Uncovering NAFLD Protein Biomarkers through Advanced Machine Learning Techniques

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✄ Poster Presentation: Yes

✄ Oral Presentation: No

INTRODUCTION

Non-alcoholic fatty liver disease (NAFLD) is a liver condition characterized by excessive fat accumulation in liver cells. Studying NAFLD is crucial because of its increasing prevalence and potential progression to severe liver diseases, such as cirrhosis and hepatocellular carcinoma, imposing significant public health burdens. Utilizing proteomics in NAFLD study allows for a comprehensive understanding of the molecular mechanisms underlying the disease, facilitating the identification of potential biomarkers and therapeutic targets for improved diagnosis and treatment. Thus, the goal of our research is to discover potential NAFLD protein biomarkers using traditional statistics and machine learning algorithms.

METHODS

A plasma proteomics dataset, PXD011839, was downloaded from ProteomeXchange, containing LC-MS/MS raw mass spectrometric files from ten healthy controls, twenty NAFLD patients, and ten cirrhosis patients. The raw files were converted into mzML format using ProteoWizard. Protein identification and quantification were performed using Fragpipe. We employed four methods to identify proteins with differential expressions among the three patients groups: differential expression analysis (DEA) with a P-value of less than 0.01, the random forest algorithm using Gini impurity (RF-Gini), the random forest algorithm using entropy (RF-Entropy), and the support vector machine (SVM) algorithm with the latter three selecting the top 20 most important proteins. We used a Venn diagram to identify the commonly selected proteins among the four methods.

RESULTS AND DISCUSSION

A total of 307 proteins were identified from healthy controls, NAFLD patients, and cirrhosis patients. Comparing healthy controls with NAFLD patients by DEA, RF-Gini, RF-Entropy and SVM, we found three commonly identified proteins: complement factor H (CFH), fibrinogen alpha chain (FGA), and hemopexin (HPX). CFH is related to pathophysiology. FGA is related to coagulation. HPX is mainly secreted by hepatocytes and is an important anti-oxidative protein. Comparing healthy controls with liver cirrhosis patients, we found four commonly identified proteins: alpha-2-macroglobulin (A2M), complement component C7 (C7), HPX, and transthyretin (TTR). A2M is related to lipid metabolism. C7 is related to lipid metabolism and immune response. TTR is mainly secreted by hepatocytes. Comparing NAFLD patients with liver cirrhosis patients, we found three commonly identified proteins: complement C3 (C3), immunoglobulin heavy constant gamma 3 (IGHG3), and TTR. C3 is related to lipid metabolism and immune response. IGHG3 is related to pathophysiology. According to the three comparison, TTR were may be a potential blood biomarker for distinguishing between cirrhosis and others. Similarly, HPX may be a potential blood biomarker for distinguishing between healthy individuals and others.

NOVEL ASPECT

Simultaneously employ classical statistical analysis and classification algorithms to identify potential protein biomarkers for NAFLD.
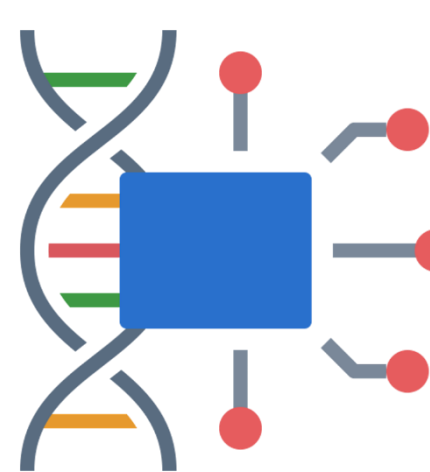
Development of Thermoresponsive Hydrogel Equipped with Antibacterial and Cell Growth-Promoting Functions for Cellulitis Wound Healing

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✍ Poster Presentation: Yes

✍ Oral Presentation: No

INTRODUCTION

In Taiwan, cellulitis is one of the common infectious diseases in the community, with about 7% of patients requiring hospitalization. Among those who have had an initial infection and completed treatment, 50% will experience a recurrence. Common risk factors include foot immunity, obesity, diabetes, and chronic edema, etc. The general treatment for cellulitis involves oral or injectable antibiotics, but wound treatment often leaves subsequent skin repair issues, and medical expenses can be quite high. We aim to develop a hydrogel that simultaneously has wound healing and skin repair functions, providing patients with an additional treatment option.

METHODS

In this study, we plan to incorporate an antibacterial agent (Polyhexamethylene Biguanide, PHMB) and Epidermal Growth Factor (EGF) into a hydrogel containing Hyaluronic Acid (HA) and HDI-PF127 (Hexamethylene Diisocyanate Pluronic F127) cross-linking, achieving a dual-purpose effect.

RESULTS AND DISCUSSION

During the wound healing process of cellulitis, it is essential to monitor for potential bacterial infection and the time required for wound healing. Results indicate that IHG-PE possesses excellent antibacterial properties and, in cell experiments, demonstrates the ability to promote cell growth and is non-cytotoxic. In summary, IHG-PE has both antibacterial properties and the ability to promote cell growth. When applied to cellulitis wounds, it not only inhibits bacteria but also accelerates wound healing. In the future wound dressing market, this injectable thermoresponsive hydrogel has promising application prospects and great potential.

NOVEL ASPECT

We aim to develop a hydrogel that simultaneously has wound healing and skin repair functions, providing patients with an additional treatment option.

A comprehensive quantitation platform for untargeted metabolomics

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- Poster Presentation: Yes
- Oral Presentation: Yes

INTRODUCTION

Metabolomics refers to the qualitative and quantitative analysis of small molecule metabolites within a biological system at a specific point in time. Liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) has become a popular analytical platform in metabolomics, and quantification stands as a crucial endeavor encompassing various stages such as noise elimination, peak identification, and peak alignment. Visualization is also important for evaluating quantitation results. We thus proposed a comprehensive platform with four implemented software tools, including MS-Picker, MS-Aligner, MS-Point, and DeNox, as important components for metabolomics quantitation.
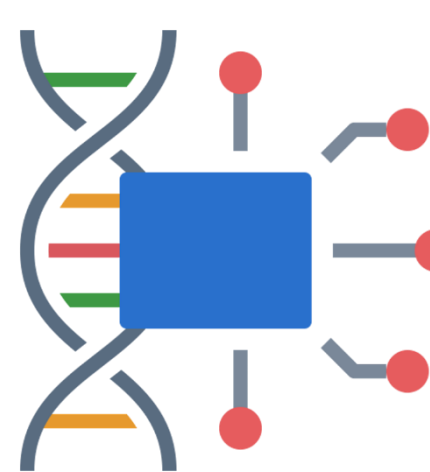
METHODS

Upon importing raw files, MS-Picker initiates feature detection by extracting their m/z, retention time, charge states, abundances. MS-Point then evaluates the quality of detected features using nine quality metrics, exporting quality scores for these features. Next, MS-Aligner aligns the detected features across files, generating an integrated feature table with features in rows and files in columns. It also summarizes the quality scores across files, providing a general quality indicator for downstream statistical analysis. DeNox empowers users to interact with the raw files and visualize quantitation outcomes. All software tools are cross-platform applications developed in Java, with MS-Picker, MS-Aligner, and MS-Point operating as command-line tools and DeNox offering a graphical user interface for ease of use.

RESULTS AND DISCUSSION

To evaluate the quantitation performance of our platform, we processed three metabolomics datasets using our platform and three public software tools, including iMet-Q, MZmine3, and XCMS Online. First, we used standard mixture dataset with two samples prepared by adding seven standard metabolites with different amount. We then calculated the technical replicate ratios and sample ratios of these metabolites, defined as the ratio of abundance between any two technical replicates and any two samples, respectively. These ratios served as the metric for assessing performance. The closer the ratio gets to theoretical value, the more accurate the quantitation is. Next, we used a public blackcurrant dataset with eleven samples downloaded from MetaboLights (MTBLS773). The eleven blackcurrant samples, each with four technical replicates, were analyzed using positive and negative ion modes. We calculated the technical replicate ratios of known metabolites detected by four tools in each mode. Additionally, we utilized a metabolomics QC dataset that included three QC sample types: LabQC, MixQC, and NC. Each sample was prepared by adding ten standard metabolites in the same amount, with eight replicates per type. We calculated the technical replicate ratios for these metabolites in each sample. The findings indicate that four platforms yield comparable quantification outcomes, and the performance is satisfactory. A uniqueness of our platform is that it provides the quality scores of detected features. Features with high-quality scores exhibit shapes that more closely resemble a bell curve, while those with low scores tend to have more irregular shapes. DeNox allows users to view both quantitation and quality assessment results. To simplify its use, we have updated the software, which includes reducing the number of operations, placing parameter settings in a collapsible page, and making the size of each section on the main page adjustable.

