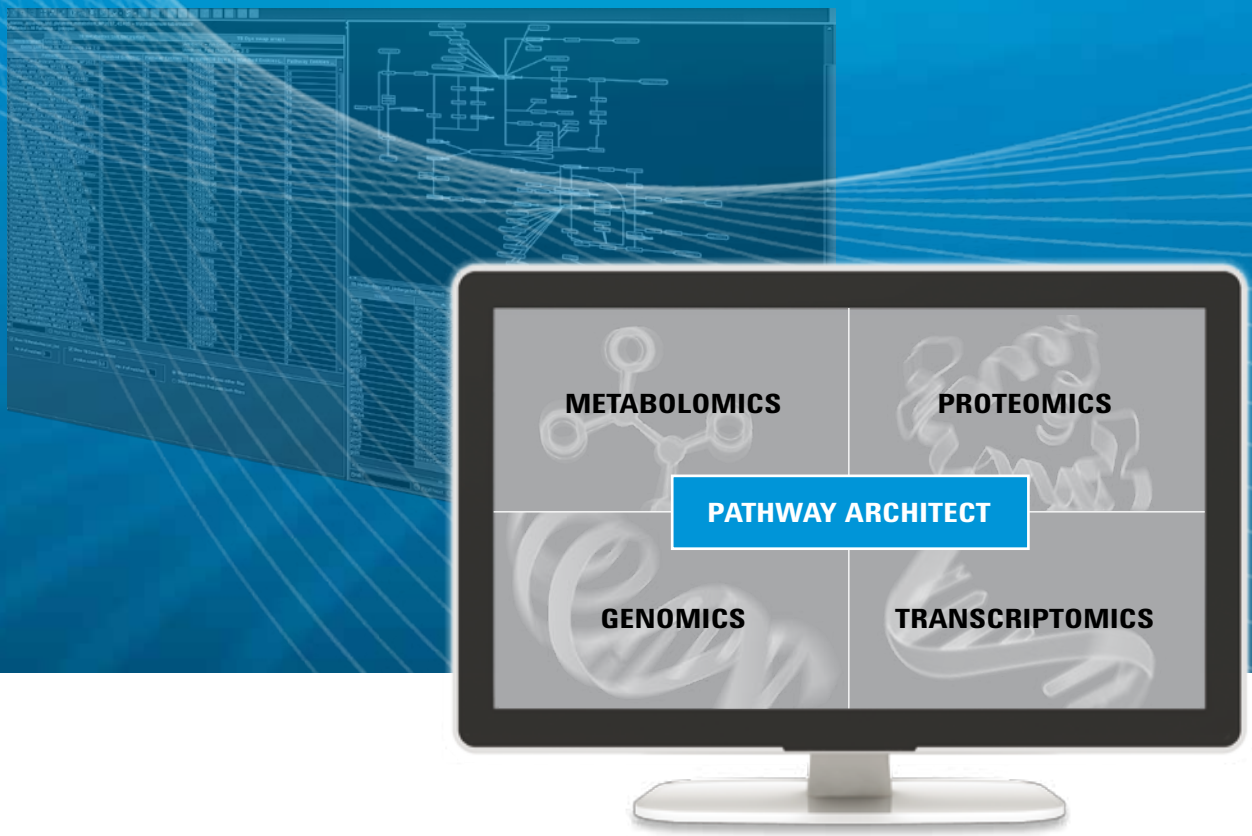
Agilent Pathway Architect

FROM DISCOVERY TO INSIGHT

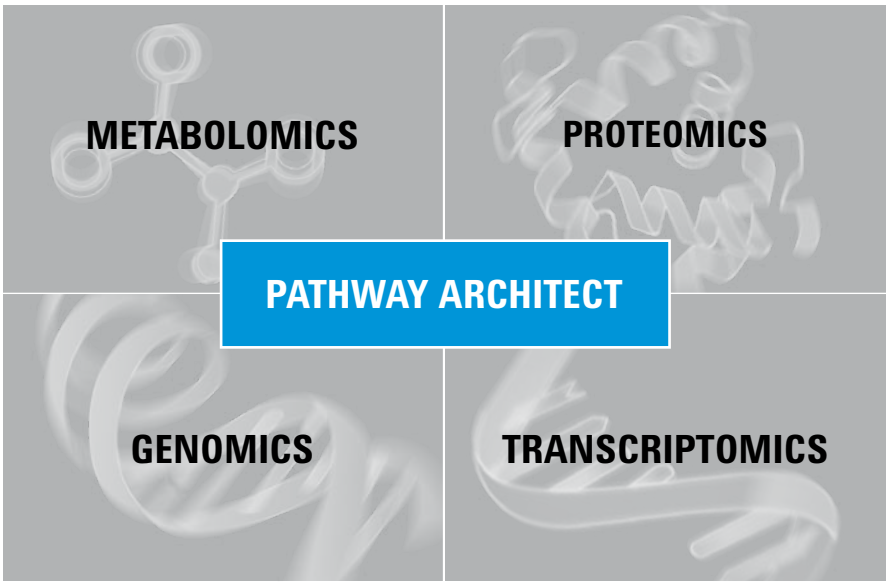
The Measure of Confidence



Agilent Technologies

SPEED DISCOVERY TO UNDERSTANDING

Today's scientists face a serious challenge as they try to analyze increasingly larger and more complex sets of data, such as those generated by genomics, transcriptomics, proteomics, and metabolomics experiments. An integrated pathway approach for analyzing data can significantly