

## **Inferring Sparse Gaussian Graphical Models for Biological Network**

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Gaussian Graphical Models provide a convenient framework for representing dependencies between variables. In this framework, a set of variables is represented by an undirected graph, where vertices correspond to variables, and an edge connects two vertices if the corresponding pair of variables are dependent, conditional on the remaining ones. Recently, this tool has received a high interest for the discovery of biological networks by  $l_1$ -penalization of the model likelihood.

In this presentation, we introduce various ways of inferring sparse co-expression networks based on partial correlation coefficients from either steady-state or time-course transcriptomic data. All proposals search for a latent structure of the network to drive the selection of edges through an adaptive  $l_1$ -penalization of the model likelihood. We focus on inference from samples collected in different experimental conditions and therefore not identically distributed.