Day 1 - Wednesday August 20th, 2025

08:20 | 19:00	Registration			
10:00 | 12:00	**Tutorial for Spatial Transcriptomics Data Analysis** Chairs: Shinn-Ying Ho and Tzong-Yi Lee ATI Room (EE building 1F)			
12:00 | 13:00	Lunch Break L.Y Room (EE building B1F)			
13:00 | 14:40	**Technical Session I: Bioinformatics** Chairs: Tzong YI Lee Room A (EE building 1F 92185)	**Technical Session II: Deep Learning** Chairs: Pang-Wei Tsai Room B (EE building 1F 92177)	**Special Session I** **i: Legal and Ethical Aspects of AI systems for biomedical** **ii: AI/CI for Biomedical Applications-1** **iii: smart circuit systems & applications** Chairs: Marco Nobile (i), I-Fang Chung (ii), Chun-Hung Yang (iii) Room C (EE building 1F 92171)	**CIS Student Grand Competition** Room D EE building 2F 92225
14:40 | 15:00	Coffee Break			
15:00 | 16:40	**Technical Session III: Multi-omics** Chairs: Andrea Tangherloni Room A (EE building 1F 92185)	**Technical Session IV: Graph Models / Network Analysis** Chair: Tzong YI Lee Room B (EE building 1F 92177)		
16:40 | 16:50	Break			
16:50 | 18:30	**Short Papers Session** Chair: I-Fang Chung ATI Room (EE building 1F)			
18:30 | 20:00	**Welcome Reception** Hall (EE building 1F)			

Day 2 - Thursday August 21st, 2025

08:20 | 17:20	Registration	
09:00 | 09:20	**Opening Ceremony** ATI Room (EE building 1F)	
09:30 | 10:30	**Keynote I** **Building predictive models with AI in radiology and digital pathology** Chair: Pau-Choo Chung Speaker：Anne Martel, Professor, University of Toronto ATI Room (EE building 1F)	
10:30 | 10:50	Coffee Break	
10:50 | 11:50	**Keynote II** **Computational Medicine for Mental and Physical Health** Chair: Tayo Obafemi-Ajayi Speaker：Rose Faghih, Associate Professor, New York University ATI Room (EE building 1F)	
11:50 | 13:10	Lunch Break L.Y Room (EE building B1F)	BBTC Meeting Meeting Room (EE building 4F 92453)
13:10 | 14:50	**Technical Session V: Machine Learning-1** Chair: Vassilis Plagianakos Room A (EE building 1F 92185)	**Special Session II: AI/CI for Biomedical Applications-2** Chair：Emily Chia-Yu Su Room B (EE building 1F 92177)
14:50 | 15:00	Coffee Break	
15:00 | 15:40	**Invitation talk** **Towards Wider Adoptions of AI/CI in the Biomedical Field - Infrastructure Building in NCHC** Chair: Pau-Choo Chung Speaker：Chau Lyan Chang, Director General, NCHC ATI Room (EE building 1F)	
15:40 | 17:10	**Panel session: Pros and Cons of AI in Medicine** Chairs: Jennifer Hallinan, Sheridan Houghten Panelists: Anne Martel, Anil Wipat, Kuo-Sheng Cheng, Lai Chao-Han, Rose Faghih, Tayo Obafemi-Ajayi ATI Room (EE building 1F)	
18:00 | 20:30	**Banquet** 3rd Floor, Cheng Kung Function Room, Shangri-La Far Eastern Plaza, Tainan	

Day 3 - Friday August 22nd, 2025		
08:20 | 12:00	Registration	
9:00 | 10:00	**Keynote III (Virtual)** **Advancing Biomedical Discovery in a Data-Driven AI Era** Chair: Pau-Choo Chung Speaker：Yang C. Fann, Director, National Institutes of Health ATI Room (EE building 1F)	
10:00 | 10:20	Coffee Break	
10:20 | 12:00	**Technical Session VI: Machine Learning-2** Chairs: Pang-Wei Tsai Room A (EE building 1F 92185)	**Special Session III** **i: Next-Generation ECG-Based Sleep Apnea Detection** **ii: Computational Intelligence for Brain-Computer Interfaces** Chairs: Kang-Ping Lin (i), Li-Wei Ko (ii). Room B (EE building 1F 92177)
12:00 | 12:40	Lunch Break L.Y Room (EE building B1F)	
12:40 | 12:50	Move to Bus	
12:50 | 17:00	**Social event：Tainan City tour**	
17:00 | 17:10	Move to Bus	
17:30 | 19:30	Dinner Chingping Seafood Restaurant, Tainan	

Return Bus Drop-off Points After Dinner:

1. Tainan Train Station (Rear Exit) / Shangri-La Far Eastern Plaza
2. National Cheng Kung University, Department of Electrical Engineering (Conference Venue)
3. Optional: Tainan High-Speed Rail Station (stop will only be made if there are enough passengers)

Day 1 - Wednesday August 20th, 2025

08:20	Hall	Registration
10:00	ATI Room	**Tutorial for Spatial Transcriptomics Data Analysis** Chairs: Shinn-Ying Ho and Tzong-Yi Lee
12:00	L.Y Room	Lunch Break
13:00 | 14:40	Room A (92185)	**Technical Session I: Bioinformatics**
	[28]	**iACP-KAN: Identifying Anticancer Peptides using Kolmogorov-Arnold Network** Hoang Nguyen, Quang Trinh, Huu-Thanh Duong, Trang Do and Binh Nguyen
	[53]	**BacCal GUI: Streamlining Virus Titration Calculations** Meng-Chi Chung, Tzong-Yuan Wu and Li-Ching Wu
	[76]	**AI-Enhanced MALDI-TOF MS Analysis for Important Peaks on Predicting Ciprofloxacin Resistance across Different Gram-Negative Bacteria** Hsin-Yao Wang, Chia-Ru Chung, Wen-Rui Zhang, Li-Ching Wu, Justin Bo-Kai Hsu, Jang-Jih Lu and Jorng-Tzong Horng
	[79]	**miSAM: Robust MicroRNA Expression Estimation Using Bi-Objective Evolutionary Learning Algorithm in Cancer Transcriptomics** Yann-Lin Ho, Shinn-Ying Ho and Tzong-Yi Lee
	[25]	**Integrative Framework for Functional analysis of multiple Traditional Chinese Medicines based on transcriptome-driven systems biology and supervised learning strategy** Yun Tang, Chia-Ru Chung, Hsi-Yuan Huang, Yang-Chi Dung Lin and Hsien-Da Huang
	[98]	**Let's Talk Bout Mutation: Evolutionary Programming for DNA Sequences** James Sargant, Michael Dubé, Sheridan Houghten and Steffen Graether
	Room B (92177)	**Technical Session II: Deep Learning**
	[03]	**An Endoscopic Lesion Segmentation Improvement** Viet Dung Nguyen, Thi Khanh Linh Do, Manh Duy Tran, Tam Anh Bui, Minh Duc Phan, Phuc Ngoc Pham and Nguyen Khang Ho
	[31]	**Continual Learning for Weakly-Supervised Histopathology Tissue Segmentation** Wei Hua Li, Huei-Fang Yang and Chu-Song Chen
	[33]	**The Brain Watching Itself: Identifying Brain Tumors with Spiking Neural Networks** Namita Achyuthan and Bhaskarjyoti Das
	[48]	**Helicobacter Pylori Infection Diagnosis from Endoscopic Images via Multi-Class Token based Multiple Instance Learning** Wei-Te Ting, Yu-Ching Tsai, Chun-Rong Huang, Hsiu-Chi Cheng and Bor-Shyang Sheu
	[58]	**Leveraging Diffusion-Based Models for Data Augmentation in Maternal-Fetal Ultrasound Classification** Shi Hao Wong and Tsung-Lu Michael Lee
	[94]	**Improving the Efficiency and the Validity of Molecular Transformers** Leone Bacciu, Matteo Grazioso, Silvia Multari, Francesca Grisoni, Angelica Mazzolari and Marco S. Nobile

	Room C (92171)		**Special SessionI** **i: Legal and Ethical Aspects of AI systems for biomedical** **ii: AI/CI for Biomedical Applications-1** **iii: smart circuit systems & applications**
	i	[6]	**Synthetic data in AI-powered medical devices – the EU regulatory implications** Tomasz Braun and Dominika Harasimiuk
		[47]	**Enhancing Clinical Decision-Making: Integrating Multi-Agent Systems with Ethical AI Governance** Ying-Jung Chen, Ahmad Albarqawi and Chi-Sheng Chen
	ii	[39]	**Towards Accurate Identification of Anti-Hepatitis C Peptides Using Stack-AHCP** Lantian Yao, Chang Liu, Jiahui Guan, Peilin Xie, Zhihao Zhao, Xingchen Liu, Yilin Guo, Yulan Liu, Yunlu Peng, Ying-Chih Chiang and Tzong-Yi Lee
		[64]	**GENESIS: Generating scRNA-Seq data from Multiome Gene Expression** Simone G. Riva, Brynelle Myers, Francesca M. Buffa and Andrea Tangherloni
		[72]	**Inductive models for structured output prediction of lncRNA-disease associations** Felipe Kenji Nakano, Livia Bertoni, Ricardo Cerri and Celine Vens
	iii Short paper	[117]	**The Impact of Min-Max and Z-Score Normalization on Prostate MRI Image Segmentation** Chun-Hung Yang and Hui-Yen Lin
		[118]	**Comparison of Prostate Region Segmentation in 2D MRI** Chun-Hung Yang and Jiu-Wei Liu
		[120]	**Virtual Healing: Counterfactual X-Ray Images Using Classifier-Free Guided Diffusion Models** Daniel Kong, Qi-Xian Huang, Hung-Min Sun, Wei-Hsin Yuan, Kuan-Yuan Chen and Wen-Ho Juang
		[124]	**Robust Blood Vessel Feature Extraction using Multispectral Imaging** Shih-Yu Chen, Siang-Yu Huang and Chun-Wei Huang
		[125]	**Machine Learning-Based Classification of CAA and Non-CAA for ICH Patients Guan-Ying** Wu, Chih-Ching Tsai, Bo-Ching Lee, Wen-Ho Juang, Chun-Hung Yang and Yung-Ming Kuo
	Room D (92225)		**CIS Student Grand Competition (13:00-17:00)**
14:40			Coffee Break
15:00 | 16:40	Room A (92185)		**Technical Session III: Multi-omics**
		[21]	**REnformer, a single-cell ATAC-seq predicting model to investigate open chromatin sites** Simone Giovanni Riva, Edward Sanders, Tom Wilson, Nicolò Stranieri, E. Ravza Gür, Matthew Baxter and Jim R. Hughes
		[75]	**EL-DRP: An Evolutionary Learning-Based Multi-Omics Framework for Drug Response Prediction with Interpretable Biomarker Selection** Yann-Jen Ho, You Sheng Paik, Yu-Ruo Chen, Yun Tang, Shinn-Ying Ho and Tzong-Yi Lee
		[86]	**Self-Attention Enhanced Deep Learning Models for Immune Cell Deconvolution from Bulk RNA-Seq** Chia-Ru Chung, Yen-Lin Chen, Yun Tang, Bo-Kai Hsu, Li-Ching Wu, Tzong-Yi Lee and Jorng-Tzong Horng
		[01]	**Decoding Aging: Multi-Omics Insights into Oxidative Stress, Mitochondrial Dysfunction, and Cellular Senescence in Fibroblasts** Rajarshi Mandal, Ning Xie and Gil Alterovitz
		[57]	**Explainable AI-Enhanced Kinase Activity Profiling Through Phosphoproteomics** Chia-Ru Chung, Ming-Feng Ho, Yun Tang, Li-Ching Wu, Justin Bokai Hsu, Tzong-Yi Lee and Jorng-Tzong Horng
		[78]	**Integrative Multi-Omics Prognostic Modeling of Glioma Recurrence Using Variational Autoencoder and Similarity Network Fusion** Phuong Lam Tran, Yun Tang, Justin Bokai Hsu and Tzong-Yi Lee

	Room B (92177)	**Technical Session IV: Graph Models / Network Analysis**
	[09]	**Spiking Neural Networks for Mental Workload Classification with a Multimodal Approach** Jiahui An, Sara Fabrikant, Giacomo Indiveri and Elisa Donati
	[54]	**SDPA++: A General Framework for Self-Supervised Denoising with Patch Aggregation** **Huy Nguyen, Triet Dao, Chau Truong and Cuong Nguyen**
	[55]	**Leveraging Graph Information for Spatially Informed Patient Data Analysis with GIST** Gospel Ozioma Nnadi, Vincenzo Bonnici, Simone Avesani, Eva Viesi and Rosalba Giugno
	[77]	**TPP Riboswitch Design Using Secondary-Structure-Informed Geometric GNN** Pradeepthi Rangineni, Nitin Manne, Nick Paradis, Ali Tekeoglu, Chen-Fu Chiang and Amirhossein Manzourolajdad
	[45]	**CombDNF: Disease-specific drug combination predictions with network-based features on clinically validated data** Pauline Hiort, Bernhard Y. Renard and Katharina Baum
	[62]	**GSDeep-DTA: A Hybrid Graph and Sequence-based Deep Learning Framework for Robust Drug-Target Affinity Prediction** Dileepa Samankula, Joanne Harvey and Binh Nguyen
16:40		Break
16:50 | 18:30	ATI Room	**Short Papers Session**
	[02]	**Can Knowledge Be Distilled from Single-cell Large Foundation Models for Efficient Cell-type Annotation?** Haohuai He, Zhi-An Huang, Jibin Wu and Kay Chen Tan
	[100]	**Segmentation and Localization of Normal and Fractured Vertebrae in Spine CT Images** Chuan-Yu Chang, Min-Hong Hsieh and Bo-Yan Lin
	[103]	**Adapting graph representation learning for cancer driver gene prediction** Thi Thuy Duong Vu and Girum Fitihamlak Ejigu
	[104]	**RGB-D Nutrient Prediction Based on Fused Cross-Modal Attention and Progressive Learning** Chao-Yang Lee and Ting-Wei Wu
	[105]	**Using Non-invasive Parameters for Bladder Outlet Obstruction Prediction by Machine Learning** Chien-Cheng Lee, Chung-You Tsai, Yun-Ci Sie, Jing-Hui Tian and Hann-Chorng Kuo
	[106]	**Low-Level Feature Integration for Robust Federated Learning in Non-IID Medical Image Analysi** Yu-Ping Gao and Pau-Choo Chung
	[107]	**Effect of Initial Weights on CT Image Registration** Rojean Noorinayer, Stephen Chen, Michael Hardisty and Teodora Vujovic
	[108]	**An Interpretable Domain Adaptation Framework using Transformers for Drug Response Prediction** Chi-Tang Wang, Yu-Kai Chiu and I-Fang Chung
	[110]	**Enhancing Large Pathology Foundation Models with Multi-Scale and Multi-Modal Integration for Cancer Prognosis Prediction** Po-Hsun Li and Yen-Hua Huang
	[112]	**A Framework for Multi-Session Virtual Psychological Counseling Syetem based on LLM** Chung-Chian Hsu, Cheng-Han Lu, Yong-Jin Chen, Yu-Huan Hsueh, Ke-Shun Chen, Ting-Yun Ke, Tin-Kwang Lin and Yu-Hsiang Huang

		[113]	**Virtual Healing: Counterfactual X-Ray Images Using Classifier-Free Guided Diffusion Models** Daniel Kong, Qi-Xian Huang, Hung-Min Sun, Wei-Hsin Yuan, Kuan-Yuan Chen and Wen-Ho Juang
		[119]	**Impact of Cross-Subject Distribution Shifts on Glucose Prediction Using Wearable Data** Nhung Huyen Hoang
		[121]	**Enhancing Gene Regulatory Network Predictions by PageRank-Weighted Graph Neural Networks** Bo-Han Wu
		[123]	**Pyramid-Pooling Multi-Resolution Learning for Automatic Pneumothorax Segmentation and Its Verification on NCKU Hospital's Dataset** Chian C. Ho and Xin-You Liao
		[126]	**Exploring Generative and Cold Adapted Amylases using VAE encoded Evolutionary Landscapes** Jennifer Hallinan and Anil Wipat
		[127]	**The Design of Intelligent Electronic Fence System with YOLOv8-Pose and Homography Algorithm** Ching-Lung Chang
		[128]	**A Comparative Analysis of Machine Learning Algorithms for Wheat Disease Classification in Taiwan Using the Orange Data Mining Tool** Jie-Long Chen, Ching-Chung Chen and Arthur Chang
		[129]	**Fluorescent-Stained Mycobacterium Detection in Sputum Smears through Computer-Assisted Analysis** Pei-Ju Yen, Ching-Fen Jiang and Ya-Ling Huang
		[130]	**Identifying Viral Adaptation Signatures Using Explainable AI in Influenza A** Allison Hsu and Yingfeng Hsu
		[131]	**Identification of Phosphorylation Sites as Predictive Biomarkers of Drug Response and Construction of Prediction Models** Chih-Yun Lin, You-Sheng Paik and Tzong-Yi Lee
		[132]	**CysPTM-GPT: A Generalized Prompt-Based Model for Predicting Diverse Cysteine Modifications** Chun-Kai Wu, Yen-Peng Chiu, Yun Tang and Tzong-Yi Lee
		[133]	**Unveiling Spatial Heterogeneity and Tumor Microenvironment of Head and Neck Squamous Cell Carcinoma** Yun-Ting Huang, Paik You Sheng, Yun Tang and Tzong-Yi Lee
		[134]	**Gut Microbiome Analysis for Predicting Cognitive Function in Older Adults: A Multi-Level Biomarker Discovery Approach** Ling-Yen Kung, Guan-Ting Chen, Yun Tang and Tzong-Yi Lee
		[135]	**F2P-DTI: A Feature Fusion and Prediction Framework for Drug-Target Interactions via Autoencoder and Multi-Layer Perceptron** Yu-Zhen Chen, Yen-Peng Chiu, Yun Tang and Tzong-Yi Lee
18:30	Hall		**Welcome Reception**

