air from outside the plane until its pressure matches that of the cabin. Next, it passes through highefficiency particulate air (hepa) filters (which remove a minimum of 99.97% of any airborne particulates, bacteria and viruses) and combining with recirculated cabin air.! The existing air onboard the aircraft is then removed by aircraft exhaust valves.
- 2) Many passenger aircraft are now designed in a way that the cabin air conditioners recirculate air from top to bottom and not forward to back, boeing and other aircraft engineers went with this design to keep air supply on aircraft localized so we won't share someone else's air across the cabin.

EPA GETS ON AIRLINES IN 2005

- 1) Federal testing in the bathrooms and kitchens of 169 passenger airplanes, found coliform in nearly 1 in 5 of the aircraft.
- 2) EPA tested planes at 12 airports, finding coliform at seven. The biggest offender was Miami International Airport, where 39 percent of the country's positive tests were found
- 3) EPA found 3.6% of the water samples tested positive for fecal bacteria

In conclusion, there is a positive correlation between diseases and aviation. The next time you're packing your carry-on for a flight, side with the disinfectant wipes and hand sanitizer over the filter mask; at the end of the day, it's coming into contact with a plane's countless potentially infected surfaces that's going to do you in — not the cabin's air supply

ACKNOWLEDGEMENTS

This study was supported by TSU College of Science, Engineering, and Technology Summer Undergraduate Research Program.

GENETIC DISTANCE BETWEEN TWO "ALLOPATIRC" ISLAND HAWK-OWLS: NINOX PHILIPPENSIS AND NINOX SPILOCEPHALA BASED ON NEARLY COMPLETE MITOCHONDRIA GENOMES

Amanda Nicole Jackson* and Hector C. Miranda Jr.[#]

Department of Biology College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



Ninox philippensis

Ninox spilocephala

ABSTRACT

Philippine Hawk-Owl Ninox philippensis is an island endemic scattered in difference islands of the Philippine achipelago. More recently, the species was split into seven allopatric species based on morphology and vocalization. This is predicted on the assumption that voice plays a major part in species recognition and species integrity. At present, no genetic studies have been conducted in this group of birds. To test pat of the taxonomic revision and the validity of voice as character in delineation of species, we sequenced the whole mitochondrial genome of two of the seven allopatric species; the Luzon Hawk-Owl Ninox philippensis found in Luzon, Samar and Leyte islands, and the Mindanao Hawk-Owl Ninox spilocephala found in Minanao Island. We sequenced the complete mitochondrial genome of N. philippensis which comprises of 16, 227 bp (not annotated), while N. spilocephala is about 80 % sequenced. We aligned both sequences with another Ninox sequence and calculated the DNA sequence similarity based on three models of molecular evolution. The Jukes and Cantor model, the HKY model, and Hasegawa model. Overall sequence divergence based on aligned 4,370 bp among N. philippensis, N. spilocephala and the reference taxa N. novaeseelandiae from New Zealand showed that genetic similarity between the allopatric species was 97.5% and that both were genetically similar to the New Zealand endemic by 90.0%. Based on the molecular clock calibration of 2 percent mutation rate every 1 million years for mitochondrial genes, we surmise the two allopatric species were separated by at least 1 million years.

Key words: Philippine Hawk-Owl, Migration, Mitochondrial genome sequencing, PCR

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Philippine Hawk-Owl *Ninox philippensis* is an island bird scattered in different islands of the Philippine archipelago. More recently, the species was split into seven allopatric species based on morphology and vocalization. This is predicted on the assumption that voice plays a major part in species recognition and species integrity. Unlike diurnal birds, nocturnal birds rely on voice for mate recognition, and less on plumage coloration. At present no genetic studies have been conducted in this group of birds. To test part of the taxonomic revision and the validity of voice as character in delineation of species, we sequenced the whole mitochondrial genome of two of the seven allopatric species; the Luzon Hawk Owl-*Ninox philippensis* found in Luzon, Samar and Leyte islands, and the Mindanao Hawk-Owl *Ninox spilocephala* found in Mindanao.

Although species delineation based on DNA sequence is a rough and temporary to all to evaluate species divergence, it is an important piece of genetic evidence. Nonetheless, mitochondrial genes have been calibrated to have a mutation rate of 2% per million years. Thus, many birds is indicative of significant lack of gene flow and speciation event.



Figure 1. Map of the Philippine islands showing the distribution of Luzon Hawk-Owl Ninox philippensis (in green) and Mindanao Hawk-Owl Ninox spilocephalus (in blue)

METHODS

Primers were designed using Primer3Plus and Genious Pro 5.5 (Biomatters , New Zealand). We did not use degenerated primers to avoid amplification of non-target loci. PCR was carried out in a total volume of 25 μ L containing 10-50ng of template DNA 4 μ L of deionized water, 4 μ L 10 mM of each dNTP, and 8 μ L of AmpliTaq 360 Gold Polymerase Master Mix (Life Technologies) . A total of 27 primer pairs were used (S1). In cases where primer pairs failed, nearest adjacent 3' end fragment that worked, or the reverse primer of the target fragment and the forward primer of the 5' end adjacent fragment (Table 1 and 2) designed new species- specific primers using the known flanking sequences for 'two-way primer walk'. The PCR cycles were as follows: one cycle of 10 min at 95° Celsius, 35 cycles of 20 second at 95° Celsius, 20 seconds at 60° Celsius and 50 seconds at 72° Celsius. The process was completed with a final elongation at 72° Celsius for 10 minutes. These parameters were adjusted depending on desired level of stringency and size of target region. All amplifications were performed on Verti Thermal Cyclr (Life Technologies). Capilary sequencing was accomplished on ABI siquencers by Operon/Eurofin (Alabama).

Chromaographs were viewed in FinchTV, imported and assemebled in Geneious Pro 5.5 using Clustal W NA reads were cross-referenced to chromatographs for verification. The finals assembly was annotated and gene position and structure defined. The correct open reading frames of coding genes were check and corrected using Expassy.

To measure the genetic divergence between the two species, we compared distances on 11 proteincoding genes sequences, as well as the two ribosomal genes; 12S rRNA and 16S rRNA based on JC (Jukes and Cantor 1969) HKY (Hasegawa et al. 1985) and Tamura-Nei (Nei 1993) DNA substitution models.



Figure 2. Flowchart to DNA sequence generation and mitogenome assembly. A)whole genome isolation, B) PCR (Veriti thermal cycler), C) gel electrophoresis, D) capillary sequencing, E) chromatograph generation, and F) sequence alignment, genome assembly, and annotations.

RESULTS AND DISCUSSION

We sequenced the complete mitochondrial genome of *N. philippensis* which comprises 16,227 bp (not annotated). While *N. spilocephala* is about 80% sequenced. We aligned both sequences with another Ninox sequence and calculated the DNA sequence similarity based on three models of molecular evolution ; the Jukes and Cantor model, the HKY model and Hasegawa model. Overall sequence divergence based on aligned 4,370 bp among *N. philippensis*, *N. spiolocephala*, and the reference taxa *N*.

novaeseelandiae from New Zealand showed that the genetic similarity between the allopatric species was 97.5% and that both were genetically similar to the New Zealand endemic by 90.0 percent. Based on the molecular clock calibration of 2 percent every 1 million years for mitochondrial genes, we surmise that the two allopatric species were separated by at least 1 million years. This divergence time estimate supports part of the recent taxonomic adjustment for the group.



Figure 3. PCR strategies to amplify missing regions. 1) PCR using forward primer of fragment 1 and reverse primer of fragment 2 (adjacent 3' end fragment), or 2) PCR using forward primer of fragment 2 and reverse primer of fragment 3. Amplitaq 360 Gold Polymerase have worked in DNA fragments larger than 2 kb.

Table 1. Genetic sequence divergence between two allopatric *Ninox* (*N. philippensis* and *N. spilocephalus*) and both with reference sequence *N. novaeseelandiae* from New Zealand. A) matrix based on Jukes and cantor model, B) HKY model, and C) Tamura Nei model. (A)

	(A)		
	Ninox nov	Ninox phili	Ninox spil
Ninox novaeseelandia		0.095	0.100
Ninox philippensis 15	0.095		0.025
Ninox spilocephalus 1	0.100	0.025	

	(B)		
	Ninox nov	Ninox phili	Ninox spil
Ninox novaeseelandia		0.097	0.103
Ninox philippensis 15	0.097		0.025
Ninox spilocephalus 1	0.103	0.025	

	(C)		
	Ninox nov	Ninox phili	Ninox spil
Ninox novaeseelandia		0.098	0.103
Ninox philippensis 15	0.098		0.025
Ninox spilocephalus 1	0.103	0.025	

ACKNOWLEDGEMENTS

This project was supported by TSU COSET Summer Undergraduate Research Program. This project is also indirectly supported by NASA URC Center for Bionanotechnology and Environmental Sciences (CBER). This project is part of the Miranda Lab initiative on Undergraduate Research on Genomics and Evolution Studies (URGES), in collaboration with Dr. Daniel Brooks of the Houston of Natural Science

TRICLOSAN IN WHITE OAK BAYOU, HOUSTON

¹Charese Jeffries* and ²Hyun-Min Hwang[#]

¹Department of Chemistry ²Department of Environmental and Interdisciplinary Sciences College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

Antimicrobial agents such as triclosan (TCS) and triclocarban (TCC) have been added to many personal care products, especially liquid hand soaps and detergents. Due to tremendous amount of consumption and less efficient removal in wastewater treatment plants, TCS and TCC have been detected at high levels in urban water ways receiving treated wastewater. This study investigated occurrence of TCS in the surface water of White Oak Bayou in Houston, TX. Water samples collected from 7 sites along the bayou covering entire White Oak Bayou. These samples were extracted using C₁₈ solid phase extraction (SPE) cartridges for the measurement of TCS. Identification and quantification of TCS was performed using gas chromatograph-mass spectrometer (GC/MS). Concentrations of TCS varied from 247 to 398 ng/L. Because TCS is a manmade chemical, its presence indicates that entire White Oak Bayou is contaminated by TCS. Higher concentrations were detected at sites below effluent outfalls of treated wastewater. This study suggests that effluents from wastewater treatment plants are a major source of TCS in urban water columns. To reduce urban water contamination by emerging contaminants like TCS, wastewater treatment processes need to be enhanced.

