CGHbase

October 25, 2011

CGHbase-package

CGHbase: Base functions and classes for arrayCGH data analysis.

Description

CGHbase: Base functions and classes for arrayCGH data analysis.

Details

Main infrastructural classes: cghRaw, cghSeg, cghCall. Full help on methods and associated functions is available from withing class help pages.

Attached data sets: WiltingData, WiltingRaw, WiltingNorm, WiltingSeg, WiltingCalled.

Author(s)

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WiltingCalled

Cervical cancer arrayCGH data called with CGHcall

Description

Cervical cancer arrayCGH data called with CGHcall with default settings, containing 3552 features for 5 samples.

Usage

WiltingCalled

Format

An object of class cghCall

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Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology*, 210, 258-259.

Mark A. van de Wiel, Kyung In Kim, Sjoerd J. Vosse, Wessel N. van Wieringen, Saskia M. Wilting and Bauke Ylstra. CGHcall: calling aberrations for array CGH tumor profiles. *Bioinformatics*, 23, 892-894.

WiltingData

Cervical cancer arrayCGH data

Description

A dataframe containing 4709 rows and 8 columns with arrayCGH data.

Usage

Wilting

Format

A dataframe containing the following 8 columns:

Name The unique identifiers of array elements.

Chromosome Chromosome number of each array element.

Position Chromosomal position in bp of each array element.

AdCA10 Raw log2 ratios for cervical cancer sample AdCA10.

SCC27 Raw log2 ratios for cervical cancer sample SCC27.

SCC32 Raw log2 ratios for cervical cancer sample SCC32.

SCC36 Raw log2 ratios for cervical cancer sample SCC36.

SCC39 Raw log2 ratios for cervical cancer sample SCC39.

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology*, 210, 258-259.

WiltingNorm 3

WiltingNorm

Normalized log2 ratios from cervical cancer arrayCGH data.

Description

Normalized log2 ratios frm cervical cancer arrayCGH data, containing 3552 features for 5 samples. These data have been normalized using the normalize function with default settings.

Usage

WiltingCalled

Format

An object of class cghRaw.

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology*, 210, 258-259.

WiltingRaw

Raw log2 ratios from cervical cancer arrayCGH data.

Description

Raw log2 ratios from cervical cancer arrayCGH data, containing 3552 features for 5 samples. These data have been preprocessed using preprocess.

Usage

WiltingCalled

Format

An object of class cghRaw.

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology*, 210, 258-259.

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WiltingRegions

Regions of cervical cancer arrayCGH data as defined by CGHregions

Description

Regions of cervical cancer arrayCGH data as defined by CGHregions with default settings, containing 90 regions over 5 samples.

Usage

WiltingRegions

Format

An object of class cghRegions

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology*, 210, 258-259.

Mark A. van de Wiel and Wessel N. van Wieringen (2007). CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. *Cancer Informatics*, 2, 55-63.

WiltingSeg

Segmented log2 ratios from cervical cancer arrayCGH data.

Description

Segmented log2 ratios from cervical cancer arrayCGH data, containing 3552 features for 5 samples. These data have been segmented using segmentData with default settings.

Usage

WiltingCalled

Format

An object of class cghSeg.

Source

Wilting, S.M., Snijders, P.J., Meijer, G.A., Ylstra, B., van den IJssel, P.R., Snijders, A.M., Albertson, D.G., Coffa, J., Schouten, J.P., van de Wiel, M.A., Meijer, C.J., & Steenbergen, R.D. (2006). Increased gene copy numbers at chromosome 20q are frequent in both squamous cell carcinomas and adenocarcinomas of the cervix. *Journal of Pathology*, 210, 258-259.

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avedist

Retrieve regions information from cghRegions object.

Description

This function accesses the regions information stored in the featureData of an object derived from the cghRegions-class.

Usage

```
avedist(object)
nclone(object)
```

Arguments

object

Object derived from class cghRegions

Value

avedist returns a vector containing the Average L1-distance of clone signatures to the medoid signature; nclone returns a vector containing the number of clones that is included in each region;

Author(s)

Sjoerd Vosse

See Also

```
cghRegions-class
```

chromosomes

Retrieve feature position data from cgh objects.

Description

These generic functions access the position data stored in the featureData of an object derived from the cghRaw-class, cghSeg-class or cghCall-class.