Day 2 - Thursday August 21st, 2025

08:20	Hall	Registration
09:00	ATI Room	**Opening Ceremony**
09:30	ATI Room	**Keynote : Building predictive models with AI in radiology and digital pathology** Speaker：Prof. Anne Martel
10:30		Coffee Break
10:50	ATI Room	**Keynote : Computational Medicine for Mental and Physical Health** Speaker：Prof. Rose Faghih
11:50	L.Y Room 4F Meeting Room	Lunch Break BBTC Meeting
13:10 | 14:50	Room A (92185)	**Technical Session V: Machine Learning-1**
	[12]	**Short-term impacts of weather conditions on biomarkers among urban adults in Greece** Katerina Tsiaktani, Panagiotis Anagnostou, Sotiris K. Tasoulis, Spiros V. Georgakopoulos, John A. Gittings, Dionysios E. Raitsos, Athanasia Sergounioti and Vassilis P. Plagianakos
	[16]	**Keypoint-Guided Ophidian Transformation for String-Shaped Data Augmentation** Tszyi Kwok, Brendan Park, Katharine Yagi, Anne Yagi, Chunsheng Yang, Min Liao and Yifeng Li
	[60]	**Alzheimer's Disease Risk Prediction in the Elderly: A Machine Learning Approach Combining Clinical Characteristics and Polygenic Risk Scores** Bo-Kai Hsu, Cheng-Yang Lee, Jia-Ruey Tsai, Vijesh Kumar Yadav, Chuan Huang and Tzu-Hao Chang
	[61]	**Development of a Generalized Model for Alzheimer's Disease Risk Prediction in the Taiwanese Population** Bo-Kai Hsu, Cheng-Yang Lee, Jia-Ruey Tsai, Vijesh Kumar Yadav, Chuan Huang and Tzu-Hao Chang
	[63]	**Balanced Benchmarking of Zero-Shot and RAG Approaches for Biomedical Term Normalization** Thanh Son Do, Daniel Hier and Tayo Obafemi-Ajayi
	Room B (92177)	**Special SessionII: AI/CI for Biomedical Applications-2**
	[44]	**SHAP-Driven Deep Learning Identifies Pre-Symptomatic Influenza A Biomarkers: An Explainable AI Framework for Clinical Genomics** Tsung-Hsien Lin, Anna Zan, Zhi-Jian Cheng, Zhong-Ru Xie and Kuan Y. Chang
	[67]	**Knowledge-Enriched Cell-Type Annotation in Single-Cell Transcriptomics via LLM Embeddings** Andrea Fabbricatore, Francesca M. Buffa and Andrea Tangherloni
	[71]	**Deep Learning-Based Object Detection System for Vocal Cords in Laryngoscopy Images** Ying-Chang Wu, Sheng-Fu Liang, Cheng-Ming Hsu and Ming-Chi Cheng
	[92]	**Explainable Machine Learning for Failed Labor Induction Prediction Using Nationwide Insurance Data** Daniel C.A. Nugroho, Septian D. Periska, Justinus A. Putranto, Jimmy I. Gunawan, Muhammad S. Muhtar, Jason C. Hsu, Yuan-Chii G. Lee and Emily Chia-Yu Su
	[93]	**Assessing Cardiac Functionality by Means of Interpretable AI and Myocardial Strain** Marco S. Nobile, Amalia Lupi, Leone Bacciu, Matteo Grazioso, Chiara Gallese, Emilio Quaia Quaia and Alessia Pepe
	[97]	**Evaluating the Feasibility of Vision-Language Models in Skin Cancer Detection: A Comparative Study with CNNs and Vision Transformers** Yu-Hxiang Chen, Ting-Ting Chang, Yao-Zhi Xue, Wei-Hsiang Sung and Chia-Yu Lin

14:50		Coffee Break
15:00	ATI Room	**Invitation talk: Towards Wider Adoptions of AI/CI in the Biomedical Field - Infrastructure Building in NCHC** Speaker：Director General-Chau-Lyan Chang, NCHC
15:40 | 17:10	ATI Room	**Panel session: Pros and Cons of AI in Medicine** Chairs: Jennifer Hallinan, Sheridan Houghten Panelists: Anne Martel, Anil Wipat, Kuo-Sheng Cheng, Lai Chao-Han, Rose Faghih, Tayo Obafemi-Ajayi
18:00	Shangri-La Far Eastern Plaza, Tainan	**Banquet**

Day 3 - Friday August 22nd, 2025

08:20	Hall		Registration
09:00	ATI Room		**Keynote Advancing Biomedical Discovery in a Data-Driven AI Era** Speaker：Prof. Yang C. Fann
10:00			Coffee Break
10:20 | 12:00	Room A (92185)		**Technical Session VI: Machine Learning-2**
		[37]	**Investigating Forecasting Models for Pandemic Infections Using Heterogeneous Data Sources: A 2-year Study with COVID-19** Zacharias Komodromos, Kleanthis Malialis and Panayiotis Kolios
		[38]	**Vertebral Fracture Risk in Spinal Metastases Patients Following Stereotactic Body Radiotherapy Using Quantitative Imaging Data and Machine Learning** Dawit Gulta, Geoff Klein, Matthew Rezkalla, Tayler Declan Ross, Daniel Palhare, Laura Burgess, Jay Detsky, Arjun Sahgal, Cari Whyne, Michael Hardisty and Stephen Chen
		[43]	**Enhancing Machine Learning Models for Medical Coding: Diagnostic Codes Mapping and Synthetic Clinical Notes** Aikaterini Bilioni, Panagiotis Anagnostou, Sotiris K. Tasoulis, Spiros V. Georgakopoulos and Vassilis P. Plagianakos
		[46]	**Finding Healthcare Provider Experts via Sheaf Laplacian** Mehmet Aktas, Iraj Moradi, Esra Akbas and Mehmet Boyno
		[50]	**Intelligent Biomechanical Simulation of Bone Healing and Remodeling** Wai Yie Leong
		[73]	**Rank Correlation and Cluster Testing in Multi-Objective Data Analysis of Medical Data** Rachel Brown, Qihao Shan, Klaus-Peter Stein, I. Erol Sandalcioglu and Sanaz Mostaghim
	Room B (92177)		**Special Session III** **i: Next-Generation ECG-Based Sleep Apnea Detection** **ii: Computational Intelligence for Brain-Computer Interfaces**
	i	[88]	**OSANet: Detection of Obstructive Sleep Apnea Episodes Using a DarkNet-Based Deep Learning Approach and Time-Frequency Spectrogram Features Derived from Single-Lead ECG** Febryan Setiawan and Che-Wei Lin
		[89]	**Development of a Sliding Window-Based Oversampling Framework for Convolutional Neural Network Sleep Stage Classification Using Polysomnographic Spectrogram Fusion** Ai Chung, Febryan Setiawan, Cheng-Yu Lin and Che-Wei Lin
		[91]	**Event-based Detection of Obstructive Sleep Apnea via YOLOv8 Nano and ECG Spectrograms: Integration with Home Sleep Apnea Test and Edge Computing** Ponpatcharee Nipattanon and Che-Wei Lin
	ii	[41]	**Drowsiness Detection based on Continuous State Transitions from Alertness to Sleep using Forehead EEG** Tsung-Hao Hsieh, Ting-Yu Chen and Sheng-Fu Liang
		[95]	**Closed-Loop Brain-Controlled Exoskeleton System with a Hybrid Model for Stroke Rehabilitation** Yu-Wei Lin, Shi-Yong Luo, Po-Hsun Cheng, Chia-Hsin Chen, Yu-Zhen Liu, Zhi-Ting Chen and Li-Wei Ko
		[96]	**Visual Game-Based Upper Limb Ergometer Therapy Associated with EEG Responses in Stroke Rehabilitation** Chiao-Hsin Chen, Li-Wei Ko, Hsuan Cheng, Yu-Lin Wang, Kai-Chiao Chi, Chih-Chung Wang and Chia-Hsin Chen

12:00	L.Y Room	Lunch Break
12:40	Hall	Move to Bus
12:50		**Social event：Tainan City tour**
17:00		Move to Bus
17:30	Chingping Seafood Restaurant	Dinner

Authors and abstracts

• Full Papers

Paper number: [1], [3], [6], [9], [12], [16], [21], [25], [28], [31], [33], [37], [38], [39], [41], [43], [44], [45], [46], [47], [48], [50], [53], [54], [55], [57], [58], [60], [61], [62], [63], [64], [67], [71], [72], [73], [75], [76] , [77], [78], [79], [86], [88], [89], [91], [92], [93], [94] , [95], [96], [97], [98]

[1] *Decoding Aging: Multi-Omics Insights into Oxidative Stress, Mitochondrial Dysfunction, and Cellular Senescence in Fibroblasts*

Rajarshi Mandal (Biomedical Cybernetics Laboratory, Harvard Medical School), Ning Xie (BCL, HMS) and Gil Alterovitz (BCL, HMS).

Abstract

This research investigates the complex biochemical mechanisms underlying aging by analyzing primary human fibroblasts using a longitudinal multi-omics dataset. This dataset includes cytology, DNA methylation and epigenetic clocks, bioenergetics, and cytokine profiling. Key findings indicate that mitochondrial efficiency declines with age, while glycolysis becomes more prevalent to compensate for energy demands. Epigenetic clocks, such as Hannum and PhenoAge, showed strong correlations with biological age ($\rho > 0.650$, $p < 1e\text{-}6$), validating the experimental setup and confirming that the cultured fibroblasts were aging appropriately. Fibroblasts with SURF1 mutations exhibited accelerated aging, marked by bioenergetic deficits, increased cell volume, and reduced proliferative capacity, underscoring the pivotal role of mitochondrial dysfunction in cellular senescence. Novel insights were gained from analyzing cytokines like IL18 and PCSK9, some of which were linked to age-related diseases such as Alzheimer's and cardiovascular disorders. Experimental treatments revealed distinct effects on cellular aging. Dexamethasone reduced inflammation but also increased DNA methylation, induced metabolic inefficiencies, and shortened cellular lifespan. By uncovering connections between mitochondrial dysfunction, epigenetic biomarkers, and immune dysregulation, this research identifies potential therapeutic targets for age-related diseases.

[3] *An Endoscopic Lesion Segmentation Improvement*

Viet Dung Nguyen (Department of Electronics, School of Electrical and Electronic Engineering, Hanoi University of Science and Technology), Thi Khanh Linh Do (HUST), Manh Duy Tran (HUST), Tam Anh Bui (Phenikaa High School), Minh Duc Phan (Thai Binh High School for the Gifted), Phuc Ngoc Pham (HUST) and Nguyen Khang Ho (HUST)

Abstract

Gastrointestinal cancer is one of the deadliest diseases all over the world. In medical imaging technology, cancer diagnosis has been evolving, especially endoscopes and currently applying artificial intelligence and deep learning on improving endoscopist's imaging abilities. By using acquisition of images of tissues and organs, physicians are able to diagnose cancer in gastrointestinal track, besides of some limitations as depending on quality of endoscopy, experience of physicians or time consuming. With the development of technology, applications of deep learning are more effective in improving imaging techniques and diagnosis. Due to the state-of-the-art of deep learning, we applied VGG16, DenseNet201, HarDNet MSEG and HarDNet MSEG with attention to obtain some better results. Our results provide the comparison with mDice, mIoU and inference time on some of our trained models on the CVC-Clinic DB and Kvasir-SEG dataset. The best obtained mDice and mIoU are over 0.9 and 0.8, respectively.

[6] *Synthetic data in AI-powered medical devices – the EU regulatory implications*

Tomasz Braun (Lazarski University, Warsaw, Poland) and Dominika Harasimiuk (University of Warsaw)

Abstract

The growing use of synthetic data in AI technologies is one of the major technological trends particularly relevant in the healthcare sector. AI -powered medical devices may be trained and evaluated with the support of synthetic data. As synthetic data applications increase, specific legal, ethical and regulatory challenges arise. The EU regulatory framework for synthetic data relies on existing provisions of Medical Devices Regulation, General Data Protection Regulation and AI Act. None of these acts defines the notion of synthetic data, nor does provide specifically tailored provisions relating to it. The legal and ethical approaches will differ depending on the type of synthetic data at stake, its generation methods and final use. The potential beneficial applications of synthetic data in healthcare regulatory processes should be carefully assessed not only from the point of view of their legality, but also from the point of view of their compliance with ethical principles of fairness, accuracy, and trustworthiness.

[9] *Spiking Neural Networks for Mental Workload Classification with a Multimodal Approach*

Jiahui An (University of Zurich and ETH Zurich), Sara Fabrikant (UZ), Giacomo Indiveri (UZ and ETHZ) and Elisa Donati (UZ and ETHZ)

Abstract

Accurately assessing mental workload is crucial in cognitive neuroscience, human-computer interaction, and real-time monitoring, as cognitive load fluctuations affect performance and decision-making. While \ac{EEG}-based machine learning (ML) models can be used to this end, their high computational cost hinders embedded real-time applications. Hardware implementations of spiking neural networks (SNNs) offer a promising alternative for low-power, fast, event-driven processing. This study compares hardware-compatible SNN models with various traditional ML ones, using an open-source multimodal dataset. Our results show that multimodal integration improves accuracy, with SNN performance comparable to the ML one, demonstrating their potential for real-time implementations of cognitive load detection. These findings position event-based processing as a promising solution for low-latency, energy-efficient workload monitoring, in adaptive closed-loop embedded devices that dynamically regulate cognitive demands.

[12] *Short-term impacts of weather conditions on biomarkers among urban adults in Greece*

Katerina Tsiaktani (University of Thessaly), Panagiotis Anagnostou (UT), Sotiris K. Tasoulis (UT), Spiros V. Georgakopoulos (UT), John A. Gittings (National and Kapodistrian University of Athens), Dionysios E. Raitsos (NKUA), Athanasia Sergounioti (General Hospital of Amfissa) and Vassilis P. Plagianakos (UT)

Abstract

In this work, we investigate the relation between weather and atmospheric conditions, and the biomarkers Platelet-Lymphocyte Ratio (PLR) and Neutrophil-Lymphocyte Ratio (NLR). In more detail, we are interested in identifying how significant weather and atmospheric changes can affect people's health over time. For this purpose we introduce a new dataset that combines data from a recent population study along with historical meteorological measurements. We initially conduct timeseries exploratory analysis and then focus on change point detection and analysis of multivariate time series data in an effort to identify major incidents and their consequences. Interestingly, the results showed that the NLR and PLR biomarkers are significantly related to major changes in weather and atmospheric conditions.

[16] *Keypoint-Guided Ophidian Transformation for String-Shaped Data Augmentation*

Tszyi Kwok (Department of Computer Science, Brock University), Brendan Park (DCS, BU), Katharine Yagi (8Trees Inc.), Anne Yagi (8Trees Inc.), Chunsheng Yang (Digital Technologies Research Centre, National Research Council Canada (Retired)), Min Liao (Aerospace Research Centre, National Research Council Canada) and Yifeng Li (DCS, Department of Biological Sciences, BU)

Abstract

Image classification tasks in scientific research often struggle with limited data, particularly when few images are available per class, necessitating effective data augmentation strategies. For snakes and other string-shaped objects, traditional augmentation methods such as flipping, adding noise, or altering colour prove inadequate in enhancing classification accuracy. This paper introduces KGOT (Keypoint-Guided Ophidian Transformation), a novel image augmentation technique designed to generate realistic, non-linear transformations of string-shaped objects. KGOT first straightens the snake image, then warps it according to a reference curve defined by key points, effectively inverting the straightening process. By utilizing advanced curve interpolation, pixel mapping, and post-processing techniques, KGOT ensures smooth, biologically plausible deformations while preserving important individual-specific features. Our experiments demonstrate that KGOT-augmented data increase accuracy compared to the traditional augmentation method using geographic transformation techniques. Although some limitations persist in scenarios where snake bodies overlap, the success of KGOT augmentation provides valuable information on factors that improve classification performance. This approach holds promise not only for snake individual identification but also for a broader range of applications involving string-shaped object classification tasks.