NOVEL ASPECT

Our platform offers accurate quantitation, quality scores for detected features, and user-friendly visualization, empowering quantification and quality assessment.

Development of Perovskite-Based Direct Current Nanogenerator Application

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✍ Poster Presentation: Yes

✍ Oral Presentation: No

INTRODUCTION

The tribo-voltaic effect is an emerging area of research that focuses on generating direct current (DC) electricity through the interaction of materials with different electron affinities. However, most of current researches in this field focus on specific polymers and metal oxides. Perovskites, with their unique crystalline structure, are already at the forefront of solar cell innovation due to their high electron transport efficiency and low-cost production. However, to our best of knowledge, no reports have been found to address the tribo-voltaic effect in perovskites. This study aims to evaluate the potential of free perovskite-based materials in generating the tribo-voltaic effect, contributing to the advancement of sustainable and environmentally friendly energy technology.

METHODS

We designed a device to demonstrate the tribovoltaic effect. Initially, the as-fabricated perovskite was deposited on an ITO substrate. X-ray diffraction (XRD) analysis confirmed the crystal structure of as-fabricated perovskite. To evaluate the tribovoltaic effect, two materials contacts back and forth, with aluminum tape were connected to the positive and negative terminals, respectively. validating the device's functionality.

RESULTS AND DISCUSSION

Herein, we successfully demonstrated a DC generator based on the as-fabricated perovskite with output voltage of 2 V and current of 6 uA. This confirms that as-fabricated perovskite can also generate the tribovoltaic effect.

NOVEL ASPECT

Tribovoltaic effect, DC, perovskite
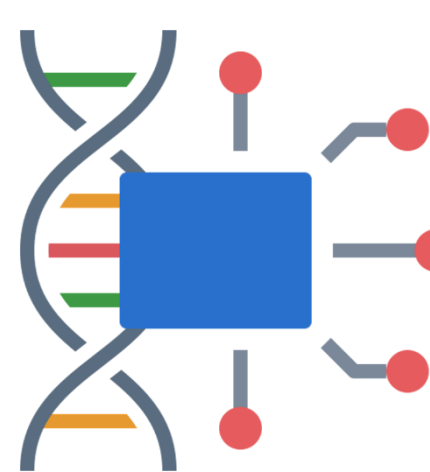
MASS SPECTROMETRY SIGNAL CALIBRATION BASED ON THEORETICAL ISOTOPE PATTERNS

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✄ Poster Presentation: Yes
✄ Oral Presentation: No

INTRODUCTION

Proteomics is a discipline that investigates the composition, structure, function, and interactions of proteins within an organism. Liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) has become a conventional technique in proteomics. Noise in LC-MS/MS proteomics data arises from various sources such as electronic and instrumental imperfections, sample impurities, and chemical interferences, which can introduce random fluctuations or distortions in the signal, potentially leading to inaccurate or misleading results. Several approaches have been proposed for noise elimination of LC-MS/MS-based proteomics data, such as MEND and the wavelet-based method, but the theoretical isotope pattern is rarely employed for this purpose. We thus developed a software tool, called NoiseZap, to improve quantitation efficiency using theoretical isotopic patterns for noise removal.

METHODS

To date, only few algorithms have employed theoretical isotope pattern matching methods to remove noise from mass spectrometry data. Therefore, we propose a new solution which fully utilize the distinct information provided by isotope patterns rather than features of noise. This unique information arises from the relative abundance of isotopes in nature, making it less susceptible to variation under different experimental conditions. We generate the theoretical isotope patterns based on identified peptide sequences, and employ the least squares method to estimate noise intensities, and correct the signal intensities mass spectrometry data. We believe this approach will enable more effective noise handling in mass spectrometry data and facilitate correction of potential errors.

RESULTS AND DISCUSSION

To evaluate the performance of NoiseZap, we conducted an analysis using a mixed human and E. coli dataset, which consisted of four samples, each injected with a protein concentration (i.e., 3, 7.5, 10, and 15 ng). The expected protein ratios between any two samples are 0.2, 0.3, 0.33, 0.4, 0.67, 0.75, 1.33, 1.5, 2, 2.5, 3.33, and 5, respectively. We fist converted the files into mzML file format using ProteoWizard and performed peptide identification and quantitation using FragPipe. Next, NoiseZap was applied for noise removal. Without using NoiseZap, we observed that the protein ratios were 0.14, 0.22, 0.44, 0.31, 0.63, 0.69, 1.44, 1.58, 2.27, 3.21, 4.63 and 7.30, respectively. After using NoiseZap, the protein ratios were 0.15, 0.30, 0.43, 0.34, 0.49, 0.88, 1.14, 2.03, 2.31, 2.97, 3.38, and 6.85, respectively. Thus, seven out of twelve protein ratios became closer to the expected ratios using NoiseZap, demonstrating the effectiveness of our software tool.

NOVEL ASPECT

Liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS), Proteomics, Theoretical isotope patterns, Noise removal
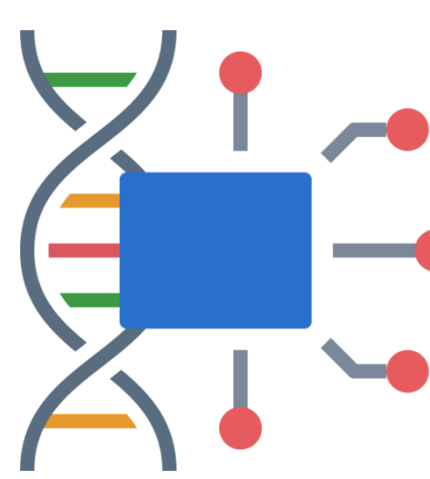
Prediction of Blood Glucose Levels from PPG Signals Using Machine Learning

- 學生：鍾秉儒
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- Poster Presentation: Yes
- Oral Presentation: No

INTRODUCTION

Currently, measuring blood glucose levels requires invasive blood sampling through glucometers, which increases the risk of infection and adds significant costs due to disposable lancets. From my literature review, I discovered that glucose levels affect blood flow and viscosity, which in turn influence PPG signals. My goal is to use non-invasive PPG signals, measured by a custom-built pulse oximeter, to predict blood glucose levels. However, PPG signals can be affected by motion, leading to motion artifacts (MA) that reduce prediction accuracy. To address this, I first distinguish between good and bad PPG signals. Then, I use the high-quality signals to predict glucose levels, aiming to achieve accurate, non-invasive glucose measurement.
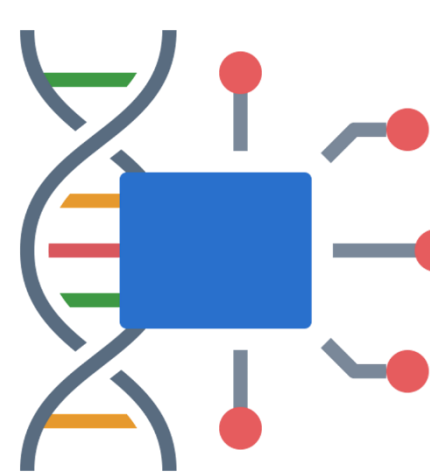
METHODS

I use three MAX30102 sensors connected to an ESP32 to collect red and infrared light signals. These signals and accurate SpO2 measurements from a commercial pulse oximeter and accurate blood glucose levels from a commercial glucometer, are sent to a Raspberry Pi 4B for machine learning. After digital signal processing, a Support Vector Machine (SVM) filters out interfered PPG segments, leaving higher-quality signals to improve SpO2 accuracy. The clean PPG signals, combined with commercial glucometer data, are then used in a multilayer perceptron(MLP) to predict blood glucose levels.

