



University of Houston-Downtown

PROGRAM

9th ANNUAL GRADUATE SCHOOL AND INTERNSHIP FAIR

Sponsored by the UHD Scholars Academy

Funded by the
Brown Foundation, National Science Foundation, U.S. Army Research Office,
U.S. Department of Education, University of Houston-Downtown



Friday, October 24, 2008
UHD Special Events Center

Welcome Address

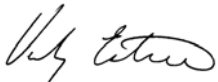
On behalf of the UHD Scholars Academy and the College of Science & Technology, we would like to welcome you to the 2008 Scholars Academy Graduate School & Internship Fair. The UHD Scholars Academy (SA) is a competitive academic program for undergraduates majoring in science, technology, engineering and mathematics (STEM) fields. The SA works to increase the number of academically capable students graduating with degrees in STEM fields and to increase the number of those choosing to pursue graduate study in these fields. This year, the Scholars Academy has grown to 166 students. Most of these students are in attendance today along with numerous other students majoring in the STEM fields.

We are proud to announce the inclusion of a Student Poster Presentation Session as part of the Graduate School and Internship Fair. The research work presented in these select scientific posters are the result of independent student research conducted on the UHD campus or at collaborating institutions. Our student driven research has served as a springboard for presentations at regional and national scientific conferences. All students in the SA are encouraged to participate in independent research projects during their undergraduate career and approximately 66% of the SA students do. This past summer, 60 students participated in independent research activities, with another 30 students in off-campus interns at the Texas Medical Center, Case Western Reserve School of Medicine, HACU, Rice University, Stanford University, and UT Medical Branch.

Last academic year, Academy students presented approximately 100 posters at local and national meetings. Within this time period, Academy students presented research posters to the regional/national conferences including ABRCMS, ACS, ASM, MAA, NCUR, RADTech, SACNAS, Sigma XI, TAS, and WAESO, and additional local meetings within their disciplines, and won several awards for their work.

We hope you enjoy your time at UHD with our students and Scholars, and we all look forward to collaborating with you and your institutions in the future.

Sincerely,

A handwritten signature in black ink, appearing to read "Vicky Estrera".

Vicky Estrera, Ph.D.
Director, UHD Scholars Academy

A handwritten signature in black ink, appearing to read "Akif Uzman".

Akif Uzman, Ph.D.
Chair, Dept. of Natural Science

Table of Contents

Welcome Address	2
Table of Contents	3
Program Schedule	4
Graduate School and Internship Programs	5
Student Poster Abstracts	7

Program Schedule Friday, October 24, 2008

8:30 - 9:00 am	Registration and Check-in
9:00 - 10:30 am	Student Poster Session and Breakfast Mixer
10:30- 12:15 pm	Graduate School and Internship Exhibits
12:15- 1:15 pm	Lunch for invited guest, faculty and student poster presenters

Conference Organizers:

Dr. Vicky Estrera, Director, Scholars Academy, UHD
Mr. Rene Garcia, Program Manager, Scholars Academy, UHD
Dr. Akif Uzman, Chairman, Department of Natural Sciences, UHD

UHD Scholars Academy Co-Directors:

Dr. Dennis Rodriguez, Chairman, Department of Computer and Mathematical Sciences
Dr. Edward Sheinberg, Chairman, Department of Engineering Technology
Dr. Akif Uzman, Chairman, Department of Natural Sciences
Dr. Richard Alo, Executive Director, Center for Computational Science
Dr. Larry Spears, Director, Urban Center for Student Success in STEM
Dr. George Pincus, Dean, College of Sciences and Technology

SJCN Scholars Academy:

Mr. Lamar McWaine, Director, San Jacinto College North Campus

Graduate School and Internship Programs

Baylor College of Medicine

Graduate School of Biomedical Sciences

Molecular and Human Genetics

Molecular Physiology and Biophysics

SMART Program: Summer Undergraduate Research Training

City of Houston – Houston Crime Lab

Exponent

Gulf Coast Consortia

Interdisciplinary Bioscience Research and Training

Kaplan Test Prep and Admissions – Graduate Programs

Our Lady of the Lake University

Student Life

Rice University

Department of Biochemistry & Cell Biology

Student Conservation Association

Houston Conservation Collaborative

Texas A & M University Health Science Center

College of Medicine

Texas Southern University

Graduate School

Texas Woman's University

Office of Admissions

University of Houston-Central

Admissions and Recruitment, College of Pharmacy

Department of Biology and Biochemistry

Department of Mathematics

Rice-Houston Alliances for Graduate Education and the Professoriate (AGEP)

