

**Held in conjunction with Deep Learning Machine Learning Journal Club and
ICHI 2022: 10th IEEE International Conference on Healthcare Informatics**



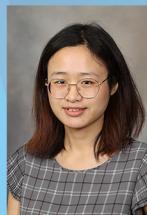
XIAOHUI ZHANG (Advisor: Prof. Mark Anastasio) - Identifying Functional Brain Networks from Spatial-temporal Wide-field Calcium Imaging Data Via a Recurrent Autoencoder

Abstract: Exploring functional brain networks (FBNs) from wide-field calcium imaging (WFCI) data is important to understand the functional architecture and organization of the brain. In the study, an unsupervised deep learning method is implemented for identifying FBNs from WFCI data. Specifically, a recurrent autoencoder is adapted to extract spatial-temporal latent embeddings of brain activity followed by use of ordinary least square regression to establish the corresponding function brain networks. Spatial similarities are shared between FBNs estimated from learned embeddings and those derived by seed-based correlation method. The proposed method allows investigations about the effect of spatial-temporal calcium dynamics on FBNs.



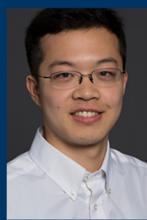
YURUI CAO (Advisor: Prof. Ravi Iyer) - Predicting ICU Admissions for Hospitalized COVID-19 Patients with a Factor Graph-based Model

Abstract: We designed a factor graph-based model that predicts intensive care unit (ICU) admission for hospitalized COVID-19 patients 3 days and 7 days in advance. This model: (i) explains relationships between different clinical features (e.g. comorbidities, labs, etc.) and provides interpretations for the disease progression; (ii) outperforms existing methods on Delta variant-affected data; (iii) maintains more robustness than existing models in predictions under the influence of the Delta variant. The proposed mode could be used as a predictive tool in clinical practice to help clinicians in decision-making by predicting which patients will need ICU support in the future.



CHANG HU (Advisor: Prof. Ravi Iyer) - Predicting Cholangiocarcinoma in Patients with Primary Sclerosing Cholangitis: An Analysis of Clinical, Laboratory, and Plasma Bile Acids Data

Abstract: Primary sclerosing cholangitis (PSC) carries a high risk of cholangiocarcinoma (CCA). We present the largest study to date aimed at developing predictive models for CCA in patients with PSC. We validated our predictive models at 2 and 5 years post-diagnosis, showing generalizability at different time points during the course of PSC. In addition, we presented the first study to explore the use of serum bile acids profiles for predicting CCA in patients with PSC, and we showed encouraging results.



CHUANYI ZHANG (Advisor: Prof. Mohammed El-Kebir) - CORSID enables de novo identification of transcription regulatory sequences and genes in coronaviruses

Abstract: Transcription regulatory sequences (TRSs), which occur upstream of structural and accessory genes as well as the 5' end of a coronavirus genome, play a critical role in discontinuous transcription in coronaviruses. We introduce two problems collectively aimed at identifying these regulatory sequences as well as their associated genes. We introduce CORSID to solve this problem, which includes a web-based visualization tool to explore the space of near-optimal solutions. We show that CORSID outperforms state-of-the-art gene finding methods in coronavirus genomes.



VAISHNAVI SUBRAMANIAN (Advisor: Prof. Minh Do) - Cross correlations in medical data for disease understanding

Abstract: Multi-modality medical data is abundant in today's world. Efforts to better understand patients' conditions by aggregating information from the different sources - such as imaging and genomics, are paving the way for personalized treatment. The correlations between the different modalities capture the joint variation of the properties of diseases. In this work, we investigate the use of canonical correlation analysis, a correlation tool, to predict patients' underlying condition utilizing histology and gene expression data from breast adenocarcinoma. Further, we propose to improve disease understanding by studying spatial proteomics data from ductal carcinoma in-situ patients, by capturing the relationship between protein expression and morphological properties of cells and cell neighborhood.



NEERAJ WAGH (Advisor: Prof. Yoga Varatharajah) - Addressing challenges in neurological disease diagnosis using domain-guided representation learning of scalp-EEG signals

Abstract: Neurological disease diagnosis (NDD) has traditionally relied on expert annotations of abnormalities in lengthy scalp-EEG recordings. This unscalable process has led to increased physician burnout, frequent misdiagnoses, and delays in patient care. This talk presents a domain-guided representation learning framework based on graph convolutions and self-supervision that can augment the NDD process by alleviating the need for visible abnormalities and labor-intensive annotations.



GRANT GREENBERG (Advisor: Prof. Ilan Shomorony) - Challenges in Single-Cell Multimodal Data Integration

Abstract: Recent technological advances have allowed the simultaneous measurement of multiple data modalities in single cells, including gene expression, DNA accessibility, and protein markers. Such multimodal sequencing provides invaluable insights into gene regulation and cellular diversity, but raises several research questions regarding the optimal processing of high-dimensional heterogeneous datasets. In this talk, we discuss several data processing tasks that arise in this context, including data integration, low-dimensional embedding, and quantification of the informational overlap between modalities.