RESULTS AND DISCUSSION

The results of my study demonstrate the potential of non-invasive blood glucose prediction using PPG signals. The primary goal was to utilize PPG signals, obtained from a custom-built pulse oximeter, to predict blood glucose levels accurately. After acquiring PPG signals and processing them through digital signal filtering, I used Support Vector Machines (SVM), to remove motion artifacts (MA) from the data. This process successfully improved the quality of the PPG signals, which in turn enhanced the accuracy of oxygen saturation (SpO2) measurements. Using high-quality, filtered PPG signals along with blood glucose data from a commercial glucometer, I applied MLP for glucose prediction. The model was able to identify key features within the PPG signals that correlated with varying glucose levels, enabling accurate glucose predictions. Overall, the study highlights that non-invasive glucose prediction using PPG signals is a viable method with promising accuracy, although challenges related to signal quality and motion artifacts remain. Future work will focus on refining the machine learning models and exploring additional features within the PPG signals to further enhance prediction accuracy. Additionally, a larger dataset will be required to validate the results across different population groups and improve the robustness of the model.

NOVEL ASPECT

Non-invasive glucose prediction via PPG with motion artifact removal for enhanced accuracy.

electrochemical sensing device for detection of drug-induced cardiotoxicity

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- Poster Presentation: Yes
- Oral Presentation: No

INTRODUCTION

Drug-induced cardiotoxicity (DICT) is a critical safety issue in drug development and clinical applications. Early detection of DICT is challenging, with traditional methods struggling to detect subtle cardiac changes. Cardiac troponin I (cTnI) is a sensitive and specific biomarker for myocardial injury. Currently, there's a lack of portable, real-time detection methods to monitor cardiotoxicity during treatment. This study aims to develop a portable electrochemical sensing device for early detection of drug-induced cardiotoxicity, enabling real-time monitoring and diagnosis of patients.
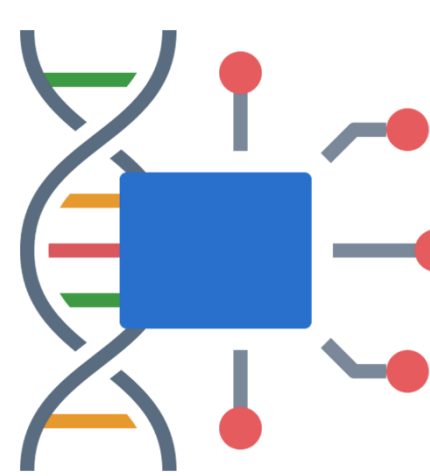
METHODS

Electrochemical detection employs potentiostat circuits and chronoamperometry, indirectly measuring target substance concentration through current changes at the electrode. A microcontroller system is designed for data processing and transmission using I2C communication protocol. An Android application is developed for data reception and visualization. The system integrates three main components: antigen extraction, electrochemical detection, and data transmission, aiming to achieve rapid and accurate cTnI detection.

RESULTS AND DISCUSSION

This study has completed the preliminary PCB concept design, laying the foundation for developing a comprehensive cTnI detection system. The system is expected to rapidly and accurately detect low concentrations of cTnI, enabling early cardiotoxicity detection following drug treatment. The high sensitivity of the system promises to enhance real-time monitoring and diagnosis of patients.Through Bluetooth technology, detection data can be wirelessly transmitted to smartphones or other devices, greatly improving operational convenience and data management efficiency. The development of an Android application will further enhance data visualization and analysis capabilities, allowing medical staff to interpret test results more intuitively.The portability and real-time features of this system are expected to play a crucial role in clinical applications, especially in chemotherapy processes requiring frequent cardiac function monitoring. It could become an effective tool for early identification of potential cardiotoxicity, helping to timely adjust treatment plans and reduce the risk of irreversible cardiac damage.However, the clinical application of the system still requires further validation and optimization. Future research will focus on improving detection accuracy, expanding detection range, and exploring application potential in various types of drug treatments. Additionally, large-scale clinical trials are needed to evaluate the system's performance and reliability in actual medical environments.

NOVEL ASPECT

electrochemical detection, and mobile applications for portable, real-time cardiotoxicity detection, enhancing patient monitoring effectiveness.

Defense Against Evasion Attacks on Biological Features Classification Model using Geometric Fast Data Density Functional Transform

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- 學系/年級：Biomedical Sciences and Engineering/Senior
- Poster Presentation: Yes
- Oral Presentation: Yes

INTRODUCTION

Adversarial attacks have been a rising issue for deep learning models, especially for biometric authentication and identification applications. Adversaries can form malicious samples that manipulate model output. Developing a defense mechanism to face and catch up with the potential confidence problem caused by the continuously newly proposed attack methods is crucial. Several methods have already aimed to resolve the issue; however, the most effective prior works consist of training procedures for unique tasks, which are inefficient regarding the usage of both time costs and computational resources. Furthermore, other methods that do not possess training procedures might still rely on empirically adjusting parameters, and most importantly, they lack consistency and overall
success rate on object recognition tasks.

METHODS

The construction of adversarial perturbation has similarities with the mathematical principle behind the g-fDDFT. To explain the relation between them, here we started with the fundamental framework of the optimization theory that supports the presented adversarial attack method. The decision boundary of a multi-label classification model can be represented as a convex polyhedron. The adversarial perturbation is the distance between the original data point and the complement of the polyhedron. Our method utilizes g-fDDFT as a preprocessing unit which use an energy density functional manifold as a solution manifold replacement for the action manifold; the energy density manifold can extend the original solution manifold boundary. This effect results in the expansion of the whole model that includes the adversarial examples.

RESULTS AND DISCUSSION

In this study, in order to analyze the effectiveness of the g-fDDFT, we recreated the same environment as the one proposed by Carlini et al. and used this as our defense target. As the original study states, the C&W method has a 100% non-targeted attack success rate when using CIFAR10 as the dataset. The results of using the proposed g-fDDFT preprocessing algorithm (please also refer to the Method section) to defend against adversarial examples created using the C&W method. The original images successfully output their correct output label, the adversarial examples generated using the C&W method have all the labels completely altered. For instance, the original image label is a cat, but after applying the C&W method to the image, the prediction label changes to a dog. For the results of using the proposed g-fDDFT algorithm as a defense technique, we can observe that more than half of the samples successfully return to their original labels. After executing the same process on every sample in the CIFAR10 dataset, the current preliminary results provided by the g-fDDFT algorithm have a 65% success rate of restoring the images and returning their correct labels. In conclusion, we first extended the mathematical structure of geometric fast data density functional transform (g-fDDT) to describe the solution manifolds of image tensors. We then implemented the g-fDDFT to be a zero-shot algorithm for the defense technique of adversarial examples. We noticed from the preliminary research results that the proposed g-fDDFT algorithm still has room for improvement. Since the g-fDDFT algorithm is heavily based on geometric deep learning with low computational complexity and high inference ability, we hope that the final result can inherit such advantages. We also expect the whole model structure can reach the demand of the lightweight learning framework.