University of Texas - MD Anderson Cancer Center

Genes and Development Graduate Program

Office of Academic Affairs

University of Texas Health Science Center Houston

**Graduate School of Biomedical Sciences
School of Health Information Sciences
School of Nursing
School of Public Health
Summer Research Programs**

University of Texas Health Science Center San Antonio

Graduate School of Biomedical Sciences

University of Texas Medical Branch

**Biochemistry and Molecular Biology Graduate Program
School of Allied Health Sciences
School of Nursing**

University of Texas Southwestern Medical Center at Dallas

Division of Basic Sciences

The following institutions have provided materials for dissemination:

Association of American Medical Colleges

Biomedical and Health Sciences Research

Gerstner Sloan-Kettering

Graduate School of Biomedical Sciences

Iowa State University

College of Engineering

The Rockefeller University

Office of Graduate Studies, Summer Undergraduate Research Program

University of Rochester Medical Center

MD/PhD Program

University of Wisconsin Madison

IGERT & SAGE Gaylord Nelson Institute for Environmental Studies

Student Poster Abstracts:

1. Can We Model Early Fenfluramine-Phentermine Valvulopathy?

Frances Acevedo* and Janet Barzilla**

Dr. K. Jane Grande-Allen, Research Mentor, Department of Bioengineering, Rice University

* Department of Natural Sciences, University of Houston-Downtown

** Department of Bioengineering, Rice University

Abstract: This research was aimed at modeling the early stages of fenfluramine-phentermine (fen-phen) valvulopathy in a mitral valve. To accomplish this, we exposed mitral valve tissues to norfen and to norfen with a serotonin blocker. The idea was that the norfen exposed tissue would develop early stages of fen-phen valvulopathy; and the tissue exposed to norfen and serotonin blocker would not show signs of fen-phen valvulopathy. The tissue was exposed to the drugs for two weeks in a bioreactor which would provide mechanical stimulation. Several histological stains were applied to the tissue samples; including a Movat pentachrome stain, Immunohistochemical stain for cell proliferation, and a hematoxylin-eosin stain. Comparisons of the tissues were then conducted using the different stains to determine the effects of the drugs on the tissue.

2. Pot1b Deletion and Telomerase Deficiency Models the Syndrome Dyskeratosis Congenita

Dennis Garcia

Hua He, Ph.D., Research Mentor, U.T. M.D. Anderson Department of Cancer Genetics; Sandy Chang, M.D., Ph.D., Primary Investigator, U.T. M.D. Anderson Department of Cancer Genetics

Abstract: Telomeres are tandem repeats (TTAGGG) located at the ends of eukaryotic chromosomes and protected from the DNA damage response by the protein shelterin complex. In the human shelterin complex, the protein Pot1 (Protection of Telomere) is a negative length regulator and is essential for maintaining genomic stability. The murine shelterin complex contains two orthologs of the human Pot1 protein, Pot1a and Pot1b. Previous studies demonstrated that Pot1a is critical for telomere end-protection. Here, we hypothesize that Pot1b is involved in telomere length regulation. Using mice engineered with the knock-out of Pot1b in a background of telomerase deficiency, various phenotypes were observed, including rapid telomere degradation, cutaneous phenotypes, testicular atrophy, male infertility, and an overall reduction in lifespan due to bone marrow failure. These phenotypes resemble the characteristic features of the rare inheritable human syndrome Dyskeratosis congenita (DC). This mouse model should be important to further understand the pathophysiology of DC.

