

Conference Abstract

2023 5th International Conference on Advanced
Bioinformatics and Biomedical Engineering (ICABB 2023)

December 11-13, 2023 | Kuala Lumpur, Malaysia--Online

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Welcome Letter

Dear participants,

It is with great pleasure that we extend a warm welcome to all of you for the 2023 5th International Conference on Advanced Bioinformatics and Biomedical Engineering (ICABB 2023). ICABB 2023, originally scheduled to take place in Kuala Lumpur, Malaysia, is now planned to be held virtually from December 11th to 13th, 2023.

The ICABB conference series is an annual event that serves as an interactive platform for the presentation and discussion of topics in Advanced Bioinformatics and Biomedical Engineering, along with related fields.

This conference promises to be a dynamic gathering, offering a unique opportunity to exchange ideas, share insights, and build collaborative relationships. Whether you are a seasoned researcher or a newcomer to the field, ICABB 2023 aims to provide an enriching experience for all participants.

Although we won't be meeting in person, we believe that the virtual format will foster meaningful connections and contribute to the advancement of research in these crucial fields.

We look forward to your active participation and meaningful contributions to the success of ICABB 2023.

Warm regards,

General Chair

Prof. Malarvili Balakrishnan, Universiti Teknologi Malaysia, Malaysia

Presentation Guidelines

Presentation Requirement

- At least one author should present for each abstract/full paper during the session.

Tips for Presentation

- English is the official language.
- Get your presentation PPT/Slides prepared.
- Keynote Speech: about 35 minutes of presentation and 5 minutes of Q&A.
- Invited Speech: about 20 minutes of presentation and 5 minutes of Q&A.
- Oral Presentation: about 12 minutes of presentation and 3 minutes of Q&A.
- One Best Oral Presentation will be selected from each session and announced at the end of the session.

Online Presentation Instruction

- **Equipment Needed:**
 - (a) A computer with an internet connection (wired connection recommended).
 - (b) USB plug-in headset with a microphone (recommended for optimal audio quality).
 - (c) Webcam (optional): built-in or USB plug-in.
 - (d) Please set up your laptop time in advance.
- **Download the ZOOM:**
 - <https://zoom.us/download>;
 - <https://www.zoom.com.cn/download>.
- **Learn the ZOOM skills:**
 - <https://support.zoom.us/hc/en-us/articles/201362033-Getting-Started-on-Windows-and-Mac>
- **How to use ZOOM:**
 - (a) Set the language.
 - (b) Test computer or device audio.
 - (c) Join a meeting: Join the meeting with the "meeting ID" provided in the program, tap the name as "paper ID+name", eg.: "M0001-XX", then click "Join".
 - (d) Get familiar with the basic functions: Rename, Chat, Raise Hands, Start Video, Share Computer Sound and Share Screen, etc.
- **Environment Requirement:**
 - (a) Quiet Location.
 - (b) Stable Internet Connection.
 - (c) Proper Lighting.
- **Test Session:**

On Dec. 11, there are test sessions. On that day, all the above functions will be taught including how to use ZOOM. If you don't know how to use, please do not worry. However, please do download ZOOM and log in the meeting room in advance, then, you can join the conference.
- **Voice Control Rules during the Presentation:**
 - (a) The host will mute all participants while entering the meeting.
 - (b) The host will unmute the speakers' microphone when it is turn for his or her presentation.
 - (c) Q&A goes after each speaker, the participant can raise hand for questions, the host will unmute the questioner.
 - (d) After Q&A, the host will mute all participants and welcome next speaker.



- **Conference Material:**
All presented papers will be issued with soft copy of conference materials: Receipt/Invoice, Participation and presentation certificate, etc.
- **Notes:**
(a) Log in the meeting room 15 minutes ahead of the session. (b) Learn the zoom skills. (c) Your punctual arrival and active involvement in each session will be highly appreciated. (d) The conference will be recorded; we will appreciate your proper behavior.

Contact Us

- Contact us by email: icabb@cbees.net or WeChat for any inquiries.



