Analysis tools for Affymetrix GeneChip®

Open resource for expression analysis

- Bioconductor
- dChip
- L2L
- RMAExpress
- TAIR's Seqviewer
- TAIR's Mapviewer
- TAIR's AraCyc Pathways
- TAIR's Chromosome map tool
- TIGR's MIDAS
- TIGR's MultiExperiment Viewer (MeV)

Commercial (http://www.affymetrix.com/ > Support > By support type > GeneChip Compatible Software > Expression)

Expression Analysis at Affymetrix web

- BioDiscovery GeneSight
- Genedata Expressionist®
- Genomatix's ChipInspector
- IMC's TeraGenomics®
- Partek's Genomics Suit™
- Rosetta Biosoftware's Rosetta Resolver System
- Spotfire DecisionSite for Functional Genomics
- Spotfire's DecisionSite® for Microarray Analysis
- Strand Genomics avadis
- Stratagene's ArrayAssist®
- VizX Labs GeneSifter

Other Expression Analysis

- Corimbia ProbeProfiler
- InforSense Kensington Discovery Edition (KDE)
- Insightful S+ArrayAnalyzer
- Stratagene's GeneTraffic™

- OmniViz
- Agilent’s GeneSpring GX

Commercial (http://www.affymetrix.com/ > Support > By support type > GeneChip Compatible Software > Pathways/Network Analysis)

Pathways/Network Analysis at Affymetrix web

- Ingenuity Pathways Analysis
- GeneGo's MetaCore™
- Genomatix's BiblioSphere Pathway Edition
- Stratagene's PathwayArchitect™

Other Pathways Analysis

- OmniViz Pathway Enterprise

Commercial (http://www.affymetrix.com/ > Support > By support type > GeneChip Compatible Software > Statistical Analysis)

Statistical Analysis at Affymetrix web

- Insightful S+ArrayAnalyzer

Commercial (http://www.affymetrix.com/ > Support > By support type > GeneChip Compatible Software > Data Management)

Data Management

- BioDiscovery GeneDirector
- Genedata Expressionist™
- Stratagene's GeneTraffic®

Other Data Management

- Agilent GeneSpring GX Workgroup
- Corimbia GenoWorks

Open resource

Bioconductor is a free program for analyzing array data. Please contact the MCF if you would like your data run through BIOConductor or would like more information on this free software. (Go to top)
(http://www.bioconductor.org)

dChip is another free program designed for statistical analysis of Affymetrix GeneChips®. If you would like to learn more about dChip, please visit the link above.
(Go to top)
(http://www.biostat.harvard.edu/complab/dchip)

L2L is a database of published microarray gene expression data, and a software tool for comparing that published data to a user's own microarray results. (Go to top)
(http://depts.washington.edu/l2l/)

RMAExpress is a standalone GUI program for Windows (and Linux) to compute gene expression summary values for Affymetrix GeneChip® data using the Robust Multichip Average expression summary. It does not require R nor is it dependent on any component of the Bioconductor project. (Go to top)
(http://stat-www.berkeley.edu/users/bolstad/RMAExpress/RMAExpress.html)

TAIR

SeqViewer is TAIR's new graphic display tool for Arabidopsis sequence and annotation. Search for names or short sequences and view search hits on the whole genome, in a close up view or at the nucleotide level. The first version displays genes, markers and clones. (Go to top)
(http://www.arabidopsis.org/servlets/sv)

MapViewer is TAIR's comprehensive map visualization and alignment tool for sequence, genetic and physical maps is available. (Go to top)
(http://www.arabidopsis.org/servlets/mapper)

AraCyc Pathways is Arabidopsis biochemical pathways visualization and querying tool. (Go to top)
(http://www.arabidopsis.org/tools/aracyc/)

Chromosome Map Tool can draw maps of your favorite gene family. (Go to top)
(http://www.arabidopsis.org/jsp/ChromosomeMap/tool.jsp)

TIGR

Microarray Data Analysis System (MIDAS), a Java application, provides users an intuitive interface to design analysis protocols combining one or more normalization and filtering steps. In this way, data from much individual hybridizations can be treated in a uniform and reproducible manner. Data analysis methods are constructed using an intuitive graphical scripting language and can be saved for application to other datasets. (Go to top)
(http://www.tm4.org/midas.html)

MultiExperiment Viewer (MeV) is a versatile microarray data analysis tool, incorporating sophisticated algorithms for clustering, visualization, classification, statistical analysis and biological theme discovery. MeV can handle several input file formats, these include the *.mev and *.tav files generated by TIGR Spotfinder and TIGR MIDAS, and also Affymetrix® (*.txt) and Genepix® (*.gpr) files. MeV generates informative and interrelated displays of expression and annotation data from single or multiple experiments and also provides many algorithms for analysis. (Go to top)
(http://www.tm4.org/mev.html)

BioDiscovery, Inc.

