#### **2021 43rd Annual International Conference of the IEEE Engineering in Medicine & Biology Society (EMBC) Oct 31 - Nov 4, 2021. Virtual Conference**

# **Mini-Symposia Title:**

Emerging Methods in Signal Processing, Machine Learning and Control for Novel Investigations of High-DImensional Brain **Networks** 

### **Mini-Symposia Organizer Name & Affiliation:**

Catherine Stamoulis, PhD Harvard Medical School

### **Mini-Symposia Speaker Name/Affiliation 1:**

Catherine Stamoulis, PhD Dept of Medicine, Harvard Medical School

### **Mini-Symposia Speaker Name/Affiliation 2:**

Jie Gao, PhD Dept of Computer Science, Rutgers University, USA

### **Mini-Symposia Speaker NameAffiliation 3:**

Prodromos Daoutidis, PhD Dept of Chemical Engineering, University of Minnesota, USA

### **Mini-Symposia Speaker Name/Affiliation 4:**

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### **Mini-Symposia Panel Discussion Speakers:**

Prodromos Daoutidis, Jie Gao, Catherine **Stamoulis** 

## **Theme:**

### Biomedical Signal Processing

 $\bigcirc$  01. Biomedical Signal Processing

- 02. Biomedical Imaging and Image Processing
- 03. Micro/Nano-bioengineering; Cellular/Tissue Engineering &  $O_{\text{Biomaterials}}^{\text{U3. PBC}}$
- 04. Computational Systems & Synthetic Biology; Multiscale modeling
- 05. Cardiovascular and Respiratory Systems Engineering
- $\bigcirc$  06. Neural and Rehabilitation Engineering
- 07. Biomedical Sensors and Wearable Systems
- 08. Biorobotics and Biomechanics
- $\bigcirc$  09. Therapeutic & Diagnostic Systems and Technologies
- 10. Biomedical & Health Informatics

## **Mini-Symposium Synopsis**

In the new era of Big Data in biology and medicine, there is a pressing need for cross-disciplinary collaborations between investigators in the Life/Medical Sciences, Data Science and Engineering. This is particularly true in Neuroscience, a field where novel signal and image processing, machine learning and statistics approach are critically needed to extract interpretable, reliable and generalizable information from highly complex brain datasets. Once appropriately translated, computational tools from fields, such as Computer Science and Engineering can be widerly applied to neurophysiological, neuroimaging and neurochemical data. At the level of the individual brain, these techniques may provide novel representations of the brain as a collection of hierarchically organized multi-layer networks, communities with a specific organization and/or as a dynamic closed-loop system. These tools can also provide a means for dataderived, unsupervised estimations of anatomical and functional features, which to date have been limited. At the cohort or collective brain level, machine learning and AI tools can identify low-dimensional manifolds and network patterns across connectomes with similar topologies and again identify common structure and organization principles in communities of brains.

This mini-symposium will bring together investigators in Computational Neuroscience, Computer Science and Engineering to present data science methods for novel investigations of large, highly heterogeneous neuroimaging and neurophysiological datasets. Novel graph signal processing approaches, such as signed and/or directional graph signal processing, machine learning techniques, such as Graph Convolutional Neural Networks and unsupervised classification methods, as well as tools/models from control theory (e.g., Stochastic Block Models) will be presented and their applications to large-scale brain data will be demonstrated. The goal of the session is to highlight the utility of these approaches, the novelty of their domain applications and potentially transformative insights they may provide into the brain's structure and function.

**<sup>978-1-7281-1178-0/21/\$31.00 ©2021</sup> IEEE 2567**

# **Speaker 1 Synopsis: Graph Signal Processing for Cross-Disciplinary Investigations of the Human Brain in the Era of Big Data**

**Abstract—** In this new era of Big Data, the Life Sciences are undergoing transformational changes that highlight not only extensive gaps in knowledge, which can now be addressed with high-dimensional data but also a significant and pressing need for crossdisciplinary investigations of complex datasets emerging from novel technologies and large studies. This is particularly true in Neuroscience, a field that is trying to stay afloat in the presence of a data deluge stemming from the development of novel technologies for studying the brain at exquisite resolutions in time and space. Novel applications of data science methods, e.g. signal processing and machine learning, are needed to extract relevant and reliable information from highly heterogeneous neuroimaging, neurophysiological and neurochemical data.

Translation of techniques and theories from other fields are needed to provide a novel perspective and insights into the brain as a dynamic system (or ensemble of networks). In particular, despite decades of investigation, information flow and processing through complex brain networks remains poorly understood, in part due to limited tools for estimating this information from noisy brain signals. In addition, only snapshots of brain network topologies are typically studied, particularly when using modalities with poor temporal resolutions such as fMRI. Thus, network dynamics and evolution across time scales during information processing remain largely elusive.

This talk will focus on graph signal processing approaches and their application to signed and directed graphs (networks) estimated from very large human neuroimaging/neurophysiological datasets. Signed and directional graphs can be used to represent dissimilarity and directional relations, respectively. In the brain, functional processing depends on an orchestrated synchronization and desynchronization of task-dependent and task-independent networks. In addition, there is well-established top-down and bottom-up (and thus hierarchical) processing in the brain. Thus, signed and directional graphs are powerful tools for representing neuronal networks. Their application for brain system identification, (dynamic) community detection and neural source localization

will be discussed, using primarily invasive and noninvasive electrophysiological data but also resting-state neuroimaging (fMRI) from large-scale studies in the developing brain.

