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ONE STEP AHEAD

A UVic microbiologist and his team play a key role in the global battle against deadly viruses

DIANA NETHERCOTT

Upton with a computer cluster used to analyse virus genomes.

by Shannon McCallum

Hardly a day goes by that we don't hear of some scary disease in the world, whether it's smallpox, West Nile virus, SARS or bird flu. All have the potential to threaten public health on a global scale.

University of Victoria microbiologist Dr. Chris Upton is working to combat this threat by designing software and database systems to analyse a particularly dangerous class of viruses—those that cause emerging or re-emerging infectious diseases, or that could be used as bioterrorist weapons.

Upton is a virologist specializing in the burgeoning field of bioinformatics, the science of analysing biological data using advanced computer techniques. In collaboration with researchers at the University of Alabama at Birmingham, he and his team are creating a first-of-a-kind viral database for use by scientists around the world.

Technically, a virus is a parasite that is not alive. It can only reproduce by injecting its genetic material into the cell of a host, causing the host to reproduce virus proteins instead of its own.

To fight viruses, researchers can create vaccines that stimulate the immune system, or design antiviral drugs that fight the infection once it's underway. Both methods require an understanding of a virus's genome—the sum of all its genetic material.

"The genomes of many of these dangerous viruses have been completely sequenced, so for the most part we can predict the proteins with some degree of accuracy," says Upton. "The question is what do these proteins do? For many of the viruses we know the basics, but not the details."

The pace of drug design is slowed by this lack of detailed information. Furthermore, the information that is available is not always readily accessible to the average microbiologist.

"Right now, we frequently depend on computer experts to analyse the data," explains Upton. "The advantage of our system is that it will not only store the information in a central, web-based repository, but it will present it in a way that is intuitive and simple to use. In essence, we're creating a library and a catalogue system of viral information that hasn't existed before."

But Upton and colleagues are more than viral librarians. "We're adding further information about where genes are on a genome, possible functions, and the proteins that are likely to be produced," he says. "In this sense, we're not just putting the information into the library and saying to users 'Here it is, go find it yourself.' We're supplying the tools to help them get around the library."

Upton's group also does bioinformatics work with the herpes and smallpox viruses. They also study insect viruses, work that may have applications in the control of forest pests.

"The exciting thing about our work is that it supports a whole series of other research centres that are doing basic research on vaccine or drug design for these types of viruses."

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This article was written by graduate student Shannon McCallum as part of the UVic SPARK program (Students Promoting Awareness of Research Knowledge).

SPARK

EDGEwise

The Spanish flu pandemic of 1918 is considered to be the most deadly viral outbreak in history. An estimated 50 to 100 million people died over the course of several years.

Bacterial diseases are often easier to treat than viral infections. One reason for this is that viruses mutate faster than bacteria, so drug researchers have to continually design new drugs to combat them.

Although the genome of viruses are quite small—the smallpox virus, for example, has 200 genes compared to several thousand in bacteria and 30-50,000 in humans—the function of many viral genes is still poorly understood.

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