

VIROLAB

A Virtual Laboratory for Decision Support in Viral Disease Treatment

ViroLab enables easy access to distributed resources as well as the sharing, processing, and analysis of virological, immunological, clinical and experimental data.

Objectives of the project

Genetic information is likely to become increasingly significant in many areas of medicine. This provides an unparalleled opportunity to advance the understanding of the role of genetic factors in human health and disease, to allow more precise definition of the non-genetic factors involved, and to apply this insight rapidly to the prevention, diagnosis and treatment of disease. Large numbers of complex genetic sequences are increasingly becoming available, providing a unique opportunity for studying the many diseases where genetic information will become important in future years, such as in the case of infectious diseases.

As a prototype the problem of HIV drug resistance is addressed. **ViroLab** integrates biomedical information from viruses (e.g., proteins and mutations), patients (e.g., viral load) and literature (e.g., drug resistance experiments), resulting in a rule-based distributed decision support system for drug ranking, as well as advanced tools for (bio)statistical analysis, visualization, modelling and simulation.

The **main objectives of ViroLab** are to:

- develop a virtual organisation that binds the various components of the **ViroLab**;
- develop a virtual laboratory infrastructure for transparent workflow, data access, experimental execution and collaboration support;

- virtualize and enhance the state of the art in genotypic resistance interpretation tools, integrating them into the virtual laboratory;
- establish epidemiological validation showing that **ViroLab** correctly and quantitatively predicts virological and immunological outcome, and disseminate the results to stakeholders.

Project Description

ViroLab is based on Grid security infrastructure, middleware and user interfaces. The virtualization of resources such as data, instruments, compute nodes, tools, and users allows full resource transparency. These resources are made available by adopting Grid computing, and building on existing tools from projects such as CrossGrid, EGEE and VL-e.

The virtual organisation spans a number of geographically separated “physical” institutions across Europe, including five hospitals. **ViroLab**

uses a uniform interface to available resources in the virtual laboratory, with functionality defined by well-defined tasks in clinical environments. The virtual lab allows users to select either pre-defined tasks or to

“ViroLab will lead to new valuable clinical data and information on treatment of HIV-infected persons”

Scenario

In **ViroLab**, a specialist member of the virtual organization logs into the virtual laboratory and accesses the distributed decision support system, which interprets the genotype of a patient by using rules developed by experts in the organization on the basis of literature mining of context sensitive data. The specialist then applies a set of multi-scale methods such as molecular dynamics modelling of HIV infection, and automatically generates new rules that are checked for consistency and redundancy. The specialist then validates the new set of rules, covering this way the fast temporal and spatial scales required to infer information from a molecular (genomic) level up to patient medical data.

compose novel tasks from repositories of workflow templates, by means of orchestration of the underlying resources. The virtual lab also provides a virtual whiteboard and experimental (provenance) logbook for scientists at geographically separate locations.

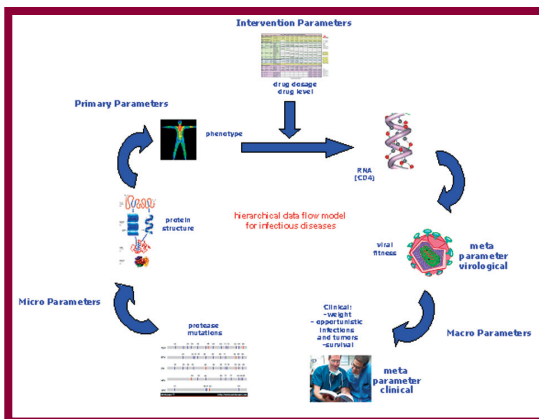
Since **ViroLab** offers access to many disparate kinds of data from many sources, much effort is devoted to providing a uniform interface to all of these resources by virtualizing them and coupling advanced modelling, simulation and analysis tools in a way that is highly accessible to specialists and researchers.

Expected Results & Impacts

The collaborative research will result in a virtual laboratory for decision support in infectious diseases treatment. We focus on HIV antiviral resistance (and thereby on a specific scientific community and patient group) for the purpose of creating a prototype for the broader application for infectious diseases.

The project will benefit from the development of innovative pharmaceutical research, (antiviral drug development and use of information of clinical trials). **ViroLab** will lead to new valuable clinical data and information on treatment of HIV-infected persons, which will provide essential insights into the prevalence of drug resistance patterns in treated individuals on a continuous basis. It is of crucial importance for future development of new drugs effective against drug resistant HIV.

ViroLab will demonstrate measurable, quantifiable benefits, respecting all aspects of confidentiality, fulfilling the urgent need for standardised rules and systems for reliable quantitative HIV-1 genotypic resistance interpretation, providing medical doctors throughout Europe with accessible and user-friendly tools for significantly improving the clinical usefulness of genotypic assay results. The virtual laboratory will function as Europe's first rule-based decision support system for drug



ranking, including advanced tools for (bio)statistical analysis, modelling and simulation, enabling prediction the temporal virological and immunological response of viruses with complex mutation patterns to drug therapy, leading to better individual based treatment.

ViroLab will be validated in epidemiological studies and will include elaborate and advanced Grid security infrastructures, respecting the aspects of confidentiality, security and trust.

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