Daily Schedule

TIME ZONE

Kuala Lumpur - GMT+8

Test Session-Dec. 11, 2023 (Monday)

Zoom ID: 827 0878 3446, Link: https://zoom.us/j/82708783446	Duration
<ul style="list-style-type: none"> •Prof. Malarvili Balakrishnan •Prof. Fangxiang Wu •Prof. Tjokorda Gde Tirta Nindhia •Dr. Abdul Fatah A. Samad •Prof. Patrick Emmanuel Meyer •Assoc. Prof. Shweta Gupta 	10:00-11:00
Online Session 1 M0012, M0016, M0020, M2004-A, M0001, M0003, M2003	11:00-11:35
Online Session 2 M0021, M0024, M0011, M0009, M0025, M2002-A	11:35-12:05

Online Session-Dec. 12, 2023 (Tuesday)

Zoom ID: 827 0878 3446, Link: https://zoom.us/j/82708783446	Duration
Opening Remarks Prof. Malarvili Balakrishnan, Universiti Teknologi Malaysia, Malaysia	09:00-09:10
Keynote Speaker I Prof. Fangxiang Wu, University of Saskatchewan, Canada Speech Title: "Deep Learning for Biomarker Discovery"	09:10-09:50
Keynote Speaker II Prof. Tjokorda Gde Tirta Nindhia, Udayana University, Indonesia Speech Title: "Development Device for The Assessment of Asthma Using Newly Develop Respiratory CO2 Measurement Device Based on Diverting Method"	09:50-10:30
Group Photo&Break	
Invited Speaker I Dr. Abdul Fatah A. Samad, Universiti Teknologi Malaysia, Malaysia Speech Title: "Harnessing High-throughput Sequencing to Develop Drought-Resistant Rice"	10:45-11:10
Invited Speaker II Prof. Patrick Emmanuel Meyer, University of Liege, Belgium Speech Title: "All-Cause Mortality and Covid-19 Vaccinations in European Populations under 65 years old"	11:10-11:35
Invited Speaker III Assoc. Prof. Shweta Gupta, Woxsen University, India Speech Title: "Effect of Indian Food on Cognitive Disease Treatment"	11:35-12:00
Break	
Online Session 1-Bioinformatics and Neurocomputational Analysis M0012, M0016, M0020, M2004-A, M0001, M0003, M2003	13:30-15:15
Break	
Online Session 2-Medical Image Processing, Wearable Devices, and Computational Models in Biomedical Sciences M0021, M0024, M0011, M0009, M0025, M2002-A	15:30-17:00

Opening Remarks



09:00-09:10, Dec. 12, 2023 (Kuala Lumpur - GMT+8)

Zoom ID: 827 0878 3446, Link: <https://zoom.us/j/82708783446>

Prof. Malarvili Balakrishnan

Universiti Teknologi Malaysia, Malaysia



Biography

Associate Professor Ir. Dr. Malarvili BalaKrishnan have acquired more than 18 years of experience in the academics as well as involvements in the biomedical industry. She received Doctor of Philosophy (Medical Sciences Engineering) from The University of Queensland, Queensland, Australia in 2008. Currently, she is attached to School of Biomedical and Health Sciences Engineering, Universiti Teknologi Malaysia. She founded Biosignal Processing Research Group (BSP-RG) in 2010 within the faculty to champion the research, development and commercialization of Biomedical Instrumentation. Dr. Malarvili is actively involved in research related to medical monitoring devices that focuses on detection of neonatal seizure, sudden cardiac death, fetal heart rate monitoring , respiratory illness screening device and many more. To date, she has published more than 130 papers. She also received 10 international awards, 16 national awards and many more appreciation certificates. In addition, she has chaired sessions in prestigious conference, editorial board member and technical reviewer by IEEE, EMBS and medical society. She was recently selected for an 'Outstanding Woman in Health and Medical Sciences' award at the 4th Venus International Women Awards - VIWA 2019, Chennai, India.

Keynote Speaker I



09:10-09:50, Dec. 12, 2023 (Kuala Lumpur - GMT+8)

Zoom ID: 827 0878 3446, Link: <https://zoom.us/j/82708783446>

Prof. Fangxiang Wu

University of Saskatchewan, Canada

Speech Info.

Speech Title: Deep Learning for Biomarker Discovery

Abstract: A biomarker, or biological marker is a measurable indicator of some biological state or condition, which has a clinical role in diagnosis, treatment, and prognosis of diseases. Advances in the high throughput biotechnologies have resulted in the creation of massive medical data, which can be utilized for biomarker discovery. Deep learning is an artificial intelligence technique that can be used to design and train computer algorithms to learn from and act on data, especially for predicting biomarker-disease associations. In this talk, after some brief introductions to biomarkers and deep learning, I will mainly talk about several deep learning models that my group developed for predicting biomarkers such as miRNAs and piRNAs.

Biography

Dr. Fangxiang Wu is currently a full professor in the Departments of Computer Science, Biomedical Engineering, and Mechanical Engineering at the University of Saskatchewan. His research interests include Artificial Intelligence, Machine/Deep Learning, Computational Biology, Health Informatics, Medical Image Analytics, and Complex Network Analytics. Dr. Wu has published about 350 journal papers and more than 130 conference papers. His total google scholar citations are over 13000, h-index is 57. He is among top 2% world's scientists ranked by Stanford University. Dr Wu is serving as the editorial board member of several international journals (including IEEE TCBB, Neurocomputing, etc.) and as the guest editor of numerous international journals, and as the program committee chair or member of many international conferences. He is an IEEE senior member.

