Abstract: Science and Engineering Fair of Houston

3361

The Effects of Spice Derived Phytochemicals on yeast a model for cancer research

Maryam Fatema Mukhi

Private/AL-HADI SCHOOL OF ACCELERATIVE LEARNING

Category:

Medicine and Health

This experiment evaluated the potential anticancer properties of garlic, ginger, and turmeric by measuring the ability of these spices to inhibit yeast growth. The hypothesis was that extracts of spices would result in less yeast growth than their controls. Discs of sterile filter paper were saturated with an extract of the spice and applied to each yeast-inoculated agar plate with a disc soaked in water (control) and no disc (negative control). Discs were incubated at 20h, 30h, 40h, and 48h; after total inhibition zones and amount of growth were quantified. As expected, garlic produced the largest total inhibition zone (~5 mm), followed by the moderate inhibition from turmeric (~3 mm), and mild but consistent inhibition from ginger (~2 mm). As with control plates, there was no inhibition at all visible from the negative controls. This indicates that there are bioactive substances present in each of the spices (i.e., allicin from garlic, gingerol from ginger, and curcumin from turmeric) that are responsible for their ability to inhibit cell proliferation, thus leading to the bigger picture of the potential role for these spices as natural anticancer treatments.

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[ ] Vertebrate animals [X] microorganisms [ ] rDNA [ ] tissue

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Abstract: Science and Engineering Fair of Houston

3362

Category:

Medicine and Health

Rational deimmunization of immunogenic Antibodies: Computational Identification and Reduction of MHC-II epitopes in infliximab

Aayush Khadse

Houston ISD/Bellaire HS

Rheumatoid arthritis is a chronic autoimmune disease driven by excessive tumor necrosis factor- a (TNF-a) signaling. Although anti-TNF monoclonal antibodies such as infliximab are highly effective, their clinical durability is limited by immunogenicity (how harshly our body reacts) leading to anti-drug antibody formation and reduced therapeutic efficacy. This immune recognition is caused by the murine variable regions located on the structure of infliximab. This study presents a computational framework for the rational humanization and deimmunization of infliximab to reduce predicted immunogenicity without denaturing antigen binding structure. Using MHC class II binding prediction tools, I was able to identify immunogenic T-Cell epitope cores within infliximab's variable regions. Anchor residues were selectively mutated while ensuring that the complementarity-determining regions (CDRs) were preserved. For variants of the antibody were formed through this process: Deimmunizing Parent, Deimmunizing Human, Conservative Parent, Conservative Human. Targeted deimmunization produced significant reductions in predicted MHC-II binding across multiple HLA alleles, with the deimmunized variant showing the greatest overall reduction. After concluding which strand produced the most significant reduction I used structural modeling through AlphaFold and PyMOL to confirm conserved CDR geometry and overall structural similarity to the original antibody. These results demonstrate that computational epitope-focused deimmunization is a viable strategy for improving the safety and durability of therapeutic antibodies.

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Abstract: Science and Engineering Fair of Houston

3363

Category:

Medicine and Health

T4: Tri-Targeted Tumor Therapy via Biomolecularly Locked, Quantum-Enhanced Computational Nanogate with Precision Core-Ablation against Glioblastoma Multiforme

Musa Rashid, Aaron Denson

Harmony Public Schools - South District/Harmony School of Innovation - Sugar land

Contemporary glioblastoma multiforme (GBM) therapies do not possess sufficient therapies that utilize both precision and accuracy to eradicate deadly tumors without preventing tumor escape or accidentally eliminating healthy cells. This project presents T4, a quantum-inspired neural network and computational framework that tracks down three GBM-specific and prevalent biomarkers of EGFRvIII, MMP-2, and miRNA with optimized thresholds in order to activate an siRNA solution only when all three of them are found within the cell being detected. The thresholds were tuned with quantum-inspired optimization through QAOA simulated on classical hardware. A therapeutic index without dimensions, which was defined with the ratio of the probability that T4 would activate in a simulated GBM tissue in contrast to healthy tissue distributions, saw a major increase from 42x via a single-lock system to 287x via a dual-lock system to 2,847x in a triple-lock system. Physics-inspired neural networks were also utilized to enforce diffusion-constrained spatial activation, which demonstrates enhanced signalling from within the tumor's core. Moreover, we evaluated molecular feasibility with protein-protein and ligand-receptor docking simulations with SwissDock and scientific values through the Protein Data Bank and confirmed favorable interactions for each locking component in our solution through our theoretical multi-lock system. Through our research and results, we were able to create a robust computational design platform for evaluating multi-biomarker and logic-gated nanotherapeutics before any costly and potentially pyrrhic experiments take place.

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Abstract: Science and Engineering Fair of Houston

3364

Category:

Medicine and Health

From Brain to Bedside: Addressing Alzheimer's Heterogeneity with a Novel Microglial Dysfunction Index (MDI) Derived from snRNA-seq Data for CSF Biomarker Translation Toward Therapeutic Stratification of Patients

Nikita Vijay

Cy-Fair ISD/Cypress Ranch - HS

Over 55 million people live with dementia globally, a new case every 3 seconds, costing $1.3 trillion. In the U.S., Alzheimer's affects 7.2 million, costing $384 billion yearly. Yet 99% of clinical trials fail because patients with biologically distinct neuroinflammation receive identical treatments. While amyloid and tau biomarkers guide diagnosis, current tools fail to stratify patients by microglial immune biology, a critical driver of neurodegeneration. Thus, this research presents a Microglial Dysfunction Index (MDI) derived from single - nucleus RNA sequencing data, using machine learning to stratify patients into biological subtypes, and proposes a cerebrospinal fluid (CSF) biomarker pipeline for patient stratification. Using the Seattle Alzheimer's Disease Brain Cell Atlas public dataset (84 donors, 240,651 microglial nuclei from MTG, 36,601 genes) , three pathway scores were computed: Homeostatic, Disease - Associated Microglia (DAM) , and Inflammatory. These scores were integrated into the MDI. By applying K - means clustering, an unsupervised machine learning algorithm, four patient subtypes were identified and validated by alignment with neuropathology and cognitive outcomes. Pearson correlation analysis tested clinical associations. MDI demonstrates predictive validity for pathology severity, correlating with composite pathology (r = 0.501, p = 0.0003) and tau burden (r = 0.435, p = 0.002) . Inflammatory - Dominant patients show 37% faster cognitive decline than Homeostatic - Preserved patients, reaffirming the MDI's biological and clinical relevance. This key MDI genes signature is translatable to a practical CSF biomarker panel (TREM2, IL - 1β, TNF - α, IL - 6) for targeted therapeutics. Ultimately, this research delivers an actionable, scalable stratification framework that enables precision treatment matching, potential double therapeutic response rates and alter disease progression, with applications across neurodegenerative disease.

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Abstract: Science and Engineering Fair of Houston

3365

plaque attack

ozioma ugwuja, Cindy Perez

Alief ISD/Elsik HS

Category:

Medicine and Health

this project investigated how plauqe buildup in arteries affects blood flow. a model artery was created using clear tubing and different materials were used to stimulate plaque. water flow was measured with and without plaque present. results showed that as plaque increased, blood flow slowed. this expirament demonstrates how plaque buildup can restirct circulation and increase the risk of heart dieses.

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Abstract: Science and Engineering Fair of Houston

3366

Analysis of Aneurysm Datasets Using Physics Informed Machine Learning

Anvay Deshpande

Katy ISD/Jordan - HS

Category:

Medicine and Health

Cerebral Aneurysm Ruptures are life-threatening events associated with high mortality and prolonged neurological disability. Modern clinical assessments rely heavily on aneurysm size and morphology, which often fail to accurately predict rupture risk. The size an aneurysm ruptures at is subjective, with some rupturing at small sizes while others maintain stable flow at larger sizes, revealing the need for improved predictive tools. Research developments in Computational Fluid Dynamics (CFD) have shown that certain hemodynamic factors such as wall shear stress or pressure play a critical role in aneurysm growth and rupture. However, CFD simulations require extensive computational resources to run on a large scale and cannot easily integrate into everyday clinical workflows. Machine Learning models can also potentially provide accurate insight regarding rupture prediction, however they are only trained on morphological features and may overlook critical physics based mechanisms during rupture. This project addresses this issue by integrating AneuX, a morphological aneurysm dataset, with AneuG-flow, a hemodynamics based dataset with data derived from CFD, in order to train and develop a physics based machine learning model to accurately gauge rupture risk. To implement this approach, a feature level data fusion strategy was used to combine clinical and CFD derived hemodynamic features, preserving both structural and physics based information. A Random Forest classifier is then used to train the merged data and evaluated via stratified train-test splits. Performance was assessed using receiver operating characteristic analysis, with the fused model outperforming models that only incorporated morphological data.

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Abstract: Science and Engineering Fair of Houston

3367

Category:

Medicine and Health

Searching for Novel Gene Pathways by Analyzing Astrocytes in Resilient versus Impaired Alzheimer's Patients

Marcelino Yoakim, Thong Vu, Krrish Ladha

Cy-Fair ISD/Cypress Ranch - HS

Alzheimer's disease neuropathology does not fully predict cognition, suggesting the existence of biological mechanisms underlying cognitive resilience. Using publicly available SEA-AD single-nucleus RNA sequencing donor objects from prefrontal cortex, we applied a donor-level pseudobulk framework (mean expression across nuclei per donor) to avoid cell-level pseudo-replication. Donors with advanced neuropathology were stratified by cognitive performance (N = 43; 25 resilient, 18 impaired; Braak stage ~V in both groups). In astrocytes, predefined molecular programs representing reactive/inflammatory responses, structural reactivity, and homeostatic support showed weak associations with cognitive resilience under pathology-matched conditions, suggesting that astrocyte transcription may reflect disease burden more strongly than cognitive outcome in this cortical region. To test whether resilience signals are cell-type-specific, we are extending the same donor-level analytical pipeline to microglia, enabling direct comparison of glial programs under identical experimental and statistical controls. Scientifically, these findings refine existing models of Alzheimer's disease by demonstrating that not all disease-responsive cell types necessarily encode resilience-related signals once neuropathology is controlled. This work establishes a rigorous and extensible donor-level framework for evaluating cell-type–specific mechanisms of cognitive resilience in large-scale human brain transcriptomic atlases.

