TPRM: tensor partition regression models with applications in imaging biomarker detection.

Summary: Medical imaging studies have collected high-dimensional imaging data to identify imaging biomarkers for diagnosis, screening, and prognosis, among many others. These imaging data are often represented in the form of a multi-dimensional array, called a tensor. The aim of this paper is to develop a tensor partition regression modeling (TPRM) framework to establish a relationship between low-dimensional clinical outcomes (e.g., diagnosis) and high-dimensional tensor covariates. Our TPRM is a hierarchical model and efficiently integrates four components: (i) a partition model, (ii) a canonical polyadic decomposition model, (iii) a principal components model, and (iv) a generalized linear model with a sparse inducing normal mixture prior. This framework not only reduces ultra-high dimensionality to a manageable level, resulting in efficient estimation, but also optimizes prediction accuracy in the search for informative sub-tensors. Posterior computation proceeds via an efficient Markov chain Monte Carlo algorithm. Simulation shows that TPRM outperforms several other competing methods. We apply TPRM to predict disease status (Alzheimer versus control) by using structural magnetic resonance imaging data obtained from the Alzheimer’s Disease Neuroimaging Initiative (ADNI) study.

MSC:

62P10 Applications of statistics to biology and medical sciences; meta analysis
62J07 Ridge regression; shrinkage estimators (Lasso)
92C55 Biomedical imaging and signal processing

Keywords:
Bayesian hierarchical model; big data; MCMC; tensor decomposition; tensor regression

Software:
ElemStatLearn; EMVS; fda (R)

Full Text: DOI arXiv Euclid

References:


Edited by FIZ Karlsruhe, the European Mathematical Society and the Heidelberg Academy of Sciences and Humanities
© 2022 FIZ Karlsruhe GmbH

This reference list is based on information provided by the publisher or from digital mathematics libraries. Its items are heuristically matched to zbMATH identifiers and may contain data conversion errors. It attempts to reflect the references listed in the original paper as accurately as possible without claiming the completeness or perfect precision of the matching.