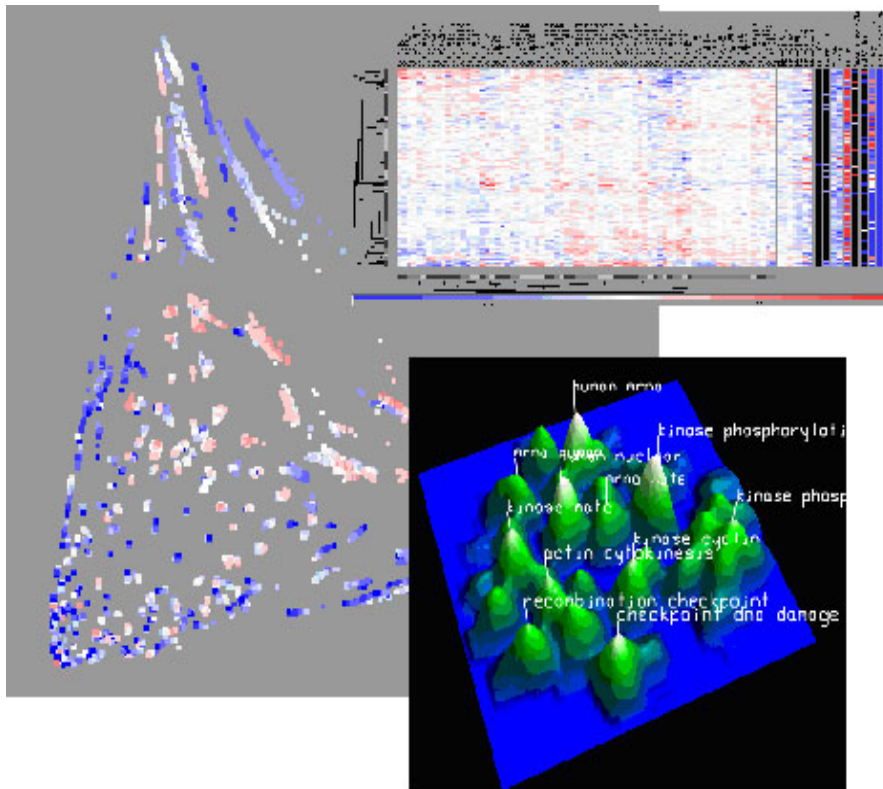


OmniViz[®] for Proteomics

Proteomic approaches have become standard in the efforts to understand potential targets and cell processes. As a logical extension to genomic level analyses, proteomics is providing a great deal of insight. However, like genomics applications, the industrial scale of data generation is leading to massive amounts of information. Not only is that information difficult to extract value from, but the best decisions require that such data be interpreted in the context of other data (such as genomics results) as well as the context provided by historical data in the form of literature and patents.

OmniViz provides the only solution that solves the problem of dealing with large volumes of data in an effective manner as well as analyzing ALL the relevant data, whether numeric data, text documents, clinical data, and more.



The OmniViz software uses intuitive, informative high-level visualizations to organize and present large volumes of data in an exploratory environment. It not only provides mathematical methods such as clustering, but also provides means for understanding the statistical basis and context within a larger framework.

The OmniViz solutions have been applied in proteomics applications ranging from protein chips to large-scale fluorescent assays (including High-Content Biology) to mass spectroscopy to biomarkers and much, much more.

Benefits

OmniViz:

- Scales to accommodate proteomic measurements across 1000's of treatments or tissues
 - **gain an understanding of the entire picture, not just 1 piece at a time**
- Quickly links to MEDLINE®, and allows clustering of the MEDLINE records to rapidly understand the context of genes of interest
 - **make faster decisions about what avenues are fruitful to pursue**
- Finds significant changes in proteins quickly by incorporation of the Stanford University SAM algorithm or understand the statistical significance using the built in Relativity™ statistical toolkit
 - **understand the significance and focus in on the most important observations**
- Processes quickly, allowing for different views of the data, and different paths that result from the analysis, to be pursued with ease
 - **make better decisions with more confidence**

Functionality Highlights

Import: In addition to reading data in comma, tab, and semicolon delimited formats, OmniViz can import data from Excel® or any JDBC compliant database. Extensive merge capabilities allow data in different formats from different sources to be retrieved and brought together in one coherent package for analysis.

Data Types: Numeric, Text, Categorical, Chemical structure, and DNA or Protein sequence information can be imported together and used to cluster and visualize.

Export: OmniViz will automatically send selected data, and ancillary information, directly to Excel or Word®. Additionally, information can be saved in FASTA or tab delimited formats for easy import into other tools.

Sharing: Sharing of analyzed data between users is via OmniViz ".xpt" files, where the completed analysis is passed in one file from one user to another.

Normalization and Clustering abilities: OmniViz has built a wide variety of normalization algorithms and steps into the software, allowing maximal flexibility. There is no broad consensus in the industry as to what the best methods are, so we endeavor to allow them all. K-means, Hierarchical (both Wards and agglomerative), and Jarvis-Patrick clustering algorithms are provided, each with multiple distance algorithms. As this field is continuing to mature, it is simple for users to plug in their own clustering algorithm.

SAM algorithm: The SAM algorithm has been licensed from Stanford University and incorporated into the software. The graphics tool that is included allows for 2 group comparisons, the changing of all parameters and linkage to other visualizations and data in order to understand where the genes of interest are in the larger context of the data.

Correlation Visualization: The correlation tool allows for the visual representation of correlations between attributes. The tool, as seen at right, can show you which proteins behaved together in a series of treatments or which diseases (based on their profiles) have correlated behaviors.

Integrated Statistics: To help make smart decisions quickly OmniViz has incorporated the most frequently used statistical tests as an integral part of our statistical analysis tool. OmniViz allows for quick analysis of 1, 2, and multi- group tests or easily send the data to any other statistical package...

Linked Visualizations: All of the OmniViz visualizations are linked, such that a selection in one tool immediately causes a selection in all other possible locations. This allows problems to be attacked from all sides.

Text Clustering: The ability to cluster based on text information, allows for the incorporation of MEDLINE information directly into an analysis. By using the telescope tool, MEDLINE records of interest for every gene can be retrieved, clustered, and understood visually. This enables rapid understanding of why genes clustered together and why those genes may be important.

In addition to the specifically mentioned tools above, OmniViz includes the: **Galaxy™** visualization - aiding the understanding of every record compared to every other record. **TreeScape™** - providing an overview of the data values and their distribution, as well as any hierarchical relationships. **™** - allowing for the understanding of what occurred with what, and would that have been expected to happen?

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