

Poster B-40

Middleware approach to data integration for plant genomics



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Short Abstract: Plant functional genomics requires efficient integration and processing of related information. The difficulty lies in the integration of this information, often semantically inconsistent or expressing different viewpoints, and, very often, only available in heterogenous formats. We present a distributed integrated environment that permits interoperability between different data sources.

Long Abstract:

The study of gene function, or functional genomics, is today one of the most active disciplines in life sciences and requires efficient integration and processing of related information. Today's biologists have access to bioinformatics resources to help them in their experimental research. For example, to identify a gene mutation and the consequences it can lead to, the biologists have to consult and compare several information sources such as biological sequencing data obtained from public or private resources. They have also to compare experimental data and data that has undergone diverse procedures to be able to refine and perfect their analyses. In genomics, several tens of public data sources can be of interest to them, each source constituting a part of the useful information. The difficulty lies in the integration of this information, often semantically inconsistent or expressing different viewpoints, and, very often, only available in heterogenous formats. In this context, informatics has a role to play in the design of systems that are flexible and adaptable to significant changes in biological data and formats.

The goal of the present work is to present a distributed integrated environment for knowledge representation that permits interoperability between different data sources by overcoming problems of heterogeneity .