**Table 1**

**Bicluster method comparison based on a bicluster set data score**

Methods are sorted by descending bicluster set data score, which is a Euclidean distance from a perfect score for the four bicluster set variables (bold column names): mean correlation, mean contrast, mean gene coverage per number of biclusters, and the mean number of experiments. The top and bottom two methods for each variable are colored red and blue, respectively. The additional columns for ‘Gene coverage’ and ‘Number’ (of biclusters) show the component data for the derived ‘Gene coverage/Number’ variable.

**Figure 3**

A scatter plot of the relationship between the mean bicluster correlation and the total data enrichment coverage by statistical enrichment in biclusters, for bicluster sets from MAK (blue), MAK starting points (black), and other methods (red). Reference data included GO terms, k-mer array gene-TF associations, KEGG pathways, and TIGR functional roles. The dashed line shows the maximum combined performance for correlation and enrichment for other methods (cMonkey) and four different MAK results to the right and above this line (bold) outperform other methods (rank in bold). The MAKchecker results incorporating all four data types showed the highest bicluster correlation and enrichment.

**Figure 4**

A bar plot showing the number of biclusters enriched for different localizations and their combinations, for different MAK results as well as other methods. Data are sorted from right to left, from most to least common cases across all bicluster results. MAK results are show in gray scale and other methods in color. The log2 value of each bicluster count is shown. ‘Unknown’ corresponds to enrichment for genes with no assigned localization and ‘none’ corresponds to cases of no significant enrichment.