Key words: Personal care products, Triclosan, Antimicrobial products, Urban water contamination

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Triclosan (TCS) is a pesticide that was first registered with the Environmental Protection Agency (EPA) in 1964. Triclosan is relatively stable, lipophilic compound with an octanol-water partitioning coefficient of 4.8. The solubility of TCS in water is 0.01 g/L. TCS has been shown to phototransform into chlorinated dibenzodioxins, such as 2, 8-dichlorodibenzo-p-dioxin (Halden and Paull 2005). It has also been known to transform into DCP (2, 4-dichlorophenol) (Halden 2014). Methyl triclosan (MeTCS) is a metabolite of TCS which is known to be more stable, environmentally persistent and more lipophilic than the parent compound with a Kow of a 5.2 (Coogan, et al. 2007) The potential risk include exposure via

inhalation and dermal contact. Due to use of cosmetic and personal care products, household products and articles containing triclosan. The ranges of TCS in cosmetics and household personal care products are from <0.01-0.5% and in household goods ranges from 0.04-0.3%; the rate of it is not expected to cause any irritant effect. (McClellan and Halden 2010).

METHODS

The samples were taken along the White Oak Bayou. The samples were collected in 1-L bottles which were placed on ice until arrival to the lab. The samples were then placed in the refrigerator at 4° C until further analysis. The samples were extracted using C₁₈ solid phase extraction (SPE) cartridges (Figure 2) and analyzed using gas chromatograph-mass spectrometer (Figure 3).



Figure 1. A personal care product containing triclosan as an active ingredient.



Figure 2. Extraction of triclosan in water samples using C₁₈ solid phase extraction (SPE) cartridges.

RESULTS AND DISCUSSION

Triclosan was detected in all samples collected along the entire White Oak Bayou. Concentrations of triclosan in White Bayou surface water were highly variable and didn't show any increasing or decreasing trends. Higher concentrations were found in samples collected from site below the treated wastewater discharge pipe. Decrease of triclosan was probably due to photodegradation in water and dilution by overflow of gardening water that entered into the bayou.

Triclosan is a manmade chemical and thus detection of this compound indicates that input of treated and/or untreated wastewater. The results showed the occurrence of triclosan in the bayou was due to the

effluent from the wastewater treatment plant. TCS can disrupt the aquatic environment because of their endocrine disruptor properties, so wastewater treatment processes need to be enhanced to reduce urban water contamination by this emerging toxic chemical.



Figure 3. Triclosan in water samples were quantified using gas chromatograph-mass spectrometer.



Figure 4. Concentrations of triclosan in water samples collected from White Oak Bayou.

ACKNOWLEDGEMENTS

This study was supported by Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

- Coogan, Melinda A., Regina E. Edziyie, Thomas W. La Point, and Barney J. Venables. 2007. "Algal bioaccumulation of triclocarban, triclosan, and methyl-triclosan in a North Texas wastewater treatment plant receiving stream." *Chemosphere* 1911-1918.
- Halden, Rolf U. 2014. "On the need and spped of regulating triclosan and triclocarban in the united states." *Environmental Society and Technology* 3603-3611.
- Halden, Rolf U., and Daniel H. Paull. 2005. "Co-Occurrence of Triclocarbana nd Triclosan in U.S. Water Resources." *Environmental Science and Technology* 1420-1426.

Lozano, Nuria, Clifford P. Rice, Mark Ramirez, and Alba Torrents. 2013. "Fate of Triclocarban, Triclosan, and Methyltriclosan during wastewater and biosolids treatment processes." *Water Research* 4519-4527.

McClellan, Kristin, and Rolf U. Halden. 2010. "Pharmaceuticals and personal care products in archived U.S. biosolids from the 2001 EPA national sewage sludge survey." *Water Research* 658-668.

COMPARISON OF DYNAMICS OF BOOLEAN NETWORKS AND NETWORKS OF ORDINARY DIFFERENTIAL EQUATIONS (ODE) SYSTEMS

Franklin Kigwe* and Yunjiao Wang[#]

Department of Mathematics College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

Networks of ordinary differential equations (ODEs) have been used widely to study activities of biological networks including gene regulatory networks. Comparing with systems of ODEs, Boolean network models need less information to set up and are relatively easy to study. It is well known that dynamics of network systems is constrained by their network structures. Networks of Boolean systems and ODEs share similar dynamics if they have the same network structures. However, the relations between the two types of systems are not very clear. In this work, we investigate such possible relations.

Keywords: Boolean network. Ordinary differential equations. Dynamical systems.

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Gene regulatory networks have attracted many attentions due to the progresses in technology. Understanding of the dynamics of gene regulatory networks may shed insights into our life and leads to novel treatments for a wide range of diseases. Mathematical modeling has shown its indispensable role in unveiling network dynamics. Both coupled differential equations and Boolean functions are popular for modeling gene regulatory networks. Coupled differential equations have the advantage that can provide more detailed information about its target biological system while Boolean models require much less information to set up. Due to constrain from their network structures, the two types of network systems share certain dynamics. The introduction of the relationships between the two types of models will enable us to leverage their advantages and better understand the target network systems. In this paper, we investigate such relations by comparing the dynamics of feedback loops.

Network systems are often represented by directed graphs, wherein nodes and interactions represent components by arrows. A *feedback loop* is a directed graph as shown in Figure 1, where an arrow with open circle end is either inhibiting or activating. If the number of inhibitory arrows is odd, then the loop is a negative feedback loop; otherwise the loop is a positive feedback loop.



Figure 1. A feedback loop where an arrow with open circle end is either inhibiting or activating.

An *n*-node Boolean network is a discrete dynamical system with the form of

$$x_i(t+1) = f_i(x_1(t), x_2(t), \dots, x_n(t))$$

where x_i is the state variable of the i^{th} node, and f_i is a Boolean function with the value being either 0 or 1. Boolean networks have been widely used to model biological regulatory networks [2, 4, 13]. They can be set up in situations where detailed kinetic characterization of interaction is not available and provide valuable insights. However, Boolean Systems cannot faithfully represents dynamics of biological networks that evolve continuous in time [7].

An *n*-node ODE network has the form

$$x_i = F_i(x_1, x_2, \ldots, x_n), \quad i = 1, 2, \ldots, n$$

where x_i is the state variable of the *i*th node, and F_i describes how x_i depends on other variables.

DYNAMICS OF NETWORKS OF ODES

In this section, we will associate to each *n*-node network a set of ODEs and Boolean functions. An associated *n*-node ODE model consists of a set of equations that are in the form of

$$\frac{dx_i}{dt} = -\gamma_i x_i + f_i(\sum_{j,i\neq j} w_{ij} x_j); \ i = 1, \dots, n$$
(1)

where $f_i(x) = \frac{1}{1+e^{-\sigma_i(a_i+x)}}$ is a monotonically increasing function, γ_i , σ_i and a_i are parameters, and w_{ij} is positive if there is a positive input from node *j* to node *i*, w_{ij} is negative if the input from node *j* to *i* is negative, $w_{ij} = 0$ if there is no arrow from node *j* to node *i*. We will investigate relations between (a) steady-states; (b) oscillations of systems of ODEs and the associated Boolean systems. We will also explore the relations between network structures and bifurcation types by using numerical and analytical bifurcation analysis methods.

Lemma 4.1 Suppose the network associated to system (1) is a negative feedback loop.

Then the system has a unique equilibrium.

Proof. An equilibrium $X_0 = (x_1, x_2, ..., x_n)$ of system (1) satisfies:

$$-\gamma_i x_i + f_i(\sum_{j,i\neq j} w_{ij} x_j) = 0$$

where $i = 1, ..., n$.

Hence,

$$x_i = f_i(\sum_{j,i\neq j} w_{ij} x_j) / \gamma_i$$

Let $h_i(x) = f_i(\sum_{j,i\neq j} w_{ij} x_j) / \gamma_i$. Then $\frac{\partial}{\partial x_j} h_i(x) > 0$ if $w_{ij} > 0$ and $\frac{\partial}{\partial x_j} h_i(x) < 0$ if $w_{ij} < 0$. i.e. $h_i(x)$ is an increasing function if $w_{ij} > 0$, and decreasing if $w_{ij} < 0$.

Since the network is a negative feedback loop as in Figure 1, node 1 has only one input from node n and node k has only one input form node k-1 for any 1 < k < n. Hence,

$$x_{1} = h_{1}(x_{n})$$
$$x_{k} = h_{k}(x_{k-1})$$

for all $1 < k \le n$. It follows that $x_1 = h_1 \circ h_n \circ h_{n-1} \circ \cdots \circ h_2(x_1)$. Since h_k

are monotonically functions and the network is a negative feedback, $h_1 \circ h_n \circ h_{n-1} \circ \cdots \circ h_2$ is a monotonically decreasing function. Hence, there is a most one equilibrium. Next we show the existence of such equilibrium. Note that when x = 0, $h_1 \circ h_n \circ h_{n-1} \circ \cdots \circ h_2(x) > 0$ and when $x \to \infty$, $h_1 \circ h_n \circ h_{n-1} \circ \cdots \circ h_2(x) > 0$. By intermediate value theorem, there exists a value of x, such that $x = h_1 \circ h_n \circ h_{n-1} \circ \cdots \circ h_2(x)$. Therefore there exists a unique solution to a negative feedback loop of the ODE system (1). Q.E.D.