Usage

```
chromosomes(object)
bpstart(object)
bpend(object)
```

Arguments

object

Object derived from class cghRaw, cghSeg, or cghCall

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Value

chromosomes returns a vector of chromosome numbers; bpstart returns a vector of basepair start positions; bpend returns a vector of basepair end positions;

Author(s)

Sjoerd Vosse

See Also

```
cghRaw-class, cghSeg-class, cghCall-class
```

cghCall

Class to contain and describe called array comparative genomic

Description

Container for aCGH data and experimental metadata. cghCall class is derived from eSet, and requires the following matrices of equal dimension as assayData members:

- copynumber Log2 copynumber ratios.
- segmented Segmented log2 ratios.
- calls Called copynumer values.
- probloss Loss probabilities as returned by CGHcall.
- probnorm Normal probabilities as returned by CGHcall.
- probgain Gain probabilities as returned by CGHcall.
- probamp Optional amplification probabilities as returned by CGHcall when run with nclass=4.

Furthermore, columns named Chromosome, Start, and End are required as featureData members, containing feature position information.

Extends

Directly extends class eSet.

Creating Objects

```
new('cghCall', phenoData = [AnnotatedDataFrame], experimentData = [MIAME],
annotation = [character], copynumber = [matrix], segmented = [matrix],
calls = [matrix], probloss = [matrix], probnorm = [matrix], probgain
= [matrix], featureData = [AnnotatedDataFrame], ...)
```

An object of class cghCall is generally obtained as output from CGHcall.

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Slots

Inherited from eSet:

assayData: Contains matrices with equal dimensions, and with column number equal to nrow (phenoData). assayData must contain the following matrices

- copynumber Log2 copynumber ratios.
- segmented Segmented log2 ratios.
- calls Called copynumer values.
- probloss Loss probabilities as returned by CGHcall.
- probnorm Normal probabilities as returned by CGHcall.
- probgain Gain probabilities as returned by CGHcall.
- probamp Optional amplification probabilities as returned by CGHcall when run with nclass=4.

with rows represening array probes and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in assayData. Class:AssayData-class

```
phenoData: See eSet
featureData: An AnnotatedDataFrame with columns Chromosome, Start, and End
    containing array element position data.
experimentData: See eSet
annotation: See eSet
```

Methods

Class-specific methods.

copynumber(cghCall), copynumber(cghCall, matrix) <- Access and set elements named copynumber in the AssayData-class slot.

segmented(cghCall), segmented(cghCall, matrix) <- Access and set elements named
segmented in the AssayData-class slot.</pre>

calls(cghCall), calls(cghCall, matrix) <- Access and set elements named calls
in the AssayData-class slot.</pre>

probloss(cghCall), probloss(cghCall, matrix) <- Access and set elements named
 probloss in the AssayData-class slot.</pre>

probnorm(cghCall),probnorm(cghCall,matrix) <- Access and set elements named
 probnorm in the AssayData-class slot.</pre>

probgain(cghCall),probgain(cghCall,matrix) <- Access and set elements named probgain in the AssayData-class slot.

chromosomes, bpstart, bpend Access the chromosomal positions stored in featureData

plot.cghCall Create a plot containing log2ratios, segments and call probabilities ordered by chromosomal position

summaryPlot Create a plot summarizing the call probabilities of all samples

See eSet for derived methods.

Author(s)

Sjoerd Vosse

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See Also

```
eSet-class, cghRaw-class, cghSeg-class
```

Examples

```
# create an instance of cghCall
new("cghCall")

# load an instance of cghCall
data(WiltingCalled)

# plot the first sample
plot.cghCall(WiltingCalled[,1])

# plot the first chromosome of the first sample
plot.cghCall(WiltingCalled[chromosomes(WiltingCalled)==1,1])

# get the copynumber values of the third and fourth sample
log2ratios <- copynumber(WiltingCalled[,3:4])

# get the names of the samples
sampleNames(WiltingCalled)

# get the names of the array elements
featureNames(WiltingCalled)</pre>
```

cghRaw

Class to contain and describe raw or normalized array comparative

Description

Container for aCGH data and experimental metadata. cghRaw class is derived from eSet, and requires a matrix named copynumber as assayData member. Furthermore, columns named Chromosome, Start, and End are required as featureData members, containing feature position information.

Extends

Directly extends class eSet.

