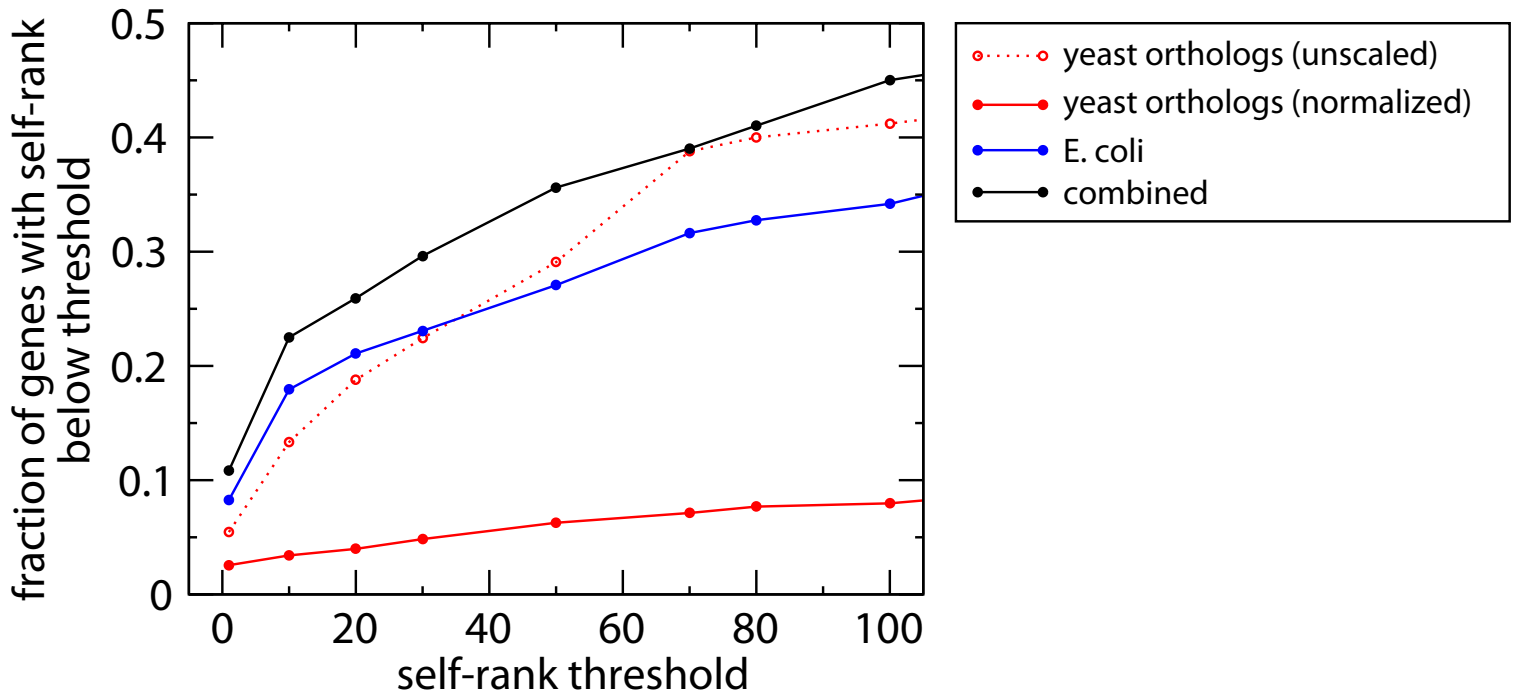


Figure 6.



Ortholog co-expression performance. *E. coli* self-rank performance is shown separately using mRNA expression data from *E. coli* microarray studies (*E. coli*), using expression of *S. cerevisiae* orthologs of *E. coli* genes in the Rosetta compendium dataset (yeast orthologs), and for the combination of the two association scores (combined). Performance is shown on the set of metabolic genes with orthologs in *S. cerevisiae* (unscaled), and also normalized to the total number of known *E. coli* metabolic genes (normalized). Prediction were generated using using ADT classifier (with 10 fold validation) based on association scores to 3 layers of the metabolic network neighborhood.