Theorem 1. Let $X_0 = (x_1, x_2, \dots, x_n)$ be an equilibrium of an *n*-node negative feedback loop with associated equations in the form of (1).

Suppose $\gamma_i = \gamma > 0$, then

1. the eigenvalues of the Jacobian matrix at the equilibrium are

$$\lambda_k = -\gamma + |\prod_{i=1}^n \gamma x_i (1 - x_i) \sigma_i v_{i,i+1}|^{\frac{1}{n}} e^{i(\frac{\pi}{n} + \frac{2k\pi}{n})}$$

where k = 0, 1, ..., n-1.

- 2. when n=2, the unique equilibrium is always stable
- 3. when $n \ge 3$, a branch of periodic solutions may occur via Hopf Bifurcation.

Proof. Without loss of generality, we can assume $\gamma = 1$. The Jacobian matrix of (1) has the form of

 $\left(\begin{array}{ccccc} -1 & 0 & \cdots & 0 & f_{1n} \\ f_{21} & -1 & \cdots & 0 & 0 \\ \vdots & \vdots & \cdots & \vdots & \vdots \\ 0 & 0 & \cdots & f_{n,n-1} & -1 \end{array}\right)$

So the characteristic equation of the Jacobian matrix at the equilibrium is

$$0 = (\lambda + 1)^n - f_{1n} f_{21} \cdots f_{n,n-1} = (\lambda + 1)^n - \prod_{i=1}^n x_i (1 - x_i) \sigma_i v_{i,i+1}$$

Hence,

$$(\lambda + 1)^n = \prod_{i=1}^n x_i (1 - x_i) \sigma_i v_{i,i+1}$$

Note that when the feedback loop is negative, the right hand side of the above equation is negative. Let

$$\Delta = \prod_{i=1}^{n} x_i (1-x_i) \sigma_i v_{i,i+1} = |\Delta| e^{i\pi}$$

then,

51

$$\lambda = -1 + |\Delta|^{\frac{1}{n}} e^{i(\frac{\pi}{n} + \frac{2k\pi}{n})}$$

for $k = 0, 1, \dots, n-1$.

Note that when n=2,

$$\begin{split} \lambda_1 &= -1 + |\Delta|^{\frac{1}{2}} e^{i(\frac{\pi}{2})} = -1 + i |\Delta|^{\frac{1}{2}} \\ \lambda_2 &= -1 + |\Delta|^{\frac{1}{2}} e^{i(\frac{\pi}{2} + \pi)} = -1 - i |\Delta|^{\frac{1}{2}} \end{split}$$

It follows that the two eigenvalues have negative real parts. Hence, negative feedback loop with only two nodes must only have a stable equilibrium.

when $n \ge 3$, the pair of conjugate roots have the largest real parts:

$$-1 + |\Delta| \cos(\frac{\pi}{n}) = -1 + |\prod_{i=1}^{n} x_i(1 - x_i)\sigma_i v_{i,i+1}| \cos \frac{\pi}{n}.$$

Note that we can vary σ_i or $v_{i,i+1}$ so that the real part changes from negative to positive and leave other eigenvalues with negative real parts. Therefore, oscillations occur through stable Hopf bifurcation. Q.E.D.

DYNAMICS OF NEGATIVE FEEDBACK LOOPS OF BOOLEAN FUNCTIONS

With a given interaction network, there are many ways to choose Boolean functions for the nodes. Here we adapt the well-cited assumptions for the related Boolean functions proposed by Albert and Othmer's [2]. We make the following assumptions, which we will refer the following assumptions as ASSUMPTIONS.

- 1. The effect of activators and inhibitors is never additive, but rather, inhibitors are dominant;
- 2. If activator is on and inhibitor is off, then the node is on in one time step;
- 3. If no activator and background activation, the node is off in one time step.
- 4. Background activation is viewed as an activator that is permanently on.

Next we consider the dynamics of negative feedback loop in Figure 2.



Figure 2. Some negative feedback loops

Dynamics of Negative feedback loop Figure 2

Following the above rule, the dynamics of the two-node network work in Figure 3 can be described by the transition graph in Figure 3. Note that this network admits a cycle.



Figure 3. Boolean network and its transition graph

We assume one of the cells having a background activation. Then there are three cases as shown in Figure 4.



Figure 4. Three-node negative feedback loop

Case I. Assume Node 1 has the background excitation as Figure 5 (left). Then following the rules we set up, the Boolean functions associated the network is Figure 5 (right).



(x_1, x_2, x_3)	$f(x_1, x_2, x_3)$
(0, 0, 0)	(1, 0, 0)
(1, 0, 0)	(1, 1, 0)
(1, 1, 0)	(1, 1, 1)
(1, 0, 1)	(0, 1, 1)
(0, 1, 1)	(0, 0, 1)
(0, 1, 0)	(1, 0, 1)
(0, 0, 1)	(0, 0, 0)
(1, 1, 1)	(0, 1, 1)

Figure 5. Three-node feedback loop and Boolean function in case1.

We can see that (1, 1, 0) is a fixed point and all other points will converge to the fixed point over the time. No cycle exists.

Case II. Assume Node 2 has the background excitation. Again, we can see easily that the system only has a stable fixed point (1, 1, 0). No cycle exists.

Case III. Assume Node 3 has the background excitation. Similarly we can determine its associated Boolean function and transition graph as. Different from other two cases, there exists a cycle with length 6.

RELATIONS OF TWO TYPES OF NETWORK SYSTEMS

Note that when a_i is relatively large, we can summarize the dynamics of negative feedback loops of ODEs systems as following: in some parameter range, the unique equilibrium is stable and no limit cycle exists. Changing the value of a parameter may lead the equilibrium loss its stability and a stable limit cycle may occur via Hopf bifurcation. The corresponding Boolean systems in the other hand, cycles exists either for two-nodes or multi-nodes negative feedback loop while no fixed point.

ACKNOWLEDGEMENTS

This study was supported by Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

- W. Abou-Jaoude, D. Ouattara, and M. Kaufman. From structure to dynamics: frequency tuning in the p53-mdm2 network: Ii differenital and stochastic approaches. Journal of Theoretical Biology, 264(4):1177–1185, 2010.
- W. Abuo-Jaoude, D. Ouattara, and M. Kaufman. From structure to dynamics: frequency tuning in the p53-mdm2 network: I. logical approach. Journal of Theoretical Biology, 258(4):561–577, 2009.
- D. Alais and R. Blake. Grouping visual features during binocular rivalry. Vision Research, 39:4341-4353, 1999.
- R. Albert and H. Othmer. The topology of the regulatory interactions perdicts the expression pattern of the segment polarity genes in drosophila melanogaster. Journal of Theoretical Biology, 233:1–18, 2003.
- B. B. Aldrige, J. M. Burke, D. A. Lauffenburge, and P.K. Sorger. Physicochemical modeling of cell signaling pathways. Nature Cell Biol, 8, 2006.
- U. Alon. Network motifs: Theory and experimental approaches. Nature Reviews Genetics, 8:450, 2007.
- J. Tyson and B. Novak. Functional motifs in biochemical reaction networks. Annu. Rev. Phys. Chem., 61(219-240), 2010.
- M. Banaji and G. Craciun. Graph-theoretic approaches to injectivity and multiple equilibria in systems of interacting elements. Comm. in Math. Sciences, 7(867-900), 2009.
- M. Banaji and G. Craciun. Graph-theoretic approaches to injectivity and multiple equilibria in general chemical reaction systems. Adv. in Appl. Math, 44:168–184, 2010.
- J. Butler, T. Sasao, and M. Matsuura. Average path length of binary decision diagrams. IEEE Trans Comput, 1041-1053(27), 2005.
- C. Campbell, J. Thakar, and R. Albert. Network analysis reveals cross-links of the immune pathways activated by bacteria and allergen. Physical Reveiw. E, Statistical physics, plasmas, fluids and related interdisciplinary topics, 84:031929, 2011.

CLONING AND SEQUENCING OF A PLANT Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) GENE

¹Ray Mbonu*, ²Abigail Newsome, ³Sodipe Ayodoton[#]

¹Department of Chemistry, Texas Southern University, Houston, TX ²Mississippi Valley State University, Itta Bena, MS ³Department of Biology, Texas Southern University, Houston, TX

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) is an enzyme that catalyzes glycolysis by assisting in the breakdown of glucose for carbon molecules and energy. This enzyme is found in both plants and animals. It has been linked to programmed cell death as well as diseases such as Alzheimer's and Parkinson's disease.

The plants chosen for experimenting were spinach, *Spinacea Oleracea*, and Pothos, *Epipremnum Aureum*. Spinach is an edible flowering plant that is rich in vitamins A, C, E, K, calcium, postassium, folic acid, copper, protein just to name a few. Pothos is a long leafy vine that can be grown both at home and in the wild. It is a flowering plant although it is rarely seen in a flower.

