

Affymetrix® Data Mining Tool (DMT) Version 3.0

Mining and analyzing Affymetrix® GeneChip® gene expression results has never been easier. Data Mining Tool (DMT) software contains a variety of new and powerful features for filtering and sorting expression results, enabling you to rapidly identify your most significant results. This software also provides the tools you need to perform more complex analyses on your data for faster and more comprehensive interpretation of results.

Replicate Sample Analysis

DMT 3.0 provides the ability to combine experiment or sample replicate results with tools for performing statistical tests. Some basic options for replicate analysis include calculating a median, mean or standard deviation; more advanced options include statistical tests such as Mann-Whitney and t-test analysis (Figure 1).

Virtual Array Sets

With DMT 3.0 you can visualize a single array out of subsets of arrays and

analyze the entire set as one large array. A virtual array allows you to combine the analysis of GeneChip® array sets composed of multiple individual arrays, such as the Human U95 Array Set, into a single analysis. This significantly reduces the time spent on analyzing array sets.

Clustering Analysis

Clustering allows you to group genes according to similarities in their expression profiles across multiple analyses. DMT 3.0 provides two types of clustering methods: Self-Organizing Maps and a modified Pearson's Correlation Coefficient method. The two methods offer different approaches to clustering genes. The clustering results are integrated with the pivoted (filtered) data view for rapid correlation with numeric results (Figure 2). The clusters are visualized using line graphs that can help you quickly find patterns in your data leading to a greater understanding and more rapid interpretation of results.

Matrix Analysis Tool

This tool provides the ability to compare two groups of probe sets and look for coincidentally occurring features, or overlaps. Overlaps are presented as a measure of significance or confidence.

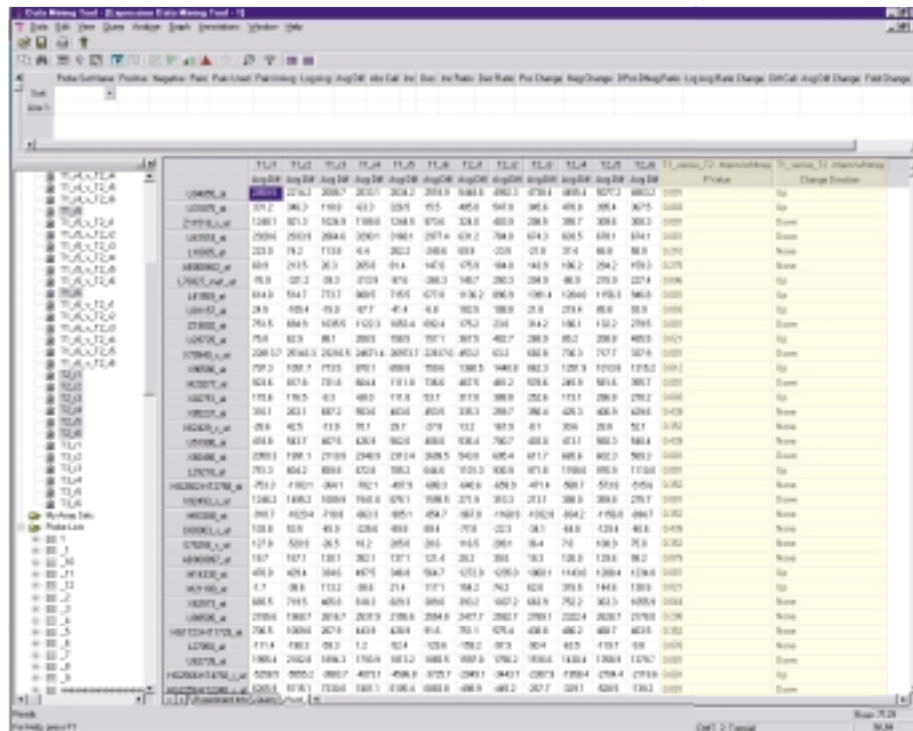
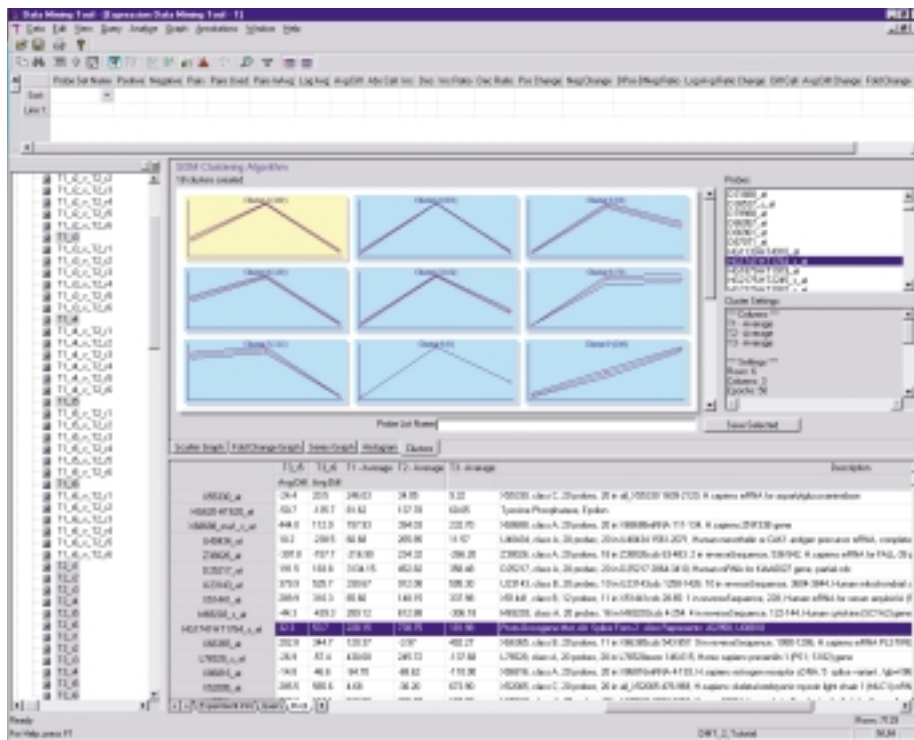


