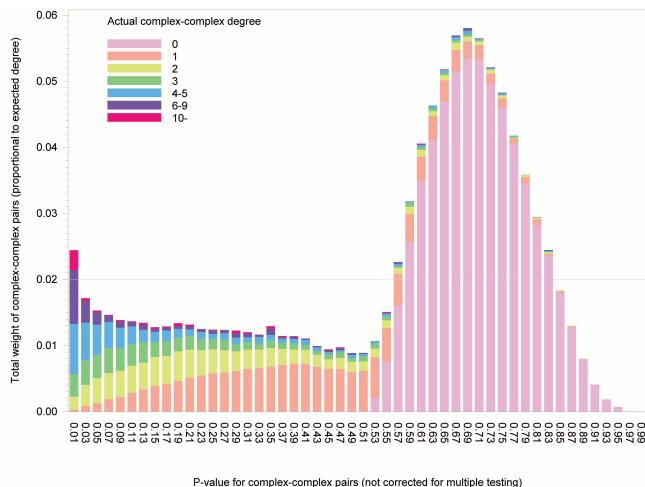


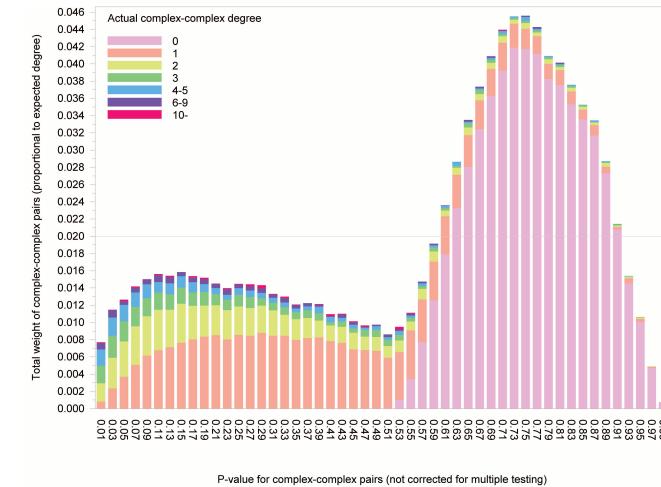
Distribution of p-values (human)

Corrected for overdispersion (colored for actual complex-complex degree)

A. Method performed on actual complexes

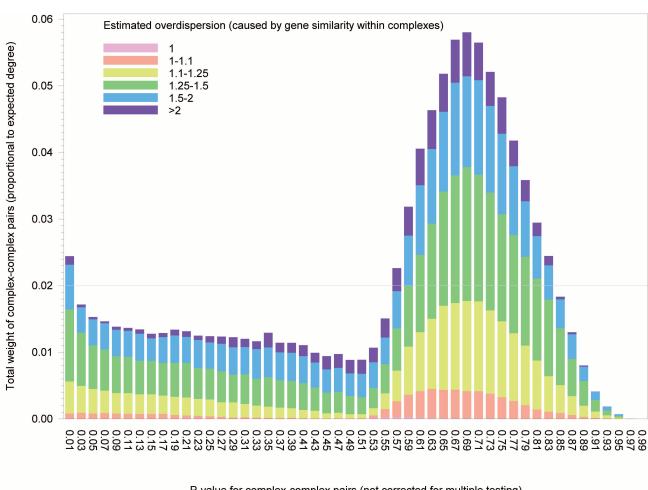


B. Method performed on random complexes

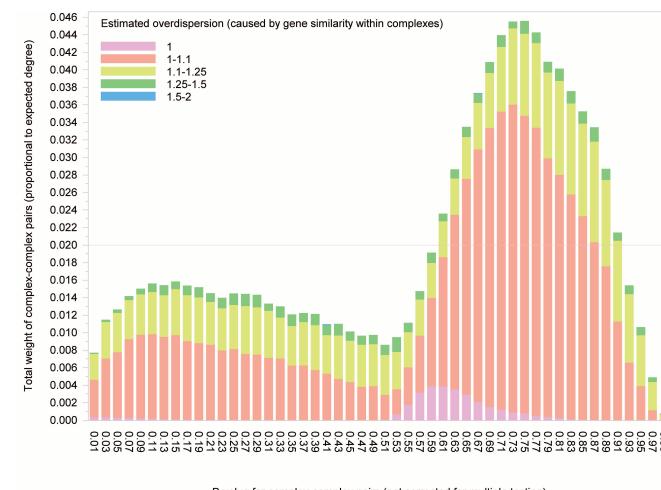


Corrected for overdispersion (colored for estimated overdispersion)

C. Method performed on actual complexes

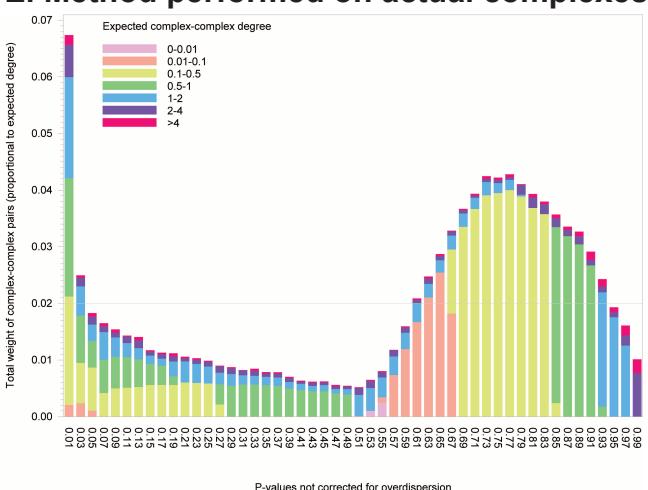


D. Method performed on random complexes

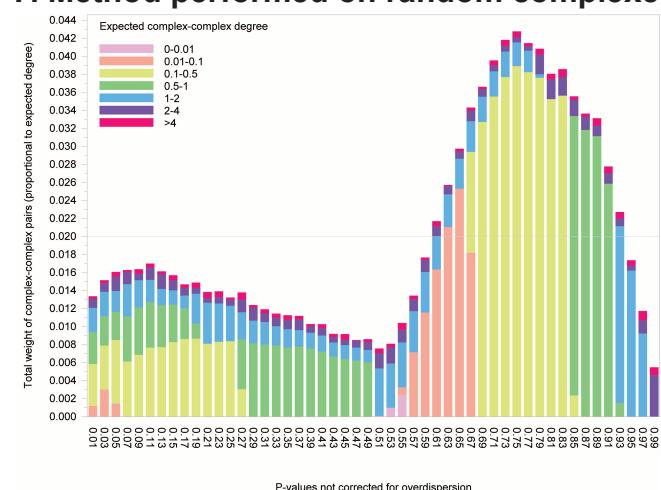


No correction for overdispersion (colored for expected complex-complex degree)

E. Method performed on actual complexes



F. Method performed on random complexes



Distribution of the raw p-values before correction for multiple testing: The weighing implies that each complex-complex pair contributes to the histograms in proportion to the weights (expected complex-complex degree) used when computing the FDR. In all analyses there is a large peak for high P-values (>0.5) due to most complex pairs having a low or zero complex-complex degree (e.g., A and B). The differences caused by the effect of overdispersion are evident in a comparison between the two histograms. The effect of overdispersion is systematically high when the method is applied on the actual protein complexes (C), and to a much lesser extent when applied on a protein-randomized version of the complexes (D). For protein-randomized analyses, the raw p-values before correcting for overdispersion look conservative when compared to the performance of the method on actual complexes (E and F).