After selecting the plant species, the GAPDH gene was isolated from their DNA, cloned, sequenced, and analyzed using bioinformatics tools. A section of the GAPDH gene was amplified via PCR, assessed, purified and ligated into a plasmid vector. The DNA was then transformed before being isolated and analyzed by restriction digestion. The resulting DNA was sequenced and analyzed.

MATERIALS & METHODS

DNA Extraction

Both the spinach and pothos leaves, in separate microcentrifuge tubes, were grinded using a micropestle and spun in a centrifuge, in silica spin columns. The supernatant was removed; ethanol was added to the DNA, which helps it bind to the silica membrane filter in the spin columns, before they were centrifuged again. The resulting purified DNA is then removed from the spin column. The positive controls used were pGAP and Arabadopsis. Sterile water was used as the negative control.

PCR (Initial and Nested) and Electrophoresis

A mixture of primers and reagents (master mix) were added to the samples and positive control, mixed, and placed on ice. This master mix contains Taq DNA polymerase, dNTPs, buffer, and salt. The blue master mix does not contain primers. The samples are then placed into the thermal cycler, where they were denatured, annealed, and extended. In order to remove unincorporated primers from the initial PCR exonuclease I is added. The samples (spinach, pothos, Arabadopsis, and pGAP) were then incubated to activate the exonuclease enzyme. A nested PCR master mix was then added to each exonuclease-treated initial PCR tube, before being placed in the thermal cycler. The resulting samples (spinach, pothos, Arabadopsis, and pGAP) are analyzed via electrophoresis.

Ligation and Transformation

A blunting reaction was set up using the purified PCR products (spinach, pothos, Arabadopsis, and pGAP), 2x ligation buffer, sterile water, and proofreading polymerase. The tubes were incubated at 70 °C and cooled before centrifuging. A ligation reaction was then set up using the blunting reaction, T4 DNA ligase, and pJet1.2 blunted vector and incubated. The ligated PCR products are used to transform 4 previously inoculated *E. coli* starter cultures and incubated overnight. The resulting bacteria colonies, tiny dots grown on the agar plates, were collected and the samples were purified and sent for sequencing.

RESULTS AND DISCUSSION

The purpose of this experiment was to isolate and sequence the GAPDH gene in spinach and pothos as well as pGAP and Arabidopsis. After transforming *E. coli* using the DNA there was only enough pGAP growth to conduct electrophoresis. There was not enough *E. coli* transformant colonies in the other DNA samples so there was nothing to isolate the DNA from to later perform electrophoresis with. Upon completion of gel electrophoresis there was no DNA band shown, this may have been due to a micropipetting error that occurred when loading the pGAP sample into the desired well in the agarose gel. Some of the sample was mixed with the buffer already in the well. After comparing the results from GenBank database with the results from BLAST, it was analyzed that the identity of the pGAP is most likely to be GAPC gene. Using the methods, the DNA was unable to be isolated and cloned in both the spinach and pothos plants because the sample grown was not enough to further the research.

Figure 1. Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene sequence in pGAP via BLAST database.

FEASIBILITY STUDY OF SMARTPHONE APPLICATIONS FOR TRAFFIC SIGNAL CONTROL

Ray Motte* and Fengxiang Qiao[#]

Innovative Transportation Research Institute College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

Traffic congestion and safety are always issues in transportation studies that call for practical solutions. The United States Department of Transportation (USDOT) has launched a Connected Vehicle (CV) program that allows vehicle-to-vehicle and vehicle-to-Infrastructure communications. One of its applications is the development of the Drivers' Smart Advisory System (DSAS), which allows communication tools such as Smartphone to provide warnings to drivers on upcoming traffic signals. With the advancement of new technology, smartphone are constantly adding or upgrading their associated applications. Apple iPhone was the first phone to have the touch screen software which was then only used in ATM machines and personal computers. With the evolutions of smartphone generations, many people rely on their phones as part of the daily routine activity, not only for communication. Typical applications. The smart use of smartphone has the potentials to regulate driving behaviors, and even decrease fatal crashes and reduce vehicle emissions on roadway segments and at intersections. In this research, an Android system based smartphone application was developed to guide drivers when approaching intersections. Driving simulator tests were conducted to evaluate the performance of drivers using such system. Results show that this application could act as a supplemental "electronic eye".

Key words: Traffic Signal, Smartphone Application, Traffic Safety, Simulator Test

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Traffic control signals are devices that are installed at roadway intersections, pedestrian crossings, and other locations to separate conflicting traffic flow in time and space. Traffic lights assign the right of

COSET SURP 2014

way to road users from different approaches by displaying lights of standard colors (red, yellow, and green) following a universal color code (Mcshane, 1999). In some cases, however, traffic signals or road users' visions are blocked by obstacles such as tree leaves, leading heavy vehicles (such as big truck and bus), and/or sever weathers conditions (like fog and storm) (Qiao, et al., 2013; Li and Qiao, 2014), which will induce incidents and even fatal crashes.

With the advancement of modern technologies, wireless communications are more and more widely used in transportation systems. The United States Department of Transportation (USDOT) lunched a "Connected Vehicle" (CV) program, aiming to connect all vehicles together through wireless network, including the invisible data exchanges between vehicle and infrastructures, and among vehicles. With this concept, a kind of Dedicated Short-Range Communication (DSRC) system, such as the Drivers Smart Advisory System (DSAS) has been developed to provide traffic control information to drivers through special devices such as the Radio Frequency Identification (RFID) (Qiao, et al., 2013; Qiao, et al., 2014). This has been partially tested at signalized intersections with sun glare in field (Qiao, et al., 2014) and in driving simulator (Li and Qiao, 2014), at stop sign controlled unsignalized intersections (Qiao et al., 2014), and in work zone area (Qiao, et al., 2013; Li, et al., 2015).

Results from these tests are very promising. However, it may not be feasible that a dedicated device is required in order to use this kind of DSAS. This calls for a new device that is always in or with current vehicles, and in the meantime is easy to implement the required functions. Smartphone, which is so populate for almost all road users, is a very idea device if its application is well designed.

METHODS

The purpose of this research is, therefore, to conduct a feasibility study on the use of smartphone application for wireless communications with roadside infrastructures such as the traffic signal. A smartphone application was developed to provide warning messages to drivers when approaching the intersections. As a first try of the entire study, the developed application was synchronized with the traffic signals at intersections. This means, the corresponding signal message (red, yellow, or green) will be pop up on the screen of the smartphone when approaching the target intersection.

The development of a smartphone application should follow a standard procedure as is illustrated in Figure 1. The first two steps are to set up the necessary environment, then to design and debug the applications, followed by the test. The last step is to program for release.



Figure 1. Standard procedure to develop a smartphone application and release

In this research, an Android smartphone was used as the test device. One of the reasons was that, the Android system is very popular in many types of smartphones (such as Google Nexus, Samsung Galaxy),

and can be used to customize applications for free. There are two important portions in designing the application for this topic: the design of button click and the design of clock timing. The click button is for the drivers to trigger and terminate the application, while the clock timing is for the synchronization and setting of traffic signals of different colors.

The developed smartphone application was also tested in a driving simulator (Figure 2). The driving simulator has a wider view of 270 degrees with full motion. The design of scene was conducted through the coding of a series of scripts. The designed elements in simulator include the location of the starting point of the test vehicle (the simulator), the layout of roadways, the settings of traffic signal, the weather. The synchronized smartphone application was used for the test of driver's reactions to traffic signals when approaching an intersection.



Figure 2. The developed smartphone application was tested in a driving simulator

RESULTS AND DISCUSSION

Figure 3 illustrates two specific functions that are used in the development of the needed smartphone application. One is the interface showing the way to develop the button click (Figure 3a), while another is for the development of clock timing (Figure 3b). The interface of the finally developed application is showing in Figure 4.



(a) The developed button click (b) Developed clock timing Figure 3. The button click and clock timing in the design interface



Figure 4. The developed display interface showing on a smartphone screen

In Figure 4, once the driver press the button "Start", the application will be triggered, and the traffic signal will display the same color as is showing on the real signal lights. The colors of light on the smartphone can alter also according to the ones on the real signal lights.

When the smartphone application was tested in the driving simulator, the instant speed and other information was recorded as a sampling rate of 60 Hz, meaning that every second there were 60 sets of driving data recorded. The subject was instructed to drive along an arterial road with six intersections, while no roadside traffic signal was clearly visible. The driver had to rely on the smartphone application to understand the color (actually the order from traffic controlled) of the signal light.

The recruited subject was a graduate student at Texas Southern University. Figure 5 shows the recorded velocity from the tests when driving along an arterial road with the guidance of colored lights showing on a smartphone.



Figure 5. The recorded velocity when driving along an arterial road with the advices from the developed smartphone application

The drops of curves in Figure 4 indicate the moment when the test vehicle (the driving simulator) stopped at intersections for the red light. In between the x-axis (a location index) 1,000 and 2,000, there is a small drop, meaning that the vehicle decelerated for a while and then accelerated again. This is related to the moment that the simulator was approaching the intersection during red signal, which causes the

59

deceleration. Shortly, the traffic signal turned to green before the simulator was fully stopped. In this case, the driver decided to accelerate and then passed the intersection.

CONCLUSION

In this research, the concept of the smart phone application is presented as a safety system that can read like the traffic street light itself and help drivers that face roadways. The application was developed in Android system and can be free downloaded to many types of phones. Simulator test shows promising results. This research implies that the smartphone application has the potential to provide advised to drivers on traffic lights.

