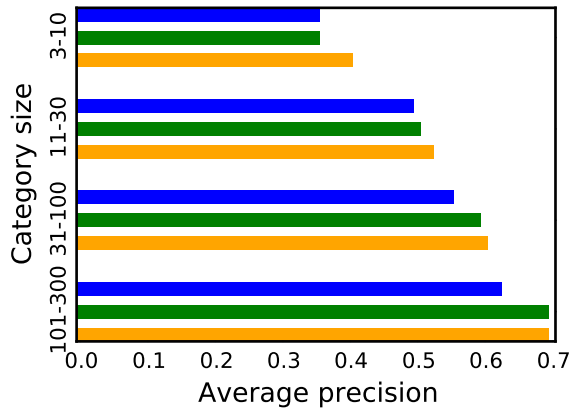


Supplementary Figures

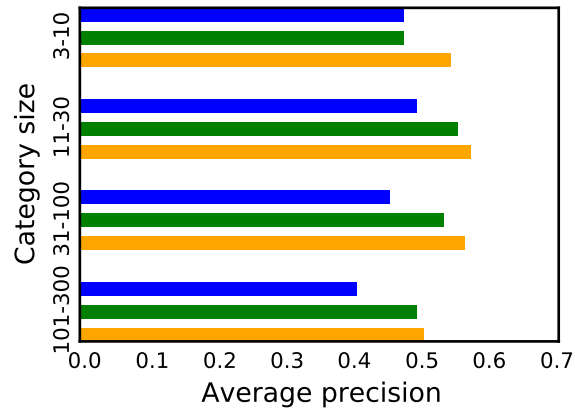
Shown are best performing (maximum) and worst performing (minimum) average precision (or area under the precision recall curves (AUC-PR)) for the three Gene Ontology (GO)-based network weighting methods implemented in GeneMANIA along with the corresponding value for the original GeneMANIA algorithm (GM-2008) described by Mostafavi and colleagues (1) and externally validated on mouse (3) and yeast (1) gene function prediction benchmarks. Each value is the average precision achieved over all GO terms in the indicated branch (Biological Process, Molecular Function, Cellular Component), for the indicated organism. GO categories were separated into bins by size, with GO categories containing 3-10 terms, 11-30, 31-200 and 101-300. In total, 1,954 GO terms were used to create the yeast graphs, 2,878 GO terms for mouse, 2,890 GO terms for human, 2,356 GO terms for fly, 572 GO terms for worm, and 1,861 GO terms for arabidopsis.

Performance on yeast

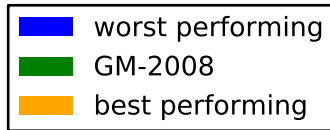
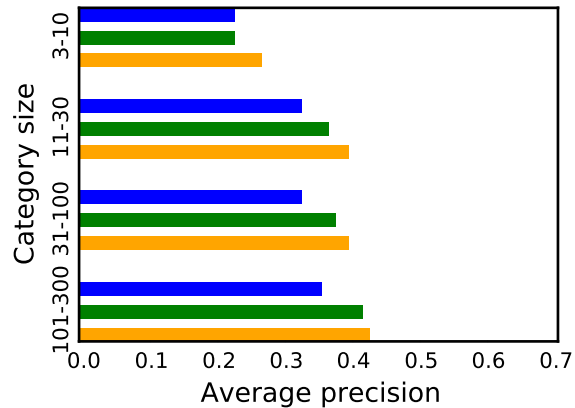
Molecular Function



