SNPchip
November 11, 2009

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addFeatureData-methods

*Method for Function* addFeatureData

**Description**
Methods to add SNP-level annotation to the featureData slot in eSets. Feature-level annotation can include chromosome, physical position, allele, strand (sense/anti-sense), etc.

**Methods**

- **object = "eSet"**  Any object that is an instance of a class extending eSet

---

**alleleA**

*Accessor for the A allele*

**Description**
Accessor for the A allele

**Usage**

```r
alleleA(object)
```

**Arguments**

- **object** one of the classes defined in SNPchip

**Value**

Returns a vector of the A alleles

**Author(s)**

R. Scharpf

**See Also**

alleleA
**alleleB**  
*Accessor for the B allele*

**Description**

Accessor for the B allele

**Usage**

```r
alleleB(object)
```

**Arguments**

- `object` one of the classes defined in SNPchip

**Value**

Returns a vector of the B alleles

**Author(s)**

R. Scharpf

**See Also**

`alleleB`

---

**centromere**  
*Coordinates of centromere*

**Description**

Extracts coordinates of centromere for a particular chromosome

**Usage**

```r
centromere(chromosome, build="hg18", verbose=FALSE)
```

**Arguments**

- `chromosome` character string: "1", ..., "22", "X", or "Y"
- `build` character string. Currently only build 'hg18' is provided
- `verbose` Logical. Displays build used to annotate the centromere coordinates when TRUE

**Value**

integer: start and stop coordinates of centromere in basepairs
**chromosome2integer**

*Converts chromosome to integer or vice versa*

**Description**

Provides a standard way of converting chromosome annotation stored in `SnpLevelSet` objects to the numeric class.

**Usage**

```r
chromosome2integer(chrom)
integer2chromosome(chrom)
```

**Arguments**

- `chrom` chromosome

**Details**

This is useful when sorting SNPs in an object by chromosome and physical position – ensures that the sorting is done in the same way for different objects.

The function currently provides the following conversions:

"X" -> 23 "Y" -> 24 "XY" -> 25 "M" -> 26

**Value**

- `integer character`

**Author(s)**

R. Scharpf
**Description**

Contains information on chromosomes 1-22, X and Y.

**Usage**

data(chromosomeAnnotation)

**Format**

A data frame with 24 observations on the following 3 variables.

- `centromereStart` a numeric vector
- `centromereEnd` a numeric vector
- `chromosomeSize` a numeric vector

**Examples**

data(chromosomeAnnotation)

---

**chromosomeSize**

*Size of chromosome in number of base pairs.*

**Description**

Size of chromosome in base pairs.

**Usage**

`chromosomeSize(chromosome, build="hg18", verbose=FALSE)`

**Arguments**

- `chromosome` character string for the chromosome, e.g., "1", ... "22", "X", or "Y"
- `build` character string: genome build. Currently only 'hg18' is provided.
- `verbose` Logical. If TRUE, build is displayed

**Value**

Numerical vector.

**Author(s)**

Robert Scharpf

**Examples**

`chromosomeSize("1", verbose=TRUE)`
Methods for Function coerce

Methods

Coercion methods for classes defined in SNPchip

crlmmOut

A data object created by the oligo vignette

Description

This data object was created by the oligo vignette from 3 Hapmap samples and then subset to include only the SNPs on chromosome 1. See the oligo vignette for additional details.

Usage

data(crlmmOut)

Examples

data(crlmmOut)

cytoband

Start and stop sites of cytoband

Description

Contains start and stop sites of cytoband for Build 35

Usage

data(cytoband)

Format

A data frame with 862 observations on the following 5 variables.

