An Integrated Visualization Tool for Heat Map and Gene Ontology Graph

Authors: Somyung Oh, Jeonghyeon Ha, Kyungwon Lee, Sejong Oh

Abstract : Microarray is a general scheme to find differentially expressed genes for target concept. The output is expressed by heat map, and biologists analyze related terms of gene ontology to find some characteristics of differentially expressed genes. In this paper, we propose integrated visualization tool for heat map and gene ontology graph. Previous two methods are used by static manner and separated way. Proposed visualization tool integrates them and users can interactively manage it. Users may easily find and confirm related terms of gene ontology for given differentially expressed genes. Proposed tool also visualize connections between genes on heat map and gene ontology graph. We expect biologists to find new meaningful topics by proposed tool.

Keywords: heat map, gene ontology, microarray, differentially expressed gene **Conference Title:** ICCB 2016: International Conference on Computational Biology

Conference Location: Tokyo, Japan Conference Dates: September 05-06, 2016