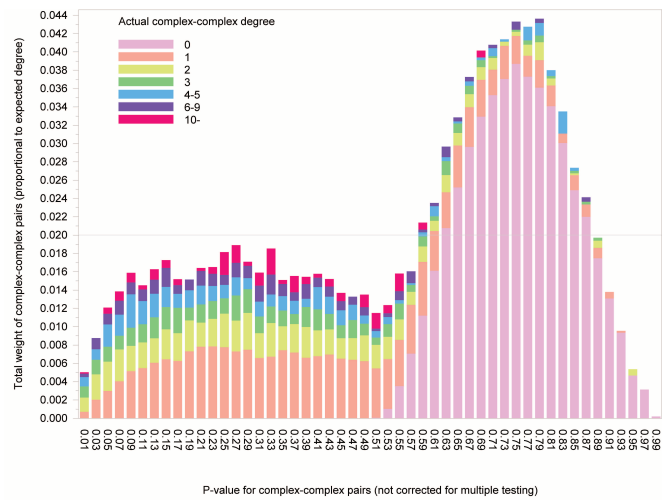
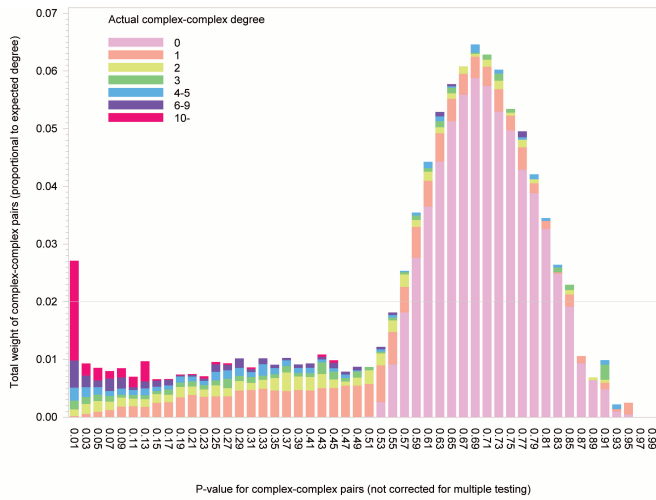


# Distribution of p-values (yeast)

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

**A. Method performed on actual complexes**

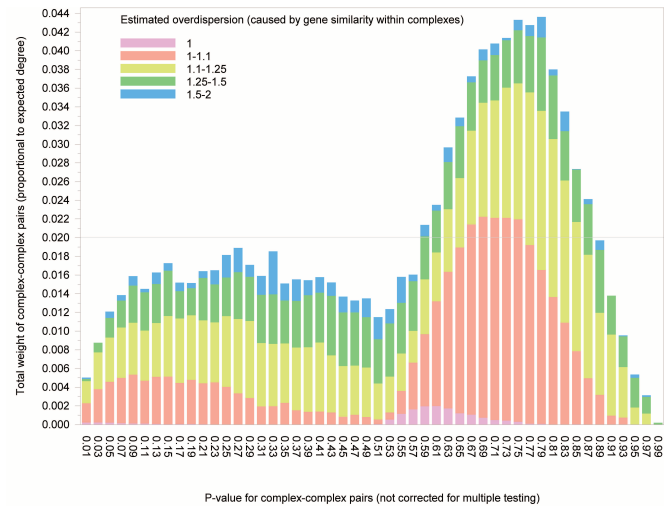
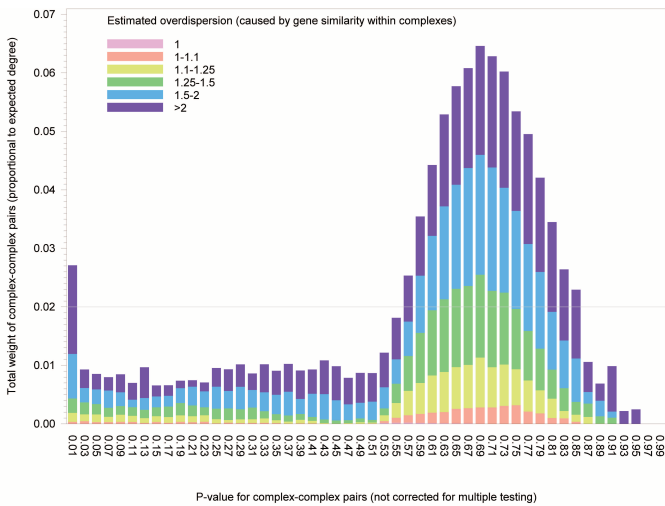
**B. Method performed on random complexes**



## Corrected for overdispersion (colored for estimated overdispersion)

**C. Method performed on actual complexes**

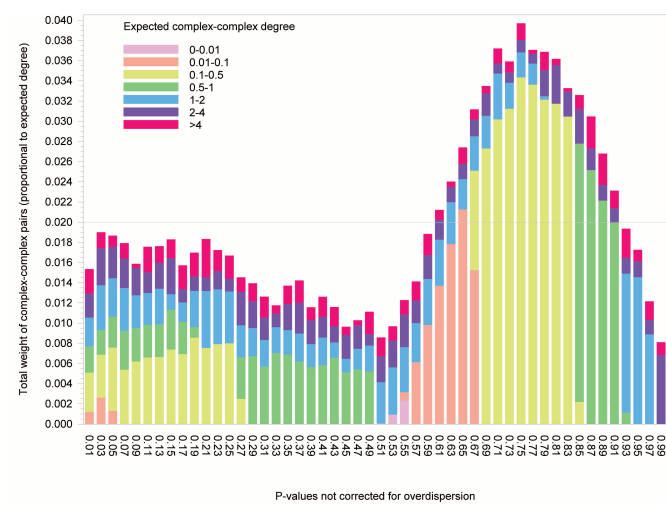
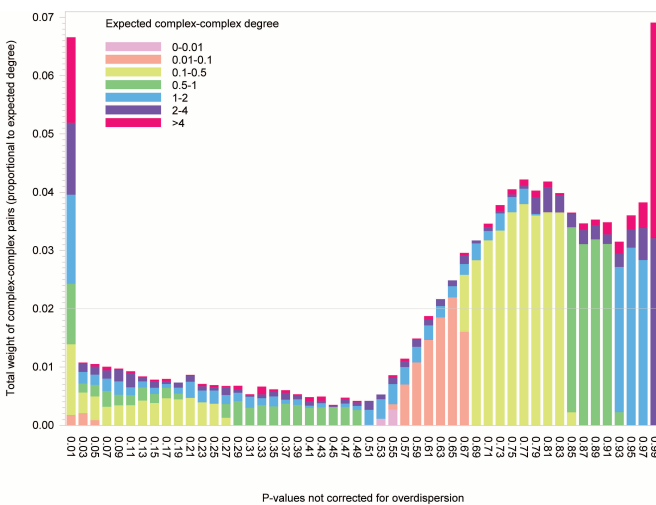
**D. Method performed on random complexes**



## No correction for overdispersion (colored for expected complex 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).