THE ANA G. MÉNDEZ UNIVERSITY SYSTEM (AGMUS) AND THE STUDENT RESEARCH DEVELOPMENT CENTER (SRDC) ARE PROUD TO HOST THE

WINTER 2009 PRE-COLLEGE RESEARCH SYMPOSIUM

SHOWCASING MINORITY HIGH SCHOOL STUDENTS’ MENTORED RESEARCH

Leadership at SUAGM Vice Presidency for Planning and Academic Affairs

Mr. Jorge L. Crespo Armáiz
Vice President for Planning and Academic Affairs

Juan F. Arratia, Ph. D.
Student Research Development Center
Executive Director

UNIVERSIDAD METROPOLITANA CAMPUS
SAN JUAN, PUERTO RICO

December 12, 2009
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National Science Foundation  
AGMUS Institute of Mathematics  
Student Research Development Center  
Ana G. Méndez University System

MISSION

The Model Institutions for Excellence (MIE) award granted by the National Science Foundation helped transform Universidad Metropolitana (UMET) into a nationally recognized undergraduate research institution, and a model in science, technology, engineering and mathematics (STEM). Mentoring of undergraduates and pre-college students by research mentors was the cornerstone of the MIE Project. We believe that creative research is one of the best ways to prepare students to become persistent and successful in graduate school and professional careers. Today, the Student Research Development Center (SRDC) is the entity that continues the MIE strategy by impacting students from the AGMUS System and universities across the nation, as well as pre-college students from the Puerto Rico Educational System.

EXECUTIVE SUMMARY

The MIE award ended, the Student Research Development Center continues the primary goal of the cooperative agreement which was to increase the number of BS degrees granted to underrepresented students in STEM fields at Universidad Metropolitana. In order to increase the number of BS degrees transferred to graduate school, we will continue with the strategy of an early undergraduate research program and partnership with key research institutions in the US mainland, Puerto Rico and abroad. Research mentoring will be the central component of the knowledge transfer and creative thinking activities at AGMUS. Cooperative and collaborative learning strategies, presentations at scientific conferences, scientific writing and co-authorship, technology literacy, and preparation for graduate school are activities that are transforming the philosophy of the institution.

GOALS

The main goals of the AGMUS Pre-College Research Symposium are to: encourage pre-college research with research mentors; develop students’ written and oral communication skills; provide a forum in Puerto Rico for students to foster interest in undergraduate education, particularly in STEM fields; and set national research standards for pre-college research presentations.
**SUNDAY, DECEMBER 13, 2009**

**AMPHITHEATER**

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<td>7:00 – 8:00 a.m.</td>
<td>Poster Session Set-Up/Breakfast, Cafeteria/Registration, Muñiz Suffront Building Lobby</td>
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<td>8:00 – 8:30 a.m.</td>
<td>Opening Ceremony, Amphitheater, Keynote Speaker Dr. Martha Bilotti Aliaga, American Statistical Association</td>
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<td>8:30 – 10:00 a.m.</td>
<td>Poster Session, Muñiz Suffront Building Lobby and Jesus T. Piñero Building Lobby</td>
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<td>10:00 – 11:40 a.m.</td>
<td>Oral Research Presentations, Amphitheater and Room MS-120</td>
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<td>12:10 – 12:50 p.m.</td>
<td>Award Ceremony and Closing Remarks</td>
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<td>1:00 p.m.</td>
<td>Lunch, Cafeteria</td>
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<tr>
<td>2:00 p.m.</td>
<td>Symposium Adjourns</td>
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**WORKSHOP**

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<td>8:00 – 3:00 p.m.</td>
<td>“Statistics and Probabilities,” Dr. Martha Bilotti-Aliaga, American Statistical Association, Investigación Científica Building, Room 301</td>
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December 12, 2009

Dear Symposium Participants:

The Ana G. Méndez University System (AGMUS) is proud to be part of the Winter 2009 Pre-College Research Symposium organized by its Student Research Development Center, a leading organization implementing early scientific research activities in Puerto Rico.

For a number of years, AGMUS has designed and offered young aspiring Hispanics like you the opportunity to learn research skills and present their research outcomes through oral and poster presentations in English in an academic environment. The experience makes you more knowledgeable and competitive as it prepares you to pursue careers in the science, technology, engineering and mathematics (STEM) fields.

We truly appreciate the support provided by the National Science Foundation, the Puerto Rico Space Grant Consortium, and the student researchers and mentors who guided you at Universidad Metropolitana, Universidad del Este and Universidad del Turabo research facilities, supported this experience, and prepared you for a world in need of innovation and committed researchers and scientists.

Congratulations to all of you for your efforts to increase our scientific knowledge.

Sincerely yours,

Mr. Jorge L. Crespo Arnaiz
Vice-President for Planning and Academic Affairs
December 12, 2009

Dear students:

Universidad Metropolitana, which is part of the Ana G. Méndez University System, thanks all of you who made a decision to become actively engaged in the fascinating world of science at a very early age. As an institution, we are committed to help students work and investigate in the fields of science, technology, engineering and mathematics (STEM) and disseminate the outcomes of your research in an academic activity.

The Winter 2009 Pre-College Research Symposium which is held at Universidad Metropolitana in San Juan Puerto Rico is a unique opportunity for all of you to share the information gathered from your research projects with peers, your parents, and the academic community. This adventure for most of you represents an opportunity to create knowledge for the benefit of society and a sign of hope for your future in careers as scientists and engineers.

Congratulations for participating in this Winter 2009 Pre-College Research Symposium. The interesting projects that you have prepared are true testimonials of this wonderful episode in your journey through high school. I am positive that this experience will spark further interest in a college education and a fascination with research and inquiry.

Yours truly,

Federico M. Mathéu, Ph. D.
Chancellor
December 12, 2009

Dear participants:

On behalf of Universidad del Turabo, I congratulate all of you who have worked very hard during this academic semester in scientific projects. You will present the outcomes of your research at the Winter 2009 Pre-College Research Symposium to be held at the Amphitheater of Universidad Metropolitana in San Juan, Puerto Rico, an event organized by the Student Research Development Center of the Ana G. Méndez University System (SUAGM according to its Spanish acronym).

I am very well pleased, as well as impressed, with the number of research projects presented by such a talented group of student researchers. It is both a privilege and an honor to have contributed to the development of scientific research skills in your development as young scientists. These experiences will pave the way for future careers in the fields of science, technology, mathematics and engineering (STEM).

We have encouraged you in your work and thank all of those who have supported you to continue providing our youth with unique opportunities that foster research and knowledge. Universidad del Turabo looks forward to continuing its preparation of scientific minds for our future generations.

Congratulations to all the participants for their excellent research projects. We thank all of the faculty mentors for their commitment and contributions in the development of the future scientists and engineers of our nation.

Sincerely,

Dennis Alicea, Ph.D.
Chancellor
December 12, 2009

Dear students:

The Ana G. Méndez University System (AGMUS) and Universidad del Este (UNE), welcome you to the Winter 2009 Pre-College Research Symposium to be held at the Amphitheater of Universidad Metropolitana in San Juan, Puerto Rico. AGMUS is proud to host this event organized by the Student Research Development Center.

The Winter 2009 Pre-College Research Symposium promotes the participation and supports the efforts of high school students who have dedicated many hours in the preparation of research projects in science. They work hard in the investigations and share the outcomes of those experiences as a contribution that inspire others and help improve knowledge in the scientific community.

We appreciate the support provided by the research mentors who guided the students at Universidad del Este facilities and set the foundation for the fruitful research experiences that our students completed. We feel proud of their accomplishments and know that we have provided a pathway to a future career in science.

Yours truly,

[Signature]
Alberto Maldonado-Ruiz, Esq.
Chancellor

ser
December 12, 2009

Pre-College Students:

The Winter 2009 Pre-College Research Symposium is the culmination of the activities and dissemination process of the Saturday Academy Program of the Ana G. Méndez University System (AGMUS). For a period of four months, since August of 2009, more than sixty-three pre-college students from private and public high schools in Puerto Rico worked long hours in the research laboratories of the Departments of Science and Technology at UMET, UNE and Universidad del Turabo with the guidance and mentorship of five college professors and student research mentors in fifty-nine research projects in the areas of biological sciences, atmospheric sciences (Global Microscope), applied mathematics and Engineering.

One of the objectives of the Winter 2009 Pre-College Research Symposium is to offer young motivated high school researchers the opportunity to learn and to practice their communication skills in a formal professional scientific meeting. A second objective is to give high school students of Puerto Rico a forum for the presentation of the results and findings of their research projects to teachers, researcher mentors, family members, and the university community at large.

The Ana G. Méndez University and the Student Research Development Center are proud of the results obtained by the pre-college students and their mentors in the Fall 2009 Saturday Academy Program and the Winter 2009 Pre-College Research Symposium. I hope your experience inspires you and your peers to select science, technology, engineering or mathematics as your field of study in the near future.

My sincere appreciation goes to the Student Research Development Center staff, student research mentors and faculty from Arizona State University, the New Jersey Institute of Technology, and the Spanish Research Council (CSIC) for their effort and commitment to implement the Fall 2009 Saturday Academy Program and the Winter 2009 Pre-College Research Symposium. This event would not have been possible without the ongoing support of the National Science Foundation and the NASA Puerto Rico Space Grant Consortium.

Sincerely yours,

Juan F. Arratia, Ph. D.
Director and Principal Investigator
ANA G. MÉNDEZ UNIVERSITY SYSTEM (AGMUS)

As an Educational Institution

The Ana G. Méndez University System is home to approximately 40,000 undergraduate and graduate students who are mainly underrepresented low-income minority students from the Metropolitan San Juan area in Puerto Rico. Three institutions form the AGMUS University System: Universidad Metropolitana (UMET), Universidad del Este (UNE), and Universidad del Turabo (UT). UMET has been a teaching institution since its foundation in 1948. Today, however, its philosophy has been changing to address the students’ study needs and the requirements of society. Our President, Mr. José F. Méndez, has set the agenda to have it become the best undergraduate research institution in Puerto Rico. Additionally, the President has set the goal to implement the MIE best practices at UNE and UT and transform AGMUS into a leading undergraduate research institution through the creation of the Student Development Center at the Vice Presidency for Planning and Academic Affairs. The Executive Director of the Student Research Development Center is Dr. Juan F. Arratia, who has set to accomplish this goal by 2010.

As an Undergraduate Research Institution

In 1995, UMET was selected by the National Science Foundation as a Model Institution for Excellence (MIE) school. At that time, a five-year Cooperative Agreement for more than $11 million was signed between UMET and the NSF. A second Cooperative Agreement was signed on October 1, 2000 for an additional three years and for $7.5 million. The third phase of the MIE grant for $2.5 million for three additional years was awarded on October 1, 2003. The main objective of the relationship with NSF has been to transform UMET into a model for Hispanic Serving Institutions in the nation. Our major goal has been to increase the number of BS degrees granted by UMET, to transfer a significant number of science students to graduate school, and to enroll them in Ph. D. programs to fulfill the goals and aspirations of a greater participation of minorities in the science, mathematics, and engineering fields. After 13 years of funding, UMET has been transformed through the MIE activities by producing an effective pipeline from pre-college to undergraduate, and from undergraduate to graduate school for hundreds of underrepresented minorities from Puerto Rico.

UMET has been transformed by the MIE Project into a leading national undergraduate and pre-college research institution where faculty research mentors are helping science students create knowledge and disseminate creative thinking among the members of the university and pre-college community. Our undergraduate and pre-college research program, sponsored by the National Science Foundation and NASA, is paving the way for research-oriented activities for the benefit of Puerto Rico students.

PROLOGUE

The sponsorship of the National Science Foundation has been fundamental for the implementation of the Pre-College Program at the Ana G. Méndez University System (AGMUS) at Universidad Metropolitana (UMET). For thirteen years, the Model Institutions for Excellence (MIE) Project organized the Saturday Academy Program. In 2006, a new dimension was established with the dissemination of the MIE best practices into Universidad del Turabo and Universidad del Este (UNE) under the Student Research Development Center. The main goal of this program is to motivate high school students to pursue careers in science, technology, engineering and mathematics at the BS and graduate levels. The Saturday Academy Program usually extends for sixteen weeks during the months of August through December. Students from public and private schools, enrolled in grades 10, 11 and 12, conduct research under the mentorship of faculty and student research mentors from AGMUS and institutions in the US mainland and abroad. More than two thousand pre-college students have learned the fundamentals of scientific research through their participation in the Saturday Academy Program at AGMUS. For the last eight years, a symposium has been organized to present the results of this activity to the university community and to motivate other Puerto Rican students to engage in scientific research.

The Winter 2009 Pre-College Research Symposium held at the campus of Universidad Metropolitana on December 12, 2009 showcases the research experiences of sixty-three (63) pre-college students from fifteen high schools in Puerto Rico. Fifty-nine research projects are presented at the Symposium in the form of posters and oral presentations. The mentorship of five faculty and student research mentors from the Department of Science and Technology at UMET, UNE and Universidad del Turabo made possible the concretization of the research projects. Their results are documented in the pages of this booklet.

