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
**ParESet-class**

**Examples**

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

---

**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

**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**

```r
showClass("ParESet")
```
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")

Class "ParSnpCopyNumberSet"

Description
Graphical parameters for plotting SnpCopyNumberSet objects

Objects from the Class
Objects can be created by calls of the form new("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")

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
**RatioSnpSet-class**

**See Also**

`oligoSnpSet-class`

**Examples**

```r
text = showClass("ParSnpSet")
```

---

**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**


**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`. 

**Class for high throughput SNP-level data. The assay data contains ratios of copy number.**
Author(s)
RS

See Also
RatioSnpSet-methods

Examples
showClass("RatioSnpSet")

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

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 "XY" -> 24 "Y" -> 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)

correct-methods

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**

```r
data(crlmmOut)
```

**Examples**

```r
data(crlmmOut)
```

---

**cytoband**

Start and stop sites of cytoband

**Description**

Contains start and stop sites of cytoband for Build 35

**Usage**

```r
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](http://pevsnerlab.kennedykrieger.org/snpscan_07_sourcecode.htm)

**Examples**

```r
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**

```r
## 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.
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 

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 

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

data(hapmap)
hmmPredict

Author(s)
R. Scharpf

Examples
data(hapmap)

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

plotCytoband

Plots cytoband 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", ...)
plotPredictions

Arguments

- chromosome: character string: 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
\textit{plotSnp}  \hspace{1cm} \underline{Plots copy number and genotype calls against physical position}

\textbf{Description}

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

\textbf{Usage}

\begin{verbatim}
plotSnp(object, hmmPredict, ...)  
## S4 method for signature 'SnpLevelSet':
plot(x, y, ...)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{object, x} \hspace{0.5cm} An object extending \texttt{ParESet}
  \item \texttt{hmmPredict, y} \hspace{0.5cm} An object of class \texttt{HmmPredict}
  \item \texttt{...} \hspace{0.5cm} Additional arguments to the initialization methods of the \texttt{ParESet} classes
\end{itemize}

\textbf{Details}

See examples in the vignette

\textbf{Author(s)}

R. Scharpf

\textbf{See Also}

\texttt{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)
```

**sample.snpset**  
Example object of class oligoSnpsSet

Description

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

Usage

```r
data(sample.snpset)
```

Examples

```r
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

```r
selectSomeIndex(object, ...)
```

Arguments

- `object` a data.frame
- `...` additional arguments

Value

a list of indices
**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  

*Description*

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

*Usage*

```r
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  

*Description*

Accessor for graphical parameters

*Usage*

```r
snpPar(object)
```
snpset

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`

**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.

Methods for updating SNP-level classes

**Description**

Methods for updating SNP-level classes
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