Keynote Speaker II



09:50-10:30, Dec. 12, 2023 (Kuala Lumpur - GMT+8)

Zoom ID: 827 0878 3446, Link: <https://zoom.us/j/82708783446>

Prof. Tjokorda Gde Tirta Nindhia

Udayana University, Indonesia



Speech Info.

Speech Title: Development Device for The Assessment of Asthma Using Newly Develop Respiratory CO₂ Measurement Device Based on Diverting Method

Abstract: This study explores the features (Area and Slope) of carbon dioxide (CO₂) waveform indices for various parts of each breath cycle. In short, the research shows some preliminary results in actual clinical circumstances that indicate that incorporation of CO₂ waveform indices into a lately developed device by our group which has the potential to be used as an indicator for severity and response in the continuous monitoring of asthmatic patients during an acute attack. Furthermore, the added advantages of this mechanism are that the monitoring device does not interfere with the ease of initiating therapy nor require active patient efforts. Further, the work now lies in recognition of proper waveform, implementation of the proposed indices into the real-time CO₂ measurement device, and the reporting of such indices in reproducible and an easily understood form that would significantly enhance the field of asthma monitoring. It is believed that this will assist a better sympathetic of asthma, improved management, and eventually a decrease in morbidity and mortality.



Biography

Tjokorda Gde Tirta Nindhia, Professor in Material Engineering at Program Study of Mechanical Engineering, Engineering Faculty, Udayana University, Jimbaran, Bali, Indonesia. Doctor Degree was granted from Gadjah Mada University Indonesia. Experienced in various Post Doc position such as at Muroran Institute of Technology Japan, Institute of Structure and Functional Ceramik (ISFK) Leoben Mining University Austria, Technical University of Vienna (TU WIEN) Austria, University Chemistry and Biochemical of Prague, Czech Republic, Michigan State University under Fulbright. Professor Nindhia was finalist at national best performance lecturer competition in 2013 and in 2017 awarded as rank III best performance lecturer in Indonesia by Ministry of Research Technology and Higher Education The republic of Indonesia. In 2016 The Government of Indonesia Granted Prof Nindhia an Award of Energy Initiative (Penghargaan Energi Prakarsa) and in 2016 received International Bern Rode Award from Association of South East Asia Uni Europa Networking (ASEA_UNINET). Prof Nindhia involving in research related with Material Engineering, Biomaterial, biomedical engineering, and various project in waste processing.

Invited Speaker I



10:45-11:10, Dec. 12, 2023 (Kuala Lumpur - GMT+8)

Zoom ID: 827 0878 3446, Link: <https://zoom.us/j/82708783446>

Dr. Abdul Fatah A. Samad

Universiti Teknologi Malaysia, Malaysia



Speech Info.

Speech Title: Harnessing High-throughput Sequencing to Develop Drought-Resistant Rice

Abstract: High-throughput sequencing is a groundbreaking tool in molecular biology, facilitating a comprehensive understanding of the genetic composition of various rice varieties and their responses to environmental stressors, particularly drought. This event aims to explore the innovative applications and methodologies of high-throughput sequencing techniques in identifying genes associated with drought resistance in rice. Six transcriptomic libraries were prepared from both control and drought-treated rice, with each group consisting of three biological replicates. Approximately 37 million reads were generated from the control group, whereas around 43 million reads were generated from the treated rice. Specifically, 2325 genes showed significant up-regulation, while 1635 genes were downregulated. Among the significantly regulated genes are those encoding regulatory and stress proteins. This data offers a comprehensive understanding of gene regulation in rice under drought stress, thereby providing a strategy to develop drought-resistant rice varieties through breeding programs.



Biography

Dr. Abdul Fatah A. Samad is a senior lecturer in the Department of Biosciences within the Faculty of Science at UTM. I hold a BSc (Hons) in Plant Biotechnology and a Doctor of Philosophy in Genetics from Universiti Kebangsaan Malaysia (UKM). Currently, I serve as the head of the Natural Product Research Group (NatPro) at the Faculty of Science, UTM. Additionally, I am a member of the American Nutrition Society (ASN). My work has been published in reputable journals, books, and chapters, and I have also served as a reviewer for several esteemed journals, including *Molecular Therapy Nucleic Acid*. To summarize my expertise, my research focuses on genetic regulation involving regulatory molecules such as miRNAs and transcription factors in plants, animals, and humans. My studies leverage high-throughput sequencing to identify significantly regulated genes and decode their functions.

