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## **Qlucore and Nebion collaboration will benefit researchers**

***The start of 2014 will see [Qlucore](#) and [Nebion](#) AG working together to promote their two products [Qlucore Omics Explorer](#) and [Genevestigator](#). These two platforms together offer an excellent combination by addressing complementary use cases.***

Qlucore Omics Explorer is a next-generation bioinformatics software program which is extremely fast and allows the user to explore and analyse high-dimensional data sets interactively and in real time. Qlucore Omics Explorer has proved to be hugely beneficial to researchers in the life science and biotech industries when it comes to analysing big data.

Nebion creates innovative systems to extract high value information from the world's genomic data for biotechnology and personalized medicine. Its Genevestigator is a high-performance Web platform which deeply integrates expression data and curated sample annotations. This allows systematic screening of the database for genes that have unique expression properties and validation of target and biomarker genes by checking how they respond to thousands of experimental conditions.

“Nebion complements the Qlucore product offering perfectly by enabling a web based systematic screening of genes across many thousand experiments, so it makes perfect sense to work together to provide a broader solution to our clients. We’re excited to be jointly promoting our complementary solutions to help researchers get better results, quickly,” says Carl-Johan Ivarsson, CEO Qlucore.

Speaking on the new relationship between the two companies, Dr Philip Zimmermann, CEO Nebion commented, “I got to know Qlucore Omics Explorer a few years ago and I have become convinced that it's one of the best tools to find patterns in data and for biomarker discovery. It is very user-friendly but at the same time statistically robust.”

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### **About Qlucore**

[Qlucore](#) was founded in 2007 as a collaborative research project at Sweden's Lund University. The firm was supported by researchers from the Departments of Mathematics and Clinical Genetics to address the vast amount of high-dimensional data generated with microarray gene expression analysis. It was recognized that an interactive software tool based on visualization was needed to conceptualize the ideas evolving from research collaboration.

The basic concept behind the software is to provide a tool that can take full advantage of the most powerful pattern recognition system that exists - the human brain. The result is an extremely fast core software engine which enables the user to handle and filter high dimensional data (big data) and instantly visualize it in 3D. This assists the user in identifying hidden structures and patterns.

The latest version of the software, [Qlucore Omics Explorer](#), is used by scientists in more than 20 countries and is a key tool among other biologists and medical doctors to creatively analyze their experiment data. The Company's customers are mainly from the Life-science and Biotech areas.

One of the key methods used by Qlucore Omics Explorer to visualize data is dynamic principal component analysis (PCA), an innovative way of combining PCA analysis with immediate user interaction. PCA analysis works by projecting high dimensional data down to lower dimensions. The specific projections of the high-dimensional data are chosen in order to maintain as much variance as possible in the projected data set. With Qlucore Omics Explorer, data is projected and plotted on the two dimensional computer screen and then rotated manually or automatically.

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**About Genevestigator**

[Genevestigator](#) started in 2003 as an academic project at the Swiss Federal Institute of Technology Zurich (ETH). The initial objective was to create fully standardized datasets of microarray gene expression combining all published studies from selected fields of research. These datasets were originally used as references in systems biology research projects.

While the datasets were originally accessible only to bioinformaticians and statisticians, it immediately became clear that biologists and biomedical researchers could greatly benefit from tools that allow a fast, intuitive and global exploration of these public datasets. As a result, Genevestigator was created as a user-friendly online platform to explore public datasets of gene expression.

As the first set of tools became widely popular and the content expanded into further organisms, novel innovative tools were needed to address the needs of each user community. Such tools could be built only provided the experiments included into Genevestigator were consistently annotated and at a very deep level of detail. The platform was therefore expanded to make use of controlled vocabularies

encapsulating detailed experimental and sample descriptions, including clinical and patient characteristics. In parallel, the increasing volume of data required search engine technology to analyze, on-the-fly, tens of thousands of microarrays simultaneously.

Since 2008, Genevestigator is developed and commercialized by Nebion. While its content is manually curated and verified by PhD level experts, its search engine represents the only platform worldwide for on-the-fly analysis and exploration of up to 100,000 full genome microarray/RNAseq samples. It offers an unprecedented flexibility and cutting-edge tools to explore and combine expression information from the global research community. In particular, it aggregates expression data in a unique way to provide summaries of expression across tissues, cell cultures, cell lines, cancers, diseases, drugs, chemicals, hormones, or genotypes. Furthermore, its search capabilities allow identifying genes expressed uniquely in a chosen condition or disease, as compared to thousands of other conditions. Finally, Genevestigator offers a unique way to compare one's own results with those of thousands of public experiments.

The main application areas are gene target prioritization, interpretation of gene lists, target/biomarker discovery, network discovery, drug repurposing, and identification of optimal genes for qPCR normalization.

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