- **chrom** a factor with levels chr1 chr10 chr11 chr12 chr13 chr14 chr15 chr16 chr17 chr18 chr19 chr2 chr20 chr21 chr22 chr3 chr4 chr5 chr6 chr7 chr8 chr9 chrX chrY
- **chromStart** a numeric vector
- **chromEnd** a numeric vector
- **name** a factor indicating which chromosomal arm
- **gieStain** a factor with levels acen gneg gpos100 gpos25 gpos50 gpos75 gvar stalk
**dbSnpId**

**Source**

http://pevsnerlab.kennedykrieger.org/snpscan_07_sourcecode.htm

**Examples**

```r
data(cytoband)
```

---

<table>
<thead>
<tr>
<th>dbSnpId</th>
<th>The dbSNP identifier</th>
</tr>
</thead>
</table>

**Description**

Unique identifier for each SNP assigned by NIH

**Usage**

```r
dbSnpId(object)
```

**Arguments**

- `object` Object possibly derived from `eSet` or `AnnotatedDataFrame` class.

**Value**

A (typically very long) character vector of SNP identifiers.

**Author(s)**

R. Scharpf

**Examples**

```r
## Not run:
data(sample.snpset)
dbSnpId(sample.snpset)[1:5]
## End(Not run)
```

---

<table>
<thead>
<tr>
<th>enzyme</th>
<th>Enzyme used to digest DNA</th>
</tr>
</thead>
</table>

**Description**

When two chips have been combined (e.g., Xba and Hind), enzyme is an accessor for whether a particular SNP was interrogated on the Xba or Hind chip. A better name for this accessor might be 'chip', suggestions welcome.

**Usage**

```r
enzyme(object)
```
**fragmentLength**

**Arguments**

object one of the classes defined in SNPchip

**Value**

Returns the enzyme for each indicated SNP.

**Author(s)**

R. Scharpf

---

**featureData-accessors**

*Accessors for feature-level SNP annotation*

**Description**

featureData accessors for classes defined in SNPchip

**Arguments**

object object inheriting from SnpLevelSet

**Details**

chromosome extracts character string of chromosome number for each SNP in the object.

position extracts the physical position (base pair number) for each SNP in the object.

**Author(s)**

R. Scharpf

---

**fragmentLength**

*Accessor for the fragment length*

**Description**

Accessor for the length of the PCR fragment on which the SNP resides.

**Usage**

fragmentLength(object)

**Arguments**

object Object, possibly derived from class SnpCallSet or SnpCopyNumberSet

**Value**

Length of the PCR fragment on which the SNP resides after enzymatic digestion.
getPar

Author(s)

R. Scharpf

getPar  Adds graphical parameters for plotting SNP data

Description

Not intended to be called directly. Adds graphical parameters for plotting SNP data to one of the graphical parameter classes (e.g., ParSnpSet, ParSnpCopyNumberSet, etc).

Usage

getPar(object, ...)

Arguments

object an object inheriting from ParESet
... additional arguments to par

Details

Adds graphical parameters to an object inherited from class ParESet that depend on the data class object (an object inherited from class SnpLevelSet). For instance, graphical parameters specifying the layout depend on the number of samples and chromosomes in the object snpset.

Value

An object of the same class as object

Author(s)

R. Scharpf

See Also

plotSnp
hapmap  

*Data from the hapmap project*

**Description**

Data obtained from the hapmap project and pre-processed by CRLMM to produce genotype calls. Due to size limitations, we only included every 10th SNP from the Affy’s 50k Xba chip. ‘Copy number’ estimates were obtained from using the calculate copy number function in the oligo-Classes package and is used solely to illustrate properties of the classes defined in SNPchip. Better approaches for estimating copy number are available in other packages, and currently under development in the oligo package.

**Usage**

```r
data(hapmap)
```

**Author(s)**

R. Scharpf

**Examples**

```r
data(hapmap)
```

---

**HmmPredict-class**  

*Class for containing output from a hidden Markov fit to SNP-level data of genotype calls and copy number estimates*

**Description**

Container for HMM predictions

**Objects from the Class**

Objects can be created by calls of the form `new("HmmPredict", assayData, phenoData, featureData, experimentData, annotation, ...)`. 