[21] *REnformer, a single-cell ATAC-seq predicting model to investigate open chromatin sites*

Simone G. Riva (MRC Molecular Haematology Unit, MRC Weatherall Institute of Molecular Medicine, Oxford University, Oxford, UK (University of Oxford)), Edward Sanders (MRC MH Unit, MRC WIMM, OU), Tom Wilson (MRC MH Unit, MRC WIMM, OU), Nicolò Stranieri (Department of Computing Sciences, Bocconi University, Milan, Italy), E. Ravza Gür (MRC MH Unit, MRC WIMM, OU), Matthew Baxter (MRC MH Unit, MRC WIMM, OU) and Jim R. Hughes (MRC MH Unit, MRC WIMM, OU)

Abstract

Genome regulatory elements are fundamental to cellular identity and cell type specific gene expression. Understanding how the underlying genetic code is differentially utilised by different cell types is central to understanding human health and disease. To better understand how DNA encodes genome regulatory elements such as promoters, enhancers, and boundary elements, we leverage the Enformer gene expression and epigenetic prediction model. We used transfer learning with high quality single cell ATAC datasets to develop REnformer, a model to predict chromatin accessibility. By introducing a benchmark for comparing performances against Enformer model, REnformer significantly outperformed Enformer in terms of higher prediction outcomes and lower error rates in all extensive analyses shown; introducing these benchmarks allowed us, and possible future works, to fairly compare such models. We further tested REnformer by predicting the effects of a well characterised alpha-thalassemia variant and found that the prediction aligned with the observed change in genome regulatory element, previously validated. We conclude that REnformer is and can be a state-of-the-art tool to predict cell type specific regulatory elements, and interrogate the effect of genome variation in health and disease.

[25] *Integrative Framework for Functional analysis of multiple Traditional Chinese Medicines based on transcriptome-driven systems biology and supervised learning strategy*

Yun Tang (National Yang Ming Chiao Tung University (Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University)), Chia-Ru Chung (National Central University), Hsi-Yuan Huang (The Chinese University of Hong Kong, Shenzhen), Yang-Chi Dung Lin (CUHK, Shenzhen) and Hsien-Da Huang (CUHK, Shenzhen)

Abstract

Traditional Chinese Medicines (TCMs) have a long history of effective clinical practice. They contain a wide variety of ingredients and are rich in bioactive chemical sources. However, their complex and unknown effects on the human body prove a challenge in TCM research. To obtain a complete map of TCM functions, rather than focusing on pure compounds, the transcriptomic profile of different TCMs extracts treated on ten cancer cell lines was acquired. Multiple genes are involved in a biological system and disease progression; therefore, transcriptome-driven systems biology approach directs our attention to perturbed pathways or enriched gene sets from whole gene expression profile, allowing more explanatory power and less analytical complexity than solely considering differentially expressed genes (DEGs). This framework integrated differential expression analysis (DEA), pathway-based expression analysis and supervised learning approaches to explore TCM functions and extract signature genes of high importance. Supervised learning approaches were employed to extract signature genes that effectively discriminate between four TCMs (92% accuracy). These signature genes were further examined through database annotations and literature survey, where some were found to be TCM compound targets, such as fatty acid synthase (FASN), thioredoxin reductase 1 (TXNRD1) and glutamate-cysteine ligase regulatory subunit (GCLM). Based on network pharmacology concept, the proposed TCM-compound-target-pathway network can link TCM compounds to signature genes, DEGs and perturbed pathways, revealing the rationale behind TCM's mechanism of action in treatment. Integrating a supervised learning strategy in identifying TCM-associated genes that were not identified in the DEG analysis can offer a new perspective for discovering potential drug targets.

[28] *iACP-KAN: Identifying Anticancer Peptides using Kolmogorov-Arnold Network*

Hoang Nguyen (Ho Chi Minh City Open University), Quang Trinh (Hanoi University of Science and Technology), Huu-Thanh Duong (HCMCOU), Trang Do (HCMCOU) and Binh Nguyen (Victoria University of Wellington)

Abstract

Anticancer peptides (ACPs) represent a promising therapeutic approach for cancer treatment, offering potential advantages over traditional methods by providing more selective targeting and reduced toxicity. However, the clinical implementation of ACPs has been hindered by insufficient effective prediction methods. This study introduces iACP-KAN, a novel computational model for identifying anticancer peptides using a Kolmogorov-Arnold Network (KAN) with innovative feature integration. The proposed methodology combines four handcrafted features: Dipeptide Composition, Binary Profile Features, Pseudo Amino Acid Composition, and K-mer Composition, with sequence embedding features learned through a Long Short-Term Memory. Utilizing two independent datasets, the model demonstrated superior performance across multiple evaluation metrics, consistently outperforming seven state-of-the-art methods. For Dataset 1, the proposed approach achieved the highest Area Under the Receiver Operating Characteristic Curve (AUROC) of 0.8551 and Area Under the Precision-Recall Curve (AUPRC) of 0.8713 on the test set. For Dataset 2, it obtained an AUROC of 0.8713 and an AUPRC of 0.5026 on the test set. The results proved its potential to advance ACP prediction and support drug discovery efforts.

[31] *Continual Learning for Weakly-Supervised Histopathology Tissue Segmentation*

Wei Hua Li (National Taiwan University), Huei-Fang Yang (National Sun Yat-sen University) and Chu-Song Chen (NTU)

Abstract

Weakly supervised histopathology segmentation is a widely studied field that aims to achieve pixel-level semantic segmentation using image-level annotations, reducing the need for labor-intensive labeling. Despite significant advances in this task, existing methods assume the availability of all training data at once during training. Since medical image collections typically expand over time in practice, such methods become impractical. Meanwhile, research on continual semantic segmentation has also made significant progress. However, most existing works still rely on pixel-level annotations to train models. As a result, integrating continual learning into weakly supervised segmentation models has emerged as a promising direction. To address this challenge, we propose CL4WSeg, a novel end-to-end transformer-based framework that employs temporal distillation to leverage features from previous models for continual weakly supervised segmentation. Furthermore, we utilize a controllable diffusion model to enable generative replay and integrate an image quality filter to collect high-quality images, alleviating catastrophic forgetting. Experiments on the LUAD-HistoSeg, BCSS-WSSS, and WSSS4LUAD datasets demonstrate that our approach outperforms state-of-the-art methods.

[33] *The Brain Watching Itself: Identifying Brain Tumors with Spiking Neural Networks*

Namita Achyuthan (PES University) and Bhaskarjyoti Das (PESU)

Abstract

This study looks at the application of spiking neural networks (SNNs) in MRI classification, in order to show their potential as an efficient, biologically inspired alternative to traditional convolutional models. Specifically, we evaluate the performance of leaky integrate-and-fire (LIF) neurons within a convolutional spiking neural network (CSNN). Additionally, we compare two encoding strategies- rate and temporal encoding- to assess their effectiveness in capturing MRI features. The findings aim to demonstrate the viability of SNNs for MRI analysis, offering insights into their computational efficiency and biological plausibility.

[37] *Investigating Forecasting Models for Pandemic Infections Using Heterogeneous Data Sources: A 2-year Study with COVID-19*

Zacharias Komodromos (University of Cyprus), Kleanthis Malialis (UC) and Panayiotis Kolios (UC)

Abstract

Emerging in December 2019, the COVID-19 pandemic caused widespread health, economic, and social disruptions. Rapid global transmission overwhelmed healthcare systems, resulting in high infection rates, hospitalisations, and fatalities. To minimise the spread, governments implemented several non-pharmaceutical interventions like lockdowns and travel restrictions. While effective in controlling transmission, these measures also posed significant economic and societal challenges. Although the WHO declared COVID-19 no longer a global health emergency in May 2023, its impact persists, shaping public health strategies. The vast amount of data collected during the pandemic offers valuable insights into disease dynamics, transmission, and intervention effectiveness. Leveraging these insights can improve forecasting models, enhancing preparedness and response to future outbreaks while mitigating their social and economic impact. This paper presents a large-scale case study on COVID-19 forecasting in Cyprus, utilising a two-year dataset that integrates epidemiological data, vaccination records, policy measures, and weather conditions. We analyse infection trends, assess forecasting performance, and examine the influence of external factors on disease dynamics. The insights gained contribute to improved pandemic preparedness and response strategies.

[38] *Vertebral Fracture Risk in Spinal Metastases Patients Following Stereotactic Body Radiotherapy Using Quantitative Imaging Data and Machine Learning*

Dawit Gulta (Sunnybrook Research Institute), Geoff Klein (SRI), Matthew Rezkalla (SRI), Tayler Declan Ross (SRI), Daniel Palhare (SRI), Laura Burgess (SRI), Jay Detsky (Sunnybrook Health Science Centre (Sunnybrook Research Institute)), Arjun Sahgal (SHSC (SRI)), Cari Whyne (SRI), Michael Hardisty (SRI) and Stephen Chen (York University)

Abstract

Vertebral compression fractures (VCFs) occur in approximately 14% of patients with spinal metastases following treatment with Stereotactic Body Radiotherapy (SBRT). The Spinal Instability Neoplastic Score (SINS) is the current clinical standard for assessing potential mechanical instability in these patients; however, it has several limitations such as it is manually assessed, has an inconsistent relationship with fracture risk and is only semi-quantitative. This study used quantitative CT imaging biomarkers derived from SBRT treatment planning imaging and machine learning models to predict vertebral compression fractures (VCF) following SBRT in spinal metastases patients (in 300 thoraco-lumbar vertebral segments from 179 patients). Fractures occurred in 18.3% of cases post-SBRT. Machine learning algorithms (Logistic Regression, Random Forest, XGBoost, SVM, Gradient Boosting, AdaBoost, Neural Network) were compared against SINS. The Random Forest model achieved the best performance (sensitivity: 0.64, specificity: 0.76, F1-score: 0.47), showing a 36% improvement in balanced accuracy over SINS. Feature importance analysis identified spinal alignment and tumour composition(lytic or blastic disease) as the strongest predictors. ML models demonstrated meaningful improvements over traditional SINS assessment.

[39] *Towards Accurate Identification of Anti-Hepatitis C Peptides Using Stack-AHCP*

Lantian Yao (The Chinese University of Hong Kong, Shenzhen), Chang Liu (CUHK, Shenzhen), Jiahui Guan (CUHK, Shenzhen), Peilin Xie (CUHK, Shenzhen), Zhihao Zhao (CUHK, Shenzhen), Xingchen Liu (CUHK, Shenzhen), Yilin Guo (CUHK, Shenzhen), Yulan Liu (CUHK, Shenzhen), Yunlu Peng (CUHK, Shenzhen), Ying-Chih Chiang (CUHK, Shenzhen) and Tzong-Yi Lee (National Yang Ming Chiao Tung University (Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University))

Abstract

Hepatitis C virus (HCV) infection remains a significant global health burden, contributing to progressive hepatic pathologies including chronic hepatitis, cirrhosis, and hepatocellular carcinoma. While anti-hepatitis C peptides (AHCPs) have emerged as promising therapeutic candidates with distinct antiviral mechanisms, conventional wet-lab approaches for AHCP discovery face critical limitations in throughput and scalability. To overcome these constraints, we present Stack-AHCP, an innovative stacked ensemble learning framework that synergistically integrates multiple machine learning algorithms through a meta-classification strategy. Our model achieves unprecedented predictive performance with 93.1% accuracy and an MCC of 0.863, substantially outperforming existing computational methods. Through comprehensive Shapley additive explanations (SHAP) analysis, we further delineate critical key intrinsic features and determinants governing AHCP bioactivity, enhancing the mechanistic interpretability of the prediction system. To facilitate translational applications, we have implemented an intuitive web interface (accessible at https://awi.cuhk.edu.cn/~biosequence/StackAHCP/index.php) that enables rapid screening and prioritization of candidate peptides. This resource is anticipated to streamline the identification of next-generation peptide therapeutics against HCV while reducing experimental validation costs. Beyond virology applications, our methodological framework establishes a paradigm for interpretable machine learning in biological sequence analysis, with potential adaptability to diverse multi-omics investigation scenarios.

[41] *Drowsiness Detection based on Continuous State Transitions from Alertness to Sleep using Forehead EEG*

Tsung-Hao Hsieh (Tunghai), Ting-Yu Chen (National Cheng Kung University) and Sheng-Fu Liang (NCKU (Department of Computer Science and Information Engineering))

Abstract

drowsiness significantly contributes to accidents and decreased performance due to its impact on attention and concentration. Various sleepiness detection methods have been proposed but have not been widely adopted in daily life due to several limitations: (1) the lack of long-term measurement capability, (2) the need for external assistance for the operation, and (3) without the capability of reliable detection from drowsiness to sleep onset. In this pilot study, we investigated the characteristics of the forehead EEG from alertness sleep. The two-phase experiment was designed. In phase 1, subjects (N=13) had to sit in a chair and play a Sudoku puzzle, representing cognitive engagement in an altered state. In Phase 2, they lay on a bed and watched a first-person-perspective driving video record, which involved transitions from alertness to drowsiness and drowsiness to sleep. Validated with video data, forehead EEG detected an increase in eye-blink frequency, and the width of eye-blink peaks was also increased. After subjects fell asleep, forehead EEG exhibited alpha rhythms and slow eye movements, the mixing patterns observed in EEG and EOG. similar to standard EEG and EOG recordings. Moreover, our participants demonstrated a shorter sleep onset latency (1.23 ± 0.83 min) than previous sleep studies without fatigue induction. By integrating these characteristics with EEG- and EOG-based sleep score methods, forehead EEG presents a practical solution as a wearable device for daily drowsiness detection.

[43] *Enhancing Machine Learning Models for Medical Coding: Diagnostic Codes Mapping and Synthetic Clinical Notes*

Aikaterini Bilioni (University of Thessaly), Panagiotis Anagnostou (UT), Sotiris K. Tasoulis (UT), Spiros V. Georgakopoulos (UT) and Vassilis P. Plagianakos (UT)

Abstract

Discharge summaries are free-text notes that outline the hospital stay of a patient, including diagnoses, treatments, and follow-up care recommendations. Through the use of International Classification of Diseases (ICD) coding, they play a vital role in communicating clinical data exchange and reimbursement. However, manually assigning ICD codes to discharge summaries can be labor-intensive and prone to errors due to the unstructured narrative format, variations in terminology, potential inaccuracies in documentation, and the limitations of the ICD coding system in capturing the complexity of patient conditions. This paper aims to improve the results of state-of-the-art automated medical coding machine learning models with two preprocessing techniques. The first technique consists of data management to maximize the amount of usable data by mapping ICD-9 codes in the MIMIC-IV dataset to their corresponding ICD-10. With a similar goal, the second technique consists of the generation with large language models (LLMs) of several synthetic discharge summaries for ICD codes with a small number of appearances in the dataset. The results of this extensive preprocessing are evaluated with the use of several well-established and state-of-the-art deep learning models, which present significant improvement.

[44] *SHAP-Driven Deep Learning Identifies Pre-Symptomatic Influenza A Biomarkers: An Explainable AI Framework for Clinical Genomics*

Tsung-Hsien Lin (National Taiwan Ocean University, Department of Computer Science and Engineering), Anna Zan (NTOU, DCSE), Zhi-Jian Cheng (NTOU, DCSE), Zhong-Ru Xie (University of Georgia, School of Electrical and Computer Engineering) and Kuan Y. Chang (NTOU, DCSE)

Abstract

Background: DeepFlu predicts symptomatic influenza onset from pre-exposure gene expression, but the contribution of individual genes remains unclear. Methods: We apply SHapley Additive exPlanations (SHAP), an explainable AI (XAI) method, to evaluate gene-level contributions in DeepFlu models trained on H1N1 and H3N2 influenza gene expression data (GSE52428 and GSE73072 datasets). Results: Five key genes—HLA-DQA1, HLA-DQB1, XIST, RPS4Y1, and KDM5D—were shared across influenza subtypes. These genes are associated with immune response and sex-linked pathways, with elevated XIST and reduced RPS4Y1/KDM5D expression suggesting higher susceptibility in females. Conclusion: Integrating SHAP with DeepFlu enhances the interpretability of influenza risk predictions, offering actionable biological insights for early intervention.