Invited Speaker II



11:10-11:35, Dec. 12, 2023 (Kuala Lumpur - GMT+8)

Zoom ID: 827 0878 3446, Link: <https://zoom.us/j/82708783446>

Prof. Patrick Emmanuel Meyer

University of Liege, Belgium



Speech Info.

Speech Title: All-Cause Mortality and Covid-19 Vaccinations in European Populations under 65 Years Old.

Abstract: The question whether Covid-19 vaccination campaigns could have had an impact on excess deaths continues to be debated two years later. When the age-stratified (anonymized) vaccination status of deceased will be publicly available, the debate should come to an end. In the meantime, we discuss various statistical analyses that shed light on the matter. Using machine learning models, all-cause mortality and google trends, we explore various hypotheses that could explain the publicly available data.



Biography

Patrick Emmanuel Meyer received the Electromechanical Engineering degree and the Ph.D. degree in Machine Learning, both from the Université Libre de Bruxelles (2003-2008, ULB, Belgium). After postdoctoral research at the Computer Science and Artificial Intelligence Laboratory of the Massachusetts Institute of Technology (CSAIL, MIT, USA, 2010) and at the BROAD Institute (USA, 2011), he became in 2014 Professor at the Université de Liège (ULiege, Belgium) where he launched the Bioinformatics and Systems Biology Lab as well as the BioAutomation Lab in the Life Science Department. Among other scientific productions, he authored the open-source R packages INFOTHEO and MINET (Mutual Information Networks), the *Drosophila* modENCODE paper (Science 2010) and the European Excess Mortality Analysis of several books focused on the aftermath of the COVID-19 crisis. His interests cover variable selection, network inference and machine learning applied to phenotypic and omics data.

Invited Speaker III



11:35-12:00, Dec. 12, 2023 (Kuala Lumpur - GMT+8)

Zoom ID: 827 0878 3446, Link: <https://zoom.us/j/82708783446>

Assoc. Prof. Shweta Gupta

Woxsen University, India



Speech Info.

Speech Title: Effect of Indian Food on Cognitive Disease Treatment

Abstract: Indian Food helps in the treatment of Cognitive Diseases which in turn helps in the regeneration of brain cells and hence, secretion of chemicals like Serotonin and Dopamine which helps in the treatment of Cognitive Diseases. The death of certain brain cells results in the inhibition of the secretion of chemicals from brain cells required for the proper functioning of the body. India has a diverse variety of food and the process of preparing it involves various condiments and food in itself provides various chemicals needed for the proper function of the body. The deficiency of these chemicals results in various Cognitive Diseases. Various Bioinspired Algorithms will be used to demonstrate the regeneration of affected brain cells and recovery from Cognitive Diseases like Depression, Parkinson 's disease, and Epilepsy. Innovative computational approaches to model complex biomedical systems and analyze big bioinformatics Cognitive data. With the help of next-generation data analytics tools, the above concept will be demonstrated. Large heterogeneous biological and health data associated with related Cognitive Diseases will be analyzed and the process will be demonstrated.



Biography

Dr. Shweta Gupta is an Associate Professor at the School of Technology, Woxsen University, Hyderabad, Telangana, India. Her research focuses on solving societal problems, including Cognitive Diseases, Bioinformatics, Bionics, Artificial Intelligence, and Machine Learning. She is a Member of the Elsevier Advisory Panel and was also awarded as Senior Scientist for her exemplary work presenting her research work pertaining to Epilepsy at ICBBT2015, Singapore by the Department of Science and Technology, Government of India. She has filed Patents which have been accepted and commercialized as products. She became Guest Editor and Editor of the reputed USA Journals and Books at a very young age. She was awarded a Certificate of Merit for Outstanding academic performance and being among the top 0.1 percent of successful candidates of the C.B.S.E. Board in XII standard. She was a Speaker at ICBBT2023, Xian, China. She is an Expert member in various research schemes in the Department of Science and Technology (DST), Government of India especially for "Start-up India" an initiative launched by the Hon'ble Prime Minister of India and worked on various research projects and provided various consultancy solutions to Government of India and reputed Companies.

