Robustness of Electroencephalography-Biomarkers for Major Depressive Disorder – an Exemplary Study with Alpha Bandpower

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Objective biomarkers for Major Depressive Disorder (MDD) are needed for diagnosis, monitoring, and treatment development. Electroencephalography (EEG) is studied for obtaining MDD biomarkers. However, results vary widely regarding the usefulness of specific features from EEG (de Aguiar Neto & Rosa, 2019). Especially the small sample sizes in many clinical studies lead to an over-estimation of diagnosis accuracy (Rakić, Cabezas, Kushibar, Oliver, & Lladó, 2020). The comparison of studies is hampered by the vast possibilities in methods. A robust biomarker for clinical application has not yet been identified.

Publicly available datasets contribute to resolving these conflicts. Some of the datasets may be combined to yield large and diverse datasets, or can be used for replication and comparative studies.

Alpha bandpower is a biomarker for MDD diagnosis with contradictory results (Cai et al., 2020; Hosseinifard, Moradi, & Rostami, 2013). The goal of the current study was to test its robustness across publicely available EEG datasets. We identified the differences between the datasets, matched the data, and varied systematically commonly used processing steps.

Two datasets with resting-state EEG from MDD patients (n=24/34) and healthy controls (n=29/30) with 13 corresponding channels were obtained (Cai et al., 2020; Mumtaz, 2016). Data was re-referenced and artifacts were removed. Subsequently, data was either not normalized, or z-transformed channel or subject-wise. Time-series were then split in 20s windows. Ten windows from each participant and channel were selected randomly and their median alpha bandpower was used as robust feature. For each variation of processing steps, we trained four classifiers (linear SVM with subject-wise 6-fold crossvalidation). Two classifiers operated on the two datasets seperately to diagnose MDD. Two classifiers tried to separate the two datasets.

Classification accuracy depends on normalization ($F_{2,60}$=15.604; p<.001) and classifier ($F_{3,60}$=3.825; p=.014). For the diagnoses in the different datasets the non-normalized data performs better across datasets ($F_{2,30}$=4.184; p=.025), which stems from only one dataset ($F_{2,30}$=9.036; p<.001). For the differentiation between datasets, normalization has a marked effect ($F_{2,30}$=12.551; p<.001.

Our results demonstrate that the normalization procedure, a common step in machine learning, has contradictory impact on the datasets. However, for combining datasets, normalization is a neccessary procedure.

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