**Slots**

- `states`: Object of class "character"
- `breakpoints`: Object of class "data.frame"
- `assayData`: Object of class "AssayData"
- `phenoData`: Object of class "AnnotatedDataFrame"
- `featureData`: Object of class "AnnotatedDataFrame"
- `experimentData`: Object of class "MIAME"
- `annotation`: Object of class "character"
- `__classVersion__`: Object of class "Versions"
**hmmPredict**

**Extends**

Class `SnpLevelSet`, directly. Class `NULLorHmmPredict`, directly. Class `eSet`, by class "SnpLevelSet", distance 2. Class `VersionedBiobase`, by class "SnpLevelSet", distance 3. Class `Versioned`, by class "SnpLevelSet", distance 4.

**Methods**

No methods defined with class "HmmPredict" in the signature.

**Author(s)**

RS

**Examples**

```r
showClass("HmmPredict")
```

---

**Description**

Accessor for HMM output

**Usage**

```r
hmmPredict(object)
```

**Arguments**

- `object` A `ParESet` instance

**Value**

An object of class `HmmPredict`

**Author(s)**

RS
ParESet-class

Class "ParESet"

Description

A class containing a list of graphical parameters for plotting objects extending SnpLevelSet.

Objects from the Class

Objects can be created by calls of the form new("ParESet", layout, col.axis, cex.main, cex.axis, cex.legend, cex, cex.lab, pch, col, bg, xакс, xaxt, yaxs, yaxt, lab, adj, bty, ann, useLayout, mar, oma, las, log, ylab, side.ylab, outer.ylab, line.ylab, cex.ylab, xlab, outer.xlab, side.xlab, cex.xlab, line.xlab, outer.axis, line.axis, main, col.centromere, border.centromere, xlim, ylim, one.ylim, add.cytoband, outer.cytoband, outer.cytoband.axis, label.cytoband, use.chromosome.size, label.chromosome, line.label.chromosome, xaxis.side, alternate.xaxis.side, mat, heights, widths, respect, firstChromosome, ...).

Slots

snpPar: Object of class list

Methods

hmmPredict signature(object="ParESet"): Accessor for HmmPredict instance. See also hmmPredict.

initialize signature(.Object = "ParESet")

plotSnp ParESet, SnpLevelSet: See also plotSnp.

snpPar signature(object = "ParESet")

snpPar<- signature(object = "ParESet")

snpset signature(object="ParESet"): Accessor for SNP data (SnpLevelSet instance). See snpset.

Author(s)

R. Scharpf

See Also

ParSnpCallSet-class, ParSnpCopyNumberSet-class, ParSnpSet-class

Examples

showClass("ParESet")
**ParSnpCallSet-class**

*Class* "ParSnpCallSet"

---

**Description**

Graphical parameters for object of class SnpCallSet

**Objects from the Class**

Objects can be created by calls of the form `new("ParSnpCallSet", ...)`.  

**Slots**

- **snpPar**: Object of class "list"  

**Extends**

Class *ParESet*, directly.

**Methods**

- `initialize` signature(.Object = "ParSnpCallSet")  
- `plotSnp` signature(object = "ParSnpCallSet", snpset = "SnpCallSet")

**Author(s)**

R.Scharpf

**See Also**

* SnpCallSet-class

**Examples**

`showClass("ParSnpCallSet")`

---

**ParSnpCopyNumberSet-class**

*Class* "ParSnpCopyNumberSet"

---

**Description**

Graphical parameters for plotting SnpCopyNumberSet objects

**Objects from the Class**

Objects can be created by calls of the form `new("ParSnpCopyNumberSet", ...)`.  

**Examples**

`showClass("ParSnpCopyNumberSet")`
ParSnpSet-class

Slots

snpPar: Object of class "list"

Extends

Class ParESet, directly.

Methods

initialize signature(.Object = "ParSnpCopyNumberSet")

plotSnp signature(object = "ParSnpCopyNumberSet", snpset = "SnpCopyNumberSet")

Author(s)

R. Scharpf

See Also

SnpCopyNumberSet-class

Examples

showClass("ParSnpCopyNumberSet")
See Also

oligoSnpSet-class

Examples

showClass("ParSnpSet")

Description

Adds cytobands to views of chromosome copy number and genotype plots.

