CDB SEMINAR

Gos Micklem

Cambridge Computational Biology Institute

Thursday, August 2, 2007
16:00~17:00   C1F Auditorium

The FlyMine and InterMine Projects

Summary

FlyMine (http://www.flymine.org) is an open-source project developed in the Departments of Genetics and Biochemistry at the University of Cambridge in collaboration with the National Institute of Biomedical Innovation, Japan.

FlyMine integrates many different genomic and proteomic data sources and allows querying of combinations of these data. It has convenient tools for working with lists of e.g. genes, as well as a library of typical queries that can be searched, executed or used as starting points for new queries.

Data currently in FlyMine include genome annotation, microarray data, protein interaction data, protein domains/families, predicted 3D protein domain structures, transcription factor binding sites, GO annotations and RNAi data. The inclusion of orthologues makes it possible to run queries across different organisms.

The basis for FlyMine is a generic system called InterMine. This makes it relatively easy to build new databases. InterMine is now being used in a number of laboratories to build other biomedical data warehouses. Many features of the design of InterMine are aimed at allowing high performance at the same time as allowing flexible querying.

Host:
Martin Jakt
Stem Cell Biology, CDB
mjakt@cdb.riken.jp
Tel:078-306-1893
(ext : 5304)

RIKEN CENTER for DEVELOPMENTAL BIOLOGY (CDB)