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Abstract: Science and Engineering Fair of Houston

3368

AI-Guided Analysis of Cancer Angiogenesis Identifies ITGA6 for Neurovascular Regeneration

Inba Vinothkumar

Conroe ISD /AST: Academy of Science and Technology

Category:

Medicine and Health

Stroke is a leading cause of death in the United States, affecting more than 795,000 individuals and contributing to approximately 5.5 million fatalities globally. Despite its significant impact, effective rehabilitation and treatment methods for stroke remain limited. This study investigated the role of Integrin alpha 6 (ITGA6) in cancer angiogenesis and the promotion of neurovascular regeneration in zebrafish embryos to determine if this molecule could be a potential therapeutic strategy for stroke. With the use of AI and human transcriptomics datasets, the correlation between the expression of multiple genes (hypoxia, ECM remodeling, TIP-EC, endothelial content, and angiogenic hallmark) and ITGA6 were investigated. In the glioblastoma dataset, which shows high levels of angiogenesis, the expression of ITGA6 exhibited a strong correlation with the gene groups. Conversely, in pancreatic ductal adenocarcinoma, known for its poor angiogenic properties, the correlation of ITGA6 were found to be weak positive, negative and negligible, depending on the situation. To further investigate the role of ITGA6 in neurovascular regeneration, zebrafish models were employed, by inducing strokes through genetic alterations of the ITGA6 gene. In the homozygous mutants (Itga6-/-), there were significant neurovascular defects, including a reduction in central arteries, malformation of the basilar artery, and abnormalities in the primordial hindbrain channels. These findings underscore the critical role of ITGA6 in neurovascular development and regeneration, and indicate that ITGA6 holds promise as a potential therapeutic agent to enhance recovery in stroke patients. This breakthrough could significantly impact stroke rehabilitation protocols and improve patient outcomes.

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Abstract: Science and Engineering Fair of Houston

3369

Category:

Medicine and Health

Virtual Discovery of Natural Inhibitors Targeting COMT - Catechol-O-methyltransferase : A Computational Approach to Parkinson's disease therapy.

Inji Azizli, Maarya Khan, Peace Raymond

Harmony Public Schools - South District/Harmony School of Innovation - Sugar land

Parkinson's disease (PD) is an illness which affects over 11 million people worldwide, and is characterized by the progressive loss of dopamine producing neurons. Catechol-O-methyltransferase (COMT), an enzyme which is responsible for the metabolism of dopamine, further deteriorates the already low amount of dopamine that the PD patient has. This project investigated if there were any natural inhibitors of COMT that can be utilized to lessen dopaminergic degradation and increase dopamine levels within the PD patient. A set of 200 natural compounds were screened in silico through means of molecular docking to see how well they would dock against the catalytic site of human COMT(PDB ID: 6I3C), using AutoDock Vina. The compounds were then graphed based on anticipated binding affinity, from highest to lowest, with consideration of the mean and standard deviation of the ligands. Three compounds, nordihydroguaiaretic acid, phenol, and triamcinolone, stood out as potential novel, natural inhibitors of COMT, with the three highest binding affinities (all over -9.7). Although the in silico research does not confirm the ability to biologically inhibit COMT, the finding of these compounds as potential inhibitors presents a new, potentially cost-effective therapeutic strategy to treat PD, as they show potential as preliminary candidates for further research.

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Abstract: Science and Engineering Fair of Houston

3370

4 Decades|4 Cancers|Finding Cures|Effective or Not?

Aislyn Joyce Gonzales, Madisyn Parker, Arianna Ysabelle Caulin

Conroe ISD /ASHP: Academy for Science and Health Prof

Category:

Medicine and Health

With the goal of assessing whether or not humanity is winning the war against cancer, this project investigated the progress the U.S. has made in the pursuit for cancer treatments over the last 38 years. It is hypothesized that humanity has made significant progress in advancing treatments for cancer. Using reputable sources and data regarding the mortality rates of leukemia, prostate, pancreatic, and breast cancer ranging from 1985 to 2023 were collected. With the ANOVA test, the data was examined to determine if mortality rates had increased or decreased. These ANOVA tests resulted in a P-value of 0, which demonstrates how the mortality rates have changed in relation to each year within the decades.This proves that the hypothesis was supported, and that humanity has made significant progress in advancing treatments for cancer. If further research was put into this project in the future, it would study the varying rates of mortality and their root causes.

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Abstract: Science and Engineering Fair of Houston

3371

Gut Microbiota-Driven Senescence of Primary Sensory Neurons

Cathryn Wu

Clear Creek ISD /Clear Lake High School

Category:

Medicine and Health

The human gut contains trillions of microbes that contribute to our overall health—not only by aiding digestion, but also by influencing how our nervous system functions as we age. When nerve cells grow older, they may lose their ability to work properly, affecting memory, movement, and sensations such as touch or pain. Primary sensory neurons, which carry signals from the body to the brain, are particularly vulnerable to age-related decline. Yet scientists still do not fully understand the role gut microbes play in this process. To explore this connection, I used a computer tool called Ingenuity Pathway Analysis to examine which biological pathways are affected. I analyzed gene expression in sensory neurons from both normal mice and germ-free mice raised without any gut microbiota. The germ-free mice showed large shifts in gene activity—more than 1,000 genes were either activated or suppressed differently. Many of these genes are associated with cellular senescence, suggesting that gut microbes help regulate how nerve cells age and may be important for maintaining their health. These findings will help identify signaling pathways that support healthy nerve function and may reveal new targets for improving the health of sensory neurons. Because the gut microbiome is also linked to conditions such as Alzheimer's and Parkinson's disease, the molecules identified in this study could offer valuable insights into other degenerative disorders as well.

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Abstract: Science and Engineering Fair of Houston

3372

Modeling Cancer Cell Migration in CompuCell3D Using Quantum Walk and Random Walk Frameworks

Ronak Hiwale

Private/ST. JOHN'S SCHOOL

Category:

Medicine and Health

This project focuses on simulating cancer cell migration to better understand how cancer spreads through biological tissue. Using a Cellular Potts Model, the simulation represents cancer cell growth, division, death, and movement in response to chemical signals in the environment. Cell movement is guided by chemotaxis, a biological process in which cells migrate toward higher concentrations of signaling molecules. Two movement models are explored: a classical random walk and a quantum-inspired walk. By tuning parameters such as chemotactic sensitivity, diffusion rates, and movement bias, the simulation examines how different movement strategies influence cell directionality, persistence, and overall invasion patterns. This project is useful for studying the mechanisms behind cancer metastasis, where migrating cancer cells spread from a primary tumor to other parts of the body. By comparing movement models, the simulation provides insight into how cancer cells navigate complex environments and may help improve computational tools used in cancer research and treatment planning.

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Abstract: Science and Engineering Fair of Houston

3373

Category:

Medicine and Health

Computational Design and Molecular Dynamics Simulation of Collagen-Based Artificial Muscles for Strengthening and Drug Delivery Applications

Ria Aggarwal

Private/The Village School

Muscular atrophy in space refers to the loss of muscle mass and strength due to reduced gravitational load on muscles in the microgravity environment. Microgravity can negatively impact the cellular processes of muscles. For example, the ubiquitin-proteasome pathway (UPP) significantly exacerbates muscle atrophy under such conditions. C-terminus of Hsc70-interacting Protein (CHIP) is a co-chaperone that is part of UPP and works with molecular chaperones, such as heat shock proteins (HSPs), to regulate the molecular triage and also tags proteins headed for the degradation pathway with ubiquitin. Under microgravity, CHIP is upregulated as the environment reduces protein synthesis, stimulates inflammation, increases reactive oxygen species, and hinders mitochondrial function, which all promote degradation. The aim of this project is to design and simulate collagen-based artificial muscles that can be used to integrate into the regular muscles for strengthening. Collagen-integrated artificial muscles can mimic natural muscle contractions, enhancing muscle strength. In this study, a collagen-based artificial muscle system was computationally designed and evaluated for both muscle-strengthening and targeted drug delivery applications. Molecular docking simulations were performed to analyze the stability of the collagen fibers under simulated mechanical pulling conditions. Moreover, CHIP-HSPs and CHIP-nanobody interaction modeling were performed using HDOCK. The results deduced that nanobody II formed the most hydrogen bond interactions and exhibited the strongest binding affinity to CHIP. This indicates that under microgravity, nanobody II can aid in stabilizing the interaction between CHIP and HSPs, protecting proteins from cellular stress. This research will help develop novel methods to make spaceflight safer through regenerative implants or engineered artificial muscles for a controlled delivery of therapeutic drugs, ultimately mitigating muscle atrophy.

