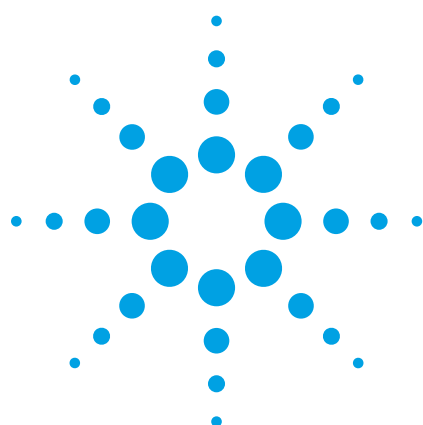




INFORMATICS GENOMICS PROTEOMICS METABOLOMICS

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Agilent CGH Analytics Software

Empowering Genomic Aberration Detection

Array Comparative Genomic Hybridization (aCGH) characterizes the genomic changes that result in developmental abnormalities, disease susceptibility, and differential drug responses. The technology enables the identification of biomarkers indicative of these genomic changes. Agilent's CGH Analytics software efficiently locates disease-implicated regions of genomic amplification or deletion from massive quantities of aCGH data. Using industry-proven statistical algorithms, CGH Analytics identifies genome-wide aberration patterns from multiple aCGH profiles. These aberration patterns can be viewed in detail and compared, using a choice of display types. The software enables oncology, neurology and cytogenetics researchers to quickly determine copy-number based biomarkers and genomic abnormalities involved in disease processes.

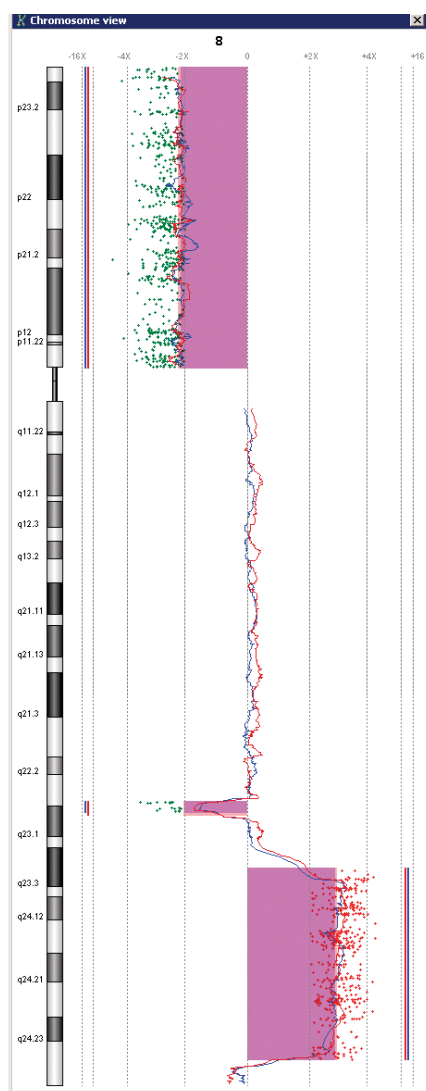


Figure 1. Intuitive visualizations quickly highlight interesting regions

At a Glance

- **Instant access to biologically relevant data** – Rapidly elucidate global patterns of interesting genomic aberrations at varying levels of detail in single or multiple microarray profiles simultaneously (Figure 1).
- **Combined CGH and expression data analysis** – Identify genes with differential expression levels that are potentially influenced by copy number changes.
- **Versatile data import** – Import data from any array platform including high-density arrays or merged arrays.
- **Flexibility and confidence** – Detect significant aberrant regions with a choice of innovative algorithms for aberration calling. Reduce false positives with Agilent's proprietary error modeling.
- **Stringent data quality control** – Select, analyze and view only the most interesting aberrations and relevant data based on user-defined quality filtering criteria.



