

## SLEEP meeting 2017, Abstract

**Title:** AUTOMATED PIPELINE FOR SPECTRAL ANALYSIS OF EEG DATA: THE NATIONAL SLEEP RESEARCH RESOURCE TOOL

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**Introduction:** The National Sleep Research Resource (NSRR, [www.sleepdata.org](http://www.sleepdata.org)) features thousands of polysomnograms (PSGs) that can be analyzed for further understanding how variations in physiological signals associate with health outcomes. Quantitative EEG analysis may help characterize physiological variation. However, analysis of large datasets collected in uncontrolled settings requires a robust pipeline including artifact detectors. To promote community-wide use of PSG data, we developed an open-source, automated pipeline for spectral analysis of sleep EEGs and tested the level of agreement with traditional analysis.

**Methods:** We used data from the C3-A2 EEG lead in a sample of PSGs from 161 women participating in the Study of Osteoporotic Fractures. The traditional approach used manual artifact removal on 4-s basis and application of commercial spectral analysis software. Automated analysis included spectral power-based artifact detection on 30-s basis and generation of summary figures for adjudication. We compared automatic and manual artifact detection epoch-by-epoch and then compared the average EEG spectral power density in six frequency bands obtained with the two approaches using correlation analysis, Bland-Altman plots and Wilcoxon test.

**Results:** The automated artifact detection algorithm had high specificity (96.8 to 99.4% in NREM, 96.9 to 99.1% in REM depending on the criterion for comparing 4-s with 30-s epochs) but lower sensitivity (26.7 to 38.1% in NREM, 9.1 to 27.4% in REM). However, we found no clinically or statistically significant differences in power density values, and results were highly correlated (Spearman's  $r > 0.99$ ). Large artifacts (total power  $> 99^{\text{th}}$  percentile) were removed with sensitivity up to 90.9% in NREM, 87.7% in REM, specificity 96.6% and 96.9%.

**Conclusion:** The automated pipeline generated similar results to those obtained with standard approach, while reducing analysis time 100-fold. This Matlab toolset, publicly available on the NSRR website, can be used to analyze thousands of recordings, allowing for its application in genetics and epidemiological research.

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