NOVEL ASPECT

Defense method against evasion attacks, Geometric deep learning, g-fDDFT

Long-Term Monitoring of Exercise Habits Using a Wrist-Worn Accelerometer and Gyroscope

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- 學系/年級：Biomedical Sciences and Engineering/Senior
- Poster Presentation: Yes
- Oral Presentation: Yes

INTRODUCTION

This study investigates adult exercise habits through the long-term collection of data using a wrist-worn device equipped with an accelerometer and gyroscope. The World Health Organization (WHO) recommends that adults engage in at least 150 minutes of moderate aerobic activity weekly, such as walking or cycling. Understanding these habits is crucial for developing effective health interventions and promoting a more active lifestyle.
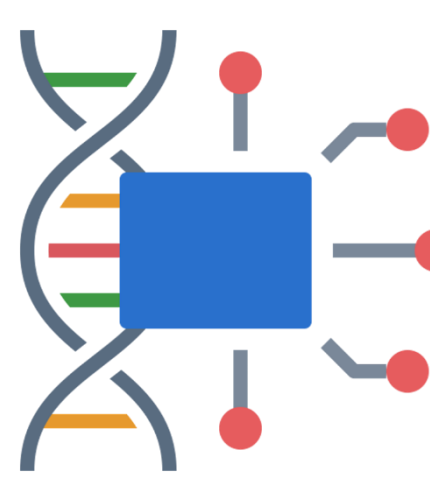
METHODS

We use a wrist-worn device with an accelerometer and gyroscope for long-term data collection. After filtering the data and extracting relevant features, machine learning algorithms were applied to classify and analyze exercise habits. The training process utilized publicly available datasets from GitHub, which included classifiers for distinguishing between walking and running, along with tools developed specifically for calculating walking speed.

RESULTS AND DISCUSSION

Long-term monitoring enabled effective classification of sedentary periods, walking, and running. The activity distribution offered valuable insights into daily exercise levels and patterns. Our analysis uncovered variations in activity intensity and frequency, which are crucial for evaluating overall exercise habits and identifying opportunities for improvement. The speed data proved particularly useful in distinguishing different exercise intensities. Long-term monitoring captures trends and fluctuations in physical activity and health over time, providing insights that short-term studies often miss. The detailed activity data underpins personalized health recommendations and interventions, which are vital for enhancing exercise habits and overall well-being.

NOVEL ASPECT

Precise long-term monitoring and intensity analysis using wearable sensors.

Estimation of Heart Rate Variability and Evaluation of Resonance Breathing Exercises using Apple Watch

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✂ 學系/年級：Biomedical Sciences and Engineering/Junior

✂ Poster Presentation: Yes

✂ Oral Presentation: No

INTRODUCTION

Heart rate variability (HRV) is a non-invasive physiologic measure of autonomic function that helps the identification of people at the risk of developing cardiovascular complications. It has been demonstrated that HRV can be improved by practicing resonance breathing exercises. Studies on the effect of resonance breathing exercises has also shown the improvement in reduced depression and better performance in cognitive tasks and functions.

METHODS

The study subject was instructed to sit quietly for 10 minutes before ECG measurement. Then, the subject was instructed to perform resonance breathing pattern of 4-second inhaling and 6-second exhaling during the ECG measurement. The breathing pattern was performed 3 times and the duration was 30 seconds in total.Our QRS wave detector consists of four steps:First,extract three 10-second ECG images from the PDF file to generate a 30-second ECG waveform.Second,the temporal electrocardiogram signal of the red band area was cultured from the culture medium.Third,use wavelet transformation to enhance QRS waveforms and automatically detect R wave peaks.Fourth,the NN interval is identified and estimated based on the position of the R wave crest.

RESULTS AND DISCUSSION

AVNN and SDNN were estimated as 997 and 88 (997 +/- 88) ms respectively.The NN-intervals have three cycles which seems to agree with resonance breathing pattern.APPLE Watch ECG measurement can be used to estimate HRV and the detected NN-interval pattern is a feasible tool for evaluating resonance breathing training.

NOVEL ASPECT

Using any smart watch that can measure ECG, you can use this method to detect heart rate variability.
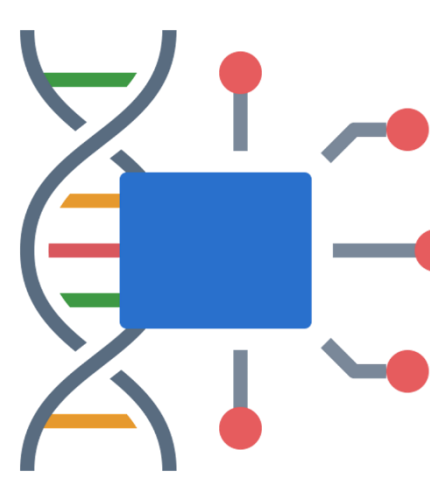
CNN-Based Detection of Diabetic Retinopathy with Attention Mechanisms.

✂ 學生：謝主韋

✂ 指導老師：陳健章

✂ 學系/年級：Biomedical Sciences and Engineering/Senior

✂ Poster Presentation: Yes

✂ Oral Presentation: No

INTRODUCTION

Diabetic Retinopathy (DR) is a complication of diabetes that damages the blood vessels in the retina, potentially leading to blindness if untreated. It affects up to 80% of individuals with long-term diabetes and is the leading cause of vision loss in working-age adults. Early detection is critical, but traditional manual examination of retinal images is time-consuming and prone to error. Recent advances in deep learning, particularly Convolutional Neural Networks (CNNs), offer a promising automated approach for detecting and grading DR with high accuracy. This project leverages CNNs to classify DR severity, enhancing early diagnosis.
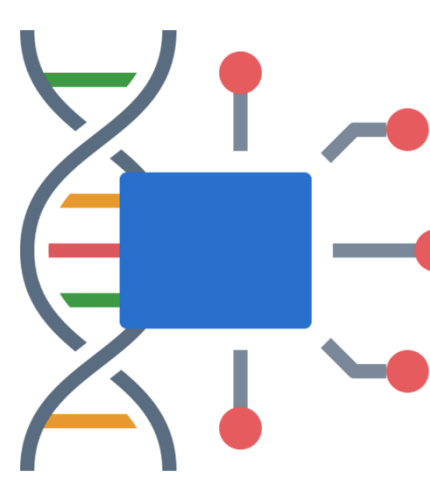
METHODS

This project uses a CNN-based model with attention mechanisms to detect diabetic retinopathy (DR) from retinal images. Due to the highly imbalanced dataset, oversampling techniques were employed to balance class distributions, ensuring that the model can effectively learn from all severity levels of DR. The images were preprocessed using data augmentation techniques like horizontal flipping, zooming, and shearing. A custom attention model was developed to focus on critical regions of the retina, enhancing the model's ability to detect subtle signs of DR. Transfer learning with InceptionV3 was also utilized to leverage pre-trained features, further improving the model's performance on this small, noisy dataset.

RESULTS AND DISCUSSION

The model demonstrated strong performance during training (training for ten epochs so far), with a final accuracy of 95.56% and an AUC of 1.00. However, a significant drop in validation accuracy to 60.00%, coupled with a high validation loss of 1.45, suggests overfitting. The model appears to have learned the training data well but struggles to generalize to unseen data. This issue is further reflected in the classification report, where precision, recall, and F1-scores hover around 0.20 for all classes, indicating poor performance across the board. The confusion matrix shows that misclassifications are widespread, with no particular class appearing as accurately predicted.The imbalance in the dataset likely exacerbated these challenges, as the model may have become biased toward the more frequent classes. Although data augmentation and oversampling were used, the results suggest that these measures were insufficient to mitigate the imbalance's impact fully. Additionally, the utilization of the attention mechanism did not sufficiently enhance the model's ability to focus on relevant features in the retina images, as indicated by the poor differentiation between DR severity levels.To improve the model performance in this study, further work should involve more times and epochs to train and more extensive data augmentation, the application of regularization techniques, and potential adjustments to the learning rate. Exploring alternative model architectures or fine-tuning pre-trained models specifically for this task might also help the model generalize better. Extending the training duration with careful monitoring of validation loss could provide additional opportunities for the model to learn from the data more effectively, potentially improving its overall accuracy and robustness.

NOVEL ASPECT

Integrating Attention Mechanisms to Enhance CNN-Based Diabetic Retinopathy Detection on Imbalanced Data.

The application of YOLO in foot arch diagnosis using x-ray images.

