



KOBIC Workshop

Bioinformatics Analysis using BioMatrix

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In post-genomics era, various technologies can be used to produce genome-scale, or 'omics', data sets that provide systems-level measurements for virtually all types of cellular components in a model organism. Analyzing the networks of interactions between genes and proteins has become a major focus of present day biology. Investigators now face serious challenge that interpreting large-scale data sets and thereby deriving fundamental and applied biological information about whole systems. Try to overcome these obstacles by using omics data, KOBIC (Korea Bioinformation Center) developed one-dimensional automatic analysis system, BioPipeline. And, KOBIC is trying to build a complex network of BioPipelines that can analyze any kind of biological data coherently with context information. We named it 'BioMatrix'. The BioMatrix is a tightly woven network of biological entities and algorithms. Also, it is the summary table of all the major omics we are generating nowadays. Each information type such as sequence, structure, expression, pathway, regulation and network is a row in the matrix, and each column represents an omics category such as genome, expressome, proteome, interactome, functome and textome. The entries in the matrix are database and/or analysis tools. Thus, BioMatrix can provide two-dimensional annotation of unknown biodata. Users can access BioMatrix via a website, BioPortal. It will provide free service of an integrated database retrieval system and an associated analysis tools.

