

## **A Functional-Genomics Information Management System**

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This project addresses the need for an Open Source Information Management System dealing primarily with functional-genomic data types, and the integration of data towards advanced visualization and analysis, allowing queries at the systems level. The system is directed towards the needs of labs gathering data in functional-genomic type applications, with extended capacity available for users with more advanced bioinformatics needs. The approach is not to duplicate existing analysis capabilities, but to reuse existing public services through transparent access to services available at eg. the EBI and NCBI, or by means of pass-through functionality to locally installed analysis suites.

A base system is being constructed providing extensive user-authentication, group management, project management and database access layers. On top of this, modules are being implemented for dealing with specific data types. Data will be curatable within the system, with versioning control available. Data modules currently include sequence data, genotype data, microarray data, structural data and proteomics data, as well as a generic laboratory notebook-type module. Each module will contain features specific to the data type, with varying degrees of analysis capability. Analysis features will be interfaced remotely / locally to existing programs and databases using a web-services-based approach.

The power and novelty of the system will be in the integrated interface to all modules / data types, and the integrative visualization of different data types.