[45] *CombDNF: Disease-specific drug combination predictions with network-based features on clinically validated data*

Pauline Hiort (Freie Universität Berlin, Institute of Computer Science, Department of Mathematics and Computer Science, Germany), Bernhard Y. Renard (Hasso Plattner Institute, Digital Engineering Faculty, University of Potsdam, Germany) and Katharina Baum (FUB, ICS, DMCS, Germany)

Abstract

Drug combinations are increasingly applied to treat a wide range of complex diseases. Drug action and thus also drug combination effects can differ between diseases, e.g., due to molecular differences. Therefore, disease-specific predictions are required for treatments. A plethora of methods based on cell-line screening data in cancer has been proposed. However, their extendability to other diseases is limited, as is their applicability in the clinical context due to the in-vivo-in-vitro gap. In contrast, only few approaches rely on clinically validated data. Here, we propose CombDNF, a novel machine-learning-based method for disease-specific drug combination prediction on clinically validated data. CombDNF is trained on and predicts both clinically approved (effective) and clinically reported adverse drug combinations from a broad collection of data sources. It can cope with the highly imbalanced label distribution in drug combination data. Further, CombDNF leverages network-derived features based on drug target and disease gene relationships. To incorporate uncertainty of the network topology it relies on edge weights in the underlying network. We systematically evaluate CombDNF against available state-of-the-art methods in four diseases with different underlying mechanisms and ground truth data characteristics. CombDNF outperforms all state-of-the-art methods in all four diseases by at least 84% in the AUPR. This translates, for example, to an enrichment of effective drug combinations in the top ten hypertension-specific predictions of four, compared to one for the best competing method. In addition, network edge weighting by interaction confidence scores indeed yields improved predictions. Further, we find evidence for biological plausibility of our top-ranked drug combinations. The Supplementary Notes, Figures, and Tables file and the training and evaluation pipeline for CombDNF are available ready-to-use at https://github.com/DILiS-lab/CombDNF.

[46] *Finding Healthcare Provider Experts via Sheaf Laplacian*

Mehmet Aktas (Kennesaw State University), Iraj Moradi (Georgia State University), Esra Akbas (GSU) and Mehmet Boyno (University of Central Florida)

Abstract

Identifying experts within healthcare provider networks is crucial for improving patient outcomes, optimizing resource allocation, and fostering medical collaboration. Traditional network-based expert detection methods primarily rely on centrality measures, which consider only structural connectivity without accounting for domain-specific expertise. In this paper, we propose a sheaf Laplacian-based expert detection method that ranks healthcare providers based on their expertise across multiple subdomains. After modeling healthcare provider networks as graphs and hypergraphs, using sheaf theory, we incorporate medical specialties into the network structure. The sheaf Laplacian diffusion model enables us to capture information propagation across providers by considering these medical specialties that facilitate a more refined ranking of experts. We evaluate our method on a benchmark dataset from the Stack Exchange healthcare community, comparing it with existing graph-based methods such as PageRank, the Susceptible-Infected-Recovered (SIR) model, and conventional Laplacian models. Experimental results using correlation and Hits$@n$ metrics demonstrate that our sheaf-based graph and hypergraph models outperform these baselines.

[47] *Enhancing Clinical Decision-Making: Integrating Multi-Agent Systems with Ethical AI Governance*

Ying-Jung Chen (georgia institute of technology), Ahmad Albarqawi (MedWrite.ai) and Chi-Sheng Chen (Neuro Industry, inc)

Abstract

Recent advances in the data-driven medicine approach, which integrates ethically managed and explainable artificial intelligence into clinical decision support systems (CDSS), are critical to ensure reliable and effective patient care. This paper focuses on comparing novel agent system designs that use modular agents to analyze laboratory results, vital signs, and clinical context, and to predict and validate results. We implement our agent system with the eICU database, including running lab analysis, vitals-only interpreters, and contextual reasoners agents first, then sharing the memory into the integration agent, prediction agent, transparency agent, and a validation agent. Our results suggest that the multi-agent system (MAS) performed better than the single-agent system (SAS) with mortality prediction accuracy (59%, 56%) and the mean error for length of stay (LOS)(4.37 days, 5.82 days), respectively. However, the transparency score for the SAS (86.21) is slightly better than the transparency score for MAS (85.5). Finally, this study suggests that our agent-based framework not only improves process transparency and prediction accuracy but also strengthens trustworthy AI-assisted decision support in an intensive care setting.

[48] *Helicobacter Pylori Infection Diagnosis from Endoscopic Images via Multi-Class Token based Multiple Instance Learning*

Wei-Te Ting (National Chung Hsing University), Yu-Ching Tsai (Tainan Hospital), Chun-Rong Huang (Department of Computer Science and Engineering, NCHU), Hsiu-Chi Cheng (NCKU) and Bor-Shyang Sheu (NCKU)

Abstract

To diagnose Helicobacter pylori (H. pylori) infection from endoscopic images, conventional methods require a time-consuming labeling process to annotate individual endoscopic images based on pathological findings. In this paper, we aim to diagnose H. pylori infection for each patient from a group of endoscopic images captured during endoscopy, where only patient-level labels are available for each patient. To achieve the goal, we propose a multi-class token-based multiple instance learning method which consists of the feature extractor, the multi-class token selector module, and the aggregator. By using learnable positive class tokens and negative class tokens with transformer encoders, the multi-class token selector module selects the proper class tokens to improve the H. pylori infection prediction performance of the aggregator. Compared with supervised methods and state-of-the-art multiple instance learning methods, the proposed method achieves the best results.

[50] *Intelligent Biomechanical Simulation of Bone Healing and Remodeling*

Wei-Te Ting (INTI International University)

Abstract

The biomechanical simulation of bone healing and remodeling is crucial for understanding the complex processes involved in bone regeneration and recovery following injuries. This study aims to advance existing biomechanical simulation methods by integrating cutting-edge artificial intelligence (AI) techniques to enhance accuracy, predictability, and clinical relevance. The research identifies key gaps and opportunities in current biomechanical models. The methodology adopted involves the design and implementation of a comprehensive simulation framework that incorporates AI-driven algorithms for improved predictive capability and simulation precision. A case study based on clinical scenarios demonstrates the applicability and effectiveness of the developed intelligent simulation approach, presenting significant improvements over traditional biomechanical models. Key findings illustrate superior accuracy in predicting bone healing timelines and remodeling outcomes, underscored by detailed comparisons and validated by empirical data. Despite substantial advancements, the research acknowledges existing technical challenges, computational limitations, and ethical considerations, emphasizing the need for continued innovation and refinement. This study highlights the potential transformative impact of AI-enhanced biomechanical simulations in clinical orthopedics, suggesting avenues for future research to further develop robust and clinically applicable predictive models.

[53] *BacCal GUI: Streamlining Virus Titration Calculations*

Meng-Chi Chung (Department of Biomedical Sciences and Engineering, National Central University), Tzong-Yuan Wu (Department of Bioscience Technology, Chung Yuan Christian University) and Li-Ching Wu (DBSE, NCU)

Abstract

Viral titer measurement is vital in virology, offering insights into viral dynamics, disease severity, and treatment efficacy. This article underscores its importance across research domains and introduces BacCal (Baculovirus Calculator), a specialized software for streamlining viral titer experiments. BacCal automates titration using the Reed-Muench method, providing a user-friendly interface for inputting parameters and analyzing results. It enables precise quantification of viral concentrations, aiding in understanding virus-host interactions and replication kinetics. BacCal enhances quality control in virology and diagnostic assay production, ensuring consistency. Analysis involves preparing plates, inoculating cells, and assessing effects, with TCID50 calculation and optional PFU conversion. BacCal features localized data storage, preserving conditions for reproducibility. By integrating automated titration and robust data management, BacCal advances virology research, facilitating efficient experimentation and safeguarding critical data.

[54] *SDPA++: A General Framework for Self-Supervised Denoising with Patch Aggregation*

Huy Nguyen (Vietnamese German University), Triet Dao (VGU), Chau Truong (VGU) and Cuong Nguyen (VGU)

Abstract

Optical Coherence Tomography (OCT) is a widely used non-invasive imaging technique that provides detailed three-dimensional views of the retina, which are essential for the early and accurate diagnosis of ocular diseases. Consequently, OCT image analysis and processing have emerged as key research areas in biomedical imaging. However, acquiring paired datasets of clean and real-world noisy OCT images for supervised denoising models remains a formidable challenge due to intrinsic speckle noise and practical constraints in clinical imaging environments. To address these issues, we propose SDPA++: A General Framework for Self-Supervised Denoising with Patch Aggregation. Our novel approach leverages only noisy OCT images by first generating pseudo-ground-truth images through self-fusion and self-supervised denoising. These refined images then serve as targets to train an ensemble of denoising models using a patch-based strategy that effectively enhances image clarity. Performance improvements are validated via metrics such as Contrast-to-Noise Ratio (CNR), Mean Square Ratio (MSR), Texture Preservation (TP), and Edge Preservation (EP) on the real-world dataset from the IEEE SPS Video and Image Processing Cup. Notably, the VIP Cup dataset contains only real-world noisy OCT images without clean references, highlighting our method's potential for improving image quality and diagnostic outcomes in clinical practice.

[55] *Leveraging Graph Information for Spatially Informed Patient Data Analysis with GIST*

Gospel Ozioma Nnadi (Department of Computer Science, University of Verona), Vincenzo Bonnici (Department of Mathematical, Physical and Computer Sciences, University of Parma), Simone Avesani (DCS, UV), Eva Viesi (DCS, UV) and Rosalba Giugno (DCS, UV)

Abstract

Patient data such as tissue samples analyzed through spatial transcriptomics have transformed our ability to study cellular subpopulations within their native microenvironments, providing unprecedented insights into tissue architecture and cellular interactions. However, accurately identifying spatial domains remains a computational challenge. Despite notable progress, no gold standard currently exists for spatial domain identification, and significant opportunities remain for further improvement. In this study, we introduce Graph Information for Spatial Transcriptomics (GIST), a Graph Neural Network (GNN)-based framework that integrates gene expression data with spatial coordinates to construct a biologically meaningful graph representation of tissue architecture. By explicitly modeling spatial dependencies and leveraging contrastive learning to optimize node embeddings, GIST substantially improves spatial domain identification. It outperforms existing methods on key clustering metrics such as the Adjusted Rand Index (ARI) demonstrating its effectiveness in capturing the true structure of spatial transcriptomic data. Furthermore, we introduce the Silhouette Spatial Score (SSS)—an extension of the traditional Silhouette Score that incorporates spatial neighborhood information. SSS enables more accurate evaluation of both transcriptomic similarity and spatial contiguity within identified domains. GIST outperforms existing methods in SSS, highlighting its ability to identify domains that are not only transcriptomically meaningful but also spatially contiguous.

[57] *Explainable AI-Enhanced Kinase Activity Profiling Through Phosphoproteomics*

Chia-Ru Chung (National Central University), Ming-Feng Ho (NCU), Yun Tang (National Yang Ming Chiao Tung University (Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University)), Li-Ching Wu (Department of Biomedical Sciences and Engineering, NCU), Justin Bokai Hsu (Department of Computer Science and Engineering, Yuan Ze University (Department of Computer Science and Engineering, College of Informatics, Yuan Ze University)), Tzong-Yi Lee (NYMCTU) and Jorng-Tzong Horng (Department of Computer Science and Information Engineering, NCU)

Abstract

Kinases play a critical role in regulating fundamental cellular processes, including metabolism, signal transduction, and cell growth, primarily through phosphorylation. The dysregulation of kinase activity is implicated in various diseases, highlighting the urgent need for robust and interpretable methodologies to profile this activity. Current approaches frequently depend on overly complex or limited datasets, lack generalizability, or fail to provide meaningful biological insights into the mechanisms governing kinase activity. To address these challenges, we developed an explainable deep learning framework that leverages mass spectrometry-based phosphoproteomics data to profile kinase activity effectively. Our study systematically evaluated Deep Neural Networks (DNNs) and Convolutional Neural Networks (CNNs), incorporating a diverse set of feature inputs, including phosphorylation sites and kinase-substrate relationships. A notable finding was that a three-layer CNN, optimized through rigorous feature selection techniques, demonstrated superior performance, achieving substantial improvements in prediction accuracy and stability when compared to established methods such as Kinase-Substrate Enrichment Analysis (KSEA) and the Kinase Activity Ranking Pipeline (KARP). We integrated SHapley Additive exPlanations (SHAP) values to enhance interpretability, illuminating biologically significant phosphorylation sites. For example, PAK2-related phosphorylation sites associated with the progression of colon adenocarcinoma and CAMK2D sites integral to adrenergic signaling were identified, thereby effectively linking computational predictions to established molecular pathways. This research illustrates the potential of explainable artificial intelligence in advancing kinase activity profiling by providing accurate and interpretable predictions. Our framework is valuable for elucidating disease mechanisms and identifying therapeutic targets, facilitating broader applications in precision medicine.

[58] *Leveraging Diffusion-Based Models for Data Augmentation in Maternal-Fetal Ultrasound Classification*

Shi Hao Wong (Southern Taiwan University of Science and Technology) and Tsung-Lu Michael Lee (STUST)

Abstract

This paper investigates diffusion models for data augmentation in fetal ultrasound image classification, addressing the critical challenge of limited medical image datasets for rare conditions. We fine-tuned Stable Diffusion with Low-Rank Adaptation (LoRA) to generate synthetic ultrasound images and systematically evaluated their impact on classification performance across multiple experimental conditions. Our results demonstrate that augmenting training data with synthetic images significantly improves classification accuracy and effectively addresses class imbalance issues. Notably, models trained with a combination of real and synthetic data showed enhanced generalization capabilities and improved performance on minority classes. These findings establish diffusion-based augmentation as a promising approach to overcome data scarcity constraints in medical imaging applications, with potential implications for clinical decision support systems.

[60] *Alzheimer's Disease Risk Prediction in the Elderly: A Machine Learning Approach Combining Clinical Characteristics and Polygenic Risk Scores*

Bo-Kai Hsu (Department of Computer Science and Engineering, Yuan Ze University (Yuan Ze University) (Department of Computer Science and Engineering, College of Informatics, Yuan Ze University)), Cheng-Yang Lee (Graduate Institute of Biomedical Informatics, College of Medical Science and Technology, Taipei Medical University), Jia-Ruey Tsai (Division of Hematology & Oncology, Department of Internal Medicine, Taipei Medical University Hospital), Vijesh Kumar Yadav (Division of Gastroenterology and Hepatology, Department of Internal Medicine, Taipei Medical University), Chuan Huang (GIBI, CMST, TMU) and Tzu-Hao Chang (GIBI, CMST, TMU)

Abstract

Motivation: Alzheimer's disease (AD) is the most common type of dementia. Given the lack of a cure, early identification of high-risk populations is crucial for timely prevention. While several studies have focused on AD risk prediction, single features (e.g., age) may dominate model performance, limiting the discovery of other potential risk factors. This study incorporates key features identified in previous research and applies propensity score matching for age and sex, aiming to improve the predictive performance of AD risk models for older adults. Methods: This study utilized data from the UK Biobank to integrate genetic and clinical data and developed 5-year and 10-year AD risk prediction models for older adults, respectively. The workflow included genome-wide association studies (GWAS) on 433,589 participants were conducted to identify significant Single nucleotide polymorphisms (SNPs) under three p-value thresholds, followed by polygenic risk score (PRS) calculation for 13,282 participants using PRSice-2 and Lassosum, and the integration of multiple features to construct prediction models. Clinical features, PRS, and significant SNPs were then incorporated into four machine learning models: Logistic Regression, LightGBM, XGBoost, and Multi-Layer Perceptron (MLP) for prediction and performance comparison. Results: For the 5-year risk prediction, the MLP model demonstrated the best performance, achieving an AUC of 0.88 based on 37 clinical features and 206 significant SNPs. For the 10-year risk prediction, the MLP model also demonstrated the best performance, achieving an AUC of 0.89 based on 37 clinical features, 206 significant SNPs, and PRS based on these SNPs. SHAP analysis revealed that key contributors across both models included ApoE genotype, urinary tract infection (N390), disorientation, depressive symptoms, and pairs matching time. The 5-year model emphasized immediate clinical and cognitive indicators such as reaction time and number of medications taken, whereas the 10-year model highlighted long-term risk factors including BMI, diabetes, and peak expiratory flow. Conclusion: This study demonstrates that integrating clinical features with PRS can effectively enhance the accuracy of AD risk prediction models for older adults. However, to further validate the utility of PRS, future research should involve collaborations across diverse populations and databases. Additionally, further exploration of other potential risk factors is needed to enhance the clinical applicability of these models.

[61] *Development of a Generalized Model for Alzheimer's Disease Risk Prediction in the Taiwanese Population*

Bo-Kai Hsu (Department of Computer Science and Engineering, Yuan Ze University (Yuan Ze University) (Department of Computer Science and Engineering, College of Informatics, Yuan Ze University)), Jia-Ruey Tsai (Division of Hematology & Oncology, Department of Internal Medicine, Taipei Medical University Hospital), Shih-Han Hung (Graduate Institute of Biomedical Informatics, College of Medical Science and Technology, Taipei Medical University), Cheng-Yang Lee (GIBI, CMST, TMU), Chaur-Jong Hu (College of Medicine, Taipei Medical University) and Tzu-Hao Chang (GIBI, CMST, TMU)

Abstract

Alzheimer's disease (AD) is the most common form of dementia worldwide, but most existing risk prediction models are based on European populations and lack generalizability to other ethnic groups. This study combined genetic and clinical data from both the UK Biobank and a Taiwanese population to develop a model more broadly applicable across populations. By selecting SNPs with similar minor allele frequencies (MAF) between groups and performing genotype imputation, models were built using polygenic risk scores (PRS), genotype, and clinical data. Logistic regression, XGBoost, and multilayer perceptron (MLP) were used for comparison. All models performed well on the UKB validation set (AUC = 0.81), and the logistic regression and MLP models showed improved performance (AUC = 0.87) in the Taiwanese test set. Key predictive features included PRSice2_PRS, lassosum_PRS, and age. The results highlight the potential of integrating genetic and clinical data to improve risk prediction for AD across populations, offering insights into AD pathogenesis and aiding the development of precision medicine strategies.

