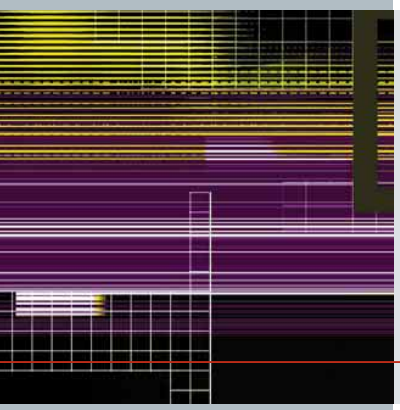
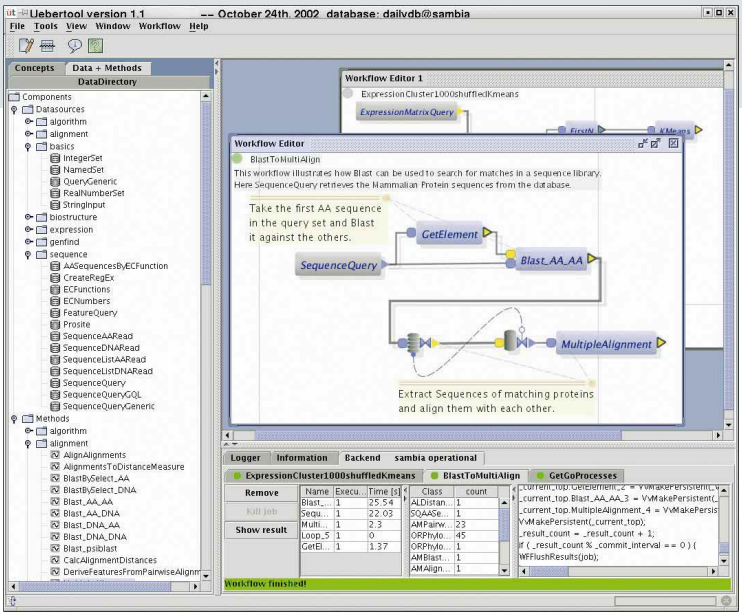
science factory



übertool

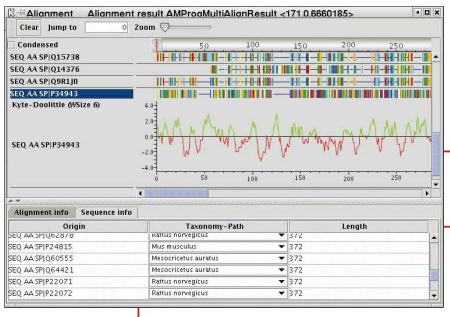
A new concept for the integration and analysis of molecular biological data



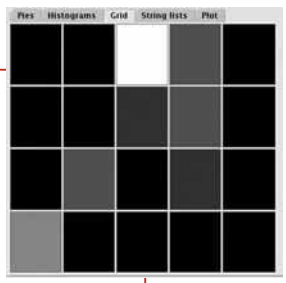
übertool ushers in a new generation of bioinformatic enterprise systems. These systems are capable of using all available information and bioinformatic methods related to diseases, genes or molecules of interest.
R&D departments need new bioinformatic infrastructures to deal with the data-avalanche emerging from in-house high-throughput systems (HTS) and an increasing number of publicly and privately available data sources.
übertool optimally supports current streamlined R&D processes, accelerating discovery and reducing costs, giving our customers the competitive advantage.
übertool has been designed to break down barriers:

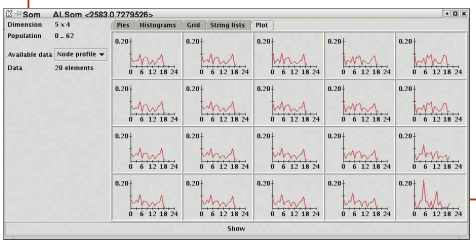
- between data integration and data analysis
- between public, licensed and proprietary data
- between sequence, expression and 3D structure analysis
- between bioinformatics and chemoinformatics
- between bioinformaticians and life-scientists
- between exploratory research and streamlined R&D processes