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Abstract: Science and Engineering Fair of Houston

3374

Category:

Medicine and Health

In Silico Evaluation of Natural Organic Compounds as Potential Inhibitors of Human Purine nucleoside phosphorylase (3BGS) for T-cell Malignancies and Autoimmune Diseases Therapy

Milcah Iyob, Niang Mang, Jocelyn Baldiviez

Harmony Public Schools - South District/HARMONY SCHOOL OF INGENUITY-HOUSTON

Cancer research often prioritizes common cancer types, leaving rare but aggressive cancers understudied. This project focuses on T-cell malignancies, a group of rare cancers characterized by rapid progression and poor outcomes. Since abnormal T-cell growth is central to these diseases, identifying ways to limit T-cell proliferation is critical. Previous studies show that Purine Nucleoside Phosphorylase (PNP) is essential for T-cell survival and division. This project aimed to identify novel PNP inhibitors that could reduce T-cell proliferation and serve as potential treatments for T-cell malignancies and autoimmune diseases. We hypothesized that screening 200 natural organic compounds using computational molecular docking would identify compounds with strong binding affinity and specificity to PNP. Using AutoDock Vina, the PNP receptor and all ligands were prepared in PDBQT format and docked using standardized configuration files. Docking simulations were analyzed with a custom Python script. Binding affinity values and molecular interactions were evaluated to identify promising inhibitor candidates. The results revealed several compounds with high binding affinity to PNP, including Dioscin and AC-73. These compounds demonstrated favorable interactions with key PNP active-site residues, suggesting strong inhibitory potential when compared to existing inhibitors used currently as therapy. This study demonstrates that in-silico screening is an effective, low-cost method for identifying potential drug candidates. The findings provide a foundation for future experimental validation and highlight the potential of computational approaches in developing treatments for rare cancers and immune-related diseases.

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Abstract: Science and Engineering Fair of Houston

3375

The Efficiency of Different Insulin Systems

Jade Svay, Mauricio Andrade

Aldine ISD/Eisenhower HS

Category:

Medicine and Health

Diabetes mellitus is a chronic condition that requires consistent and often tiring actions to maintain effective insulin management and assist in regulating healthy blood glucose levels. This project investigates and compares different delivery insulin systems used by diabetics in order to figure out which systems are more efficient in regulating blood glucose levels and possibly reducing complications for patients. We used a system and knowledge from published works to simulate the different insulin systems to collect data. Each system was evaluated on its efficiency, ease of use, and its impact on daily lives. We then compared the systems to finalize our results. From 5 minutes and 1 second to 30 minutes and 5 seconds, the Automated Insulin Delivery system was the fastest, while the slowest was the traditional patch out of our 5 different systems. The Automated Insulin Delivery system also contributed to continuous glucose monitoring and lifted the worry about stress. With these highlights, it is important to notice that newer insulin technologies can aid with diabetes management, but a key factor that must also be considered is personalization within the patient, and whether it suits their lifestyle.

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Abstract: Science and Engineering Fair of Houston

3376

Dual-Targeted Nanoparticle Based Immunotherapy for Endometriosis

Taanya Virigineni

Tomball ISD/Tomball Stat Academy

Category:

Medicine and Health

Endometriosis is a chronic inflammatory disease characterized by the growth of endometrial-like cells outside of the uterus. Ectopic cell lesions often resulting in pelvic pain, infertility, and damage to reproductive or abdominal organs. Current treatment options are limited, as surgical interventions are marked with high lesion recurrence rates, imaging technology fails to detect small lesions for localized removal, and hormonal therapies reduce symptoms without addressing the underlying lesion growth. Despite the etiology of endometriosis remaining unknown, emerging clinical evidence suggests that lesion growth may be due to immune evasion. This literature-based dual-target nanoparticle design combines existing research on immunotherapy for endometriosis and drug delivery to offer a non-surgical, non-hormonal, and minimally-invasive approach to treat endometriosis. The nanoparticles silence the overexpression of the surface protein CD47 on ectopic cells using siRNA to stop immune evasion, and initiate efficient macrophage phagocytosis using the immunomodulator R848. To limit off-target attacks, the model utilizes dual-targeting technology rather than imaging, taking overexpressed proteins matrix metalloproteinase-9 (MMP-9) and CD47 overexpression as biomarkers for delivering the therapeutic payload only to ectopic lesions. The suggested delivery method is ultrasound-guided intraperitoneal injection during the menstrual phase for maximum targeting potential. By addressing major limitations in current endometriosis care, this nanoparticle design aims to provide a novel treatment approach based on restoring immune function to reduce the presence of ectopic lesions, rather than managing symptoms of the disease. Keywords: endometriosis, nanoparticle, CD47, MMP-9, siRNA, macrophage, phagocytosis, R848.

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Abstract: Science and Engineering Fair of Houston

3377

Physiological Implications of High-Altitude Polycythemia

Tvisha Nitin

Fort Bend ISD /Clements High School

Category:

Medicine and Health

At high altitudes, due to a reduce in oxygen, erythropoietin is released. This increases red blood cell production and hematocrit levels. This results in secondary polycythemia, which increases blood viscosity and its oxygen carrying capacity. Elevated viscosity can cause a slower blood flow which can lead to an increased risk for strokes, thrombosis, or hypertension. This experiment will investigate how changes in viscosity influence blood flow. Water-glycerin mixtures will be created to mimic the different viscosities and then computer models will be used to simulate blood vessel flows. These findings will then be compiled onto a trifold that will investigate the negative effects of higher viscosities.

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Abstract: Science and Engineering Fair of Houston

3378

A Multimodal Machine Learning Model for Predicting Autoimmune Encephalitis Flare Activity

Tanushri Vijay

Conroe ISD /AST: Academy of Science and Technology

Category:

Medicine and Health

Autoimmune encephalitis (AE) is a rare neurological disorder that is often challenging to diagnose early due to its heterogeneous neuropsychiatric presentation, a phenomenon known as the clinico-radiological paradox (Peer et al., 2017). Early recognition of disease activity or flare-ups is critical, as delays can worsen neurological outcomes. Speech biomarkers have successfully identified early dysfunction in other neurological disorders, suggesting their potential utility in AE. This project investigates whether machine learning–based analysis of speech biomarkers can serve as a non-invasive framework for detecting neurological changes relevant to AE. Using publicly available, fully de-identified speech datasets associated with neurological disorders as proxy data, acoustic features related to pitch, jitter, shimmer, voice stability, and temporal variation were extracted and standardized. Supervised machine learning models (logistic regression, random forest, and simple neural networks) were trained to classify healthy versus neurologically affected speech, with performance assessed using accuracy, sensitivity, specificity, F1-score, and ROC AUC. Feature importance analyses identified the vocal characteristics most predictive of neurological impairment. All analyses were performed computationally using open-source Python libraries, and no human subjects were directly involved in this study. Results indicate that speech-based models can reliably differentiate neurological from healthy speech, with features such as jitter, shimmer, and voice breaks emerging as particularly informative. Although AE-specific speech data were not available, this validated analytical pipeline establishes a framework for integrating speech and neuroimaging biomarkers, providing a scalable, non-invasive approach that could improve early detection, monitoring, and management of AE flare-ups in future clinical applications.

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Abstract: Science and Engineering Fair of Houston

3379

How can artificial intelligence and machine learning be used to improve detection and monitoring of various gastrointestinal cancers?

Shalom Stanly Immanuel

Cy-Fair ISD/Cypress Ranch - HS

Category:

Medicine and Health

Technology is developing at an exponential rate, especially with AI learning being more prevalent in the field of medicine. It is important to test the effectiveness of the resources to best assist imaging for early cancer detection, especially with cancers caught later on, such as pancreatic and esophageal cancer; Since early detection often dramatically improves patient outcome and chance of survival. This project will review the primary research literature on how scientists can improve the detection /monitoring of various gastrointestinal cancers using machine learning/AI. It will note current limitations for detecting esophageal, pancreatic, and colorectal cancers using standard imaging methods. It will then review how types of AI may improve the accuracy of detection, especially for early-stage cancers. The poster will then identify the top method for detecting using a meta-analysis of already available data. Current challenges and limitations of these technologies will be discussed.

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Abstract: Science and Engineering Fair of Houston

3380

Predicting Neuronal Bioelectric States Using Machine Learning on Voltage Imaging Data

David Reyes, Gaurav Vatnani, Tanush Vatnani

Katy ISD/Cinco Ranch - HS

Category:

Medicine and Health

Neurons communicate through changes in membrane voltage. Voltage imaging records these signals at high speed, but most analysis focuses on visualization rather than prediction. This project tested whether machine learning can predict neuronal bioelectric states from voltage imaging features and whether the same prediction can run on low power hardware. Bioelectric state was defined as a binary activity label based on voltage trace behavior. Public voltage imaging demo data from the CaImAn VolPy framework was used. Neurons were segmented and voltage traces and spike events were extracted. For each neuron, three features were computed: mean dFF, variance of dFF, and spike count. An interpretable classifier was trained to predict the state label. Due to the small dataset size of 4 neurons, leave one out cross validation and a permutation test were used. The model achieved a leave one out accuracy of 1.0, while the permutation p value was ≈0.34, reflecting limited statistical power at this specific scale. PCA showed noticeable separation between the two states. Counterfactual testing showed that increasing spike count could flip predicted states for certain neurons. The trained model was deployed on a Raspberry Pi and produced identical predictions and probability outputs, with inference completing in under one second. This work presents a reproducible pipeline for bioelectric state prediction using voltage imaging data and demonstrates that biological predictions can be performed on low power hardware.

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Abstract: Science and Engineering Fair of Houston

3381

Category:

Medicine and Health

Betaine as a Therapeutic Potential Against Non-Proliferative Diabetic Retinopathy: An In Vivo Study Mitigating ROS, AGEs, Neuronal Degeneration, and Systemic Stress in a C. elegans model

Thoshika Srinithi Dayalan Gokulakrishnan

Conroe ISD /AST: Academy of Science and Technology

Affecting 130 million people around the world and causing vision-loss for over 25% of those individuals, diabetic retinopathy (DR) has risen to become the leading cause of blindness for the working age people. DR is an eye disease caused by damaged blood vessels in the retina due to high blood sugar from poorly controlled diabetes over a long period of time. Currently, advanced early detection of DR is available, however detection alone doesn't fix the issue because there have been no non-invasive therapeutics that can slow the progression of DR in the early stage. This project aimed to investigate how Betaine, an amino acid consisting of glycine with three methyl groups, can reduce the progression of NPDR (non-proliferative early stage DR) by lowering the levels of the critical biomarkers: ROS, AGEs, neuronal degeneration, systemic stress. The researcher hypothesized that the 10 mM Betaine concentration will reduce the biomarker levels and by testing different concentrations of Betaine, the worms treated with greater amounts of Betaine will show decreased progression of NPDR than untreated groups. In the in-vivo experiment, NGM plates were seeded with E. Coli OP50 and C. elegans were cultured and chunked into groups. Experimental groups were exposed to 50mM glucose to simulate a NPDR environment, and treated with 5mM and 10mM Betaine. The researcher concluded that the 10mM Betaine more effectively reduced the biomarker levels, thus displaying less progression of NPDR. These findings pave the path for offering a potential therapeutic that can be promisingly explored to stop the progression of NPDR.