ACKNOWLEDGEMENTS

This study was supported by Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University. We also express our gratitude to the Innovative Transportation Research Institute (ITRI) for supporting this study and providing equipment. We also would like to thank Graduate Students at ITRI, including Po-Hsien Kuo, Ruksana Rahman, Johora Munni, and Qing Li for their helps.

REFERENCES

- Li Q. and Qiao F. (2014). How Drivers' Smart Advisory System Improves Driving Performance? A Simulator Imitation of Wireless Warning on Traffic Signal under Sun Glare. LAMBERT Academic Publishing. ISBN-13: 978-3-659-57193-0
- Li, Q., Qiao F, Yu L. (2015). Socio-demographic impacts on lane-changing response time and distance in work zone with drivers' smart advisory system, Journal of Traffic and Transportation Engineering (English Edition), Volume 2, number 5, October 2015. Elsevier Publishing.
- Mcshane C. (1999). The origins and globalization of traffic control signals. Northeastern University. Journal of Urban History. March 1999. Website: http://sites.tufts.edu/carscultureplace2010/files/2010/09/McShane-traffic-signals-1999.pdf.
- Qiao F, Jia J, Yu L, Li Q, and Zhai D. (2014). Drivers' Smart Assistance System Based on Radio Frequency Identification. Transportation Research Record: Journal of Transportation Research Board, No. 2458, Transportation Research Board of the National Academies, Washington, DC, 2014, pp. 37-46.
- Qiao F. Wang X, Yu L. (2013). Using Radio Frequency Identification to Improve Drivers' Awareness of Stop Sign at Unsignalized Intersections. Proceedings of Transportation Research Board (TRB) annual meeting of National Science of Academy, January 13-17, 2013. Washington DC.

CREATING AN APPLICATION ON GOOGLE ANDROID PLATFORM

Samuel Teferra* and Moshen Javadian[#]

Department of Computer Sciences College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



*SURP Fellowship Recipient #Faculty Mentor

61

INTRODUCTION

Obtaining the best platform for the development of an application that would be efficient and easy to use. Eclipse (for android) and x codec (for apple) are a popular choice. These are Softwares used to design applications we have in the apple store (apple) and google play (for android). To create an app that would serve as a tool for patron in restaurants and venues alike to know exactly what percent to tip their servers. Make app appear to be user friendly, while still being able to perform its intended function.

METHODS

The feasibility of using the best software that would be required to complete the design and coding of the application. Getting the pros and cons of using different application development platforms. After choosing the appropriate platform, proceeding to designing the user interface of the application. Make a rough sketch of what the app should look like. Downloading the eclipse software form the oracle website and optimizing it to specifically code for android based phones and tablets. Carefully designing the user interface since it is as important as to the application. Switching back and forth from the main activity xml (the code part of the design) to the graphical layout page to see if the code we wrote actually made a difference graphically to the application. Coding various aspects of the app like giving functionality to each of the buttons.

ite Edit Refector Source I	Navigute Search Project Run Window Help			H	_
3-8-446-61	5 X * 3 X 9 * 9 * 9 * 6 * 6 6 * 6 6 X * 7 7 2 1 1 1 1 * 7 * 7 9 * * 7		Quick Access	1 11	a line
Respective X □ □ □ □	<pre>CM Detectionspace 1: (</pre>	•	Outlies 21 Bend 1 Be	e Vent inhet sprot en i Imagebalte : Gall fon : Gall fo	= []
travoble-hdpi travoble-hdpi travoble-mdpi travoble-hdpi 9 gg2_prg 4 gg2_prg 4 subtrepting travoble-pohde	(E) Problems 団 Console 出 ① Consulta y 知 Lug Col Andread				
	1. Contract of the second s	1	Shar (Mar		

STEPS:

- setting the view to scroll view so we have one fluid page that can be scrolled up and down.
- giving id handle to each button so we can refer to them later in our main activity java codes
- manipulating the gravity, parameters, padding etc. to set up the positions and alignments for the buttons.
- go to the mainactivity java file and begin coding
- importing bundles, activities, menus etc from android.
- connecting out xml file with the java file using 'set content view'.
- setting up a class called 'main activity' that would inherit all its aspects from the activity we imported.
- casting, using if-then codes, using for loops and while loops,
- giving functionality to the each button by first inheriting 'on click' then use onclicklistener method.
- debugging many lines of codes that is very time consuming.

 ava - sametoswirestavouti 	57//Y #31 ## - E056				T SA D E	2 III enti			♥@9:10 :
Re Edt Refector Source I	avigate Search Project Ram Window Help 2 B B 2 × 1 × 1 × 10 + 0 + 0 + 0 + 0 + 0 + 0 + 0 + 0 + 1 + 1		Quick Access	1 Pina		mount Before Tax		c	1 10
Changing 2: Imaging 2: Imagin	i.	È Costec 21 } Souther, ¢-isby	9 ° U		Patron 20% Tip: Tax: Final Bill: Split Check Patron	Restart	80.00 30.00 30.00 0.00 0.00	0	
ets + (Generated Java Files)	<textview (<="" td=""><td></td><td></td><td></td><td>- +</td><td>. 1</td><td>2</td><td>3</td><td>-63</td></textview>				- +	. 1	2	3	-63
dmwable-hdpi dmwable-hdpi dmwable-ndpi	Consta 20 ginnerson Consta 20 ginnerson Consta 20 ginnerson Consta 20 ginnerson Consta 20 ginnerson	180-0-0			* /	, 4	5	6	Next
dawate-shapi Bi gogi proj Bi gogi proj Bi k_Suncherung dawate-shapi T	a					*	0	#	

RESULTS AND DISCUSSION

Essentially by going to a restaurant, ordering food and using our simple app, the patron is able to find out what percentage tip he should leave the server based on the quality of service and performance. Know what to tip by inputting first the 'Amount before tax' on the bill handed to him by his server, then input the tax on his bill, finally the app will give the user the option to choose what percentage tip to leave his server using the hover shown on the screenshot of the app.

This app is easy to utilize and user friendly and has social, economic, and/or scientific significance. Computer science students may be inspired to engage in developing applications for phones and tablets. Developing an application requires a lot of time and dedication a great learning experience for the developers on this project. Eventually after further debugging and user interface fix ups, it will be available to download on the google play store for android.

ACKNOWLEDGEMENTS

This study was supported by Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

https://developer.android.com/sdk/installing/index.html https://www.eclipse.org/downloads/ https://www.virtualbox.org/ http://developer.android.com/tools/help/sdk-manager.html http://developer.android.com/reference/packages.html http://stackoverflow.com/

63

MAKING MORE EFFICIENT PHOTOVOLTAIC CELLS USING MATERIALS ABSORBING DIFFERENT COLORS OF LIGHT

Fernando Valdez* and Graham Thomas #

Department of Electronics Engineering Technology College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

The photovoltaic industry is experiencing rapid growth as people around the world turn to alternative energy. Photovoltaic energy is the science of converting light energy into electrical energy and is achieved through the use of semiconductors. In this research, a method was developed and tested to increase the efficiency of solar cells using various materials that absorb different colors of light. Strips of different absorbent light materials were placed side by side on different solar cells to investigate the possibility of making the cells more efficient. Different color materials attract light differently, therefore it was hypothesized that if the colors were place next to Silicon (used in solar cells) then the efficiency would increase because each color attracts different amount of energy given by the rays of sun. Several different solar cells were used to test out different materials and their colors. After conducting several trials in the sun, the data obtained from the used method revealed that the solar cell efficiency from the materials tested either decreased or remained the same in all trials.

Key words: Photovoltaic energy, solar cell efficiency

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Photovoltaic energy is the science of converting light energy into electrical energy and is achieved through the use of semiconductors. When light strikes the cell, a certain portion of it is absorbed within the semiconductor. The rest for the most part is lost. An average solar panel has an efficiency of about

12% to 20%. In recent works, there has been improvements where solar efficiency reaches 40.7%, 43.6% and even 44.7%.

METHODS

Ultra-thin microscope slides were used as a support to place the colors or ink in the cell. Layers of different colors of materials were placed along the slides to create a single layer that were placed on top of the silicon of each cell.

Cell 1 Control Cell: The control cell remained the same throughout the experiment. No changes were made to keep a constant control of the experiment.

Cell 2 Cello-Sheet Plastic: Visible sheets of plastic (red, green, orange, blue, yellow and violet) were cut into 0.5" by 1.75" strips. Each strip (different color) were placed aside to create a 3" by 1.75" layer that could be added to the silicon.

Cell 3 Dye-Ink: To properly place ink in the microscope slides, about two drops of ink were placed in a clear strip of normal tape. The strips of tape (now colored) were placed aside each other on the slides to provide a single multi-color layer for the silicon

Cell 4 Chlorophyll: To obtain chlorophyll pigments, a normal bottle of Chlorophyll supplement was used. The slide was dipped in a tray with enough liquid to cover the slide. The slides were left on the open for a few days until the liquid evaporated, leaving green pigments behind, hence make our slides dark green and ready to be used.

Experimental Method: The voltage provided by the cells was measured individually before placing the different colored materials next to the silicon, data was recorded in the tables below. After placing the colored materials, once again, more data was recorded. Based on the charts and graphs below, conclusions were obtained.

RESULTS AND DISCUSSION

Based on the data obtained from the chart and graphs, it was concluded that the method performed to increase the efficiency did not function as expected. The voltage obtained after the color either remained constant or decreased by a small amount. The material that reduced the efficiency the most was the chlorophyll pigments. In all trials, the pigments reduced the amount of voltage provided by the solar cell. This is a material that would not be very good to use in following trials. The materials that performed the best was the visible color plastic sheets. By increasing the visibility of the material, the voltage provided with increase or remain constant as it was before the material was placed.