[62] *GSDeep-DTA: A Hybrid Graph and Sequence-based Deep Learning Framework for Robust Drug-Target Affinity Prediction*

Dileepa Samankula (Victoria University of Wellington), Joanne Harvey (VUW) and Binh Nguyen (VUW)

Abstract

Robust prediction of drug-target binding affinity (DTA) is essential for accelerating drug discovery pipelines, as it reduces experimental failures in cold-start scenarios where novel compounds or targets are involved. Although existing DTA models primarily rely on sequence-based or graph-based representations, a limited number of studies have explored the integration of both approaches. However, to effectively encode and integrate the diverse features of drugs and proteins, while enhancing predictive performance, is a challenging task. This work proposes a new hybrid graph- and sequence-based framework for robust DTA prediction, GSDeep-DTA. The model integrates graph neural networks to represent drug molecular structures and protein contact maps, and cascades Convolutional Neural Network - Bidirectional Long Short-Term Memory modules with transformer embeddings to hierarchically capture sequential dependencies. To integrate these heterogeneous features, we adopt a weighted sum fusion mechanism, which balances effectiveness and simplicity compared to more complex fusion techniques. Experimental results on the Davis benchmark dataset shows that our model outperforms state-of-the-art DTA prediction models. In addition, we evaluate its ability to generalize in cold-start scenarios, assessing its performance on novel drugs and/or proteins. Our findings highlight the potential of hybrid graph and sequence-based deep learning models for improved DTA prediction.

[63] *Balanced Benchmarking of Zero-Shot and RAG Approaches for Biomedical Term Normalization*

Thanh Son Do (Missouri State University), Daniel Hier (Missouri University of Science & Technology) and Tayo Obafemi-Ajayi (MSU)

Abstract

Normalization of medical concepts to an ontology is a key aspect of the natural language processing of biomedical text. It enables the mapping of medical expressions to standardized ontology terms and their identifiers, thereby enhancing the interoperability and computability of medical concepts. Although large language models (LLMs) can identify and standardize medical terms, they may struggle to accurately map ontology terms to their corresponding ontology identifiers. These challenges arise from the stochastic nature of LLMs, their limited exposure to uncommon ontology identifiers during training, and their lack of an integrated lookup mechanism. We generated test sets of synthetic terms to assess normalization performance by both zero-shot prompted and retrieval-augmented generation (RAG) prompted methods across two ontologies (Human Phenotype Ontology and Gene Ontology) and three LLMs (GPT-4o, LLaMA 3.3 70B, and Phi-4). To ensure a calibrated and fair evaluation of normalization, the test set was balanced along two axes: (1) term prevalence in biomedical literature, as estimated by PubMed Central frequency counts, and (2) semantic proximity to ontology terms, as assessed by cosine similarity of BioBERT embeddings. Our results demonstrate that RAG consistently outperforms zero-shot prompting, particularly on low-prevalence terms that are infrequently encountered in the biomedical literature. This highlights the value of RAG in compensating for gaps in model exposure to uncommon medical concepts. We demonstrate that a synthetic test set can be a valuable tool for evaluating biomedical term normalization across LLMs.

[64] *GENESIS: Generating scRNA-Seq data from Multiome Gene Expression*

Simone G. Riva (MRC Molecular Haematology Unit, MRC Weatherall Institute of Molecular Medicine, Oxford University, Oxford, UK (University of Oxford)), Brynelle Myers (University of Oxford), Francesca M. Buffa (Bocconi University) and Andrea Tangherloni (BU)

Abstract

Single-cell technologies have significantly advanced our understanding of cellular heterogeneity by allowing the examination of individual cells at high resolution. Traditional single-cell RNA sequencing (scRNA-Seq) methods, which utilise whole cells, capture comprehensive RNA content. In contrast, emerging Multiome technologies, which simultaneously profile multiple omics such as gene expression (GEX) and chromatin accessibility, rely on nuclear RNA, potentially missing key cytoplasmic information. This discrepancy leads to substantial technical and biological differences between GEX and scRNA-Seq datasets, making it difficult to integrate data and perform downstream tasks like cell-type classification. To address this challenge, we introduce GENESIS (Gene Expression Normalisation and Enhancement for Single-cell Integrated Sequencing), a novel computational framework designed to transform GEX data from Multiome experiments into enhanced, scRNA-Seq like profiles. Utilising advanced generative models--including Variational Autoencoders, Generative Adversarial Networks, and a tailored VAE_UNet architecture--GENESIS can generate high-quality data by modelling and compensating for the inherent differences between nuclear and cytoplasmic RNA. Our comprehensive evaluations show that GENESIS, particularly through the VAE_UNet model, generates synthetic scRNA-Seq data that closely resembles the resolution and biological accuracy of whole-cell sequencing, improving downstream tasks, especially cell-type classification.

[67] *Knowledge-Enriched Cell-Type Annotation in Single-Cell Transcriptomics via LLM Embeddings*

Andrea Fabbricatore (Bocconi University), Francesca M. Buffa (BU) and Andrea Tangherloni (BU)

Abstract

Single-cell RNA sequencing (scRNA-seq) has profoundly reshaped our understanding of cellular diversity and functionality; however, accurate cell-type annotation is required for biological interpretation. Current annotation methods, predominantly reliant on gene expression alone or manual curation, suffer from subjectivity and limited biological context.

Here, we introduce a novel approach that integrates textual biological knowledge via gene embeddings, derived from fine-tuning Large Language Models (LLMs), with gene counts for automatic cell-type classification using Machine Learning supervised models. In particular, we trained an XGBoost model and a multi-layer perceptron (MLP) to classify the cell populations automatically. We show that combining ModernBERT embeddings and raw counts improves the MLP performance, particularly in complex classification scenarios involving subtle cell-subtype distinctions. Our results also show that ModernBERT generated better embeddings than smaller LLM architectures, underlining the value of enriched, biologically informed embeddings. By embedding prior knowledge from curated biological databases and literature, our approach enhances the MLP's ability to distinguish sub-cell populations and biological signals. This work provides a scalable framework for integrating broader biological context into scRNA-seq analyses, offering new opportunities for downstream tasks such as gene regulatory network inference and cross-species annotation.

[71] *Deep Learning-Based Object Detection System for Vocal Cords in Laryngoscopy Images*

Ying-Chang Wu (Department of Computer Science and Information Engineering , National Cheng Kung University), Sheng-Fu Liang (DCSIE , NCKU), Cheng-Ming Hsu (Department of Otolaryngology-Head and Neck Surgery , Chiayi Chang Gung Memorial Hospital) and Ming-Chi Cheng (DCSIE , NCKU)

Abstract

Accurate localization of the vocal folds is critical for diagnostic and therapeutic applications in medical imaging. This paper developed a deep learning-based object detection system to address different tasks related to vocal fold detection. A two-step transfer learning approach was proposed for model training. The YOLOv8 was pre-trained with a large scale of high-speed video recordings available in a public dataset. Then, we fine-tuned the model using a 1:1 combination of the data from the public dataset and the low-frame rate (30 frames/sec) dataset collected from the hospital CGMH in Taiwan to fine-tune the final optimized glottis detection model. The results show that the recall and precision of ROI multiple bounding box predictions are 97.6% and 98.3%, respectively. In comparison, the recall and precision of single bounding box predictions are 97.5% and 100%, respectively. These results demonstrate the successful use of deep learning technology for vocal fold localization with superior performance. Our study provides valuable information for selecting appropriate object detection modalities in medical imaging applications for diagnosis and treatment planning in laryngology and otorhinolaryngology.

[72] *Inductive models for structured output prediction of lncRNA-disease associations*

Felipe Kenji Nakano (KU Leuven Kulak), Livia Bertoni (Federal University of Sao Carlos), Ricardo Cerri (Instituto de Ciências Matemáticas e de Computação (ICMC/USP)) and Celine Vens (KU LK)

Abstract

Long non-coding RNAs have gained significant attention due to their crucial roles in the pathogenesis of complex human diseases, such as neurological diseases, cardiovascular diseases, AIDS, diabetes, and various types of cancer. In the machine learning literature, lncRNA-disease association (LDA) has been widely investigated as a binary classification problem, where each lncRNA-disease pair is seen as an independent instance. This approach presents drawbacks as it does not exploit the correlation among the diseases, aggravates the already imbalanced dataset, and substantially increases the execution time. Furthermore, the literature focuses on the transductive setting where new disease associations are predicted in lncRNAs already seen by the model, which naturally restricts its application to already seen lncRNAs. As a solution, we propose to address LDA prediction as a structured output prediction problem, namely (hierarchical) multi-label classification, where all LDAs are predicted at once for a given lncRNA. We compared several LDA methods and their structured output variants with recent (hierarchical) multi-label classification methods in an inductive setting, e.g., disease associations are predicted in unseen lncRNAs. Our experiments reveal that approaching LDA prediction with structured output prediction leads to superior or competitive results while drastically reducing the running time.

[73] *Rank Correlation and Cluster Testing in Multi-Objective Data Analysis of Medical Data*

Rachel Brown (Otto von Guericke University Magdeburg), Qihao Shan (OvGUM), Klaus-Peter Stein (OvGUM), I. Erol Sandalcioglu (OvGUM) and Sanaz Mostaghim (OvGUM)

Abstract

Multi-Objective Data Analysis is a method of exploring conflicting patterns in static data. This method is used to explore complex relationships commonly found in medical data, where human body systems often have overlapping variables, creating a complex web of relationships. Within multi-objective optimization, a relationship is usually described as conflicting if an increase in optimality in one objective leads to a subsequent decrease in the other. This relationship is difficult to extract from static data, where no optimization is taking place. Multi-Objective Data Analysis extracts conflicting relationships using non-dominated sorting to find multiple fronts that represent the gradient of the fitness landscape between the decision and objective spaces, and checks to see if this gradient is related to variables in the decision space that are of interest. In this work, we showcase the use of the Wilcoxon (or Proportions) test and the Pearson Correlation test as objective measures of the usefulness of a found conflicting pair of objectives by comparing the distributions of a chosen response variable relative to the sorting. The shown examples include a clean synthetic dataset, a synthetic dataset with noise in the objective space, and a real-world dataset consisting of breast cancer data. From these examples, the argument is made that the statistical tests are compatible with Multi-Objective Data Analysis.

[75] *EL-DRP: An Evolutionary Learning-Based Multi-Omics Framework for Drug Response Prediction with Interpretable Biomarker Selection*

Yann-Jen Ho (National Yang Ming Chiao Tung University), You Sheng Paik (NYMCTU), Yu-Ruo Chen (NYMCTU), Yun Tang (NYMCTU (Institute of Bioinformatics and Systems Biology)), Shinn-Ying Ho (NYMCTU) and Tzong-Yi Lee (NYMCTU (IBSB))

Abstract

Cancer is a complex disease driven by diverse genetic, epigenetic, and microenvironmental alterations that result in dysregulated cell proliferation and therapeutic resistance. Both inter- and intra-tumoral heterogeneity further complicate treatment outcomes, highlighting the critical need for effective and efficient drug response prediction in precision oncology. While deep learning models have yielded robust predictive performance, their limited interpretability remains a critical barrier to clinical translation. To overcome this, we propose EL-DRP, an evolutionary learning framework for drug response prediction that integrates multi-omics data, including gene expression, copy number variation (CNV), and single nucleotide polymorphisms (SNPs). Central to EL-DRP is the use of an Inheritable Bi-objective Combinatorial Genetic Algorithm (IBCGA) for optimized feature selection within each omics modality. The IBCGA identifies a minimal yet informative subset of biomarkers, which are subsequently integrated to construct a unified multi-omics predictive model. EL-DRP achieved accurate drug response prediction using a minimal subset of biomarkers, many of which align with known drug mechanisms of action (MOA). For instance, among the camptothecin response–associated biomarkers, KDM4A and SCML2 are known to participate in camptothecin-induced DNA damage response, whereas SALL2, RBM10, BAHCC1, and PBRM1 regulate chromatin structure and genome maintenance, corroborating their mechanistic relevance. Importantly, this minimal biomarker panel alone retains robust predictive power with explainable biomarkers. These results provide a new perspective for discovering potential biomarkers associated with drug response prediction and lay the groundwork for future studies integrating clinical data with translational potential.

[76] *AI-Enhanced MALDI-TOF MS Analysis for Important Peaks on Predicting Ciprofloxacin Resistance across Different Gram-Negative Bacteria*

Hsin-Yao Wang (Chang Gung Memorial Hospital at Linkou), Chia-Ru Chung (National Central University), Wen-Rui Zhang (NCU), Li-Ching Wu (Department of Biomedical Sciences and Engineering, NCU), Justin Bo-Kai Hsu (Department of Computer Science and Engineering, Yuan Ze University (Department of Computer Science and Engineering, College of Informatics, Yuan Ze University)), Jang-Jih Lu (Division of Clinical Pathology, Taipei Tzu Chi Hospital, Buddhist Tzu Chi Medical Foundation (Taipei Tzu Chi Hospital Buddhist Tzu Chi Medical Foundation)) and Jorng-Tzong Horng (Department of Computer Science and Information Engineering, NCU)

Abstract

Rapid identification of antibiotic-resistant infections is crucial, as antimicrobial resistance is a global health crisis. Yet, conventional antibiotic susceptibility tests (AST) often require days to yield results. Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) has emerged as a rapid, cost-effective tool for bacterial identification and shows promise for resistance profiling by detecting spectral biomarkers. In this study, we harness MALDI-TOF MS with machine learning and deep learning to predict ciprofloxacin resistance across four Gram-negative bacteria, Escherichia coli, Klebsiella pneumoniae, Acinetobacter baumannii, and Acinetobacter nosocomialis, using a cross-species “basket-wise” approach. We extracted features from mass spectra using kernel density estimation-based peak detection and m/z binning, then trained a random forest (RF) classifier and a convolutional neural network (CNN) to distinguish ciprofloxacin-resistant and susceptible isolates. To interpret the models, we employed dual feature importance analyses: gradient-weighted class activation mapping (Grad-CAM) for the CNN to highlight critical m/z regions and an ensemble RF-based method to identify significant peak features. The CNN achieved higher overall accuracy than the RF, especially in three of four species, while the ensemble RF approach identified interpretable sets of around 20 important m/z peaks per organism. Several informative peaks overlapped between species, indicating some common resistance-associated spectral signatures. However, no single universal marker was found across all species. These findings demonstrate an AI-enhanced MALDI-TOF MS framework for rapid AMR detection, yielding accurate predictions and interpretable spectral markers. The approach highlights clinical potential to guide effective therapy and bolster antimicrobial stewardship, particularly for underrepresented pathogens such as A. nosocomialis.

[77] *TPP Riboswitch Design Using Secondary-Structure-Informed Geometric GNN*

Pradeepthi Rangineni (State University of New York Polytechnic Institute), Nitin Manne (SUNYPI), Nick Paradis (Rowan University), Ali Tekeoglu (Leidos & Johns Hopkins University), Chen-Fu Chiang (SUNYPI) and Amirhossein Manzourolajdad (SUNYPI)

Abstract

RNA inverse design is an essential part of many synthetic biology applications. The current machine learning approaches can effectively predict sequence of the RNA from its 3D atomic-scale information and generate hypothetical sequences. Natural riboswitches are RNA molecules capable of switching their conformation upon sensing an environmental signal and are great candidates for synthetic RNA devices. Design of a novel riboswitch, however, is a formidable challenge, given the uniqueness of structural and functional characteristics of a riboswitch. In this work, we explore the capabilities of the GNN-based structure-informed RNA inverse design tool, to inverse design the Thiamine Pyrophosphate (TPP) riboswitch from its backbone geometry. Results show that sequence recovery of TPP riboswitches is higher for models containing solo RNA structures compared to those containing other types of riboswitches as well as those containing RNA-Protein complexes. Design of a bound state required further modeling of ligand binding as well as impact of metal ions on structure.