Usage

plotCytoband(chromosome, cytoband, cytoband.ycoords, xlim, ylim=c(0, 2),
new=TRUE, label.cytoband=TRUE, label.y=NULL, srt, cex.axis=1,
outer=FALSE, taper=0.15, verbose=FALSE, build="hg18", ...)

Arguments

chromosome character string or integer: which chromosome to draw the cytoband
cytoband data.frame containing cytoband information
cytoband.ycoords numeric: y coordinates
xlim x-axis limits
ylim y-axis limits
new logical: new plotting device
label.cytoband logical: if TRUE, labels the cytobands
label.y numeric: height (y-coordinate) for cytoband label
srt string rotation for cytoband labels. See par
cex.axis size of cytoband labels. See par
outer logical: whether to draw the labels in the outer margins. See par
taper tapering for the ends of the cytoband
verbose Logical. If TRUE, displays human genome build used to annotated the cytoband
coordinates.
build Character string. Currently only "hg18" is allowed.
...

Author(s)

Robert Scharpf and Jason Ting

See Also

plotSnp, cytoband
plotSnp

**plotSnp**  
Plots copy number and genotype calls against physical position

### Description

Returns an object inheriting from class ParESet – essentially, a list of default graphical parameters that can be modified as needed. The `show` method for this class plots the copy number and genotype calls versus physical position for an arbitrary number of samples and chromosomes.

### Usage

```r
plotSnp(object, hmmPredict, ...)  
## S4 method for signature 'SnpLevelSet':  
plot(x, y, ...)  
```

---

plotPredictions  
Plots the predictions from the HMM

### Description

Plots the predictions from the HMM. This function is usually not called directly.

### Usage

```r
plotPredictions(object, op)  
```

### Arguments

- **object**  
  object of class HmmPredict

- **op**  
  an object inheriting from ParESet

### Value

Nothing

### Author(s)

R. Scharpf

---

Examples

```r
##See the VanillaICE vignette
```

---

plotCytoband("1")
**RatioSnpSet-class**

**Arguments**

- `object, x` An object extending `ParESet`
- `hmmPredict, y` An object of class `HmmPredict`
- `...` Additional arguments to the initialization methods of the `ParESet` classes

**Details**

See examples in the vignette

**Author(s)**

R. Scharpf

**See Also**

`par`, `ParESet-class`, `ParSnpCallSet-class`, `ParSnpCopyNumberSet-class`, `ParSnpSet-class`

**Examples**

```r
data(sample.snpset)
chr1 <- sample.snpset[chromosome(sample.snpset) == "1", 1]
graph.par <- plotSnp(chr1)
class(graph.par)
## Not run:
graph.par
## End(Not run)
```

---

**RatioSnpSet-class**  
Class for high throughput SNP-level data. The assay data contains ratios of copy number.

**Description**

Container for high throughput SNP data for platforms that provide ratios as SNP-level summaries of copy number

**Objects from the Class**

Objects can be created by calls of the form `new("RatioSnpSet", calls, callsConfidence, ratio, ratioConfidence, ...)`. 

**Slots**

- `assayData`: Object of class "AssayData"
- `phenoData`: Object of class "AnnotatedDataFrame"
- `featureData`: Object of class "AnnotatedDataFrame"
- `experimentData`: Object of class "MIAME"
- `annotation`: Object of class "character"
- `__classVersion__`: Object of class "Versions"
RatioSnpSet-methods

Extends


Methods

`cnConfidence` signature(object = "RatioSnpSet"): Accessor for confidence scores for the ratios

`cnConfidence<-` signature(object = "RatioSnpSet", value = "matrix"): Replacement method for ratio confidence scores

`copyNumber` signature(object = "RatioSnpSet"): Accessor for ratios. See also `ratio`.

`copyNumber<-` signature(object = "RatioSnpSet", value = "matrix"): Replacement method for ratios.