Online Session 1

Bioinformatics and
Neurocomputational Analysis

13:30-15:15, Dec. 12, 2023 (Tuesday), GMT+8

Zoom ID: 827 0878 3446
Link: <https://zoom.us/j/82708783446>

Session Chair: TBA

<p>S1-1</p>	<p>M0012 13:30-13:45</p>	<p>Discrete Wavelet Transform Based Multiview Screening Analysis of scRNA-seq Data Enhance Early-Stage Lung Adenocarcinoma Separation in Lung Tumor Microenvironment Ecotyping Daniel Li, Luke Peng, Yongzhong Zhao, Tong Liu, and Xiaodi Wang Western Connecticut State University, USA</p> <p>Abstract-Tumors can be viewed as ecosystems consisting of diverse cells within a host environment. Tumor microenvironment ecotyping can be investigated through gene expression at single cell level. In this study, we leverage the benefits of state-of-art analytic tools, discrete wavelet transforms (DWT) and Uniform Manifold Approximation and Projection (UMAP), in signal processing and apply them to a publicly available whole-genome single-cell RNAseq dataset of 58 lung adenocarcinoma and lung squamous carcinoma at various stages. We identified cell type composition clusters in both the untransformed and the discrete wavelet transformed (DWT-ed) data and performed pattern clustering analysis by UMAP. Our findings show that the DWT-based ordination plots provide a clear spatial separation between early adenocarcinoma tumors and advanced adenocarcinoma /squamous tumors. In contrast, traditional untransformed data-derived ordination plots fail to clearly separate early adenocarcinoma from advanced cancer groups. This difference in separation between DWT-ed and non-DWT-ed methods was confirmed by both independent DWT models by using approximation and detail components of DWT-ed data. Our DWT-based composition data also revealed novel cell type signatures between different tumor histologies, with higher significance compared to the non-DWT analysis. Taken together, our approach of utilizing DWT Multiview Screening Analysis of sc-RNAseq data enhances early-stage lung adenocarcinoma prediction, which adds value to future early diagnosis and precision treatment.</p>
<p>S1-2</p>	<p>M0016 13:45-14:00</p>	<p>Recognition of Escherichia Coli Promoters Based on Attention Mechanisms Dan Li, Yanchun Yuan, and Yuhan Li Changchun Institute of Education, China</p> <p>Abstract-Recognition of the promoter of Escherichia coli is significant due to it indirectly controls the activity of genes. Several computational promoter prediction methods have been proposed these years, and they have mainly focused on the recognition of the Escherichia coli $\sigma 70$ promoter. In this paper, we proposed a novel Escherichia coli</p>

		<p>promoter recognition method based on a deep-learning model, which can recognize all types of Escherichia coli promoters. The method encodes sequences using k-mers component information, DNA structure information, and a natural language feature. It extracts both the global information of the sequence and short sequence segments, and uses a convolutional neural network and multi-head self-attention network to extract the position information for promoter recognition. The model gets an accuracy of 90.07%, a sensitivity of 90.29%, a specificity of 89.86%, and a Matthews correlation coefficient score of 0.8021.</p>
S1-3	M0020 14:00-14:15	<p>A Wavelet-Based Approach Reveals Host-Cell-Type-Specific Multi-omics Networks in Inflammatory Bowel Disease Stephanie Chang, Adeethya Shankar, Yongzhong Zhao, Tong Liu, and Xiaodi Wang Massachusetts Institute of Technology, USA</p> <p>Abstract-The interplay between microbiome metabolites and human cells is crucial and mechanistically linked to human health and disease. Inflammatory bowel disease (IBD) is linked to microbiome metabolite and host gene expression. However, details of the microbiome and host interplays remain elusive. We carry out microbiome metabolome-wide and host transcriptome-wide association studies of IBD with microbiome metabolite targeted cell types discovery via leveraging the publicly available IBD data sets from Human Microbiome Project 2 (HMP2). By performing deconvolution on the transcriptomic data and applying discrete wavelet transform (DWT), we obtained cell type-metabolite correlations, which we visualize in the form of heatmaps and networks. We also carried out both targeted and untargeted approaches by mean of correlating the microbiome data matrix to host transcriptomic data. Given the limited sample size, in addition to visualizing a global picture of the interplay landscape between microbiome metabolites and host genes alongside distinct clusters of IBD and healthy controls with UMAP and t-SNE, we found a set of microbiome metabolites most likely linked to IBD and the transcriptomic signature of IBD. For the targeted approach, we also refer to the single-cell gene signature dataset, i.e., the MSigDB C8, uncovering a bile acid, namely, lithocholate, targeted cell types, including intestine lymphoid cells and enterocytes. Moreover, we utilized Mendelian Randomization causality tests with ursodeoxycholic acid (UDCA), RUNX1 gene, and IBD, resulting in a putative causality network of RUNX1, UDCA, and IBD. Taken together, our approaches shed light on the mechanistic interplay of microbiome metabolites and host cells in human health and disease.</p>
S1-4	M2003 14:15-14:30	<p>A Neurocomputational Analysis Review of Dorsolateral Prefrontal Cortex rTMS Treatments of Neurological Disorder Hany Alashwal, Julian Maciaszek, Dorota Frydecka, Blazej Misiak, and Ahmed A Moustafa United Arab Emirates University, UAE</p> <p>Abstract—Repetitive transcranial magnetic stimulation (rTMS) to the dorsolateral prefrontal cortex (DLPFC) has been used as a treatment for several psychiatric and neurological disorders, including depression, bipolar disorder, anxiety, eating disorders, obsessive</p>



