

I have presented our recent approach for epistasis-based gene network inference at [ISMB 2014](#). We propose a factorized model of interactions that is used for scoring of different types of gene-gene relationships, such as epistasis, parallelism and partial interdependence, and assembly of gene networks that are consistent with estimated pairwise relationships. Detailed derivation of the method and its empirical comparisons with existing approaches [are described in our paper published by Bioinformatics.](#)