alleviate bottlenecks and fulfill the ultimate purpose of biological research—understanding the biology behind the measurements. One successful method for translating diverse analytical data into biological understanding can be achieved by projecting and visualizing processed data onto the biological pathways accumulated over the last century and a half of research.

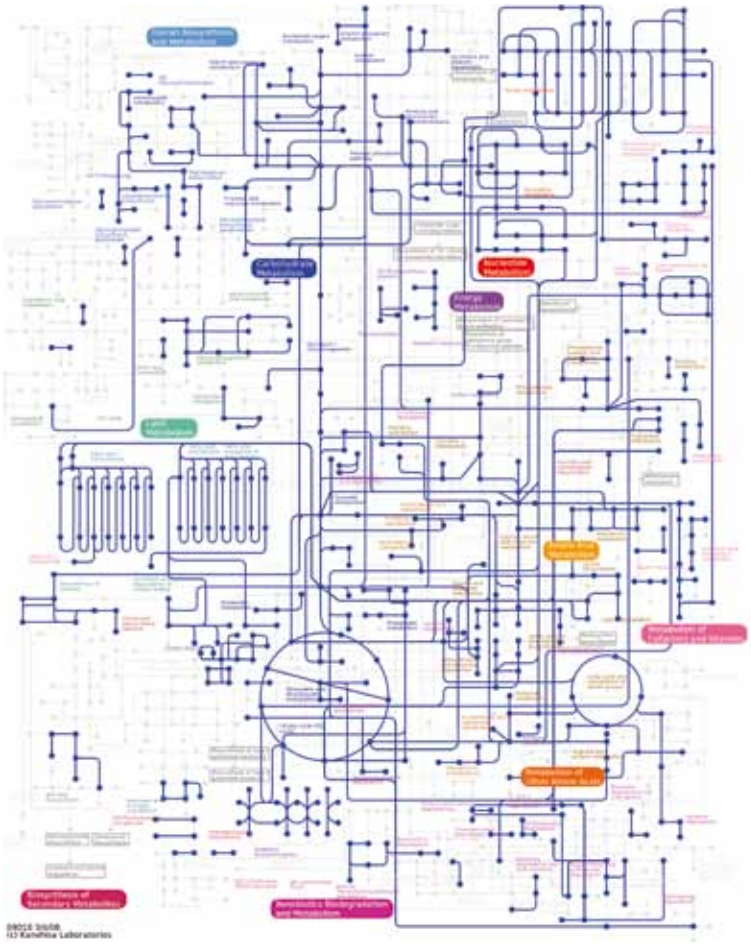


The ability to analyze data using a pathway-centric view allows scientist to:

