

Report of Scalar-on-Network Regression

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Abstract There is a growing trend in learning the association between individuals' brain connectivity networks and their clinical characteristics as well as symptoms. It requires a kind of model whose response variable is scalar, and the predictors are networks or adjacent matrices. Therefore, in this research, we developed a new boosting method for variable screening. The performance of our method was demonstrated through analysis of the rs-fMRI data.

Introduction

Functional connectome fingerprinting (Finn et al., 2015) has aroused heated discussion over recent years since it implies some clinical symptoms or demographic characteristics. Previous research used various regression methods (Dubois, Galdi, Han, et al., 2018; Dubois, Galdi, Paul, et al., 2018; Tozzi et al., 2021) or dimension reduction approaches (Sripada, Angstadt, et al., 2020; Sripada, Rutherford, et al., 2020) to extract relevant information from functional connectivity. However, they either failed to perform variable screening or omitted the brain structure information, which is deficient for the identification of sub-networks or edges that contribute to certain diseases. Thus, our research goal is to find biomarkers of certain diseases or brain functions, while extracting their information as much as possible.