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In this paper we develop a computational method for the prediction of functional modules in microbial genomes. We first quantify the functional relatedness among genes based on their distribution across different microbial genomes, and obtain a gene network in which every two genes are associated with a score representing their functional relatedness. We then apply a threshold-based clustering algorithm to this gene network, and obtain modules within each of which the number of genes is upper-bounded by a pre-specified value and the inside genes are more strongly functionally related to each other than to the outside genes. We use the gene ontology (GO) information to assess the prediction results. The GO similarities among the genes that are predicted to belong to the same functional module are compared with the GO similarities among the genes that are randomly clustered together. Such comparisons reveal that our predicted functional modules are statistically significant, and the genes within the same predicted functional module share much commonality in terms of biological process. We also look into the predicted functional modules that are common to both *Escherichia coli* K12 and *Bacillus subtilis* subsp. *subtilis* str. 168, and provide explanations for some functional modules. (Received August 22, 2005)