Figure 1- Results for Trial 1 of solar cell efficiency



Figure 2- Results for Trial 2 of solar cell efficiency





Figure 4. Solar cells with the color materials as they are being tested for efficiency

COSET SURP 2014

ACKNOWLEDGEMENTS

This study was supported by the Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

C. Strümpel, M. McCann, G. Beaucarne, V. Arkhipov, A. Slaoui, V. Švrček, C. del Cañizo, I. Tobias, "Modifying the solar spectrum to enhance silicon solar cell efficiency– An overview of available materials", Solar Energy Materials and Solar Cells, Volume 91, Issue 4, 15 February 2007, Pages 238-249

Floyd, Thomas L., Electronic Devices (Conventional Current). Pearson Education. 2009. Print

Per I. Widenborg and Armin G. Aberle, "Polycrystalline Silicon Thin-Film Solar Cells on AIT-Textured Glass Superstrates," Advances in OptoElectronics, vol. 2007, Article ID 24584, 7 pages, 2007.

Swatowska B, Stapinski T, Drabszyk K, Panek P. "The role of antireflective coating in silicon solar cells—the influence on their electrical parameters" Optica Applicata, Vol. XLI, No. 2, June 2011; 41 (2): 487-492.

A USER CENTERED APPROACH TO MANAGING IDENTITIES IN ONLINE SOCIAL NETWORK

Terence Vaughn* and Lila Ghemri[#]

Department of Computer Science, College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

In this work, we propose to use Vickrey auction principle to bid "your true value" is applied to managing online identities and to allow the user to create multiple profiles within one account, and posts are made to a specific profile.

Key words: Online Social network, Vickrey auction

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

While they offer convenience to connect to friends and share content, opinions and views, online social networks disclose personnel information, violate person's privacy, current solution for users is to create multiple accounts and violates terms of use. In this paper, we propose to use Vickrey auction principle to bid "your true value" is applied to managing online identities and to allow the user to create multiple profiles within one account, and posts are made to a specific profile. The goal of our research is provide a way to obey the OSN terms of use and protection of the user privacy.

METHODS AND RESULTS

Phase 1:Account and Profile Creation





Phase 2:User Interaction Management



Phase 1 is fully implemented Web Interface: Implemented using HTLM, JavaScript and JQuery Database : User table and Profile table fully implemented using MySQL, PHP Data Capture and validation: implemented using PHP. We will implement Phase 2 components and test System in the future.

ACKNOWLEDGEMENTS

This study was supported by Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

- Conti, M., Hasani, A., and Crispo, B. 2013. Virtual private social networks and a Facebook implementation. ACM Trans. Web Vol 7,14 (09/2013)
- 2.Facebook Query Language Reference. *Facebook Developers*. Retrieved 7/25/2014, https://developers.facebook.com/docs/reference/fql/
- 3. Lampe, C., Ellison, N., & Steinfield, C. A Familiar Face(book): Profile Elements as Signals in an Online Social Network, 10.
- 4. Sandholm, T.W. *Limitations of the Vickrey auction in computational multi-agent systems*. In Proceedings of the 2sd International Conference on Multi-Agent Systems, Tokyo, Japan Dec, 1996, pp 299-306
- 5. Zheleva, E., & Getoor, L. To Join or Not to Join: Illusion of Privacy in Social Networks with Mixed Public and Private User Profiles IW3C2, April 20–24, 2009, Madrid, Spain
J-COUPLING AND IMAGING WITH EARTH FIELD NUCLEAR MAGNETIC RESONANCE

¹Eric Wilson* and ²Daniel Vrincianu[#]

¹Department of Electronics Engineering Technology ²Department of Physics College of Science, Engineering, and Technology Texas Southern University 3100 Cleburne Street, Houston, TX 77004



ABSTRACT

This research was conducted in the hope that Earth field nuclear magnetic resonance (NMR) can be used effectively to solve many of the same problems that high field NMR solves, but at considerably less cost. This study focused upon calibrating the Magritek Terranova MRI device to image small objects, and learn basic NMR techniques. By using water the system is set up to gain a signal of hydrogen, improve signal strength through shimming, and learn about J-coupling and chemical shifts. By using a small electromagnetic pulse it was possible to manipulate polarized nuclear spin properties of water, isopropyl alcohol, and boron trifluoride diethyl ethernate. These experiments were found to be successful by finding the identifying doublet markers of the isopropyl alcohol, finding that the hydrogen in water shows up at 2230 Hz, seeing the chemical signature of boron trifluoride diethyl ethernate, and getting 2D and 3D images of fruit (an orange and a lemon). All in all this study showed that a compact Earth field NMR device is sensitive enough to be able to perform at a level useful enough to explore many of the same areas as high field devices, but at a fraction of the cost.

Keywords: Magritek, Earth Field Nuclear Magnetic Resonance, J-coupling, spin dynamics

*SURP Fellowship Recipient #Faculty Mentor

INTRODUCTION

Many people have played with tops as children. They watch in glee as the top whirls and wobbles before it inevitably falls over motionless. What they have observed is analogous to the behavior of

COSET SURP 2014

subatomic particles. These particles all possess a quantum number called spin which has the characteristics similar to the angular velocity of a top, the wobble of the top correlates to precession in the subatomic particle and it can be manipulated with a magnetic field and an alternating pulse of electromagnetic radiation (usually radio frequency). The particles of interest are nuclei which have a spin of 1/2. When subjected to a magnetic field B_0 the spin is split into two energy sub-levels +1/2(spin-up) and -1/2(spin-down). In Nuclear Magnetic Resonance (NMR) after the nuclei are aligned in a polarization magnetic field, a radio signal knocks the nuclei out of alignment or causes nutation, what that means is that the pulse induces transitions between the energy levels mentioned earlier. The energy difference is given by the equation: $\Delta E = \gamma \hbar B_0$ where γ is the gyromagnetic ratio (for instance, the gyromagnetic ratio for hydrogen is, $2.675 * 10^8 T^{-1} s^{-1}$). After a while the nuclei align again with a static magnetic field in the Terranova device's case it is the Earth's magnetic field. The resonant frequency of the precession of the nuclei is governed by the equation: $\omega = \gamma B_0$ which is called the Larmor frequency (Meghan E. Halse). The frequency in which the hydrogen nuclei in water were found the most during this research was at 2230Hz therefore $\Delta E \approx 1.45 \times 10^{-11} eV$. That value is the photon energy of the pulse. Indirect spin-spin coupling, also known as, J-coupling is caused by the influence of bonding electrons on the magnetic interactions between the spins of nuclei (Levitt). J-coupling is governed by the Hamiltonian equation, $\hat{H}_{jk}^{J,full} = 2\pi \hat{I}_j \cdot J_{jk} \cdot \hat{I}_k$, where \hat{I}_j and \hat{I}_k , are spins on the same molecule and J is a 3x3 matrix called the J-coupling tensor (Levitt). Using various methods an enormous amount of data can be collected and analyzed pertaining to frequency, capacitance, chemical composition, etc. Also, imaging in one, two or three dimensions is possible. This study's main purpose was to ascertain whether or not a low cost NMR device was capable of advanced operations like J-coupling, chemical shift analysis, and three dimensional imaging.

MATERIALS AND METHODS

All experimental procedures carried out during this research required the use of the Terranova-MRI Earth Field Nuclear Magnetic Resonance apparatus. This device consists of a probe made up of three coils that fit inside each other that are connected to a spectrometer that provides signal processing and power. There are also a 570 ml sample bottle, a dual chamber sample bottle, a Magnaprobe 3D compass, and a computer running the *Prospa*, software package.

First, by placing the device in the most optimal area in the laboratory electromagnetic noise can be reduced. This is essential in order to find weak signals. The earth's magnetic field is more or less homogenous; however, the great amount of human-made metallic items can cause anomalies in the local field which is detected by the B_1 coil (the innermost coil). The polarization coil (B_n) , is the outermost

coil provides a polarizing field that is approximately 350 times that of the Earth's magnetic field (which is about 52 μ T). Using the Magnaprobe compass it was possible to align the z-axis of the device to that of the Earth's magnetic field in that location. The wooden stand also aided in alignment of the device by allowing greater freedom of movement. After the device was positioned correctly, a noise monitoring program was run to verify device placement. If the noise read above 10 μ V then the device was rotated on its vertical axis until the noise was well below that noise level. A noise level below 5 μ V was optimal. To calibrate the probe (coils) a program (macro) called analyzeCoil (see Table 1 for results) was used to form a curve of frequency versus capacitance in order to find the Larmor frequency.

Next, a macro named autotune (Table 2) was run to find the timing capacitance and resonant frequency. These values were used in another macro called spinEcho. The spinEcho macro (Figure 1 and Figure 2), allows refocusing of the de-phasing of the magnetization caused by the inhomogeneous detection field (Meghan E. Halse). Besides allowing for a more accurate spin-spin relaxation time, it also allows for a more accurate measure of the resonant frequency.

After using spinEcho, it is necessary to improve the quality of the NMR signal by using a macro known as autoShim (Table 3 and Figure 5). Even though the Earth's magnetic field is very homogeneous it is very weak. Any magnetic sources will be detected and disturb the homogeneity of the detection magnetic field. The NMR signal comes from the phase coherence of an enormous number of precessing nuclear spins (Meghan E. Halse). The signal decays exponentially in a homogeneous field, but decays at a greater rate in areas of inhomogeneity. Spin-spin relaxation is also a source of decay caused by loss of phase coherence over time. It happens because of magnetic dipole coupling to adjacent spins. The detection field homogeneity can be improved by a called shimming (Meghan E. Halse). Tiny magnetic fields are induced in gradients along specific axes across the sample. This allows for three dimensional shimming. Once the macro completes its function the new shims are saved by Prospa. There are two iterations of shimming, one with spin echo and one without. Both macros are used to enhance signal to noise ratio.

