Probabilistic modelling of cellular processes on undirected graphs

Lorenz Wernisch

MRC Biostatistics Unit, Cambridge and School of Crystallography, Birkbeck College

Undirected graphs are a useful model for biological processes: metabolic networks, protein interaction graphs, sequence and phylogenetic similarities. We present and compare methods for estimating the covariance matrix on graphs from biological data, for example, on gene expression. Graph kernels, as used in support vector machine learning, provide a range of covariance structures suitable for estimation and inference on metabolic networks, as we demonstrate on the example of metabolic control in Mycobacterium tuberculosis.