BFRM 2.0

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BFRM is a comprehensive implementation of sparse statistical models for high-dimensional data analysis, structure discovery and prediction.

The framework of sparse latent factor modelling coupled with sparse regression and anova for multivariate data is relevant in many exploratory and predictive problems with very high-dimensional multivariate observations. Bayesian analysis utilising sparsity-inducing models, and computational methods able to efficiently explore and fit large-scale models, now allow these approaches to be used in increasingly complex and high-dimensional problems.

The statistical methods and computational analysis represented in BFRM are generic and will apply in many areas of application. Some recent applications include studies in finance and econometrics and other areas. A major focus for applications is in biological studies using gene expression data coupled with outcomes (phenotypes) to be predicted based on patterns underlying gene expression, and especially for biological pathway analysis and the evaluation of subpathway structure. Examples of the use of the program in this area will be provided shortly.

Key manuscripts with examples

- Carvalho et al, 2008, High-dimensional sparse factor modelling: Applications in gene expression genomics, in *JASA*
- Lucas et al 2006, Sparse statistical modelling in gene expression genomics, in *Bayesian Bioinformatics*
- Seo et al 2008, Of mice and men: Sparse statistical modelling in cardiovascular genomics, in *Annals of Applied Statistics*
- Lucas et al 2009, Bench-to-bedside and cross-study projections of genomic biomarkers: An evaluation in breast cancer genomics, in *PLoS One*
- Lucas et al 2009, A Bayesian analysis strategy for cross-study translation of gene expression biomarkers, in *Statistical Applications in Genetics and Molecular Biology*
- Merl et al 2009, Trans-study projection of genomic biomarkers in analysis of oncogene deregulation and breast cancer, in *The Handbook of Applied Bayesian Analysis*
- Useful additional discussion and examples appear in the 2006 PhD theses of Carlos Carvalho and Joe Lucas.

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This software is made freely available to any interested user. The authors can provide no support nor assistance with implementations beyond the details and examples here, nor extensions of the code for other purposes. The download has been tested to confirm all details are operational as described here.

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More software from the West group