Abstract

Real-time PCR is one of the most important methods used in functional genomics. As one of the leading assays it has a large dynamic range, great sensitivity, and avoids the need for post-PCR processing. The requirement for analyzation, in oder to get significant results, produced a number of different analyzers, which mostly run in a separate software. Drawing conclusions is often done by comparing analyzed results of different experiments and usually consists of dealing with several printed sheets that are hard to handle, store, and organize.

This thesis describes the design and implementation of an application capable of managing and analyzing all relevant real-time PCR data. Based on the three tiered J2EE platform it is developed as a Web application using a model driven architecture approach. It allows the storage of general component descriptions, plate definitions, fluorescence measurements, and analyzer results.

Files produced by PCR machines contain information about the plate and the detected fluorescence measurements. The developed application integrates a parser that is able to read in those files and therefore provides a rapid and error-free insertion of important data. A newly developed system using Web 2.0 features allows to graphically view the inserted fluorescence measurements.

Already existing analyzers were integrated into the system and can be launched from a central point in the application. A plug-in manager ensures that new analyzers can be added to the system without having to change existing parts in the application. Results generated by analyzers can be easily compared and exported to files for further analyses. User interactions are managed using the Model-View-Controler framework Struts and Message Driven Beans are used to perform long lasting business tasks, which run in the background.

The incorporated parser and the possibility to analyze one's date using several different analyzers in combination with an user-friendly interface provides an application capable of managing, storing, comparing, and analyzing real-time PCR experiments. All these features combined in one single application make up an unique tool the certainly improves the daily work of biologists.

Keywords: *real-time PCR*, *qPCR*, *analyzers*, *Web 2.0*, *J2EE*