- Link compounds and omics results to their biological significance
- Focus research goals with direct linkage to biological relevance
- Integrate multi-omics results for holistic overviews
- Generate hypotheses and guide future experiments

Gain Deeper Insight

Agilent Pathway Architect is an optional module for GeneSpring and Mass Profiler Professional (MPP) that was developed to offer scientists a seamless platform for gaining deeper insights into their data. It allows users to take the results from single or multi-omics experiments and map them onto canonical biological pathways, concurrently analyzing, visualizing, and interpreting pathway information. This pathway-centric workflow speeds the route from discovery and insight to validation. It also enables researchers to efficiently plan and execute their next series of experiments.



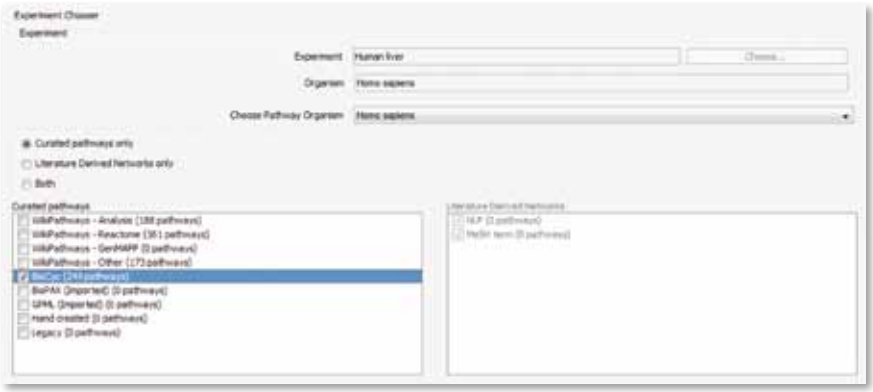
Graphical representation of central carbon metabolism in pathway form. *(Courtesy of KEGG)*

VISUALIZE YOUR RESULTS

Pathway Architect is a visualization tool that uses publicly available pathway databases to facilitate the understanding of biological results. The software maps metabolites, proteins, and genes onto curated pathways, graphically projecting data onto pathway nodes or edges for interactive user analysis. Researchers can specify search criteria for particular organisms and browse a table of pathway results before projecting data onto a particular pathway.

Pathway Databases Supported

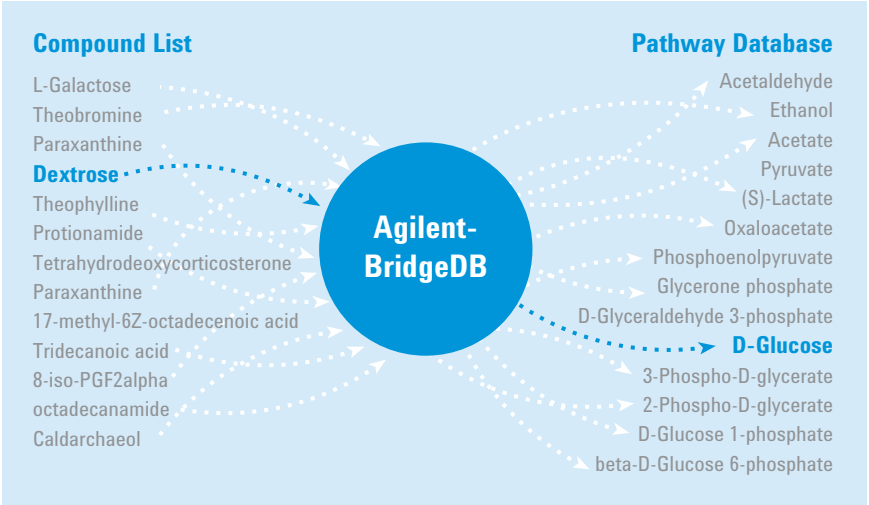
- WikiPathways
- BioCyc
- PathVisio custom pathways
- GPML format
- BioPAX format



Choose among the curated pathways available within Pathway Architect.