GeneSight combines advanced normalization, visualization, and statistical decision support tools into a single powerful package. Its unique Confidence Analyzer tool can use replicated gene expression data for identifying genes having true differential expression. Its Significance Analyzer tool can determine genes with statistically significant expression patterns and differentiate between classes of experimental conditions, such as disease states. Its Integrated Annotation Complier supports Affymetrix annotation files and annotations from other public databases. Runs on Windows 9x / NT4 / Win2000 / WinXP, Linux, and Mac OSX. Integrated for direct use with Affymetrix GeneChip result files. (Go to top)
(http://www.biodiscovery.com/genesight.asp)

GeneDirector is comprehensive solution for management of all data generated throughout the entire array experiment workflow including, sample preparation, protocols, hybridization, image analysis, and data analysis. It also features integrated

tools and features which provide direct import of Affymetrix data. Agilent's Bioanalyzer data and software are also integrated for tracking of RNA quality control. It provides standardized tools for the entire lab, department, or organization which means more time spent can be spend analyzing results and less time learning new software. It has been designed to be flexible and customized to any laboratory's requirements. Its centralized data management allows immediate data access, impenetrable security and cross experiment analysis. Runs on Windows 9x / NT4 / Win2000 / WinXP, Linux, and Mac OSX. Supports Oracle 8i or 9i. Integrated for direct use with Affymetrix GeneChip result files. (Go to top)
(http://www.biodiscovery.com/index/genedirector)

Genedata, Inc.

Expressionist® provides one platform for investigating data from transcriptomics, proteomics, and metabolomics. Compatible with all major commercial microarray, 2D-PAGE, and MS platforms, Expressionist spans the workflow from experiment planning to biomarker documentation: Sample tracking, technology-specific quality assessment, analysis, interpretation, and results handling. Automated quality control, probe-level analysis exceeding 500 chips a day, and step-by-step report generation make Expressionist the system of choice for companies engaged in high-throughput expression analysis. Other analysis-level benefits include: clustering, classification and cross-validation with thousands of chips in parallel. Extensive pathway analyses provide the biological context required to validate findings. Key applications of the Expressionist software include identification and validation of novel biomarkers, evaluation and prediction of bioactive molecules, and stratification of patient groups for clinical trials. (Go to top)

Genedata Expressionist® provides a comprehensive solution for biological data management. The open database, built on Oracle RDBMS technology, supports the structured storage and retrieval for gene, protein, and metabolite expression data and relevant associated information — from sample registration and experimental design, to raw and metadata management, annotation, and analysis results. Automated report generation, electronic signatures, access control, and audit trails actively support FDA 21 CFR Part 11 compliance. Additionally, the database serves as a single-point-of-access for analyzing data from all major commercial microarray, 2D-PAGE, and MS platforms.

Key applications of the Expressionist software include identification and validation of novel biomarkers, evaluation and prediction of bioactive molecules, and stratification of patient groups for clinical trials. (Go to top)
(http://www.genedata.com/productoverview/expressionist/index_eng.html)

Genomatix

ChipInspector. Microarray analysis software using Affymetrix raw data files. ChipInspector carries out significance analysis on the level of single probes rather than predefined probe-sets. This results in heavily reduced false positive rates. Probes are checked against Genomatix' regularly updated ElDorado genome annotation. Mismatching or multiple matching probes are excluded from the analysis. The output of the program is a list of significantly regulated transcripts including alternative transcripts as far as resolvable. The software includes several clustering features. A direct link to GenomatixSuite allows further analysis of the ChipInspector results through pathways and networks down to the molecular mechanisms of gene regulation. (Go to top)
(http://www.genomatix.de/products/ChipInspector/index.html)

BiblioSphere Pathway Edition. Dynamic data-driven gene network construction and analysis based on Genomatix Knowledge Base Ontology, literature, and sequence analysis. BiblioSphere PE automatically creates the entire network of biological connections between input and correlated genes. The user is supported by various tools to facilitate focusing on functional sub-nets. He is assisted in finding the biological context most relevant for his research. There is no size limit for networks to be analyzed. Integration of sequence analysis provides additional independent lines of evidence. This is achieved by applying Genomatix' proprietary genome annotation and its unique promoter and transcription factor binding site database. (Go to top)
(http://www.genomatix.de/products/BiblioSphere/BiblioSpherePE1.html)

