# Free online software helps speed up genetic discoveries

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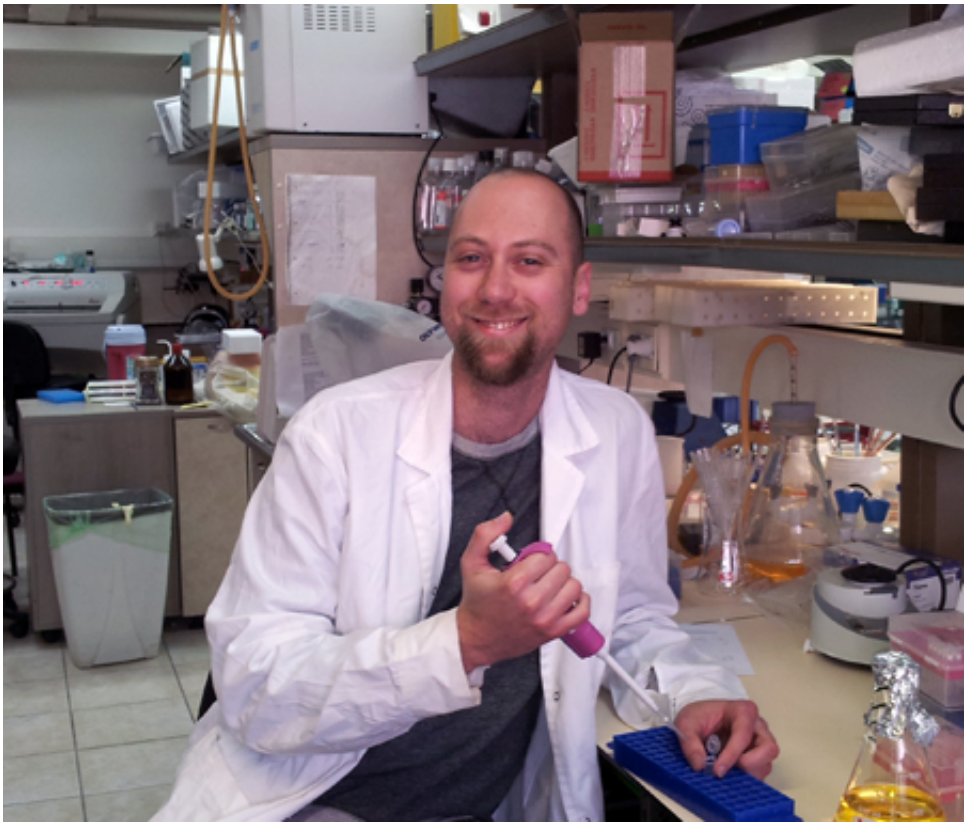

Sagi Abelson.

DNA microarray analysis, a high-speed method by which the expression of thousands of genes can be analyzed simultaneously, was invented in the late 1980s and developed in the 1990s. Genetic researchers used a glass slide with tiny dots of copies of DNA to test match genes they were

trying to identify. Because the array of dots was so small, it was called a "microarray." There is a strong correlation between the field of molecular biology and medical research, and microarray technology is used routinely in the area of cancer research and other epidemiology studies. Many research groups apply it to detect genetic variations between biological samples and information about aberrant gene expression levels can be used in what is called "personalized medicine." This includes customized approaches to medical care, including finding new drugs for gene targets where diseases have genetic causes and potential cures are based on an individual's aberrant gene's signal.

An article written by Abelson published in the current issue of *BMC Bioinformatics* (2014,15:53) describes the new software tool and provides examples of its uses.

"Eureka-DMA combines simplicity of operation and ease of data management with the rapid execution of multiple task analyses," says Abelson. "This ability can help researchers who have less experience in bioinformatics to transform the high throughput data they generate into meaningful and understandable information."

Eureka-DMA has a distinct advantage over other software programs that only work "behind the scenes" and provide only a final output. It provides users with an understanding of how their actions influence the outcome throughout all the data elucidation steps, keeping them connected to the data, and enabling them to reach optimal conclusions.

"It is very gratifying to see the insightful initiative of Sagi Abelson, a leading 'out-of-the-box' thoughtful Technion doctorate student whom I have had the privilege of supervising," said Prof. Karl Skorecki, the Director of the Rappaport Family Institute for Research in the Medical Sciences at the Technion Faculty of Medicine and Director of Medical and Research Development at the Rambam Health Care Campus. "Over

and above his outstanding PhD thesis research project on cancer stem cells, Sagi has developed – on his own – a user-friendly computer-based graphical interface for health and biological research studies. Eureka-DMA enables users to easily interpret massive DNA expression data outputs, empowering researchers (and in the future, clinicians) to generate new testable hypotheses with great intuitive ease, and to examine complex genetic expression signatures of genes that provide information relevant to health and disease conditions. This was enabled by combining outstanding insight and expertise in biological and computer sciences, demonstrating the unique multidisciplinary strengths and intellectual freedom that fosters creative innovation at the Technion."

According to Abelson, Eureka-DMA was programmed in MATLAB, a high-level language and interactive environment for numerical computation, visualization, and programming. Advanced users of MATLAB can analyze data, develop algorithms, and create models and applications to explore multiple hypotheses and reach solutions faster than with spreadsheets or traditional software. Eureka-DMA uses many of MATLAB's toolbox features to provide ways to search for enriched pathways and genetic terms and then combines them with other relevant features.

Raw data input is through Windows Excel or text files. This, says Abelson, spares the user from dealing with multiple and less common microarray files received by different manufacturers. Results can then be exported into a 'txt' file format,' or Windows Excel, making Eureka-DMA a unified and flexible platform for microarray data analysis, interpretation and visualization. It can also be used as a fast validation tool for results obtained by different methods.

Eureka-DMA loads and exports genetic data, "normalizes" raw data, filters non-relevant data, and enables pathway enrichment analysis for

mapping genes on cellular pathways. The user can browse through the enriched pathways and create an illustration of the pathway with the differentially expressed genes highlighted.

After identifying the differentially expressed genes, biological meaning is ascribed via the software so that the identification of significant co-clustered genes with similar properties - cellular components, a biological process, or a molecular function - can be achieved.

**More information:** The full paper is available online: www.biomedcentral.com/content/ … /1471-2105-15-53.pdf

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