To show the distribution of edges, we partition the graph consisting of human and yeast genes into subgraphs of equal size, using a multi-level bisection algorithm implemented by METIS.

Figure 1: Histogram of number of edges in subgraphs.

It can be seen there are only two densely connected subgraphs consisting of \( \sim 200 \) nodes and \( \sim 250 \) nodes respectively. The rest of the subgraphs are relatively sparse, even when the graph is divided into smaller subgraphs (\( \sim 50 \) nodes).