IMC, Inc

TeraGenomics® is a high-performance and highly-scalable data warehousing solution for managing, analyzing, and sharing Affymetrix GeneChip® expression data. TeraGenomics supports rich annotation through a MIAME-compliant metadata structure comprised of 140+ data fields using controlled vocabularies (e.g., for

organism, anatomy, disease type, experimental conditions, etc.). The solution uses .CEL files to compute gene expression levels, calls, associated statistics, and probe-level analysis among chips through a rapid point-and-click interface. RMA analysis can be performed on an unlimited number of microarrays. TeraGenomics is a browser-based thin client solution with an extensive visualization support that can be securely deployed over the web or on an intranet as an installed or hosted solution. It is seamlessly integrated with the Affymetrix GCOS and supports exports in multiple formats. Its architecture enables customization and integration with other data sources. TeraGenomics is an ideal solution for collaborating scientists in multiple locations and for organizations that need to manage thousands of microarrays on an enterprise basis. (Go to top)
(http://www.teragenomics.com/)

Partek Incorporated

Genomics Suit™ is an integrated statistical and visual analysis solution for GeneChip® experiments, optimized for fast and memory-efficient processing of large, ultra high-dimensional data. Proven, rigorously tested statistical methods are integrated with 2-D and 3-D interactive visualization allowing you to reliably explore, identify, and present important patterns in your data. The Partek Genome Browser™ provides dot plots, box & whiskers, profiles, exon-level, gene-level, and alternative splicing summaries. All graphs can be exported in publication-quality vector graphic format. Multiple classification methods are integrated with gene selection for accurate diagnostic/prognostic prediction. Seamless integration with .CEL, .CDF, .CHP, and .EXP files includes fast, memory-efficient RMA and probe-level import. Partek GS automatically annotates all results and provides hyperlinks to NetAffx and other internet databases. (Go to top)
（http://www.partek.com/html/products/products.html）

Rosetta Biosoftware

The **Rosetta Resolver system** is a comprehensive gene expression analysis solution that incorporates powerful analysis tools with a robust, scalable database designed for pharmaceutical and biotechnology companies and research centers of excellence. The rigorous analysis methods, scalable database and extensive management tools of the Resolver system offer many opportunities for workflow and ad hoc-driven gene

expression analyses. The Resolver system is an overall solution for gene expression analysis that is customizable and extendable to an organization's informatics platform and to the unique research goals of its scientists. (Go to top)
(http://www.rosettabio.com/products/resolver/default.htm)

Spotfire

Spotfire DecisionSite® for Functional Genomics offers scientists a powerful visual analytic environment for exploring and finding unexpected relationships in gene expression and other types of genomic data. To better understand the large amounts of data from microarray experiments, rt-PCR and proteomic studies, DecisionSite for Functional Genomics provides rapid normalization, interactive filtering, clustering and statistical capabilities that give scientists deeper, more reliable insights into the biological relevance of the data. DecisionSite for Functional Genomics provides direct access to Affymetrix databases and chp files, NetAffx files and a number of other data sources. (Go to top)
(http://www.spotfire.com/products/decisionsite_functional_genomics.cfm)

DecisionSite® for Microarray Analysis combines DecisionSite's visual analytics with high-power statistics that are at the leading edge of how scientists want to be able to analyze gene expression and biomarker data. DecisionSite for Microarray Analysis provides multiple methods of probe level analysis, normalization, quality assessment and advanced statistics for secondary analysis of both Affymetrix and 2-Channel microarray experiments. With DecisionSite for Microarray Analysis, DecisionSite for Functional Genomics and DecisionSite, Spotfire now offers a continuum of solutions for microarray experiment analysis to address the complete range of needs and skill levels of scientists involved in genomic research. (Go to top)
(http://www.spotfire.com/products/decisionsite_microarray_analysis.cfm)

Strand Genomics

Avadis brings the very best in data mining techniques and the finest in software engineering to microarray gene expression data analysis. Prebuilt Affymetrix workflows combine powerful mining algorithms with ready-to-explore views of data. This makes avadis the only software that provides algorithmic and visual inquiry techniques in an intuitive and easy-to-use framework. Avadis is highly tuned to work

with Affymetrix GeneChip® data. It supports multiple probe-level analysis algorithms such as PLIER™, GC-RMA, RMA and MAS5. avadis seamlessly imports .CEL and .CHP files from within/outside GCOS and integrates with NetAffx™ gene annotations. In addition to these functions, avadis helps researchers in deriving biological insights from the expression data through its automated annotation engine, interactive GO browser and pathway viewers. Avadis also offers a range of clustering and class prediction algorithms. (Go to top)
(http://avadis.strandgenomics.com/)

