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## Press Release

### BLUEFUSE TO IMPROVE OBJECTIVITY AND THROUGHPUT AT WORLD LEADING PATHOLOGY DEPARTMENT

#### First orders for BlueFuse follow extensive beta testing

Cambridge University's world leading Pathology Department is amongst a growing group to install groundbreaking statistical software that will speed up genetics research and give more accurate results.

BlueFuse for Microarrays, the first product from Cambridge based specialist bioinformatics company BlueGnome, is used in microarray experiments. DNA microarrays enable the activity of all 30,000 of the body's genes to be measured in a single experiment. Britain's largest pathology unit estimates the software will make the initial stages of their microarray analysis up to 6 times faster.

Dr. Nabeel A Affara, Group Leader Human Molecular Genetics Group, University of Cambridge, Department of Pathology, believes BlueFuse will improve the accuracy of the results and reduce the tedium of much of the analysis for his team.

He explained: "One DNA microarray contains around 17,000 spot shaped features. Currently researchers have to manually examine each spot to make a judgement on the quality of each feature. A researcher could spend two hours fitting a grid on a single microarray slide and ruling out bad features. BlueFuse takes just 20 minutes to do it automatically, with greater accuracy and consistency."

BlueFuse is unique as it not only automates this visual inspection but also assigns confidence values to results for each feature. This enables more informed conclusions to be made on the basis of all the data.

He said: "BlueFuse cuts down on the degree of manual intervention required to get reliable data which is time consuming and therefore a real bottleneck. Also, unlike other software we have trialled, which looks primarily at the shape of the spot, BlueFuse can distinguish signal from background very effectively. This means that data that would previously have been discarded due to contamination, will now be considered and BlueFuse will effectively extract useful information from all the features on a microarray."

Dr Affara said that researchers are now planning to re-examine large data sets using BlueFuse in the hope it will uncover promising information in data that had previously been discarded. He believes BlueFuse will give researchers a morale boost by allowing them to draw more reliable conclusions more quickly.

He explained: "The evaluations we have carried out with the beta versions of BlueFuse show a major improvement upon the techniques we have used previously. We are getting more data which means BlueFuse is doing a better job of quantifying the lower expressing genes. This is where new biological findings will come from, and so is particularly exciting for our researchers."

Dr Nick Haan, CEO of BlueGnome, believes BlueFuse has far reaching implications for research laboratories and commercial biotech organisations across the world. He said: "BlueFuse increases the throughput of first stage experiments, slashing research time and costs. This could help bring important drugs to market sooner."

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BlueFuse employs Bayesian statistical models of the microarray process. This moves analysis from a black and white world of 'accept' or 'reject' to a situation where the many shades of experimental variability are clearly visible and can be exploited to make better research and drug discovery decisions.

The benefits of BlueFuse have been recognised by both commercial and academic laboratories. Sygen International plc, leader in the application of quantitative genetics to animal breeding, has also licensed BlueFuse for Microarrays. Dr Gary Evans, research manager at their Cambridge laboratory, confirmed. "BlueFuse has delivered automated analysis of our microarray experiments, from spot finding through to the provision of meaningful confidence estimates in the results. This gives us more biological information of higher quality, from our existing process, at a much lower cost."

**21st April 2004**