BioInfra : System for Large Scale Genome Analysis

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BioInfra is the first ever bioinformatics integrated analysis system that provides biological information from genome sequence to protein-protein interaction prediction. Its comprehensive automated annotations cover eukaryotic, prokaryotic genomes and EST data. For genomic sequence analysis, it uses repeat region finding, ab initio gene prediction, EST based on gene prediction, protein domain finding, and disease relativity search. Importantly, it provides insight into the prediction of gene functions by predicting protein-protein interaction using Protein Structural Interactome Map (PSIMAP). The system provides the basis for further interactive data mining to extract meaningful biological information to further advances in life science research. Bioinfra also provides genome visual tools, an easy! -to-use protein domain assignment module, and protein-protein interaction navigation tool. Users can retrieve possible interaction partners of their proteins of interests if a significant homology assignment is made with their query sequences. Bioinfra was designed and developed by National Genome Information Center (NGIC) of Korea Research Institute of Bioscience and Biotechnology (KRIBB), Object Interaction Technologies, Inc. (OITEK), and Biomatics Laboratory of Korea Advanced Institute of Science & Technology (KAIST).