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Researchers develop innovative, freely available software to purify mass spectrometry data

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Researchers at University of Toronto and the Samuel Lunenfeld Research Institute of Mount Sinai Hospital, as well as colleagues in Michigan and Scotland, have developed an innovative computational approach -- the first of its kind worldwide -- designed to analyze mass spectrometry data. The software, called SAINT (Significance Analysis of INTeractome), will allow researchers globally to quickly assess the reliability and accuracy of protein binding data, helping to further their studies of cancer and other illnesses.

SAINT is described online in the leading international journal Nature Methods, published Nov. 5.

The tool was developed by Professor Anne-Claude Gingras of molecular genetics and principal investigator and Lea Reichmann Research Chair in Cancer Proteomics at the Samuel Lunenfeld Research Institute and Professor Alexey Nesvizhskii of the University of Michigan, Ann Arbor, to meet a key challenge in the field of protein mass spectrometry (a technology that helps researchers separate, identify and quantify specific proteins): namely, to identify and quantify “true” protein interactions gleaned from mass spectrometry data and filter them from protein-based contaminants in the sample data. Previously, other approaches to analyze mass spectrometry data have not allowed for a probability-based model to measure and account for errors in a data set.

“SAINT allows researchers to identify the real protein interactions in their sample and to exclude the false positives generated through contaminants,” said Gingras. “In effect, the software applies a much needed filter to purify the data and remove ‘noise.’”

SAINT was introduced earlier this year by Gingras, Nesvizhskii and Professor Mike Tyers of molecular genetics when their teams generated a comprehensive road map of the signalling proteins that control many aspects of cellular behaviour in yeast cells (www.yeastkinome.org) — a discovery reported in a May issue of *Science*. However, the updated approach can be applied to a wider variety of datasets of various sizes and levels of protein network density.

“The first version of SAINT was intended to help us analyze very large scale datasets, which is something that only a few laboratories worldwide are generating,” said Nesvizhskii. “We then realized that, with some modifications, the same approach could be extended to researchers specifically interested in knowing what a few proteins interact with inside the cell. This makes our approach very useful to most cancer biologists using mass spectrometry, as it enables them to quantify their interaction data.”

Gingras and Nesvizhskii are former research associates and have collaborated on various research projects over the past eight years and bring together their expertise in biology and computational modelling, respectively.

“We come from completely different directions but have focused on this problem together,” said Gingras.

Gingras has encouraged many other scientists to use SAINT and the software is being implemented at research institutes internationally. Gingras and Nesvizhskii, with study first author Hyungwon Choi (a post-

doctoral research fellow in the Nesvizhskii lab), recently held a workshop at the Lunenfeld Research Institute at which almost 100 Toronto-based scientists and industry representatives learned of the advantages offered by SAINT.

“SAINT is a new and important software tool that — for the first time — allows us to assign a confidence value to every protein-protein interaction that we identify in our mass spectrometry studies,” said Professor Brian Raught of medical biophysics, Canada Research Chair in Proteomics and Molecular Medicine and a scientist at the Ontario Cancer Institute. Raught attended Gingras’ workshop and uses the tool in his research.

“It has been truly instrumental in our work on deciphering the protein-protein interactions within complex intracellular regulatory networks, and thus represents a major advance in our field.”

More information: The software is available for downloading at sourceforge.net/projects/saint-apms .

Provided by University of Toronto

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