The National Science Foundation, NASA/Puerto Rico Space Grant Consortium, the Ana G. Méndez University System, and the Student Research Development Center are proud of the research work conducted by the Saturday Academy Winter 2009 participants. We hope this Symposium will be a vehicle by which the scientific productivity of high school youngsters from Puerto Rico will be disseminated in future years.
Dr. Martha Bilotti-Aliaga is Director of Education at the American Statistical Association in Washington DC. She received a B.A. in Mathematics from Universidad de Buenos Aires, Argentina, an M.A. in Statistics from Universidad de Chile, in Chile, and a Ph.D in Statistics from the University of Michigan. Her dissertation was on the Use of a Side Effect as a Covariate in a Problem of Sequential Analysis. She was director and instructor at the Summer Institute for Mathematics Enhancement (SIME), National Science Foundation Teacher Enhancement for High School Teachers Program at The University of Michigan (1990-1995), Training University Graduate Student Instructor on Interactive Teaching Techniques with Graphing Calculators. The University of Michigan (1997-May 2001), Training University Professors on Cooperative Teaching Techniques in Mathematics (1999), Associate Professor of Statistics, School of Public Policy at The University of Michigan (2001-2003), Creator of the following ASA programs: Educational Ambassadors (2005-Present), Meeting Within the Meeting(MWM) (2007-present), STEW (2008-Present), Census@School (2009-Present). She was the co-founder of MATHWORK, an Enrichment Program on the study of Mathematics at Ann Arbor, MI. She has served on national panel reviews for the Mathematical Association of America (MAA) (1998-1999) and for the National Science Foundation (1992, 1994, 1997, 2008).
Dr. Juan F. Arratia was born in Pomaire, Chile. He graduated from Universidad Técnica del Estado with a BS in Electrical Engineering in 1973. He was awarded an MSc in Engineering from Louisiana Tech University, Ruston, Louisiana, in 1979 and a Ph.D. in Electrical Engineering from Washington University, St. Louis, Missouri in 1985. He has taught and conducted research at universities in Chile (Universidad Técnica del Estado and Universidad Austral de Chile), Puerto Rico (Universidad Interamericana de Puerto Rico and the University of Puerto Rico-Mayaguez), and in the US mainland at Washington University, St. Louis, and Louisiana Tech University, Ruston, Louisiana. He has lectured and given conferences on advanced automation, robotics, vision systems, artificial intelligence, total quality management and science and engineering education in Chile, Bolivia, Ecuador, Guatemala, Panama, Mexico, Brazil, Nicaragua, Perú, Canada, Spain, the Netherlands, Turkey, Japan, Philippines, Singapore, Australia, China, Puerto Rico and in the US mainland. He was the Advanced Manufacturing Manager for Medtronic, Inc., a leading pacemaker company, and is a consultant in advanced automation for pharmaceutical and medical devices companies in Puerto Rico. Since 1998, he has been the Director and Principal Investigator of the Model Institutions for Excellence (MIE) Project, a National Science Foundation sponsored program based at Universidad Metropolitana in San Juan, Puerto Rico. Since 2007, he is the Executive Director of the Ana G. Méndez University System (AGMUS) Student Research Development Center, designed to disseminate MIE best practices at Universidad del Turabo and Universidad del Este. In November 2007 he was awarded the Presidential Award for Excellence in Science, Mathematics and Engineering Mentoring at a ceremony in the White House in Washington DC.
Dr. César Banderas studied his Bachelor’s and Master’s Degrees in Electrical Engineer at the University of Buffalo in New York and was certified in Executive Development at Harvard School of Management in Boston, Massachusetts. He is the President of BanDeMar Networks, a minority owned small company specializing in advanced video solutions for e-learning markets. Dr. Banderas’ technical background is in active perception, which combines real-time computer vision and other sensor modalities with machine learning and behavioral control. He is interested in all aspects of active vision, including algorithms for signal processing and control, sensor VLSI, and multiprocessing architectures. His experience in active perception comes largely from his work in foveal vision, which exploits in the machine setting the multiacuity properties prevalent in vertebrate vision. Since the peak of broadband multimedia investments by the telecommunications industry, Dr. Banderas has been active in the field of pervasive rich media. This field endeavors to provide spatiotemporally coordinated multimodal streams to an audience with diverse demographics, player platforms and channel access (e.g., broadband-connected PCs, wireless PDAs, set-top boxes). In 1990, Dr. Banderas formed a research department at Amherst Systems dedicated to the development and application of active vision. This work yielded operational platforms with algorithms for video understanding and automaton behavior control, matching multiprocessor architectures, and smart VLSI imaging sensors ( imagers with monolithic signal processing). He has had profit/loss responsibility, and was able to secure external funding for all R&D (over twenty customer grants and contracts) while exceeding growth and profit estimates. To date, this active vision research has yielded six Ph.D. and four M.S. degrees, several patents, highest distinction in the Air Force Small Business Innovative Research Accomplishments Report to the U.S. Congress, a Small Business of the Year nomination from Rome Lab, and the 1999 NASA Space Act award from Johnson Space Center. In 2001, he formed a research department at Manhattan-based Sorceron (now BanDeMar) dedicated to the synthesis and delivery of object-oriented rich media. As CTO, Dr. Banderas is member of the Association for Computing Machinery, Institute of Electrical and Electronics Engineers, and the International Society for Optical Engineering.
Dr. Sudhir Kumar is professor of biology at Arizona State University, where he teaches undergraduate-level evolutionary biology and graduate-level evolutionary genomics classes. He is a standing member of the NIH review panel and a member of many journal editorial boards, including Molecular Biology and Evolution, Genome Research, Evolutionary Bioinformatics Online, and Gene: Functional Genomics. Dr. Kumar is currently the webmaster for the Society for Molecular Biology and Evolution and the American Genetic Association. He received his B.E. in Electrical/Electronics Engineering and M.Sc. in Biological Sciences from the Birla Institute of Technology and Sciences in India, and his Ph.D. in Genetics from Pennsylvania State University.

Dr. Kumar leads a team of interdisciplinary scientists who are developing new computer-based methods of studying and analyzing the tens of thousands of genes in humans and related species, enabling researchers to learn their functions and origins. Dr. Kumar is a renowned expert in the field of evolutionary bioinformatics, who received an Innovation Award in Functional Genomics from the Burroughs Wellcome Fund in 2000. In 2004 he joined the elite ranks of most-cited researchers, being among the top ten in number of citations in the field of computer science over the last decade. Among his more than 70 papers and books are three “Hot Papers,” which were cited among the most of any in their fields.

Dr. Kumar is an interdisciplinary scientist who brings the problem-solving skills from his undergraduate engineering background together with his knowledge of evolutionary genetics from his doctoral work to tackle long-standing problems in functional genomics and evolutionary biology. He has made pioneering efforts in developing bioinformatics tools and databases for the analysis of gene expression patterns from early stages of the fruit fly development. He has also conducted breakthrough work using protein molecular clocks to illuminate the Evolutionary Timescale of Life. Over the last decade, Dr. Kumar has led the team that developed the Molecular Evolutionary Genetics Analysis (MEGA) software in order to make useful methods of comparative sequence analysis easily accessible to the scientific community for research and education. His research is funded by National Institutes of Health and the National Science Foundation, among other agencies.
AGMUS INSTITUTE OF MATHEMATICS

BS Degree in Applied Mathematics

Bio-Mathematics

Benefits:

- National Science Foundation Scholarship for up to $4,000/year
- Tutoring, mentoring and academic advising through the AGMUS Institute of Mathematics
- Summer Research Internship opportunities at major US universities: Arizona State University, Rice University, University of California at Berkeley, Howard University, Cornell University, among others
- Transfer to Master and Ph.D Program in Biomathematics at US research institutions after graduation
- BS in Applied Mathematics started in August 2009

For more information, please contact Dr. Juan F. Arratia, Executive Director, Institute of Mathematics, Tel. (787) 766-1717 Ext. 6000, email: um_jarratia@suagm.edu, PO BOX 21150, San Juan, PR 00928-1150
SCHEDULE OF EVENTS

SATURDAY, DECEMBER 12, 2009                UNIVERSIDAD METROPOLITANA

7:00 – 8:00 am.                  POSTER SESSION SET-UP                LOBBY MUÑIZ
Continental Breakfast                SOUFFFRONT BUILDING
REGISTRATION

POSTER SESSION SET-UP

8:00 – 8:30 a.m.        OPENING CEREMONY                AMPHITHEATER
Welcome : Dr. Juan F. Arratia
Executive Director
Student Research Development Center

Keynote Speaker: Dr. Martha Bilotti-Aliaga
American Statistical Association

8:00 a.m. – 4:00 p.m. WORKSHOP FOR SCIENCE AND MATH TEACHERS INVESTIGACIÓN CIENTÍFICA BUILDING
“STATISTICS AND PROBABILITIES” ROOM 301

8:30 – 10:00 a.m. POSTER SESSION                LOBBY MUÑIZ SOUFFFRONT BUILDING
BIOLOGICAL SCIENCES
ATMOSPHERIC SCIENCES (GLOBAL MICROSCOPE)
APPLIED MATHEMATICS
ENGINEERING

Chairperson: Dr. Juan F. Arratia
Executive Director
Student Research Development Center

BIOLOGICAL SCIENCES

Yanisse Aponte, María Auxiliadora School, San Juan, Puerto Rico. (1)
Species Comparison and Substitution Tolerance of SCAX1 Protein
Christian R. Báez, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico.  
Study of Gram-Positive *Staphylococcus aureus* and its Divergence to Related Strains

Alan D. Bernier, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico. 
Agammaglobulinemia Protein (AGMX2), A Study Using MEGA and SIFT

Yamitza Carrillo, José Aponte De La Torre School, Carolina, Puerto Rico.  
Comprehensive Computational Study of the Amino Acid Substitution Effects in Interferon Regulatory Factor 6 Gene (IRF6)

Dinorah Carrión, Thomas Alva Edison School, Caguas, Puerto Rico.  
Evolutionary Analysis of Disease Associated Mutations in the Homo sapiens Gene (SLC12A3) Gytelman Syndrome, NM_000339

Noel O. Carrión, Thomas Alva Edison School, Caguas, Puerto Rico.  
Evolutionary Analysis of Disease Associated Mutations in the Transthyretin Disease, Amyloidosis Type I (TTR) NM_000371

Kiara M. Delgado, José Aponte De La Torre School, Carolina, Puerto Rico.  
A SIFT Analysis of Amino Acid Substituent-Effect on Myocilin

Gabriela Fenollal, Notre Dame School, Caguas, Puerto Rico.  
Analysis of MSH6 Protein with Comparison of the Protein Sequence and the Homogeniety Pattern
Danechka Izquierdo, José Aponte De La Torre School, Carolina, Puerto Rico. (9)

A Study of an Amino Acid Substitution Effect on the Biotinidase Gene

Natalie Jiménez, María Auxiliadora School, San Juan, Puerto Rico. (10)

Protein Tolerance and Species Comparison of the BBS5 Protein

Natalia Manzano, San Antonio School, San Juan, Puerto Rico. (11)

Serotonin Receptor 2 A Protein Analyzed SIFT and MEGA4

Giselle Martínez, María Auxiliadora School, San Juan, Puerto Rico. (12)

Evaluation of CFTR Protein by SIFT and Mega 4

Jaynee M. Mendoza, Bautista de Caguas School, Caguas, Puerto Rico. (13)

Evolutionary Analysis of Disease Associated Mutations in the Homo sapiens Tyrosinase (Oculocutaneous Albinism IA), (TYR), MRNA, NM_000372

Alexander P. Molina, Bautista de Caguas School, Caguas, Puerto Rico. (14)

Evolutionary Analysis of Disease Associated Mutations in Homo sapiens Calcium-Sensing Receptor, (CASR), NM_000388

Frances C. Negrón, Bautista de Levittown School, Toa Baja, Puerto Rico. (15)

Study of the IL2RG Protein: Tolerance Evaluation and Homolog Species Comparison
**Julyannette O’Neill**, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico. (16)

Study of the 8-Oxoguanine Glycosylase Using SIFT, MEGA and Grantham’s Distance

**Enrique A. Pérez**, Thomas Alva Edison School, Caguas, Puerto Rico. (17)

Evolutionary Analysis of Disease-Associated Mutations in the Gene Phosphomanomutase Disease, Type IA (PMM2), NM_000303

**Eduardo Rodríguez**, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico. (18)

Species and Protein Comparison of Neurofibromatin

**Itzamar Romero**, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico. (19)

Myosin Biding Protein C: Comparison, Mutation Tolerance and Biochemical Distance

**Mónica Santos**, Notre Dame School, Caguas, Puerto Rico. (20)

BRAC2 Protein: Analysis of Substitution Tolerance, Species Comparison and Biochemical Distance

**Valeria Velázquez**, Notre Dame School, Caguas, Puerto Rico. (21)

Evolutionary Analysis of Disease Associated Mutations in the Homo Sapiens Gene KCNQ1, NM_000218

**ATMOSPHERIC SCIENCES (GLOBAL MICROSCOPE)**

**Joseph P. Class**, Nuestra Señora de Lourdes School, Carolina, Puerto Rico. (22)

Modeling Rainfall Dynamics Over the Caribbean Zone
Andrea de los Santos, Petra Zenón de Fabery Vocational School, Trujillo Alto, Puerto Rico. (23)

The Effect of the Phytoplankton Bloom on the Ocean

Luis Reyes, Petra Zenón Vocational School, Trujillo Alto, Puerto Rico. (24)

Picture in Picture Morphing Using the Global Microscope

Camila del Mar Rodríguez, Puertorriqueño de Niñas School, Guaynabo, Puerto Rico. (25)

Deforestation and its Effects on Atmospheric and Natural Behaviors

Kermit Toro and Alex Caminero, Petra Zenón de Fabery Vocational School, Trujillo Alto, Puerto Rico. (26)

Modeling NH₃ Renewable Energy Using Geoscience Techniques in the Global Microscope

**APPLIED MATHEMATICS**

Xaymara E. Arroyo, María Auxiliadora School, San Juan, Puerto Rico. (27)

What Variables Influence Diabetes Susceptibility?: Female Pima Indians Study Model

Carlos J. Cancel, Petra Zenón de Fabery Vocational School, Trujillo Alto, Puerto Rico. (28)

Statistical Study of Estradiol Exposure in Breast Cancer Cells

Jonathan García, Petra Zenón de Fabery Vocational School, Trujillo Alto, Puerto Rico. (29)

Multi-Alignment of Sequences: A Comparison of Ten Species Based on the RAG1 Sequence

Emanuel Hernández, Petra Zenón de Fabery Vocational School, Trujillo Alto, Puerto Rico. (30)

The Use of Short Tandem Repeat Polymorphism for Classification
Jonathan Irizarry, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico. (31)

Does the NTP-2000 Diet Influence Mouse Weight?

Luis R. Santos, Notre Dame School, Caguas, Puerto Rico. (32)

Statistical Study of the Endemic Tortoises in the Galápagos Islands

Myriam Soto, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico. (33)

Study of Mouse Obesity with the NIH-07 Diet

ENGINEERING

Salvador Álvarez, Calvary Baptist Christian School, Carolina, Puerto Rico. (34)

Equation of Motion used to Mathematically Model the Motion of an Arm of a Mechanical Turtle

José A. González, José Aponte De La Torre School, Carolina, Puerto Rico. (35)

Explaining the Mechanics of a Turtle Movement Using Mathematical Principles
<table>
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<th>Time</th>
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| 10:00 – 10:10 a.m. | **Stephanie Betancourt**, José Aponte De La Torre School, Carolina, Puerto Rico.  
*Ataxia telangiectasia* as a Progressive Cerebellar Degenerative Disease |
Evolutionary Analysis of Disease Associated Mutations in the *Homo sapiens* Gene TTR Disease, Amyloidosis Type 1, NM_000371 |
| 10:20 – 10:30 a.m. | **Nelimar Cruz**, Notre Dame School, Caguas, Puerto Rico.  
Making an Evolutionary Genetic Analysis of Park2 Protein |
| 10:30 – 10:40 a.m. | **José L. Díaz**, CIEM School, Carolina, Puerto Rico.  
Predicting Amino Acid Substitution for Diseases Associated in the Mutation on MYO7A Gene |
| 10:40 – 10:50 a.m. | **Christian Echevarría**, Notre Dame School, Caguas, Puerto Rico.  
Evolutionary Analysis of the LMNA Gene |
| 10:50 – 11:00 a.m. | **Gianna Gómez**, CIEM School, Carolina, Puerto Rico.  
Tolerance and Intolerance for Amino Acids Changes in the GAA Gene |
| 11:00 – 11:10 a.m. | **Carla A. López**, Notre Dame School, Caguas, Puerto Rico.  
Analyzing the Neuregulin Protein with SIFT and MEGA 4 |
| 11:10 – 11:20 a.m. | **Elvin A. Méndez**, José Aponte De La Torre School, Carolina, Puerto Rico.  
Computational Study of Amino Acid Changes on BRCA2 |
11:20 – 11:30 a.m.  **Juan Carlos Torres**, Notre Dame School, Caguas, Puerto Rico.

