The *ClustScan* program package architecture

Janko Diminić, *Faculty of Food Technology and Biotechnology*

Abstract

The ***ClustScan*** program package was developed as *Java* client and *Linux* server application. To develop the *Linux* server application several programming languages (*Java*, *Perl*, *PHP*, etc.) were used and implemented as a Web service (SOAP) that acts as a wrapper for a number of command-line bioinformatics tools (*HMMER*, *GeneMark*, Glimmer, *ClustalW*, etc.) specific for *Linux* operating system. On the other hand, for the database (*DBMS*) implemented within the ***ClustScan*** program package the *PostgreSQL* was used. To develop the backbone of *Java* client application the *eclipse RCP* (Rich Client Platform) technology was used featuring fast SWT graphical interface. In the near future we will develop the ***ClustScan*** database (***CSDB***) as a publically available Web application. The ***CSDB*** will allow browsing, searching and manipulation of data from polyketide and peptide gene clusters annotated by ***ClustScan*** program package using bioinformatics programs such as *BLAST*, *ClustalW*, *Phylip* and others. The ***ClustScan*** program package and the ***CSDB*** database will offer novel and user friendly approaches for the presentation of the biological data.