**Introduction**

- We used SNP data and gene expression data of *S. cerevisiae* to detect eQTLs using three different mapping methods
  - Non parametric regression
  - Mixed models
  - Elastic net
- Using a physical interaction network, we prioritized eQTLs spanning multiple genes to individual causal genes using a graph node kernel based approach
- Evaluating using knockout pairs, and when compared to random assignment or a shortest path approach, we obtained superior results
- Published in Bioinformatics:
- Software available at bioinformatics.intec.ugent.be/epsilon

**Method**

- Genetic polymorphism associated with differentially expressed target gene
- Local neighborhood on chromosome

  **Step 1.** Find candidate causal genes within a fixed distance of eQTL and construct a local sub-network connecting the target gene with all candidate causal genes.

  **Step 2.** Calculate a similarity measure for each candidate-target pair and select candidate that yields the highest similarity.

  - $r_{g1}$
  - $r_{g2}$
  - $r_{g3}$
  - $r_{g4}$
  - $r_{g5}$
  - $r_{g6}$

**Results**

- Three different eQTL mapping methods
- Evaluation using Hughes (2000) knockout dataset
- Local kernel based prioritization consistently outperforms both reference methods
- Maximum number of retrievable knockout pairs depends on the eQTL mapping method and the network at hand
- Results are comparable or superior to results mentioned in literature, see e.g.