

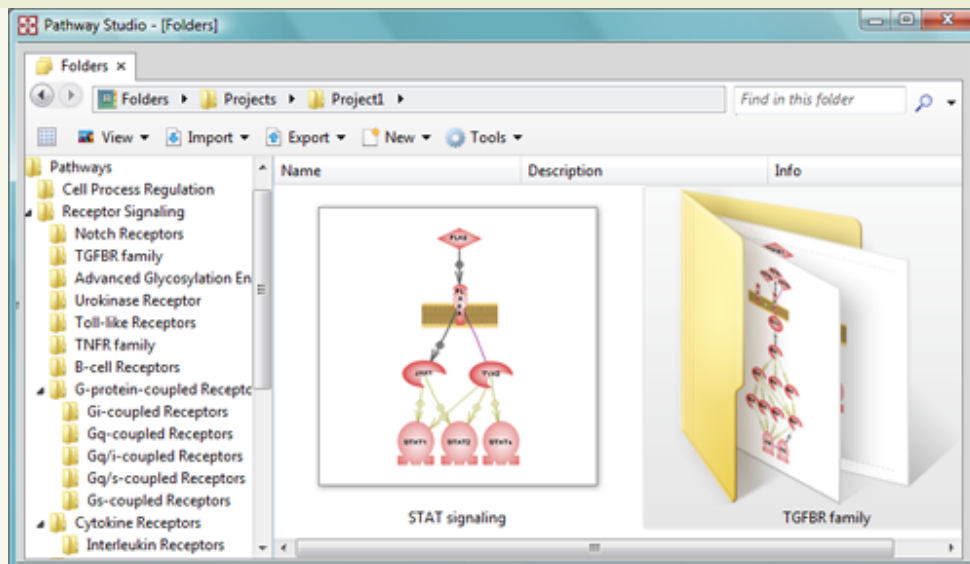
# PATHWAY STUDIO 7

Pathway Studio pathway analysis software helps you to:

- Interpret gene expression and other high throughput data
- Build, expand and analyze pathways
- Find relationships among genes, proteins, cell processes and diseases
- Draw publication-quality pathway diagrams

Pathway Studio comes with the [ResNet Mammalian Database](#) with access to other [databases](#) including [ResNet Plant](#), and enables pathway analysis for most model organisms. Pathway Studio also supports [KEGG](#), [Science Signaling](#), and [Prolexys HyNet](#) protein-protein interaction database.

You can keep the ResNet databases up-to-date with newly published facts with [Ariadne MedScan](#) technology or use our Quarterly database updates.



*Pathway Studio pathway analysis software: visualizing the science.*

Pathway Studio enables in-depth analysis of any interrelated biological data. This is particularly useful for the interpretation of gene expression or proteomics experiments. Import the experimental data into Pathway Studio and use it to find relationships based upon biological knowledge extracted from the entire PubMed.

Pathway Studio finds common regulators and associates pathway components with like-behaving biological entities and processes. All relationships are supported and validated by citations, linked to their references of origin.

With advanced data analysis algorithms, Pathway Studio enables pathway analysis of the entire probe set, associating genes into like-functioned or like-associated biological properties.



- Display specific upstream and downstream events
- Find interaction paths among molecules, cell objects and processes
- Determine and identify common targets and regulators for a group of proteins

## MOLECULAR INTERACTION NETWORKS FROM THE LITERATURE

- Analyze pathways with ResNet database, compiled from PubMed abstracts and articles
- Access more than 1,000,000 facts of regulation, interaction and modification
- Validate the facts by clicking on the link to an original sentence, abstract or source

## PATHWAY RECONSTRUCTION ALGORITHMS

- "Build Pathway" is a powerful search tool with flexible options to navigate the network database and build pathways. Choose from multiple algorithms for assembling a pathway such as "find only direct interactions", "find shortest paths", "find common targets" or "find common regulators".
- "Find relevant networks" - finds pathways related to a list of molecules
- Find differentially expressed networks (pathways) for a microarray experiment.

