SNPchip

April 19, 2010

`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

```
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

```
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

```
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

Author(s)

R. Scharpf

Examples

```
centromere("1")
```

`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

```
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

`chromosomeAnnotation`
chromosome annotation

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)
```

`coerce-methods` *Methods for Function coerce*

Description

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`

Source

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

Examples

```
data(cytoband)
```

`dbSnpId` *The dbSNP identifier*

Description

Unique identifier for each SNP assigned by NIH

Usage

```
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

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

## End(Not run)
```

`enzyme` *Enzyme used to digest DNA*

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

```
enzyme(object)
```

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.

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 oligoClasses 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

```
data(hapmap)
```

Author(s)

R. Scharpf

Examples

```
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"`

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

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

`hmmPredict` *Accessor for HMM output*

Description

Accessor for HMM output

Usage

```
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, xaxs, 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`

`hmmPredict`**:** Object of class `list`

`snpset`**:** Object inherited from class `SnpLevelSet`

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", ...)`.

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")
```

`ParSnpSet-class` *Class "ParSnpSet"*

Description

Graphical parameters for `oligoSnpSet` objects

Objects from the Class

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

Slots

`snpPar`: Object of class `"list"`

Extends

Class `ParSnpCopyNumberSet`, directly. Class `ParESet`, by class "ParSnpCopyNumberSet", distance 2.

Methods

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

plotSnp `signature(object = "ParSnpSet", snpset = "oligoSnpSet")`

Author(s)

R. Scharpf

See Also

`oligoSnpSet-class`

Examples

```
showClass("ParSnpSet")
```

`plotCytoband` *Plots idiogram for one chromosome*

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.
`...`	additional arguments to plot

Author(s)

Robert Scharpf and Jason Ting

See Also

`plotSnp`, `cytoband`

Examples

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

`plotPredictions` *Plots the predictions from the HMM*

Description

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

Usage

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

Arguments

`object`	object of class `HmmPredict`
`op`	an object inheriting from `ParESet`

Value

Nothing

Author(s)

R. Scharpf

Examples

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

`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

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

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

```
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"`

Extends

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

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

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

`RatioSnpSet-methods` *Accessors for RatioSnpSet objects*

Description

Accessors and replacement methods for RatioSnpSet objects.

Usage

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

Arguments

`object`	`RatioSnpSet` object
`value`	matrix

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

```
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)
```

`snpset` *Accessor for SNP data*

Description

Accessor for SNP data.

Usage

```
snpset(object)
```

Arguments

`object`	A `ParESet` instance.

Value

A `SnpLevelSet` instance.

Author(s)

RS

`summary-methods` *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.

`updateObject-methods` *updateObject methods*

Description

Methods for updating SNP-level classes

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