Reveal human-growth patterns in transcriptomic data

OVERVIEW

Dr. Adam Stevens, a human development systems biologist working in Professor Peter Clayton's group at the UK's University of Manchester.

The research aims to bring more understanding to the growth process. Humans are the only animals that return to rapid growth in puberty. Other animals – even other mammals that have a long juvenile phase – grow rapidly after birth and then their growth rate slows down until eventually tailing off as they reach their adult size. Understanding how children grow is key to understanding many childhood diseases and conditions, particularly those affecting growth. A child is very different at two than at four or 10 but medically they are often treated the same.

In addition to industrially-funded and commercially-sensitive research into drug responses, Dr. Stevens and colleagues have published a number of papers on the pharmacogenomics of growth hormones.

"Qlucore forms a key role in our research," Dr. Adam Stevens

TECHNICAL SITUATION

Dr. Stevens is doing both bench studies and in silico studies on a range of omics datasets derived primarily from blood samples throughout human childhood. The datasets include transcriptomic data – which measures RNA and microarray RNA sequencing, looks at the integration of genetic data and other omics data (such as proteomics and phosphor proteomic data).

These datasets are used to study both normal childhood growth and growth with various impairments. For example, at short stature, where there is a growth hormone deficiency, and chromosomal syndromes, for example Turner syndrome, where girls are often treated with growth hormones.

Dr. Stevens has experienced that a fundamental problem is that if you're running a project and realize you need statistics expertise you find statisticians but they don't always understand the biology.

SOLUTION

The group started to use Qlucore Omics Explorer to analyze their data. One of the key drivers for this decision was the visually-driven interface which allowed biologists to do parts of the analysis by themselves. Dr. Stevens concluded that Qlucore, already from a standing start, is very intuitive and visual but there's an advanced component with powerful statistics too. However, you don't need to be advanced in mathematics or statistics but it's a very powerful tool. The fact that the user interface is both accessible to new users and a gateway to powerful capabilities makes it easy to deploy the program in the organization. Dr. Stevens works with data sets of sizes of around 400 microarrays, each with 55,000 data points and uses the program for various types of analysis. The approach varies with the question they are asking. "If we come in with a hypothesis, it's simple to use and includes the necessary functionality but the real power of Qlucore is in assessing structure when we are coming in with hypothesis-free data."

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"The power of Qlucore is in assessing structure with hypothesis-free data," Dr. Adam Stevens

TABM666, 4579 probe-sets, Horizontal axis = age in years of sample

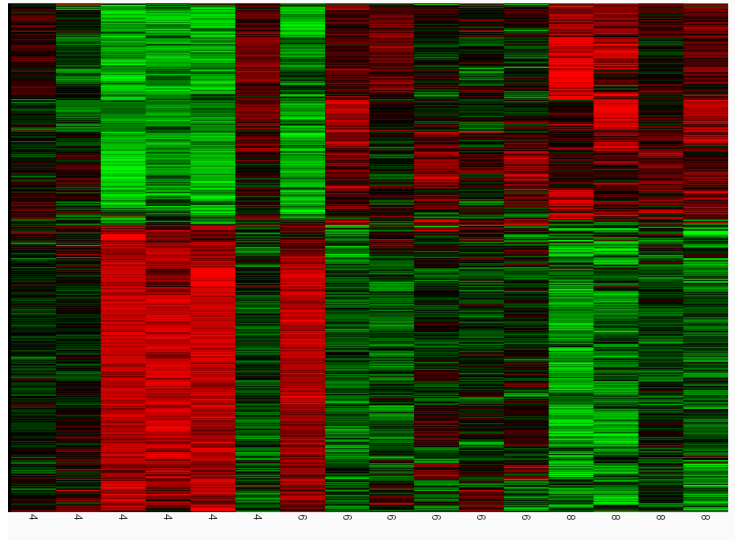For More information Contact Qlucore at www.qlucore .com.

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BENEFITS
The versatile data import and the ease of use are important benefits. The program is designed to deal with big data and nothing we have used slowed the program down.

Since the visualization drives the analysis it makes the software also accessible to non-statisticians.

The benefits, of the visualization, are in helping the researchers to explore, interpret and explain to others their research findings.

Another aspect of the visual approach is that it makes it easier to explain the study and the methodology used in the study to reviewers, who are not experts in statistics and mathematics.

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