## DATA MINING AND SEARCHES

- Find all interacting molecules for a protein or other biological entity
- Find all networks/pathways for a query protein
- Use context and field-specific database searches
- Filter to see only specific types of biological objects to be included in your pathway, such as proteins, complexes, small molecules, cellular processes etc.
- Filter to see only specific types of biological interactions such as binding interactions, post-translational regulation, expression regulation, enzymatic activity, molecular synthesis, transport, and others.
- Review original literature sources for every relation within a pathway via direct links to PubMed abstract and exact source sentence where each finding is referenced.

## IMPORT AND ANALYSIS OF GENE & PROTEIN LISTS

- Import/export gene and protein lists
- Map gene lists on signaling and metabolic pathways, and GO groups
- Build and analyze pathways from imported lists
- Work with protein IDs, names or aliases from various sources: Unigene IDs, Accession Numbers, LocusLink, Swiss-Prot, Affymetrix GeneChip® IDs, Gene Names and Gene Symbols

## LITERATURE MINING

- Use integrated MedScan software to extract biological interactions from scientific text
- Mine PubMed and build pathways from extracted facts
- Update pathways using data from recent publications

## MICROARRAY GENE EXPRESSION DATA ANALYSIS

- Import data from all popular microarray analysis software packages
- Reconstruct molecular networks from gene expression and proteomics data
- View how genes in a pathway are up or down regulated through various biological states to identify key regulators or targets of interest

## SUPPORTED DATA FORMATS

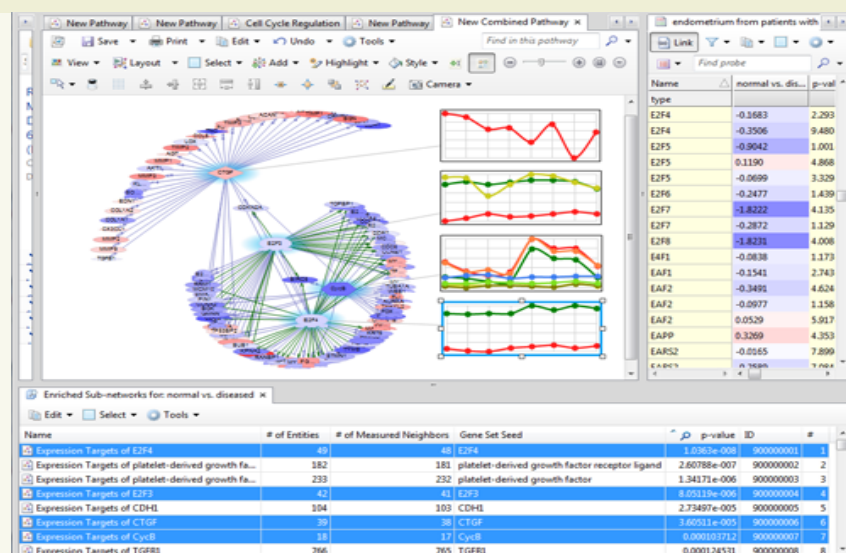
- ResNet Exchange (RNEF) XML and SBML formats for molecular network data
- Simple tab-delimited format for molecular interaction data import from KEGG, BIND, DIP, Science Signaling, GO and other leading pathway databases
- Flexible tab-delimited format for microarray data import
- Multiple microarray platforms including Affymetrix, Agilent and Amersham
- Both raw and pre-processed microarray data

## GENE EXPRESSION DATA ANALYSIS

Pathway Studio enables gene expression data analysis within the biological context of protein-protein interactions, pathways and pathway components.

- Are there key regulators that explain my gene expression modulation?
- Is the regulation acting coordinately on downstream targets?
- What key biological processes are regulated in my experiment?
- What proteins should I look at? What do they do?
- What kinases and phosphatases modify proteins in my gene list?

These and many other questions you can answer with Pathway Studio, starting with either raw gene expression data, or a list of significant genes.



