Computers aid in cracking deception in plants

June 25 2009

Dmitry Korkin is an assistant professor of bioinformatics at the University of Missouri-Columbia. Credit: Photo courtesy of Dr. Korkin

If the growing presence of computer 'geeks' on television crime shows is any indicator, computers are increasingly becoming essential tools for detecting and combating skullduggery. However, television detectives are not the only ones taking advantage of these tools. Researchers also are beginning to collaborate with computer scientists to help uncover biological forms of deception, known as molecular mimicry.

"Molecular mimicry is a biological mechanism that a pathogen, such as a bacterium, uses to trick a host organism into accepting it and, in some cases, to alter the host's function to its own benefit," said Dmitry Korkin, assistant professor in the University of Missouri Informatics Institute

and Department of Computer Science in the College of Engineering. "All this mimicry occurs among proteins."

Korkin recently received a five-year, $613,000 CAREER Award from the National Science Foundation to apply his computational research to the study of molecular mimicry in an important plant pathogen, the soybean cyst nematode.

The soybean cyst nematode is a small parasitic roundworm that infects the roots of a soybean plant. As part of its modus operandi, the nematode secretes proteins into the soybean that change the plant's cellular function and causes it to create a specialized cell from which the nematode feeds. Scientists think molecular mimicry may be involved in this host-pathogen interaction, but detecting it experimentally is difficult due to the sheer volume of proteins involved.

By applying concepts of machine learning and pattern recognition, Korkin will narrow the field of potential protein candidates by identifying protein binding sites in the soybean that match with those in the nematode.

"The problem is similar to trying to detect a face in a group of people," Korkin said. "To match the face, you need to know specific features about it: the color of the face, the color of the eyes, the shape of the nose, and so on. In our case, we're trying to find a specific protein binding site among a group of proteins from the nematode that match a particular binding site in the soybean using a set of chemical features."

Once potential binding sites are identified computationally, Korkin will work with Melissa Mitchum, assistant professor of plant sciences in MU's Interdisciplinary Plant Group (IPG), to verify them experimentally.

"We expect that information resulting from the research will help scientists improve soybean cultivars for disease resistance by accelerating the pace of discovery on resistance to this pathogen," said Korkin, who also is a member of the IPG and an investigator in the Christopher S. Bond Life Sciences Center.

He will be applying similar computational methods in studies of Shigella flexneri, a bacterium that can cause diarrhea in humans. For this research, he will be working closely with William Picking, professor at the University of Kansas.

Additional benefits of the project will be the interdisciplinary training of MU students, which may encourage them to consider careers in either the biological or computer sciences.

"This project provides a great environment to train students to think across disciplines," Korkin said. "Students from the life sciences will be working closely with students from computer science, and vice versa, to apply their individual expertise to solve a common research problem."

Source: University of Missouri-Columbia (news : web)