

Documentation for Software Package SBAMS

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1 Introduction

Software package SBAMS (**S**tructured **B**ayesian **M**odel **S**election) implements the Bayesian statistical methods discussed in [1], and provides the functionality to perform structured Bayesian model selections in the Multivariate Linear Regression (MVLRL) models. The relevant technical details are discussed in the paper and its supplementary materials. The purpose of this documentation is to explain the software implementation and corresponding input/output format.

2 Approximate Bayes Factor Computation

2.1 R implementation

The file `mvlr.R` implements the approximate Bayes factor calculation for the MVLRL model. The code is self-explanatory and it is convenient to use model comparisons in a set of candidate MVLRL models.

2.2 C++ implementation

We also implement the C++ class MVLRL, which can be conveniently re-used in other software implementations. The public and private interfaces of the MVLRL class is documented in `MVLRL.h` file. The compilation of the object file requires GNU Scientific Library (GSL).

3 MCMC Algorithm for Bayesian Model Selection

We also implement the MCMC algorithm to perform Bayesian model selection for MVLRL model. The program, *sbams-mvlr*, can be used for some rather general purposes. Because multiple linear regression

model is a special case of MVLRL, *sbams_mvlr* can be applied for variable selection problems in multiple linear regression context.

3.1 Input Files

3.2 Running Program

3.3 Program Parameters

3.4 Input/Output Options

3.5 Program Options

3.6 Output from Program

References

- [1] Wen, X. “Bayesian Model Selection in Complex Linear Systems, as Illustrated in Genetic Association Studies”, submit to Biometrics.