

Genevestigator—Commentary

Zimmermann P, Hirsch-Hoffmann M, Hennig L, Gruissem W (2004) GENEVESTIGATOR. Arabidopsis microarray database and analysis toolbox. *Plant Physiol* **136**: 2621–2632

Science has changed dramatically over the last decades. Numerous genomes have been sequenced, giving us the “blueprint” to many organisms. Deciphering the function of those genes and determining their physiological relevance continues to be a major challenge. The continued improvement and development of gene expression analysis tools as well as the establishment of standards and databases for experimental data are instrumental in this. Much of the data generated from gene expression experiments have been deposited in publicly accessible databases, resulting in a wealth of available data that can now be combined with other experiments, increasing the surety of the results. This is a boon to researchers; large candidate gene lists can be narrowed before validating function, hypotheses can be tested, and “virtual” experiments can be performed before committing time and resources to bench work. Although many array analysis tools are available for analyzing publicly available databases, one that stands out is Genevestigator.

Genevestigator is the result of a multidisciplinary project from Wilhelm Gruissem’s lab at ETH Zurich and was originally developed by a team including Peter Zimmermann, Matthias Hirsch-Hoffmann, and Lars Hennig, as described in the above-mentioned article. Genevestigator is a suite of Web-based analysis tools that allow researchers to “rapidly find out in which tissues, at which stages of development, and to what

stimuli, drug treatments, diseases, or genetic modifications genes of given organisms are activated.” Although initially centered on Arabidopsis, Genevestigator has been rereleased and now provides gene expression metaprofiles for not only plants (Arabidopsis, soybean, rice, barley) but also animals (mice, rats, humans) and microorganisms (yeast and *Escherichia coli*; Hruz et al., 2008). It is also now JAVA based, so there is no software to download (unless you do not have JAVA runtime environment, a free download), it is platform independent, and it allows for faster data management than HTML or Javascript.

Public databases contain a wealth of information, but not all data are equal. Data from microarrays can be of low technical quality either due to the microarray itself or to sample quality. Low-quality data can give false associations and can also lead to problems with reproducibility. Data and pathways included in Genevestigator are manually curated and quality controlled before inclusion into the database, ensuring high-quality data. As more gene expression data become available and statistical methods for comparing data originating from different technologies, the accuracy of “virtual laboratories” will continue to improve, enabling further advancement of functional genomics.

LITERATURE CITED

Hruz T, Laule O, Szabo G, Wessendorp F, Bleuler S, Oertle L, Widmayer P, Gruissem W, Zimmermann P (2008) Genevestigator V3: a reference expression database for the meta-analysis of transcriptomes. *Adv Bioinformatics* **2008**: 420747

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