

Probabilistic modelling of data on undirected graphs

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Many problems in bioinformatics involve weighted undirected graphs: metabolic networks, interaction graphs, or indeed any binary relationships derived from similarity scores. For example, gene expression data can be modelled by a multivariate Gaussian distribution with a covariance structure informed by the graph. We explore ways of constraining and estimating kernels for given graph structures and evaluate their usefulness for graph selection and graph partitioning problems. Such problems emerge, for example, in assigning roles within metabolic networks to genes, or in delineating active metabolic pathways.