

# Researchers create powerful new tool for research and drug development

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(Medical Xpress) -- A University of Saskatchewan research team led by Tony Kusalik and Scott Napper have harnessed bioinformatics and molecular biology to create powerful software that promises to become a “must have” tool in drug development research labs the world over.

The software is used to analyze kinases – a type of enzyme involved in virtually every cellular function, from energy use and reproduction to modifying gene expression. Licensing of the patented technology is currently underway, and a demonstration of its effectiveness recently appeared in the journal *Science Signalling*.

“This is a premiere example of what can be achieved through interdisciplinary and collaborative research,” says Kusalik, a professor in the computer science department.

Kinases are often involved in cellular functions that go awry, such as when pathogens such viruses or bacteria “hijack” a cell’s functions for their own purposes. Pathogens also have kinases of their own.

"Kinases have a central role in controlling cellular processes and are associated with many diseases. They're logical points for understanding biology and represent important treatment targets," says Napper, an associate professor of biochemistry with the U of S and senior scientist at the Vaccine and Infectious Disease Organization-International Vaccine Centre (VIDO-InterVac).

The standard lab tool in kinase research is the microarray, which allows researchers to analyze many different kinases within a sample simultaneously. A microarray looks like a standard microscope slide with rows of spots, each spot representing a different molecular test.

“With older methods, it was like having a little flashlight in a cave – you can see, but it doesn’t tell you all that is there,” Napper says. “These arrays give you the whole picture – but you end up with absolutely mountains of data.”

The problem for Napper and fellow VIDO-InterVac senior scientist Philip Griebel was that the mountains of data were making no sense. Griebel is also a faculty member with the U of S School of Public Health.

“They knew there were problems with the methodology they were following, because the results ‘weren't working out,’ but they didn't have sufficient expertise in bioinformatics to come up with an alternate method. That's where we came in,” Kusalik says.

Kusalik is an expert in bioinformatics, which is the application of computers and information technology to biology and medicine. One well-known application of bioinformatics is DNA sequencing, including the Human Genome Project.

For Kusalik, the problem wasn’t the volume of data, but how it was being handled. Standard software for analyzing DNA microarrays doesn’t work well with other microarrays. He explains that it’s like using a descrambler box from one cable company to try watch television from another company. You might get fuzzy glimpses of the picture, but it will be impossible to view the entire program with any clarity.

The solution was to build software tailor-made for [kinases](#).

“By developing a technique specifically designed for kinase microarrays we are able to get more data, and with more accuracy,” Kusalik says.

This claim is borne out in the research described in the *Science Signalling* paper, as well as by colleagues in the field. Napper says that other research groups have approached them to run their existing data sets through the new software.

“It’s very brave of them – it may prove some of their earlier conclusions wrong,” he says.

“We’re going to leave it up to other people to decide if they want to re-analyze their data. I bet there’s a lot more interesting biology that’s going to come out of their studies.”

**More information:** "A Systematic Approach for Analysis of Peptide Array Kinome Data" *Science Signalling*, 17 April 2012 Vol. 5, Issue 220, p. pl2

[stke.sciencemag.org/cgi/content/abstract/5/220/pl2](http://stke.sciencemag.org/cgi/content/abstract/5/220/pl2)

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