Stratagene

ArrayAssist® Expression Software is an easy to use desktop software application for the analysis of Affymetrix GeneChip® expression data. ArrayAssist offers the latest probe-level analysis algorithms to calculate gene expression values from GeneChip® microarrays including PLIER™, GC-RMA and RMA and also supports the MAS5 algorithm. ArrayAssist also generates comprehensive quality reporting including native Affymetrix RPT file and experimental quality metrics based on Affymetrix internal controls. ArrayAssist can perform statistical analysis with p-value corrections, cluster and visualize your data in multiple different ways including volcano plots. ArrayAssist also offers searchable database of current gene annotations for all Affymetrix GeneChip microarrays based on the latest NetAffx annotation. (Go to top)
(http://www.stratagene.com/products/displayProduct.aspx?pid=731)

GeneTraffic is fully integrated with the Affymetrix platform and import GeneChip® files (CEL, CHP) in text and binary format. GeneTraffic provide state-of-the-art probe-level analysis methods, it includes PLIER, GC-RMA and RMA. GeneTraffic also provides powerful statistical analysis tools and rich experimental annotation. (Go to top)

GeneTraffic® Software is a client-server based microarray data management and analysis software package intended for core facilities or large-scale microarray users with support for Affymetrix GeneChip® microarrays. It has an intuitive interface for rich data mining, visualization and statistical analyses. All data, including raw images, are stored on the server and accessed using your PC. Multiple users can access the data at the same time, and work on projects simultaneously. Experimental annotation within GeneTraffic is MIAME compliant with MAGE-ML support. Integration with the

Affymetrix GCOS software is seamless. Included are the latest probe-level analysis algorithms (GC-RMA, RMA, MAS5) optimized for speed and scalable to process hundreds of GeneChip microarrays for better precision and accuracy. GeneTraffic has a complete Application Programming Interface (API) to integrate data with other software applications to complete any core facility's workflow. GeneTraffic is an ideal product for facilities that need to easily archive and analyze data in a multi-user environment. (Go to top)
(http://www.stratagene.com/products/showProduct.aspx?pid=538)

PathwayArchitect™ allows you to build, visualize and explore pathways and biological interaction networks (BINs). A BIN is an interactive diagram showing biological relationships among different proteins, small molecules and cellular processes from a range of organisms. PathwayArchitect™ build interaction networks with multiple algorithms including direct interactions, shortest path, putative targets and putative regulators and provides multiple filter options to view pertinent interactions. PathwayArchitect also provides gene/protein annotations that includes Entrez gene annotations, alias (synonyms), subcellular locations, gene ontology terms and microarray IDs. (Go to top)
(http://www.stratagene.com/products/displayProduct.aspx?pid=733)

VizX Labs

GeneSifter, the only microarray data analysis system optimized for biomedical research, won the 2005 "Best Practices Award for Product Innovation" in Bioinformatics in Drug Discovery from Frost & Sullivan. They noted that "the flexible nature of web-based GeneSifter enables scientists to better understand the biology behind their gene expression data," and that scientists using GeneSifter products have testified to improved research, savings in training time, reduction in costs, and faster results. The GeneSifter product line includes GeneSifter Lab Edition, for individual researchers; GeneSifter Core Edition, for core facilities that prefer to administer their own accounts while taking advantage of GeneSifter's lower training and support costs; GeneSifter JumpStart, for scientists seeking to accelerate initial analysis efforts; the GeneSifter Data Center, an opportunity for any researcher to analyze high-quality, published data using the GeneSifter system for free; and

MicroarraySuccess.com, for researchers new to microarrays. Free GeneSifter trial accounts are currently available. (Go to top)
(http://www.genesifter.net/web/)

Corimbia, Inc.