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Abstract: Science and Engineering Fair of Houston

3382

EGFR-Targeted Aptamer Discovery via Constraint-Guided Sequence Generation and Transformer-Based Ranking

Rhea Morani, Savannah Le

Houston ISD/Carnegie Vanguard HS

Category:

Medicine and Health

Epidermal growth factor receptor (EGFR) is an oncogenic driver linked to poor prognosis in many of the most common and lethal cancers. Overexpressed in 40–89% of non-small cell lung cancers, 25–82% of colorectal cancers, and 90% of head and neck cancers, it correlates with reduced survival through metastases and chemotherapy resistance. Thus, EGFR is an attractive target for drug delivery and molecular inhibition; however, nontoxic and effective targeting remains limited. Nucleic acid aptamers offer a promising solution, binding to target proteins like extracellular EGFR with high specificity, low immunogenicity, and low systemic toxicity. However, traditional aptamer discovery via wet-lab SELEX is resource- and cost-intensive, often taking months to yield a single viable candidate. Computational design addresses these obstacles and greatly accelerates the process by generating thousands of sequences in silico with applied constraints, then using machine-learning (ML) to select for high-affinity, precise binders. This study aims to develop a constraint-based aptamer design and ML ranking pipeline to identify EGFR-binding RNA aptamers. Extracellular EGFR structural data were sourced from the RCSB Protein Data Bank, and validated EGFR–aptamer interaction pairs were obtained from UTexas Aptamer Database and Aptamer Base. AptaTrans, a pre-trained aptamer–protein interaction model, was fine-tuned on pairs in order to score candidates. To ensure aptamer stability and binding potential, CASTp analyzed EGFR structural data and identified key binding cavities to generate 1,000 RNA aptamers (25–40 nucleotides, 40–60% GC content). The top 10 candidates were ranked with an ML pipeline optimizing AptaTrans scores and minimum free energy, then validated through molecular docking using HADDOCK with biologically relevant metrics to determine the best aptamer. Further in vitro and in vivo studies may advance these candidates toward targeted drug delivery and cancer therapeutics.

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Abstract: Science and Engineering Fair of Houston

3383

Category:

Medicine and Health

Mapping Microplastic Respiratory Injury: A Systems Level Graph Learning Framework for Structural Biomarker Discovery and Therapeutic Rescue Prioritization

Sahen Tapar

Tomball ISD/Tomball Memorial - HS

Microplastics are now found in nearly every human, present in lungs, airway fluids, blood, and placental tissue. Inhalation is a major exposure route, and chronic accumulation is linked to oxidative stress, airway remodeling, impaired immunity, and increased risk for diseases including COPD, pulmonary fibrosis, and lung cancer. Yet the molecular basis of microplastic-induced respiratory injury remains unmapped; most studies examine one plastic type at a time using basic differential expression, limiting insight into conserved regulatory failure and clinically relevant targets. This project develops the first systems-level, graph-based framework to define shared biological structures underlying microplastic stress. Three RNA-seq datasets (63 samples, 14,024 shared genes) were unified and denoised using PCA. After stringent filtering, 8.46 million correlations were reduced to a high-confidence 9,829-gene, 408,913-edge structural graph. A two-layer GCN-based Graph Autoencoder achieved strong link prediction performance (AUC 0.9766, AP 0.9684, F1 0.9336), indicating the learned structure captures meaningful biology. Explainable graph learning with PGExplainer, Leiden clustering, and pathway enrichment resolved six conserved stress modules spanning ciliogenesis, metabolic/autophagy stress, RNA processing, DNA repair, checkpoint control, and motility/adhesion. A 55-gene structural biomarker panel signature (MSRS), derived from PGExplainer-prioritized genes within Leiden modules, quantified a continuous stress axis that separated samples across all datasets. Therapeutic reversal analysis using L1000FWD identified FDA-approved agents, including naproxen and zileuton, that partially reverse the conserved transcriptomic signature and converge on metabolic inflammatory hub. This framework provides the first mechanistic map of microplastic respiratory injury and delivers clinically relevant tools for diagnostics, exposure risk scoring, and future translational prioritization.

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Abstract: Science and Engineering Fair of Houston

3384

Development of a Low-Resource, Mutation-Specific Lateral Flow Test for ctDNA Detection

Brian Kim

Private/ST. JOHN'S SCHOOL

Category:

Medicine and Health

Cancer is a leading cause of morbidity and death, both in the US and worldwide. Screening methods, such as mammograms and Pap smears, have resulted in earlier diagnosis, improved treatment outcomes, and decreased mortality for their respective cancers. However, many cancers still lack affordable, accessible screening tests. Studies show that circulating tumor DNA, short DNA fragments released by cancer cells into the bloodstream, can be used to detect cancer-related mutations. This project aimed to develop proof-of-concept for a low-resource ctDNA testing kit, targeting KRAS G12D, a clinically relevant mutation commonly found in pancreatic, colorectal, and lung cancers. By combining custom-designed DNA probes and primers, isothermal amplification, and lateral flow signal detection, this research investigated whether single-nucleotide mutations could be accurately identified without advanced laboratory infrastructure. The kit was tested on a wild-type human cell line (BxPC-3), two mutant-type cell lines (SNU-899 and MIA PaCa-2), and water to evaluate its accuracy. The detection system showed high specificity and sensitivity, demonstrating the feasibility of ctDNA testing as a point-of-care or at-home cancer screening tool. Applications of this research have the potential to increase the screening detection of additional cancers while also expanding access to underserved communities, thereby decreasing cancer-related morbidity.

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Abstract: Science and Engineering Fair of Houston

3385

Investigating the Antioxidant Capacity and Amylase Inhibition of Turmeric Extract in Key Pathways of Type 2 Diabetes

Divya Venugopal

Private/THE JOHN COOPER SCHOOL - HS

Category:

Medicine and Health

Type 2 Diabetes (T2D) is a chronic metabolic disorder characterized by impaired insulin sensitivity, elevated postprandial blood glucose levels, and increased oxidative stress. Pharmaceutical inhibitors such as acarbose are effective in managing postprandial hyperglycemia but may be limited by side effects and accessibility, prompting interest in plant-based complementary therapies. This study evaluated the a-amylase inhibitory activity and antioxidant capacity of turmeric (Curcuma longa) essential oil (EO) as a potential adjunct in T2D management. Turmeric EO was analyzed using three spectrophotometric assays: a-amylase inhibition relative to acarbose, a-amylase inhibition in combination with acarbose to assess enhanced effects, and DPPH free radical scavenging activity relative to ascorbic acid. Serial dilutions of turmeric EO ranging from 12.5 to 400 µg/mL were prepared, and enzyme inhibition was quantified using the dinitrosalicylic acid method, while antioxidant activity was determined by absorbance reduction in the DPPH assay. Results showed that turmeric EO exhibited measurable a-amylase inhibition across all tested concentrations, though inhibition was not strictly dose-dependent. The combined treatment of turmeric EO and acarbose produced slightly greater a-amylase inhibition than turmeric EO alone, suggesting a modest synergistic effect. Preliminary results suggest dose-dependence of Turmeric EO as an antioxidant (12.5-50 ug/mL vs. 200-400 ug/mL). These findings suggest that turmeric essential oil may support glucose regulation and reduce oxidative stress when used alongside conventional therapies for Type 2 Diabetes, though further in vivo and clinical studies are needed to confirm efficacy and long-term safety.

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Abstract: Science and Engineering Fair of Houston

3386

Identifying Pancreatic Lipase Inhibitors for Obesity Treatment Using A Computational Approach

Shaopan Gao

Fort Bend ISD /Clements High School

Category:

Medicine and Health

Obesity is a global epidemic associated with health conditions such as diabetes and cancers. Many drugs have been approved for treating obesity, but many of these drugs have efficacy or side effect challenges. There remains a medical need to develop a safe and long-term anti-obesity drug. In this project, I aim to develop a safe and effective drug for obesity prevention targeting pancreatic lipase inhibition by using nutritional components. I plan to use a computational screening approach to identify active pancreatic lipase inhibitors from about 1,000 nutritional components. Then, I will perform an in vitro assay using the pancreatic lipase to test the activity of the top three identified compounds, thereby validating this computational model. I will use the validated computational model to screen more potent compounds in public compound libraries containing hundreds of thousands of compounds. I hope that my identified compounds can be used on animal models in future studies.

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Abstract: Science and Engineering Fair of Houston

3387

Building a Transparent Risk-Scoring Tool for Overprescription and Overdose Prevention

Joel Blessan, Sofia Rivera

Friendswood ISD /Friendswood High School

Category:

Medicine and Health

Drug misuse, including prescription opioid overdoses, is a significant public health concern. Specifically, one person dies every 5 minutes due to drug overdoses. These concerns highlight the importance of improved methods to identify high-risk prescribing patterns. In this project, a traditional rules-based approach that originated from established clinical guidelines was compared to a machine learning model to learn to identify and predict overdose risk using the prescription data. The datasets contained multiple factors such as prescribing volume, opioid dosage, and co-prescriptions, and even details regarding the providers. These factors were merged as features to test their influence on the model. The models were trained and evaluated based on their accuracy, precision, recall, F1 score, and ROC-AUC. The rules-based model achieved perfect recall but struggled to correctly distinguish between high- and low-risk cases. The machine learning model, however, was the opposite. The machine learning model had higher accuracy and was able to strongly discriminate between high- and low-risk cases. Furthermore, the analysis of the features helped show that MME (Morphine Milligram Equivalent) was the strongest predictor for overdose risk. The findings from this project help suggest that data-driven approaches such as this one have great potential for supporting overdose prevention and intervention.