Predicting Possible Mutations and Strain Comparison Using SIFT and MEGA 4 in *Clostridium tetani*’s Toxin

11:30 – 11:40 a.m.  **Edgardo Vázquez**, José Aponte De La Torre School, Carolina, Puerto Rico.

A Computational Study of Amino Acid Substitution in the SMPD1 Gene
10:00 – 11:30 m.  ORAL PRESENTATIONS II  MUÑÍZ SOUFFRONT 120

Chairperson: Dr. Marlio Paredes  
Universidad del Turabo

APPLIED MATHEMATICS

10:00 – 10:10 a.m.  Nelson Ciuró, San Antonio School, San Juan, Puerto Rico.

Comparative Study of Hawksbill Nesting on Mona Island and Other Nesting Sites in Puerto Rico

10:10 – 10:20 a.m  Wilfredo Cruz, Notre Dame School, Caguas, Puerto Rico.

Study of Transcriptional Change in the Arabidopsis thaliana Leaf Development

10:20 – 10:30 a.m.  David Morales, Nuestra Señora de la Altagracia School, San Juan, Puerto Rico.

Statistical Study of the Presence of the Cystic Fibrosis Transmembrane Receptors (CFTR) Gene

10:30 – 10:40 a.m.  Mario V. Ramos, Nuestra Señora de la Altagracia School, San Juan, Puerto Rico.

Phosphate Levels in Blood: Important Indicator of Disease

ATMOSPHERIC SCIENCES (GLOBAL MICROSCOPE)

10:40 – 10:50 a.m.  Lysander Borrero, Notre Dame School, Caguas, Puerto Rico.

The Epidemiology Dynamics Spread Increase of the A H1N1 Virus Around the World Represented with the Global Microscope

10:50 – 11:00 a.m.  Astrid Díaz, Notre Dame School, Caguas, Puerto Rico.

Modeling the Effects of the Increasing Melting of Poles in Superficial Ocean Currents
11:00 – 11:10 a.m.  **Valeria A. Rodríguez**, Petra Zenón de Fabery Vocational School, Trujillo Alto, Puerto Rico.

Modeling the Effects of a Tsunami in the Caribbean Region


Using the Global Microscope for Modeling Particles Dynamics in the CAPECO Explosion in Bayamón, Puerto Rico.

**ENGINEERING**

11:20 – 11:30 a.m.  **Carlos Molina**, Bilingüe Padre Rufo School, San Juan, Puerto Rico.

Mathematical Model of Neuronal Firing

12:10 – 12:50 p.m.  AWARD CEREMONY

AND CLOSING REMARKS

AMPHITHEATER

1:00 p.m.  LUNCH

GAZEBOS

2:00 p.m.  SYMPOSIUM ADJOURNS
Spinocerebellar ataxia is a degeneration of the spinal cord and the cerebellum, which can be noted by a genetic defect. The autosomal dominant cerebellar degenerative disorders are generally referred to as 'spinocerebellar ataxias,' (SCAs) even though 'spinocerebellar' is a hybrid term, referring to both clinical signs and neuroanatomical regions. Neuropathologists have defined SCAs as cerebellar ataxias with variable involvement of the brainstem and spinal cord, and the clinical features of the disorders are caused by degeneration of the cerebellum and its afferent and efferent connections, which involve the brainstem and spinal cord. The objective of this research was to evaluate the tolerance of the SCA1 protein using SIFT and compare the protein in question with homologous species using MEGA4. MEGA4, Molecular Evolutionary Genomic Analysis, is a program that compares the sequence of homologous genes and protein of different species. SIFT is a program that predicts whether an amino acid substitution affects protein function. Results of SIFT indicated a 25.9% of amino acids that had zero tolerance to substitution. According to MEGA4, the most similar species are *Homo sapiens* and *Canis lupus familiaris* in terms of protein and species. In conclusion, the results may suggest that there are less tolerable amino acids because they may be important for the function of the protein, and that there is an evolutionary difference between proteins and the species tested.
STUDY OF GRAM-POSITIVE *STAPHYLOCOCCUS AUREUS* AND ITS DIVERGENCE TO RELATED STRAINS

**Christian R. Báez**, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico.

Student Research Mentor: Krizia Cabrera, Universidad Metropolitana, San Juan, Puerto Rico.
Student Research Mentor Assistant: Ashley González, Universidad Metropolitana, San Juan, Puerto Rico.

Septic Shock is the result of a systemic response to an overwhelming amount of bacteria in the bloodstream. There are two known causes for septic shock: Streptococcal Toxic Shock Syndrome (STSS-group A) caused by its bacteria, *Streptococcus aureus* and Toxic Shock Syndrome (TSST–group B) caused by its bacteria, *Staphylococcus aureus*. They are different according to their way of infiltrating the body. The toxin’s sequence was first analyzed using the program Molecular Evolutionary Genetic Analysis (MEGA). This program is primarily used to understand the evolution and adaptation of genes, protein in species. It works in inferring evolutionary relationship of homologous sequences, exploring basic statistical properties of genes and estimating neutral and selective evolutionary divergence among sequences. The features from this program that allowed to build a phylogenetic tree, and compare the original sequence with other strains of the toxin, was used. Phylogenetic trees were built by comparing different strains of the bacteria. First, comparison of the protein in the different strains of *Staphylococcus aureus* was done, followed by a comparison of the strain. Strain comparison was determined by the means of using the software MEGA4.

AGAMMAGLOBULINEMIA PROTEIN (AGMX2), A STUDY USING MEGA AND SIFT

**Alan D. Bernier**, Bautista de Puerto Nuevo Academy, San Juan, Puerto Rico.

Student Research Mentor: Krizia Cabrera, Universidad Metropolitana, San Juan, Puerto Rico.
Student Research Mentor Assistant: Ashley González, Universidad Metropolitana, San Juan, Puerto Rico.

The focus of this research was agammaglobulinemia (AGMX2), which is a rare disorder that threatens the health of the immune system. It is characterized by failure to produce mature lymphocytes cells, which play a large role in defending the body against disease. Since the growth of lymphocytes is stunted, the immune system is adversely affected and people with this disorder suffer from repeated infections unless treated. The study of this disorder was done through SIFT (Sorting Intolerant From Tolerant), which is a program that predicts whether an amino acid substitution affects protein function by taking into consideration the chemical properties of the amino acids. This program was used to determine the percent of amino acids which have zero tolerance to any substitution. Also, MEGA 4 (Molecular Evolutionary Genomic Analysis 4) was used, a program that is aimed for comparative analysis of homologous gene sequences with a special emphasis on evolutionary relationships and patterns of DNA and protein evolution. The SIFT results show that 11% of the amino acids in the protein sequence are intolerant to mutations. Specifically, 76 amino acids out of a total of 693 amino acids have zero tolerance of mutations. These results show that there is a low number of amino acids that do not tolerate mutations; these may also indicate that 76 amino acids may be essential for the protein function. It can be concluded from this that the protein sequence of agammaglobulinemia protein is very susceptible to mutations.
ATAXIA TELANGIECTASIA AS A PROGRESSIVE CEREBELLAR DEGENERATIVE DISEASE

Stephanie Betancourt, José Aponte De La Torre School, Carolina, Puerto Rico.

Research Mentor: Dr. Ángel R. Arcelay, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Carol J. Diaz, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Amir M. Rodríguez, Universidad Interamericana, San Juan, Puerto Rico.

This gene under study is the ATM gene, associated with the disease Ataxia telangiectasia and how it affects infants. The protein encoded by this gene belongs to the kinase family. Protein kinases are the key controllers of cell behavior. The ATM protein controls the cell behavior by sending signals and modifying proteins in the cell, which then alters the function of others proteins. Ataxia telangiectasia is a genetic disorder which mainly affects the control center of the brain and compromises the immune system in many cases. This disease affects the brain and other body parts. Because it is an inherited disease, there is no specific treatment for it. An immunodeficiency disease is one that causes the immune system to break down, making the body susceptible to diseases. Ataxia refers to uncoordinated movements. Telangiectasia is the enlargement of blood vessels just below the surface of the skin. ATM is an autosomal recessive disorder, which means two copies of an abnormal gene, must be present in order for the disease to develop. The program SIFT was used to predict whether the amino acid substitution of the gene affects protein function based on sequence homology and the physical properties of amino acids. A total of 20 different positions in one amino acid substitution were chose at random. They revealed that 52% of these positions are intolerant and affect the protein function.

COMPREHENSIVE COMPUTATIONAL STUDY OF THE AMINO ACID SUBSTITUTION EFFECTS IN INTERFERON REGULATORY FACTOR 6 GENE (IRF6)

Yamitz Carrillo, José Aponte De La Torre School, Carolina, Puerto Rico.

Research Mentor: Dr. Ángel R. Arcelay, Universidad del Este, School of science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Carol J. Diaz, Universidad del Este, School of science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Amir M. Rodríguez, Universidad Interamericana, San Juan, Puerto Rico.

The interferon regulatory factor 6 (IRF6) is a gene whose function has been related to the formation of the connective fine weave, for example, the palate formation. The mutations in this gene can cause the Van der Woude Syndrome and the Popliteal Syndrome of the Pterigio. The Van der Woude Syndrome is characterized by the presence of lip holes. Like the previous Popliteal of the Pterigio Syndrome, it practically consists of the same condition, but in this syndrome it displays bony anomalies and deformities in the genitals. Moreover, these diseases are hereditary. This research focused on the study on tolerance and intolerance that the amino acid exchange creates in the IRF6 gene. SIFT (Sorting Intolerant From Tolerant), a program that predicts whether an amino acid substitution affects protein function, so that users can prioritize substitutions for further study, was used. Predictions had been calculated for this gene. Fifteen were selected to further study the levels of tolerances and gene function effects.
EVOLUTIONARY ANALYSIS OF DISEASE ASSOCIATED MUTATIONS IN THE \textit{HOMO SAPIENS} GENE (SLC12A3) GYTELMAN SYNDROME, NM\_000339

Dinorah Carrión, Thomas Alva Edison School, Caguas, Puerto Rico.

Research Mentor: Raúl M. Navedo, Universidad del Turabo, Gurabo, Puerto Rico.

The comparative genomics project focuses on the research of gene mutations and their effects on humans in terms of health, whether it is beneficial or not. There are two types of mutations: disease associated mutations (DAM’s) and associated single nucleotide Polymorphism (nSNPs). The evolutionary rates of amino acid positions play a crucial role in determining whether a mutation is a harmful one, which occurs on low evolutionary rates positions or simply irrelevant; meaning that it provokes the development of disease phenotypes. The latter are usually present on high evolutionary rates. This project focused on the evolutionary rates of DAMs and nSNPs, their role, and how they affect the NM\_000339 gene in contrast with other genes. This gene mutates and causes the Gitelman Syndrome, a mild variant of Bartter syndrome, which affects the kidneys. In order to obtain the evolutionary rates of the gene, computational tools are needed. The gene bank offers the data necessary to calculate the evolutionary rates of a gene in several species. Polyphen is the most widely used method for estimating potential lethal effects of amino acid mutations. During this research, not only the gene’s variation in \textit{Homo sapiens} are being investigated, but also forty-four species such as primates, reptiles, and others are included. As more information is collected, the computational tools become more efficient in understanding the mutations that occur in genes and how they affect health. This can possibly revolutionize how these rare inherited diseases are treated. To determine the difference between observed and expected values for DAMs, the p-value is crucial. DAMs are more likely to be found in low evolutionary rate level which is in accordance with expectations. The outcome of the study points out that the nSNPs p-value is too low to be taken into consideration since it is not statistically significant.

EVOLUTIONARY ANALYSIS OF DISEASE ASSOCIATED MUTATIONS IN THE TRANSTHYRETIN DISEASE, AMYLOIDOSIS TYPE I (TTR) NM\_000371

Noel O. Carrión, Colegio Thomas Alba Edison, Caguas, Puerto Rico.

Research Mentor: Raúl M. Navedo, Universidad del Turabo, Gurabo, Puerto Rico.

The Comparative Genomics Project has as main point to help in the understanding of gene mutations and whether they are beneficial or not to an individual’s health. To know the answers, there have been several projects and numerous investigations and experiments. Evolutionary rates of amino acid positions between clinical and population genetic analyses are considered to determine consistency and predictability of genome wide patterns and help to understand the relationship between mutations and the development of disease phenotypes. There are two types of mutations: disease associated mutations, better known as DAMs, and associated single nucleotide polymorphism, better known as nSNPs. Computational tools help to learn about the types of mutations and how mutations benefit the human body.
EVOLUTIONARY ANALYSIS OF DISEASE ASSOCIATED MUTATIONS IN THE HOMO SAPIENS GENE TTR DISEASE, AMYLOIDOSIS TYPE I, NM_000371

Diego A. Chamorro, Thomas Alva Edison School, Caguas, Puerto Rico.

Research Mentor: Raúl M. Navedo, Universidad del Turabo, Gurabo, Puerto Rico.

Genome sequencing provides help in the analysis and identification of disease-associated genes. Even though it is not a 100% perfect process, genome sequencing can help create better ways to diagnose, treat and prevent certain diseases. PolyPhen is among the computational tools used to identify the threat to genes, which has helped identify disease associated mutations (DAMs), and non-disease associated single nucleotide polymorphism (nSNPs), as benign, possibly damaging or probably damaging. It is expected that the DAMs are going to be present in amino acid positions that have been conserved in vertebrates while the nSNPs are found at amino acid positions that are not in human vertebrates. EPAs of the nSNPs need to be verified since nSNPs found in the EPA are less severe than those that are not found. This could also help to make more accurate classifications. This work is based on evaluating if the evolutionary rates of the DAMs and nSNPs are different in the Transthyretin gene (TTR). The p-value for DAMs was 1.194E-5 which is considered a significant difference between observed and expected values for DAMs while nSNPs are too few for a statistical significance. The evolutionary frequencies show that there are more observed DAMs than expected at low evolutionary rate levels, which is consistent with the expected results for evolutionary rates for DAMs. The predictions for the DAMs in the NPC1 gene have 24.75% of error while nSNPs do not have a significant quantity of this gene for statistical significance. These observations are important to improve the accuracy of functional prediction tools.

