Upton with a computer cluster used to analyse virus genomes.

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).