Resolve Mismatches

Pathway Architect makes it easy to resolve nomenclature inconsistencies by providing a powerful built-in tool, Agilent-BridgeDB. This resource automatically links an annotated metabolite, protein, or gene identifier in the experiment to the corresponding identifier used by the pathway database. Pathway Architect uses only identifiers instead of common names to minimize errors. Agilent-BridgeDB has been optimized for BioCyc and WikiPathways databases.

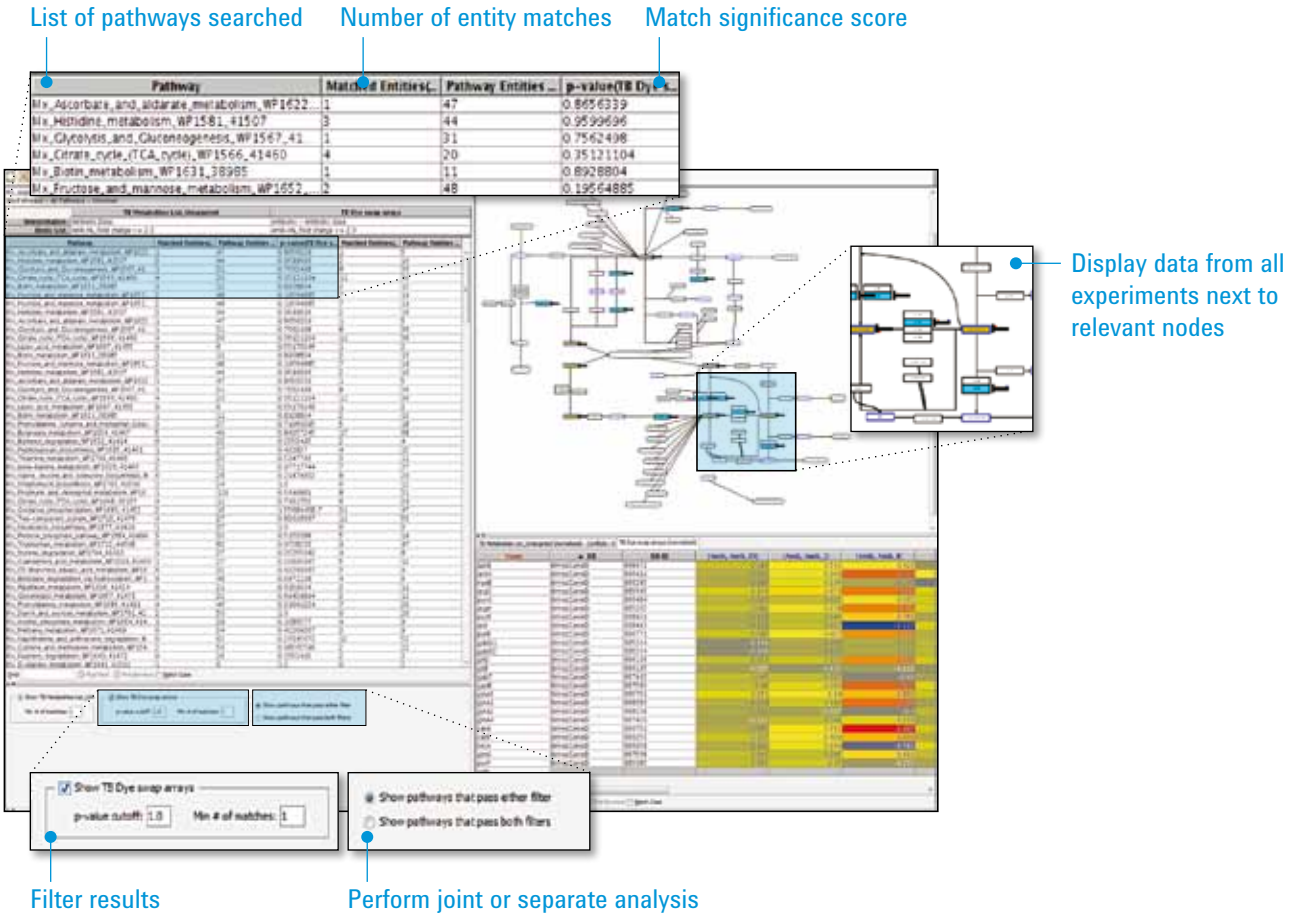


Agilent-BridgeDB automatically links annotated metabolites, proteins, and gene identifiers used in the experiment to those in the pathway database.

Simplified Pathway Analysis

Once the software is ready to perform pathway analysis, users can execute a single or multi-omic analysis in three simple steps:

1. Choose the data and interpretation
