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Press Release

CANCER RESEARCH GIVEN BOOST BY NEW SOFTWARE

BlueGnome demonstrates BlueFuse for Batch Analysis with arrayCGH

BlueGnome, the specialist bioinformatics company, is to demonstrate the new version of its microarray analysis software, BlueFuse for Microarrays, on stand 826, American Society Human Genetics, Toronto, 26-30th October 2004.

New features include the capacity to automatically analyse 20 or more slides at a time, enabling a series of experiments to be analysed overnight and a summary showing all the results to be displayed graphically on the screen. This batch functionality is particularly well suited to Comparative Genomic Hybridisation (CGH), an exciting new technique which is rapidly becoming prominent in the microarray community.

Rather than measuring the levels of gene expression, CGH aims to understand which genetic sequences are present or absent in the underlying genomic DNA. For example, many cancers are believed to occur from mutations either inherited or environmental. CGH provides a means of comparing DNA from healthy cells to those in a cancerous cell. This provides a useful tool in determining the physiology of the cancer and also a potential tool for early diagnosis.

The DNA to be analysed together with the normal reference sample are differentially labelled with a stain, typically fluorescein 'green' and Texas Red. Digital image analysis is used to compare the ratio of red:green banding down the chromosome in order to determine the relative presence/absence of genetic sequences. Currently many users have to set a threshold to distinguish between valid biological signal and extraneous noise present on the microarray, disregarding results below this.

In arrayCGH the setting of this threshold has a huge affect on the results: set too high and genomic sequences will be called absent even though they were present; too low and poor quality results will be included. BlueGnome's BlueFuse technology addresses this fundamental problem by using a statistical framework which eliminates rigid thresholds from the analysis.

BlueFuse uses knowledge of how signal and noise are generated in the microarray process to tell the difference between the two and provide a useful measure of confidence in the result. This enables very low level signals to be consistently detected and high level signals to be more accurately measured. In customer trials this has enabled researchers to extract up to 10 per cent more data from their trials.

Dr Nick Haan, CEO of BlueGnome, is delighted that this breakthrough is attracting great interest from customers: "Research labs that would normally take a month to analyse 120 slides, are reporting that the same trial analysed with BlueFuse with batch processing took only a couple of days and revealed significantly more data.

"The analysis is highly visual, interesting results can be interrogated on screen by a simple 'point and click' technique, and all slides in a trial can be viewed simultaneously. This tool allows more information to be extracted from the data and is creating great excitement in the industry. Progress in CGH is rapid and we are working with leading practitioners in this field to extend further the scope of the statistical analysis."

26th October 2005