Researchers can assemble specific analysis procedures from more than 200 modules with a few mouse clicks. Our rapidly growing repository contains sophisticated algorithms for sequence, expression and structure analysis e.g. BLAST, Multiple Alignment, Hidden Markov Models (HMM), clustering methods, Self Organizing Maps (SOM), Support Vector Machines (SVM), 3D superposition and many more.
All workflows are processed automatically. They can be stored together with their results. Results can be used as data sources for new procedures.



Various interactive viewers give you diverse perspectives onto your results.





Our Technology

Integration means more than simply collecting data: sciencefactory has developed a sophisticated biological object model which stores all data with their respective relations. A network of classes stores molecular and experimental datatypes including sequences, expression data, metabolic pathways, chemical information, literature references and more. All of this data can be processed in a seamless workflow environment in which you can combine diverse analysis methods however you choose.

Your übertool

übertool is an expandable platform technology. An application programmer interface (API) is available for implementing your own datatypes and proprietary algorithms in Python.
sciencefactory´s team of experts provides services for adapting übertool to your special requirements and integrating it into your existing R&D infrastructure seamlessly.

Your Opportunity

übertool is under active development. Please check our website regularly where you can find more details and view live demo viewlets.
If you are interested in demo license of übertool please contact our sales team (sales@science-factory.com). One-month trial licenses are available free of charge.

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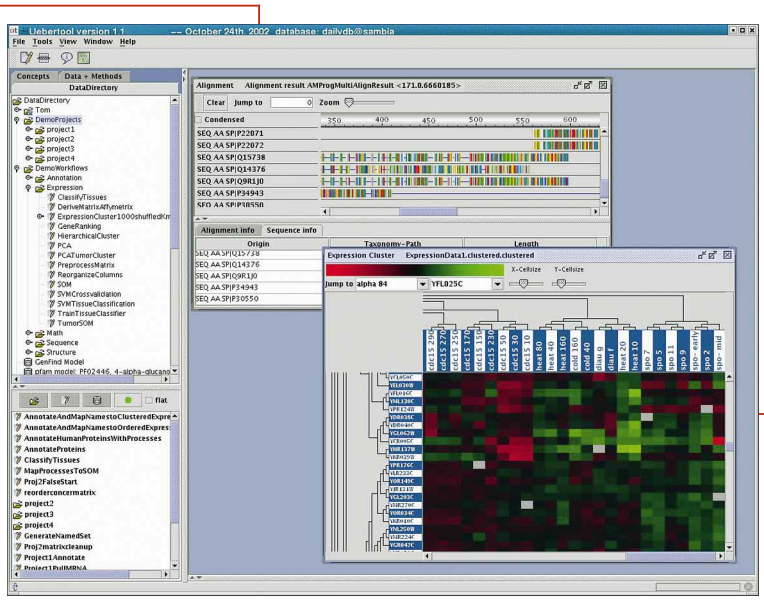

data analysis with übertool

Facts

Data Integration

- flexible biological object model
- XML in- and output
- interface to relational databases

Data analysis

- automatic data format conversions
- data compatibility checks
- >200 connectable modules covering sequence, expression and 3D-structure analysis
- easy-to-learn workflow approach, no programming required
- workflows can be stored, rerun and triggered
- interactive viewers
- application programmer interface (API) for custom enhancements

System features

- easy server administration
- zero effort client Installation
- migration and customization consulting
- scalable architecture
- distributed computing options
- multiple servers, multiple platforms

Complimentary Services

- installation and support
- basic training
- technical support
- application community support list

Optional Services

- in-depth bioinformatics training by experts
- custom programming (viewers, modules)
- migration support
- remote administration
- project consulting

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