3. Incorporating Protein Flexibility in Virtual Screening

Edgar Alan Gatica

Dr. Claudio N. Cavasotto, Research Mentor, School of Health Information Sciences, University of Texas Houston Health Science Center

Abstract: Typical structure-based virtual screening uses a flexible ligand-rigid receptor docking approach. This method fails to account for the induced-fit effects, in which the receptor flexes upon ligand binding. As a result, the docking algorithm may fail to dock a known binder to a rigid receptor. Incorporating receptor flexibility may be necessary to ensure proper docking in cases where rigid receptor docking is unsuccessful. However, explicit flexible-ligand:receptor docking is computationally too expensive for use in large-scale virtual screening experiments. An alternative strategy is the use of multiple rigid receptors to simulate a single flexible one. The docking scores are then merged, and the resulting list is condensed to a size equivalent to that of a single screening (the merging-shrinking procedure). Unfortunately, previous attempts to use this method have shown mixed results. We hypothesize that this is due to the inclusion of redundant receptor combinations, which dilutes the performance of the method.

4. The Spontaneously Hypertensive Rat (SHR) Model and Investigation of Glutathione Levels in Association with Renal Injury

Micaela Gilbert

Dr. Peter A. Doris, Research Mentor, Institute of Molecular Medicine at the University of Texas Houston Health Science Center

Abstract: The kidney is capable of significant glutathione synthesis, a major anti-oxidant molecule. Hypertension is associated with renal oxidative stress, indicating that aspects of renal anti-oxidant mechanisms may be altered. The experimental model of hypertension exploited was the spontaneously hypertensive rat, SHR, from several distinct genetic sub-strains. Most of these strains resist the end-organ injury associated with hypertension; however, the SHR-A3 strain is susceptible to renal injury and stroke. The present project compares the renal glutathione content of SHR-A3 animals with those in the injury resistant SHR-B2 strain during and after the development of hypertension (and renal injury in SHR-A3)

to address the hypothesis that reduced renal anti-oxidant protection in SHR-A3 is associated with the emergence of renal injury. Heritability of renal glutathione content was estimated at 27%, indicating the renal glutathione levels in the SHR lines we have compared is subject to genetic influence, in addition to environmental influence.

5. Multivariate Analysis of the Factors Affecting the Spread of Pierce's Disease Across Texas

Audrey Gonzalez, Ali Abedi, Shawn Luce, Lauren Gracia

Dr. Lisa Morano, Research Mentor, Department of Natural Sciences, UHD

Abstract: Pierce's disease (PD) is caused by *Xylella fastidiosa* (Xf) a plant pathogen that infects grapevines. The bacterium is transferred by sharpshooter insects which multiply in the xylem (water-conducting vessels) causing plant death. PD is an agricultural threat to both the Texas and California grape industries. The objective of this study is to analyze the significance of the factors which are most responsible for the spread of PD across Texas. The multivariate data set includes information about disease incidence, sharpshooter insect frequencies and environmental variables (ie. elevation, precipitation, cold hardiness, plant community classification). Ordination methods (Principal Components Analysis, Correspondence Analysis) and ordination combined with regression methods (Redundancy Analysis and Canonical Correspondence Analysis) will be utilized to determine which variables explain the epidemiology of PD spread across the state. Analyses will be completed numerically with the aid of XLSTAT and CANOCO software packages.

6. Multivariate Data Analysis for Ecological Applications

Lauren Gracia

Dr. Jeong-Mi Yoon, Research Mentor, Department of Computer and Mathematical Sciences, UHD

Abstract: Ecologists have encountered a problem with how to analyze complex ecological data sets which are typically organized in rows corresponding to sample sites, and columns representing the variables describing the biological communities, or the physical environment. This type of data is called multivariate data. To analyze such types of data, mathematicians support ecologists to find the best numerical methods based on the data. We'll discuss the following five numerical methods with chosen data sets: Multiple Regression; Principal Component Analysis; Correspondence Analysis; Redundancy Analysis; and Canonical Correspondence Analysis. The first two methods represent the ordered relationships between sample, sites, and species. The last two methods show the relationship between a first table describing species and a second table of environmental descriptors combining the concepts of ordination and regression, observed at the same sites. The obtained results will be analyzed and compared by using two chosen statistical software, XLSTAT and CANOCO.

