

**511/E1**

### **Development of a Virtual Bioinformatics Workbench for Sequence analysis**

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Use of Bioinformatics in tasks of molecular sequence analysis involves heavy usage of multiple computational tools and databases. This could be very time consuming when multiple tasks are needed to be done. Navigation between multiple analytical tools also consumes a considerable amount of time. Therefore there is a need to develop an integrated system which combines a variety of analytical tools into a single component. The main aim of this project was to develop a virtual analysis workbench, by integrating a number of available bioinformatics software tools into a single web application which would permit single-point access to a variety of software tools.

The implementation was done using java and related technologies. In addition, a 'rich' component framework called Rich Faces was used in order to create a better and a faster navigation system between tools. Throughout the project, none of the bioinformatics software tools were actually developed. The workbench makes heavy usage of already developed software tools through a distributed computing technology called web services which can allow access to incompatible software services over the web. The web services utilized by this workbench are provided by DNA Data Bank of Japan (DDBJ) through their web API for biology (WABI). Each web service was called using Rest method and then each software tool was made accessible as a separate software component.

With this virtual application a user could access several software tools through a single web interface. When one tool is in active mode other related software tools are also displayed to the user. Incorporation of rich components to the application has caused much faster performance compared to a regular web application.

As large number of biological data and biological software tools are being continuously developed, more software from different data services can be incorporated to this workbench in the future. This will result in a highly usable and complex integrated system which would largely reduce the time wastage in conducting complex molecular biological analyses.