[78] *Integrative Multi-Omics Prognostic Modeling of Glioma Recurrence Using Variational Autoencoder and Similarity Network Fusion*

Phuong Lam Tran (Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University), Yun Tang (IBSB, NYMCTU), Justin Bokai Hsu (Department of Computer Science and Engineering, Yuan Ze University (Department of Computer Science and Engineering, College of Informatics, Yuan Ze University)) and Tzong-Yi Lee (IBSB, NYMCTU)

Abstract

Gliomas represent the most prevalen form oft malignant brain tumors, with glioblastoma (GBM) classified as the most aggressive subtype and lower-grade gliomas (LGGs) showing a high recurrence rate despite better survival outcomes. Traditional prognostic methods rely on clinical and molecular markers, yet they often fail to leverage the predictive potential of integrative multiomics data. Hence, early and accurate identification of glioma recurrence is critical for optimizing treatment strategies and improving patient outcomes. To address this challenge, we developed a deep learning-based approach that integrates multiomics data with clinical features to enhance recurrence risk stratification. Multiomics data, including mRNA, miRNA, DNA methylation, and CNV profiles from 512 LGG and 350 GBM patients in The Cancer Genome Atlas (TCGA), were processed using the variational autoencoder for nonlinear feature extraction, followed by similarity network fusion to capture cross-omics relationships. Recurrence-guided feature selection identified a robust biomarker panel consisting of TMBM1, EMP3, STEAP3, TRIP6, EFEMP2, PDPN, CLIC1, ANXA1, SLC2A1, TAGLN2, C1RL, PYGL, and S1PR3. This panel effectively categorized patients into high- and low-risk recurrence groups, with Kaplan-Meier survival analysis demonstrating a notable significant difference with p-value less than 0.001. Integration of clinical factors (age, tumor grade, IDH mutation status) further improved predictive performance, yielding a C-index of 0.695 ($p < 2e\text{-}16$) for LGG and 0.619 ($p = 3.346e\text{-}11$) for GBM. Together, these findings establish a multiomics-based predictive model that enables refined glioma recurrence risk assessment, offering personalized treatment strategies for LGG and GBM patients.

[79] *miSAM: Robust MicroRNA Expression Estimation Using Bi-Objective Evolutionary Learning Algorithm in Cancer Transcriptomics*

Yann-Lin Ho(National Yang Ming Chiao Tung University) , Shinn-Ying Ho (NYMCTU) and Tzong-Yi Lee (Institute of Bioinformatics and Systems Biology, NYMCTU)

Abstract

MicroRNAs (miRNAs) play crucial regulatory roles in cancer biology, but accurately quantifying their expression remains a significant unmet challenge in single-cell and spatial transcriptomics. Current sequencing technologies predominantly capture polyadenylated messenger RNAs (mRNAs), rendering them incapable of directly profiling miRNAs, which lack poly(A) tails. To address this gap, we thus propose miSAM, a novel computational framework for estimation of miRNA expressions based on a bi-objective combinatorial genetic algorithm in conjunction with support vector regression. The miSAM jointly optimizes the selection of a minimal subset of mRNAs, called signatures, while maximizing the Spearman correlation coefficient (SCC) between inferred and actual miRNA expression levels. Evaluation on The Cancer Genome Atlas (TCGA)-BRCA dataset, comprising 1,095 breast cancer samples with expression profiles of 1,881 miRNAs and 19,937 mRNAs, demonstrates the effectiveness of miSAM. Using the top five prognostic miRNA biomarkers for breast cancer, miSAM achieved a mean SCC of 0.633 on the test set while utilizing only 32.6 mRNAs in average, significantly outperforming baseline approaches including: (1) differential expression filtering-based SVR using 887 mRNAs (SCC = 0.562), and (2) LASSO-based SVR using 147.4 mRNAs (SCC = 0.470). miSAM also outperformed XGBoost, which yielded a SCC of approximately 0.45–0.50 across various cancer types. Furthermore, the identified mRNAs signatures offer explainable insights into the regulatory associations between miRNAs and their corresponding mRNA targets. These results underscore miSAM's potential as a robust, interpretable, and scalable tool for miRNA inference in spatial transcriptomics, single-cell sequencing analyses, and precision oncology.

[86] *Self-Attention Enhanced Deep Learning Models for Immune Cell Deconvolution from Bulk RNA-Seq*

Chia-Ru Chung (National Central University), Yen-Lin Chen (NCU), Yun Tang (Institute of Bioinformatics and Systems Biology, National Yang Ming Chiao Tung University), Bo-Kai Hsu (Department of Computer Science and Engineering, College of Informatics, Yuan Ze University), Li-Ching Wu (Department of Biomedical Sciences and Engineering, NCU), Tzong-Yi Lee (IBSB, NYMCTU) and Jorng-Tzong Horng (Department of Computer Science and Information Engineering, NCU)

Abstract

Accurate immune cell composition profiling is crucial for understanding immunological dynamics and disease mechanisms. Bulk RNA sequencing (bulk RNA-seq) is widely employed due to its cost-effectiveness and scalability; however, it lacks the resolution to identify cell-specific gene expression. To address this limitation, we propose a self-attention enhanced deep learning model designed for precise immune cell deconvolution from bulk RNA-seq data. We systematically annotated immune cell types from four single-cell RNA-seq (scRNA-seq) peripheral blood mononuclear cell (PBMC) datasets and validated these annotations against established automated identification tools (SingleR, Seurat, scPred, ScType). Leveraging these annotations, we generated realistic pseudo-bulk RNA-seq training samples using Dirichlet-distribution-based composition sampling, significantly enhancing the model's performance, particularly for rare cell populations. Comparative evaluations demonstrated that our self-attention enhanced deep learning model consistently outperformed existing approaches, including CIBERSORTx and Scaden, achieving lower prediction errors and higher correlations on benchmark PBMC datasets. Integrating multi-head self-attention allowed the model to dynamically capture intricate dependencies among gene expression features, substantially improving deconvolution accuracy for specific cell subsets. While demonstrating robust performance on PBMC datasets, we acknowledge that broader validation is essential due to potential limitations in generalizability across different tissue types and conditions. Our study highlights the potential of self-attention mechanisms and realistic training data generation strategies to enhance computational deconvolution techniques, providing valuable tools for clinical diagnostics and translational immunology research.

[88] *OSANet: Detection of Obstructive Sleep Apnea Episodes Using a DarkNet-Based Deep Learning Approach and Time-Frequency Spectrogram Features Derived from Single-Lead ECG*

Febryan Setiawan (Department of Biomedical Engineering, College of Engineering, National Cheng Kung University, Tainan) and Che-Wei Lin (DBE, CE, NCK, Tainan)

Abstract

An OSA detection algorithm has successfully been developed employing bag-of-features (BoF) extracted from an ECG spectrogram alongside a deep learning (DL) framework, yielding a commendable classification accuracy and exceptional temporal resolution. Validation of this study utilized overnight ECG recordings from 33 subjects sourced from the Physionet Apnea-ECG database (PAED), exhibiting an average apnea–hypopnea index (AHI) of 30.23 (/h). The investigation focused on determining the optimal spectrogram window duration, examining 60-s intervals to achieve the desired accuracy level. Moreover, specific frequency bands (0.1–50, 8–50, 0.8–10, and 0–0.8 Hz) were isolated to generate BoF, identifying the most suitable frequency band for precise OSA detection. Employing the DarkNet-based CNN classification model, named OSANet, the algorithm was trained and validated to discern AH and non-AH events. The 5-fold cross-validation (5fold-CV) results demonstrated impressive accuracies of 91.9% for the 0.8–10 Hz frequency bands using BoF derived from ECG spectrograms with 60-s time windows.

[89] *Development of a Sliding Window-Based Oversampling Framework for Convolutional Neural Network Sleep Stage Classification Using Polysomnographic Spectrogram Fusion*

Ai Chung (Department of Biomedical Engineering, College of Engineering, National Cheng Kung University, Tainan), Febryan Setiawan (DBE, CE, NCKU, Tainan), Cheng-Yu Lin (Department of Otolaryngology, College of Medicine, NCKU, Tainan) and Che-Wei Lin (DBE, CE, NCKU, Tainan)

Abstract

This study proposed an oversampling framework based on a sliding window approach for CNN-based sleep stage classification using PSG spectrogram fusion. Continuous Wavelet Transform (CWT) was employed as the feature transformation method to convert raw EEG and EOG signals into time-frequency spectrograms. To address the issue of class imbalance commonly found in sleep datasets, the sliding window method was applied as a data augmentation technique, resulting in a more balanced distribution of samples across sleep stages. Multi-channel, multi-epoch spectrograms were used as input to three CNN-based classifiers: AlexNet with SVM, AlexNet, and ResNet-18. The results demonstrated that the sliding window method significantly enhanced classification performance across all stages, particularly in the N1 stage, achieving an average accuracy of 98.53%. The highest overall average accuracy of 95.81% was obtained using ResNet-18.

[91] *Event-based Detection of Obstructive Sleep Apnea via YOLOv8 Nano and ECG Spectrograms: Integration with Home Sleep Apnea Test and Edge Computing*

Ponpatcharee Nipattanon (NCKU BME) and Che-Wei Lin (DBE, CE, NCKU, Tainan)

Abstract

Obstructive sleep apnea (OSA) remains significantly underdiagnosed due to limitations associated with traditional polysomnography (PSG), including complexity, high cost, and patient inconvenience. To overcome these challenges, this study introduces a novel event-based detection method using the YOLOv8 Nano object detection model applied to electrocardiogram (ECG) spectrograms. ECG features were generated via Continuous Wavelet Transform (CWT) with the Morlet wavelet, enabling precise identification and temporal localization of individual apnea and hypopnea events within the signal. Model performance was rigorously validated using datasets comprising 50 subjects from clinical source: clinical ECG data collected at the National Cheng Kung University Hospital Sleep Center (NCKUHSC).

Evaluation involved both 5-fold and Leave-One-Subject-Out (LOSO) cross-validation methods to assess generalization. Experimental results demonstrated that the YOLOv8 Nano model achieved a mean average precision (mAP) of 0.480 for event detection on 135-second segments, significantly surpassing traditional epoch-based classification methods by providing accurate temporal granularity. Additionally, apnea-hypopnea index (AHI) estimation, derived from counting precisely localized events, strongly correlated with clinical ground-truth values (Pearson correlation coefficient R = 0.86, RMSE = 12.16 events/hour for detection on 135-sec ECG spectrogram segments), highlighting clinical accuracy and reliability. The compact model size (~6 MB, 3.2M parameters) facilitates seamless integration with Home Sleep Apnea Tests (HSAT) and edge computing platforms, enabling accessible, cost-effective, and patient-friendly diagnostic solutions. Furthermore, the event-based nature of the results allows for extraction of richer, event-specific clinical parameters beyond AHI. Future research directions include enhancing feature extraction, improving model generalization with larger datasets, exploring these extended clinical parameters, and optimizing embedded computing implementations for real-world clinical use.

[92] *Explainable Machine Learning for Failed Labor Induction Prediction Using Nationwide Insurance Data*

Daniel C.A. Nugroho (Faculty of Medicine, Universitas Kristen Duta Wacana, Yogyakarta, Indonesia), Septian D. Periska (FM, UKDW, YI), Justinus A. Putranto (FM, UKDW, YI), Jimmy I. Gunawan (FM, UKDW, YI), Muhammad S. Muhtar (College of Management, Taipei Medical University Taipei, Taiwan), Jason C. Hsu (CMTMU Taipei, Taiwan), Yuan-Chii G. Lee (College of Medical Science and Technology, TMU) and Emily Chia-Yu Su (Institute of Biomedical Informatics, National Yang Ming Chiao Tung University, Hsinchu, Taiwan)

Abstract

Failed labor induction presents a significant challenge, posing considerable risks for maternal health. The development of accurate predictive models is essential for assisting healthcare providers in determining the most suitable delivery methods. This study explores the application of machine learning (ML) models to predict failed labor induction, utilizing data from the Indonesian National Health Insurance (INHI). A retrospective cohort of 9-month period of pregnancy was established using INHI Sample Data, comprising 27,953 pregnancy cases. Failed labor induction was identified through ICD-10 codes (O61). The features considered included demographic data (age, insurance class, region) and binary-encoded diagnoses. Various ML models were assessed for their predictive performance. The ensemble model demonstrated a high area under the curve (AUC) of 0.759 (95% CI , with a balanced trade-off between sensitivity (0.816) and specificity (0.589). SHAP analysis was used to interpret feature contributions, highlighting both clinical and demographic factors influencing model predictions. ML models showed strong potential in predicting failed labor induction using administrative data. While the ensemble model achieved the best overall performance, simpler models such as logistic regression or XGBoost may offer greater practicality for clinical integration in Indonesia.

[93] *Assessing Cardiac Functionality by Means of Interpretable AI and Myocardial Strain*

Marco S. Nobile (Ca' Foscari University of Venice), Amalia Lupi (University of Padua), Leone Bacciu (Ca' FUV), Matteo Grazioso (Ca' FUV), Chiara Gallese (University of Turin), Emilio Quaia Quaia (UP) and Alessia Pepe (UP)

Abstract

Cardiac Imaging is a powerful methodology for the accurate assessment of heart functionality. Among the possible approaches, Myocardial Strain assesses the functionality of the heart by tracking the movement and deformation of myocardium during the cardiac cycle. This information, that can be acquired also by means of Cardiac Magnetic Resonance, can pave the way to the development of predictive models using machine learning. In this work, we developed a predictive model of left ventricular ejection fraction, which is a measure of the heart's function to pump oxygen-rich blood to the body, trained using strain data. Specifically, we developed a fully interpretable model based on a rule-based Fuzzy Inference System, coupled with a novel methodology for the disambiguation of the rules. Our results show that the developed model is able to accurately estimate the ejection fraction, and can provide physicians with additional insights about the role of strain features.

[94] *Improving the Efficiency and the Validity of Molecular Transformers*

Leone Bacciu (Ca' Foscari University of Venice), Matteo Grazioso (Ca' FUV), Silvia Multari (Ca' FUV), Francesca Grisoni (Eindhoven University of Technology), Angelica Mazzolari (University of Milan) and Marco S. Nobile (Ca' FUV)

Abstract

Since their advent, Transformer models have been applied across a wide range of fields, including cheminformatics. In this context, drug discovery has benefited from using Molecular Transformers by leveraging diverse string representations of molecules, although with some limitations such as low validity of generated molecules and slow computation times. In this study, we present a model focused on improving the efficiency and yield of valid predictions of a formerly developed Molecular Transformer specifically dedicated to metabolism prediction. Metabolism refers to all the biotransformations a drug undergoes once inside the human body, directly influencing its therapeutic effect and potential toxicity, and therefore represents a key topic in medicinal chemistry. Our previous work framed molecular transformation prediction as a sequence-to-sequence translation problem using the Simplified Molecular Input Line Entry Systems (SMILES) notation to represent substrates and predicted metabolites. While the approach proved to be very promising, as the model demonstrated the ability to learn how to metabolize (or not) molecules with high accuracy, the evaluation was limited to syntactically valid SMILES, that could be converted into the corresponding molecular structure, leaving room for improvement in ensuring the validity of generated metabolites. To address this limitation, we here propose an optimized model that integrates pre-training, transfer learning, and fine-tuning techniques, already improving validity and reducing computation time. Finally, by separating the metabolism prediction task from the SMILES syntax learning, we ensure broader applicability of the proposed model across diverse datasets and a variety of SMILES-based tasks beyond metabolic transformations, expanding its potential utility.

[95] *Closed-Loop Brain-Controlled Exoskeleton System with a Hybrid Model for Stroke Rehabilitation*

Yu-Wei Lin (Institute of Electrical and Control Engineering, National Yang Ming Chiao Tung University), Shi-Yong Luo (IECE, NYMCTU), Po-Hsun Cheng (Service Systems Technology Center, ITRI, Dept. of Software Engineering, National Kaohsiung Normal University), Chia-Hsin Chen (Department of Kaohsiung Medical University Chung-Ho Memorial Hospital), Yu-Zhen Liu (DMKMU), Zhi-Ting Chen (DMKMU) and Li-Wei Ko (Electrical and Control Engineering, NYMCTU, Service Systems Technology Center, ITRI)

Abstract

Stroke (Cerebrovascular Accident, CVA) is one of the diseases with the greatest impact on human health, particularly due to the neurological dysfunctions that often follow, such as upper or lower limb paralysis, foot drop, muscle weakness, and cognitive impairment, which significantly affect patients' daily lives. Existing research indicates that the first three months after a stroke is the "golden period" for treatment, during which rehabilitation training can greatly improve a patient's quality of life and promote neuroplasticity. However, some stroke patients are unable to engage in active rehabilitation training due to physical limitations and can only rely on passive rehabilitation methods. To address this issue, this study proposes a closed-loop brain-controlled exoskeleton system based on brain-computer interface (BCI) technology to enhance rehabilitation in post-stroke patients. This study designed a brain-controlled exoskeleton system consisting of open-loop control and closed-loop feedback. In the open-loop control stage, patients control the exoskeleton's standing, walking, and sitting commands through electroencephalogram (EEG) signals; in the closed-loop feedback stage, the rehabilitation effect is evaluated through brainwave analysis and clinical evaluation. Experimental results demonstrate that the system can effectively assist patients in regaining motor control during training and elicit significant neurophysiological responses in the preparation and execution stages of movement. Additionally, clinical evaluation results showed that patients made notable progress in muscle strength and functional recovery. Although the study sample size was small (n=3) and the treatment period was short, the study highlights the potential application of brain-controlled exoskeleton systems in post-stroke rehabilitation. Future studies should expand the sample size and include long-term follow-up to further assess its clinical feasibility and long-term effects.