Probe Profiler is a software solution for biologists who want to reduce variability of the data generated from the Affymetrix GeneChip system and to increase the overall quality and efficiency of the downstream analysis. It also generates alternative signal for Affymetrix GeneChip data using rigorous statistical analysis of probe performance. (Go to top)
(http://www.corimbia.com/Pages/ProbeProfiler.htm)

GenoWorks™ offers a complete process tracking software solution and data delivery system for laboratories engaged in gene expression profiling experiments using Affymetrix® GeneChip® systems. The system enables the users to automatically track sample handling and project billing and provides facilities for the users to share generated data over the internet. (Go to top)
(http://www.corimbia.com/Pages/GenoWorks.htm)

InforSense Limited

KDE enables analysts to accelerate their research by accessing and integrating all their tools through the intuitive InforSense analytical workflow interface. It also includes flexible and interactive visualizations in combination with a comprehensive suite of normalizations (including RMA, Li&Wong methods), pre-processing, statistical analysis, unsupervised (clustering) and supervised analysis procedures. (Go to top)
(http://www.inforsense.com/kde.html)

Insightful Corporation

S+ArrayAnalyzer® provides a comprehensive suite of statistical and graphical methods for analysis of GeneChip microarray data. It includes methods for data access, probe-level summary, QA/diagnostics, filtering, normalization, differential expression testing, class discovery (unsupervised learning), class prediction (supervised learning), machine learning and (interactive) annotation. S+ArrayAnalyzer is extendable using S-PLUS® scripts, and well-documented C++,

Java, SOAP, JavaServer Pages Tag API's. S+ArrayAnalyzer runs on Windows® , Linux, and Solaris and includes web (server) and desktop deployment options. (Go to top)
(http://www.insightful.com/products/s-plus_arrayanalyzer/default.asp)

OmniViz, Inc.

OmniViz is designed to comprehensively analyze huge amounts of data in a manner that allows a global overview coupled with rapid identification and interpretation of the details. OmniViz supports the analysis of numeric, categorical, and full-text documents (including patents) and for the scientist, it also supports analysis of chemical structures and genome sequences. (Go to top)
(http://www.omniviz.com/applications/omni_viz.htm)

OmniViz Pathway Enterprise is a full featured pathway drawing and analysis package, incorporating the best of a stand alone drawing tool with enterprise wide sharing and searching. OmniViz Pathway Enterprise can import multiple data sources, with standardization and linking of related genes and proteins. The biological object model allows for mapping of clones to genes to proteins. (Go to top)
(http://www.omniviz.com/applications/pathways.htm)

Agilent technologies

GeneSpring GX is widely regarded as the gold standard for expression data analysis and designed to meet the needs of the individual researcher. GeneSpring GX is part of an integrated analysis suite that enables visual and analytical comparisons between different data types. The GeneSpring platform is designed to break through bottlenecks in the analysis process and to help identify genes/pathways that are truly relevant to your biological question by comparing analysis results from expression, genotyping, protein, metabolite and other data types. (Go to top)
(http://www.chem.agilent.com/scripts/pds.asp?lpage=27881)

GeneSpring GX Workgroup software is a highly scalable analysis platform for managing and mining expression data in a workgroup or an enterprise setting. The workgroup software streamlines microarray research at large and multicampus organizations, and provides facilities for robust data analysis, collaborative workflow management, automating research procedures, and secure data administration. (Go to top)

(http://www.chem.agilent.com/scripts/pds.asp?lpage=34668)

Ingenuity Systems

Ingenuity Pathways Analysis. Now scientists can simultaneously analyze multiple genomic and proteomic datasets to rapidly gain biological insight and understanding. Scientists are using this innovative technology to make better and faster decisions in all areas of drug discovery and development, from target identification and validation to biomarkers, predictive toxicology, and patient stratification. The application makes use of the Ingenuity Pathways Knowledge Base, the world's largest curated database consisting of millions of individually modeled relationships between proteins, genes, complexes, cells, tissues, drugs, and diseases. Ingenuity Pathways Analysis is available as a web-delivered, hosted, or deployed solution. (Go to top)

(http://www.ingenuity.com/products/pathways_analysis.html)

GeneGo Inc.

MetaCore™ enables life science researchers to analyze microarrays, SAGE, proteomics, metabolomics and phenotypic experimental data in the context of biological mechanisms in norm and disease. The platform is based on the most comprehensive up to date, expert curated database of ?small experiments?, mammalian protein interactions, enzymatic reactions and bioactive molecules (drugs, metabolites and toxins). This includes millions of data points. The content includes the largest collection of unique maps with thousands of signaling, regulation and metabolic pathways established for human. Our customers are empowered by an intuitive analytical toolkit for data import, visualization and exchange; with eight unique networking algorithms, multiple specificity filters and a networks comparison module. MetaCore™ is available via web access and as a stand-alone server for in-house installations. (Go to top)

(http://www.genego.com/about/products.shtml#metacore)