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- 指導老師：黃輝揚
- 學系/年級：Biomedical Sciences and Engineering/Senior
- Poster Presentation: Yes
- Oral Presentation: No

INTRODUCTION

The human foot is a complex anatomical and biomechanical structure. The arches of the foot provide quantitative measurements for the effectiveness of the lower extremity function. Manual interpretation of foot bone images is inefficient and may have some inter-rater variability. We hope to utilize YOLO to assist in detecting bones in the foot using X-ray images, thereby improving efficiency and reducing inter-rater variability in foot arch measurement.
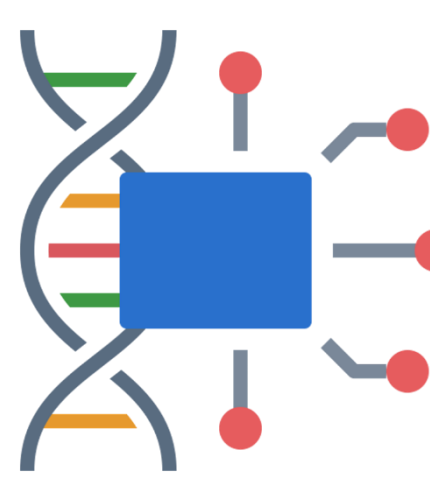
METHODS

X-ray Images of 1836 feets were annotated by a radiologist. The lower boundaries of calcaneal and the fifth metatarsal bones were refined by using the a level set method. The data set was divided into 1549,192, and 195 for training, validation, and test respectively. The training data was augmented by flipping the foot images horizontally to create mirrored images. The YOLO model was trained with different image resolutions and epochs to select the module metaparameters that generated the best results, and use this module for X-ray image detection. Finally, perform statistical analysis on the error values compared to the ground truth.

RESULTS AND DISCUSSION

Image resolution of 1024 pixels and trained at 20 epochs generated the best results. The arch angle measurement error at the fifth metatarsal bone was 0.34 degrees with 95% confidence interval [-0.82,1.50]. The arch angle measurement error at the calcaneal bone was 1.45 degrees with 95% confidence interval [-0.82, 3.37]. It was found that the angle error of the calcaneal bone was larger, which can subsequently affect the detective results.

NOVEL ASPECT

The YOLO model can detect bones for X-ray foot images for diagnosing foot arch angle with good accuracy.

Contactless Detection of Physiological Signal using a 4-Transmitter Phased Array Ultrasound System

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✍ 指導老師：林澂

✍ 學系/年級：Biomedical Sciences and Engineering/Senior

✍ Poster Presentation: Yes

✍ Oral Presentation: Yes

INTRODUCTION

Accurate heart rate measurement and monitoring are crucial for diagnosing diseases, yet traditional equipment like ECG is often costly and inconvenient for regular use. To overcome these challenges, we have developed a cost-effective, contactless heart rate monitoring system utilizing a 4-transmitter ultrasound phased array. This system focuses its beam around the chest area to monitor respiratory motion over extended periods. It is particularly beneficial for long-term care facilities or home care settings, providing a practical and accessible solution for continuous heart rate monitoring.

METHODS

In our system, we use 4 ultrasound transmitters and 1 receiver to focus the ultrasound beam around the chest by adjusting the transmission delay between transmitters. The signal is processed using band-pass filters and half-wave rectifier to reduce noise. The resulting image is constructed with additional software. In order to construct the image, we apply interpolation to estimate the undetected angle and we also remove the grating lobe artifacts to enhance image accuracy.

RESULTS AND DISCUSSION

In our study, we successfully constructed a one-dimensional image parallel to the emitters and estimated the object's distance. To validate our experimental results and mitigate grating lobe artifacts, we simulated the ultrasound imaging system with the same specifications as the real system. This simulation allowed us to rectify the data and eliminate areas affected by grating lobes. Furthermore, we applied the system to monitor respiratory motion in human subjects. The system effectively captured movement both back and forth and left and right. However, the detection area was constrained by the use of only four transmitters. Our next goal is to enhance the system's capability to estimate heart rate under various conditions. To achieve this, we plan to increase the number of transmitters and adjust the array structure to improve both lateral and axial resolution. Additionally, we aim to develop a robust signal processing algorithm tailored to our specific needs. These advancements will enable more accurate and reliable heart rate estimation, broadening the system's applicability and effectiveness in real-world scenarios.

NOVEL ASPECT

Acoustic sensing, Contactless detection, Long-term
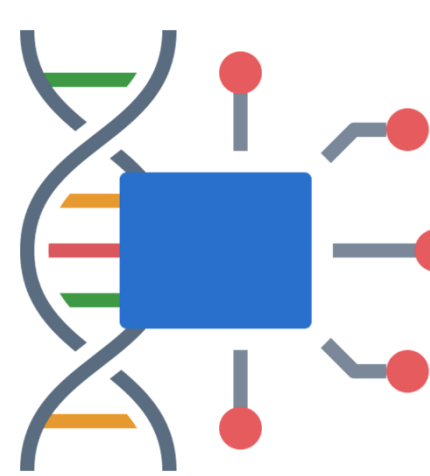
Detecting R-wave in Electrocardiograms with a 2D Image based Deep Learning Approach

✄ 學生：鄭喬憶
✄ 指導老師：黃輝揚
✄ 學系/年級：Biomedical Sciences and Engineering/Senior

✄ Poster Presentation: Yes
✄ Oral Presentation: No

INTRODUCTION

Traditionally, ECG signal processing has primarily been based on direct analysis of the voltage-time signals from the electrodes, treating them as one-dimensional time signals data. With the widespread adoption of portable ECG devices, current ECG outputs are mostly recorded as two-dimensional images of 12-lead ECG waveforms over 10 seconds.Since R-wave detection involves processing the amplitude and periodic characteristics of ECG signals, the features of the ECG must be represented on a one-dimensional time axis. Converting two-dimensional images to one-dimensional time signals involves complex software and hardware image processing, leading to higher demands on hardware and increased development costs for the devices. Therefore, we want to investigate whether two-dimensional image deep learning, using convolutional neural networks and other models, can automatically learn to detect features.
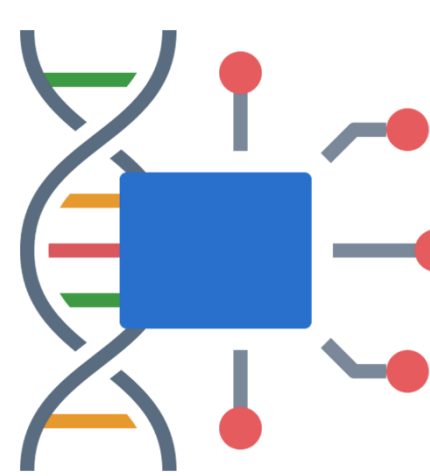
METHODS

In this experiment, two methods for R-wave detection are employed: traditional one-dimensional time signal processing and two-dimensional image deep learning. Two Python programs are constructed for comparison. Additionally, Hausdorff distance statistics are used to quantify the error in R-wave detection by calculating the Hausdorff distance from the detected time positions to the reference points. This approach allows us to evaluate which method is more advantageous for medical diagnosis by assessing the accuracy of R-wave position detection.

RESULTS AND DISCUSSION

The data for this study comes from a publicly available dataset collected by a research team from Pakistan using the "EDAN SERIES-3" ECG equipment. The collected data includes a dataset of 12-lead ECG images. The traditional one-dimensional time signal processing use the Python Neurokit2 toolbox module to detect R-waves. For YOLO processing, 80 ECG images from healthy individuals were annotated in MATLAB with RR intervals, and each annotated RR interval was normalized with bounding box dimensions. Out of these 80 samples, 606 R-wave peak positions were manually annotated as a ground truth for training the YOLO model. Comparing the Hausdorff distance between Neurokit2 and YOLO methods, it can be inferred that after upsampling the ECG to a resolution of 2048x2048, YOLO performs better in detecting R-waves, indicating greater accuracy and stability in R-wave detection. In contrast, Neurokit2 shows higher variability in its results. Therefore, for high precision and stability in R-wave detection, YOLO is a more preferable tool.

NOVEL ASPECT

Deep learning models can accurately detect R-waves in 2D ECGs, aiding cardiovascular disease diagnosis.

