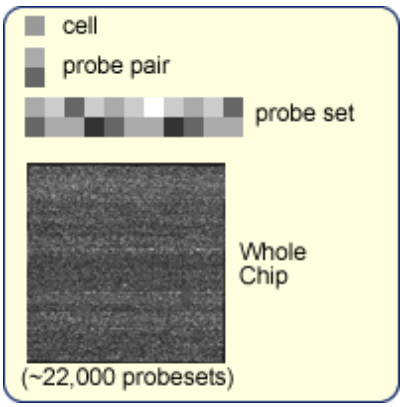
Genstat Knowledge Base 2024

Introduction to Affymetrix microarrays

The microarray menus provide facilities for the design and analysis of microarray experiments. Microarray experiments are used in genetics to screen RNA samples against libraries of DNA/RNA samples/fragments.

Affymetrix/One Channel Microarrays

Affymetrix produce chips which have just a single target added to each chip. A single level of intensity is read from each spot or cell on the chip. Each gene is presented on the chip by multiple short sections of DNA (**probes**) which match the gene at various locations. The set of sections is known as a **probe set**. For each matching section of DNA (the **perfect match** (PM)), as a control, a corresponding section of DNA with a single base change near the middle of the sequence is also put on the chip (the **mismatch** (MM)). The pairs of PM/MM spots are then summarized over to obtain an average reading for the presence of each gene. The images below show an Affymetrix chip and its components.



Further help can be found on the Affymetrix GeneChips help page or by visiting the Affymetrix web site at http://www.affymetrix.com.

Affymetrix chips can be very large (for example they can have about 500,000 spots on them), so analysing a series of Affymetrix chips can be time consuming, and can require a large amount of RAM when the CEL files are processed within Genstat. As an alternative, Affymetrix supplied soft-

ware can be used to summarize over the PM/MM pairs and store the results in summary files (CHP files), which can then be read into Genstat.

A CEL file provides data for each physical location, or cell, (defined by row and column coordinates) and intensity. In addition it contains the name of the CDF file needed for the location-probe-set mapping. The CDF files store the probe set related to each location on the array. The computation of summary expression values from the probe intensities requires a mapping/merging of the probes set (CDF) data to the location (CEL) data. When opening a series of CEL files in Genstat the corresponding CDF file name needs to be specified. CDF files can be downloaded from the Affymetrix web site at https://www.affymetrix.com

See the Affymetrix microarray example to view how the menus can be used to analyse an Affymetrix microarray experiment.

Menu Items

The microarray menu has been designed so that you can progress easily through each step of an analysis. For example, the first section is for designing an experiment. This is followed by a section for importing data and then calculating expression values. Further sections are available for exploring the data and then normalizing. The data is explored and then normalized. The **Analyse** section can then be used to perform a robust means analysis or single channel analysis of variance. The final two sections can be used to graphically visualize the results and to cluster probes and targets to look at groups or for structure in the experiment.

Only the menus appropriate for Affymetrix/single colour microarrays are listed below. The excluded menus are used for analyzing two colour microarrays.

Design

- Generate One Channel Design

Data

- Open Microarray Data Files

Calculate

- Affymetrix Expression Values

Explore

- Histograms
- Density Plot
- 2D Plots
- Spatial Plot

Normalize

- One Channel

Analyse

- One Channel ANOVA
- Robust Means Analysis

Display

- Volcano Plot
- Q-Q plot

Cluster

- Probes/Genes
- Targets/Slides
- Two-way

Updated on April 29, 2019