		<p>compulsive disorder, schizophrenia, addiction and Parkinson’s disease. However, the precise mechanism of action of DLPFC rTMS and how it translates to the effectiveness of treatment of these disorders is not fully understood. In this study, we provide a review of computational explanations of how DLPFC rTMS may treat several clinical disorders. The review show that DLPFC rTMS can ameliorate several symptoms in different psychiatric and neurological disorders via the following mechanisms of action: (a) modulating the activations of several cortical and subcortical areas, (b) increasing dopamine levels in both cortical and subcortical structures, and (c) modulating connectivity among several brain areas. In addition, we discuss future directions on experimental and computational studies of DLPFC rTMS. Specifically, future computational modelling should take into account the multi-dimensional nature of DLPFC rTMS effect on the brain and behaviour.</p>
<p>S1-5</p>	<p>M2004-A 14:30-14:45</p>	<p>Classification of Tumor Metastasis mRNA Data by Using Quantum SVM Algorithm Aninda Astuti, Venugopal Reddy Mekala, Ezra Wijaya, and Kalok Ng Asia University, Taiwan</p> <p>Abstract—Metastasis is a major cause of cancer mortality and requires early and accurate detection of biomarkers foreffective treatment. Messenger-RNAs (mRNAs) have been used as prognostic biomarkers in various cancers becausetheir abnormal expression can influence cancer development. Support vector classifier (SVC) is a machine learningalgorithm that performs well in many classification tasks. Quantum-enhanced SVC (QSVC) is a novel algorithm thatcould offer higher classification accuracy in a shorter time when quantum computing becomes more advanced.We retrieved the kidney cancer (KIRC) mRNA expression from the Xena database. Then, we apply PCA to the KIRCmRNA expression data that show differential expression and reduce the dimensionality to 9-12 principal components.We also deal with the data imbalance problem (unequal number of samples for M0 and M1 classes). Next, we use theneural network algorithm to train the input data and use SVC and QSVC as classifiers to predict the tumor metastasisstatus of the KIRC patients. We optimize both SVC and QSVC and compare their performance on different dimensions.We find that QSVC performs better on dimensions 9 and 10, while SVC performs better on dimensions 11 and 12. Inthis work, we show that using neural networks to preprocess the input data and applying QSVM can improve theclassification performance compared to SVM under certain conditions.</p>
<p>S1-6</p>	<p>M0001 14:45-15:00</p>	<p>A Multiclass Method for Selecting Differentially-Expressed and Cell-Type-Discriminative Genes from Scrna-Seq Data Grace Yee Lin Ng, Chia Sui Ong, and Shing Chiang Tan Multimedia University, Malaysia</p> <p>Abstract-Log fold change (LFC) is a common measure used in differential expression analysis to examine the differences in gene expression between two experimental classes, as in the data generated by microarray or bulk RNA sequencing. Many single-cell RNA-seq (scrna-seq) data are labelled with three or more classes in terms of cell types, cell states, or cell stages. Several differential expression methods have been introduced to select differentially expressed genes (DEGs) among different classes in scrna-seq data while accounting for the technical and biological variations. However,</p>



		<p>these methods are only applicable to perform comparisons between two classes. Methods to select DEGs with multiclass comparisons have also been introduced in the literature, but different measures are used instead of LFC. Thus, this study aims to impose the impactful LFC measure as a multiclass DEGs selection method. The majority voting concept is incorporated to aggregate the DEGs from every pairwise class comparison. Cell type classification using the selected genes has been performed to evaluate and validate the genes selected by the multiclass LFC method. The results show that the proposed method is capable of reducing the number of genes to as low as 26.05% of the initial scRNA-seq data. Moreover, the selected genes can classify cells into their respective cell types more accurately (an accuracy of 0.9425) as compared to the existing scRNA-seq gene selection method (an accuracy of 0.9137).</p>
<p>S1-7</p>	<p>M0003 15:00-15:15</p>	<p>Predicted Drug-Drug Interactions in Diabetes Mellitus Rashini Maduka, Rupika Wijesinghe, and Ruvan Weerasinge University of Colombo School of Computing, Sri Lanka</p> <p>Abstract-Drug-drug interactions (DDIs) can happen when two or more drugs are taken together. Today DDIs have become a serious health issue due to adverse drug effects. In vivo and in vitro methods for identifying DDIs are time consuming and costly. Therefore, in silico based approaches are more popular in DDI identification. Most machine learning models of DDI prediction use chemical and biological properties of drugs as features. However, some properties of drugs are not available and costly to extract hence automatic feature engineering of drugs is important. Furthermore, people who suffer from diabetes mostly suffer from some other diseases as well and take more than one medicine together leading to adverse drug effects in diabetic patients. In this study we present a model with a graph convolutional auto encoder and a graph decoder using a dataset from DrugBank version 5.1.3 to predict DDIs. Main objective of the model is to identify unknown interactions between antidiabetic drugs and the drugs taken by diabetic patients for other diseases. We considered automatic feature engineering and used Known DDIs only as the input for the model. Our model has achieved 0.86 in AUC and 0.86 in AP.</p>

