We got accepted a paper on *Imputation of Quantitative Genetic Interactions in Epistatic MAPs by Interaction Propagation Matrix Completion* to RECOMB 2014 .

Epistatic Miniarray Profile (E-MAP) is a popular large-scale gene interaction discovery platform. E-MAPs benefit from quantitative output, which makes it possible to detect subtle interactions. However, due to the limits of biotechnology, E-MAP studies fail to measure genetic interactions for up to 40% of gene pairs in an assay. Missing measurements can be recovered by computational techniques for data imputation, thus completing the interaction profiles and enabling downstream analysis algorithms that could otherwise be sensitive to largely incomplete data sets. In the paper, we introduce a new interaction data imputation method called interaction propagation matrix completion (IP-MC). The core part of IP-MC is a low-rank (latent) probabilistic matrix completion approach that considers additional knowledge presented through a gene network. IP-MC assumes that interactions are transitive, such that latent gene interaction profiles depend on the profiles of their direct neighbors in a given gene network. As the IP-MC inference algorithm progresses, the latent interaction profiles propagate through the branches of the network. In a study with three different E-MAP data assays and the considered protein-protein interaction and Gene Ontology similarity networks, IP-MC significantly surpassed existing alternative techniques. Inclusion of information from gene networks also allows IP-MC to predict interactions for genes that were not included in original E-MAP assays, a task that could not be considered by current imputation approaches.

Presentation is available at Prezi.