[96] *Visual Game-Based Upper Limb Ergometer Therapy Associated with EEG Responses in Stroke Rehabilitation*

Chiao-Hsin Chen (National Yang-Ming Chiao Tung University), Li-Wei Ko (Electrical and Control Engineering, NYMCTU, Service Systems Technology Center, ITRI), Hsuan Cheng (Department of Kaohsiung Medical University Chung-Ho Memorial Hospital), Yu-Lin Wang (Department of Physical Medicine and Rehabilitation, Chi Mei Medical Center), Kai-Chiao Chi (DKMU Chung-Ho MH), Chih-Chung Wang (DKMU Chung-Ho MH) and Chia-Hsin Chen (DKMU Chung-Ho MH)

Abstract

This longitudinal EEG study demonstrates that integrating interactive visual gaming with conventional upper limb resistance training enhances motor recovery in post-stroke patients compared to traditional rehabilitation alone. The game-based approach resulted in superior behavioral outcomes, with significantly greater improvements in specific muscle groups. Notably, among participants in the game-based group, those who exhibited peripheral motor improvement also showed significantly greater alpha-band suppression in the lesioned motor cortex compared to non-improved individuals. EEG signals were preprocessed using Independent Component Analysis (ICA), and Power Spectral Density (PSD) analysis was performed to evaluate cortical activation during the rehabilitation period. The findings suggest a positive association between motor cortex activation and improvements in muscle strength. This study presents a clinically feasible rehabilitation model that incorporates game-based feedback without modifying standard protocols, supporting its potential as a more interactive and effective approach for early neurorehabilitation.

[97] *Evaluating the Feasibility of Vision-Language Models in Skin Cancer Detection: A Comparative Study with CNNs and Vision Transformers*

Yu-Hxiang Chen (National Central University), Ting-Ting Chang (NCU), Yao-Zhi Xue (NCU), Wei-Hsiang Sung (NCU) and Chia-Yu Lin (NCU)

Abstract

This study presents a comprehensive evaluation of vision-language models (VLMs) for skin lesion classification, comparing them with conventional convolutional neural networks (CNNs) and Vision Transformer (ViT) architectures. Using the HAM10000 dataset, we assess six models across four critical dimensions: classification accuracy, robustness to visual perturbations, zero-shot generalization to unseen lesion types, and the quality of semantic explanations. While traditional vision-only models achieve higher accuracy on clean images, their performance degrades significantly under various types of image distortion. In contrast, VLMs, particularly Qwen2.5, demonstrate stronger resilience and produce more coherent and clinically relevant explanations. However, these models still lag behind in overall classification performance and exhibit limited generalization capabilities in zero-shot settings. The results reveal key trade-offs between task-specific accuracy and multimodal adaptability, offering practical insights into the current capabilities and limitations of VLMs in dermatological artificial intelligence applications.

[98] *Let's Talk Bout Mutation: Evolutionary Programming for DNA Sequences*

James Sargant (Brock University), Michael Dubé (Otto-von-Guericke-University), Sheridan Houghten (BU) and Steffen Graether (University of Guelph)

Abstract

Self-driving automata (SDAs) are extensions of finite state automata that both read and output symbols. Previously, genetic algorithms were used to evolve SDAs to generate sequences that closely matched given DNA sequences, with the eventual goal of finding patterns in those sequences that were not achievable using traditional biological methods. Previous work demonstrated that improvements in fitness were almost exclusively due to mutation not crossover. This paper evaluates the use of evolutionary programming (EP) using SDAs as the representation. EP allows for easy handling of multiple types of mutation, including changes in the number of states, which was not available in earlier approaches. This work uses three fitness metrics: primary sequence matching fitness, secondary sequence similarity fitness, and a relative fitness function known as bout score. Tested on a set of six target DNA sequences, the approach matched 84.4–98.2% of each sequence, and discovered some features of the sequences for future exploration.

Authors and abstracts

• Short Papers

Paper number: [2], [100], [103], [104], [105], [106], [107], [108], [110], [112], [113], [117], [118], [119], [120], [121], [123], [124], [125] , [126], [127], [128], [129], [130], [131] , [132], [133], [134], [135]

[2] *Can Knowledge Be Distilled from Single-cell Large Foundation Models for Efficient Cell-type Annotation?*

Haohuai He (The Hong Kong Polytechnic University), Zhi-An Huang (City University of Hong Kong (Dongguan)), Jibin Wu (HKPU) and Kay Chen Tan (HKPU).

Abstract

Single-cell analysis has been revolutionized by foundation models, yet their deployment faces significant computational challenges. We present an efficient knowledge distillation framework that transfers knowledge from large foundation models to a lightweight multilayer perceptron for single-cell analysis. Our approach achieves superior performance in cell type annotation while reducing training time by 7.4-fold compared to foundation models. Experimental results across multiple datasets demonstrate that our lightweight model maintains or even exceeds the accuracy of foundation models, providing a practical solution for resource-efficient single-cell analysis.

[100] *Segmentation and Localization of Normal and Fractured Vertebrae in Spine CT Images*

Chuan-Yu Chang (National Yunlin University of Science and Technology), Min-Hong Hsieh (Dalin Tzu Chi Hospital, Buddhist Tzu Chi Medical Foundation) and Bo-Yan Lin (NYUST, Yunlin, Taiwan).

Abstract

Vertebral compression fractures caused by osteoporosis are one of the causes of pain and disability in the elderly. Therefore, early diagnosis and treatment are crucial in managing osteoporotic compression fractures. Although MRI images can effectively diagnose related conditions, the cost of diagnosis is relatively high. In contrast, CT images have a lower diagnostic cost but are less accurate than MRI in segmenting vertebral fractures. This paper proposed a YOLO-based instance segmentation method to segment and localize normal and fractured vertebrae in spinal CT images, aiming to achieve fast and accurate segmentation, and to provide valuable diagnostic suggestions and references for clinicians. Experimental results showed that the proposed YOLO-GAM method achieves an accuracy of 99.5%, outperforming the baseline YOLO11, which achieves 96.6%.

[103] *Adapting graph representation learning for cancer driver gene prediction*

Thi Thuy Duong Vu (Faculty of Fundamental Sciences, University of Medicine and Pharmacy at Ho Chi Minh City) and Girum Fitihamlak Ejigu (Department of Computer Science and Engineering, Kyung Hee University).

Abstract

Identifying cancer driver genes is crucial for elucidating the molecular mechanisms underlying cancer development and for proposing effective therapeutic strategies. In recent years, deep graph learning methods tailored for driver gene detection have emerged, particularly focusing on learning gene representations from biological networks and multi-omics features, which are then used to predict driver genes. However, the quality of these learned gene representations still requires improvement to enable more accurate predictions while maintaining computational efficiency. In this study, we adapted a recent general-purpose graph Transformer architecture, NAGphormer, originally developed for node classification, to the task of driver gene prediction. To the best of our knowledge, this is the first application of NAGphormer for classifying cancer driver genes. Experimental results show that the adapted algorithm outperforms existing driver gene prediction models in both AUPR and AUC evaluation metrics, while also reducing computational time compared to two recent comparison methods. These findings highlight the potential of further deep graph representation learning algorithms to enable more accurate and efficient driver gene identification in future studies.

[104] *RGB-D Nutrient Prediction Based on Fused Cross-Modal Attention and Progressive Learning*

Chao-Yang Lee (National Yunlin University of Science and Technology) and Ting-Wei Wu (NYUST)

Abstract

In modern society, extended working hours often drive people to rely on takeout or fast food as their primary meal option, and prolonged unhealthy eating patterns can lead to health risks such as hypertension and diabetes. Traditionally, nutritional intake has been managed using labels on packaged foods, but takeout and fast food rarely provide such information. To bridge this gap, this study proposes a deep learning approach based on RGB images for simultaneous food classification and nutrient prediction. Unlike conventional methods that depend solely on food categories and assume fixed portion sizes, our method feeds both RGB images and their derived depth maps into a learning model to jointly predict food types and nutritional values. The RGB images supply rich texture, contour, and color cues, while the depth maps capture object distance and volume information, enabling the model to dynamically adjust nutrient estimates according to the actual food size.

[105] *Using Non-invasive Parameters for Bladder Outlet Obstruction Prediction by Machine Learning*

Chien-Cheng Lee (Yuan Ze University), Chung-You Tsai (Far Eastern Memorial Hospital), Yun-Ci Sie (YZU), Jing-Hui Tian (Hualien Tzu Chi Hospital) and Hann-Chorng Kuo (Buddhist Tzu Chi Medical Foundation and Tzu Chi University).

Abstract

Bladder outlet obstruction (BOO) is a common cause of lower urinary tract symptoms (LUTS) in aging males, typically diagnosed through invasive video urodynamic studies (VUDS). To reduce reliance on such procedures, we propose a novel, non-invasive predictive method that combines clinical parameters with advanced machine learning. Our approach applies Synthesized Minority Oversampling by Mode (SMOM) for data augmentation and uses a Tabular Prior-Fitting Network (TabPFN)—integrating structural causal modeling and Bayesian neural networks within a Transformer architecture—to predict VUDS-based BOO (VBOO). Experimental results show an AUC of 0.73, indicating strong potential as a clinical decision support tool.

[106] *Low-Level Feature Integration for Robust Federated Learning in Non-IID Medical Image Analysi*

Yu-Ping Gao (National Cheng Kung University) and Pau-Choo Chung (NCKU).

Abstract

Federated Learning facilitates collaborative model training across medical institutions while ensuring data privacy. However, the non-IID nature of pathological images presents significant challenges for model training and generalization. To address this issue, this study refines the data consistency process in HarmoFL by integrating the low-level features of the original image into the Fourier transformation strategy. The experimental results, obtained using Camelyon17 for classification and real-world liver tumor datasets for segmentation, demonstrate that the enhanced federated learning method achieves a superior performance and robustness under extreme data heterogeneity than HarmoFL.

[107] *Effect of Initial Weights on CT Image Registration*

Rojean Noorinayer (York University), Stephen Chen (YU), Michael Hardisty (Sunnybrook Research Institute) and Teodora Vujovic (SRI).

Abstract

We study the effect of initial weights on a simple 3D convolutional neural network (CNN) for lung CT image registration. The model predicts a displacement field to align moving and fixed scans. Instead of building complex deep learning registration models, we begin with a baseline model that is a simple one-layer 3D CNN optimized by using a variable learning rate schedule. While the baseline performs well on easy cases, it struggles with harder ones. Our results show that improved initial weights can greatly reduce Total Registration Error (TRE), particularly for challenging cases.

[108] *An Interpretable Domain Adaptation Framework using Transformers for Drug Response Prediction*

Chi-Tang Wang (Institute of Biomedical Informatics National Yang Ming Chiao Tung University), Yu-Kai Chiu (IBINYMCTU) and I-Fang Chung (IBINYMCTU).

Abstract

Predicting anticancer drug response faces domain discrepancies between cell-line models and patient samples. We propose an interpretable framework integrating variational autoencoders, Explainable Substructure Partition Fingerprints (ESPF), and Transformers. Our model aligns genomic distributions across domains, identifies drug molecular substructures, and integrates these features via Transformer encoders. Results demonstrate superior predictive performance, effectively mitigating out-of-distribution issues while offering enhanced interpretability through attention mechanisms.

[110] *Enhancing Large Pathology Foundation Models with Multi-Scale and Multi-Modal Integration for Cancer Prognosis Prediction*

Po-Hsun Li (National Yang Ming Chiao Tung University, Taipei, Taiwan) and Yen-Hua Huang (NYMCTU, Taipei, Taiwan).

Abstract

We proposes a framework to improve large pathology foundation models for cancer prognosis by integrating multi-scale whole slide image (WSI) features and multi-modal information from tissue and cellular levels. Utilizing cross-attention mechanisms and multiple instance learning (MIL), our method is validated on the TCGA-LUAD dataset, demonstrating effective improvement in survival risk prediction.

[112] *A Framework for Multi-Session Virtual Psychological Counseling Syetem based on LLM*

Chung-Chian Hsu (Department of Information Management, National Yunlin University of Science and Technology, Yunlin, Taiwan), Cheng-Han Lu (DIM, NYUST, Yunlin, Taiwan), Yong-Jin Chen (DIM, NYUST, Yunlin, Taiwan, Yu-Huan Hsueh (DIM, NYUST, Yunlin, Taiwan), Ke-Shun Chen (DIM, NYUST, Yunlin, Taiwan), Ting-Yun Ke (DIM, NYUST, Yunlin, Taiwan), Tin-Kwang Lin (Dalin Tzu Chi Hospital, Buddhist Tzu Chi Medical Foundation, Chiayi, Taiwan) and Yu-Hsiang Huang (DTCH, BTCMF, Chiayi, Taiwan).

Abstract

Global mental health challenges are exacerbated by a scarcity of professional counseling resources. To address this issue, we propose and evaluate a multi-session virtual psychological counseling system grounded in Cognitive Behavioral Therapy (CBT) and Large Language Models (LLMs). The core innovation is a structured, multi-session, multi-turn conversational framework that simulates professional counselor-patient interactions over an entire course of therapy. Based on evaluation results, we selected Claude 3.5 Sonnet for dialogue generation after comparing several LLMs, finding it superior in adhering to complex instructions. The system generated dialogue datasets for six distinct patient personalities. The system's efficacy was validated through two analyses: (1) a dialogue word count analysis to confirm personality consistency, and (2) an emotional judgment consistency analysis. The latter compared five leading LLMs against ratings from three professional personnels. Results show that ChatGPT 4o achieved the highest consistency with expert emotional judgments, attaining the best overall rank score. This work presents a complete framework from generation to evaluation, demonstrating a viable pathway for creating LLM-based tools to support mental health services.

[113] ***Virtual Healing: Counterfactual X-Ray Images Using Classifier-Free Guided Diffusion Models***

Daniel Kong (Department of Computer Science, National Tsing Hua University), Qi-Xian Huang (Institute of Information Systems and Applications, NTHU), Hung-Min Sun (Institute of Information Security, NTHU), Wei-Hsin Yuan (Division of Radiology Taipei Municipal Gan-Dau Hospital), Kuan-Yuan Chen (Department of Medical Education Taipei Veterans General Hospital) and Wen-Ho Juang (Department of Computer Science and Information Engineering, National Formosa University).

Abstract

We introduce a classifier-free guided diffusion model architecture for detecting pleural effusions in chest X-ray images. The resulting anomaly is displayed by reconstructing a pseudo-healthy version of the X-ray scan and subtracting it from the original image. By eliminating the classifier, in conjunction with image deblurring in the data pipeline, we reduce model complexity while attaining performance matching or surpassing that of classifier-guided DDIM models. We evaluate this approach on metrics used for generative models, together with qualitative input from medical experts.

[117] ***The Impact of Min-Max and Z-Score Normalization on Prostate MRI Image Segmentation***

Chun-Hung Yang (Department of Electrical Engineering, National Formosa University) and Hui-Yen Lin (DEE, Southern Taiwan University of Science and Technology
(Southern Taiwan University of Science and Technology)).

Abstract

This study investigates the impact of different normalization techniques on prostate MRI image segmentation models, with a particular focus on comparing the performance of Min-Max normalization and Z-Score standardization. Experiments were conducted using the publicly available PROSTATEx dataset and MRI images from a single medical institution, employing the U-Net3+ architecture for segmentation training. The results indicate that while both normalization methods yield comparable average Dice scores, Z-Score standardization produces a smaller standard deviation, suggesting more consistent performance. These findings highlight that the choice of normalization technique can influence the robustness of deep learning models in medical image segmentation tasks.

[118] ***Comparison of Prostate Region Segmentation in 2D MRI***

Chun-Hung Yang (Department of Electrical Engineering, National Formosa University) and Jiu-Wei Liu (DEE, Southern Taiwan University of Science and Technology (Southern Taiwan University of Science and Technology)).

Abstract

Prostate cancer (PCa) is one of the leading causes of cancer-related mortality in men. Accurate prostate segmentation is essential for precise tumor localization, risk assessment, and treatment planning. However, the segmentation of the base and apex regions remains challenging due to their indistinct anatomical features. This study proposes a regionspecific approach by dividing MRI images into three anatomical zones: base, middle, and apex. Separate models are trained for each region, and their predictions are subsequently integrated. UNet and U-Net3+ architectures are employed as the segmentation frameworks. The proposed method demonstrates improved stability in terms of standard deviation for base and apex regions compared to conventional single-model approaches, along with a marginal improvement in Dice Similarity Coefficient (DSC) scores.

