

OVERVIEW

Steven Kornblau, a Professor of Medicine in the Department of Leukemia & Department of Stem Cell Transplantation and Cellular Therapy at UT MD Anderson Cancer Center in Houston, Texas, US, uses proteomics – the large-scale study of proteins – in the fight against leukemia. The approach that he and his colleagues take is to look simultaneously at hundreds of proteins to define patterns of protein activation in acute myeloid leukemia (AML) and identify proteins whose function are key to the survival of leukemic cells.

“QluCore allows me to do analysis on my own. There are things that I know are biologically relevant that I can check on the fly.”

Using QluCore Omics Explorer for interpreting leukemia proteomics data

TECHNICAL SITUATION

There are many things that can be limiting factors in the research process. In the case of medical, professor Steven Kornblau, the time pressures of the biological infomaticians he works with have been significant limitations. His laboratory developed the techniques required to use a reverse phase protein array (RPPA), which measures the relative expression levels of a protein in many samples simultaneously, for the study of leukemia and he is recognized as the leader in this field. Another key feature of his work is the vast repository of leukemia patient samples that he has collected and can use for studies. Gaining insight from these many experiments is a complex task. The repository includes samples from over 2000 AML patients and the RPPA that Kornblau’s team has built uses samples from 511 AML cases. This approach enables many studies to go on simultaneously, speeding up research and enabling patterns to be uncovered. However, the volumes of data are huge, particularly considering that there are around 80 different fields of clinical information for each patient, which all need to be treated differently depending whether they are simple details like the patient’s name or more complicated features such as the patient’s response to a particular drug or combination chemotherapy regimen.

The volumes and complexities of the data prevent patterns being spotted without in-depth statistical analysis that is outside the normal range of expertise of biologists. As a result, data is taken to statistician colleagues for analysis, a process that can take time as these colleagues’ expertise is very much in demand.

SOLUTION

All this changed in June 2013 when Kornblau purchased QluCore Omics Explorer. ‘QluCore allows me to do analysis on my own,’ he said. ‘I can now check things that I know are biologically relevant on the fly.’ This, he said, has ‘speeded up the process and facilitated discovery. It has definitely been a big enabler.’

Steve Kornblau Case study
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"I was always having to rely on statisticians. They did a great job but it involved a lot of going back and forth,"

"The more I use the software the more I keep discovering new things."

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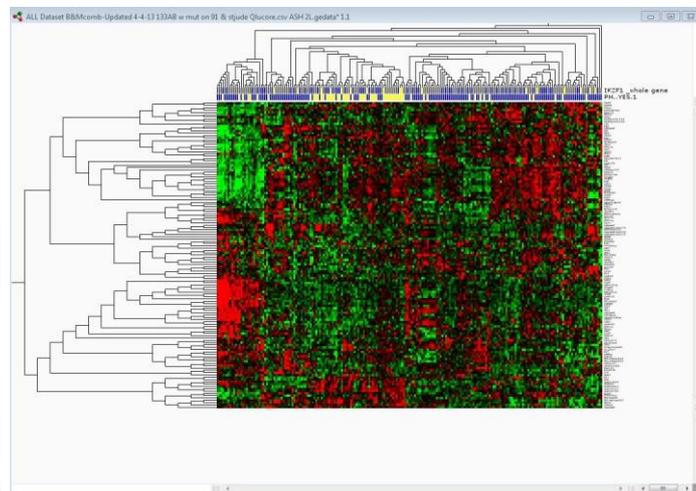
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The software allows Kornblau to explore his data statistically and, for example, change outlier parameters. It also enables him to generate heatmaps that quickly show relevant patterns. "We can look at proteins, see why some are particularly important compared with other functionally-related proteins and look for correlations between protein clusters from one functional group. We can see how proteins are interacting with antibodies and can classify them into groups. Formerly my statistician would do all this," he observed.

BENEFITS

The change has been dramatic. "I've been working with protein arrays for seven years and always had to get bioinformaticians to do the analysis. They are very much in demand so they are a rate-limiting step."



In fact, he said that it usually took a couple of months to get results. "Now it is pretty easy to put my data in and I can get results within an hour – and I play with my dataset more now that I can do it myself."

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