7. Induction of β -lactamase Genes of *Bacillus cereus* Group Species in Response to Cell-wall Damaging Antibiotics

Claudia Jiménez López

Drs. Cana L. Ross and Theresa M. Koehler, Research Mentors, The University of Texas - Houston Health Science Center Medical School

Abstract: Of the 80 *Bacillus cereus* group species include *B. cereus*, *B. thuringiensis*, and *B. anthracis*. Despite their overall genomic similarity they exhibit different phenotypes, including synthesis of β -lactamases. All three species harbor β -lactamases (*bla*) genes. Nevertheless, prototypical *B. anthracis* strains are penicillin-susceptible while *B. cereus* and *B. thuringiensis* strains exhibit inducible penicillin-resistance. To determine if *bla* gene expression is induced in response to β -lactama antibiotic-mediated cell wall damage or by the presence of the antibiotic itself, we examined *bla* gene expression during growth in the presence of antibiotics that interfere with different stages of cell wall synthesis. Each species harbored a plasmid-borne *B. anthracis bla2* promoter followed by a promoterless *lacZ* gene. In this way, antibiotic induction of *bla2* promoter would produce β -galactosidase. The results showed that in *B. cereus* and *B. thuringiensis* cultures *bla2* promoter was only induced by the β -lactams ampicillin and cefazolin, suggesting that *B. cereus* and *B. thuringiensis*, but not *B. anthracis*, produce β -lactamases in response to β -lactam antibiotics. Consequently, β -lactamase synthesis is not induced by cell wall stress.

8. Inhibition of Dental Biofilms Using Commercial Mouthwashes

Uffaf Khan*, Neeraj Salhotra**, Natalie Sirisaengtaksin*, Claudia Jiménez López*, Syeda Kazmi*, Evelin Vaquiz*, Chau Nguyen***, and Laura Lucio*

* Department of Natural Sciences, University of Houston-Downtown, Houston, TX

** St. John's School, 2401 Claremont Lane, Houston, TX

*** Northbrook High School, #1 Raider Circle Houston, TX

Dr. Dr. Poonam Gulati, Research Mentor, Department of Natural Sciences, UHD

Abstract: Dental plaque is a community of bacteria living within extrapolymeric substances (EPS) synthesized and secreted by them, also called biofilms. In this project, we were interested to study the effects of commercial mouthwashes on biofilm versus planktonic cells. Plaque bacteria were collected from student volunteers of different demographics.

These samples were grown as planktonic cells or as biofilms on 12-well plates. We tested three mouthwashes at different concentrations to see the minimum bactericidal concentration (MBC) for each mouthwash on the planktonic cells and on biofilms. The planktonic cells were plated on LB agar medium after the treatment. The biofilms were scraped off the wells, resuspended in media and plated. Colony forming units were counted the next day. The preliminary results showed that Scope did not cause complete biofilm inhibition but Crest and Listerine did. The data also indicated that different people respond to different mouthwashes. However, with planktonic cells Scope mouthwash worked better. The difference seen may be due to the accessibility of the cells.

9. Antibiotic Inhibition and Mathematical Modeling of *Mycobacterium smegmatis* Biofilms

Benedict Khoo, Jamal Dawson, Whitney Bass

Drs. Youn-Sha Chan* and Poonam Gulati**, Research Mentors, *Department of Computer and Mathematical Sciences, **Department of Natural Sciences, UHD

Abstract: In nature, most microbes live in communities called biofilms, embedded in a self-produced and secreted matrix of extracellular polymeric substances (EPS). The biofilm facilitates bacterial survival under harsh conditions and environmental insults. In the clinical setting, formation of these sessile easily-formed recalcitrant bacterial biofilms on implanted devices such as artificial joints can lead to bacterial colonization, and systemic infection, serving as a pertinacious bacterial reservoir while affording an inherent resistance to antimicrobial agents. This investigation sought to study the inhibitive effects of the antibiotics Streptomycin and Tetracycline on *Mycobacterium smegmatis* in its planktonic form and as biofilms. Mathematical modeling explored the dynamic system to provide insight into the system dynamics under antibiotic stress treatment. By studying the effective antibiotic doses with the help of mathematical models, a better understanding of the dynamic system can be achieved, and future modes of application can be developed for treating diseases such as tuberculosis.

10. Mathematical Modeling of the BMP4 and FGF Signaling Pathways during Neural and Epidermal Development in *Xenopus laevis*

Marsida Lisi and Tung Bui

Drs. Edwin Tecarro* and Akif Uzman**, Research Mentors, *Department of Computer and Mathematical Sciences, **Department of Natural Sciences, UHD

Abstract: During embryonic development, ectodermal cell fate in *Xenopus laevis* is determined by the mitogen-activated protein (MAP) kinase and bone morphogenetic protein-4 (BMP-4) signaling pathways. In an attempt to further understand the interactions between these two pathways, a mathematical model consisting of coupled, nonlinear ordinary differential equations has been developed. Properties of this model are described by using linear stability analysis and bifurcation theory. Numerical computations, including bifurcation studies, have been carried out to elucidate the interaction between the two signaling pathways.

