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Bioinformatic Infrastructure for Maintaining Proteome Information

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Extracting the most out of omics databases requires automated pipelines. Modern biological science requires such an automated platform for handling data with proper a information technology infrastructure. We introduce an integrated bioinformatic pipeline scheme for processing genomic, proteomic, and RNA data. These pipelines incorporate a data mapping part: BioMatrix, automation part: BioPipeline, daemoninzing part: BioEngine, and information distribution part: BioPortal. As a specific BioPortal application for a processing raw proteomic data we have built a web service called MassNet.kr. As the fusion of biological fields is accelerated, data glueing methods and integrated databases are becoming the key issues in bioinformatics. We introduce a distributed approach of sharing biological data using P2P for heterogeneous groups of researchers. Distributed resources architecture is fast and robust for projects that have a very large number of participants. This approach is suitable for Asian and Oceanian regions.