VIROLAB – a Virtual Laboratory for Decision Support in Viral Diseases Treatment

Peter Sloot\textsuperscript{1}, Charles Boucher\textsuperscript{2}, Marian Bubak\textsuperscript{3,4}, Alfons Hoekstra\textsuperscript{1}, Pawel Plaszczak\textsuperscript{5}, Alice Posthumus\textsuperscript{6}, David van de Vijver\textsuperscript{2}, Stefan Wesner\textsuperscript{7}, Alfredo Tirado-Ramos\textsuperscript{1}

\textsuperscript{1} Universiteit van Amsterdam, The Netherlands
\textsuperscript{2} Universitair Medisch Centrum Utrecht, The Netherlands
\textsuperscript{3} Institute of Computer Science AGH, Krakow, Poland
\textsuperscript{4} ACC CYFRONET AGH, Krakow, Poland
\textsuperscript{5} Gridwise Technologies, Krakow, Poland
\textsuperscript{6} Virology Education B.V., Utrecht, The Netherlands
\textsuperscript{7} Universitaet Stuttgart, Germany

Abstract
The main objective of the ViroLab project is developing a Virtual Laboratory for Infectious Diseases that facilitates medical knowledge discovery and decision support for e.g. HIV drug resistance.

Large, high quality, clinical and patient databases have become available which can be used to relate genotype to drug-susceptibility phenotype. The relevant data has two main characteristics: it spans in a rule-based decision support system for drug ranking. The Virtual Laboratory supports tools for statistical analysis, visualization, modelling and simulation, to predict the temporal virological and immunological response of viruses with complex mutation patterns to drug therapy. The Virtual Laboratory provides the medical doctors with a decision support system to rank drugs targeted at patients. It provides the virologists with an advanced environment to study trends on an individual, population and epidemiological level. By virtualizing the hardware, compute infrastructure and databases, the virtual laboratory is a user friendly environment, with tailored workflow templates to harness and automate such diverse tasks as data archiving, data integration, data mining and analysis, and modelling and simulation. HIV drug resistance is one of the few areas in medicine where genetic information is widely used for a considerable number of years. Large numbers of complex genetic sequences are available, in addition to clinical data. ViroLab offers a unique opportunity as a blueprint for the potentially many diseases where genetic information becomes important in future years.

References

1. VIROLAB – EU IST STREP Project 027446; http://www.virolab.eu

33