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A system for the analysis of EEG data and brain state modeling

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Electroencephalographic (EEG) data modeling is useful for developing applications in the areas of healthcare, as well as in the design of brain-computer interface (BCI). In this study, we aim to build an efficient self-adjusting brain wave modeling system that can seamlessly capture and analyze EEG brainwave data using various custom developed tools and off the shelf software and hardware components. The platform provides user friendly interface with secure data storage and analytics capabilities for wave analysis, statistical analysis, and categorical classification using a number of well-established machine learning algorithms. We also present a systematic method to understand how the variation of raw data sets used in training models affects the accuracy of machine learning algorithms, and then analyze the performance of machine learning algorithms under various computational implementations. Additionally, we compared this finding with the efficiency of common machine learning algorithms on normalized mean data sets. Our results strongly indicate that Random Forest algorithm yields the highest accuracy for the both raw and normalized mean data sets. The data analysis result shows the distinctive pattern of delta and beta waves during active and idle brain states. Overall, the study describes a successful built of an incorporated data analysis platform, and provides preliminary insights into the performance of common machine learning algorithms on the brain wave (EEG) data sets.

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Pathway and gene identification from integrative analysis of omics data

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In the era of big data, as the individual patient data (IPD) become more accessible, integrative analyses using IPD from multiple studies are now extensively conducted to identify prognostic genes. It has been recognized that genes do not work alone but through pathways. In this talk, I will present a general statistical framework for pathway and gene identification from integrative analysis. Our framework employs a hierarchical decomposition on genes' effects followed by a proper regularization to identify important pathways and genes across multiple studies. Asymptotic theories are provided to show that our method is both pathway and gene selection consistent. We explicitly show that pathway selection consistency needs milder statistical conditions than gene selection consistency, as it would allow false positives/negatives at the gene selection level. Finite-sample performance of our method is shown to be superior to other ad hoc methods in various simulation studies. We further apply our method to analyze five cardiovascular disease studies.

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