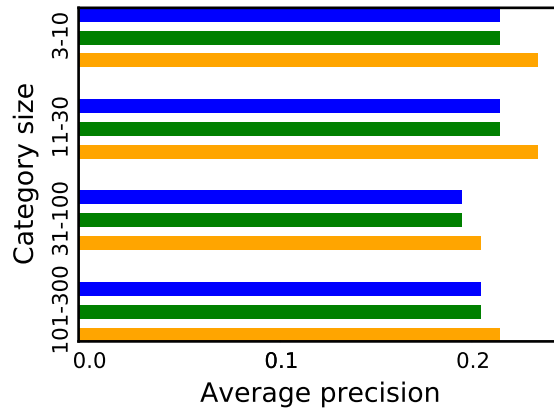
Cellular Component



Biological Process

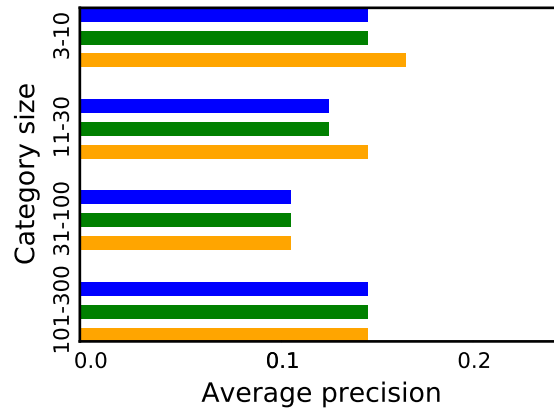


Molecular Function

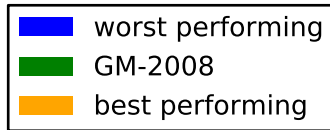
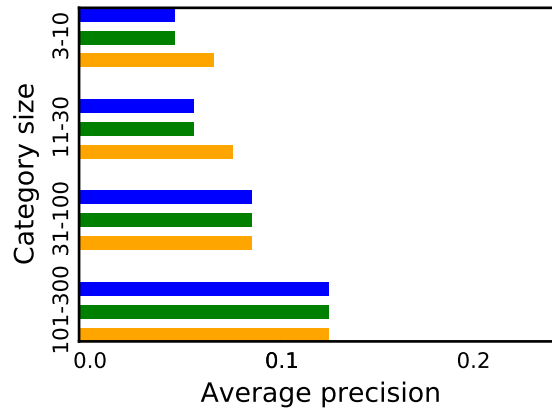


