

# SNPchip

October 25, 2011

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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, yaxt, 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 = "SnpSet")

**Author(s)**

R.Scharpf

**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

**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")
```

---

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")
```

---

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	<i>Size of chromosome in number of base pairs.</i>
----------------	--

---

**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	<i>Methods for Function coerce</i>
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**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](http://pevsnerlab.kennedykrieger.org/snpscan_07_sourcecode.htm)

**Examples**

```
data(cytoband)
```



---

dbSnpId	<i>The dbSNP identifier</i>
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---

**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	<i>Enzyme used to digest DNA</i>
--------	----------------------------------

---

**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	<i>Adds graphical parameters for plotting SNP data</i>
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---

**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**

<code>object</code>	an object inheriting from <code>ParESet</code>
<code>...</code>	additional arguments to <code>par</code>

**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	<i>Data from the hapmap project</i>
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---

**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	<i>Accessor for HMM output</i>
------------	--------------------------------

---

**Description**

Accessor for HMM output

**Usage**

```
hmmPredict(object)
```

**Arguments**

object            A ParESet instance

**Value**

An object of class HmmPredict

**Author(s)**

RS

---

integer2chromosome	<i>Converts integer representation of chromosome number back to letter</i>
--------------------	--

---

**Description**

Coerces integer representation for chromosome in the pd.annotation packages to character strings

**Usage**

```
integer2chromosome(chrom)
```

**Arguments**

chrom            chromosome

**Value**

character

**Author(s)**

R. Scharpf

**Examples**

```
integer2chromosome(1:26)
```

---

plotCytoband	<i>Plots idiogram for one chromosome</i>
--------------	--

---

**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 <code>par</code>
cex.axis	size of cytoband labels. See <code>par</code>
outer	logical: whether to draw the labels in the outer margins. See <code>par</code>
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 <code>HmmPredict</code>
op	an object inheriting from <code>ParESet</code>

**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)
graph.par <- plot(sample.snpset[chromosome(sample.snpset) < 5, ])

class(graph.par)
## Not run:
## to plot the data, the following are equivalent
graph.par
# or
show(graph.par)
# or
print(graph.par)

## End(Not run)
```

---

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
```

---

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

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

### 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**

<code>object</code>	Object derived from <code>AnnotatedSnpSet</code>
<code>...</code>	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)
options(error=recover)
chr23=sample.snpset[chromosome(sample.snpset) == 23, ]
object <- plot(sample.snpset[chromosome(sample.snpset) == 23, ])
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      *Summary statistics for various SNP classes that extend eSet*

---

**Description**

Methods for function `summary`

**Methods**

**object = "SnpSet"** 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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