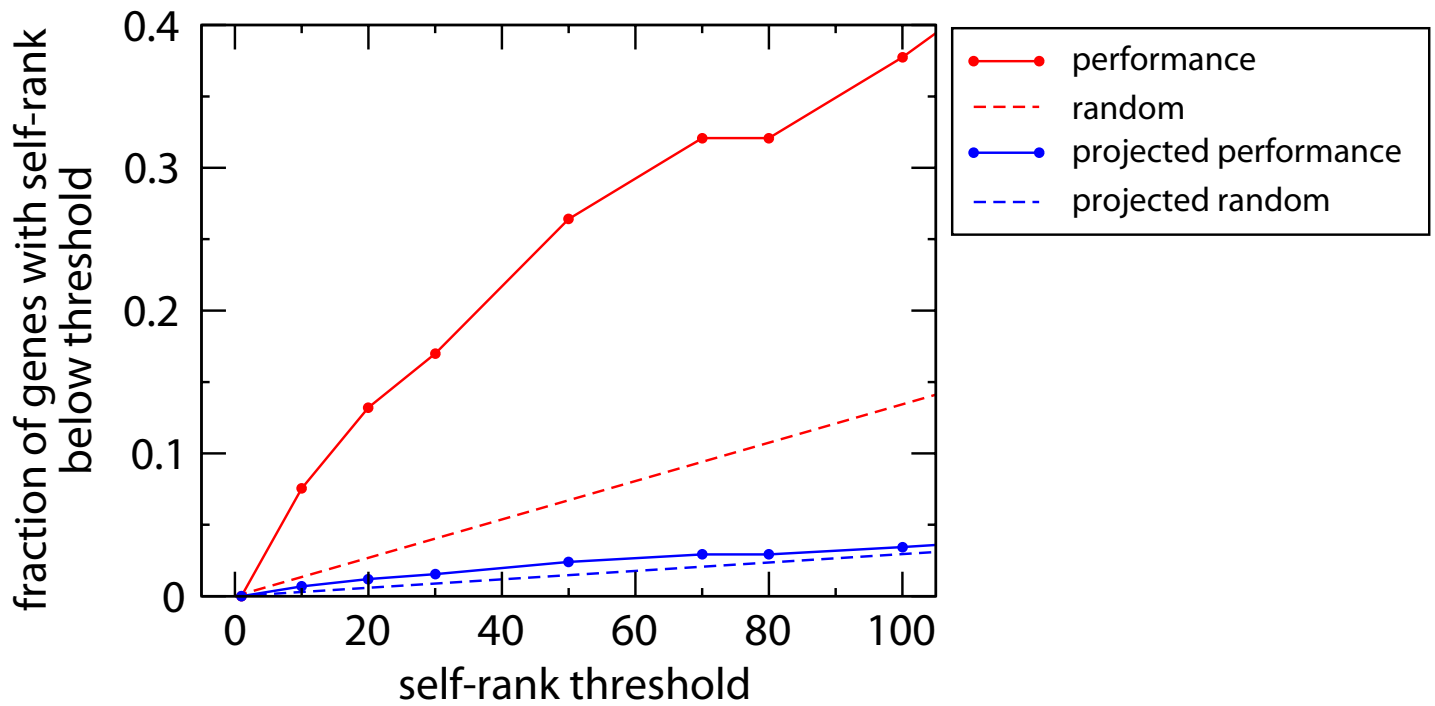




Self-rank performance of phenotypic profiles. *S. cerevisiae* self-rank performance based on similarity of phenotypic profiles is shown for the set of genes for which phenotypic data is available (red). Overall, normalized performance on a set of all metabolic enzymes is estimated (blue). Unlike all other presented results, the set of metabolic enzymes was not filtered to exclude homologous enzyme pairs. Performance of a completely noninformative (random) scores is shown by the dashed lines for each case. Predictions were generated based on association scores with 3 layers of the metabolic network neighborhood, combined using ADT classifier with 10 fold validation.