*Pathway Studio helps you to easily find common regulators for your most differentially expressed genes.*

## WITH PATHWAY STUDIO YOU CAN:

- Find pathways and gene ontology groups affected in an experiment
- Overlay expression data on canonical pathways and visualize the effects
- Identify significant genes from a network relevance prospective
- Build new pathways/regulation networks using molecular and functional relationship information extracted from publicly available literature

Pathway Studio has convenient data import tools and algorithms that allow you to identify pathways and biological processes affected in the experiment. With Pathway Studio you can build pathways and regulation networks, and identify mechanisms responsible for your observed phenotypic change.

## DATA IMPORTER

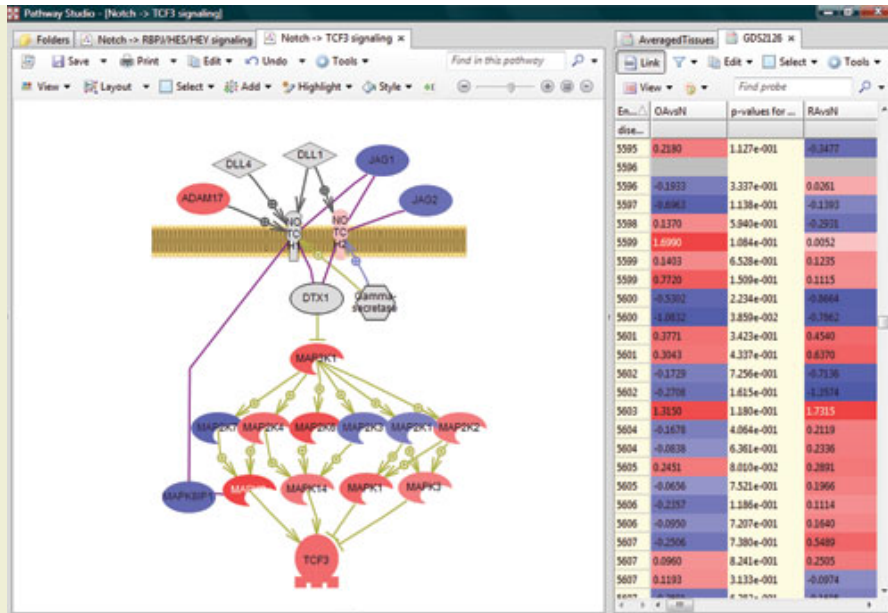
- Pathway Studio can import data from Affymetrix, Illumina, and other major gene expression platforms, as well as text and Excel, GEO, .cdf files.
- Sample Correlation Viewer helps to group samples and identify potential outliers at the stage of data import.

## RESULTS AND DISPLAYS

- Lists of affected pathways or significant genes, with numerical measure of confidence and score
- Ready-for-publication pathway diagrams; automatic layouts help to arrange upstream and downstream events, or display entities according to their cellular localization
- Multiple Expression viewer displays multiple channels of experimental data on a network diagram

## DATA ANALYSIS ALGORITHMS

- **Gene Set Enrichment Analysis (GSEA)** finds pathways affected in the experiment
- **Subnetwork Enrichment Analysis** helps to identify expression targets, binding partners, disease regulators, etc. to create pathways for the most differentially expressed genes using data from the ResNet database
- Fisher Exact Test helps to find the most relevant groups affected in the experiment
- Build Dense Expression Networks searches the ResNet database for dense expressed clusters (only available in Pathway Studio Enterprise)



Find pathways and gene ontology groups most affected in the experiment.

## MEDSCAN: INFORMATION HARVESTING

High-throughput data generation methodologies like microarray gene expression require new approaches for gathering information for data analysis. For the best results, computational approaches used for high-throughput data analysis require that biological information from the literature be a coherent and integrated part of the analysis software itself.

Pathway Studio meets this challenge through its MedScan Technology and underlying ResNet database. All editions of Pathway Studio contain **MedScan Technology** to harvest information from the literature and to save this information in the Pathway Studio ResNet database ready for data analysis.

MedScan is more than a web search engine. Indeed, the output of a Google search can be channeled into MedScan for example. Web searches, like Google, are excellent at finding items as a result of a query. A quick look at the output list usually locates the item for which you are looking. This approach however, is not well suited for information and knowledge gathering. Also, once information is gathered, where do you put it for later computational use? MedScan meets this challenge for the area of biomedical literature and biomedical online information.

