

Abstract

The volume of biological related data, which is for instance derived from DNA sequencing, is exponentially growing over the years. At the same time large amounts of data is generated due to the increased application of high-throughput methods like DNA-microarray or mass spectroscopy. The strong increase of biological related data raised the demand for analyzing applications and bioinformatic software, which supports a scientist by doing data analysis. Especially for the analysis of DNA-microarrays various programs, which differ in functionality, have been developed. Many programs are too widespread, too complex, difficult to use, limited to certain operating systems or not for free.

During this thesis the internet application OrfMapper, which provides unique functionality for analyzing, querying and visualizing gene metadata, has been developed. OrfMapper is a free, operating system independent and easy-to-use web tool. It includes many special features, like fast querying by a variety of gene specific data for instance gene IDs, EC-numbers, nucleotide sequences, or general keywords. These data can be linked to different colors in order to simplify visualization. Therefore it is also possible to generate individually colored metabolic pathway maps. These can be downloaded as interactive PDF files which include hyperlinks. A genome browser has been developed in order to analyze genomes and the environment of genes. Accessibility is provided by specific interfaces for different user groups. Besides other features OrfMapper offers an automated translation of gene-expression values from DNA-microarrays to color values.

A DNA-microarray experiment for the organism *Anabaena* PCC7120 has been performed during this thesis. Data resulting from this experiment is exemplarily analyzed with OrfMapper. The functionality of OrfMapper is presented using the microarray dataset.