MAKING AN EVOLUTIONARY GENETIC ANALYSIS OF PARK2 PROTEIN

Nelimar Cruz, Notre Dame School, Caguas, Puerto Rico.

Student Research Mentor: Krizia Cabrera, Universidad Metropolitana, San Juan, Puerto Rico.
Student Research Mentor Assistant: Ashley González, Universidad Metropolitana, San Juan, Puerto Rico.

The PARK 2 gene is one of the largest human genes. This is a gene of protein coding that is found in humans in chromosome 6, which carries one of the most important regions in the genome for fighting disease. This gene provides instructions for making a protein called Parkin. Parkin plays a role in the cell machinery that breaks down unwanted proteins by tagging damaged and excess proteins with molecules called Ubiquitin. Mutations of this gene in chromosome 6 are responsible for a form of childhood Parkinson's, epilepsy and some cancers. Parkinson's Disease is a neurological illness, a progressive disorder caused by the gradual loss of cells in a small part of the brain. The loss or death of these cells produces a reduction in a vital chemical called Dopamine that controls movement and balance and is essential to the proper functioning of the central nervous system. The objective of this research was to analyze the Parkin protein by comparing the human protein to other homolog species and test for pattern homogeneity. The Parkin protein was analyzed using the MEGA4 program. MEGA 4 (Molecular Evolutionary Genomic Analysis) is an integrated tool for conducting automatic and manual sequence alignment and inferring phylogenetic trees, among other features. MEGA indicated the relations between the species compared in terms of the Parkin protein and in terms of species. Similarities and difference observed may be due to evolutionary changes. Future research may be needed to corroborate these facts.
A SIFT ANALYSIS ON AMINO ACID SUBSTITUENT-EFFECT ON MYOCILIN

Kiara M. Delgado, José Aponte De La Torre School, Carolina, Puerto Rico.

Research Mentor: Dr. Ángel R. Arcelay, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Carol J. Díaz, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Amir M. Rodríguez, Universidad Interamericana, San Juan, Puerto Rico.

The myocilin (MYOC) gene provides instruction for producing a protein called myocilin. Myocilin is found in certain structures of the eye called trabecular meshwork inducible glucocortoid response. The myocilin function is not well understood but it is believed to have a role in cytoeskeletal function such as to supply structure to cells and to act as scaffolding for the attachment of many organelles. It is also responsible for disability of cells to move and required for the proper division of cells. Myocilin is expressed in many ocular tissues, including trabecular meshwork. This tissue is located around the base of the cornea, near the ciliary body, and is responsible for draining the aqueous humor from the eye via the anterior chamber. Mutations in MYOC gene have been identified as the cause of hereditary juvenile-onset open-angle glaucoma that causes disease were selected affects the optic nerve and involves a loss of retinal ganglion cells in a characteristic pattern. The juvenile-onset open-angle glaucoma (JOAG) is a rare form of open-angle glaucoma (OAG), which is associated with inherited conditions such as myopia and demonstrates an autosomal dominant inheritance. The objective of this work was to observe predictions in amino acid changes made with the SIFT program. The amino acid substitutions produce tolerance and intolerance predicted with SIFT. Ten substitutions in amino acid positions were selected and these were tested for the tolerance and intolerance of the amino acid change.
PREDICTING AMINO ACID SUBSTITUTION FOR DISEASES ASSOCIATED IN THE MUTATION ON MYO7A GENE

José L. Díaz, CIEM School, Carolina, Puerto Rico.

Research Mentor: Dr. Ángel R. Arcelay, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Carol J. Diaz, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Amir M. Rodríguez, Universidad Interamericana, San Juan, Puerto Rico.

The Myosin VIIA (MYO7A) gene encodes a protein classified as an unconventional myosin. Unconventional myosins are motor molecules with structurally conserved heads that move along actin filaments. Their highly divergent filament tails are presumed to be tethered to different macromolecular structures that move relative to actin filaments, thus enabling them to transport cargo. Defects in this gene are associated with the human Usher Syndrome 1B characterized by deafness, reduced vestibular function, and (in humans) retinal degeneration. Disease mutations occur when an amino acid changes: consequently producing a phenotypic disease. This research focuses on tolerance and intolerance that the amino acid exchange creates. The application of the SIFT program unveils a sequence homology-based tool that sorts intolerant from tolerant amino acid substitutions and predicts whether an amino acid substitution in a protein will have a phenotypic effect. Possible causes for mutations for this gene were evaluated. Scores were calculated for positions 1 to 4,430 within the alignment of the protein sequences. SIFT results showed that most of the substitutions chosen did not tolerate changes. From the prediction, 15 positions were chosen for further study of their tolerance levels, and 73% proved to be intolerant to changes in amino acids.

EVOlUTIONARY ANALYSIS OF ATHE LMNA GENE

Christian Echevarría, Notre Dame School, Caguas, Puerto Rico.

Student Research Mentor: Krizia Cabrera, Universidad Metropolitana, San Juan, Puerto Rico.
Student Research Mentor Assistant: Ashley González, Universidad Metropolitana, San Juan, Puerto Rico.

The Lamin family of proteins makes up the nuclear lamina and are protected and conserved during evolution. The lamin proteins are thought to be related to nuclear stability, chromatin structure and gene expression. They are encoded by the gene known as the LMNA gene, or Lamin A/C. A mutation in this gene may lead to Hutchinson-Gilford Progeria Syndrome, which is a rare, fatal genetic condition characterized by an appearance of accelerated aging in children. The objective of this research project was to make a molecular evolutionary analysis of the LMNA gene. To do this, MEGA 4 (Molecular Evolutionary Genomic Analysis 4), integrated software for conducting automatic and manual sequence alignment, inferring phylogenetic trees, among other features was used. This software compared the lamin protein of humans to that of other species and to test for pattern homogeneity. Comparison was done by selecting homolog species and conducting an alignment which produces phylogenetic trees that can be analyzed. Both species and protein comparison were obtained by means of MEGA4 followed by pattern homogeneity of the lamin protein. This evolutionary analysis may give insight into changes of the lamin protein.
ANALYSIS OF MSH6 PROTEIN WITH COMPARISON OF THE PROTEIN SEQUENCE AND THE HOMOGENIETY PATTERN

Gabriela Fenollal, Notre Dame School, Caguas, Puerto Rico.

Student Research Mentor: Krizia Cabrera, Universidad Metropolitana, San Juan, Puerto Rico.
Student Research Mentor Assistant: Ashley González, Universidad Metropolitana, San Juan, Puerto Rico.

The colon/rectum is responsible for the final stages of the digestive process. Colorectal cancer is a disease in which normal cells from the walls of the colon begin to change, grow without control, lose their normal function and are immortal. The MSH6 gene provides instructions for making a protein that plays an essential role in repairing DNA. This protein fixes mistakes that are made when DNA is copied (DNA replication) in preparation for cell division. When the MSH6 protein is absent or ineffective, the number of mistakes that are left unrepaired during cell division increases substantially. If the cells continue to divide, errors accumulate in DNA; the cells become unable to function properly and may form a tumor in the colon. The purpose in this research was to compare the human MHS6 protein to that of other species, and test the pattern of homogeneity. A program called Molecular Evolutionary Genomic Analysis version 4 (MEGA4) was used. MEGA4 works by conducting of automatic and manual sequence alignments, inferring phylogenetic trees, mining web-based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses. Comparisons between protein and species was obtained using MEGA 4. These results may indicate evolutionary patterns of the MSH6 protein.
TOLERANCE AND INTOLEANCE FOR AMINO ACIDS CHANGES IN THE GAA GENE

Gianna Gómez, CIEM School, Carolina, Puerto Rico.

Research Mentor: Dr. Ángel R. Arcelay, Universidad del Este, School of science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Carol J. Díaz, Universidad del Este, School of science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Amir M. Rodriguez, Universidad Interamericana, San Juan, Puerto Rico.

The acid alpha-glucosidase or GAA gene which is located on the long (q) arm of chromosome 17, is essential for glycogen degradation. This enzyme is active in lysosomes, which are structures that serve as the cells’ recycling center. Lysosomes are organelles that use digestive enzymes to break down complex molecules into metabolites needed by the cells for optimum performance. Acid alpha-glucosidase normally breaks down a complex sugar called glycogen into a simpler sugar called glucose which is an important energy source for cells. Any defects in this gene cause Pompe disease. The Pompe diseases are responsible for muscle weakness, feeding difficulties, failure to thrive (prosper), respiratory distress, and hearing loss. Treatment by enzyme replacement therapy is necessary to avoid death within the first year of life from progressive left ventricular outflow obstruction. The non-classic variant of infantile-onset Pompe disease usually is present within the first year of life with motor decays and/or slowly progressive muscle weakness, typically resulting in the death from ventilator failure in their early childhood. Most of these mutations change one or more of the protein building blocks (amino acids) used to make acid alpha-glycosidase, which reduces the enzyme activity. This disease is characterized by proximal muscle weakness and respiratory insufficiency without cardiac involvement. The purpose of the use of the SIFT (Sort Tolerant from Intolerant) program is to predict the severity of an amino acid change and toleration to possible mutations. Scores were calculated for positions 1 to 1,911 within the alignment of the protein sequences. The predictions obtained resulted in 35.7% tolerant and 64.3% intolerant.
A STUDY OF AN AMINO ACID SUBSTITUTION EFFECT ON THE BIOTINIDASE GENE

Danechka Izquierdo, José Aponte De La Torre School, Carolina, Puerto Rico.
José Aponte School, Carolina, Puerto Rico.

Research Mentor: Dr. Ángel R. Arcelay, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Carol J. Díaz, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Amir M. Rodríguez Mujica, Universidad Interamericana, San Juan, Puerto Rico.

The Biotinidase gene is responsible for the recycling of biotin from biocytin or biotinylated small peptides and the liberation of protein-bound vitamins in the diet. In humans, biotin acts as a carboxylase prosthetic group for essential metabolic processes such as gluconeogenesis, fatty acid synthesis and catabolism of amino acids. Mutations or deficiencies in this gene result in biotinidase deficiency. Biotinidase deficiency is an autosomal recessive disease characterized by neurological symptoms and skin problems. Children with biotinidase deficiency cannot recycle endogenous biotin, an essential water soluble B vitamin. Biotin is covalently attached to epsilon-amino groups of residues of four carboxyl lamisil, which are subsequently degraded to biocytin (biotin-Epsilon-lysine). Biotinidase joins biocytin to biotin and lysine, thereby completing the cycle of biotin. The symptoms of biotinidase deficiency can be solved or prevented by treatment with biotin. Therefore, it is important that biotinidase deficiency is diagnosed early so that permanent neurological damages can be avoided. Many states and countries currently perform newborn screening for biotinidase deficiency. The focus of the research was to predict amino acid exchange that might be responsible for the mutation which causes profound biotinidase deficiency. These predictions have been produced through the use of SIFT (Sorting Intolerant From Tolerant). SIFT uses sequence homology to predict whether an amino acid substitution will affect protein function and hence, potentially alter phenotype; therefore, producing causes of mutations. Predictions were calculated for the 543 positions within the gene by the SIFT application. Fifteen amino acid predictions were chosen in order to evaluate their range in tolerance level and effect on the gene.
PROTEIN TOLERANCE AND SPECIES COMPARISON OF THE BBS5 PROTEIN

Natalie Jiménez, María Auxiliadora School, San Juan, Puerto Rico.

Student Research Mentor: Krizia Cabrera, Universidad Metropolitana, San Juan, Puerto Rico.
Student Research Mentor Assistant: Ashley González, Universidad Metropolitana, San Juan, Puerto Rico.

The BBS5, Bardet-Biedl Syndrome 5, gene encodes a protein that has been directly linked to Bardet Biedl Syndrome. BBS5 is a protein-coding gene that has been found in humans in chromosome two, locus 2q13.1. Features of this syndrome include retinal dystrophy, obesity, polydactyly, renal abnormalities and learning disabilities. The objective of this research was to determine the percentage of zero tolerance of BBS5 protein and compare it with homolog species. Two programs used were: MEGA4 and SIFT. The Molecular Evolutionary Genetics Analysis (MEGA) software is an application designed for comparative analysis of homologous gene sequences. It was used to compare the BBS5 protein in the following species: Homo sapiens, Mus musculus, Xenopus laevis, Bos Taurus, Rattus norvegicus. SIFT (Sorting Intolerant From Tolerant) is a program that predicts whether an amino acid substitution may affect protein function base of the chemical properties of the amino acids so that users can prioritize substitutions for future study. SIFT was used to determine the tolerance of mutations found and indicated which amino acids had zero tolerance to substitutions. The percentage of zero tolerance of the BBS5 protein was 18.5% according to SIFT. Of the mutations evaluated, only Arg207His was found tolerable. According to MEGA4, the species with more similarity in terms of species were the Homo sapiens and Bos Taurus, while in terms of species the most related were the Homo sapiens and Rattus norvegicus. In conclusion, the protein can tolerate some change, yet other amino acids may be essential to the function or structure of the protein, hence this may be due to evolutionary changes that the BBS5 protein may have suffered.
ANALYZING THE NEUREGULIN PROTEIN WITH SIFT AND MEGA 4

Carla A. López, Notre Dame School, Caguas, Puerto Rico.

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Student Research Mentor Assistant: Ashley González, Universidad Metropolitana, San Juan, Puerto Rico.

The gene for the neuregulin protein is found in chromosome 8, locus 8p12, in humans. It is a protein-coding gene for a signaling protein that mediates cell-cell interactions and plays a critical role in the growth of organ systems. The gene deregulation has been linked to diseases such as cancer, schizophrenia and bipolar disorder. Since the neuregulin has been linked with the functioning and development of the nervous system, it has been considered as a major cause for schizophrenia. Symptoms of schizophrenia are depression, oversleeping or insomnia, extreme reaction to criticism, forgetfulness, inability to concentrate, hallucinations, delusions, deterioration of personal hygiene, and others. The objective of this research was to evaluate the neuregulin protein using SIFT and MEGA4 to observe the protein tolerance to substitution and comparison between homolog species. SIFT (Sorting Intolerant From Tolerant) is a program that predicts whether an amino acid substitution affects protein function by comparing the biochemical properties of amino acids. It was used to determine the percentage of amino acid substitution tolerance of the neuregulin protein. MEGA 4 (Molecular Evolutionary Genomic Analysis 4) is a program that edits DNA sequence data from auto sequencers, mining Web-databases, performing automatic and manual sequence alignment, analyzing sequence alignments to estimate evolutionary distances, inferring phylogenetic trees, and testing evolutionary hypotheses. MEGA4, also known as Molecular Evolutionary Genetics Analysis, is an integrated tool for conducting automatic and manual sequence alignment, inferring phylogenetic trees, mining web-based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses. After evaluating the protein sequence on SIFT, it was determined that 21.24 % of amino acids are not tolerant to change. Furthermore, the neuregulin protein can tolerate some change, due to amino acids that may be essential to the function or structure of the protein. This may be due to evolutionary changes that the protein may have had.

