# Modelling signaling networks

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Marc Bailly-Bechet et al. have developed a new algorithm for the signaling network inference problem, and applied it to transcriptomic and proteomic data in yeast. The predictions of the new algorithm are confirmed experimentally. This new method can be applied to many network inference problems, and the algorithm performance in terms of speed and complexity make it able to treat large-scale networks such as the human signaling network.

Bailly-Bechet M, Borgs C, Braunstein A, Chayes J, Dagkessamanskaia A, François JM, Zecchina R. Finding undetected protein associations in cell signaling by belief propagation. Proc Natl Acad Sci U S A. 2010 Dec 27.