PubMed meets the needs for a central repository of biomedical literature. Researchers can go to PubMed and search for any topic and articles of interest, much like a web type of search. However, just like a web type of search, PubMed also provides a list of all the hits with a link to the articles. If a single article, or even just a few, are sought, this search approach is useful. Alternatively, MedScan will list all the articles of interest but additionally scans the text for "relationships", highlights these relationships in the articles and then lists these relationships and the biological molecules and processes involved in the relationships in separate tables. The tables of relationships can be viewed graphically in Pathway Studio and can be saved into the ResNet database for use in experimental data analysis.

## JOURNAL COVERAGE

Pathway Studio powered by MedScan therefore can be assigned to search all literature sources that you have available to you online. For example, to create and maintain the ResNet Databases, Ariadne uses Pathway Studio Enterprise with MedScan Enterprise. MedScan reads the entire PubMed and 47 full-text journals. You may have access to additional journals and also to additional internal information and sources.

While it takes Ariadne several days to build the ResNet database we provide ResNet with Pathway Studio to save you this trouble. However, as mentioned there may be additional information that you may need in your database and you may wish to make sure this information is as up-to-date as possible. MedScan provides you this functionality.

## HOW GOOD IS MEDSCAN?

The best testament to the ability of MedScan to provide coverage of all the facts in the literature with few false positives, is in the number of researchers that use the software and have published in peer review journals. We can't tell you all of our customers but we can use MedScan to search in the literature for "Ariadne" and "Pathway Studio" and older software versions, to find these publications. This list of **PUBLICATIONS** is provided.

## BENEFITS OF MEDSCAN

- Create targeted databases for specific topics, organisms, diseases etc
- Highlight proteins, chemicals, cell processes, diseases, and other terms in the text
- Get instant informational snapshots or digests of your documents
- Detect entity co-occurrences in documents or sentences
- Set up automatic data extraction pipelines for regularly updating information content

### • **PATHWAY COLLECTION**

- Pathway Studio includes 227 Receptor Signaling and 21 new Cellular Process Regulation pathways. You can edit, expand, and modify these pathways using Pathway Studio's pathway building functionality.
- These pathways are also useful for interpretation of your microarray and other experimental data. A sample of these pathways is presented here. All pathways contain additional information which can be accessed by clicking on the entities or the relationships.

[Actin Cytoskeleton Regulation](#)

[Activin Receptor -> SMAD Signaling](#)

[Apoptosis Regulation Pathway](#)

[Axon Guidance](#)

[B-cell receptor -> NFATC signaling](#)

[B-cell receptor -> NF-kB signaling](#)

Dopamine receptor -> NF-kB signaling

Dopamine receptor signaling via MAPK cascade

EGF receptor signaling in myogenesis

Gap Junction Regulation

Growth factors signaling via MAPK cascade

Hedgehog Signaling

IGF receptor signaling via MAPK cascade

IL-1 -> NF-kB signaling

IL-6 signaling via MAPK cascade

IL-6 -> STAT signaling

IL-7 -> Akt signaling

Insulin -> Akt signaling I

Insulin -> STAT signaling I

Insulin -> STAT signaling II

Insulin Signaling Pathway

Integrin -> beta-catenin signaling

Interferon gamma signaling

Macrophage receptor signaling

NK Cell Activation

Notch -> HES/HEY signaling

Notch Pathway

Prostaglandin receptor signaling

Protein tyrosine phosphatase receptor signaling

Serotonin receptor 1 signaling

Serotonin receptor 2 signaling

Somatostatin receptor signaling

T-cell receptor -> NF-kB signaling

TGF-beta -> SMAD signaling

TGF-beta signaling in myogenesis

TNF receptor (Death receptor) -> NF-kB signaling

TNF receptor (Death receptor) signaling via MAPK cascade

Toll-like receptor -> AP-1 signaling

Toll-like receptor -> NF-kB signaling

WNT -> beta-catenin signaling

WNT signaling via MAPK cascade