

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.

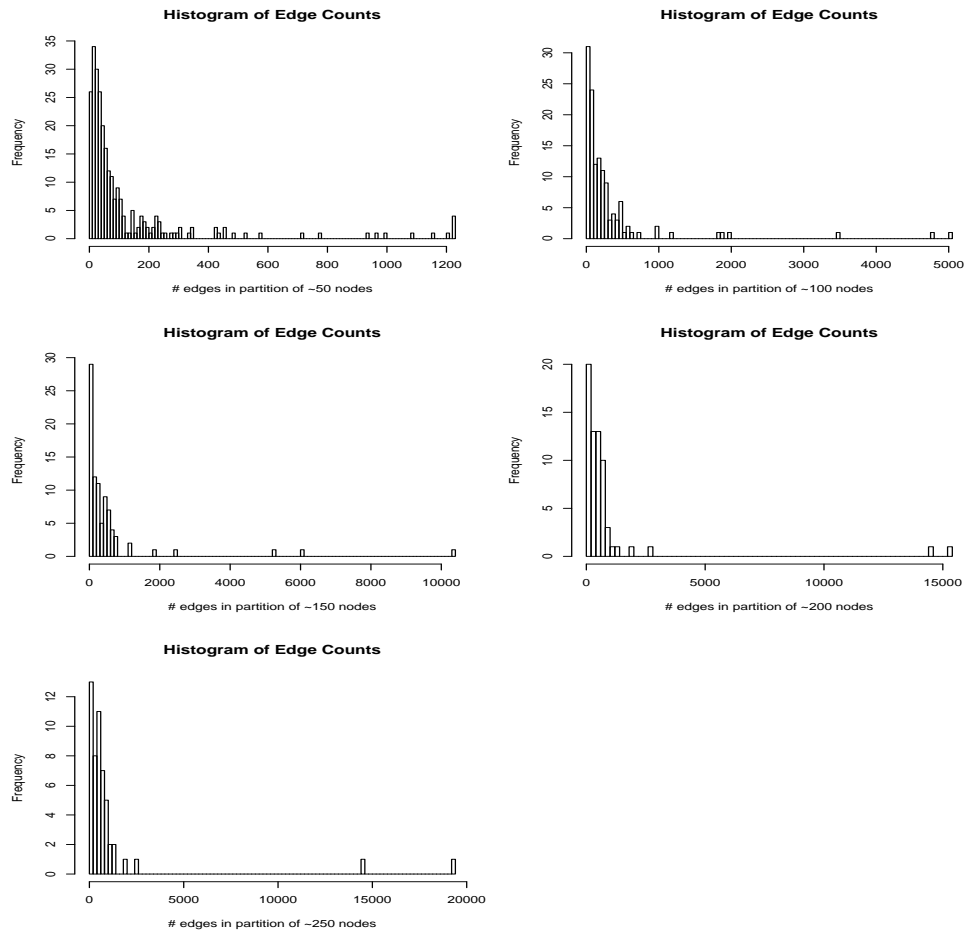


Figure 1: Histogram of number of edges in subgraphs.

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).