Abstract

Electroencephalography (EEG) is one of the oldest techniques used for studying the brain that continues to be used today because of the several advantages it offers. The EEG device is inexpensive, compact and specializes in capturing the functional activity of the brain. Although it was extremely prominent in the last century, its clinical use has largely been restricted to investigating epilepsy. As opposed to imaging modalities like CT scan and MRI, EEG more naturally lends itself to quantitative techniques because it dynamically captures brain function. However, it is in this aspect that EEG remains largely underutilized.

Techniques aimed at quantitative analysis of EEG have primarily explored three distinct specialization areas within the study of epilepsy, namely, epilepsy diagnosis, seizure prediction and seizure/abnormality detection. This thesis focuses on the first two of the three application areas by trying to identify novel computational biomarkers that help identify pathological features in EEG that are not visible to the naked eye. Although decades of research activity has preceded the work presented in this thesis, we aim to fill some of the gaps that have prevented the studies carried out in the past from translating into tools in the clinic. The most pressing issues were found in the case of epilepsy diagnosis where a single benchmark data set with several shortcomings has been in use for more than a decade for building predictive models.

In this thesis, we begin with the creation of a new data set that overcomes the shortcomings of the previous benchmark data set for epilepsy diagnosis and correcting the flaws in the model evaluation methodology of past studies. Characteristic response vector (CRV) is proposed that extends the notion of an impulse response of a linear system to positive definite matrices. This vector is used to reduce sample covariance matrices of EEG obtained through sliding window technique to single vectors. A novel computational biomarker is discovered in these vectors that helps in distinguishing epilepsy patients from healthy individuals. The predictive model is

evaluated on an external test data set, which, to the best of our knowledge, has not been done in previous studies.

Extending the sliding window technique employed in the predictive model described above, we propose recursive dynamic functional connectivity (rdFC) that builds a multi-scale hierarchical network for neurophysiological data. The rdFC technique is used to build 5-point connectivity patterns in a 3-dimensional Cartesian coordinate system. Using rdFC, a specific correlation structure is discovered that is present universally in a diverse range of human EEG records. This correlation structure is represented using three equivalent rdFC patterns. The dynamics of these patterns is found to be linked with that of seizures and used to build a seizure forecasting system for scalp EEG. The system is highly computationally efficient and satisfies all the guidelines widely accepted for evaluation of seizure prediction systems.