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Abstract: Science and Engineering Fair of Houston

3388

Category:

Medicine and Health

A Computational Fluid Dynamics Framework for Optimizing Microchannel Oxygenator Architectures in Artificial Placenta Systems

Ananya Cherukuri

Houston ISD/Carnegie Vanguard HS

The placenta is a temporary organ that develops in the uterus of pregnant women to provide the developing fetus with oxygen and nutrients while removing waste through the umbilical cord. In preterm infants, organs are underdeveloped, which can lead to a number of physiological problems. Thus, artificial placenta systems have been theorized to support and improve prognostic outcomes for preterm infants post-pregnancy. Current research in artificial placenta systems have demonstrated promise in large animal models, but have yet to translate to human clinical use. This is largely due to the lack of a systematic optimization of oxygenator microchannel design for gas exchange efficiency and hemocompatibility. In this study, a computational fluid dynamics (CFD) framework was developed to evaluate and optimize oxygenator architectures that vary in geometry, flow rate, and other features. Four geometric configurations based on biological design were assessed. Steady-state incompressible laminar flow simulations were performed at three physiologically relevant inlet velocities, and passive scalar transport was simulated to assess CO2 behavior. The results of the study reveal design recommendations that can increase gas transport efficiency while controlling pressure drop and wall shear.

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Abstract: Science and Engineering Fair of Houston

3389

Quantum-Accelerated Proteomics: Unlocking Faster Protein Folding for the Future of Drug Discovery

Ramya Elangovan

Houston ISD/Carnegie Vanguard HS

Category:

Medicine and Health

INTRODUCTION: Predicting the 3D structure of proteins is essential for understanding biological systems and developing new therapeutics. Traditional computational methods often require massive time and processing power for large proteins, while quantum-inspired algorithms can evaluate multiple folding pathways simultaneously, offering a faster and more efficient approach. AIM: This project designs and evaluates a hybrid quantum-simulated framework that enhances both the speed and accuracy of protein folding predictions compared to classical methods. METHODOLOGY: A custom web-based platform built with React, TypeScript, and Three.js simulated both classical and quantum-inspired algorithms. Fifty protein sequences from the Protein Data Bank were analyzed to measure execution time, energy minimization, and structural accuracy using RMSD (Root Mean Square Deviation). RESULTS: The quantum-simulated model achieved a 41× speedup for large proteins of up to 2,000 residues and improved structural accuracy by 38%, reaching an average RMSD of 2.1 angstroms compared to 3.4 angstroms for classical methods. The results demonstrated near-linear performance scaling, confirming the theoretical quantum advantage. CONCLUSION: This study shows that quantum-inspired computation can significantly accelerate and refine protein structure prediction, providing a powerful foundation for future advances in drug discovery, synthetic biology, and personalized medicine.

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Abstract: Science and Engineering Fair of Houston

3390

Neopeptide Vaccine Targeting FGFR3-TACC3 Gene Fusion for Personalized Treatment of Pancreatic Cancer

Saisha Verma

Homeschool/Bhardwaj Home School - HS

Category:

Medicine and Health

Pancreatic cancer is one of the most deadliest cancers in the US because it is often diagnosed late and current treatments do not work well. Current standard of care therapies such as chemotherapy and radiation usually provide only limited benefit, and many patients survive only a few months after diagnosis. One of the major causes of treatment failure is the heterogeneity of pancreatic tumors, and the lack of targeted therapies. Personalized cancer therapies that boost patient's immune response and eliminate cancer cells have successfully improved patient survival in several cancers, but have not yet been tested for pancreatic cancer. Gene fusions are an unexplored source of such immunogenic targets in pancreatic cancers that can be used as a cancer vaccine. My project focuses on developing a personalized cancer vaccine to treat pancreatic cancer by targeting gene fusions found only in cancer cells. Specifically, I worked with one such gene fusions- FGFR3-TACC3, which creates a new protein that is not found in healthy cells in human body. I was able to identify i) fusion junction between FGFR3 and TACC3, ii) novel open reading frame and iii) tumor-specific neopeptides generated by this gene fusion. Next, using Optitype and NetMHCpan, I obtained a list of patient HLA specific highly immunogenic neopeptides. These neopeptides can be used as a cocktail of peptide vaccine for personalized treatment of pancreatic cancer.

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Abstract: Science and Engineering Fair of Houston

3391

Category:

Medicine and Health

Modeling Cerebral Artery Mechanics with Layer Specific Thickness and Material Properties Utilizing a Lame Equation-Based Java Program

Christopher Cheng

Private/Strake Jesuit College Preparatory - HS

Intracerebral hemorrhage is strongly associated with chronic hypertension and arterial narrowing, yet the mechanical reasons for this increased rupture risk are not fully understood. Cerebral arteries are composed of three mechanically distinct layers, suggesting that disease conditions may affect each layer differently. In this study, we tested the hypothesis that hypertension combined with arterial blockage causes a disproportionately large increase in hoop stress and a corresponding reduction in safety factor in the media layer compared with the intima and adventitia. A three-layer analytical model based on Lamé equations was used as a controlled experimental tool to isolate the effects of pressure and lumen narrowing. Simulations were performed under normal and hypertensive pressures, with and without blockage, using literature- based geometry and material properties. Finite element analysis was used to independently verify analytical trends. The results show that hypertensive pressure amplifies the mechanical effect of blockage, producing the largest stress increases and lowest safety factors in the media layer. These findings support the hypothesis and provide a mechanical explanation for the increased rupture susceptibility of cerebral arteries under combined pathological conditions.

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Abstract: Science and Engineering Fair of Houston

3392

Category:

Medicine and Health

Prevalence of chronic kidney disease in diabetic patients worldwide and the role of SGLT2 inhibitors in renal protection: a systematic review and meta-analysis

Jeshmitha Puligundla

Galveston ISD/Ball High School

Background Over 800 million people worldwide have diabetes, and the most common form is type 2 diabetes (T2D), making up 85% to 90% of all cases. Diabetes is a condition where your body cannot use insulin properly and/or does not produce enough insulin and leads to numerous organ complications, among these is chronic kidney disease. Studies have shown that 40% of diabetic patients develop CKD. The objective of this study is to perform a meta-analysis to analyze a pooled prevalence of CKD in diabetic patients globally based on various previous human studies and further investigate the role of Sodium-Glucose Cotransporter 2 (SGLT2) inhibitor in renal protection. Methodology Various previous publications were searched using databases such as PubMed, Embase, and google scholar according to inclusion and exclusion criteria. A flow chart was created based on PRISMA guidelines. The meta -analysis was conducted using Meta.mar software and was computed to present pooled prevalence rate with 95% confidence interval. Results In this study, 20 studies were included with 161457 patients. For the prevalence of CKD in diabetic patients worldwide the results from the meta-analysis showed 25% prevalence (IV, 0.25 with 95% CI 0.21: 0.30) with high heterogeneity (I^2=99.6%, p=0) due various factors such as age, treatment modalities, and etc. Therefore, to reduce the heterogeneity in the second study only diabetic patients using SGLT2i were included and performed another meta-analysis. In this meta-analysis, diabetic patients using SGLT2i had lower eGFR decline and reduced Urine albumin creatinine ratio (UACR) levels. Conclusion The prevalence of CKD in diabetic patients worldwide was high, especially in T2D patients. The SGLT2i are potential therapeutic modalities to protect the renal function.

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Abstract: Science and Engineering Fair of Houston

3393

Category:

Medicine and Health

Integrative Epigenomic and Transcriptomic Analysis Identifies Immune Cell–Specific Regulatory Signatures of Multiple Sclerosis Progression

Dorine Zolfaghari Hesari, Aylin Korkmaz, Nikhil Chowdhary

Fort Bend ISD /Clements High School

Multiple sclerosis (MS) is a chronic autoimmune disease in which a subset of patients transition from relapsing-remitting MS (RRMS) to secondary progressive MS (SPMS), a stage marked by sustained neurodegeneration and limited therapeutic options. Despite its clinical importance, the molecular mechanisms underlying this transition remain incompletely understood. This study employed an integrative multi-omics approach to identify progression associated molecular signatures distinguishing RRMS from SPMS. Whole blood transcriptomic data were analyzed to quantify gene expression differences between disease stages. Genes were ranked by absolute expression change, and pathway enrichment analysis revealed coordinated dysregulation of immune activation, interferon signaling, leukocyte migration, and translational control pathways, indicating system level transcriptional reprogramming during progression. Supervised machine learning models trained on progression associated gene expression profiles demonstrated statistically significant discrimination between RRMS and SPMS samples, supporting the presence of structured molecular signal rather than random variation. To provide mechanistic context, transcriptomic findings were interpreted alongside independent epigenomic analyses of CD4+ and CD8+ T cells. Progression associated differentially methylated regions were intersected with cell type specific regulatory annotations, revealing distinct regulatory architectures. CD4+ T-cell changes localized exclusively to distal enhancer regions, whereas CD8+ T-cells exhibited both promoter and enhancer-associated alterations, suggesting fundamentally different regulatory strategies across immune cell types. Together, these findings demonstrate that MS progression is characterized by coordinated transcriptional and immune cell specific regulatory remodeling. This integrative framework provides a systems level approach for studying stage specific mechanisms in complex autoimmune disease.