Figure 1. DMT Replicate Statistical Analysis

An example of Mann-Whitney analysis of two different replicate sets representing two experimental conditions. Results are displayed as a direction of change in expression: up/down/none and *p*-value for confidence.

SOFTWARE SOLUTIONS



An example of Self-Organizing Map clustering results. Clustering results are integrated with probe set information, description or annotation information, and expression results.




Figure 2. DMT SOM Clustering

Annotations

The ability to annotate genes has been expanded in DMT 3.0. Single annotations can be added “on the fly” or large sets of annotations can be batch-loaded into the software. Annotations can also be brought in from the NetAffx™ Analysis Center (www.affymetrix.com), a unique online resource created by Affymetrix to enable researchers to correlate results from their GeneChip® array experiments with array design and annotation information. The annotation information can be customized and the annotations are integrated with every step of the analysis workflow.

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System Requirements

Hardware Requirements:

- Meets or exceeds
 - 400 MHz Pentium III® Processor
 - 128 MB RAM
 - 100 MB hard disk space

Required Third-Party Software:

- Microsoft Windows NT® 4.0, Service Pack 6.0 or Windows 2000
- Oracle® Client Utilities (if using Oracle)

Required Affymetrix® Software:

- MicroDB™ Version 3.0 or
- LIMS Version 3.0 (Compatible with MAS 4.0 or 5.0)

Ordering Information:

Part No.	Description
690004	Data Mining Tool 1 seat license

Please see our product catalog for additional combination packages.

AFFYMETRIX, INC.
3380 Central Expressway
Santa Clara, CA 95051 USA
Tel: 1-888-362-2447 (1-888-DNA-CHIP)
Fax: 1-408-731-5441
sales@affymetrix.com
support@affymetrix.com

AFFYMETRIX UK Ltd.,
Voyager, Mercury Park,
Wycombe Lane, Woodburn Green,
High Wycombe HP10 0HH
United Kingdom
Tel: +44 (0)1628 552550
Fax: +44 (0)1628 552585
sales@affymetrix.com
support@affymetrix.com

www.affymetrix.com