#### ACKNOWLEDGMENT

This work is supported by the National Science Foundation, grants # 1940094 and 1649865.

## **Speaker 2 Synopsis: Graph Convolutional Neural Networks for Large-Scale Brain Connectome Analyses**

**Abstract -** In classical machine learning, signal or image features are typically extracted from data to learn common rules. Related techniques are routinely applied to neurophysiological and neuroimaging data, to extract patterns of neural activity in the time and/or space domains. In contrast, graph learning aims to extract features that encode graph topological structures. This is of significant interest to Neuroscience, where the brain's topology and related network features directly impact neural information processing and cognitive function.

This talk will specifically focus on using advanced geometric features for graph analysis and learning as well as application to the brain data (described as a set of interconnected nodes). For individual brain networks, we analyze the network topology and identify community structures (i.e., clusters of wellconnected nodes). We also apply *multi-layer Graph Convolutional Network (GCN)* At each layer the features of the nodes are propagated to the neighbors and then aggregated to form the next layer's features. The advantage of aggregated features, compared to those estimated with more traditional tools, is that they encode both node features and their connection patterns.

The utility of the GCN in the analysis of individual brain connectomes as well as cohorts of brains will be demonstrated. One immediate application of significant interest to the community is parcellation with minimal a priori assumptions of anatomical constraints and landmarks between brain regions (e.g., those imposed by independently derived brain atlases). The GCN may be used for unsupervised parcellation of individual brains, based on their functionally similar components (network nodes.

Across brains, particularly in large and heterogeneous datasets, the GCN may be used to identify topologically similar connectome clusters that may support statistically similar behavioral patterns, providing valuable insights into the neural basis of the commonality and individuality of human behaviors.

ACKNOWLEDGMENT This work is supported by the National Science Foundation, grant OAC-1939459.

Prodromos Daoutidis, PhD, Department of Chemical Engineering, University of Minnesota

## **Speaker 3 Synopsis: Cognitive brain efficiency: A sparse optimal feedback control perspective**

Abstract— There is significant interest in Neuroscience to establish a mapping between cognitive and network control. Brain network control is a topic that is currently attracting significant attention in the field. Brain networks have certain topological properties, such as sparsity, which favor stability and computational efficiency but from a mechanistic point of view, the emergence of these properties remain elusive. This talk will describe the brain as a closed-loop dynamic system from the perspective of control, including its topological properties that optimize control cost. It will describe the investigation of network structures on sparse feedback control and application to brain networks (Constantino, 2019). The overarching aim of the talk is to highlight the translation of concepts from control theory to network Neuroscience, with the goal to elucidate how the brain achieves a parsimonious and efficient structural and functional topology that minimizes its control and how the latter is perturbed by neurological/neurodevelopmental disorders that alter these topologies leading to aberrantly increased control.

### ACKNOWLEDGMENT

This work is supported by the National Science Foundation, grants # OAC 1939459

#### **REFERENCES**

[1] P. H. Constantino, W. Tang, and P. Daoutidis, "Sparse Control of Complex Networks Favors Organized Topological Structures," Scientific Reports, doi: 10.1038/s41598-019-45476-6 (2019).

[2] Mitrai, I., C. Stamoulis and P. Daoutidis, A sparse  $H<sup>∞</sup>$  controller synthesis perspective on the reconfiguration of brain networks, Proceedings of the 2021 American Control Conference, New Orleans, Louisiana, in press, 2021.

Skylar Brooks, BS, Department of Medicine, Division of Adolescent Medicine, Boston Childrens Hospital

# **Speaker 4 Synopsis: Unsupervised Classification of Functional Networks for Data Derived Parcellations of the Human Brain**

**Abstract—** Big neuroimaging data are rapidly being generated by several ongoing large-scale national and international studies, including the Human Connectome Project (HCP) and the Adolescent Brain Cognitive Development (ABCD) study, both measuring thousands of children and adults with neuroimaging. Although these data promise to provide unprecedented opportunities for studying brain structure and function in large cohorts, their inherent heterogeneity poses challenges for representing the brain as a network of discrete interconnected regions. One of these challenges is the data-derived (and even brain-specific) identification of individual brain regions from fMRI data. Although a number of connectivity-based approaches have been proposed for this purpose, they all make a number of assumptions, without which brain parcellations would not be comparable across individuals.

This talk will discuss unsupervised classification approaches for high-dimensional (voxel-level) spatial clusters based on time series similarity in the presence of significant inter-brain variability and cohort heterogeneity. It will thus provide a different approach to the AI-based tools discussed by Speaker 3. Furthermore, it will show that connectivity/similaritybased classification depends on a number of factors, including the choice of threshold for identifying edge maps and non-linear relationships between similarity and edge map sparsity. It will demonstrate the utility of connectivity-based classifications for identifying statistically similar brain regions and consequently parcellations. Finally, it will present an application of unsupervised classification of resting connectomes for the parcellation of developing brains into functionally distinct regions that comparable across individuals. The specific application to data from the large-scale ABCD cohort (a highly heterogeneous sample of almost 12,000 brains) will be discussed.

#### ACKNOWLEDGMENT

This work is supported by the National Science Foundation, grants # 1940094 and 1649865.