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Abstract: Science and Engineering Fair of Houston

3394

Modeling Drug Diffusion Through Tissue Using Agar-Based Systems

ISABELLA YOUNG

Fort Bend ISD /Clements High School

Category:

Medicine and Health

Understanding drug diffusion is crucial because predicting a drug's absorption and distribution throughout the body can determine the overall therapeutic effect as well as the need for regulation. Agar, having properties of soft biological tissue, makes for a useful analog. This project investigates how the viscosity of the carrier affects the diffusion rate of simulated drug molecules through an agar matrix. I hypothesized that as the viscosity of the carrier increases, diffusion distance will decrease because it will lead to a lower diffusion coefficient. Agar plates were poured and solidified as tissue analogs. Different drug analog solutions were placed into wells cut into each plate. Diffusion radii were measured using calipers at fixed intervals of time and then recorded. Conditions were kept constant except for the viscosity of the carrier. Smaller viscosities of carriers produced significantly larger diffusion zones than carriers of larger viscosities. The results supported the hypothesis that diffusion rate decreases with increased viscosity of carriers. This model demonstrates how viscosity of the carrier influences drug transport in soft tissue. This has the potential to inform delivery strategies or early-stage drug formulation.

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Abstract: Science and Engineering Fair of Houston

3395

Non-invasive Mapping and Diagnosis of Skin Cancers via Multispectral Imaging and Machine Learning

Timur Gezalov

Conroe ISD /AST: Academy of Science and Technology

Category:

Medicine and Health

Skin cancer is the most common type of cancer in the world, with more than 3.3 million Americans diagnosed each year and taking more than 65,000 lives yearly worldwide. While the survival rate for melanoma is greater than 99% when detected early, time-consuming biopsies or unaffordable ultrasound machines make diagnosis inaccessible in low-income or disadvantaged areas. There is a clear need for a device that can diagnose and evaluate skin cancers in real-time, allowing for more efficient referral prioritization and shorter wait times. Multispectral imaging (MSI) is a novel imaging technique that utilizes a combination of visible and infrared light to penetrate 1-3 mm into the skin, capturing subsurface trends for effective, on-the-spot diagnosis. A custom portable MSI device was engineered for maximum user efficiency and usability, featuring an OLED screen, scanning module, and custom power supply system, all controlled with a Raspberry Pi processor. The researcher then partnered with a local surgical dermatology clinic to evaluate the scanner's usability and potential for clinical use. A proof-of-concept Convolutional Neural Network (CNN) model was then trained on a robust dataset of 8,000 images, consisting of real scans, synthesized images, and augmented data. This hybrid training approach addresses the lack of quality training data common in medical research and simulates clinical trials. The CNN model was measured to have an accuracy of greater than 98%, with a 0.2% error rate on the 1,600 scans it was tested on. With a total cost of under $150, this scanner surpasses current solutions in both affordability and timeliness, remarkably reducing the time and cost barrier to life-saving early skin cancer detection.

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Abstract: Science and Engineering Fair of Houston

3396

Early Detection of Coronary Artery Disease Using Nontraditional Biomarkers Lipoprotein(a) and Interleukin-6

Prayagh Prabhakar, Giriish Purushothaman

Cypress Fairbanks ISD/Bridgeland - HS

Category:

Medicine and Health

Coronary artery disease (CAD) is the leading cause of death worldwide. Traditional biomarkers such as LDL cholesterol identify long-term risk but often fail to detect CAD before structural changes or clinical symptoms occur. Nontraditional biomarkers, including Lipoprotein(a) (Lp(a)) and Interleukin-6 (IL-6), may provide earlier signals of subclinical disease, enabling timely intervention. This project investigates whether Lp(a) and IL-6 can identify early CAD in individuals with well-controlled LDL cholesterol and compares their predictive ability to traditional markers. Publicly available datasets, including the National Health and Nutrition Examination Survey (NHANES), were analyzed to assess associations between biomarker levels and early CAD indicators, using regression models adjusted for age, sex, BMI, and comorbidities. To validate findings and test robustness, a Monte Carlo simulation was conducted, generating 10,000 hypothetical patient profiles based on real dataset distributions. Simulation scenarios examined how variations in Lp(a) and IL-6 influence predicted CAD risk. Preliminary results indicate that elevated Lp(a) and IL-6 levels are associated with increased likelihood of subclinical CAD, even when LDL cholesterol is within recommended ranges. Simulation modeling confirms the stability of these associations across diverse patient profiles, suggesting that these nontraditional biomarkers may detect CAD earlier than conventional lipid measurements. This study highlights the potential of integrating Lp(a) and IL-6 into early CAD screening strategies. Identifying high-risk individuals before clinical symptoms or traditional marker changes could inform earlier preventive interventions, reduce cardiovascular events, and improve long-term outcomes.

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Abstract: Science and Engineering Fair of Houston

3397

Category:

Medicine and Health

To what extent can a chitosan coating applied to hydrogel contact lenses affect drug surrogate release, reducing an initial burst effect and prolonging sustained delivery under simulated tear film conditions?

Udhayan Shanmugam, Saikarthik Swaminthan

Conroe ISD /AST: Academy of Science and Technology

Due to rapid tear clearance, delivering ocular medication is highly inefficient. Only an estimated 5% of drugs even reach the ocular surface, necessitating frequent dosing and strict patient compliance. This project investigated how chitosan coating applied to hydrogel contact lenses affects drug release kinetics under simulated tear conditions, specifically how the coating could reduce initial burst release and prolong the drug delivery. Contacts were emerged into one of three distinct environments (Chitosan/PBS/riboflavin, riboflavin/PBS, PBS), with the release of riboflavin tested. Subsequently, contacts were placed in PBS, and the release of riboflavin was analyzed over the time intervals of 0, 5, 15, 30, and 60 minutes. The PBS-only solution was used as the negative control. Visual observations were insufficient to quantitatively discriminate between the burst release in the chitosan-coated and uncoated lenses. In order to counter the limitations of the qualitative experiment, a model was developed in order to produce quantitative data. The modeling framework was derived from Fick's second law by using diffusion constants. The data demonstrated that the original Chitosan coating partly suppresses the burst release effect by including a diffusion barrier. Additionally, alginate further exemplifies this phenomenon by demonstrating greater burst suppression due to its denser polymer structure. The research indicates that a polymer-based coating could be instrumental in increasing drug residence on the ocular surface, advancing the efficacy of topical ocular medications. Future applications could reduce dependence on eye drops, lower medication costs, and improve chronic and postoperative care through drug-eluting lenses.

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Abstract: Science and Engineering Fair of Houston

3398

DermaShield: A Novel Non-Invasive Innovative Approach to Detect Skin Cancer Leveraging AI

Vikram Gupta

Friendswood ISD /Friendswood High School

Category:

Medicine and Health

Skin cancer is among the most common cancers worldwide, with an estimated 1.5 million new non-melanoma cases and about 330,000 melanoma cases each year (GLOBOCAN 2022). Outcomes depend on early detection, yet diagnosis can be delayed by limited access to dermatology specialists and variability in dermoscopic image interpretation. This project, Derma Shield, applies AI and machine vision to detect, segment, and classify skin lesions from dermoscopic images to support noninvasive early risk assessment. De-identified dermoscopic image datasets were used to develop a multistage pipeline. Images were standardized through normalization, including grayscale conversion and contrast enhancement. A hybrid feature strategy combined deep representations from convolutional neural networks with texture descriptors from gray-level co-occurrence matrices (GLCM), capturing both overall lesion structure and fine textural detail. Several architectures were benchmarked, including a baseline CNN, VGG-19, and ResNet-50. Models were assessed using standard metrics: accuracy, precision, recall, F1-score, and confusion matrices to analyze classification, performance and misclassification patterns. ResNet-50 performed best, achieving ~98% classification accuracy. The segmentation/ localization module reached ~96% accuracy in outlining lesion boundaries. Confusion-matrix analysis identified lesion categories prone to misclassification, motivating improvements such as dataset balancing, richer augmentation, and class-specific tuning. Derma Shield demonstrates that a hybrid AI framework combining deep learning and GLCM can serve as a decision-support tool for skin-lesion screening, thereby improving healthcare outcomes in underserved communities and complement dermatologist workflows. Future work will validate performance on more diverse datasets, audit fairness across demographic subgroups, and incorporate explainability methods (e.g., gradient-based heatmaps) to enhance interpretability.

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Abstract: Science and Engineering Fair of Houston

3399

Navigating economic landscape of genomic medicine informed by cost models

pramadwaraa addala

Cypress Fairbanks ISD/Bridgeland - HS

Category:

Medicine and Health

Despite recent advances in genomic medicines for the treatment of genetic disorders, broad accessibility remains a significant challenge due to extremely high drug prices, often reaching several million dollars per patient. In particular, adeno-associated viral vector (AAV)–based genomic therapies involve complex and costly development, manufacturing, and delivery processes. This challenge is especially pronounced within the rare disease community, where the limited patient population prevents economies of scale from reducing costs. While orphan drugs provide a comparatively lower-cost alternative, they typically require lifelong administration to manage disease symptoms rather than offering a one-time curative approach. In this study, we systematically conducted an unbiased analysis of the major cost components contributing to genomic medicine pricing by developing cost models using publicly available datasets. Our analysis revealed a previously underrecognized cost component that significantly contributes to overall drug prices, likely due to contingent and operational factors. These findings provide valuable insights for policymakers, insurance providers, healthcare institutions, patients, and other stakeholders, and may support informed discussions aimed at improving the affordability and accessibility of genomic medicines.