SEROTONIN RECEPTOR 2 A PROTEIN ANALYZED BY SIFT AND MEGA4

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The 5-hydroxytryptamine serotonin receptor 2-A, also known as 5-HTR2A, is a protein-coding gene. The 5-HTR2A gene is located on chromosome 13q 14- q21. The receptor is expressed in the central nervous system. The hydroxytryptamine 2A receptor-5 functions as a hormone that is a neurotransmitter. This receptor mediates its action by association with G proteins that activate a phosphatidylinositol-calcium second messenger system. It is also a receptor that binds an extracellular ligand and transmits the signal to a heterotrimeric G-protein complex. The program SIFT, Sorting Intolerant From Tolerant, is a program that predicts whether an amino acid substitution affects function. SIFT considers the position at which the change occurred and the type of the amino acid change. MEGA4, also known as Molecular Evolutionary Genetics Analysis, is an integrated tool for conducting automatic and manual sequence alignment, inferring phylogenetic trees, mining web-based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses. After evaluating the protein sequence on SIFT, it was determined that 21.24 % of amino acids are not tolerant to change. Comparison of the Serotonin receptor protein between the human protein and other species, and species comparison itself, was successful. These results may give more insight about the 5-HTR2A protein.
EVALUATION OF CFTR PROTEIN BY SIFT AND MEGA 4

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Cystic Fibrosis is a hereditary disease that affects the respiratory system and the digestive system. Symptoms of this disease are: chronic cough, mucus secretion, and an increase of appetite, loss of weight, intestinal disorders, acid-flavored skin and repeated attacks of pneumonia. In severe cases, the deterioration of the illness can impose the need of a lung transplant. Most people die from pulmonary infections. The objective for this research was to evaluate the tolerance of amino acid substitutions using SIFT and compare the CFTR protein with other homolog proteins by means of MEGA 4. SIFT (Sorting Intolerant From Tolerant) is a program that predicts whether an amino acid substitution affects protein function so that users can prioritize substitutions for further study. SIFT indicates which amino acids have tolerance to substitutions based on the biochemical properties of amino acids. It was used to determine which amino acids are less tolerable to amino acid substitutions. The Molecular Evolutionary Genetics Analysis (MEGA) software is designed for comparative analysis of homologous gene sequences either from multigene families or from different species with emphasis on evolutionary relationships and patterns of DNA and protein evolution. MEGA4 was used in order to compare the CFTR protein of humans to that of other species. The percentage of zero tolerance was approximately 6 percent. In MEGA4, similarity in term of protein between Mus musculus and Homo sapiens is more than with Rattus norvegicus and Thermococcus gammatolerans. The same cannot be said in terms of species, which indicated that the Rattus norvegicus and Mus musculus are more similar. These results may suggest that the CFTR protein may have certain amino acids that may be important for the protein function due to the percent given by SIFT. In terms of comparison, the CFTR protein may have evolved due to the difference in species and protein similarities indicated by MEGA4.
The BRCA2 is considered a tumor suppressor gene which was recently localized in chromosome 13q12 – q13. The BRCA2 protein contains several copies of a 70 amino acid (recessive) motif called the BRC motif. These motifs mediate binding to the RAD51 recombinases, which function in DNA repair. Mutation or allelic loss of this chromosome is associated with poor prognosis in familial and sporadic breast and ovarian cancer. The BRCA2 gene confers increased risk of developing breast or ovarian cancer. Men who have harmful BRCA2 mutations may be at increased risk of other cancers, such as prostate and pancreatic cancer. A small proportion of breast cancers, in particular in those cases arising at a young age, are due to inheritance of dominant susceptibility which confers a high risk of the disease. The objective of this research was to examine changes on the amino acids using SIFT (Sort Intolerant from Tolerant), which predicts whether an amino acid substitution affects protein function. Substitutions were studied with SIFT. Twenty positions of the gene were taken and the levels of intolerance were observed, concluding that an average of 77.3% amino acids from this gene are intolerant.
The difference in positions of amino acids and the mutation number will determine the level of critical damage in each species. If the position changes through the years, it will be considered as a non-disease associated site (nSNPs), but if the position presents a low level of change, it will be considered a disease-associated site (DAMs). To find the categories in which each position is set, they need to be investigated, calculated, and compared together. In this specific gene, it is expected for DAMs to be present, especially on the eleventh chromosome. It is important to be alert, observe and calculate those evolutionary rates. Oculocutaneous albinism is a genetically heterogeneous congenital disorder characterized by decreased or absent pigmentation in the hair, the skin, and the eyes. Albinism is the result of the biological inheritance of genetically recessive alleles passed from both parents of an individual, though some rare forms are inherited from only one parent. The term albinism includes specific ocular changes that are the result of reduced amounts of melanin in the developing eye. These abnormalities in the eye and optic system are specific and necessary for the diagnosis. To determine the difference between observed and expected values for DAMs and nSNPs, the p-value was calculated. The non-associate disease mutations nSNPs are too few for statistical significance. The p-value for DAMs was 1.24E-5 which is a significant difference between observed and expected values. It was observed that DAMs have more frequency at low evolutionary rate levels while nSNPs are observed more abundantly at high levels. PolyPhen diagnosis analysis was applied to predict phenotypic expression of DAMs and nSNPs in the gene. The PolyPhen diagnosis for DAMs have 28.3% of error which is a significant value that decrease while sequencing projects adds data with new investigations.
EVOLUTIONARY ANALYSIS OF DISEASE ASSOCIATED MUTATIONS IN *HOMO SAPIENS* CALCIUM-SENSING RECEPTOR, (CASR), NM_000388

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The most important issue in the analysis of molecular evolutionary patterns using genome sequence projects is to make a good structure based on factors of the evolution of genetically-based diseases. The analysis of evolution rates in amino acid positions between clinical and population genetics can help to understand the phenotypes caused by disease mutations using computational tools. This investigation allows for the understanding of the difference between DAMs and nSNPs of the evolutionary rates of diseases. To present and compare the position of both, the evolutionary rates need to be calculated. The gene calcium-sensing receptor (CASR) is located on chromosome three. The protein encoded by this gene is a G protein-coupled receptor that is expressed in the parathyroid hormone (PTH)-producing chief cells of the parathyroid gland, and the cells lining the kidney tubule. It senses small changes in circulating calcium concentration and couples this information to intracellular signaling pathways that modify PTH secretion or renal caution handling, thus this protein plays an essential role in maintaining mineral ion homeostasis. The nSNPs observed and expected are too few for a statistical significance. Meanwhile, the p-value of DAMs is 1.55E-6 which establishes a difference between them. The results for evolutionary rates for DAMs are expected in low rate levels and reveal the evolutionary frequency levels. The number of nNSPs is so small that they are not significant; on the other hand, the DAMS in calcium-sensing receptor genes have 20.5% of error. Diagnosis tools are based on structure and chemical composition and its predictable accuracy is an important goal to clinical advances.
STUDY OF THE IL2RG PROTEIN: TOLERANCE EVALUATION AND HOMOLOG SPECIES COMPARISON

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The Interleukin 2 Receptor Gamma, also know as IL2RG, is a protein coding gene located in chromosome X, locus Xq13.1. The receptor is found in the plasma membrane of the immune cells. This protein works with other receptors in the immune system; and in the synthesis of subtypes of lymphocytes like: T cells, B cells and natural killer cells. Mutations in the gene IL2RG can be related to a health condition that is X-linked Sever Combined Immunodeficiency (SCID), which also affects the IL-2 receptor system. Humans born with SCID have a fault in the protein that constructs a receptor whose job is to establish communication between immune cells: T cells and B cells. If there is no receptor to warn T cells and B cells about invaders, the body stays defenseless to attack. The purpose of this research was to determine the percentage of non-tolerance to substitutions using SIFT, and a homolog species comparison of the IL2RG protein. SIFT (Sorting Intolerant From Tolerant) predicts whether an amino acid substitution affects protein function by comparing the biochemical properties of amino acids. SIFT was used to determine the percentage of amino acid substitution tolerance in the IL2RG protein. The Molecular Evolutionary Genetics Analysis (MEGA) version 4.0 is software that compares DNA or protein sequences of homolog species to estimate evolutionary rates using phylogenetic trees. Grantham Distance is a score system used to determine the biochemical distance of an amino acid when a mutation occurs. The percentage of non-tolerance was determined using SIFT, which indicated an 11% of amino acids with zero tolerance to substitution. The mutation R224W resulted with a SIFT of score 0.00 and a Grantham’s Distance of 101. Comparison between species and species’ protein was analyzed using MEGA 4, which suggested that Rattus norvegicus and Sus scrofa are the closest in terms of similarity between species; yet in terms of protein, the closest relation was observed between Homo sapiens and Macaca mulatta. These results may suggest that the amino acids that have zero tolerance to substitutions indicated by SIFT may indeed be conserved sites. Also, the IL2RG protein may have evolved due to the similarity in protein that is not observed in species.
STUDY OF THE 8-OXOGUANINE GLYCOSYLASE USING SIFT, MEGA AND GRANTHAM’S DISTANCE

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The major reason for mutant base lesion in DNA caused by exposure to reactive oxygen species is 8-oxoguanine. DNA glycosylases, like 8-oxoguanine glycosylase (OGG1), are enzymes that initiate the multistep base excision repair (BER) pathway by removing damaged or inappropriate bases, including oxoguanine, from the phosphodiester backbone. DNA glycosylases initiate the first step of BER, thereby creating an AP (apurinic/apyrimidinic) site in the DNA. The purpose of this research was to analyze the OGG1 protein using SIFT, MEGA4 and Grantham’s Distance. The program SIFT (Sorting Tolerant From Intolerant) was used to study the severity of changes in amino acids and if the mutations found are tolerable or not to the protein function and structure. A search for other homolog species was conducted. Using MEGA4 (Molecular Evolutionary Genetics Analysis 4), the evolutionary change in the OGG1 protein of species was compared. Each substitution was evaluated for biochemical severity using Grantham Distance, the distance between the original amino acid and the mutated amino acid. MEGA4 was used to do a protein alignment of these sequences. The mutations found and the percentage of zero tolerance of the OGG1 was determined by SIFT, the protein comparison between a homolog species was given by MEGA4. Theses results obtained may imply that these amino acids are very important for the function of the protein due to the evolutionary changes that the OGG1 may have suffered over time.
EVOLUTIONARY ANALYSIS OF DISEASE-ASSOCIATED MUTATIONS IN THE GENE PHOSPHOMANOMUTASE DISEASE, TYPE IA (PMM2), NM_000303

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Genomic projects have revealed that every individual carries thousands of amino acid–altering nucleotide mutations. The evolutionary rates of amino acids positions are thought to be the most practical tool to understanding and predicting how genomes are going to mutate. The evolutionary rates are the method of choosing a fraction of amino acid sites that is conserved even among distantly related species. Certain amino acids have been through the process of purifying the selection and have not been eliminated from the specific locations of the species gene. These prove that they were essential throughout the evolutionary process. The amino acids that were variations were compared to the ones that were essential and throughout their evolutionary history were eliminated. This study was associated with two types of mutations, the disease associated sites (DAMs) and non-disease associated sites (nSNPs). Studies have proven that the DAMs are the mutations that have taken the position of an essential amino acid by another and affect the cell’s basic functions. The nSNPs are the mutations that have occurred in the genome, but instead of replacing vital amino acids, they replace other amino acids and do not cause diseases. The Polyphen diagnosis method has been used to find probably potential defective effects of mutations classifying them into three categories: benign, possibly damaging and probably damaging. The patients that do not have the proper alignment in their amino acid pairs suffer many physiological problems. The p-value statistics have proven that the significance of nSNPs is too small compared to what was expected in the DAMs. As expected, the evolutionary frequencies showed that there were more mutations at low evolutionary rates which are consistent with the expected results of evolutionary rates of DAMs. The evolutionary frequencies showed that there are more observed DAMs than expected at low evolutionary rate levels which are consistent with the expected results for evolutionary rates for DAMs.

SPECIES AND PROTEIN COMPARISON OF NEUROFIBROMATIN

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Neurofibromatosis type 1, also known as NF1, is gene found in chromosome 17 in humans. Neurofibromatosis is a hereditary disorder that affects development and growth of nerve cell tissues. It occurs as a result of a mutation in the gene NF1, which may be inherited as part of the disease or in cases where neither parent does not have the disease or are not carriers it is said to be germ cell mutations. The objective of this research was to evaluate the neurofibromatin protein using MEGA4. MEGA4 (Molecular Evolutionary Genetic Analysis 4) is a program that compares the protein sequences of random species to estimate rates, and uses phylogenetic trees to compare the information. It was used to compare the NF1 protein with other homolog species by means of phylogenetic trees. Two different comparisons were done: a parsimony species comparison and a protein comparison. Comparison of species and protein comparison was done by MEGA4, which indicated the similarities between protein and species compared. These types of comparison may give insight of the evolutionary changes of the neurofibromatin protein.
HYPERTECHRONIC CARDIOMYOPATHY

Hypertrophic cardiomyopathy is a disease of the myocardium in which a portion of this muscle is hypertrophied. One of the causing genes of this disease is the myosin binding protein C (MYBPC3), located in chromosome 11, locus 11p 11.2. The protein is expressed only in the heart muscle. Mutations in this gene are one cause of familial hypertrophic cardiomyopathy. The objective of this research was to test the pattern of homogeneity of the MYBPC3 protein after it was evaluated by SIFT, MEGA4 and Grantham’s Distance. SIFT (Sorting Intolerant From Tolerant) was used to predict whether the amino acid substitutions will affect the protein function. Past research has found the following mutations that were evaluated for tolerance by SIFT: V771M, V342D, A627V, E344K, Q998E, T1046M, P147L, S236G and R1138H. These mutations were later analyzed by Grantham’s Distance system. Grantham’s Distance system is a program that measures the biochemical change between amino acids when a mutation occurs. MEGA 4 (Molecular Evolutionary Analysis) was used to evaluate how the sequences of DNA and proteins change with time. Using a minimum phylogenetic tree to make a comparison of protein between species and a maximum phylogenetic tree to establish a comparison between species, comparisons between the following species were evaluated: Homo sapiens, Mus musculus, Danio rerio, Gallus gallus and Xenopus tropicalis. The species more similar to the Homo sapiens was the Mus musculus. Also, with MEGA 4, the test pattern of the homogeneity between sequences of the species mentioned before was used to determine the probability of rejecting the hypothesis that sequences evolved with the same pattern of substitution. Finally, SIFT indicated that 22% of the mutations found are tolerable to the mutations and Grantham Distance shows that mutation V342D had the largest distance of all. This may suggest that the protein in question may have evolved permitting a certain grade of susceptibility.
BRCA2 PROTEIN: ANALYSIS OF SUBSTITUTION TOLERANCE, SPECIES COMPARISON AND BIOCHEMICAL DISTANCE

