Future Directions
Agilent: A Focused Measurement Company
Serving Diverse End Markets

Electronic Measurement
2008 Revenue: $3.6 Billion

- General Purpose: 37%
- Communications: 25%
- Other General Industry
  - Computers & Semiconductors
  - Aerospace & Defense
  - Wireless Mfg.
  - Other Comms
  - Wireless R&D
  - Broadband R&D/Mfg

Bio-Analytical Measurement
2008 Revenue: $2.2 Billion

- Chemical Analysis: 20%
- Life Sciences: 18%
- Other General Industry
  - Environmental
  - Forensics
  - Food
  - Petrochemical
  - Academic & Government
  - Pharma & Biotech

June 4, 2010
Agilent Genomics Portfolio

DNA

- aCGH/CNV: Study chromosomal aberrations and measure gene copy number.
- CH₃: Methylation patterns across and study effects on transcription.
- ChIP: Measure protein/DNA interactions and to better characterize transcription, replication and repair.
- Target Enrich Sys.: Enrich for genomic regions or transcripts for high throughput DNA sequencing.
- Splice Variants: Identify the splice forms of specific genes and study their effect on protein translation.
- GE: Make high sensitivity measurements of gene transcription and correlate results with other genomic data.
- miRNA: Identify the presence of microRNAs and measure the effect of knockouts and correlate this activity with gene transcription.

RNA

- Targeted sample prep: Enrich for genomic regions or transcripts for high throughput DNA sequencing.
Agilent Bioinformatics Software
A comprehensive suite of applications

Transcriptome
*GeneSpring*
miRNA, qPCR, Exon, Copy#, LOH, GWAS

RNA

Protein

DNA

CH$_2$OH

Genome
*AGW*
ChIP, Methyl, CGH

Proteome
*Mass Profiler Pro*

Metabolome
*Mass Profiler Pro*
GeneSpring: Data Analysis Solution for Omics Research
GeneSpring Value

- GeneSpring provides powerful, accessible statistical tools for fast visualization and analysis of expression and genomic structural variation data.

- Designed specifically for the needs of biologists, GeneSpring offers an interactive desktop and enterprise computing environments that promotes investigation and enables understanding of microarray data within a biological context.

- Developed on avadis™ from Strand Life Sciences, GeneSpring is part of Agilent’s life sciences informatics portfolio for systems-level research.
GeneSpring in Genomics Research
A Standard in Biological Interpretation

GeneSpring has **7,800 references** in Google Scholar and over **1,600** in peer reviewed publication.

GeneSpring has **10 years of history** in RNA-based applications:
- mRNA expression analysis
- miRNA analysis with TargetScan gene target identification
- Exon splicing analysis

GeneSpring is an **open-platform** application:
- Support Agilent, Affymetrix, Illumina and other vendors
- Supports custom format import
- Supports custom scripting using Jython and the R-Project for Statistical Computing (including Bioconductor)

Source: Google Scholar:
GeneSpring GX
Platform Strengths

Powerful Statistical Tools and Sophisticated Data Visualizations

Biological Contextualization (pathway module)

Strategic Partners Include:

INGENIUTY®
SYSTEMS

GeneGo. Your GPS in pathway analysis

Agilent Technologies
GeneSpring Workgroup: Scalable Enterprise Solution
GeneSpring 11 represents a significant advance in data analysis software for life sciences. Here we see for the first time an all-wheel driving machine for multi-omics technologies that shape a new roadmap for integrative systems biology.”

Customer quote:
Bruce Aronow
Director of the Center for Computational Medicine
Cincinnati Children’s Hospital
GeneSpring Platform Transformation
Modular System for Integrated Biology

Integration Module
Pathway Module
Cytoscape

GeneSpring Platform
(Common Code Base, Common Middle Tier, Visualizations, APIs, Installer)

Enterprise (Workgroup) Server: Computation, Data Management, Collaboration


mRNA  miRNA  qPCR  CGH  CNV  SNP  GWAS  MPP  CH3  ChIP  NGS
Multi-omic Analysis
Cytoscape is an open source software platform for integrating, analyzing, and visualizing measurement data in their biological context.

- 80000+ downloads for 2.x release; 25,000 downloads in 2007 alone; 3500/month
- Currently 100 registered plugins, developed by leading research groups, freely available
- Community development of plugins strongly encouraged and actively supported by core development team.

freely available at http://www.cytoscape.org

Cytoscape is a collaboration between
University of California, San Diego
Institute for Systems Biology
Memorial Sloan-Kettering Cancer Center
Institute Pasteur
Agilent Technologies
University of Toronto
Gladstone Institute for Cardiovascular Disease
University of California, San Francisco
Unilever
National Center for Integrative Biomedical Informatics
Agilent Genomics Workbench
Enabling Genomics Applications

- **OLS**
  - Oligo Library Synthesis (OLS)
  - Gene Silencing
  - Protein Mutagenesis
  - Whole Gene Synthesis
  - Genome Partitioning

- **aCGH/CNV**
  - Copy number
  - Cancer Research
  - Cytogenetics
  - Population Studies