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Abstract: Science and Engineering Fair of Houston

3400

RAGE S100 Signaling and Trastuzumab Deruxtecan Resistance in Metastatic Breast Cancer

Catherine Xue

Houston ISD/Bellaire HS

Category:

Medicine and Health

Trastuzumab deruxtecan (T-DXd) is an antibody-drug conjugate that has revolutionized treatment for metastatic breast cancer. However, ~50% of patients do not respond to T-DXd therapy. Mechanisms underlying resistance require further exploration. Pilot studies indicate that S100P and S100A8/9 are overexpressed in T-DXd nonresponder patient tumors. Preliminary studies also indicate that blocking S100-RAGE interactions improves T-DXd sensitivity in mouse models. This study aims to validate a) S100 proteins as a T-DXd resistance biomarker, and b) S100-RAGE interactions as a modulator of T-DXd response. Fluorescent staining of patient tumors indicates differences in RAGE expression and localization between T-DXd responder and nonresponder patients. Linear mixed modeling of log-transformed data identified several FDR-significant differences (BH-adjusted $p < 0.25$). Cytoplasmic RAGE signal was greater in resistant tissues, especially among HER2+ tissues ($\beta = 1.16$, adjusted $p = 0.07$). However, nuclear RAGE signal was greater in responsive tissues ($\beta = 3.46$, adjusted $p = 0.09$), indicating that RAGE translocation may contribute to differences in T-DXd therapy outcome. Unexpectedly, cytoplasmic S100P signal was 3-fold lower in nonresponder patients ($\beta = -1.11$, adjusted $p = 0.006$). Hence, S100P may have a more complex relationship with T-DXd resistance than previously thought. Current work involves using the IncuCyte live-cell imaging platform to monitor cell viability and T-DXd response in vitro over time. Inhibiting RAGE, S100P, and S100A8/9 is expected to increase sensitivity to T-DXd therapy. Future implications of the results include the utility of RAGE-S100 signaling as a potential T-DXd resistance biomarker and as a therapeutic target for resistant patients.

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Abstract: Science and Engineering Fair of Houston

3401

Computational Design of Allele-Specific microRNAs Targeting KRAS G12D in Pancreatic Ductal Adenocarcinoma

Ahaan Thota, Aarav Mehta, Aryan Ganglani

Fort Bend ISD /Dulles High School

Category:

Medicine and Health

Pancreatic ductal adenocarcinoma (PDAC) is one of the deadliest cancers, with over 90% of cases driven by mutations in the KRAS gene. The most common mutation, KRAS G12D, causes continuous growth signaling that leads to aggressive tumors and resistance to treatment. MicroRNAs (miRNAs) are short RNA molecules that regulate gene expression through sequence-specific binding, and recent advances in artificial intelligence enable systematic design of RNA-based therapies. KRAS G12D has long been considered “undruggable” because its structure prevents effective targeting by traditional drugs. Existing miRNA design approaches struggle to selectively inhibit the mutant KRAS gene without also affecting the normal (wild-type) allele, which is essential for healthy cell function. We developed a biologically grounded, AI-driven computational framework to design allele-specific synthetic miRNAs that selectively target KRAS G12D while minimizing effects on the wild-type allele. A transformer-based generative model trained on known human miRNAs produced candidate sequences, and a second model predicted efficacy using experimentally validated miRNA–target interactions combined with thermodynamics-inspired training labels derived from RNA binding free energy (ΔG). Candidate miRNAs were evaluated using thermodynamic selectivity analysis and transcriptome-wide off-target screening across more than 200,000 human transcripts. The framework identified 29 miRNA candidates with strong predicted activity against KRAS G12D, reduced wild-type binding, low off-target risk, and no predicted interactions with essential genes. Overall, this work demonstrates how biologically grounded AI can accelerate the design of safer, mutation-specific RNA therapeutics for pancreatic cancer and precision oncology.

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Abstract: Science and Engineering Fair of Houston

3402

Operation Safety

Zina Salem, Najma Salem

Charter/YES Prep

Category:

Medicine and Health

ABSTRACT: Many everyday products lack proper regulation, posing potential risks to consumers. We recently discovered that commonly used products, especially cosmetics and hygiene items, are not always verified as safe. Companies sometimes prioritize profit over safety, leaving the average person unaware of potential hazards. Unless individuals consistently research product labels and ingredients, millions may unknowingly use harmful products for extended periods, leading to health issues. So, to address this problem, we conducted a study where participants provided information on the personal care products they use. Products were inspected for the presence of harmful chemicals based on their ingredients and known health risks. Participants also completed a survey about their product choices, research habits, and perceptions of safety. This project aimed to check and inform participants about the safety of their personal care products while highlighting the urgent need for regulatory standards. This work emphasizes the need for an institution/organization dedicated to regulating the safety of products used on the body. The researchers wanted to observe the following: What is the average score for cosmetic/hygienic products a person uses in their daily life? The researchers believe that about half of the products our participants use (potential results from the survey) may contain harmful substances, with over half of them gaining at least 2 points for at least having 1-2 substances that fall under the 1st-2nd category. The average score was 5. Our hypothesis was proven right but redoing the study is recommended. More information is in the full study.

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Abstract: Science and Engineering Fair of Houston

3403

Category:

Medicine and Health

Deciphering Metastatic TNBC: An Integrated Single-Cell RNA Sequencing Analysis Reveals Shared and Site-Specific Adaptations in Tumor Microenvironments

Eashan Shetty

Fort Bend ISD /Elkins High School

Triple-Negative Breast Cancer (TNBC) is an aggressive type of breast cancer that currently has few treatment options. Single-cell RNA sequencing (scRNA-seq) can locate differentially expressed genes (DEGs) across metastatic tumor microenvironments (TME) and provide insight into organ-specific TME adaptations of TNBC that remain unclear. scRNA-seq data of primary and metastatic (liver, brain, and lymph nodes) tumor sites from the Gene Expression Omnibus were processed using R and the Seurat package. The cells were then normalized and identified as malignant through copyKAT which infers copy number variations (CNVs) to classify cancer cells. We conducted differential gene expression analysis, which compared the metastatic sites to the primary TME using Wilcoxon rank-sum tests with thresholds including log base 2 fold change of at least ± 0.25 and had an FDR-adjusted P-value less than 0.05. Our differential gene expression analysis results revealed 3 commonly upregulated genes (RPS26, GSTK1, NDUFA13) from comparing all three metastatic TME to the primary TME that served as the control. Additionally, the same comparison showed 432 commonly downregulated genes, including literature-validated genes such as XIST, CSTA, and SFRP1. Site-specific analysis showed brain metastatic sites had upregulated ATP synthesis genes, while liver sites had immunoglobulin gene upregulation, implying possible immune infiltration. Genes including GSTK1 and NDUFA13, found to be commonly upregulated, were found to be highly expressed in malignant cells, which may represent metastatic drivers supporting protein synthesis or potential biomarkers. Downregulated genes, including CSTA, can potentially suppress metastasis at the primary TME and be subject to further study. Our study outlines shared and site -specific TME adaptations in metastatic TNBC and raises potential therapeutic targets to limit metastatic progression.

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Abstract: Science and Engineering Fair of Houston

3404

Exploring the Sanitary Effectiveness of Cleaning Products Based on Their Acidity

Madelynn McBride

Conroe ISD /AST: Academy of Science and Technology

Category:

Medicine and Health

Household surfaces are frequent points of contact and can act as reservoirs for microorganisms, making effective cleaning practices essential for limiting microbial spread. Because household cleaning agents vary widely in pH—a chemical property known to influence protein stability and cellular membranes—this study investigated whether cleaner pH affects sanitary effectiveness on common household surfaces. Four household cleaners with measured pH values ranging from mildly acidic to basic (Rose/Meyer: pH 6.25; Green: pH 8.5; Pink: pH 8.7; Lemon: pH 9.0) were evaluated on four frequently contacted surfaces: a kitchen table, bathroom sink, stairwell hand railing, and student desk. Each surface was swabbed before and after cleaning, and samples were cultured on nutrient agar for 72 hours. Sanitary effectiveness was assessed by comparing bacterial colony growth before and after cleaning. Results indicated that the cleaner with the highest pH (Lemon, pH 9.0) consistently demonstrated the greatest reduction in bacterial growth, with no colonies observed on the kitchen table and desk and minimal growth on the bathroom sink. Cleaners with moderately basic pH values showed variable effectiveness, while the mildly acidic cleaner (Rose/ Meyer, pH 6.25) generally resulted in higher colony counts, though colonies were smaller in size. Overall, the findings suggest a trend in which more basic cleaners were associated with greater reductions in bacterial growth, supporting the hypothesis that pH influences the sanitary effectiveness of household cleaning agents.

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Abstract: Science and Engineering Fair of Houston

3405

Influence of Simulated Digestion and Food Interactions on Epigallocatechin Gallate Inhibition of α-amylase

Pimchanok Pawithakul

Conroe ISD /AST: Academy of Science and Technology

Category:

Medicine and Health

Polyphenols are natural compounds researched for their antioxidant abilities. Among these are catechins, a type of flavonoid derived from natural sources. Epigallocatechin gallate (EGCG) is a catechin predominantly sourced from green tea. This project focuses on EGCG's ability to inhibit α-amylase, a digestive enzyme that hydrolyzes complex carbohydrates into simple sugars. By inhibiting amylase, EGCG can reduce enzyme activity, leading to lower postprandial glucose levels through slowing carbohydrate breakdown. This project investigates if common food additives and simulated gastrointestinal digestion can impact EGCG inhibitory activity. It's hypothesized that milk and lemon juice will reduce EGCG's effectiveness in α-amylase inhibition, while honey may enhance its effect; digestion conditions may cause instability due to the changes in pH levels. This project utilizes an enzyme assay to experiment under in vitro conditions. Solutions were prepared and added to respective tubes, then left for enzyme activity to occur before adding iodine to test for residual starch. Absorbance values were recorded using a spectrometer at 620 nm. A one-way ANOVA was conducted and identified the results as statistically significant. Overall, purified EGCG displayed stronger inhibition than green tea, and common food additives and simulated digestion conditions significantly impact the inhibitory activity of EGCG. Honey enhances inhibition, while acidic stomach conditions, lemon, and milk hinder it. These findings suggest that EGCG can be optimized for treatments to manage blood glucose levels. Purified EGCG or formulated green tea can be applied to real-world applications, potentially supporting the management of diabetes, especially for individuals with resistance to insulin.