Online Session 2

Medical Image Processing, Wearable Devices, and Computational Models in Biomedical Sciences

15:30-17:00, Dec. 12, 2023 (Tuesday), GMT+8

Zoom ID: 827 0878 3446
Link: <https://zoom.us/j/82708783446>

Session Chair: Assoc. Prof. Shweta Gupta, Woxsen University, India

<p>S2-1</p>	<p>M0021 15:30-15:45</p>	<p>Impact of Training Data Quality on Deep Speckle Noise Reduction in Ultrasound Images Fajar Astuti Hermawati, Elsen Ronando, and Dwi Harini Sulistyowati Universitas 17 Agustus 1945 Surabaya, Indonesia</p> <p>Abstract-Speckle noise reduction is an essential step in ultrasound image analysis. One of the challenges in speckle noise reduction is removing noise without significantly losing image detail. Various studies have been conducted using image processing and deep learning approaches. This research offers a simple framework using a deep learning method, which shows that the quality of the images used in the training process influences the performance of the denoising results using the trained network. The training data in the form of ultrasound images in this study was processed separately using various speckle noise reduction methods. We also compare with one of the pre-trained networks, namely denoising convolutional neural networks (DnCNNs). The research shows that denoising results using training data processed using the hybrid speckle noise method provide high image edge preservation performance. The tests in MATLAB reveal a significant reduction in the speckle noise of the ultrasound image, with a peak signal-to-noise ratio of 20.68 dB, a mean structural similarity index measure (MSSIM) of 0.83, and Pratt's Figure Of Merit metric indicating an edge preservation index value reaching 91.76%. Reducing speckle noise using this approach takes less time, ensuring well-maintained edge information and clear visibility of image details, making it applicable for ultrasound diagnosis.</p>
<p>S2-2</p>	<p>M0024 15:45-16:00</p>	<p>Classification of Capnogram for Respiratory Assessment Using Entropy Measures M. B. Malarvili, Mushikiwabeza Alexie, and K Thulasi Universiti Teknologi Malaysia, Malaysia</p> <p>Abstract-Capnography reveals significant information useful for the assessment of respiratory conditions. Previous studies have analysed quantitatively the shape of the capnogram waveform and proposed various features to differentiate asthma from normal subjects while also classifying asthma severity levels. However, those indices are not always clearly defined in deformed capnograms. Therefore, this research presents two parameters for the characterization of capnogram waveforms. Those parameters include two types of entropy measures: approximate entropy (ApEn) and sample entropy (SampEn). Entropy measures were used for the analysis of the regularity of capnogram waveforms. This research makes use of the CO2 samples recorded from 36 patients with respiratory diseases (i.e., 12</p>