After shimming, a macro called pulseandCollect (Table 4) is used to fine-tune NMR probe. This optimizes the free-induction decay (FID) and increases signal amplitude by allowing the operator to change the center frequency to match as closely as possible the Larmor frequency. After pulseandCollect macro is complete, more advanced experiments (like 2D/3D imaging) can commence (Meghan E. Halse).

In the course of this research, the lab group followed the following process:

- 1. Draw a block diagram of the Terranova MRI (Figure 7).
- 2. Design and build a wooden stand for the probe.
- 3. Measure the Earth's local magnetic field.
- 4. Find the optimal position for the EFNMR device in the lab.
- 5. Run the various macros to set up the device.
- 6. Run the pulse and collect experiment.
- 7. Run detection coil optimization experiment.
- 8. Run T_1 and T_2 determination experiments.
- 9. Run CPMG experiment (Figure 6).
- 10. Perform MRI experiments (2D and 3D imaging, Figures 3 and 4).
- 11. Investigate chemical shifts, k-space, and j-coupling.

RESULTS AND DISCUSSION

To draw the block diagram, it was necessary to take the Terranova device apart. It was not very difficult, but one had to be careful not to bend the circuit card pins when putting the device back together. The detection coil forms a parallel LCR circuit in receive mode. This resonant circuit picks up the EFNMR signal. The precessing nuclear magnetism of the sample induces a voltage (V_s) . Impedance in

the LCR circuit equals, $Z = R + i \left(\omega L - \frac{1}{\omega C} \right)$, and then the current in the circuit has to be,

 $I = \frac{V_s}{Z} = \frac{V_s}{R + i \left(\omega L - \frac{1}{\omega C}\right)}$. When the circuit is at resonance, the imaginary term in current will go to

zero and thus will be, $I = \frac{V_s}{R}$. The output voltage is, $V_{out} = |IZ| = \frac{|V_s|}{R\omega_0 C} = \frac{|V_s|\omega_0 L}{R} = |V_s|Q$. Q is the

quality factor in where the resonant circuit amplifies the signal voltage by a factor of Q (Meghan E. Halse).

Designing the wooden stand did take a bit of time. The lab team had to measure the device, decide how to mount it, and then cut the supplied wood. It was designed where it was possible to easily adjust the Z-axis by simply rotating the device. Getting to know the *Prospa* software macros was necessary in order to

set up the Terranova MRI device and to perform all of the experiments required. The lab team was able to successfully gain results from the MRI experiments and image an orange and a lemon and also look into the concepts of k-space and j-coupling. The chemical shift poses a problem on the Terranova MRI device as it is 10000 times smaller than the EFNMR signal, so the shift gets lost in the noise.

In the investigation of k-space, it is important to define some events. A localized group of spins all precessing at the same frequency is known as an isochromat. Straight from the EFNMR Student Manual, "The signal generated by the isochromat within a sample in the presence of a magnetic field gradient G_q is proportional to: $\exp\{-i\omega(x)\} = \exp\{-i\gamma(B_0 + G_q q)t\}$, where q represents any frame of reference along the gradient or combination of vectors along the gradient. The equation that governs the spin density of the NMR signal at each point in space is: $S = \int_{-\infty}^{\infty} \rho(x) \exp\{-i\gamma(G_q q)t\} dq$. The spin density is the "image" of the sample. In order to get this data from the signal the k-vector must be used. The k-vector is: $\vec{k}(G,t) = \frac{\gamma}{2\pi} \int_{-\infty}^{\infty} \vec{G}(t) dt = \frac{1}{2\pi} \gamma \vec{G}t$. Substituting the k-vector equation into the equation with spin density will reveal a Fourier relationship between $\rho(q)$ and S(k). Applying a Fourier transform and generalizing the resulting expression into three dimensions yields: $\rho(\vec{r}) = \iiint S(\vec{k}) \exp\{-i2\pi \vec{k} \cdot r\} dk_x dk_y dk_z$. (Meghan E. Halse)

In the study of j-coupling, the lab team was successful in the imaging of the double doublet structure of isopropyl alcohol (Figure 2); however, we were only able to see the –CH3 coupling in the boron trifluoride diethyl etherate. There is more to discover with this molecule. The hypothesis is that the oxygen bond with boron trifluoride and the fact that boron is a Quadrapole nucleus interferes with our ability to find fluorine in this molecule with the EFNMR device. That being stated, the signature of this molecule every time we imaged it is what is shown in Figure 1. The lab team under the advisement of Dr. Vrinceanu delved far deeper into the capabilities of the Terranova MRI device than expected. Most of the experiments were successful and those that were not we were able to find out why. We overcame early technical issues (I had to repair the detection coil lead with solder), and schedule problems to be able to complete our research properly. These graphs and figures show that the goals of the research were met.

Table 1. B1 Coil Analysi

B1 Coil Analysis	
Results	
B1 Coil Capacitance	(3.72 +/- 0.02)nF
_	(0.4249 +/-
B1 Coil Inductance	0.0005)H
B1 Coil F0	(4000 +/- 10)Hz

autotune Results				
B1 Freq	Capacitance			
2358.19	7			
2305.05	7.5			
2255.34	8			
2208.72	8.5			

autoShim Results	
x_shim	-2.04
y_shim	-39.03
z_shim	37.13
peak	20.4766
iters	80
time	0:06:18

Table 3. Autoshim results.

Table 4. Pulse and Collect results

Pulse and Collect	t				
Results					
Max	Freq		Phase	Integral	
	69.5	2240	168	181.6	
	69.7	2240	168	181.6	
	69.7	2240	166	181.6	
	69.4	2240	165	182.1	
	69.2	2240	165	182.3	
	69.1	2240	165	182.3	



Figure 1. SpinEcho example of Boron triflouride diethyl etherate profile which shows j-coupling with –CH3 portions of the molecule.



Figure 2. SpinEcho example of Isopropyl Alcohol profile FID and Magnitude.



Figure 3. 2D Image of an Orange with K-space data.



Figure 4. 3D Image of a Lemon.



Figure 5. Example of AutoShim.



Figure 6. Example of CPMG.



TERRANOVA BLOCK DIAGRAM

Figure 7. Terranova block diagram.

ACKNOWLEDGEMENT

This study was supported by the Summer Undergraduate Research Program (SURP) of the College of Science, Engineering, and Technology at Texas Southern University.

REFERENCES

Adrian C. Melissinos, Jim Napolitano. *Experiments in Modern Physics*. San Diego, California: Elsevier Science, 2003. Print. Edwards, John. *Process NMR Associates*. 01 01 2012. blog. 29 07 2014. http://www.process-

nmr.com/NMR%20Blog%20on%20the%20Web.htm>.

Hass, M. Organicchem.org. 12 April 2004. digital. 22 July 2014.

Levitt, Malcolm H. Spin Dynamics: Basics of Nuclear Magnetic Resonance. The University of Southampton, UK: John Wiley & Sons, Ltd, 2007. Book.

Meghan E. Halse. Terranova-MRI EFNMR Student Guide. Kelburn, Wellington, New Zealand: Magritek Limited, 2006. Print.

Terranova-MRI EFNMR User's Manual. Kelburn, Wellington, New Zealand: Magritek Limited, 2006. Print.

William R. Hendee, E. Russell Ritenour. Medical Imaging Physics. New York: Wiley-Liss, Inc, 2002. Print.

APPENDIX

The attached research article was published in *Mitochondrial DNA*, which is a peer-review journal, by Mr. Tommy Quatch (Senior, Biology Major) who participated in the COSET Summer Undergraduate Research Program (SURP) in 2013. After he successfully completed the SURP, he continued working with his mentor (Dr. Hector C. Miranda Jr., Department of Biology) to generate more data for a publication in a peer-review journal.



Mitochondrial DNA, Early Online: 1–2 © 2014 Informa UK Ltd. DOI: 10.3109/19401736.2014.928870 informa healthcare

MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of Palawan peacock-pheasant *Polyplectron napoleonis* (Galliformes, Phasianidae)

Tommy Quach¹, Daniel M. Brooks², and Hector C. Miranda Jr¹

¹Department of Biology, Texas Southern University, Houston, TX, USA and ²Department of Vertebrate Zoology, Houston Museum of Natural Science, Houston Museum of Natural Science, Houston, TX, USA

Abstract

The complete mitochondrial genome of the Palawan peacock-pheasant *Polyplectron napoleonis* is 16,710 bp and contains 13 protein-coding genes, 2 rRNA genes, 22 tRNA genes and a control-region. All protein-coding genes use the standard ATG start codon, except for *cox1* which has GTG start codon. Seven out of 13 PCGs have TAA stop codons, two have AGG (*cox1* and *nd6*), and three PCGs (*nd2*, *cox2* and *nd4*) have incomplete stop codon of just T– – nucleotide.