`initialize` signature(.Object = "RatioSnpSet")

`ratioConfidence` signature(object = "RatioSnpSet"): Accessor for confidence scores of the ratios. See also `cnConfidence`.

Author(s)

RS

See Also

`RatioSnpSet-methods`

Examples

```r
showClass("RatioSnpSet")
```

Description

Accessors and replacement methods for RatioSnpSet objects.

Usage

```r
ratio(object)
ratio(object)<-value
ratioConfidence(object)
ratioConfidence(object) <- value
```

Arguments

<table>
<thead>
<tr>
<th>object</th>
<th>RatioSnpSet object</th>
</tr>
</thead>
<tbody>
<tr>
<td>value</td>
<td>matrix</td>
</tr>
</tbody>
</table>

Value

Matrix with R rows (SNPs) and C columns (Samples) containing ratios of allele intensities
sample.snpset 

Example object of class oligoSnpSet

Description

Example object of class oligoSnpSet created from 5 HapMap samples assayed on the Affymetrix 100k platform.

Usage

data(sample.snpset)

Examples

data(sample.snpset)
sample.snpset

selectSomeIndex 

Method from Biobase for selecting indices

Description

Method from Biobase for selecting indices in a data.frame. This method is not currently exported in Biobase.

Usage

selectSomeIndex(object, ...)

Arguments

object 
a data.frame

... 
additional arguments

Value

a list of indices
show-methods  show methods

Description
Show methods

Details
The show methods can be used to plot instances of the ParESet classes. An object of the class is created using plotSnp.

Methods
- `object = "oligoSnpSet"`  show method for `oligoSnpSet` objects
- `object = "ParESet"`  show method for objects inheriting from the `ParESet` class

See Also
- `plotSnp`

showSummary  Displays descriptive statistics for a sample.

Description
Displays descriptive statistics for a sample as a legend.

Usage
```r
showSummary(object, where, bty, legend.panel, cex, col, digits)
```

Arguments
- `object`  Object of class `oligoSnpSet`
- `where`  Character string indicating where to put the legend. See `legend`
- `bty`  See `bty`
- `legend.panel`  Logical for plotting the legend on a separate panel.
- `cex`  See `par`
- `col`  See `par`
- `digits`  Argument to `round`

Author(s)
Robert Scharpf

See Also
- `legend`, `round`, `\par`
smoothSnp

A simple nonparametric smoother for genotype and copy number

Description

A loess smoother for finding regions of reduced copy number and loss of heterozygosity.

Usage

smoothSnp(object, ...)

Arguments

- object: Object derived from AnnotatedSnpSet
- ...: For additional arguments see details.

Details

Additional arguments include the chromosomes (character vector) and samples (numerical vector) to smooth. Options for smoothing are set by specifying the span and the method. See the SNPchip vignette.

See the R package VanillaICE for a hidden Markov model for more formal inference regarding regions of LOH and copy number alterations.

Value

An object of the same class, e.g., AnnotatedSnpSet, where assayData elements copyNumber and calls are replaced by the smoothed values.

Author(s)

Robert Scharpf

References

RS

snpPar

Accessor for graphical parameters

Description

Accessor for the list of graphical parameters in objects of class ParESet.

Usage

snpPar(object)
Arguments

object object of class ParESet

Value

list

Author(s)

RS

See Also

par.layout

Examples

data(sample.snpset)
object <- plotSnp(sample.snpset)
str(snpPar(object))
## Not run:
show(object)
## End(Not run)
Methods for Function `summary`

**Description**

Methods for function `summary`

**Methods**

- **object = "ANY"** describe this method here
- **object = "SnpCallSet"** calculates percent homozygous calls, and percent heterozygous calls for each chromosome, and then aggregated over all autosomes.
- **object = "AnnotatedSnpSet"** calculates average copy number, standard deviation of copy number, percent homozygous calls, and percent heterozygous calls for each chromosome, and then aggregated over all autosomes.

**Description**

Methods for updating SNP-level classes
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