Hogeschool van Arnhem en Nijmegen

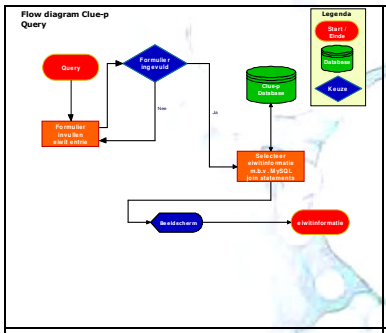
Integrating data sources for the functional clustering of proteins

Bioinformatics

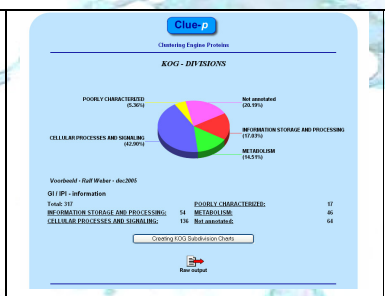
Querying biological data sources is an essential part of any biological study.
A well-known example of this is BLAST, which is frequently used to compare proteins at sequence level.

In cooperation with Nijmegen Proteomics Facility, which is part of the Laboratory for Paediatrics and Neurology, the Bioinformatics Studies Department at HAN University has developed a web-based application for the functional clustering of proteomics data. Cluster information has been retrieved from existing cluster databases, including COG (Cluster of Orthologous Groups) and Pfam. Researchers can cluster sets of proteins into functional categories by submitting the accession numbers of the proteins. The application presents the clustering results as distribution charts.

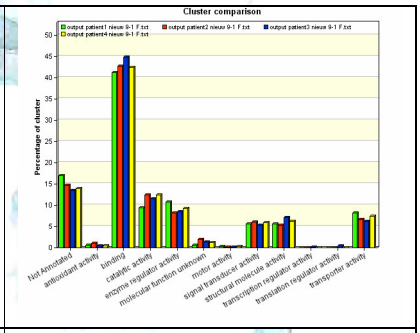
The figures below depict the design of the data flow, the user website's user interface and the distribution charts, respectively.



Design



Implementation



Analysis

The HAN BioCentre offers the following areas of expertise within the field of bioinformatics:

- Advice on the application of bioinformatics for applied research.
- Development and implementation of databases and software.
- Analysis of high-throughput data by applying standard statistical methods and tools.

HAN BioCentre