

Free, open virtual laboratory for infectious diseases

June 4 2010



(PhysOrg.com) -- Doctors around the world will soon have a powerful new tool at their disposal in the fight against HIV and other infectious diseases: a virtual laboratory that will help them match drugs to patients and make treatments more effective.

The ViroLab Virtual Laboratory, the core components of which are scheduled to be available online in 2010, uses the latest advances in machine learning, data mining, [grid computing](#), modelling and simulation to turn the content of millions of scientific journal articles, disparate databases and patients' own medical histories into knowledge that can effectively be used to treat disease.

Developed by a multidisciplinary team of European researchers working

in the EU-funded ViroLab project, the virtual laboratory is already being used in seven hospitals to provide personalised treatment to HIV patients and is eliciting widespread interest as a potent decision-support tool for doctors.

“ViroLab finds new pathways for treatment by integrating different kinds of data, from genetic information and molecular interactions within the body, measured in nanoseconds, up to sociological interactions on the epidemiological level spanning years of [disease progression](#),” explains Peter Sloot, a computational scientist at the University of Amsterdam and the coordinator of ViroLab.

Sloot came up with the idea for ViroLab a decade ago when he met a virologist at a scientific conference who told him about the problems doctors face when trying to find the right cocktail of [antiretroviral drugs](#) to treat people infected with HIV, the virus that causes AIDS. Because HIV frequently mutates and can quickly become resistant to drugs, doctors need to know which medications are likely to be effective in slowing the progression of the disease. For that, they must take into account not only the strain of the virus the person is infected with but also the patient’s own medical history, [genetic information](#) and even sociological factors.

Unlocking the potential of personalised medicine

“It’s like a lock and key. Drugs are keys made to fit certain locks, which are part of the viruses. If the locks change then the key no longer fits - and each lock is different for each patient. That is why we need personalised medicine,” Sloot explains.

The ViroLab Virtual Laboratory uses a combination of technologies and methods to help doctors make decisions about the best medication to give each individual patient, accessed through a simple-to-use web

interface.

The system continuously crawls grid-connected databases of virological, immunological, clinical, genetic and experimental data, extracts information from scientific journal articles (such as the results of drug resistance experiments) and draws on other sources of information. This data is then processed to give it machine-readable semantic meaning and analysed to produce models of the likely effects of different drugs on a given patient. Each medication is ranked according to its predicted effectiveness in light of the patient's personal medical history.

Crucially, the system incorporates the concept of provenance, ensuring that every step a doctor takes in creating a workflow to find the right drug for a patient and every step the system takes to provide a recommendation is recorded. Because of the distributed nature of the virtual laboratory, cases can be compared to those of other patients living a few streets or thousands of kilometres away. And the system can even generate models simulating the likely spread and progression of different mutations of viruses based not only on medical data but also on sociological information.

“Say a government has 500 million euros to spend on HIV research and wants to know whether they should focus on funding the development of new drugs or on preventive measures such as encouraging people to change their sexual behaviour. We can give them an answer as to what would be more effective,” Sloot says.

The ViroLab coordinator says the project's focus on HIV was driven not only by the scale and importance of the epidemic but also by the wealth of information about it. “I make mathematical models and for models you need data,” Sloot notes.

The ViroLab Virtual Laboratory could be equally effectively used to

create personalised drug rankings to aid in the treatment of people suffering from other diseases. It is something Sloot and other members of the ViroLab consortium are exploring in DynaNets, a follow-on EU-funded project that will look at drug dynamics in groups people infected with the H1N1 flu virus and co-infections, in addition to drug-resistant HIV.

Sloot, who “went back to school” during the project to study virology and epidemiology, puts the success of ViroLab, which received funding from the EU’s Sixth Framework Programme, down to the multidisciplinary nature of the team involved. It has proven to be a productive collaboration that is set to continue.

“We are committed to continuing our work with whatever funding we can get. We are not at present interested in commercialising this technology,” Sloot says. “We want it to be open and free. The goal is not to make money from it but to contribute something to the world.”

More information: ViroLab project - www.virolab.org/

Provided by ICT Results

Citation: Free, open virtual laboratory for infectious diseases (2010, June 4) retrieved 23 April 2024 from <https://medicalxpress.com/news/2010-06-free-virtual-laboratory-infectious-diseases.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
--