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BRCA2, also known as breast cancer early onset, is a tumor suppressor gene that reduces the probability that a cell in a multi-cellular organism will turn into a tumor cell. This gene is located in chromosome 13 belonging to Homo sapiens. Inherited mutations of this gene can increase the risk of developing breast or ovarian cancer as well as prostate cancer. Treatment of breast and ovarian cancer in individuals with BRCA 1 or BRCA 2 related tumors is similar to that for appearing in scattered or isolated instances forms of these cancers. The purpose of this investigation was to determine the percentage of zero tolerance, comparison of the BRCA2 protein and biochemical distance. The investigation involved the use of SIFT (Sorting Intolerant From Tolerant), a program that evaluates the tolerance of amino acid substitution of a certain protein. It gives a score that ranges between 0.00-0.05 as intolerable and 0.06-1.00 as tolerable. MEGA 4 (Molecular Evolutionary Genetics Analysis) is a program that compares the gene sequences between homologous animals and it includes tools for visual presentations of the results obtained. Grantham is a score system that measures a biochemical change between the amino acids on a mutation using a table. SIFT predicted two mutations to be one intolerable and the other tolerable. MEGA 4 made a phylogenetic tree ranking Homo sapiens at the top and the Trypanosoma brucei at the bottom, the Salmon Salar and the Mus musculus interchanged their positions on the diagram. Grantham’s score system evaluated the mutations with a score of 81. In conclusion, BRCA2 is a tumor suppressor gene whose mutations may have risks. Different methods are used to investigate the protein’s function in an organism and its future evolution.
PREDICTING POSSIBLE MUTATIONS AND STRAIN COMPARISONS USING SIFT AND MEGA 4 IN CLOSTRIDIUM TETANI’S TOXIN

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Clostridium tetani is an anaerobic pathogenic bacterium that is primarily found in soil and animal intestinal tracts. It is a bacillus, gram-positive single-celled bacteria, and does not contain any membrane-bound organelles, such as a nucleus. There are currently eleven identified strains of Clostridium tetani, and they are all known to produce an identical neurotoxin known as tetanospasmin. It spreads through tissue spaces into the lymphatic and vascular systems. It enters the nervous system at the neuromuscular junctions and migrates through nerve trunks and into the system by retrograde axonal transport. This toxin is the cause of the condition known as tetanus, which is commonly fatal unless treated. The purpose of this research was to determine possible mutations in order to gain insight into the susceptibility of the Clostridium tetani toxin and to compare the strains to determine conserved sites. SIFT (Sorting Intolerant From Tolerant) predicts whether an amino acid substitution affects protein function based on sequence homology and the chemical properties of amino acids. MEGA4 is an integrated tool for conducting automatic and manual sequence alignment, phylogenetic trees, mining web-based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses. The results of the amino acid predictions using SIFT was approximately 17.79%. The analysis done using SIFT was the Analysis of zero, which measures the amount of amino acids with zero tolerance to substitutions compared by the entire amount of amino acids in the protein sequence. On MEGA 4, conserved sites were estimated by comparing two sequence alignments of a Clostridium tetani strain: Clostridium tetani and Clostridium tetani E88. It was determined eighty-four conserved sites were found. These may indicate that the tetanospasmin protein has conserved sites that may be targets for further study.
Shingomyelin phosphodiesterase is a hydrolase enzyme involved in shingolipid metabolism reactions which is responsible for the production of phosphocholine and ceramide that is an important lipid in the brain. The sphingomyelinase phosphodiesterase 1 (SMPD1) gene is located in chromosome 11 and has a base pairs size from 6,368,230 to 6,372,801. The protein within the gene is an acid lysosomal shingomyelinase with a phospholipase C activity. The phospholipase reaction takes place in the plasma membrane and the Golgi apparatus. When mutation occurs on this gene, it causes Niemann Pick disease, which is the lack of enzyme activity. The lack of enzyme functions can lead to the accumulation of shingomyelins, cholesterol and other types of lipids within the cell and tissues. Mutations in the gene can cause two different types of Niemann Pick diseases: Type A and Type B. Niemann Pick disease Type A (NPA) causes the enzyme to be inactive. The symptoms in type A may produce abdominal swelling within 3-6 months, loss of motor skills, feeding difficulties and a cherry red spot in the eye. The Niemann Pick disease type B is the production of defective enzymes. The symptoms that may occur in early childhood or adolescence are abdominal swelling, loss of motor skills and respiratory infections. SIFT (Sorting Intolerant From Tolerant) is a program that predicts whether an amino acid substitution affects protein function so that users can prioritize substitutions for further study. The aim of the study was to determine whether the predictions presented by SIFT are links to the mutation or lack of phospholipase activity. Fifteen different positions within the gene were chosen from SIFT predictions which concluded that 43% of the changed amino acids were intolerant to the substitution.
EVOLUTIONARY ANALYSIS OF DISEASE ASSOCIATED MUTATIONS IN THE *HOMO SAPIENS* GENE KCNQ1, NM_000218

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Genome sequencing projects are expensive procedures that provide extensive data that is impossible to analyze with conventional methods. The design of the genome sequencing projects provide the opportunity to manage and conduct a research plan based on important factors in genetic-based disease patterns while the cost lowers. The use of computational tools helps understand the relationship and development of mutations that cause disease with the evolutionary rates of amino acid position. The amino acid positions between clinical and population genetic analysis help to determine consistency and predictability that will also help in the understanding of mutation developments. This research was focused on determining if DAMs (disease associated sites) and the nSNPs (non-disease associated sites) are different in the *Homo sapiens* gene KCNQ1, encoding potassium voltagegated channel. The DAMs are expected to be at positions that have been retained in multiple vertebrate species while the nSNPs are expected to be overabundant at positions that have been lost in non-human vertebrates. In order to see those observations with the DAMs and nSNPs in gene KCNQ1, it is necessary to calculate the evolutionary rates for the improvement of the accuracy of functions. The difference between observed and expected values for DAMs and nSNPs is expressed in terms of p-value. For DAMs it was $1.318E-6$ while nSNPs are too few to apply statistical analyses. Evolutionary frequencies demonstrated that the gene has less observed DAMs than expected at high evolutionary rational level rates with the expected results. The PolyPhen diagnosis was 23.2% of error predicting DAMs behavior for the KCNQ1 gene. For the nSNPs, the PolyPhen diagnosis does not have a statistical significance to achieve a statistical analysis. These results become part of a multidisciplinary force in the improvement of the diagnosis of genetic diseases.
ATMOSPHERIC SCIENCES (GLOBAL MICROSCOPE)

THE EPIDEMIOLOGY DYNAMICS SPREAD INCREASE OF THE A H1N1 VIRUS AROUND THE WORLD REPRESENTED WITH THE GLOBAL MICROSCOPE

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Different kinds of influenza viruses such as type A, type B, and type C, especially the one that has been a pandemic since April 2009, the A H1N1 virus, are found around the world. This new virus has been studied in how it works, infects, and spreads dynamically throughout the world using humans and animals as hosts, and how the immune system responds to this virus compared to other influenza viruses. In this research, different kinds of demographic maps and the Global Microscope were used to represent the dynamic spread of the virus throughout the world. The research objective was the modeling of the Influenza A virus spread over the world and predicting how the population will be infected over the future years. The common flu or influenza is a contagious disease caused by different types of viruses from the orthomyxovirus family (Osores et al, 2009). In the orthomyxovirus, there are different types of influenza viruses such as type A, type B, and type C. The type A flu or influenza is capable of infecting humans as well as animals. Wild birds commonly act as a host for this kind of flu (cdc.org, 2009). The type B flu, unlike type A, is only found in humans and cause less severe action than type A flu, but this flu can still be extremely harmful, although it does not cause pandemics. According to the Center for Disease Control and Prevention, type C flu is found in people and it is milder than Type A or B; people generally do not become very ill from this type of flu and it does not cause epidemics. The objective of this research was to represent the dynamics of the A H1N1 virus to spread in the world using the Global Microscope. Since April 2009, there has been an epidemic due to a new kind of flu or influenza, the type A subtype H1N1 or “swine’’ flu. This A H1N1 virus or flu is a combination pig (swine) genes, bird (avian) genes, and human genes (cdc.org, 2009); this fusion is called by the scientists the “quadruple reassortant” virus. This flu or influenza has been spreading worldwide because it is transferred from human to human; either by a person coughing or sneezing that is already infected. Since it is a virus, it cannot be killed and there is still no vaccine or antivirus to reduce the symptoms in the infected human.
MODELING RAINFALL DYNAMICS OVER THE CARIBBEAN ZONE

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Rainfall is the amount of precipitation of any type, mostly liquid. Rainfall is an important factor in the ecosystem, mainly because it affects the lives of many living beings. There are numerous ways to analyze rainfall data using the satellites, such as: mapping the boundaries of areas probably affected by rain; mapping estimated totals of rainfall accumulated through unit periods of time; assessing, monitoring and forecasting extreme rainfall events; assessing the climatology of rainfall distributions; and forecasting rainfall, especially in areas open to systems from relatively poorly observed regions. Using satellites for estimating rainfall data is difficult because different authors apply different methods and data. The objective of this research was to model the rainfall patterns over a tropical zone, specifically the Caribbean, using the Global Microscope Program. It also included comparing these patterns of precipitations with the last agricultural/land use changes in the research zone.

THE EFFECT OF THE PHYTOPLANKTON BLOOM ON THE OCEAN

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Phytoplanktons are microscopic plants that live in all healthy aquatic systems including freshwater ponds and lakes capable of producing photosynthesis. Phytoplanktons are due to the oxygen from the other organisms that live in the water. Phytoplankton bloom occurs when they develop too much due to excess of nutrients in the water. The objective in this research was to use the Global Microscope to model the effect of the phytoplankton bloom in the ocean, showing how the phytoplankton bloom by excess of nutrients multiply quickly. These masses of phytoplanktons move forming a layer that covers a part of the ocean making the aquatic animals receive no sunlight. This affects the animals. If the phytoplankton use oxygen for the aquatic animals, when the phytoplankton bloom occurs these animals may die. The phytoplankton bloom is very dangerous because it can cause a massive loss of animals such as fish. The effects of the phytoplankton bloom in the North Atlantic Ocean, why they affect the aquatic animals, and all the possible data or variables were studied. After having all this data entered in MATLAB to have a model of the results of the effect on the aquatic animals they were projected in the Global Microscope. Sunlight is necessary since, like terrestrial plants, phytoplankton use solar radiation to convert carbon dioxide and water into organic molecules such as glucose (Spokes 2003).
The science that studies all aspects of oceans is oceanography. This science has studied the ocean currents that are the main force that moves water mass around the whole planet. This science gives past, present and future data from the oceans that are approximately seventy percent of the earth’s surface area. There is an enormous wealth of natural resources hidden in the ocean’s depths. It includes a vast reserve of food and energy sources (Bruno & Hires, 2006). The world’s oceans are divided in three main water bodies: the Atlantic Ocean, the Pacific Ocean and the Indian Ocean. Currents in the northern circular motion to the right and in the southern hemisphere move to the left because of the Coriolis force. Currents move water from tropic regions to polar regions; these have a direct influence on the climate and disperses nutrients and organisms through the ocean (Brooks & Cole, 2006) The superficial currents are caused mostly by the winds, every layer beyond them is moved more slowly by friction (Ekman Spiral). Currents near the bottom of the ocean are regulated by the force of gravity and move very slowly, sometimes almost imperceptibly, and they are called thermohaline circulation or density-driven deep ocean currents (Bruno & Hires 2006). According with Brooks & Cole (2006), density is mainly a function of temperature and salinity if the ice in the polar regions melts, and it could affect the ocean currents. The polar regions are formed by water in solid state, but the icebergs or other solid bodies in polar zones are made by marine water; that is water without saline solutes. When the water is changing from liquid to solid all the solutes precipitate to the bottom. If this ice bodies melts, some surface currents will be affected by the sweet water that is homogenizing with salt water. With these homogenizing, the temperature of the currents could change and the thermal balance in the planet could get affected. The surface water can move more fluidly through currents but the ones near the ocean floor do not have flow by their density altering the currents dynamics in the ocean. Water temperatures in them are regulated by currents that can be cold or warm depending on the part of the planet. This circle transports warm water from the tropic to the poles and vice versa to maintain the balance of temperatures around the world. The Arctic pole is formed by water in solid state that maintains the water with large quantities of solutes at the bottom. If the temperatures in this area decrease, the marine water will homogenize with the high solute containing water and these will affect all the arctic pole balance. The ecosystems in this polar region will get affected because there is going to be a change in their habitat. In fact, the whole planet will be affected by this ice melting because the marine water could change the whole current flow and their temperatures. In this research the changes in the arctic pole if the ice melts and homogenizes with the marine water were predicted. This data was used to represent the effects in the global microscope. The objective of the research was to predict and represent, using the Global Microscope instrument, how the superficial ocean currents could be affected if the ice on polar regions melts and homogenizes with marine water. If the ice melts, the currents that are supposed to be warmer may become colder and this could cause weather and climate changes in the ecosystems that may have a direct impact on ocean currents.
PICTURE IN PICTURE MORPHING USING THE GLOBAL MICROSCOPE

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The Global Microscope (GM) is mostly used by teachers and students for educational purposes such as analyzing phenomena in the Earth’s surface, from global warming indicators to atmospheric changes to hurricane formations. It is mostly used by students or teachers for educational purposes such as analyzing phenomena across the Earth’s surface, from global warming indicators to atmospheric changes to hurricane formation. The Global Microscope can zoom in or load information on a certain place using the Picture in Picture (PIP) function. Picture in picture is a function that allows to view a photo or video inside another picture. When it is situated near the poles, the image may come out to long or wide or not where it is supposed to be. This occurs because the image is being displayed in a round object instead of a flat object. The GM can achieve this by using MATLAB which is used to make software for the GM. To work on it, input must be provided through a code which will pre-warp the image so that when the image is placed in the GM, it will come out the right size and shape. This project developed tools to fix those problems that occur when using the PIP function. It morphed the images so that when PIP was used, the image or video stayed rectilinear and did not become distorted. The Global Microscope (GM) uses data from NASA’s earth observatory.

