Tools for high throughput SNP chip data

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Introduction

SNPchip includes methods for visualizing copy number and inferred copy number alterations from high-throughput genotyping arrays.

1 Simple Usage

```
> library(SNPchip)
> data(oligoSet)

> snpset <- oligoSet[chromosome(oligoSet) %in% as.character(1:3), 1:4]
```

Plot the first few chromosomes for samples 1-4:
The samples are plotted by row. For each sample, the copy number (vertical axis) is plotted against the physical position of the SNP in the chromosome. Here, the chromosome labels are plotted beneath the cytobands.

2 Examples

2.1 Genome-wide plots for multiple samples

A genome-wide view of copy number and genotype calls versus physical position can be made using `plot`. Here, we plot autosomes 1-22 of samples 1 - 3 in the object `oligoSet`:
Note that we suppress the cytobands in the above plot (the resolution is too poor at this level) by the argument `add.cytoband` in the function `getPar`. The default plot layout generally works well, but can be adjusted through additional arguments to par and layout.
A plot of just the p-arm in sample 2 of chromosome 1.
Note that the cytoband is automatically subsetted appropriately. Had we instead specified `use.chromosome.size=TRUE`, the x-axis limits would include the entire chromosome (and cytoband) though only the SNPs on the p-arm would be plotted.
Adding a legend for the genotypes

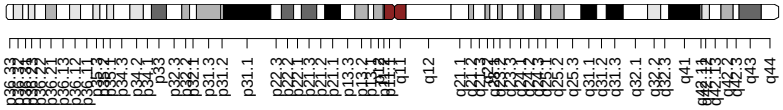
```
> data(oligoSet)
> x <- oligoSet[chromosome(oligoSet) == "1", 1]
```

2.2 Plotting cytoband

To plot the cytoband of chromosome 1,

```
> plotCytoband("1")
```

```
NULL
```



Hidden Markov models for objects of class `SnpSet`, `CopyNumberSet`, and `oligoSnpSet` are available in the package *VanillaICE* available at Bioconductor. A more detailed description of the hidden Markov models fit in the *VanillaICE* package are discussed elsewhere (**?**). Here we provide an example of a lowess smoother for copy number estimates. The following code chunk first assigns heterozygous calls to the integer 1 and homozygous calls to the integer zero. It follows that regions of deletions will have homozygous calls of zero. We simulated a deletion of 50 consecutive SNPs and converted the `oligoSet` to a list where each element in the list is an `oligoSnpSet` object for one chromosome.

3 Session Information

The version number of R and packages loaded for generating the vignette were:

- R Under development (unstable) (2011-12-18 r57922), `x86_64-apple-darwin11.2.0`
- Locale:
  `en_US.US-ASCII/en_US.US-ASCII/en_US.US-ASCII/C/en_US.US-ASCII/en_US.US-ASCII`
- Base packages: base, datasets, graphics, grDevices, methods, stats, utils
- Other packages: Biobase 2.15.3, BiocGenerics 0.1.4, BiocInstaller 1.3.5, oligoClasses 1.17.11, SNPchip 2.0.0
- Loaded via a namespace (and not attached): affyio 1.23.1, Biostrings 2.23.4, IRanges 1.13.19, tools 2.15.0, zlibbioc 1.1.0