Agilent Technologies

Visualize Aberrant Regions in Single or Multiple Samples

Visualization tools can be used to reveal amplifications and deletions that are common to all samples (Figure 2) or to specific samples. Aberrations are displayed in a heatmap-like view relative to their cytogenetic positions. The software can report detected aberrations with probe-based or interval-based aberration scores. A list of genes associated with regions containing aberrations can be saved for further analysis.

Leverage CGH and Gene Expression Data

Explore the interaction between gene copy numbers and gene expression levels. The joint analysis tool compares CGH aberration calls with gene expression values to quickly correlate

aberrant regions with regions showing significant expression change. The results are summarized in a single display showing aberrations, gene expression heat map and a plot of statistical relevance (Figure 3).

Check the Quality of Your Data

Use a color-coded table or graph view of QC metrics (Figure 4) to assess the relative data quality of individual Agilent aCGH microarrays in an experiment. Statistics on nine QC metrics and special spike-in control probes facilitate the detection of problematic data resulting from potential sample or processing issues.

Use Multiple Data Views

CGH Analytics provides multiple views of the data (Figure 5) including a data and experiment browser; three levels

of zoom-in including genome, chromosome, and gene views; and a tabbed view of feature by feature probe data and annotations. A toolbar displays the major settings currently in use for the analysis. Features include:

- Co-visualization of both CGH and expression data
- Tabular and graphical views
- Dockable, hideable panes



Figure 4. QC Metrics Plot

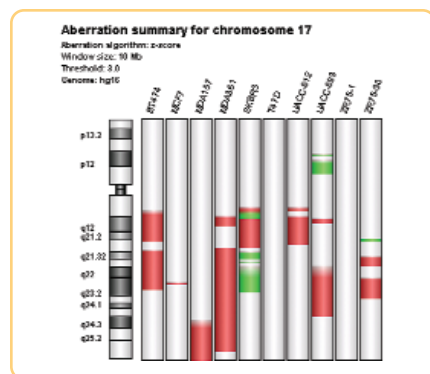


Figure 2. Aberration Summary Report



Figure 3. Joint Gene Expression and CGH Analysis

Advantages

Accuracy

Multiple features enhance the accuracy of your data. Filters remove unreliable data leaving only what's relevant, so that you have more confidence in the results. Unique noise detection and error-weighted replicate combining improves confidence in aberration calls. Additionally, the flexibility to work with data in multiple microarray design formats enables data to be pooled from broader sources, significantly improving accuracy and confidence. These sources can include specialized microarrays that target specific aberrant regions as well as data from gene expression microarrays.

Accuracy-enhancing features

- Filter aberrations – Built-in filtering mechanisms enable you to design,

name, save and apply selection criteria for features, microarrays, and aberrations that will be analyzed.

- Penetrance plot (Figure 6) – The penetrance plot visually summarizes the percentage that a given aberration is present in selected samples.

Speed

Don't wait all day for your data. CGH Analytics employs fast, high-performance statistical calculations based on hypergeometric Z-scores or alternative aberration detection algorithms for a quick turnaround, so you can plan your next set of experiments sooner.

Flexibility

Researchers, not software, should dictate which kinds of experiments to run. Flexible CGH Analytics software imports and analyzes both Agilent and

non-Agilent files, so you are not locked into one design. Analyze catalog and custom gene expression data as well as aCGH data, using multiple aberration detection methods, or the flexible plug-in architecture. Through flexibility, your data analysis is more powerful because you can identify genes that change in both expression and copy number, more precisely locate aberration breakpoints, and detect smaller aberrations.

Portability

Results from analysis or visualization tools are readily available for other uses. Results can be organized into gene lists to enable further analysis and saved and linked to the web for future information mining. Images can also be easily exported for publication.

