Carnegie Mellon engineering researchers automate analysis of protein patterns

May 12 2008

Carnegie Mellon University's Justin Y. Newberg and Robert F. Murphy have developed a software toolbox that is intended to help bioscience researchers characterize protein patterns in human tissues.

Newberg, a Ph.D. student in biomedical engineering, described the automated protein pattern recognition tool and its underlying methods as important for identifying biomarkers that could be useful for cancer diagnosis and therapy.

"Distribution of proteins in a cell or group of cells can be used to identify the state of surrounding tissue, whether it is healthy or diseased," said Newberg, the newsletter editor for Carnegie Mellon's Graduate Biomedical Engineering Society. "So, our tools can be used to develop novel approaches to screen tissue, which could have an immense benefit in such things as cancer diagnosis."

Newberg, a member of Murphy's research group, added that researchers are increasingly collecting large numbers of images due to the availability of automated microscopes. These images provide an excellent opportunity for improving the understanding of biological processes, but also create a need for automated bioimage analysis tools. Development of such tools has been a major focus of Carnegie Mellon's Center for Bioimage Informatics for many years.

Newberg said the Human Protein Atlas is an excellent example of a large scale dataset ripe for automated analysis. The atlas consists of more than

3,000 proteins imaged in 45 normal and 20 cancerous human tissues.

In a research article in the Journal of Proteome Research, Newberg and Murphy, the Ray and Stephanie Lane Professor of Computational Biology and a professor in the departments of Biological Sciences, Biomedical Engineering and Machine Learning at Carnegie Mellon, described how they applied their tools to analyze images of eight major subcellular location patterns with a high degree of accuracy. They pointed to their work as a strong indication that automated analysis of the whole atlas is feasible, and they plan to continue to study and characterize all of the proteins in the atlas.

“Knowing the exact location of thousands of proteins in human cells will enable a much better understanding of how these cells work and could ultimately advance the detection and diagnosis of serious diseases,” Murphy said.

Source: Carnegie Mellon University