		<p>asthmatics, 12 COPD, and 12 pulmonary edema patients). The results show that pulmonary edema recordings demonstrated higher ApEn and SampEn values compared to asthma and COPD. Increased values of entropy measures are associated with higher irregularities in pulmonary edema capnograms. This research provides features for differentiating capnogram waveforms, which may serve clinically for the assessment of respiratory diseases.</p>
S2-3	M0011 16:00-16:15	<p>COViT: Convolutions and ViT based Deep Learning Model for Covid19 and Viral Pneumonia Classification using X-ray Datasets Athar Shahzad Fazal, Somaiya Khan, and Ali Khan Nottingham Trent University, UK</p> <p>Abstract-Artificial Intelligence based Covid19 through X-ray scans has revolutionized early diagnosis and treatment since the outbreak. There have been remarkable achievements in the research of Covid19 from Normal or other Pneumonia X-ray image classification using a convolutional neural network (CNN). CNN alone face problems in describing low-level features and can miss important information. Moreover, accurate diagnosis is important in the medical field with minimum false alarms. To answer the issue, the researchers of this paper have turned to self-attention mechanism inspired by the ViT, which has displayed state-of-the-art performance in the classification task. The proposed COViT method uses convolutions of 3×3 instead of patch embedding as in ViT, then alternate self-attention and MLP with hardswish function are added, and finally, MLP head is proposed which has average pooling, fully connected (FC) layer with ReLU function and kernel L2 as a classifier which improves the accuracy. Exhaustive experiments are carried out on three datasets. We have only considered Covid19 and Viral Pneumonia classes for our problem. The proposed model has achieved 98.98% classification accuracy on dataset1, 99.50% on dataset2 and 99.18% on dataset3, which validates the efficiency of COViT The proposed COViT which uses self-attention and CNN shows superiority over other SOTA models and has better accuracy than the methods in the literature.</p>
S2-4	M0009 16:15-16:30	<p>Design of a Pulsed-Wave Doppler Ultrasound Blood Flow Detector Based on a Programmable System-on-Chip (PSoC) Demetrio Fabian Garcia Nocetti, Pedro Jesus Acevedo Contla, Martin Fuentes Cruz, and Adalberto Joel Duran Ortega Universidad Nacional Autónoma de México, Mexico</p> <p>Abstract-Doppler ultrasound systems are medical diagnostic equipment that measure blood flow in veins and arteries. These systems are widely used because they are considered non-invasive. This paper describes the design of a Pulsed Wave (PW) Doppler ultrasound blood flow detector for a bi-directional system, implemented in a Programmable System-on-Chip (PSoC-5LP) device that operates at 8MHz. In the PSoC-5LP, control signals, amplification, filtering, analog to digital conversion are implemented, and the digitized blood flow Doppler signals are transferred to a Personal Computer via an USB data communication port, for further processing in order to generate the Doppler spectra waveform. The transmission driver, the RF amplifier and the mixers for quadrature demodulation are implemented using external components.</p>



		<p>The implemented Doppler detector is reconfigurable; parameters of the system can be programmed, such as: operation frequency of the transducer, quadrature signals for demodulation, repetition frequency, number of pulses of the transmission burst and receiver enable pulse, which allows measuring a vessel at a certain depth.</p>
S2-5	M0025 16:30-16:45	<p>IoT-Enabled Wearable Prototype: Detecting Signs of Depression K Thulasi, Sumathi Balakrishnan, Yue Lu, Rattana Monpreeyadee, Syeda Rahmathunnisa Fatima, Mohammad Izhar Shafiq Rosli, Qi Wei Giok, and M.B Malarvili Universiti Teknologi Malaysia, Malaysia</p> <p>Abstract-The emergence of the Internet of Things (IoT) offers new possibilities for mental health care, including remote monitoring and early detection of depressive symptoms. This paper presents the design and development of "MindTrack", a smart monitoring system aimed at addressing the long-term treatment and monitoring challenges of depression. MindTrack is composed of smart wearable devices integrated with a real-time monitoring desktop application. It passively monitors patients' behavioral and physiological data, enabling objective assessment of depressive symptoms. The proposed architecture combines ADCs and WIFI IEEE 802.11ah protocol for efficient data transmission, incorporates edge computing and cloud connectivity for storage and analysis, utilizes various sensors in the perception layer to track the patient's well-being, and includes a patient-oriented smart wearable device operating system and a desktop application for psychologists to monitor and aid in treatment planning. None of the existing studies utilized a comprehensive combination of sensors specifically tailored for monitoring MDD patients. Moreover, there's limited focus on efficient power resources and security risk management. Hence, this paper proposes Mindtrack as a reliable and usable solution for improving specialized mental health care and addressing the challenges associated with MDD treatment and monitoring.</p>
S2-6	M2002-A 16:45-17:00	<p>The Study of Non-Invasive Blood Information Measurement and Monitoring Method via Wearable MWPPG Device Cheng Chun Chang, Chi Fu Chung, Xiang Jun Zhang, and Po Wen Lu National Taipei University of Technology, Taiwan</p> <p>Abstract—In recent years, with the proliferation of wearable devices, wearable watches and wristbands capable of detecting physiological information have been considered indispensable tools of modern civilization. These wearable devices enable individuals to monitor real-time physiological data such as heart rate, blood pressure, and blood oxygen concentration to maintain their health. However, there is currently no non-invasive method available on the market for measuring blood-related information within the human body. Therefore, this study aims to investigate whether wearable devices can provide a non-invasive means of acquiring blood-related information through related signal processing algorithms and neural network models. The research is divided into three main components: the development of a non-invasive wearable device, the collection of blood information in a clinical setting, and the exploration of one-dimensional signal algorithm models. Currently, we have collected blood-related data at the hospital using our self-developed MWPPG measurement device. We have also trained artificial intelligence models for various blood</p>



		<p>parameters. The accuracy rate for blood glucose is seventy percent, while for hemoglobin, platelet count, sodium ion concentration, calcium ion concentration, and total protein content, the accuracy rate is approximately sixty to seventy percent.</p>
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