Predictive Modeling of Hepatocellular Carcinoma Recurrence Post-Ablation: A Machine Learning Approach Integrating DNA Methylation and Biochemical Data

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- 指導老師：蘇立仁
- 學系/年級：Biomedical Sciences and Engineering/Senior
- Poster Presentation: Yes
- Oral Presentation: No

INTRODUCTION

According to the 2022 statistics from the Ministry of Health and Welfare, liver cancer and chronic liver diseases, including cirrhosis, caused 11,888 deaths in Taiwan, with liver cancer being the second leading cause of cancer-related deaths, accounting for approximately 15% of all cancer fatalities. Curative treatments for liver cancer include liver transplantation, surgical resection, and local ablative therapies such as radiofrequency ablation and microwave ablation, with liver transplantation having the lowest recurrence rate. Even after successful treatment, regular follow-up is recommended for patients. DNA methylation testing has emerged as a more sensitive method compared to traditional alpha-fetoprotein (AFP) testing, offering potential advantages in predicting recurrence and providing additional information on cancer malignancy and staging.

METHODS

In this study, we developed a predictive model for hepatocellular carcinoma recurrence within two years after ablation. We collected biochemical test results and CT values of 12 methylation genes, categorizing continuous variables by quartiles and using medical guidelines to classify biochemical values. CT values above 55 were also binarized. We applied various machine learning models, including Bayes Net, Naive Bayes, Logistic Regression, Decision Tree, and Random Forest, and evaluated their performance using leave-one-out cross-validation to predict recurrence effectively.

RESULTS AND DISCUSSION

Data from 95 patients who underwent hepatocellular carcinoma ablation were analyzed, including 13 biochemical test parameters and CT values of 12 methylation genes. Among the biochemical parameters, 7 had associated medical thresholds, which were used to classify these parameters into binary outcomes (0, 1). Continuous variables were discretized into six levels using quartile concepts, resulting in a total of 20 biochemical features. For the 12 methylation genes, the CT values from three experimental replicates were averaged. Two genes (S01 and S33) with high experimental missing values were excluded, leaving 10 methylation genes. M1 gene served as a control; the CT values of the other 9 methylation genes were adjusted by subtracting the M1 gene's CT value, resulting in 9 new features. These 9 features were then binarized using a CT value threshold of >55, producing a final set of 28 methylation gene features. We used machine learning models to train a predictive model for early progression (recurrence within two years after ablation) using the 48 features from the 95 patients. The models were evaluated with leave-one-out cross-validation, yielding the following accuracy rates: Bayes Network: 71.58%, Naive Bayes: 76.84%, Logistic Regression: 67.37%, Decision Tree: 73.68%, and Random Forest: 78.95%. Our findings suggest that using Random Forest models would likely to predict recurrence effectively.

NOVEL ASPECT

Combining DNA methylation testing with machine learning to predict liver cancer recurrence post-ablation.
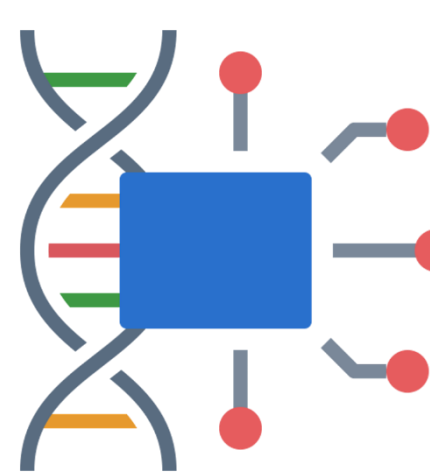
Geometric Lightweight Approximation Topology Encoding and Decoding Network Model

- 學生：曾友亭
- 指導老師：陳健章
- 學系/年級：Biomedical Sciences and Engineering/Senior
- Poster Presentation: Yes
- Oral Presentation: No

INTRODUCTION

Accurately describing how cells change shape and move when interacting with other cells helps researchers understand biomechanical patterns in cell migration and morphology. By analyzing temporal images of segmented moving cells, researchers can compare normal and abnormal tissue development, identifying key factors influencing diseases. In the era of AI-driven medical IoT, fast and accurate cell tracking, recognition, and segmentation models still require extensive computational resources, such as GPUs and high-capacity storage, for training. These models are then adapted to lightweight platforms like TensorFlow Lite (TFlite). However, performance often suffers due to reduced parameters and architectural changes.
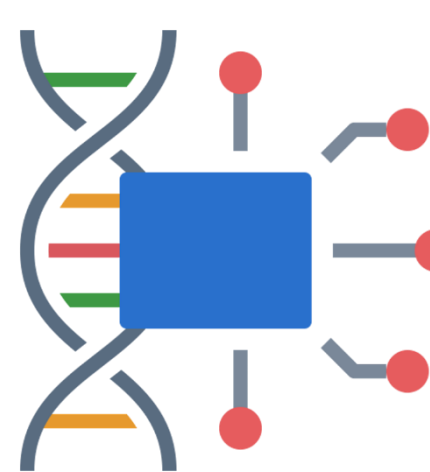
METHODS

By combining Graph Convolutional Neural Networks (GCN) with lightweight neural network models such as MobileNetV3, a variant of U-net context encoder network (CE-net), and variational inference priors, it is integrated into fast Data Density Functional Transform (fDDFT) equipped with edge computing capabilities.

RESULTS AND DISCUSSION

In previous research, this model has been proven to significantly improve speed in cell tracking.Due to the heavy computational load of GCN networks, we aim to optimize data compression by utilizing more efficient network architectures, such as ShuffleNet and MobileNet. These architectures leverage optimization techniques like integer-arithmetic-only quantization methods, which ensure that no features are lost. We plan to integrate these techniques into our proposed lightweight feature-preserving topology encoding network.

NOVEL ASPECT

Technology for rapid and accurate cell image recognition and tracking, focusing on cell identification, tracking, and segmentation.

Electrochemical System for Detecting C-Reactive Protein Using Self-Assembled Monolayer-Modified Interdigitated Electrodes

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✄ 指導老師：黃貞翰

✄ 學系/年級：Biomedical Sciences and Engineering/Senior

✄ Poster Presentation: Yes

✄ Oral Presentation: No

INTRODUCTION

C-reactive protein (CRP) is a cyclic protein found in plasma and produced primarily by the liver. Clinically, it is considered an important biomarker related to the prognosis of various diseases, such as cardiovascular inflammation, diabetes, cancer, arthritis, etc. However, current biosensors require a lot of time to detect CRP. This study designed and developed a simple, fast, high-sensitivity, low-detection-limit biosensor for CRP detection based on an electrochemical sensing method and system of interdigitated electrode chips.
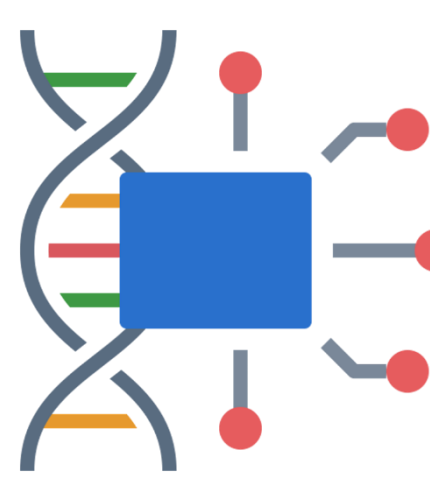
METHODS

This study uses the electrochemical sensing method and a system of interdigitated electrode chips for detection. An immune sensing chip composed of anti-CRP functionalized interdigitated electrodes modified with gold nanoparticles measures CRP molecules in the sample. This measurement relies on changes in electrochemical impedance caused by the immune response between CRP and anti-CRP.

RESULTS AND DISCUSSION

This immunoassay measures CRP reach a linear range of 0.5-150 nM, a detection limit of 0.1 nM (S/N = 3), and a high sensitivity of 105.7 nA/nM under optimal conditions. Additionally, it demonstrates good reproducibility and stability. The study verified the immunoassay's analytical applicability by measuring CRP in simulated human serum samples at clinically relevant concentrations. This research paves the way for a low-cost, safe, easy-to-use point-of-care immune sensor test for CRP measurement.

