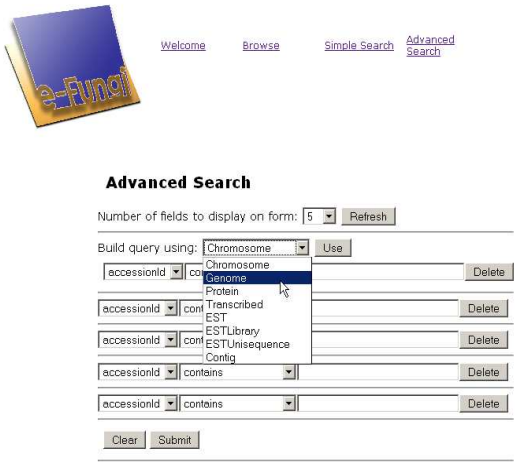
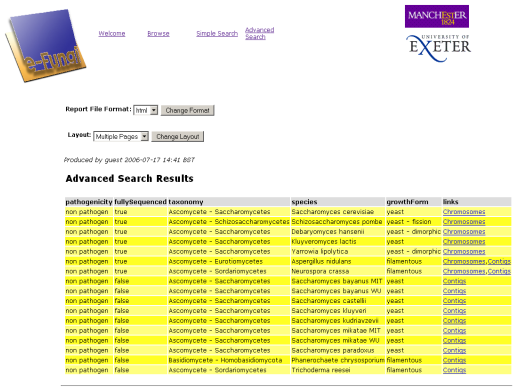
e-Fungi: An e-Science Infrastructure for Comparative Functional Genomics

e-Fungi integrates sequence and functional data from multiple fungal species, facilitating the systematic study of less well understood species with reference to model organisms.

Simple Searches

Advanced Searches





Database Details

The e-Fungi database has been built using FastObjects, a commercially available object database.

The database includes complete genome sequences, sequence clusters, ESTs, protein domains and protein localization data.

The Web based interface for the e-Fungi database has been developed using Pierre (http://pierredownload.man.ac.uk).

The first database in July 2006 allowed sequence based queries over 25 genomes.

A second release in November 2006 allowed function-based queries over an increased number of genomes.

For later releases, there will also be access via a Java application. This will enable the user to compose more complex queries.

Web site:

http://www.e-fungi.org.uk

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