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Title: "Inferring biological regulation network by model selection"

Abstract.

A current challenge in Systemic Biology is to infer the regulation network of a family of  $p$  genes from a  $n$ -sample of microarrays, with  $n$  (much) smaller than  $p$ . Gaussian graphical models are simple models to describe these regulation networks.

We propose a procedure that performs Gaussian graph estimation by model selection. We introduce a collection of candidate graphs and then select one of them by minimizing a penalized empirical risk. We pay a special attention to the maximum degree of the graphs that we can handle and asses the performance of the procedure in a non-asymptotic setting. The good theoretical properties of the procedure are confirmed on numerical examples.

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