Abstract

After the previous thesis the biological-information integration system, in particular focusing on the task of rice biological data was constructed. In addition, the web-based application “RiceGeneThresher” was developed for mining rice genes and finding the most promising candidate genes for the trait of interest underlying QTLs. However, this web-based application and associated computation services were designed to be accessed by humans via WWW interface, not by machine, which means that it is troublesome for the researchers and software developers who want to use this database in an automate manner. Besides, from the database and software developer’s side, it is impossible to prepare all the CGI programs that satisfy a variety of users’s needs. To solve this problem, the middleware (GeneThresher APIs) was developed. I developed five major GeneThresher APIs by using Perl object-oriented methodology. They were prepared for other software developers who want to develop theirs new Perl based applications which run on the top of RiceGeneThresher database. Once, the completion of GeneThresher APIs, RiceGeneThresher web-based application was reconstructed to employ those APIs for visualizing, analyzing, browsing, and mining the rice biological data in same theme as the first thesis. In addition, RiceGeneThresher is migrated into the modular software that runs on the top of other datawarehousing platforms such as the Generic Model Organism (GMOD) and it provides the database schema and software for other crop genomes.

Keywords: RiceGeneThresher / GeneThresher APIs/ rice biological data integration system /