Performance on mouse

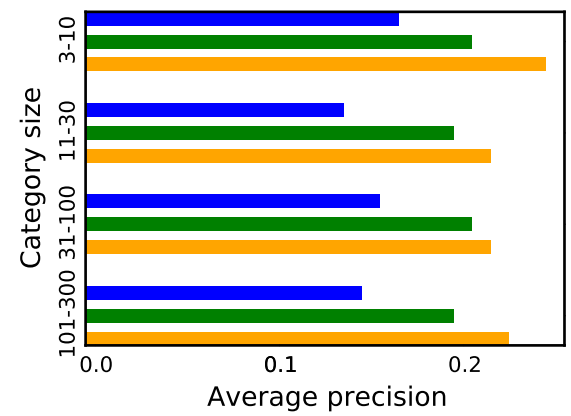
Cellular Component



Biological Process

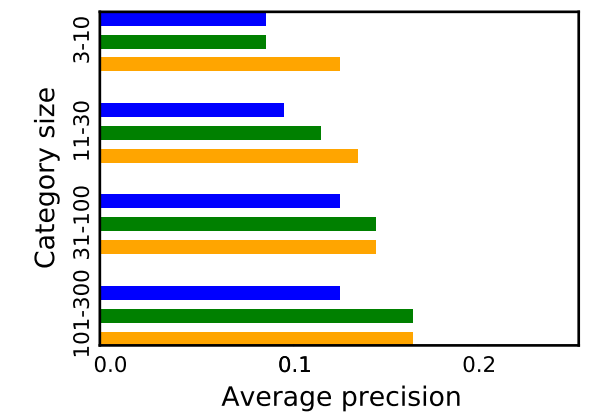


Molecular Function

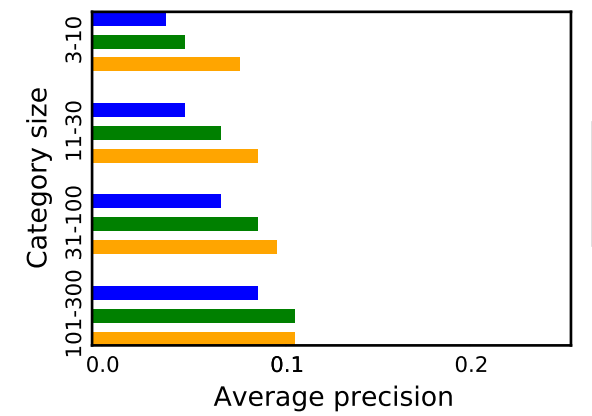


Performance on human

Cellular Component

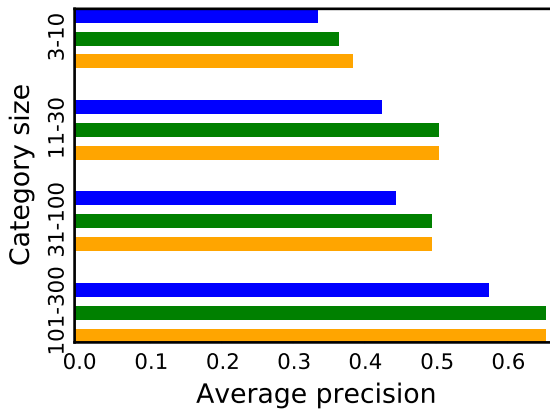


Biological Process

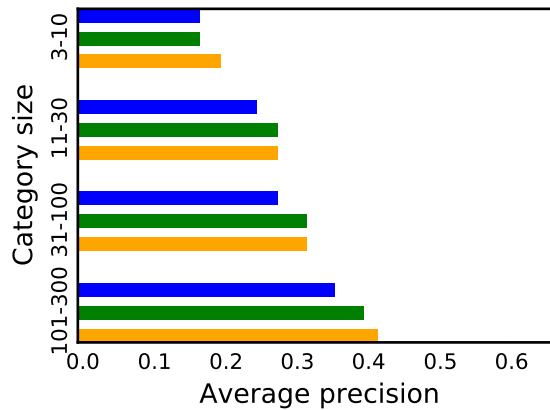


Performance on fly

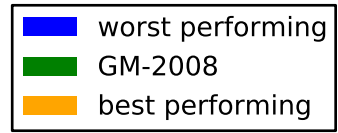
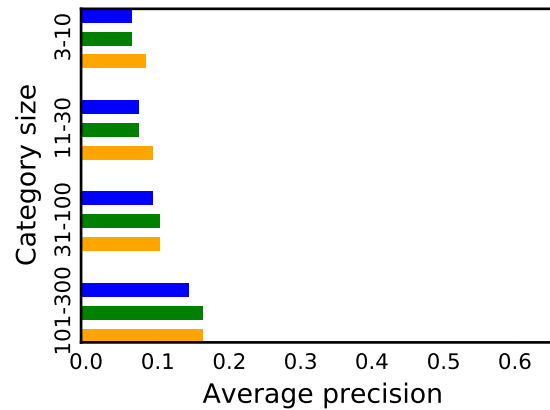
Molecular Function



Cellular Component

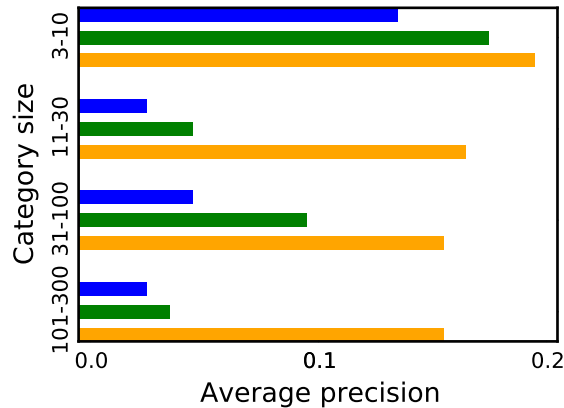


Biological Process

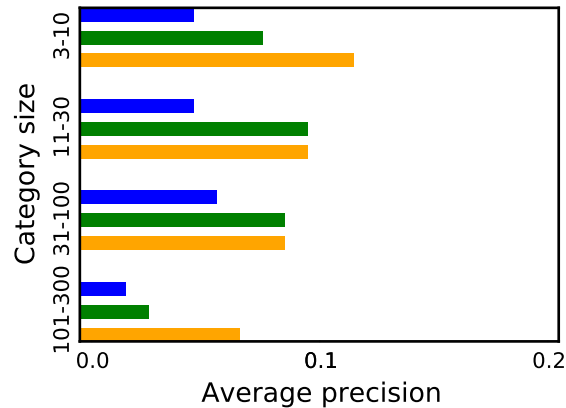


Performance on worm

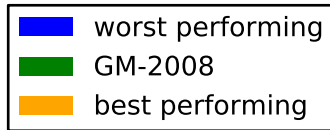
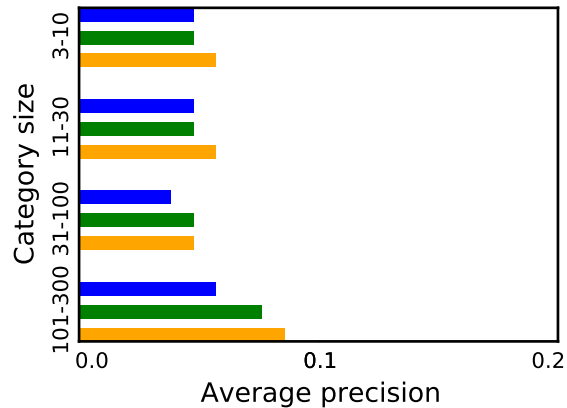
Molecular Function



Cellular Component

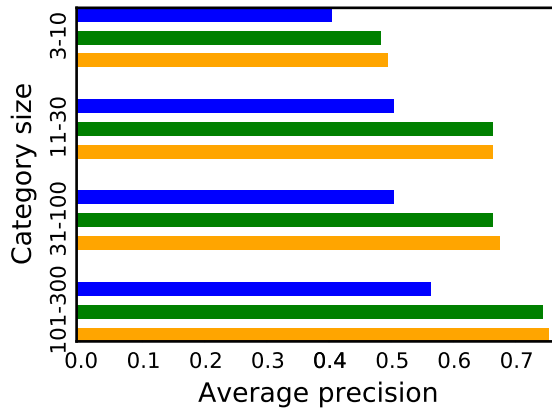


Biological Process

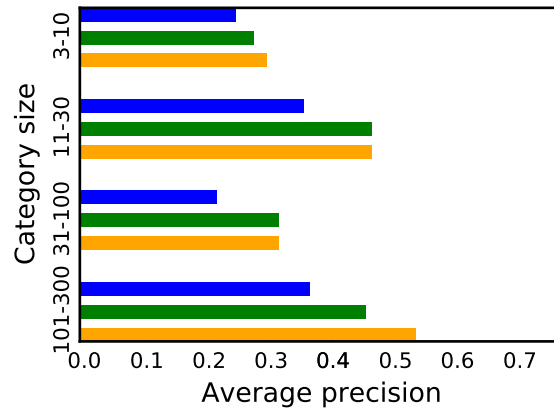


Performance on arabidopsis

Molecular Function



Cellular Component



Biological Process

