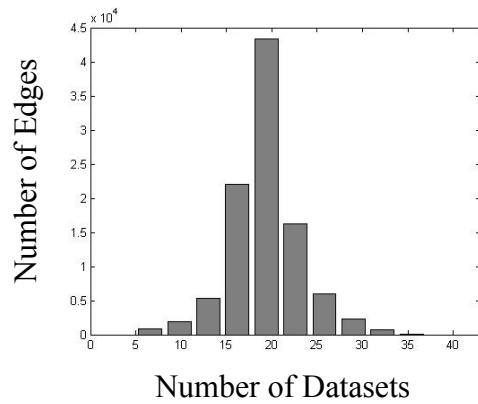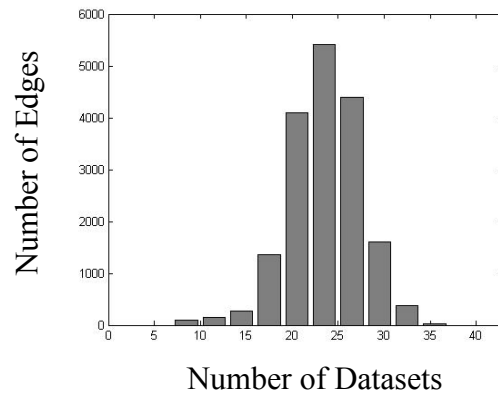A

B



**Distribution of the number of datasets that contribute to each edge**
For each edge connecting a pair of genes in the 0.3 (A) and 0.4 (B)
networks, connecting a pair of genes, we calculated the number of
datasets in which the two genes appear co-regulated. The data in the
histogram shows the number of edges confirmed per number of datasets.