- **CH₃**
  - Methylation
  - Discover and monitor epigenetic changes that play a role in cellular processes

- **ChIP**
  - Transcription Factors
  - Elucidate the role that protein-DNA interaction plays in transcription, replication, and repair

- **GX**
  - Gene Expression
  - Explore gene transcription on a genome-wide basis across a variety of model systems

- **miRNA**
  - RNA interference
  - Profile microRNAs and explore the role they play in gene regulation

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**eArray**

- Sample Manager
- Workflow Manager
- Feature Extraction
- DNA Analytics

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Agilent Technologies
The Agilent Genomic Workbench (AGW) is a suite of desktop applications (client/server model) that provide Agilent customers with a single user environment to design microarrays, manage sample information, run feature extraction, perform quality and do analysis from scanned image onward.
AGW – FE 10.9

Overview

Sophisticated image analysis application that is used to generate raw intensity values from scanned microarray images

New Features

- Merged database for FE, AGW and QC Tool
- Full version FE can be launched within AGW or outside of AGW
- Merged installer for FE, AGW
- Design file “load once” to support FE (grid template), Analytics and eArrayXD.
- Automatic software version check and updates
- Migration tool to migrate previous custom protocol and metric sets
- Provide stats (like AF Hold, PMT Voltages) from Tiff Header to AGW
Superior Spot Finding and Pixel Outlier Rejection

Raw Image – All pixels

Post-Processing Image – Only pixels used in analysis are shown

All pixels

Cookie cutter

After pixel outlier rejection
AGW Core

**Sample Manager**

Enables users to easily associate meta data (patient/sample information) with individual slides. The meta data is then persisted through the analysis process.

**Workflow Manager**

Desktop utility that enables users to easily associate meta data (patient/sample information) with individual slides. The meta data is then persisted through the analysis process.

**Quality Module**

- **Array QC Tool**: Quality control reporting tool that helps customer to assess microarray quality and analyze trends: calculates QC metrics and metrics sets, applies QC thresholds, plots QC trends

- **Target Enrichment QC Tool**: Quality control reporting tool that helps customer to assess pull down quality: QC reports; metrics for library complexity
DNA Analytics

Designed to examine data generated from DNA-based experiments. Analytics is comprised of “modules” that contain analysis packages for specific biological applications (i.e. CGH, ChIP, Methylation)
ChIP
Transcription Factors
Elucidate the role that protein-DNA interaction plays in transcription, replication, and repair

CH$_3$
Methylation
Discover and monitor epigenetic changes that play a role in cellular processes

Copy number
\begin{itemize}
  \item Cancer Research
  \item Cytogenetics
  \item Population Studies
\end{itemize}

AGW – DNA Analytics
Analysis of Agilent Arrays

DNA Analytics

GeneSpring

DNA Analytics

DNA

RNA

Pro

Proteomics

Metabolomics

miRNA

Exon

GWAS

CNV
eArray.com

**eArray XD**

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**Search**

- Microarray
- Probe Group
- Simple Probe

**Create Design Wizards**

- Create a Microarray Design by Uploading Probes
- Create a Microarray Design from Existing ProbeGroup(s)
- Create a Microarray Design from Target Transcripts

**Search Results:**

<table>
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<th>Wizard Name</th>
<th>Status</th>
<th>Created Date</th>
<th>Action</th>
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<td>Enqueued</td>
<td>03-Nov-2007</td>
<td>Delete</td>
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<td>03-Nov-2007</td>
<td>Delete</td>
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</table>

**Pending Jobs**

- Search Results: 0 matching results found

**My Designs**

- Search Results: 10 matching results found

**eArray Contact Support** Site Information *Terms of Use* FAQ © Copyright Agilent Technologies, Inc. 2002-2002
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OpenLAB ELN for Genomics

Create

Analyze

Share

Helping customers:

- Increase data trace-ability
- Decrease time to find results
- Protect intellectual property
GeneSpring
Support for Multiple Platforms

**MICROARRAY (mRNA and miRNA)**
- Agilent, Affymetrix, Illumina,
- .GPR files; **Any custom format**

**qPCR**
- ABI + Stratagene, Roche, BioRad, etc

**SNP Arrays (Copy #, LOH, GWAS)**
- Affymetrix and Illumina

**MASS SPEC**
- *‘Mass Profiler Professional’* application
- Agilent + Waters, Thermo, ABI, etc
The Agilent LCMS & GCMS Workflow

- Separate detect
- Peak find quantitate
- Statistics
- Identify
- Pathways

**GCMS**
- GC/MSD
- GC-QQQ

**LCMS**
- LC-TOF/QTOF
- LC-QQQ

**Software**
- AMDIS
- Mass Profiler Professional
- MassHunter Qual
- MFE
- ID Browser
Multi-omics Analysis in GeneSpring 11.5 (Summer 2010)
Data Analysis Workflow in GeneSpring & MPP

1. Start with raw data
2. Load data into GX or MPP
3. Use powerful but easy-to-use statistics to filter the list
4. Find biological relevance of your entities

Transcription factor over-expressed!