2. Select the pathway database
3. Define the species and analyze



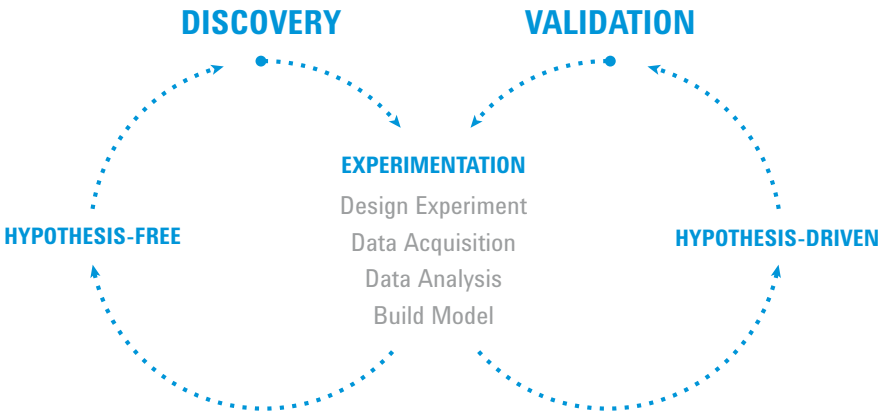
Pathway Architect provides an interactive, user-friendly graphical display.

PATHWAYS TO INFORM YOUR EXPERIMENTS

The addition of the Pathway Architect module to GeneSpring and MPP facilitates the move from hypothesis-free to pathway-driven studies. This approach has been demonstrated for both single omic and multi-omic experiments. The results of primary data analysis from one or multiple omic-level experiments can be analyzed by Pathway Architect to easily and robustly identify pathways that are involved in different biological phenomena. The results of such pathway analysis can be used to quickly direct and design the next experiment using an exported list of metabolites, proteins, or genes from a selected significant pathway.

