

New challenges for (biological) network inference with sparse Gaussian graphical models

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Network inference methods based upon sparse Gaussian Graphical Models (GGM) have recently emerged as a promising exploratory tool in genomics. They give a sound representation of direct relationships between genes and are accompanied with sparse inference strategies well suited to the high dimensional setting. They are also versatile enough to include prior structural knowledge to drive the inference. Still, GGM are now in need for a second breath after showing some limitations: among other questionings, the state-of-the-art reconstruction strategies often suffer a lack of robustness and are not fully appropriate for treating heterogeneous data. In that perspective, we will discuss recent approaches that try to overcome the limitations essentially induced by the nature of the genomic data and of the underlying biological mechanisms.

Keywords: Graphical Model · Sparse Method · Heterogeneous data · Genomics