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Using Mathematical Algorithms To Save Lives

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Advances in molecular biology, proteomics and genetic testing have brought us closer to personalized health care that can tailor treatments to an individual patient's needs. Data gathering capabilities have greatly surpassed data analysis techniques, creating a need for more effective methods to analyze a vast and growing amount of data.

Bioinformatics, the use of computer science methods and tools in the life sciences, has exploded as modern high-throughput methods have generated a deluge of information, including sequence data, structural data, chemistry data, assay results and imaging data. While pharmaceutical and biotechnology companies have begun to appreciate the potential benefit of information technology systems in improving the productivity of drug discovery and research, several hurdles must be overcome to fully capitalize on the impact this data may have on the health care industry.

With the help of more than $3 million in competitive grants from the National Institutes of Health (NIH) and the National Science Foundation, Sorin Draghici, Ph.D. is working to develop new and effective approaches to analyze these data and identify impacted gene signaling pathways in a given condition. Draghici holds joint appointments as professor in the Department of Computer Science, College of Engineering; and the departments of Clinical and Translational Science, and Obstetrics and Gynecology in the School of Medicine at Wayne State University. In recent years, Draghici has developed several bioinformatics software tools that utilize mathematical algorithms to extract relevant intelligence from genomics data by combining statistical analysis with existing knowledge about how these pathways work. Correctly identifying the significantly impacted gene signaling pathways in a given condition can lead to better decision-making capabilities for drug development and personalized health.

According to Draghici, current methods that aim to bridge the gap between data collection and data analysis are unsophisticated. "Many if not all existing methods treat the pathways as simple sets of genes, and either ignore or underutilize our current understanding about how the body's systems work, as well as the gene expression values made available by current technologies," he said. Draghici has developed bioinformatics tools that will lead to reliable approaches to identify the most impacted gene signaling pathway in a given condition, which ultimately will facilitate pinpointing the molecular causes of a given disease, and identifying potential therapies and possible side effects.

Using a systems biology approach, Draghici's approach identifies pathways that are significantly impacted in any condition, which may be monitored through high-throughput gene expression. His more sophisticated algorithms can also identify relevant signaling cascades that can be potentially targeted for therapeutic intervention.

Access to these tools by biotechnology and pharmaceutical companies will increase efficiency in the drug discovery pipeline and, most importantly, reduce development costs of new therapeutics. Such tools can help organizations make early decisions on pursuing clinical trials.

The technology has been licensed to Advaita Corporation, where Draghici serves as chief executive officer and chief technology officer. Advaita has received additional funding from the NIH in the form of a Small Business Technology Transfer grant.

Draghici's novel analysis method can identify the significantly impacted gene regulatory pathways in a given condition, such as lung cancer, obesity and diabetes. Classical methods fall short and neglect to take into consideration the roles the genes play in each pathway. These classical methods can produce both false positives, pathways that are reported as being relevant when in reality they are not, as well as false negatives, relevant pathways that are not identified as being significant in the given condition.

Current analysis methods rely too heavily on the number of differentially regulated genes that fall on each pathway, rather than taking into consideration where each gene is positioned and what each gene does. Draghici's method pays close attention to these aspects and can potentially identify regulatory pathways that can open the way to new therapeutic interventions in a large variety of conditions such as cancer, pre-term labor, obesity and more, ultimately benefiting millions of people suffering from these conditions.

"Currently, most patients with health conditions such as cancer are diagnosed because of a clinical

change, such as detecting a malignant tumor," said Draghici. "By the time the tumor is found, treatment can be an uphill battle because of complex changes including the need to kill tumor cells that might have already spread. If a physician could identify a departure from the healthy state well before the tumor is present, these changes in cells may possibly be reversed. We aim to identify qualitative changes in the state of a biological system, with the ultimate goal of eradicating diseases not by finding a cure for them, but by preventing them from ever occurring in the first place."

About Dr. Sorin Draghici:

Dr. Draghici received a B.Sc. in computer engineering and an M.Sc. in computer science – software engineering from Politehnica University of Bucharest, Romania, and a Ph.D. in computer science – artificial intelligence from University of St. Andrews, United Kingdom. He joined Wayne State University in 1996. He was recently appointed the first Robert J. Sokol, M.D. Endowed Chair in Systems Biology.

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