

Bioinformatics just published a [special issue devoted to ISMB 2014 proceedings papers](#) that will be presented next month at the world's premier conference on computational biology -- [ISMB 2014 in Boston, MA, USA](#)

Our paper, [Gene network inference by probabilistic scoring of relationships from a factorized model of interactions](#), which you will find in this issue of Bioinformatics, describes a conceptually new probabilistic approach to gene network inference from quantitative interaction data called Red. Red is founded on epistasis analysis. Epistasis analysis is an essential tool of classical genetics for inferring the order of function of genes in a common pathway. Typically, it considers single and double mutant phenotypes and for a pair of genes observes if a change in the first gene masks the effects of the mutation in the second gene. Despite the recent emergence of biotechnology techniques that can provide gene interaction data on a large, possibly genomic scale, very few methods are available for quantitative epistasis analysis and epistasis-based network reconstruction.

The features of Red are joint treatment of the mutant phenotype data with a factorized model and probabilistic scoring of pairwise gene relationships that are inferred from the latent gene representation. The resulting gene network is assembled from scored pairwise relationships. In an experimental study, we show that the proposed approach can accurately reconstruct several known pathways and that it surpasses the accuracy of current approaches.