DEFORESTATION AND ITS EFFECTS ON ATMOSPHERIC AND NATURAL BEHAVIORS

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Nowadays, approximately 8.5 of rainforest are deforested all around the globe in a period of one year (UNFA, 2008). The deforestation process active in the world is a consequence of various factors. The most noticeable one is urbanization and the development of cities, factories, etc. Other than this, deforestation is also provoked in a much lesser scale by naturally fuelled fires. These fires, even though not directly, are also provoked by humans through the emission of CO₂ and the increase of greenhouse gas emissions causing the raise of temperatures that provoke the “natural” fueling of rainforests all around the globe (IEA, 2009). Deforestation has always been an important factor in determining atmospheric and natural changes such as rain patterns, temperature changes, and animal extinction (Campbell & Reece, 2005). The objective of this research was to determine how deforestation in certain regions of the globe affects atmospheric and natural behaviors. The study was done through the use of the Global Microscope by making a model of different levels of deforestation in various important rainforests in the world and modeling the impact that it had on the ecosystem. The program MATLAB was use to encode the different degrees of deforestation as well as the exact place where deforestation occurs. It was expected that the modeling of the different degrees of deforestation would prove that if the proportion at which different landscapes on Earth are being deforested is reduced and possibly stopped completely, the greenhouse effect, with all it consequences, could be greatly reduced as well as the conservation of different species that are in danger of extinction.
MODELING THE EFFECTS OF A TSUNAMI IN THE CARIBBEAN REGION

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Puerto Rico is located in a high seismic area. The Puerto Rico Seismic Network (PRSN) Department of Geology at UPR-Mayaguez reported last year 2574 tectonic movements in the local area, 9.6% more than in 2007. The objective of this research was to predict the run-up and model the consequences of a tsunami in the Caribbean area, especially on the main island of the archipelago of Puerto Rico. When an earthquake occurs, the land starts shaking because the tectonic plates are moving. According to intensity of the earthquake, it may be very disastrous or catastrophic (Wood & Neuman, 1931). That is when a tsunami occurs. A tsunami is giant wave that surpasses from the perimeter and affects a coast destroying properties and human life. Tsunamis are classified into three categories, distant (> 750 km from the source), regional (100–750 km from the source), and local (< 100 km from the source (Fernandez M. et al., 2000). Tsunamis depend on where the epicenter is localized. Using a seismograph, scientists can determine the time, location and magnitude of earthquakes (Milne, 1880). The extent of vertical run-up of seawater depends on near shore bathymetry, beach profile, land topography, and the frequency and velocity of tsunami waves (CHoi et al., 2003). Puerto Rico is located in a region where there is a lot seismic activity (USGS, 2009. This research focused on which areas of Puerto Rico are more prone to this phenomenon, in case that a tsunami wave hits the island area; and which areas are more exposed according to the elevation, topography and geomorphology. After studying all this data or variable, the data was entered on MATLAB to obtain a model. Using the Global Microscope Project System, and mathematical models, the range of a tsunami was demonstrated using images and data depending on the magnitude of an earthquakes and the distance from the epicenter. The results indicate that Puerto Rico is not prepared for an atmospheric catastrophe. If a tsunami occurs in Puerto Rico, there will be much damage because the Island is not prepared for it. Moreover, Puerto Rico does not have a drainpipe system and water will be stagnant, thus bringing about many diseases.
Since the year 2000, there has been a petroleum decrease around the entire world. Scientists came up with the idea of renewable energy to solve this problem. Renewable energy is energy generated from natural resources such as sunlight, wind, rain, tides, and geothermal heat. Ocean Thermal Energy Conversion (OTEC) is a base load renewable energy source particularly suited for tropical zones. It uses the temperature difference between the warm surface ocean water and the cold deep ocean water to generate electricity and, if desired, potable water. In 2006, about 18% of global final energy consumption came from renewable, with 13% coming from traditional biomass, such as wood-burning (Global Status Report 2007). Hydroelectricity was the next largest renewable source, providing 3% of global energy consumption and 15% of global electricity generation (Global Status Report 2007). Ocean Thermal Conversion (OTEC) is a base load renewable energy source particularly suited for tropical zones. It uses the temperature difference between the warm surface ocean water and the cold deep ocean water to generate electricity and, if desired, potable water (OTEC, 1997). The research objective of this project was to determine how usable ammonia is and how it can be made to work with the use of water and nitrogen to make energy, and thus resolve the energy problem using geoscience techniques. This was made using the Global Microscope. Ammonia was chosen for this research because after combustion represents a clean energy in comparison hydrocarbons. Ammonia is a water-created solution made of nitrogen and three elements of hydrogen (NH₃). Ammonia is also a colorless gas with a characteristic pungent smell. It is lighter than air, its density being 0.589 times that of air. It is easily liquefied due to the strong hydrogen bonding between molecules; the liquid boils at 33.3 °C, and solidifies at 77.7 °C to white crystals. Another reason is because it does not burn readily or sustain combustion, except under narrow fuel-to-air mixtures of 15-25% air (Cleeton, 1934).
USING THE GLOBAL MICROSCOPE FOR MODELING PARTICLES DYNAMICS IN THE CAPECO EXPLOSION IN BAYAMON, PUERTO RICO

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This research studied the wind, which is caused by the differences in pressure and varies all over the world. Wind is air flowing across the Earth's surface created by differences in atmospheric pressures that force it to move from zones of higher pressure to zones of lower pressure (Astwood, 2003). The differences of pressures in the Earth’s surface are the result of unequal heating of the surface by solar energy. Besides pressure, wind also differs in speed and direction. In the Northern hemisphere, wind currents tend to flow to the right direction eventually forming counterclockwise circular currents and in the south of the equator they also move in circular currents but to the opposite way caused by the Coriolis effect which is the result from inertial forces that are applied to bodies moving on the Earth (Encyclopedia Britannica, 2009). Those wind currents are divided into three wind belts: the Polar Easterlies (from 60-90 degrees latitude), the Westerlies (from 30-60 degrees latitude), and the Trade Winds (0-30 degrees latitude). Wind is responsible for redistributing heat and water across the surface of the Earth (Gedzelma, 1980); this is why it has an important role on continents because it gives them their specific climates. Wind is also a way of transporting nutrients, dust and other substances (IUGS, 2002). The enormous explosion of the CAPECO refinery in Puerto Rico caused serious consequences to the people near it and the company. On September 16, the Caribbean Petroleum Corporation (CAPECO) located in Bayamón, Puerto Rico had an incident in which some of their tanks exploded and needed almost three days to put out the fire (ENDI, 2009). To understand the explosion that occurred in the Caribbean Petroleum Corporation (CAPECO) refinery of located in Puerto Rico, it was necessary to study the directions of the wind currents in Puerto Rico and the Caribbean. Since they have different speeds and directions, it was easier to know why the particles of the explosion behaved the way they did. Maps were used to guide and to understand the location of the currents. The global microscope was used to identify how the smoke and the particles of the explosion traveled through the air depending on the wind currents and the wind patterns that were present that day. Since the wind patterns of that day were northwest, the possible result would be that the particles traveled to the west and that the Dominican Republic and other islands located on the west of Puerto Rico received some particles of the explosion. Based on the wind currents of the area where it exploded and the wind currents of the Caribbean, the research objective was to locate in the global microscope where the particles of the explosion were directed and what they caused in the places near it.
APPLIED MATHEMATICS

WHAT VARIABLES INFLUENCE DIABETES SUSCEPTIBILITY?: FEMALE PIMA INDIANS STUDY MODEL

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Pima Indians are American Indians who have lived at least 2,000 years at the Indian Community of the Gila River, southern Arizona. Their ancestors were among the first people to set foot in the Americas 30,000 years ago. Members of the Gila River Indian Reservation have participated in 30 years of research of the National Institute of Diabetes and Digestive and Kidney Diseases, research that will help people avoid diabetes. The reason why Pima Indians are so important in this research is because diabetes is a disease that is influenced by genes and the individual lifestyle. Pima Indians often marry other Pimas and have lived in the Gila River Indian Community for generations. Therefore, there is not much variation in genes and lifestyle and permits the study of the disease progress through generations. This study used the data of 768 female Pima Indians analyzed, provided by the National Institute of Diabetes and Digestive and Kidney Diseases. The variables taken into account were the number of times pregnant, glucose concentrations, age, if diagnosed with diabetes. The program “R” was used to calculate the mean, and standard deviation, which will be used to see if there is some relation between the times a female Pima was pregnant and being diagnosed with diabetes. The program “R” is a language and environment for statistical computing and graphics. The results demonstrated that the information on female Pimas that had been pregnant was not enough to conclude that it is a determinant variable to identify the individual is susceptible to develop the disease, but that other variables do have an affect such as glucose concentration and diastolic blood pressure.

STATISTICAL STUDY OF ESTRADIOL EXPOSURE IN BREAST CANCER CELLS


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Estradiol is a form of estrogen, which is a female sex hormone necessary for many processes in the body. Long-term estradiol treatment may increase the risk of breast cancer, heart attack, or stroke. The expression levels of a gene can be used as indicators of possible development of a disease, such as cancer. This study used the data provided by the National Center for Biotechnology Information from Lin Cy et al. The data describes the expression levels of important oncogenes measured at different time points from the MCF-7 breast cancer cell line. The MCF-7 cell line was obtained in 1970 from a woman patient of breast cancer. The mean and range of the gene expression levels were obtained using the ‘R’ program. The ‘R’ program is a language and environment for statistical computing and graphics. After comparing the mean values for the gene expression for estradiol, it was found that high levels are indicating possible development or susceptibility to breast cancer. The question now is if one of the samples were individuals that had long-term treatment with estradiol and how this affected susceptibility to the disease.
COMPARATIVE STUDY OF HAWKSBILL NESTING ON MONA ISLAND AND OTHER NESTING SITES IN PUERTO RICO

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The hawksbill, also known for its scientific name *Eretmochelys imbricatta*, is among the six endangered species of sea turtles. The hawksbill has been listed as endangered in the Endangered Species Act (ESA). The hawksbill is known to nest mostly in the Caribbean. This project focused on the different locations of hawksbill in Puerto Rico’s Archipelago. A recent report of nesting on Mona Island has shown an increment of hawksbill nesting. The goal of this project was to perform a statistical study of the increment in nesting of the hawksbill through the years 1974 to 2005 and compare it with other nesting locations in Puerto Rico. The data was obtained from the Diez, C. E., van Dam, R. P. report of 2005 for the Natural Resources Department of Puerto Rico. This data was taken to the ‘R’ program, which was used as the statistical software tool to calculate the mean, standard deviation and range of the data. The ‘R’ program is a language and environment for statistical computing and graphics. The results showed an increase of nesting for the hawksbill. Compared to the different nesting sites in Puerto Rico, the number of nests was below the number of nests on Mona Island. These set the bases for a study that would deal with the facts that affect hawksbill nesting if this has to do with the human interference or if they are more factors that can affect hawksbill nesting.

STUDY OF TRANSCRIPTIONAL CHANGE IN THE *ARABIDOPSIS THALIANA* LEAF DEVELOPMENT

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*Arabidopsis thaliana* is a small flowering plant that has been used as a genetic model for many years in plant biology. *Arabidopsis* offers important advantages for basic research in genetics and molecular biology. The *Arabidopsis* genome sequencing revealed the presence of at least three extensive gene families that may encode protein ligands. This research focused on the S-protein homologue (SPH), although there has not been found much information regarding the function of these genes. There is one member of the family, SPH1, which is involved in leaf vascular development. The data used in this research was downloaded from the microarray database NASC Arrays of Nottingham Arabidopsis Stock Centre. This database contains a large number of microarray experiments for *Arabidopsis thaliana* with 24,000 representing genes, each gene having a single expression value for each condition. The program ‘R’ was used to group the different gene expression for each condition. The ‘R’ program is a language and environment for statistical computing and graphics. The population was seen as a population of *Arabidopsis* with a specific condition. The gene expression for the different conditions was compared within each population and with the overall population.
MULTI-ALIGNMENT OF SEQUENCES: A COMPARISON OF TEN SPECIES BASED ON THE RAG1 SEQUENCE


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The recombination activation of genes-1 (RAG1) has the function of the re-ordering of half the genome and is essential for adaptive immunity in vertebrates. In humans a mutant RAG1 gene is known to result in the Ommen Syndrome. Sequences can be aligned to identify regions of similarity that may result as a consequence of functional, structural or evolution between sequences. The objective of this research was to compare the RAG1 sequence between ten different species. The sequence of ten species was multi-aligned. These species are: *A. sinensis* (a type of alligator), *A. ferreus, A. lugubris, D. tenebrosus* (types of salamanders), *B. balearicus, X. borealis, S. baudinii* (types of frogs), *B. constrictor* (type of snake), *B. taurus* (common bull), *T. rubripes* (type of fish). The sequences were obtained from the National Center for Biotechnology Information and the multi-alignment was performed using ClustalW through the MEGA 4.0 program. A comparative statistical study was performed between the different species sequence for RAG1. The mean represented the level of similarity compared to the RAG1 sequence and then compared with the other sequences. This analysis was performed using the ‘R’ program which is a language and environment for statistical computing and graphics. The results of comparison to other sequences were represented with the use of a phylogenetic tree to see how close the different species are.

THE USE OF SHORT TANDEM REPEAT POLYMORPHISM FOR CLASSIFICATION

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DNA is identical among individuals and also there are specific sequences common of a certain population. On the other hand, there are variations in the sequence between individuals which are termed as polymorphisms. The inheritance of a class or type of DNA polymorphisms is known as Short Tandem Repeats (STR). Short Tandem Repeats are short sequences of DNA, normally of length 2-5 base pairs, that are repeated numerous times. The data used in this research was obtained from the article Bruce B. et al 1999. The data consisted of 13 STR loci data in sample populations of African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians. This data was used to classify into each population based on the STRs polymorphisms using the ‘R’ program, which is a language and environment for statistical computing and graphics. The classification was performed successfully and plotted on a graph to show and compare the 13 Short Tandem Repeats loci data for the different populations. The comparison was performed within the sample population and between populations.
DOES THE NTP-2000 DIET INFLUENCE MOUSE WEIGHT?

