

Abstract

Genomic studies ask for a number of molecular biology approaches that rely on different cloning procedures, PCR-based detection mechanisms and immunochemical methods. Additionally the use of different model organisms and tissues deepens the informational content in these projects. The extensive information of all components applied in an interdisciplinary research approach and the resulting data need to be organized and stored in a comprehensive way.

Organized data storage is inevitable for any laboratory which is involved in active research. So, a database exclusively for storing the information about the biological stocks used in the Institute of Genomics and Bioinformatics was planned and subsequently implemented. The ultimate aim of this database is to facilitate a concerted and powerful information use that allows easy access to all possible information sets as well as sharing and exchange of the same by a variety of different users.

The database was implemented based on three-tier architecture with a database backend (MySQL), an application server (JBoss) as the middle tier and a Web Interface as the client tier using the J2EE platform. The design and implementation builds upon an UML model. The code generator AndroMDA was used to convert the UML model into Java source code. The presentation layer was implemented using the Struts framework. Currently, the application facilitates storage of primer and plasmid related data.

Keywords: Cloning, PCR, J2EE, UML, LIMS, AndroMDA, Struts, Stocks, Primer, Plasmid