Accelerate Future Experiments

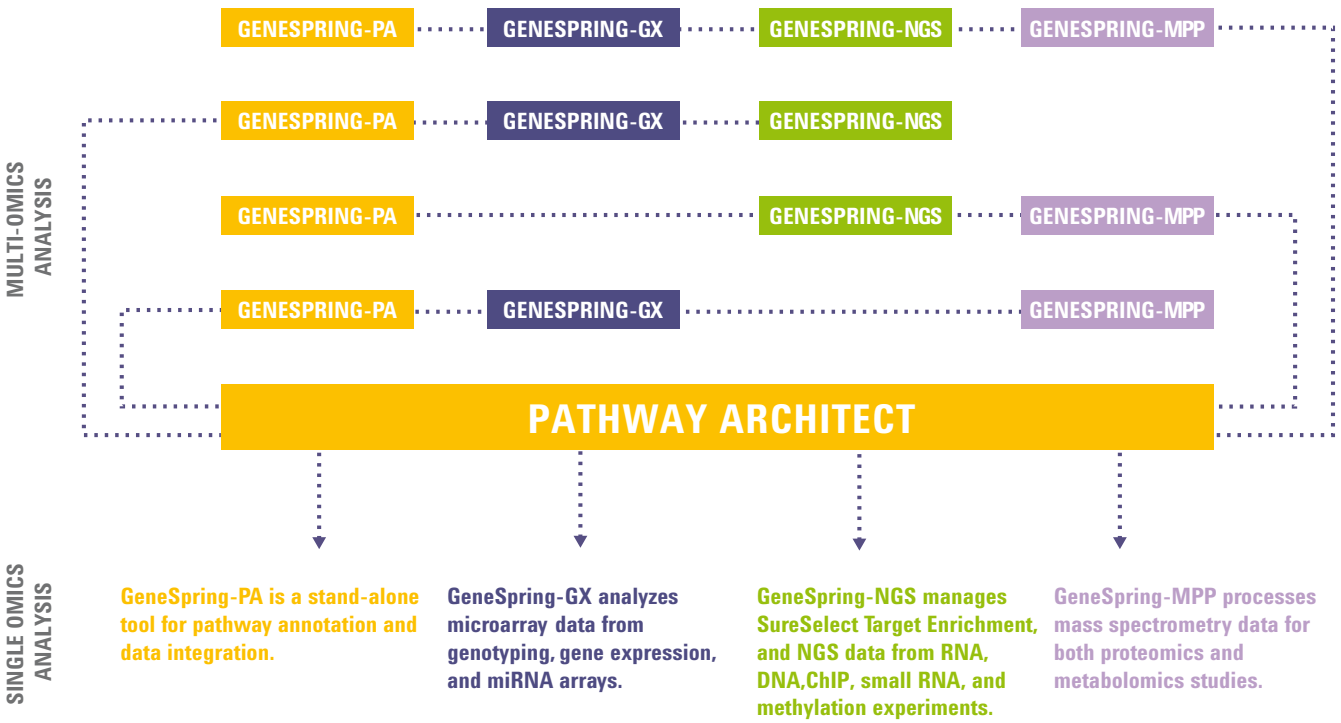
A list exported from Pathway Architect can be brought into other Agilent software to enable your next experiment. For example, a list of protein accession numbers can be imported into Agilent's Spectrum Mill software and a triple quadrupole MRM experiment can be designed and loaded into Agilent's MassHunter Acquisition software to run the experiment. The same concept applies to genes, where a list of genes can be transferred to Agilent's eArray website to build a custom microarray. These useful software linkages accelerate the planning and execution of the next set of experiments.



Agilent supports and integrates single and multi-omic experiments, simplifying the cyclical journey from hypothesis-free discovery to pathway-driven validation.

Integrate Multi-Omics

Agilent's Integrated Biology software suite, which includes GeneSpring, Mass Profiler Professional, and Pathway Architect, simplifies the joint analysis of multi-omic data. These software modules jointly process the data from genomics, transcriptomics, proteomics, and metabolomics studies and efficiently map entities onto their corresponding pathways. Intuitively explore, verify, and quickly find the biological pathways that are over-represented in the multi-omics data you are generating. Gain more insight by integrating your pre-existing knowledge of biological pathways with multi-omics data, speeding the process from discovery to validation.



Learn more
www.agilent.com/chem/metabolomics

Find a local Agilent customer center
www.agilent.com/chem/contactus

USA and Canada
1-800-227-9770
agilent_inquiries@agilent.com

Europe
info_agilent@agilent.com

Asia Pacific
inquiry_lsca@agilent.com

This information is subject to change without notice.

© Agilent Technologies, Inc., 2012
Printed in the USA, November 16, 2012
5991-1459EN

Agilent Technologies