11. Fungal Communities along the Buffalo Bayou: Influence of Salinity and other Environmental Gradients

Van Nguyen, Pantea Mohammadi, and Nida Rizvi

Drs. Shishen Xie* and Phil Lyons**, Research Mentors, *Department of Computer and Mathematical Sciences, **Department of Natural Sciences, UHD

Abstract: We consider the correlation between environmental gradients such as salinity, pH, elemental composition, and the diversity of soil fungal communities along Buffalo Bayou. Upon determining which correlations exist mathematical models will be formulated representing the relationship between specific environmental factors and different fungal taxa. We are using biological analyses such as direct isolation of soil fungi and indirect determination of fungal taxa based on DNA sequence variations to determine the diversity of fungi within the Buffalo Bayou ecosystem. As a sufficient data is accumulated, efforts will be directed toward mathematical analyses including statistical model and multivariate analysis.

12. Characterization of EB1-P150^{Glued} Interactions

David Nanyes

Drs. Yan-Min Yang and Wei Wang, Department of Neurology, Stanford University School of Medicine

Abstract: The microtubule (MT) network plays an important role in cell structure and cellular trafficking. Acquiring information on proteins that interact with microtubules is essential and may lead to a better understanding of cell physiology. End Binding Protein 1 (EB1) is a protein that binds to the microtubule network and may play a vital role in regulating microtubule dynamics. EB1 has a significant binding affinity for the growing plus ends of the microtubule (+TIPs). P150^{Glued} is the largest subunit of the dynein/dynactin complex and is a binding partner of EB1. Its function with EB1 may hold further information on microtubule-protein interactions. Previous research suggested that Lysine 220, Arginine 222, and the last 4 amino acids of EB1 are required for binding to P150^{Glued} (Hayashi et al. 2005). We constructed point mutations on EB1 to assess effects that would have on the binding of P150^{Glued}. My results showed decreased binding

activity between EB1 mutants and P150^{Glued}. A complete loss of binding to P150^{Glued} was observed with EB1 mutation (KR-DEL), this may suggest that Lysine 220, Arginine 222, and the last four amino acids on EB1 are essential for P150^{Glued} binding. Several experiments were undertaken to see whether the microtubule network would be affected by over-expressing EB1 wt, EB1 mutations, or P150^{Glued}. I found that over-expression of EB1 wt may change some MT network characteristics, suggesting that normal EB1-P150^{Glued} function may be inhibited.

13. **A Comparison in Diatom Assemblages between Anahuac National Wildlife Refuge (ANWR) and Greens Bayou Wetland Mitigation Bank (GBWMB)**

Justine Onyedebelu, Harold Lee, and Elzary Asberry

Dr. Brad Hoge, Research Mentor, Department of Natural Sciences, UHD

Abstract: The diatom death assemblage was studied in the Green's Bayou Wetlands Mitigation Bank (GBWMB) in Harris County, Texas and compared to the Anahuac National Wildlife Refuge (ANWR) in order to determine the extent of succession in the GBWMB. Wetland mitigation aims to replace wetland functions which provide public benefits, such as flood storage, water quality protection, and fish and wildlife habitat. It may be possible to determine the success of wetland mitigation through a study of the succession of non-introduced organisms in the GBWMB. Diatoms, which are found in all wetlands, are expected to provide evidence of succession in the GBWMB as the water and soil chemistry of the wetland change over time. Anahuac is an undisturbed natural wetland so it provides a good example of a climax community to check the mitigation success of GBWMB, an artificial wetland, by comparing the diatom assemblages from Anahuac and the GBWMB.

