



ArrayUnlock Rule your data, free the knowledge

A tool for functional analysis of gene expression data sets.

ArrayUnlock™ is an advanced data analysis tool designed by Integromics to extract biological knowledge from gene expression data. This software allows researchers to explore vast gene expression data sets 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 gene expression data sets. This powerful software is using data mining methods to automatically extract associations among gene annotations and expression patterns as well as to determine the main biological properties associated to lists of genes.

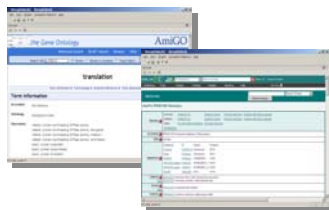
Key Features

> Annotate genes

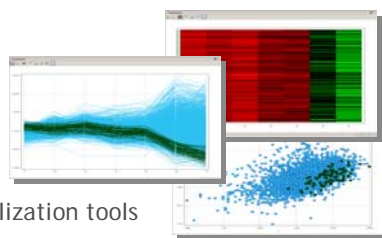
ArrayUnlock™ provides the ability to annotate gene lists with several biological topics of interest such GO terms, InterPro motifs or biological Pathways. This software is able to work with gene IDs from different sources.

> Association 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.



External Databases



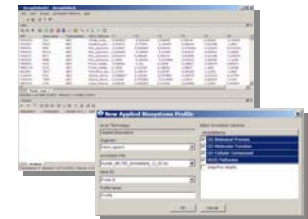
Visualization tools

> Link to external databases

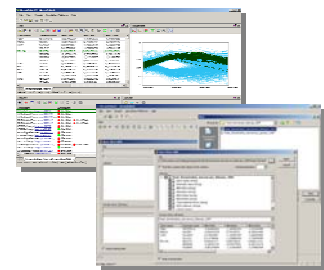
ArrayUnlock™ allows the user to link genes and annotations to main biological databases (NCBI, GO or InterPro) in order to visualize summary information from different resources.

> Visualization tools

Several visualization tools (Profile plot, Scatter plot, Heatmap, Hbar and Pie Chart) allow the user a full interaction for browsing and exploring the obtained results.



Annotate genes



Annotations and gene expression rules

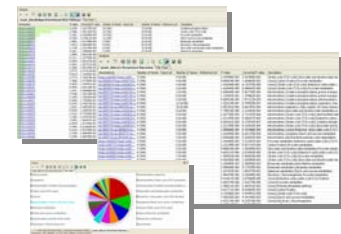
> Biological enrichment

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

As with single annotation, it is useful to discover the significant co-occurrences of biological annotations in lists of genes (for example biological pathways and cellular localization).

ArrayUnlock™ provides rank scores for statistical significant combination of annotations in a list of genes.



Biological Enrichment and Co-Occurrence Discovery

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