

Rare event analysis: A Case Study with the University of Pittsburgh

The Organisation

Basic Research for the Heart, Lung and Esophageal Surgery Institute at the University of Pittsburgh
Flow Cytometry Facility at the University of Pittsburgh Cancer Institute.

The Challenge

Rare event analysis has been an important requirement of flow cytometry users for some time. Researchers such as Albert and Vera Donnenberg of the University of Pittsburgh Cancer Institute have been at the fore-front of these applications. The latest flow cytometry instruments allow a higher number of parameters to be collected on large numbers of cells, although the native software struggles to analyse the data. Dr. Vera Donnenberg, Director of Basic Research for the Heart, Lung and Esophageal Surgery Institute at the University of Pittsburgh, says, "With our current system, just opening a file takes so long that I can get up, go get a cup of coffee - which is not close by! - come back, and the computer screen is still being refreshed."

At the Donnenberg laboratories, large or complex projects might require researchers to look at tens of markers on hundreds of patients with tens of thousands or even millions of cells on each sample. As a result, the files that are created are very large. These files are growing to hundreds of megabytes in size as researchers work with more data. "Although the software as it exists now can technically do everything that we want it to do, it is so difficult to use because of the speed issue," adds Dr. Albert Donnenberg, Director of the Flow Cytometry Facility at the University of Pittsburgh Cancer Institute. "If we didn't have the bottleneck of speed, we could perhaps be analysing these files in minutes. Instead, it literally takes us hours."

Dr. Albert Donnenberg says, "We've been working heavily in the area of cancer stem cells, dealing with about 6 million to 10 million cells with about 11 different parameters. We worked on the data every morning for 10 days using our fastest workstation, and only analysed 30 files."

A typical example of the problems facing the Donnenberg's is one of their cancer stem cell investigations; this required the analysis 6 samples each of which contained 11 parameters with 250,000 to 5 million events being collected.

This required around 50 hours of analysis time. Causing an analysis backlog due to them being able to spend less time in the lab, forcing them to look at the data in a limited way and experienced "countless crashes and much marital strife"

The Solution

Dr's Albert and Vera Donnenberg have advised Applied Cytometry in the development of VenturiOne™ software, since first seeing an early version of the software they have been impressed "Applied Cytometry ran a demo of its VenturiOne™ software for us, using a file that we provided, and it ran more than 10 times faster. It was amazing".

VenturiOne™ software includes new techniques (U.S. patent pending) to increase the speed and efficiency of the software. This allows efficient use of the latest multi-core processors. Available for 32bit or 64bit Windows platforms (Windows XP or Windows Vista) VenturiOne™ software is scalable so will make use of all available processors within your PC. The design of workflow within VenturiOne™ means that you do not need a high specification PC, users will benefit from VenturiOne™ software on any Windows XP or Windows Vista capable PC.

VenturiOne™ has an innovative preview display of all parameters that allows extensive exploration of your generated data files. Point and click gating and powerful colour eventing allow users to explore possibilities on even the largest data files.

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