

Bioinformatics

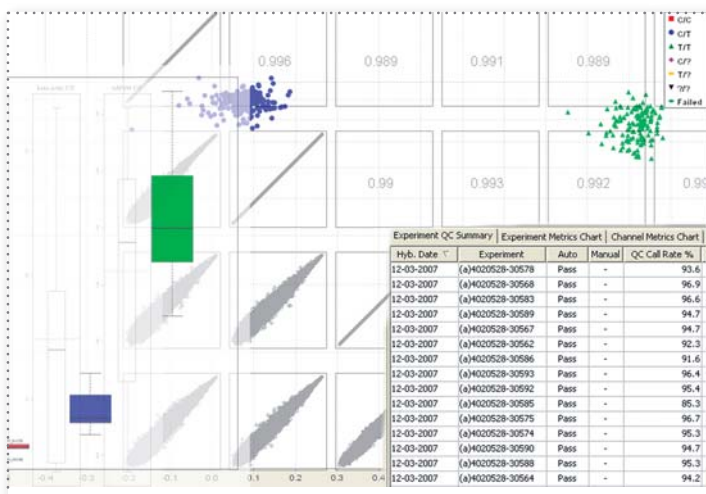
In the last few decades, advances in molecular biology and the equipment available in the field have resulted in increasingly rapid generation of a wide variety of data. Nowadays, whole gene expression profiles or hundreds of thousands of single nucleotide polymorphisms (SNPs) can be obtained within a few days. In-depth analysis and interpretation of such datasets can only be obtained by using high level computational and statistical techniques.

DNA Vision is a multidisciplinary research team composed of molecular biologists, bioinformatics experts and other computer scientists who, using state-of-the-art techniques, both analyze your data and develop new algorithms.

Quality control

For both SNPs and expression data, the first step in effective data analysis is to check the quality of the data with reference to international guidelines (ISO17025, MAQC).

Statistical and exploratory data analysis for quality control.



Expression profiles

An effective expression profile analysis requires a set of different statistical and bioinformatical approaches.



Statistical analysis includes

- ▶ Supervised and unsupervised cluster analysis
- ▶ Parametric (t-test, ANOVA) and non-parametric tests
- ▶ Correction for multiple factors (FDR)
- ▶ Principal component analysis (PCA)
- ▶ Class prediction (k-nearest, SVM, median/centroid)
- ▶ Delta delta Ct

One of the most important parts of the analysis is the biological interpretation of data. You can rely on the combined expertise of our multidisciplinary team to perform

- ▶ Gene ontology (GO) analyses
- ▶ Pathway inference
- ▶ GEO profile concordance
- ▶ OMIM links
- ▶ Cross literature analyses

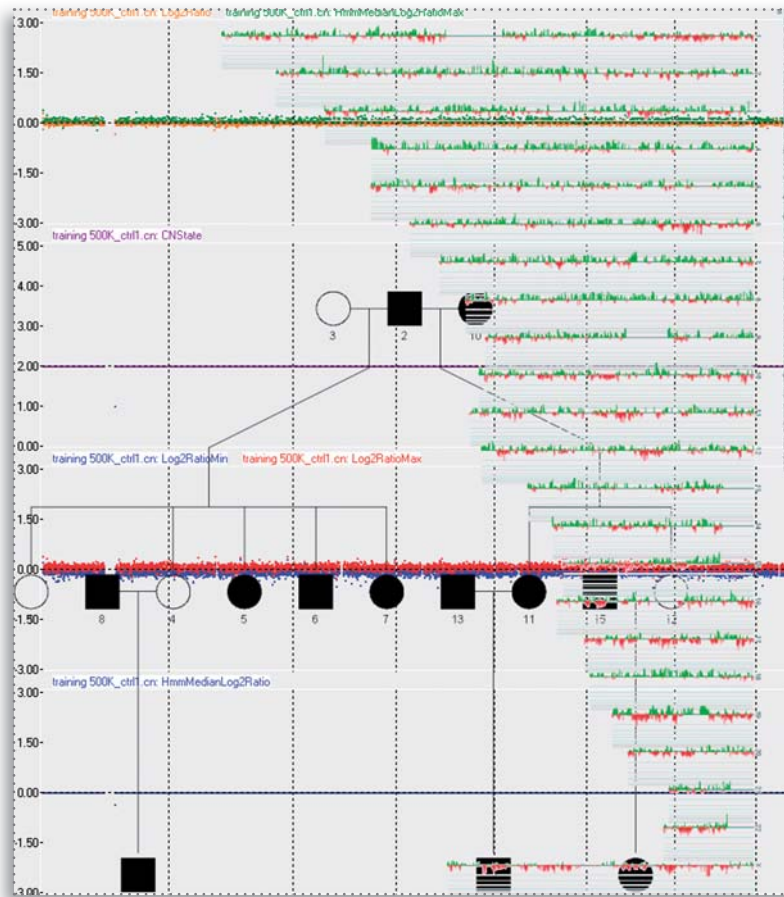
Single nucleotide polymorphism

SNPs are the most common type of genetic variation and are most frequently used in pharmacogenetics to determine disease susceptibility by measuring the efficacy of drug therapies based on the patient's genetic background.

Using SNP genotyping, we perform

- ▶ In silico haplotyping
- ▶ Comparative genomic hybridization (CGH) to analyze copy number variations (gains /losses) across the genome
- ▶ Loss of heterozygosity (LOH) to estimate the loss of one parent's contribution to the genome
- ▶ Pedigree analysis to identify common homozygote regions in recessive homozygote patients
- ▶ Associative studies in families
- ▶ Other studies on request

Plots of associative studies and copy number variations.



Final report

The final report includes QC metrics, description of analyses done, discussion of results and general conclusions. The results (lists of differentially expressed genes, clusters, heat maps, normalized expression intensities) are attached as individual files in personalized user-friendly formats. All raw data files are available on CD/DVD-ROM and/or are directly and securely downloadable from our website.