NOVEL ASPECT

This research paves the way for a low-cost, safe, and user-friendly point-of-care immune sensor for CRP measurement.

Classification for Prostate Cancer diagnosis via Deep-Learning-Enabled Raman Spectroscopy

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⌇ 指導老師：黃貞翰

⌇ 學系/年級：Biomedical Sciences and Engineering/Senior

⌇ Poster Presentation: Yes

⌇ Oral Presentation: No

INTRODUCTION

Prostate cancer (PCa) is a prevalent malignancy, particularly in developed countries, where timely diagnosis and treatment are vital for patient survival. Despite the effectiveness of prostate-specific antigen (PSA) screening, its lack of specificity results in unnecessary biopsies and overtreatment. In this study, surface-enhanced Raman spectroscopy (SERS) emerges as a promising diagnostic tool, offering molecular insights with high accuracy and non-invasiveness. However, challenges persist in its application for PCa diagnosis. This study aims to develop a machine learning structure integrating 1D convolutional neural network (1D CNN) and spatial pyramid pooling (SPP) for enhanced SERS signal analysis. By combining advanced machine learning techniques with SERS, this research seeks to improve PCa diagnosis accuracy and efficiency, providing a valuable contribution to clinical practice
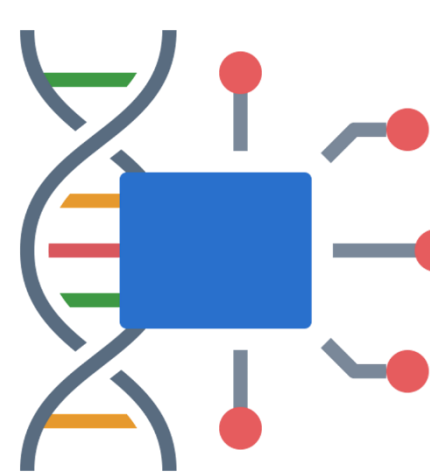
METHODS

To classify prostate cancer using deep learning-enabled Raman spectroscopy, the study proposes a method combining 1D convolutional neural networks (1D CNN) with spatial pyramid pooling (SPP). The process begins with data collection using surface-enhanced Raman spectroscopy (SERS) on patient serum samples. Data preprocessing involves augmentation and normalization techniques. The 1D CNN-SPP structure is then developed to extract features and handle variable input sizes. Performance metrics such as accuracy, specificity, and sensitivity are calculated using a confusion matrix. The trained model is then applied to new patient data for prostate cancer identification. Finally, the method's performance is compared to traditional PCA-LDA analysis to assess its robustness, accuracy, and efficiency in prostate cancer diagnosis.

RESULTS AND DISCUSSION

The proposed 1D CNN-SPP model for prostate cancer diagnosis using SERS data showed promising results in distinguishing between cancerous and non-cancerous samples. These results indicate a significant improvement over traditional PCA-LDA methods. The high performance of the 1D CNN-SPP model can be attributed to its ability to automatically extract relevant features from the SERS spectra and handle variable input sizes. This flexibility allowed the model to adapt to slight variations in spectral data that may occur due to different experimental conditions or equipment. Data augmentation techniques proved effective in enhancing the model's performance, particularly in addressing the limited sample size often encountered in clinical studies. The augmented dataset provided a more robust training set, leading to improved generalization of the model. In conclusion, the 1D CNN-SPP model shows great promise for enhancing prostate cancer diagnosis using SERS data. Its high accuracy, particularly in challenging diagnostic scenarios, suggests potential for improving patient care and reducing healthcare costs associated with unnecessary procedures. Future work should focus on external validation and exploring methods to increase model interpretability for clinical implementation.

NOVEL ASPECT

Exploring Medical Diagnostic Projects Integrating Deep Learning and Optics.

Employing Machine Learning for the Peak Quality Assessment in Untargeted Metabolomics Data

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- Poster Presentation: Yes
- Oral Presentation: Yes

INTRODUCTION

Metabolomics is a study that investigates the complete set of small molecules within a biological system. Liquid chromatography coupled with tandem mass spectrometry (LC-MS/MS) is a powerful technique used in metabolomics to identify and quantify small molecules with high sensitivity and precision. Several software tools have been proposed for metabolite quantitation from LC-MS/MS-based metabolomics data, but only few tools focus on peak quality evaluation. Thus, we conducted an analysis of peak quality assessment, employing nine metrics and five machine learning algorithms, aiming to identify an appropriate algorithm and key metrics for evaluating peak quality.
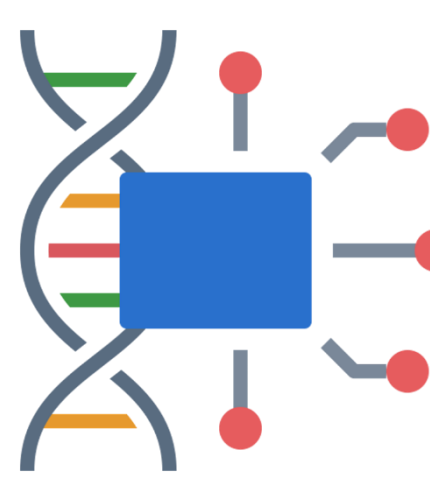
METHODS

In our peak quality assessment analysis, we integrated nine metrics, including Shapiro-Wilk (SW) test, intensity slope (SL), signal-to-noise ratio (SNR), sharpness (SP), peak significance level (PSL), symmetry (SM), triangle peak area similarity ratio (TPASR), zig-zag index (ZZ), and apex boundary ratio (ABR), along with five machine learning algorithms, including logistic regression, support vector machine, AdaBoost, random forest, and multilayer perceptron. We utilize accuracy as the measurements for performance evaluation which measures the ratio of correctly classified instances to the total instances. We conducted the analysis using an in-house metabolomics dataset, comprising 360 LC-MS/MS-based samples, each pooled with human serum and ten internal standards.

RESULTS AND DISCUSSION

The 360 LC-MS/MS samples were first converted into mzML file format using ProteomeWizard, and quantified using MS-Picker, generating a feature list with detected metabolite features in rows. We found a notable difference in the distribution validated by the nine quality metrics between internal standards and detected features, indicating that the nine metrics are good features for model building. We then categorized these features into "good" or "bad" based on manual assessment. A feature was considered "good" if it garnered at least six positive evaluations across the nine metrics; conversely, receiving fewer than three positive evaluations relegated a feature to the "bad" category. The criteria for these evaluations included considerations like SW values below 0.05, intensity slope exceeding 15.82, SNR greater than 3, sharpness over 0.44, peak significance level above 0.996, symmetry higher than 1, TPASR lower than 0.06, zig-zag index under 1.15, and apex boundary ratio below 0.86. Unlabeled peaks were excluded from consideration. Next, we applied the five machine learning models, using a five-fold cross-validation approach. The outcomes indicated that logistic regression achieved an accuracy of 0.984. Random forest and AdaBoost excelled with an accuracy of 1. Support vector machine posted results of 0.994 in accuracy, while multilayer perceptron reached an accuracy of 0.999. The computational times for these algorithms were recorded as 0.159 minutes for logistic regression, 4.056 minutes for random forest, 40.415 minutes for support vector machine, 19.988 minutes for AdaBoost, and 8.736 minutes for multilayer perceptron, highlighting random forest as the top performer among the evaluated algorithms. We also conducted an analysis of nine metrics utilizing logistic regression, AdaBoost and random forest, and observed that the peak significance level, apex boundary ratio and zig-zag index as crucial metrics for assessing peak quality.

NOVEL ASPECT

We employ nine metrics as feature attributes to compare the accuracy of five machine learning algorithms and provide a comprehensive analysis.