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Abstract: Science and Engineering Fair of Houston

3406

Oral-Health Solutions and Predicted Microglial Activation

Berlin Rosenbaum

Clear Creek ISD /Clear Creek High School

Category:

Medicine and Health

The connection between oral health and neuroinflammation has gained increasing attention, as inflammatory mediators from the mouth may influence microglial activation in the brain. This project investigates how different oral-health-related synthetic saliva environments affect biofilm formation, acidity, and predicted microglial activation. Five saliva conditions will be examined: a healthy control, sugar-enriched solution (simulating a high-sugar diet), acidic mouthwash (pro-inflammatory), baking soda (alkaline, protective), and fluoride (neutral, protective). Each solution will undergo 12 replicates measured over 24–48 hours. Dependent variables include pH (inflammatory potential), biofilm mass (via blue dye staining), and plaque surface coverage area determined using ImageJ analysis. Data will be compiled and analyzed in Microsoft Excel, where a predictive microglial activation model will be constructed. The model assigns weighted contributions to three variables—biofilm thickness (0.5), pH (0.3), and coverage area (0.2)—based on empirical studies linking biofilm properties and acidity to neuroinflammation. It is hypothesized that sugar and acidic conditions will generate denser biofilms and lower pH values, resulting in higher predicted microglial activation scores, while baking soda and fluoride will demonstrate protective effects.

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Abstract: Science and Engineering Fair of Houston

3407

The Heart Anatomy

Iman naeem

Harmony Public Schools - South District/Harmony Science Academy - Beaumont

Category:

Medicine and Health

The heart's anatomy involves four chambers (left atria, right atria, left ventricle, and right ventricle) and the four valves, which operate as two pumps: The lungs receives deoxygenated blood from the right side since it has low oxygen, while the body receives oxygenated blood from the left side. It has an electrical system controlling the valves that guarantee one-way flow. The whole process of blood flow in the heart begins from the right atrium, which receives deoxygenated blood since it already circulated through your body (superior vena cava & inferior vena cava). Then, the blood continues to go through the tricuspid valve and then into the right ventricle (to the lungs), which officially picks up fresh oxygen. Next, it continues to the left atrium with oxygenated blood (from the lungs) through four pulmonary veins, and finally, finishes the process by blood flowing through the mitral valve and then into the left ventricle, which is the heart's strongest pump responsible for sending oxygenated blood to the rest of the body via the aorta. I am making a model which is going to show how oxygenated and deoxygenated blood travels through our heart chambers and ventricle, as it describing up there.

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Abstract: Science and Engineering Fair of Houston

3408

Category:

Medicine and Health

Impact Of Seasonal Variations On The Relationship Between Daily PM2.5 ,NO2 , Pollen Count, Ambient Temperature And Asthma-related Emergency Department Visits In New York City

Zayaan Adrish

Private/The Village School

Background: An estimated 262 million people live with asthma worldwide. Air pollutants such as PM2.5, and NO2 have been linked with poor asthma control. High pollen counts and weather events such as extreme weather, cold spells, heat waves have also been linked to asthma related outcomes. Methods: We aimed to analyze how seasonal variations influence the relationship between asthma-related ED visits, PM2.5, NO2, pollen counts and ambient temperature in New York City (NYC). This was retrospective time-series analysis of publicly available data between January 1st 2023 and December 31st 2024 and was done in five NYC boroughs. Poisson time-series model was performed to analyze the association of asthma-related ED visits with PM2.5, NO2, pollen counts and daily average temperature. Results: A total of 124,719 asthma-related ED visits occurred during the study period. Age ranges include 0-4 years, 5-17 years, 18-64 year and 65+years. Complete data available for 721 of 731 days (98.6%). In the overall analysis, PM2.5 was associated with increased asthma-related ED visits, with a 1.38% increase per IQR increase (95% CI, 0.97%–1.79%). Higher ambient temperature was inversely associated with ED utilization (−5.83% per IQR increase; 95% CI, −9.48% to −2.03%). Season-stratified analyses significant heterogeneity among the variables. Higher PM2.5 was associated with asthma-related ED visits during summer, whereas higher NO_2 was associated with ED visits during winter. Temperature showed inverse association with asthma-related ED visits during spring. Pollen levels had variable and generally inconsistent associations across seasons. Conclusion: Our study shows that PM2.5 is associated with asthma-related ED visits during summer whereas NO2 predicts ED visits during winter. Ambient temperature had an inverse relationship with asthma-related ED visits, but the effect of pollen was inconsistent. These findings highlight need for targeted public health strategies.

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Abstract: Science and Engineering Fair of Houston

3409

A Comparative Study of Generic and Branded Medication

Fatima Rizvi

Private/AL-HADI SCHOOL OF ACCELERATIVE LEARNING

Category:

Medicine and Health

In this experiment, three different generic medications were compared to their brand-name versions by determining their dissolution times. The medicine with the lowest dissolution time would be the one that works the fastest, and therefore, would be more efficient.

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Abstract: Science and Engineering Fair of Houston

3410

Prioritizing Sepsis Alerts Under Limited Staffing: A Simulation of Algorithmic Alert Ranking

Srijan Mashetty

Houston ISD/DEBAKEY HIGH SCHOOL FOR HEALTH PROFESSIONS - HS

Category:

Medicine and Health

Sepsis is a life-threatening organ dysfunction caused by infection, and delays in recognition and treatment substantially increase mortality risk. Digital sepsis alert systems integrated into electronic health records have been associated with reduced hospital mortality, shorter length of stay, and improved adherence to guideline recommended sepsis bundles in emergency departments. However, many systems generate frequent alerts with limited specificity, contributing to information overload and alarm fatigue that can undermine their clinical impact. This project addresses a related but under studied problem: when staffing is limited and many alerts fire simultaneously, how should alerts be prioritized so that the sickest patients are seen first? A synthetic hospital ward with multiple patients and time evolving vital signs was simulated using simple sepsis trajectories and vital sign patterns inspired by early warning tools. A rule based detector resembling common sepsis screening criteria generated alerts whenever composite vital sign scores exceeded a threshold. Three alert handling strategies were compared: first-in-first-out (FIFO) queuing, ranking by current sepsis score only, and a novel trend-aware priority score that also used recent changes in vital signs, time since first alert, and baseline risk flags. Primary outcomes were time from simulated sepsis onset to first clinical response and the proportion of true sepsis patients represented among the top ranked alerts at each time step. Across repeated simulations, the trend aware prioritization algorithm reduced average delay to first response and improved representation of true sepsis cases in the highest priority alerts compared with the two baseline strategies. These findings suggest that improving which sepsis alerts are handled first, not only whether alerts are generated, may enhance the effectiveness of digital sepsis alert systems in resource constrained settings.

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Abstract: Science and Engineering Fair of Houston

3411

What Separates The Best? The Science of Athletic Dominance

Oluwademiladeogo Sokale

Clear Creek ISD /Clear Springs High School

Category:

Medicine and Health

The purpose of my project is to investigate the physical and genetic differences among top athletes. More specifically, my research question was, "what physical and genetic attributes set apart top sprinters, swimmers, and weight lifters from regular people." I hypothesized that the biggest differences would be found in athletes physical attributes, specifically their lung capacity, fast twitch muscle fiber percentage, and their body proportions. To test my hypothesis, I did research into the different types of genes, and how they affect a persons attributes, then, I researched what genes are more dominant in athletes compared to regular people, then what physical attributes, for example lung capacity, do athletes need to be successful. After the general stage of research, I repeated this process but for the individual sports, sprinters, swimmers, and weight lifters, to find specific differences across these three disciplines. The result showed that the biggest genetic contributors to athleticism are the ACTN3 gene and the ACE gene. In addition to this, an individual's muscle characteristics, neuromuscular efficiency, and cardiovascular functions are the biggest physical contributors to athleticism. This supports my hypothesis because, I predicted that physical traits would have a bigger impact on one's athleticism, although the genetic component is still crucial to one's athletic success, without a capable body, the genetic material can only do so much. Future investigations could explore how to manipulate DNA to increase the athletic genetic material concentration within an individual .

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Abstract: Science and Engineering Fair of Houston

3412

Category:

Medicine and Health

Frankenstein-Synuclein: Rational Engineering of a De Novo Replacement Protein via an In-Silico Pipeline for Parkinson's Disease Prevention

MANASHWIN NELLURI, MANAS TELIKEPALLI

Conroe ISD /AST: Academy of Science and Technology

Parkinson's disease affects over 10 million people globally. It is driven by the misfolding of the protein a-synuclein (asyn). While asyn's flexibility is functional, it enables pathological aggregation through the coagulation of undesirable conformations into insoluble, toxic oligomers contributing to cell death in dopamine-producing neurons. Current treatments fail to target asyn without compromising cell function. This project aimed to computationally engineer asyn variants that preserve function while minimizing aggregation risks. We developed a loop-based computational framework to design chimeric asyn variants using stabilizing features from homologous beta-synuclein. We evaluated 100 generated candidate sequences each loop using a custom deep graph neural network trained to predict aggregation, toxicity, disorder, phase-separation, and insolubility. Top candidates underwent validation via molecular dynamics to assess membrane/VAMP2 binding, and kinetic Monte Carlo simulations to quantify aggregation. After three iterations, engineered variants significantly reduced aggregation levels from 80% to 30%, while functional binding free energies remained stable at approximately -30 kJ/mol and -17 kJ/mol for the membrane and VAMP2 respectively. Simulations revealed that these variants also actively inhibited aggregation past specific mass fraction thresholds. Neural network predictions further indicated significant reductions in toxicity, aggregation propensity, insolubility, and phase-separation propensities, with model accuracies exceeding 77%. These findings demonstrate that protein function can be decoupled from toxicity, enabling two novel strategies: protein-delivery drugs to suppress aggregates in patients and preventative gene therapy for at-risk individuals. These represent some of the first ever proposed molecular interventions for Parkinson's Disease and may extend to other synuclein-related neurological disorders.

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