14. **Advancing Computational Methods for Protein Structure Determination: Rosetta + Footprinting**

Nicolle Patterson

Drs. Xiaojing Zheng and Mark R. Chance, Case Center for Proteomics, Case Western Reserve School of Medicine

Abstract: There are millions of sequences coding for proteins that are responsible for different functions in the human body and other living organisms. Understanding the structures of these proteins will allow us to understand the functions that these proteins serve as well as their mechanisms of reaction. Although protein structure information is extremely important, obtaining structural information is challenging using current methods. Currently computation tools are becoming increasingly popular for the prediction of protein structure. However computational approaches are not without problems. They are time consuming and computationally expensive. In addition to that, several lowest energy structures are generated making the prediction of the structure difficult and sometimes impossible. The purpose of this project is to develop a novel idea for computer based structure determination. This is based on the hypothesis that a combination of Rosetta software and footprinting methods will result in faster and more accurate structure prediction. For this project we took 15 Protein Structure Initiative (PSI) targets with the aim of using the aforementioned methods on them. Through various processes, we were able to utilize 6 of the PSI targets, and successfully determine the structure of all of them. The results suggest that this method can be used for fast and accurate protein structure determination.

15. **The Early Effects of Maxillary Expansion - A Clinical and Conebeam Computed Tomography Report**

Kristi Pennington

Drs. Carin Domann and Chung How Kau, Research Mentor, Dental Branch, University of Texas Houston Health Science Center

Abstract: The effects of rapid maxillary expansion have been studied since its first documentation in 1860. Maxillary expansion devices are used routinely. Rapid maxillary expansion (RME) is a valuable treatment with a variety of benefits including correction of transverse discrepancies, increase of arch length, correction of sagittal discrepancies and improved nasal breathing. The purpose of this study is to investigate the initial effect of maxillary expansion on the dental alveolar region and midpalatal suture system using expansion appliances on the maxillary complex. The investigation was conducted using a Cone Beam Computed Tomography (CBCT) device. Retrospective evaluation of twenty clinical records already present in an orthodontic clinic took place. Measurements for the amount of dental expansion, the axial inclination of the palatal root of the maxillary first molar, and the thickness of the buccal plate at the level of the first molar roots were performed on pre and post CBCT scans. The results of this study are still pending the arrival of a few post scans that have not been taken. Following the completion of the data sets, a paired t-test will be used to analyze the data on the following criteria: amount of expansion, dental alveolar bone/buccal bone, and molar angulation.

16. **Regulation of HOX gene expression by SAFB1**

Laura Sanchez

Drs. Benny Kaiparettu and Steffi Oesterreich, Breast Center, Baylor College of Medicine

Abstract: SAFB1 is a large multifunctional protein. Genetic deletion of SAFB1 in mice results in dramatic pleiotropic defects, and high rates of lethality. It is also involved in many cellular processes such as chromatin organization,

transcriptional regulation, RNA splicing and stress response. In breast cancer though, SAFB1 functions as an estrogen receptor co-repressor and growth inhibitor. Loss of SAFB1 was associated with high grade breast cancer and in almost 20% of breast tumors undetectable SAFB1 protein levels have been observed. Loss of SAFB1 is also associated with worse overall outcome of breast cancer patients. Using cDNA, microarray data of RNA from immortalized SAFB1 knockout (KO) and wild type (WT) mouse embryonic fibroblasts (MEFs), several HOX genes have shown to be significantly affected by the deletion of SAFB1. This was further confirmed by quantitative real time PCR (q-PCR). However, this difference was not so evident in the primary MEFs. This suggested that long term depletion of SAFB1 might regulate HOX gene's expression. q-PCR analysis confirmed the microarray observation that several HOX genes are either up-regulated or down-regulated upon the deletion of SAFB1. In order to know whether HOX gene alteration in SAFB1 KO MEFs is a gradual process or a sudden change during immortalization a q-PCR analysis was done. The results showed that the change in HOX expression is a gradual process and it altered corresponding to the increase in passage. In one KO MEF, the expression of HOXB6 and HOXC8 gradually increased and the other KO MEF the same HOX genes were gradually decreased. However, this change was not evident in the WT MEF. Further analysis and future questions are intended in order to derive an accurate mechanism for the regulation of HOX genes.