[119] *Impact of Cross-Subject Distribution Shifts on Glucose Prediction Using Wearable Data*

Nhung Huyen Hoang (KUAS)

Abstract

Wearable sensors hold promise for non-invasive glucose monitoring by leveraging physiological signals such as heart rate, skin temperature, and electrodermal activity. However, many existing studies suffer from data leakage, where training and testing data come from the same individuals, potentially inflating performance and limiting generalizability to unseen individuals with differing physiological patterns. This study investigates how cross-subject distribution shifts influence the performance of glucose prediction models based on wearable data. We used the BIGIDEAs Lab dataset, comprising simultaneous recordings of glucose levels and multimodal physiological signals from 16 subjects. Ten personalized XGBoost models were trained, each using data from a single subject, resulting in a total of 10 distinct models. These were then tested on the 6 held-out subjects to evaluate cross-subject generalization. To quantify distribution shifts in glucose profiles between training and test subjects, we employed the Anderson-Darling (AD) statistic. Model performance was assessed using root mean squared error (RMSE), normalized root mean squared error (NRMSE) and mean absolute relative difference (MARD). Results indicate that models trained on one subject performed poorly when applied to other subjects. Repeated measures correlation analysis showed a significant positive correlation between the AD statistic and each of the error metrics. These findings highlight the challenges of cross-subject generalization and the necessity of adopting distribution-aware modeling techniques.

[120] *Virtual Healing: Counterfactual X-Ray Images Using Classifier-Free Guided Diffusion Models*

Daniel Kong (Department of Computer Science, National Tsing Hua University), Qi-Xian Huang (Institute of Information Systems and Applications, NTHU), Hung-Min Sun (Institute of Information Security, NTHU), Wei-Hsin Yuan (Division of Radiology Taipei Municipal Gan-Dau Hospital), Kuan-Yuan Chen (Department of Medical Education Taipei Veterans General Hospital) and Wen-Ho Juang (Department of Computer Science and Information Engineering, National Formosa University).

Abstract

We introduce a classifier-free guided diffusion model architecture for detecting pleural effusions in chest X-ray images. The resulting anomaly is displayed by reconstructing a pseudo-healthy version of the X-ray scan and subtracting it from the original image. By eliminating the classifier, in conjunction with image deblurring in the data pipeline, we reduce model complexity while attaining performance matching or surpassing that of classifier-guided DDIM models. We evaluate this approach on metrics used for generative models, together with qualitative input from medical experts.

[121] *Enhancing Gene Regulatory Network Predictions by PageRank-Weighted Graph Neural Networks*

Bo-Han Wu (Department of Computer Science and Information Engineering, National Central University)

Abstract

Accurate deciphering of gene regulatory networks (GRNs) is crucial for understanding complex biological mechanisms and the processes underlying diseases. In this study, we developed a computational framework that integrates the PageRank algorithm with graph neural networks (GNNs) to enhance the prediction of gene regulatory links. Initially, edge flux scores, derived from PageRank, highlight the global centrality of the network. These scores enrich the GNN model by capturing both topological and contextual patterns of gene interactions. The proposed method demonstrated an improvement in predictive performance, merging the interpretability offered by network theory with the predictive capabilities of deep learning, as evidenced by benchmarks across multiple GRN datasets.

[123] *Pyramid-Pooling Multi-Resolution Learning for Automatic Pneumothorax Segmentation and Its Verification on NCKU Hospital's Dataset*

Chian C. Ho (National Yunlin University of Science & Technology) and Xin-You Liao (NYUST).

Abstract

Based on lots of conventional well-known deep learning models for automatic pneumothorax segmentation, this paper develops a novel method of "pyramid-pooling multi-resolution learning" to improve the training and prediction stages of the deep learning model used for automatic pneumothorax segmentation. The proposed "pyramid-pooling multi-resolution learning" adds a pyramid pooling module into the deepest layer of the encoder to capture feature maps at multiple resolutions. It can enhance the deep learning model to perceive both local and global spatial contextual information during training and prediction stages. It makes the deep learning model not only aggregate multi-resolution contextual information effectively to extract global feature and deep details, but also alleviate the conditions of highly-uncertainty or abnormal pneumothorax segmentation common to conventional deep learning models of automatic pneumothorax segmentation. Experimental results show that, against "ensemble multi-resolution learning" and "progressive multi-resolution learning", the proposed "pyramid-pooling multi-resolution learning" can raise the feature adaptability, segmentation accuracy, and segmentation reliability of deep learning model more effectively, in terms of 8 well-known deep learning models for automatic pneumothorax segmentation. On the other hand, the paper has also performed and tested the proposed "pyramid-pooling multi-resolution learning for automatic pneumothorax segmentation" on NCKU Hospital's dataset. The testing results show that the proposed method also works well on NCKU Hospital's dataset and improves the accuracy and reliability of automatic pneumothorax segmentation in chest radiographs.

[124] *Robust Blood Vessel Feature Extraction using Multispectral Imaging*

Shih-Yu Chen (National Yunlin University of Science and Technology), Siang-Yu Huang (NYUST) and Chun-Wei Huang (NYUST).

Abstract

Feature extraction is a fundamental task in image processing and computer vision, aiming to derive discriminative and representative information from raw image data for further analysis. In medical image analysis, blood vessels—essential components of the human circulatory system—are of particular interest. However, traditional feature extraction methods often struggle with challenges such as poor image quality and the intricate, branching structure of vascular networks. To address these issues, this paper proposes a novel blood vessel feature extraction method based on the Low-rank Sparse Orthogonal Subspace Projection (LSOSP) algorithm. LSOSP is a subspace learning technique designed to project high-dimensional image data into a lower-dimensional subspace while preserving essential structural and discriminative features. The algorithm incorporates low-rank and sparse constraints to filter out noise and redundancy, while orthogonality constraints ensure the resulting subspace is both independent and complete. By solving an optimization problem, LSOSP yields an optimal projection matrix that maps original image data into a compact subspace, thereby enhancing the extraction of blood vessel features. To evaluate the performance of the proposed method, manually annotated vessel ground truths were used as a reference. Experimental results demonstrate that the LSOSP-based approach achieves an Area Under the Curve (AUC) of 76% and an overall accuracy (ACC) of 87%, validating its effectiveness and robustness in vascular feature extraction.

[125] *Machine Learning-Based Classification of CAA and Non-CAA for ICH Patients*

Guan-Ying Wu (Department of Computer Science and Information Engineering, National Formosa University), Chih-Ching Tsai (Department of Electronic Engineering, NFU), Bo-Ching Lee (Department of Medical Imaging, National Taiwan University Hospital), Wen-Ho Juang (DCSIE, NFU), Chun-Hung Yang (Department of Electrical Engineering, NFU) and Yung-Ming Kuo (DEE, NFU).

Abstract

This study presents a classification approach that integrates clinical data and machine learning to differentiate cases of cerebral amyloid angiopathy (CAA) among patients with intracerebral hemorrhage (ICH). A total of 299 patient records were analyzed, including 32 CAA cases, reflecting a highly imbalanced dataset. To address this, random oversampling and cross-validation techniques were employed to compare multiple classification models. The experimental results indicate that the XGBoost model achieved the best performance, with a Youden's index of 0.6791, demonstrating strong discriminative capability. This method offers a potential clinical decision support tool for CAA identification in settings lacking access to PET imaging.

[126] *Exploring Generative and Cold Adapted Amylases using VAE encoded Evolutionary Landscapes*

Jennifer Hallinan (BioThink) and Anil Wipat (School of Computing, Newcastle University & Insiligence Ltd.).

Abstract

Amylase is an important enzyme, which catalyzes in the breakdown of starch to the oligosaccharides maltose and maltriose. Although amylase genes are ubiquitous, new amylases are still required by biotech industry. In order to develop a method to identify promising cold adapted generative amylases, we constructed an amylase evolutionary landscape, and used it to identify generative amylases which mapped close to natural psychrophilic enzymes. We found that characterisation of the generative landscape will aid in the screening and selection of in silico candidates prior to in vitro and in vivo characterisation, saving time, money and effort in the design of novel enzymes.

[127] *The Design of Intelligent Electronic Fence System with YOLOv8-Pose and Homography Algorithm*

Ching-Lung Chang (National Yunlin University of Science and Technology).

Abstract

This research proposes a novel intelligent electronic fence system that implements personnel activity monitoring and alarm capabilities for specific spaces by integrating YOLOv8-Pose skeletal prediction with Homography transformation algorithms. The system, based on the YOLOv8-Pose model, can detect human skeletal keypoints in camera footage in real-time, with particular focus on the midpoint position of the ankles to determine whether personnel have entered the warning zone. The system first establishes a virtual warning zone by defining four points through an interactive interface, then employs the Homography algorithm to convert camera pixel coordinates to actual ground coordinates, establishing a correspondence relationship between the two coordinate systems. Additionally, the system supports multiple cameras and integrates a web interface, facilitating remote monitoring by management personnel. The research outcomes provide substantial practical value for industrial safety, construction sites, museum exhibit protection, and similar applications

[128] *A Comparative Analysis of Machine Learning Algorithms for Wheat Disease Classification in Taiwan Using the Orange Data Mining Tool*

Jie-Long Chen (Dept. of Information Management, National Yunlin University of Science and Technology), Ching-Chung Chen (DIM, National Pingtung University) and Arthur Chang (DIM, NYUST).

Abstract

Amid intensifying food security concerns and the impacts of climate change, wheat diseases pose a significant threat to Taiwan's agricultural resilience. This study employs image enhancement techniques and the Orange Data Mining platform to classify five prevalent wheat diseases using five machine learning algorithms. Neural networks with Inception v3 embeddings attained the highest accuracy (93.3%), closely followed by SVM (93.2%). Notably, even with lightweight SqueezeNet embeddings, neural networks remained the top performers (92.3%). These results underscore the promise of integrating deep feature embeddings with user-friendly ML tools for effective plant disease diagnosis in Taiwan.

[129] *Fluorescent-Stained Mycobacterium Detection in Sputum Smears through Computer-Assisted Analysis*

Pei-Ju Yen (Graduate Degree Program of Smart Healthcare and Bioinformatics, I-Shou University, Kaohsiung, Taiwan), Ching-Fen Jiang (GDPSHB, I-Shou University, Kaohsiung, Taiwan) and Ya-Ling Huang (Department of Laboratory Medicine, E-Da Hospital, Kaohsiung, Taiwan).

Abstract

Early detection of tuberculosis (TB) is critical for effective treatment and infection control. Auramine-Rhodamine (AR) staining, which offers faster and more efficient screening compared to Ziehl-Neelsen (ZN) staining, is commonly adopted for frontline sputum smear microscopy. This study presents an automated AR stain recognition method designed to support microscopic screening. The proposed approach aims to enhance diagnostic accuracy, reduce analysis time, and alleviate laboratory workload, thereby expediting TB detection in clinical settings.

[130] *Identifying Viral Adaptation Signatures Using Explainable AI in Influenza A*

Allison Hsu (Osaka YMCA International School) and Yingfeng Hsu (Osaka University).

Abstract

Influenza A viruses (IAVs) threaten global health due to their ability to cross species barriers and mutate rapidly. This study explores the use of explainable artificial intelligence (XAI) to interpret a convolutional neural network (CNN) trained on avian and human IAV protein sequences. Our model achieved 97% classification accuracy and identified amino acid positions important for host adaptation using Saliency Maps, Integrated Gradients, and SHAP. These positions matched known host-specific mutations with up to 99% accuracy. The results highlight the potential of XAI-enhanced deep learning to uncover biologically meaningful features, supporting future zoonotic surveillance and vaccine research.

[131] *Identification of Phosphorylation Sites as Predictive Biomarkers of Drug Response and Construction of Prediction Models*

Chih-Yun Lin (National Yang Ming Chiao Tung University), You-Sheng Paik (NYMCTU) and Tzong-Yi Lee (Institute of Bioinformatics and Systems Biology, NYMCTU).

Abstract

The advancement of personalized cancer therapy relies on the accurate prediction of drug sensitivity. While numerous models have utilized gene expression data for drug response prediction, the utility of phosphoproteomic features remains insufficiently explored. Here, we analyzed transcriptomic, proteomic, phosphoproteomic, and pharmacological profiles from 210 patient-derived AML samples to identify phosphorylation sites associated with drug sensitivity. Using Sorafenib as a representative drug, candidate phosphosites were enriched in cytoskeletal and immune-related pathways. These phosphorylation sites will be further used to build predictive models for drug response.

[132] *CysPTM-GPT: A Generalized Prompt-Based Model for Predicting Diverse Cysteine Modifications*

Chun-Kai Wu (National Yang Ming Chiao Tung University), Yen-Peng Chiu (NYMCTU), Yun Tang (Institute of Bioinformatics and Systems Biology, NYMCTU) and Tzong-Yi Lee (IBSB, NYMCTU).

Abstract

Proteins are fundamental biomolecules whose sequences resemble sentences in a language. PTMs, especially those on cysteine, significantly influence protein function. However, experimental identification of PTM sites is labor-intensive, creating a need for efficient computational prediction. Recent advances in protein language models, such as ProtGPT2 and PTMGPT2, have enabled prompt-based fine-tuning for PTM site prediction. Unlike PTMGPT2, which is typically trained for a single PTM type, we propose CysPTMGPT2, enables a single model to predict multiple cysteine PTM types simultaneously from sequence context.

[133] *Unveiling Spatial Heterogeneity and Tumor Microenvironment of Head and Neck Squamous Cell Carcinoma*

Yun-Ting Huang (National Yang Ming Chiao Tung University), Paik You Sheng (NYMCTU), Yun Tang (Institute of Bioinformatics and Systems Biology, NYMCTU) and Tzong-Yi Lee (IBSB, NYMCTU).

Abstract

Understanding intra-tumoral heterogeneity is essential for improving treatment strategies in head and neck squamous cell carcinoma (HNSCC). Here, we applied spatial transcriptomics to clinical HNSCC samples to examine gene expression within tumor-enriched regions. Clustering and cell-type annotation revealed transcriptionally distinct tumor subpopulations with spatially variable pathways, including immune signaling and ECM organization. Cell–cell communication analysis further highlighted active interactions, particularly involving macrophages and malignant cells. Our results offer a spatially resolved view of the tumor microenvironment and identify localized signaling dynamics that may inform targeted therapeutic approaches.

[134] *Gut Microbiome Analysis for Predicting Cognitive Function in Older Adults: A Multi-Level Biomarker Discovery Approach*

Ling-Yen Kung (National Yang Ming Chiao Tung University), Guan-Ting Chen (NYMCTU), Yun Tang (Institute of Bioinformatics and Systems Biology, NYMCTU) and Tzong-Yi Lee (National Yang Ming Chiao Tung University (IBSB, NYMCTU).

Abstract

Cognitive decline is a growing public health concern among aging populations, with increasing interest in the gut-brain axis as a modifiable factor. This study aims to identify gut microbiome biomarkers for predicting cognitive status and to develop a machine learning framework for cognitive function classification. We analyzed 16S rRNA sequencing data from fecal samples of 376 participants stratified by Montreal Cognitive Assessment (MoCA) scores into cognitively normal and impaired groups. Taxonomic composition profiling revealed that genera such as Klebsiella, Dialister, and Proteobacterial taxa were significantly enriched in cognitively impaired individuals, while Tyzzerella, Sellimonas, and Eubacterium siraeum group were more prevalent among cognitively preserved groups. Functional predictions using PICRUSt2 demonstrated differential enrichment in pathways related to short-chain fatty acid metabolism and neurotransmitter biosynthesis. In addition, microbial co-occurrence networks constructed via FastSpar exhibited diminished connectivity and altered community modules in the cognitively impaired group. These compositional, functional, and network-based features were selected for integration into a supervised machine learning model.

[135] *F2P-DTI: A Feature Fusion and Prediction Framework for Drug-Target Interactions via Autoencoder and Multi-Layer Perceptron*

Yu-Zhen Chen (National Yang Ming Chiao Tung University), Yen-Peng Chiu (NYMCTU), Yun Tang (Institute of Bioinformatics and Systems Biology, NYMCTU) and Tzong-Yi Lee (National Yang Ming Chiao Tung University (IBSB, NYMCTU).

Abstract

Accurately predicting drug-target interactions (DTIs) is a challenge in drug discovery. To address this, we propose F2P-DTI, a framework that improves DTI prediction by integrating multi-dimensional features from both proteins and drugs. The framework extracts physicochemical and structural features from protein sequences and generates molecular fingerprints from drug SMILES. These features are combined into a unified input vector, which is then processed using an Autoencoder for dimensionality reduction and to generate latent representations. The final latent features are fed into a Multi-Layer Perceptron (MLP) classifier to predict the interactions between drugs and targets. Benchmark testing showed that F2P-DTI performed better than existing methods (CPI-GNN), providing a practical tool for the drug discovery process.