



BISP8

**Eighth Workshop on
BAYESIAN INFERENCE IN STOCHASTIC PROCESSES**

Sparse latent factor models with interactions: analysis of gene expression data

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Sparse latent multi-factor models have been used in many exploratory and predictive problems with high-dimensional multivariate observations. Because of concerns with identifiability, the latent factors are almost always assumed to be linearly related to measured feature variables. Here we explore the analysis of multi-factor models with different structures of interactions between latent factors, including multiplicative effects as well as a more general framework for non-linear interactions introduced via Gaussian Process. We utilize sparsity priors to test whether the factors and interaction terms have significant effect. The performance of the models is evaluated through simulated and real data applications in genomics. Variation in the number of copies of regions of the genome is a well known and important feature of most cancers. We examine interactions between factors directly associated with different chromosomal regions detected with copy number alteration in breast cancer data. In this context, significant interaction effects for specific genes suggest synergies between duplications and deletions in different regions of the chromosome.

**ABSTRACT
TYPE**

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Young researcher Vinicius Diniz Mayrink invited to contribute