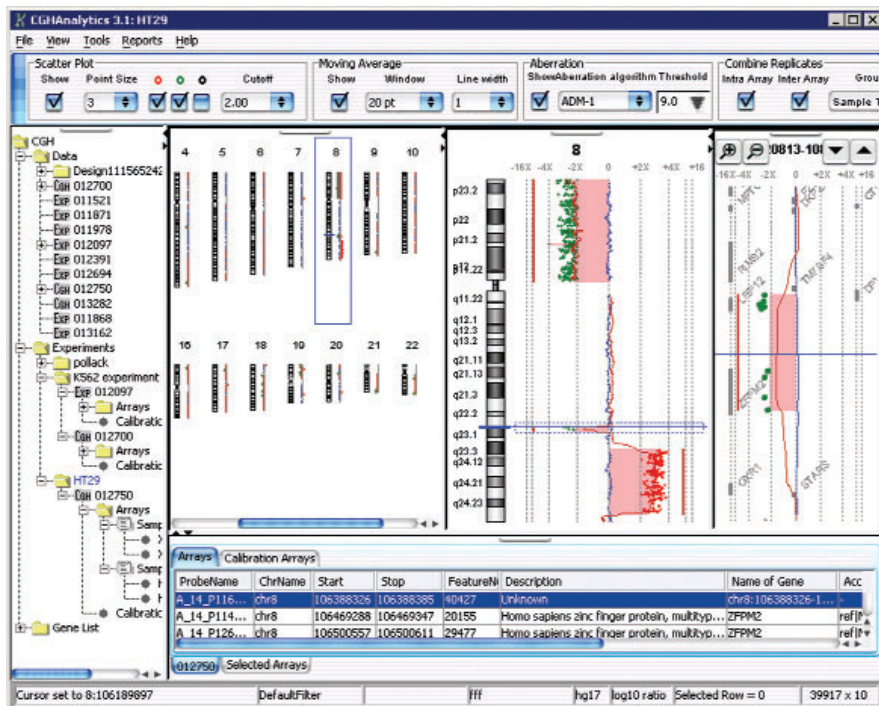


Figure 5. CGH Analytics Software provides an intuitive environment for aCGH visualization and analysis

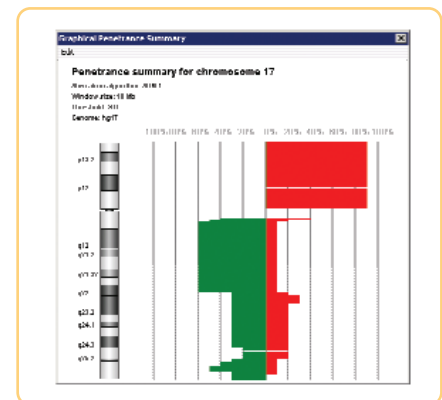


Figure 6. The Aberration Penetrance Report quickly highlights regions with aberrations in multiple samples

Store and Handle Data in One Dedicated Location

Don't lose valuable time searching for data files stored all over your server. CGH Analytics conveniently categorizes and stores data according to design format in one central location, and facilitates the analysis of microarray subsets which are grouped by experiment. Find what you are looking for fast with easy handling and recall.

Robustness

Agilent provides a commercial solution to your aCGH analysis needs. The software's robustness is confirmed through extensive testing to validate the performance, reliability and accuracy of the results. CGH Analytics has an integrated online help system to provide additional information on operating the software efficiently. Purchase of the software includes access to a world-wide Agilent support organization, with email and phone access to regional support specialists that know the software and aCGH application, and are ready to assist you with your research questions.

Specifications

Windows XP/2000 with Pentium IV or faster

or

Mac OS X version 10.4.x with JVM 1.5.0

or

Redhat Linux version 9

2 GB RAM

1024 x 768 display

4 GB of free disk space

Dual CPU (recommended)

About Agilent's Integrated Biology Solutions

Agilent Technologies is a leading supplier of life science research systems that enable scientists to understand complex biological processes, determine disease mechanisms, and speed drug discovery. Engineered for sensitivity, reproducibility, and workflow productivity, Agilent's integrated biology solutions include instrumentation, microfluidics, software, microarrays, consumables, and services for genomics, proteomics, and metabolomics applications.

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Printed in the U.S.A. July 28, 2006

5989-4006EN

