



## ArrayUnlock Rule your data, free the knowledge

A tool for functional analysis of gene expression data sets within Spotfire DecisionSite®.

ArrayUnlock™ is an advanced data analysis tool designed to discover biological knowledge from gene expression data. The software allows researchers to explore vast data sets of genes along with multiple experimental conditions in order to understand the underlying biological processes. ArrayUnlock™ uses the information contained in local and external databases to annotate and analyze large lists of genes or protein expression data. Powerful data mining methods are applied to automatically extract associations among gene annotations and expression patterns. This application is seamlessly integrated with Spotfire DecisionSite® to facilitate interactive biological understanding of gene expression data sets.

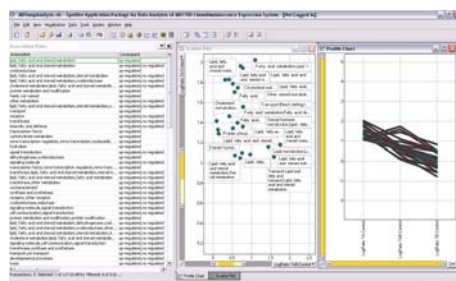
### Key Features

#### > Annotate genes

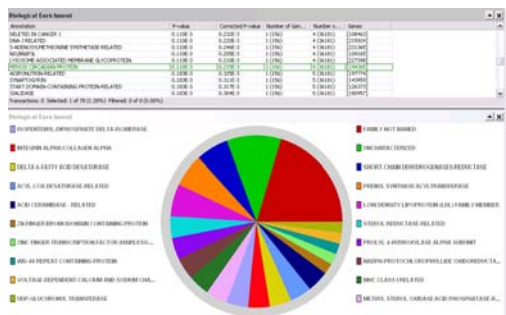
ArrayUnlock™ provides the ability to annotate gene lists with several biological topics of interest such as GO terms or biological pathways. Probe IDs from most-extended platforms are supported (Affymetrix®, Agilent®, etc.).

#### > Association discovery among gene annotations and expression patterns

ArrayUnlock™ uses data mining methods to integrate biological annotations and expression data, being able to automatically extract associations among functional annotations and gene expression patterns.



Gene expression rules that highlight significant associations between annotations and gene expression fold changes.



Biological Enrichment and Co-Occurrence  
Discovery to make assessments on  
annotation abundance.

#### > Biological enrichment

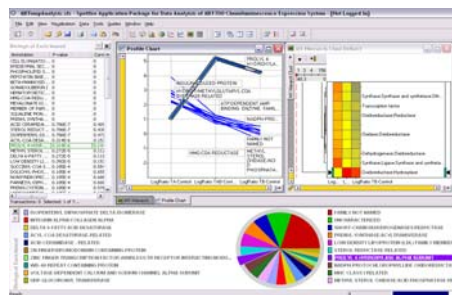
ArrayUnlock™ provides statistical analysis to determine the enrichment of biological annotations in a list of genes of interest with respect to a list of reference genes, such as full arrays or whole genomes.

#### > Gene Annotation co-occurrence discovery

ArrayUnlock™ implements an innovative algorithm to discover novel associations from different biological annotation sources in your set of genes. Annotations that frequently co-occur in the list are ranked according to their statistical significance.

#### > Full Integration with Spotfire DecisionSite®

The Spotfire DecisionSite® suite of products offer researchers in life sciences, a direct, interactive and visual approach to data analysis that rapidly reveals insights and unexpected relationships. ArrayUnlock™ empowers DecisionSite® with new algorithms and visualizations that can be used in conjunction with standard data mining procedures.



Visualization tools integrated with  
state-of-the-art data mining.

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