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Mouse lines such as TG.AC of transgenic mice and p53 have been used by the National Toxicology Program as models for toxicology and carcinogenesis studies. In the years 1980 to 1994, the diet used for these mice was the NIH-07. The NIH-07 is a complete and balanced diet designed to meet the nutritional needs of most laboratory rodents. It has been claimed that the NIH-07 has resulted in obesity in mice. A new diet was designed for the rodents called NTP-2000 and started being used in 1994. The NTP-2000 diet contains less protein and more fiber than the NIH-07. This project had the objective to study the effect in obesity of the NTP-2000 diet and compare it with the NIH-07 diet. The methodology consisted of using data sets that indicate the weight of mice during the years 1994 to 2003. The data set was obtained from the National Toxicology Program of Historical Control Tumor Incidence mice. The mean, standard deviation and range were obtained using the program “R”. The program “R” is a utility for statistical studies. The use of the NTP-2000 diet for rodents solved the weight problem with the control rodents. There was not a significant increase in weight; therefore, the weight was not affected by the NTP-2000 diet.

STATISTICAL STUDY OF THE PRESENCE OF THE CYSTIC FIBROSIS TRANSMEMBRANE RECEPTOR (CFTR) GENE

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There are 70,000 people worldwide affected by Cystic Fibrosis and it is a fatal genetic disease. Cystic Fibrosis affects the lungs, digestive track and pancreas. It causes the body to produce thick, sticky mucus that clogs the lungs, leading to infection. It also blocks the pancreas, which stops digestive enzymes from reaching the intestine where they are required in order to digest food. This disease is caused by a defective Cystic Fibrosis Transmembrane Receptor (CFTR) gene. There are around 900 different mutations for this gene. The purpose of this investigation was to determine how many individuals have the mutated CFTR gene, based on the single base pair mutation. The data was provided by a Kerem study on the identification of the CFTR gene. The “R” program was used to obtain the mean, standard deviation and range for the individuals with the mutated gene. The “R” program is a language and environment for statistical computing and graphics. The results are expected to be high in the number of individual with the mutated gene. This is because of the variation of the mutated gene.
PHOSPHATE LEVELS IN BLOOD: IMPORTANT INDICATOR OF DISEASE

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Phosphate levels in the blood serve as indicators of a possible kidney problem and low calcium levels. High levels of phosphate in the blood can cause kidney failure and weak bones. On the other hand, low levels in phosphate concentrations can result in Hypophosphatemia. This in consequence results in anemia, heart muscle damage and muscle weakness. This project focused on the effect of high levels of phosphate levels. The data of phosphate levels in blood of 33 individuals after the first change in glucose in different periods of time was studied statistically. The mean of the phosphate levels of each individual was calculated and compared with the population. The data was provided by An R and S-plus Companion to Multivariate Analysis book, which includes the phosphate levels of 20 controls and 13 patients. The data was analyzed with the “R” program, a language and environment program for statistical computing and graphics. The mean of phosphate levels in blood for each individual was calculated as well as the range per individual and the total population. Results of the 13 patients show high phosphate levels when compared with the controls. In order to make a more precise conclusion, research is needed to study the reason for the high levels in phosphate.

STATISTICAL STUDY OF THE ENDEMIC TARTOISES IN THE GALAPAGOS ISLANDS

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The Galapagos tortoises are symbolic animals of the fauna of the Galápagos and a principal center of attraction to any tourist. Tortoises are similar to turtles, but tortoises tend to be larger in size and weight. A tortoise can weight over 300 kilograms (661 pounds) and measure about 4 feet long. They also have a long life expectancy of about 100-150 years. Today the tortoises in Galapagos are in a period when their population is very small. There are 16 species, 8 of them endangered, as a result of the arrival of the colonists centuries ago, bringing with them new animals and diseases, which may have affected the tortoises. The purpose of this project was to perform a statistical study of the endemic species of the Galapagos Islands. The data used in this project was obtained from the “farway R package.” The total number of species for each island in the Galapagos was compared to the total of endemic tortoises for each island based on the area. The “R” program is a language and environment for statistical computing and graphics. The mean, range and standard deviation were measured for the data and they were also plotted into a graph to compare the endemic species in the 30 islands of the Galapagos. The results show that the endemic population of tortoises is rising and the endemic tortoises are getting closer to extinction. Their life expectancy is what has helped the tortoise to exist over the years, the problem being that after all these years the tortoises can disappear.
The National Toxicology Program has used the TG.AC transgenic mouse line and p53 mouse line as models for toxicology and carcinogenesis studies. The diet used for these mice was the NIH-07 for the studies performed in the period of 1980 to 1994. The NIH-07 is a complete and balanced diet designed to meet the nutritional needs of most laboratory rodents. It has been claimed that the NIH-07 has resulted in obesity in mice. This project seeks to find out if the NIH-07 diet has a significant effect on mouse weight. The methodology consisted of using data sets that indicate the weight of mice during the years 1982 to 1994. The data set was obtained from the National Toxicology Program of Historical Control Tumor Incidence mice. The mean, standard deviation and range were obtained using the program “R”. The program “R” is a utility that it has a primary purpose for statistical study. As a result, an increase in rodents weight was expected.
ENGINEERING

EQUATION OF MOTION USED TO MATHEMATICALLY MODEL THE MOTION OF AN ARM OF A MECHANICAL TURTLE

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\[ \text{Mass Force} + \text{Damper Force} + \text{Spring Force} = \text{External Force} \]
\[ m \frac{d^2x}{dt^2} + c \frac{dx}{dt} + kx = \text{external force}. \]

The mass force is the mass of the free body in the system times the acceleration of that body; this is done by using Newton’s second law of motion. The mass is denoted \( m \), and the acceleration is denoted \( \frac{d^2x}{dt^2} \) using Leibniz notation because it is the second derivative of position. The damper force is the approximation of the friction caused by the drag of the free body in the system; it is synchronous with the velocity of an object but opposite in direction to it. Damper force is the viscous damping coefficient \( c \) times the velocity \( \frac{dx}{dt} \), which is the first derivative of position. Spring Force, described by using Hooke’s law, is the displacement of the end of the spring from its equilibrium position \( x \) and the spring constant or force constant \( k \). This spring constant is always negative because the restoring force always acts in the opposite direction of its displacement. Since \( \frac{d^2x}{dt^2} \) and \( \frac{dx}{dt} \) are both derivatives of the displacement \( x \), then the system parameters are the mass \( m \), the spring stiffness \( k \), and the damping coefficient \( c \). The purpose of this project was to use the equation of motion to mathematically model how a mechanical turtle’s arm moves.

EXPLAINING THE MECHANICS OF A TURTLE MOVEMENT USING MATHEMATICAL PRINCIPLES

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Mathematical principles can be applied to conduct a research on the movement of a mechanical turtle. The movements of the turtle can be expressed by means of equations and principles, since they involve physics, Newton’s second law, potential energy and kinetic energy. In this project we used the spring-mass-damper system differential equation to model the movement of a mechanical turtle. The Laplace transformation was applied to set the solutions in the frequency domain and in the time domain and the solutions were graphed in MATLAB software. A second approach was demonstrated in this project by applying MATLAB software to the solution of differential equations of the system.
MATHEMATICAL MODEL OF NEURONAL FIRING

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Research Mentor: Prof. Isis S. Laham Bauzó, Universidad Del Este, Carolina, Puerto Rico.

A neuron is a nerve cell which is the integral element of the five senses and other physical and mental faculties. It consists of a body (or soma), short branching fibers called dendrites, an elongated projection called axon, and axon terminals that store chemical messengers called neurotransmitters. Neurons receive nerve signals through the dendrites, integrate these signals, and transmit them to other neurons by means of the axon. Neuronal firing is the process that takes place and enables communication between neurons. This investigation focused on the study and application of neuronal mathematical models to explain the effect of alcohol in the neuron firing process. Three different neural models were studied: the Hodgkin-Huxley model, the Fitzhugh and Nagumo model, and the Morris-Lecar model. The Morris-Lecar set of differential equations was modeled using Matlab.
UNDERGRADUATE BIOLOGY

THE RELATION BETWEEN CALPAIN 3 AND LIMB-GIRDLE MUSCULAR DYSTROPHY TYPE 2A

Zoimillie G. Morales, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.

Research Mentor: Dr. Ángel R. Arcelay, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Carol J. Díaz, Universidad del Este, School of Science and Technology, Carolina, Puerto Rico.
Student Research Mentor Assistant: Amir M. Rodríguez, Universidad Interamericana, San Juan, Puerto Rico.

The gene under research is Homo sapiens calpain 3, p94 or CAPN3, which is a protein important to the muscle fibers and located in chromosome 15, called calpain 3. Calpain 3 is a heterodimer (which is a protein complex formed by two different polypeptide chains) composed of a large and a small subunit. Calpain 3 is a member of the calpain family of calcium-dependent intracellular proteases (enzyme that degrades the proteins). This gene encodes a muscle specific member of the calpain family that specifically binds to titin, which is important in the contraction of striated muscle tissues. It has been found that CAPN3 protease is not obligatory for muscle formation, but it is a pre-requisite for muscles to remain healthy in muscular function. Mutations in this gene are associated with limb-girdle muscular dystrophies type 2A, an autosomal recessive condition (means two copies of an abnormal gene must be present in order for the disease to develop). The disease also known as Calpainopathy, or LGMD2A, is characterized by the progressive loss of muscular mass and weakness, as in shoulders, thighs and hips. This can result in frequent falls, difficulty in running, climbing stairs and rising from the floor. At least two main forms of Limb-girdle muscular dystrophy have been identified: autosomal dominant or type 1 LGMD and autosomal recessive or type 2 LGMD. Changes in amino acids alterations from this mutation were examined to correlate the loss of protein function related to the disease by the SiFT program. The program results showed intolerance on the substitutions of the amino acids that could cause major damages to the genes and provoke DAM mutations.
When streams are surrounded by urbanization, sediments can alter the water dynamics, habitats, and ecosystems in the streams. The development of the urbanization surrounding the stream can affect the growth of the ecosystems in these; it can also change the dynamics of the water flow causing damages to the macro-invertebrate habitat. This research was based on the study of the macro-invertebrates, phosphorus, and Total Suspended Solids (TSS) present in the streams, located at the Puerto Nuevo basin on the north side of Rio Piedras, Puerto Rico. The site streams selection on the surroundings of these are classified into residential and commercial areas. There are various factors needed to be taken into consideration when it comes to streams; for example, the polluting factors surrounding them and the sediments carried. The samples were collected twice per month from September to November. There were around twenty water samples and macro-invertebrates. The sampling consisted of two bottles of 125 mL (4 ounce) of phosphorus and two of TSS of each stream. There was a sampling of macro-invertebrates. The method used was to catch the macros that would swim towards a net, a methodology taken from the Vermont Stream Assessment (V.S.A.). The insects collected were classified, and identified for phosphorus and TSS. They were sent to UVM for more analysis. The result of the macro samples showed a wide biodiversity in the residential stream and a poor diversity in the commercial site. Species like *Sphaerium simile* and *Goniobasis livescens* and *Laccophilus testaceus* were commonly found in the collected samples.
UNDERGRADUATE ENGINEERING

ROBOTICS: COMPLEX PARAMETER ON A SPRING-MASS-DAMPING SYSTEM

Raúl O. Colón, Universidad Metropolitana, San Juan Puerto Rico.

Research Mentor: Dr. Juan F Arratia, Executive Director, Student Research Development Center, Ana G. Méndez University System, San Juan, Puerto Rico.

This project was focused on a mathematical model of a turtle. To understand the dynamics of a system, the equation for the spring-mass-damping system

\[ M \frac{d^2x}{dt^2} + f \frac{dx}{dt} + Kx = f(t) \]

was used. The objective was to find and solve the case when the solution for the equation is in its complex form. Using the Laplace Transformation, the equation was transformed to a more simple algebra equation that can be solved. Transforming the equation requires different processes such as

\[ ((x' = 0), (x = 0)) \text{ on the transformed equation } M \{s^2X(s) - sx(c) - x(c)\} + D\{sX(c) - x(c)\} + K\{X(s)\} = F(s). \]

Then, there is the equation in the frequency domain \( X(s) = \frac{F(s)}{sM + sD + K} \). After that, there is the equation in the frequency domain. The denominator of the simplified equation looks like a quadratic function. The quadratic equation is applied for getting a solution for s. Then the equation is changed back to the time domain using the invert Laplace transformation. To get the results, MATLAB is used to program, plot and solve the problem. A manual solution is also implemented. MATLAB is a programming language used for solving mathematical problems.

UNDERSTANDING AND ANALYZING BLACK HOLE DYNAMICS AND FUNCTION

Eduan E. Martínez, Fernando Martínez, and Giancarlo Mendoza, Universidad Metropolitana, San Juan, Puerto Rico.

Research Mentors: Prof. Isis Laham, Universidad del Este, Carolina, Puerto Rico, and Dr. Juan F. Arratia, Executive Director, Student Research Development Center, Ana G. Méndez University System.

A star has different life cycles. One of the most interesting to study is the black hole. A black hole is a region of space in which the gravity is deep, the density is infinite and the escape velocity is higher than the speed of light, creating distortion in space time. But black holes do not only distort space; they actually have functions in galaxies and cycles. This research focused on the chemical and physical states of the star and the dynamics of the death of a massive star, which is a black hole. MATLAB, a high-level language and interactive environment that enables to perform computationally intensive tasks faster than with traditional programming languages, and the Schwarzschild radius equation, was used. The second part of this project consisted on researching black holes dynamic properties, understanding structural analysis and simulating the event.
APPLYING NEWTON'S SECOND LAW OF MOTION IN A MATHEMATICAL MODEL OF A MECHANICAL TURTLE

Jesús O’Neill, Universidad Metropolitana, San Juan, Puerto Rico.

Research Mentors: Prof. Isis Laham, Universidad del Este, Carolina, Puerto Rico, and Dr. Juan F. Arratia, Executive Director, Student Research Development Center, Ana G. Méndez University System.

The objective of this investigation was to understand the physics and mathematical equations behind the mathematical modeling of a mechanical turtle. Since the turtle has several degrees of freedom, a two degree of freedom model was developed. The mathematical model was developed using physical principles. One of these principles is the Isaac Newton’s Second Law of Motion. Newton’s Second Law describes how the velocity of an object changes when it is under an external force. A mathematical model consisting of differential equations was developed and the methodology of Laplace Transformation was used to obtain the solution in the time domain for the displacement, velocity and acceleration of the two degree of freedom system. A MATLAB simulation was implemented to obtain a graphical solution of the displacement of the system.
ACKNOWLEDGMENTS

Faculty research mentoring is the main driving force behind the scientific products (posters and oral presentations) presented in this symposium. Our greatest appreciation and gratitude to all the mentors who took part in the Winter 2009 Pre-College Research Symposium by working and training the next generation of scientists whose efforts are presented in this booklet, as well as to the many other faculty members who support the Student Research Development Center and its goals and objectives. Our most sincere thanks are also extended to the following individuals who helped to make this Winter 2009 Pre-College Research Symposium possible.

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American Statistical Association

Workshop Speaker:

Dr. Martha Bilotti-Aliaga
American Statistical Association

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