

Seminar III: R/Bioconductor

The geneplotter package from Bioconductor

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Abstract

A brief description of the `geneplotter` package from Bioconductor.

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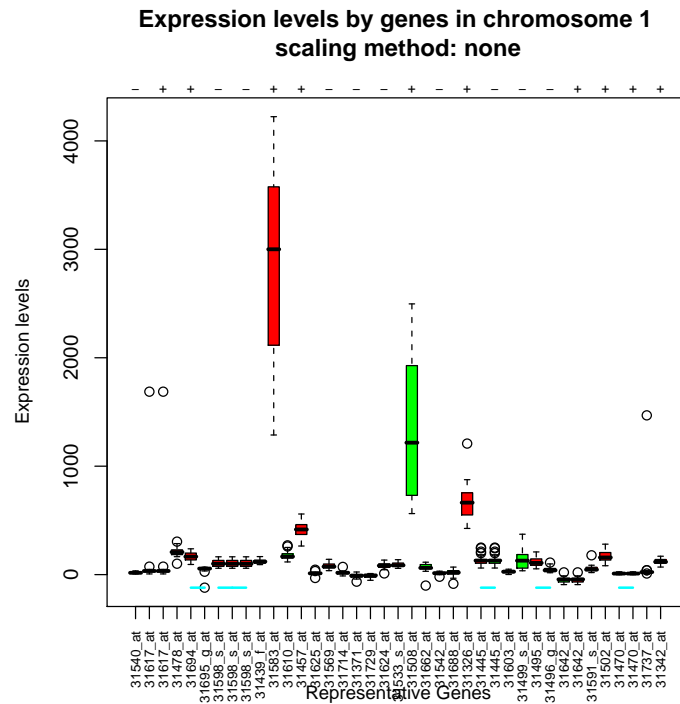
1 What the geneplotter package is?

It is a very useful graphics related package which contains some basic functions for plotting genetic data.

2 What can geneplotter do?

This package contains a variety of functions that allow you to visualize genetic information in a graphic way, here I show you some of them and what you can create using them.

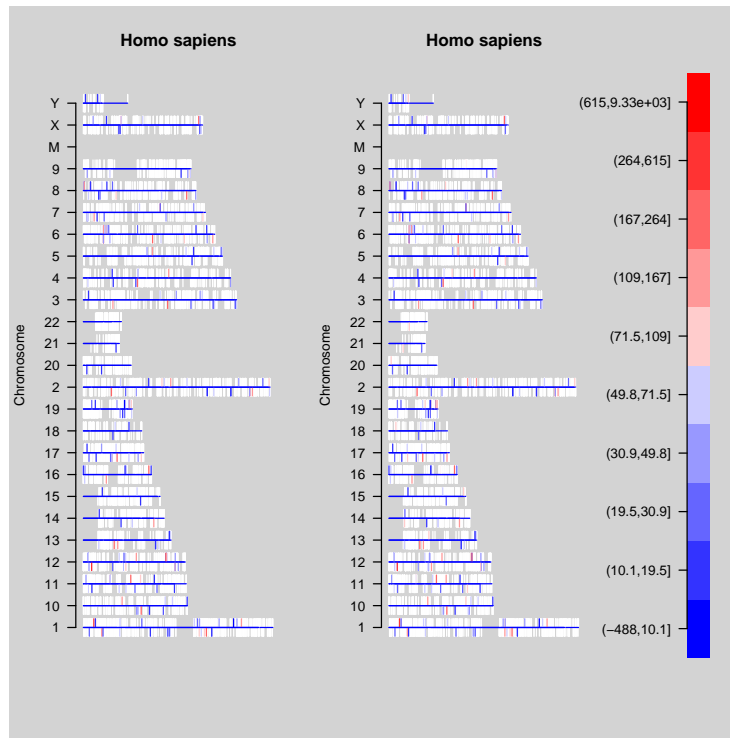
- The `alongChrom` function: Given a particular `ExpressionSet` object, a `chromLocation` object, and a chromosome name, will plot selected `ExpressionSet` data using various methods. Here a little example:



This figure was done using the function `alongChrom`. It shows the expression levels of different representative genes from chromosome 1.

- The `cPlot` and `cColor` functions: allow you to associate microarray expression data with chromosomal location. Chromosomes are represented by straight lines parallel to the x axis, genes are represented by short perpendicular lines.

In the plot below we can compare the mean expression levels for genes in Group 1 with those in Group 2. The Group 1 values are in the lefthand plot and the Group 2 values are in the righthand plot. The original setup is done using `cPlot`. The subsequent coloring is done using `cColor`.



3 Why is it worth knowing the geneplotter package?

As you have seen, this package offers interesting functions if you want to visualize genomic data in a friendly way. For example you can analyse the expression levels of all genes from a microarray experiment using the `cPlot` function. There are other useful functions within this package, I encourage you to explore them.

Finally, the `geneplotter` package depends (end user can see the functions) on `Biobase`, `annotate` and `lattice`.

It imports (uses but does not let the user see) the `annotate`, `AnnotationDbi`, `graphics`, `grDevices`, `grid`, `methods`, `RColorBrewer`, `stats` and `utils`.

And it suggests (useful for some expanded workflows) `Rgraphviz`, `fibroE-set`, `hgu95av2.db`, `hu6800.db` and `hgu133a.db`.