Low-Cost, Infrastructure-Free Indoor Mapping with a Single Phone IMU: Ideal for Hospitals and Care Facilities

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- 指導老師：羅孟宗　林澂
- 學系/年級：Biomedical Sciences and Engineering/Senior
- Poster Presentation: Yes
- Oral Presentation: Yes

INTRODUCTION

Nowadays, it is increasingly common for children and elders to become disoriented in mazy hospital. In addition, attendants may struggle to locate elders in vast care facilities. Both hospitals and care facilities typically lack outside signal, making it difficult to locate individuals accurately using Global Positioning System(GPS). Therefore, it is needed to develop an indoor locating system. There are various approaches such as BLE, Beacons, Wi-Fi, or high-intensity signal transmitters. However, all of these options require numerous costly sensors installations throughout the buildings. In my research work, I propose a low cost and infrastructure-free indoor mapping system only utilizing a phone's IMU sensor for children and elders.

METHODS

The system uses IMU's acceleration and gyroscope data as input, and the sensor puts in front of the chest. The system is composed by Mapping, Orientation and Step Length Detection. I get the R3's floor plan, drawing particle-exist and non-particle area. This mapping system distinguishes the place where particles can show up. Moreover, using Madgwick filter and Particle filter updates the heading way. Madgwick filter is a gradient descent method to calibrate the quaternion which is a four dimensions vector representing space vector. Particle filter randomly gives particle's radius and heading angle. After numerous sampling, the system gets the most possible location. Lastly, detecting acceleration's peak defines the foot touching moment. Segmentation to every steps attenuates some high frequency noise.

RESULTS AND DISCUSSION

Our software is capable of capturing a phone's IMU data at a 100Hz sample rate and transferring it to a computer. Before starting the experiment, the device must be held in a fixed position to calibrate the quaternion. Once calibration is done, the program begins identifying the foot's touchdown moments. This approach divides the entire data set into individual steps. Madgwick filter is applied to each step, updating the quaternion with a small beta coefficient. This updated quaternion is then used to convert the acceleration data into the correct heading direction, providing directional information that the original acceleration data lacks. To demonstrate, I use the R3 first floor as an example, setting the side entrance as the starting point. With the map, the program eliminates any particles that are located inside walls, as these are impossible positions. In the final video, we can observe numerous particles moving accurately in both direction and movement. The Particle filter then aggregates the XY locations of all possible particles and sends the results to the mapping system. Looking ahead, there are several tasks that need to be addressed. The mapping system needs to be updated in real-time, displaying the user's location on the phone. So, I need to convert the current offline version to a real-time Android application. Besides, it is difficult to request users holding the phone in front of their chest in real-world scenarios. In short, we need to explore alternative methods to improve our mapping system and become more user-friendly.

NOVEL ASPECT

Indoor Tracking, Particle Filter, Madgwick Filter, Quaternion, Android Software, Single IMU
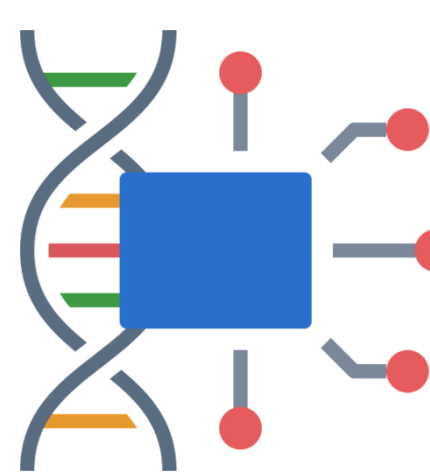
Development of a Portable Low-Power Impedance Cardiography Measurement System for Long-Term Care of Heart Failure and Myocardial Infarction Patients

- 學生：洪至寬
- 指導老師：羅孟宗　林澂
- 學系/年級：Biomedical Sciences and Engineering/Senior

- Poster Presentation: Yes
- Oral Presentation: Yes

INTRODUCTION

Stroke volume (SV) is one of the important hemodynamic parameters for assessing the function of the heart as a pump. Several decades ago, Kubicek proposed impedance cardiography (ICG) as a noninvasive technique for continuous measurement of SV. SV is low in heart failure (HR) patients, and ICG also reveals beneficial effects of cardio rehabilitation (CR) of these patients. Abnormal ICG wave is found to be a sign of poor prognosis in patients with acute myocardial infraction. So, I aim to develop a portable, low-power ICG measurement system for monitoring hemodynamic function to help CR and prevention for Patients with HR and myocardial infraction.
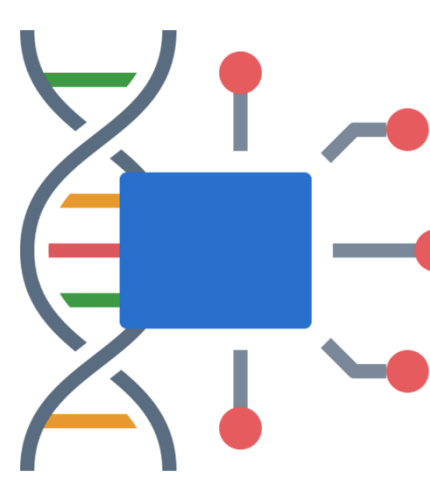
METHODS

A ICG system is proposed, including of the emission and receiver circuit. Since ICG and ECG share overlapping bandwidth, the ICG should be modulated to 50kHz via emission current source. Then, the receiver unit performs biopotential amplifier and demodulator to record the cardiac contraction related thoracic impedance variation. First, emission circuit generates a 1mA, Vpp, 50 kHz sinusoidal current into the body. Later, the receiving circuit contains instrumentation amplifier, bandpass filter and precision demodulator (AD630, Analog Device) to collect ICG and ECG simultaneously. Last, the digital circuit is also considered. A microcontroller should host the overall data flow, where ICG/ECG are collected with precision analog to digital converter(ADS1298R, TI) and transmitted via Bluetooth (BLE, DA154431, Renesas) to IOT devices.

RESULTS AND DISCUSSION

The signals are successfully and stably collected by the ADC. The output impedance of the current source is very important to achieve the desired high performance in impedance measurement. Bioimpedance analysis assumes fat mass is anhydrous and that conductivity reflects fat-free mass. In one measurement, a subject weighing 80 kilograms is tested, and the ICG is successfully observed. I also test the system under Valsava maneouver. In this test, the amplitude of ICG is observed to decrease and flat due to reduced cardio output.

NOVEL ASPECT

My circuit is capable of providing a precise ICG waveform while maintaining low power.

Bio-inspired Structures in Portal Frame Building Design

- 學生：陳萱
- 指導老師：陳健章
- 學系/年級：Biomedical Sciences and Engineering/Senior
- Poster Presentation: Yes
- Oral Presentation: No

INTRODUCTION

Inspiration for new, innovative ideas are often found in the world around us, including natural life. The honeycomb is a natural home and structure that has inspired many ideas in scientific fields, such as the benefits of the hexagonal shape in math and the comb structure in biomaterials. The design of efficient and sustainable structural systems is a critical aspect of modern engineering. This study investigates the potential of natural structures, specifically the honeycomb pattern, to inspire the design of a steel portal frame structure.

METHODS

The primary objective is to explore and determine optimal dimensions that balance structural integrity with material efficiency. The research begins with a preliminary design phase, where geometrical configurations inspired by the honeycomb structure are considered. Subsequent analysis focuses on the structural behavior of these designs under typical loading conditions. Specifically, the study aims to determine the required sizes of columns and rafters to ensure stability and safety while minimizing material use. Additionally, Revit is used to draw the designs.

RESULTS AND DISCUSSION

The analysis stage and calculations show the potential of using the honeycomb as a bio-inspired structure in steel portal frame design. The honeycomb as a biomaterial is not, at current standards, suitable to replicate in large structural form, but the material considered in this study, steel, in portal frame buildings, proves to adopt the proposed design well. The initial conditions set in the preliminary design allow for flexible numbers in the analysis stage, so a future study may strive to calculate the most optimized figures for a more complete combination of design elements. Further studies require extended analysis and consideration of other possible load combinations, for a more extensive and concrete design. Given additional professional resources for the structural analysis segments, it is possible that further studies could implement more complicated structural designs also inspired by the honeycomb structure. In future endeavors, it is worth to considering these design concepts in the production of biomedical technology, such as smaller structures in the bone, or artificial tissue.

NOVEL ASPECT

Honeycomb structure in Portal Frame Design