The genomic tree of gene contents using the functional classification of KEGG orthology

김진식*, 이상엽
한국과학기술원
(jinsikkim@kaist.ac.kr*)

We have performed a genome-scale clustering to identify whole genome relationships using the functional groups given by the KEGG Orthology (KO). The capabilities of metabolism were assigned by using the number of genes in the functional categories. Two-step clustering method, which is comprised of a self organizing tree algorithm followed by hierarchical clustering, was used simultaneously. As a result, we obtained a consistent clustering results with various phenotypic characteristics of the organisms. The capability of this approach to collect and cluster the metabolic functional capabilities can be a useful tool in the prediction of the relationships among the organisms. [This work was supported by from the Korean Systems Biology Research Project of the Ministry of Science and Technology and by the Brain Korea 21 Project. Further supports by the LG Chem Chair Professorship, Microsoft, and IBM SUR program are appreciated]