

TOOLS AND RESOURCES TUTORIAL

An Introduction to Taverna

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The World Wide Web has brought a whole new world of databases and tools within easy reach of scientists. With this wealth of information, however, scientists and bioinformaticians can quickly become overwhelmed with the volume, diversity and complexity of data. Many bioinformatics resources are available to scientists through web interfaces, which require no programming knowledge. In this post-genomic era, however, web interfaces are limiting in many ways, such as when performing complex or very large analyses. An increasing number of resources are now becoming available as **Webservices**, which provide a programmatic interface for web-based services and are gradually being used more and more in biology and bioinformatics to automate the execution of services, circumventing many of these limitations. These Webservices can be chained together to create complex **Workflows**. **Taverna** (<http://taverna.sourceforge.net/>), which was written by Tom Oinn at the European Bioinformatics Institute (EBI) is a sophisticated, but easy to use application, developed for biologists to organise, automate and visualise these workflows. Taverna makes it simple enough to design the workflow of services you require, load your data in and click “go”.