Keywords

Mitochondrial genome, Palawan peacock-pheasant, Polyplectron napoleonis DNA sequencing

History

Received 22 May 2014 Accepted 25 May 2014 Published online 26 June 2014

The Palawan peacock-pheasant Polyplectron napoleonis is endemic to the island of Palawan and is currently categorized by the International Union for the Conservation of Nature (IUCN) as Vulnerable (Bird Life International, 2001). The population estimates for P. napoleonis ranges from 10,000 (McGowan & Garson, 1995) to 50,000 individuals (Mallari et al., 2011). The complete mitochondrial genome of P. napoleonis is a closedcircular molecule of 16,700 bp (GenBank accession number KJ939353). The genome contains 13 protein-coding genes, 2 rRNA genes and 22 tRNA genes. Gene order and gene coding strand is consistent with those observed in galliformes and other birds, with tRNA^{Glu} and nd6 found immediately adjacent to the control region instead of being located between the nd5 and cytb genes as in other vertebrates (Desjardins & Morais, 1990). Except for nd6, all protein-coding genes (PCGs) are transcribed at the complementary Heavy (H) strand. The overall base composition is 23.9% T; 29.5 A, 32.3% C, and 14.3% G with a total A + T content of 53.4%. Two reading frames overlaps occur on the same strand: atp8 and atp6 overlap by 8 nt, nd4L and nd4 by 5 nt. The initiation and stop codons are shown in Table 1. All protein-coding genes use the standard ATG start codon, except for cox1 which has GTG start codon. This differs from P. germaini which has the typical

ATG start codon (Omeire et al., 2014). Seven out of 13 (PCGs) have TAA stop codon and two PCGs have AGG (cox1 and nd6). Three PCGs (nd2, cox2 and nd4) have incomplete stop codon of just T-- nucleotide. TAA termination of the incomplete T-- by post-transcriptional polyadenylation is assumed to be operational (Ojala et al., 1981). The P. napoleonis contains the typical set of 22tRNA genes, which are interspersed between rRNAs and protein-coding genes. As inferred from tRNAscan-SE 1.21 (Lowe & Eddy, 1997), about 20 tRNA genes can fold into a typical cloverleaf structure, except for tRNA-Ser (AGN) which may lack the DHU arm. Eight tRNAs are coded on the complementary Light (L) strand, while the remaining 14 tRNAs are transcribed at the Heavy (H) strand. The three tRNA clusters (IQM, WANCY and HSL) are well conserved in P. napoleonis, typical of vertebrate mitochondrial genomes. As in all metazoans, there are two rRNA genes in P. napoleonis, the small and large ribosomal genes (12S rRNA and 16S rRNA). The 12S rRNA (981 bp) is located in between tRNA-Phe and tRNA-Val, and the 16S rRNA (1598 bp) is located between tRNA-Val and tRNA-Leu (UUR). The control region is 1169 bp long, one bp shorter than that reported for *P. bicalcaratum* (Shen et al., 2009), and 4 bp longer than P. germaini (Omeire et al., 2014).

Correspondence: H. C. Miranda, Jr., Department of Biology, Texas Southern University, 3100 Cleburne St., Houston TX 77004, USA. Tel: 713-313-1031. Fax: 713-313-7932. E-mail: mirandahc@tsu.edu

Table 1. Mitochondrial genome characteristics of P. napoleonis.

Position				Codon				
Gene	From	То	Size (bp) Nucleotide	Amino Acid	Initiation	Stop	Intergenic nucleotides	Strand
Control region	1	1169	1169				0	N/A
tRNA ^{Phe}	1170	1236	67				0	Н
12S rRNA	1237	2215	979				0	Н
tRNA ^{Val}	2216	2289	74				0	Н
16S rRNA	2290	3887	1598				-1	Н
tRNA ^{Leu} (UUR)	3887	3960	74				+9	Н
nd1	3970	4944	975	325	ATG	TAA	0	Н
tRNA ^{Ile}	4945	5018	74				+6	Н
tRNA ^{Gln}	5025	5095	71				-1	L
tRNA ^{Met}	5095	5163	69				0	Н
nd2	5164	6202	1039	346	ATG	T	0	Н
tRNA ^{Trp}	6203	6281	79				+6	Н
tRNA ^{Ala}	6288	6359	72				-2	L
tRNA ^{Asn}	6358	6420	63				+12	L
tRNA ^{Cys}	6433	6498	66				-1	L
tRNA ^{Tyr}	6498	6568	71				+1	L
coxl	6570	8120	1551	517	GTG	AGG	-7	Н
tRNA ^{Ser} (UCN)	8112	8186	75				+2	L
tRNA ^{Asp}	8189	8257	69				+1	Н
cox2	8259	8942	684	228	ATG	TAG	+1	Н
tRNA ^{Lys}	8944	9010	67				0	Н
atp8	9011	9176	165	55	ATG	TAA	-8	Н
atp6	9167	9850	684	228	ATG	TAA	-1	Н
cox3	9850	10,633	784	261	ATG	T	+1	Н
tRNA ^{Gly}	10,635	10,702	68				0	Н
nd3	10,703	11,054	352	117	ATG	TAA	+1	Н
tRNA ^{Arg}	11,056	11,124	69				0	Н
nd4l	11,125	11,421	297	99	ATG	TAA	-5	Н
nd4	11,415	12,792	1377	459	ATG	T	0	Н
tRNA ^{His}	12,792	12,860	69				+1	Н
tRNA ^{Ser} (AGY)	12,862	12,926	65				+2	Н
tRNA ^{Leu} (CUN)	12,929	12,999	71				0	Н
nd5	13,000	14,817	1818	606	ATG	TAA	+4	Н
cytb	14,822	15,964	1143	381	ATG	TAA	+3	Н
tRNA ^{Thr}	15,968	16,036	69				0	Н
tRNA ^{Pro}	16,037	16,112	76				+5	L
nd6	16,118	16,639	522	174	ATG	AGG	+1	L
tRNA ^{Glu}	16,641	16,709	69				0	L

Declaration of interest

The study was supported by TSU University Research Center (URC)-NASA Center for Bionanotechnology and Environmental Research (CBER) – NASA Cooperative Agreement NNX0BA47A and the TSU College of Science and Technology 2013 Summer Undergraduate Research Program. Kind thanks to Christine Miller and James Dunster at Zoo Miami for donating the specimen (HMNS 3464). The authors report no conflicts of interest and are responsible for the writing and content of this paper.

References

- Bird Life International. (2001). Threatened birds of Asia: The Bird Life International Red Data Book. Cambridge, UK: Bird Life International. Desjardins P, Morais R. (1990). Sequence and gene organization of the
- chicken mitochondrial genome. A novel gene order in higher vertebrates. J Mol Biol 12:599–634.

- Lowe TM, Eddy SR. (1997). tRNAscan-SE: A program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 25:955–64.
- Mallari NAD, Collar NJ, Lee DC, McGowan PJK, Wilkinson R, Marsden SJ. (2011). Population densities of understorey birds across a habitat gradient in Palawan, Philippines: Implications for conservation. Oryx 45:234–42.
- McGowan PJK, Garson PJ. (1995). Pheasants: Status survey and conservation action plan, 1995–1999. Gland, Switzerland: International Union for Nature Conservation and Natural Resources and World Pheasant Association.
- Ojala D, Montoya J, Attardi G. (1981). tRNA punctuation model of RNA processing in human mitochondria. Nature 290:470–4.
- Omeire D, Abdin S, Brooks D, Miranda Jr HC. (2014). Complete mitochondrial genome of Germain's Peacock-Pheasant *Polyplectron* germaini (Aves, Galliformes, Phasianidae). Mitochondrial DNA. [Epub Ahead of Print]. doi: 10.3109/19401736.2013.830292.
- Shen YY, Shi P, Sun YB, Zhang YP. (2009). Relaxation of selective constraints on avian mitochondrial DNA following the degeneration of flight ability. Genome Res 19:1760–5.

STEM EXCELLENCE MOVING FORWARD – NEXT STEPS



For Information Please Contact:

Dr. Hyun-Min Hwang Department of Environmental and Interdisciplinary Sciences

> Texas Southern University 3100 Cleburne Street Houston, Texas 77004

Tel: 713 313 1028 Email: hwangh@tsu.edu

WWW.COSET.TSU.EDU

COSET ADMINISTRATION



Lei Yu Professor and Dean

OFFICE OF THE DEAN



Professor and Interim Associate Dean



Charlotte Whaley College Business Admin. III



Shishir Shishodia Associate Professor and Interim Associate Dean



Dolly Spencer Sr. Administrative Assistant



Desirée A. Jackson Associate Professor and Assistant Dean



Tioka Freeman Administrative Assistant



Evangeline Pearson Director of Advisement



Peter Olamigoke Tech. Support Specialist

AVIATION SCIENCE AND TECHNOLOGY



David Olowokere Professor and Interim Chair



Gertrude Florent Administrative Assistant



BIOLOGY

Warren E Williams Associate Professor and Interim Chair



Helen P. Cockrell Administrative Assistant

INDUSTRIAL

TECHNOLOGY

Jessie E. Horner

Associate Professor and

Interim Chair

Lulueua A. Nasser

Administrative Assistant



John B. Sapp Professor and Chair

CHEMISTRY



Delois S. Johnson Administrative Assistant

MATHEMATICS



A. Serpil Saydam Associate Professor and Chair



Nia Eakins Administrative Assistant

COMPUTER SCIENCE



Wei Wayne Li Professor and Interim Chair



Nadereh Jahedmotlagh Administrative Assistant

PHYSICS



Carlos Handy Professor and Chair



Gertrude Florent Administrative Assistant





David Olowokere Professor and Chair



Lulueua A. Nasser Administrative Assistant

TRANSPORTATION STUDIES



Yi Qi Associate Professor and Chair



Paula Eakins Administrative Assistant



Shishir Shishodia Associate Professor and Interim Chair



Rachel Mizzell Administrative Assistant