17. PID Controller for a Tank System

Daniel Siddiqui

Dr. Heider Malki, Research Mentor, College of Engineering Technology, University of Houston

Abstract: This project presents the application of a Proportional-Integral-Derivative (PID) Controller for controlling water level in a tank. The PID Controllers are widely applied in industry. A controller output is generally based on the error between a set-point and the actual output of the plant. The proposed PID controller was used to control the flow-level of water from Tank 1 to Tank 2 in a Twin Tank System. The tank level system was simulated in LabVIEW. The proposed controller demonstrated satisfactory results in controlling water level between the two tanks. The proposed PID controller will be implemented in a real-world tank system by next summer as part of the NSF-REU SITE at UH-College of Technology.

18. Molecular-based Identification of Bacteria Within Dental Biofilms Before and After Treatment with Commercial Mouthwashes

Natalie Sirisaengtaksin and Evelin Vaquiz

Dr. Poonam Gulati, Research Mentor, Department of Natural Sciences, UHD

Abstract: Plaque is a type of dental biofilm that forms on the surface of teeth. Microbial organisms involved in dental plaque formation are the leading cause of dental caries, which lead to the development of cavities and tooth decay. Biofilms are the preferred mode of existence for most microbes, in contrast to a planktonic, free-floating lifestyle. Biofilms are a community of microorganisms that are encased within extrapolymeric substances (EPS), which they secrete when stressed by their environment. EPS protects cells exposed to extreme temperatures, pH levels, and nutrient-deficient environments. They also increase bacterial resistance to antimicrobials, such as antibiotics and mouthwash. This project focuses on identifying bacteria within dental biofilms, and comparing the bacterial populations before and after exposure to commercial mouthwashes. The 16s rRNA sequence was isolated from dental plaque samples and cloned into competent cells to separate sequences from different species. The DNA were recovered from the cells and sent for identification. Both cultured and uncultured species of *Streptococcus* were found.

19. A Natural Language Processing Application

Mark Smithers

Dr. Ping Chen, Research Mentor, Department of Computer and Mathematical Sciences, UHD

Abstract: Natural Language Processing is a subfield in artificial intelligence that addresses the problem of computers understanding natural human languages. Information Technology, Biomedicine, Criminal Justice, and Marketing are examples of fields using application of Natural Language Processing. I am using c++ to implement a natural language processing program that evaluates the strength of pairs of words obtained from free text.

20. Study of Transitional Metal Based Detector for Carbohydrates

An Vo

Dr. Mian Jiang, Research Mentor, Department of Natural Science, UHD

Abstract: Mono-, oligo-, and poly-saccharides are essential components in life circle. The detection of these carbohydrates varies from assay kit, sophisticated HPLC to x-ray analysis. We systematically examined transition metals Co, Ni, Cu, Pd, Au, and their alloys, for their sensing capacity toward carbohydrates. Voltammetry was used for qualitative and quantitative comparisons. The results have shown the highest sensory effect of these metals for monosaccharides can only occur at alkaline media, and polysaccharides revealed no response. We found thin nickel layer coated electrodes exhibited a stable

and sensitive voltammetric peak for monosaccharides with minimal surface fouling effect. This response is based on catalytic oxidation of sugar molecules at around Ni (II/III) moieties and shows linearity depending on the analyte concentration. Following these findings, we developed a new selective detection of simple carbohydrates in the presence of polysaccharides. Our protocol can be extended into monitoring the decay/decomposition of polysaccharides such as starches.

21. An Excellent Electrocatalyst for Fabrication of Sensors Used in Alkaline Media

Desirée S. Wilson

Dr. Mian Jiang, Research Mentor, Department of Natural Science, UHD

Abstract: Most of this study thus far concentrated on application in ambient condition where most sensing layers and targets are active, which offers compatibility between the measurement operation and storage of the sensors. In this work we tackled this issue and present nickel hydroxide as a simple, stable, and reusable sensing material for variety of potential targets that have not been reported before. The theoretic foundation of our study was based on the high insolubility of nickel hydroxide in aqueous media. Our practical approach was through (1) the chemical “dipping” preparation, or (2) the electrochemical in situ fabrication. Both protocols generated identical results, though the latter offered better control of the film thickness. The resultant nickel hydroxide film displays an excellent, well-defined, reduction-oxidation behavior in strong alkaline media. Our study indicated a variety of chemical and biochemical molecules can be catalyzed on this film, ranging from hydrazine, hydrogen peroxide, aldehydes, sulfite, to vitamine B, acetaminophen. Moreover, the catalytic current displays a concentration dependence that can be used for analytical and sensing application.