Creating Objects

```
new('cghRaw', phenoData = [AnnotatedDataFrame], experimentData = [MIAME],
annotation = [character], copynumber = [matrix], featureData = [AnnotatedDataFra...)
```

make_cghRaw is a function to convert a dataframe or textfile to an object of class cghRaw. The input should be either a dataframe or a tabseparated textfile (textfiles must contain a header). The first three columns should contain the name, chromosome and position in bp for each array target respectively. The chromosome and position column must contain numbers only. Following these is a column with log2 ratios for each of your samples. If the input type is a textfile, missing values should be represented as 'NA' or an empty field.

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Slots

```
Inherited from eSet:
```

```
assayData Contains matrices with equal dimensions, and with column number equal to nrow (phenoData).

assayData must contain a matrix copynumber with rows represening array probes and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in assayData. Class:AssayData-class

phenoData: See eSet

featureData: An AnnotatedDataFrame with columns Chromosome, Start, and End containing array element position data.

experimentData: See eSet

annotation: See eSet
```

Methods

Class-specific methods.

```
\label{lem:copynumber} \mbox{\tt copynumber(cghRaw,matrix)$<-$ Access and set elements named copynumber in the $\tt AssayData-class slot.$
```

chromosomes, bpstart, bpend Access the chromosomal positions stored in featureData **plot.cghRaw** Create a plot containing log2ratios ordered by chromosomal position

See eSet for derived methods. Annotation functionality is not yet supported.

Author(s)

Sjoerd Vosse

See Also

```
eSet-class, cghSeg-class, cghCall-class
```

```
# create an instance of cghRaw
new("cghRaw")

# create an instance of cghRaw from a dataframe
data(WiltingData)
cghobj <- cghRaw(WiltingData)

# plot the first sample
plot.cghRaw(cghobj[,1])
# first three chromosomes
plot.cghRaw(cghobj[chromosomes(cghobj)==1,1])

# get the copynumber values of the third and fourth sample
log2ratios <- copynumber(cghobj[,3:4])

# get the names of the samples
sampleNames(cghobj)

# get the names of the array elements
featureNames(cghobj)</pre>
```

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cghRegions	Class to contain and describe array comparative genomic hybridization

Description

Container for aCGH regions data and experimental metadata. cghRegions class is derived from eSet, and requires a matrix named regions as assayData member. Furthermore, columns named Chromosome, Start, End, Nclone, and Avedist are required as featureData members, containing region and position information.

Extends

Directly extends class eSet.

Creating Objects

```
new('cghRegions', phenoData = [AnnotatedDataFrame], experimentData
= [MIAME], annotation = [character], regions = [matrix], featureData
= [AnnotatedDataFrame], ...)
```

An object of this class is generally obtained by running the function CGHregions.

Slots

Inherited from eSet:

```
assayData: Contains matrices with equal dimensions, and with column number equal to nrow (phenoData).

assayData must contain a matrix regions with rows represening regions and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in assayData. Class:AssayData

phenoData: See eSet
```

 $\label{lem:columns} \begin{tabular}{ll} feature Data: An Annotated Data Frame with columns \end{tabular} Chromosome, Start, End, Nclone, and Avedist containing region and position information. \\ \end{tabular}$

```
experimentData: See eSet
annotation: See eSet
```

Methods

Class-specific methods.

regions (cghRegions), regions (cghRegions, matrix) <- Access and set elements named regions in the AssayData-class slot.

chromosomes, bpstart, bpend, nclone, avedist Access the region and position information stored in featureData

plot.cghRegions Create a plot displaying chromosomes on the Y-axis and base pair position on the X-axis. A new region is displayed by a slight jump with respect to the previous region. Each region is displayed as a bi-colored segment, the lower and upper part of which correspond to the proportions pl and pg of samples with a loss (red) or gain (green), respectively. The color coding is displayed as well: 1: pl (pg) < 10%; 2: 10% = pl (pg) < 30%; 3:30% = pl (pg) < 50%; 4: pl (pg) = 50%.

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frequencyPlot Create a frequency plot

See eSet for derived methods. Annotation functionality is not yet supported.

Author(s)

Sjoerd Vosse

See Also

```
eSet, cghRaw, cghSeg, cghCall
```

Examples

```
# create an instance of cghRegions
new("cghRegions")

# load an instance of cghRegions
data(WiltingRegions)

# plot all region data
plot.cghRegions(WiltingRegions)

# make a frequency plot
frequencyPlot(WiltingRegions)

# extract the region values
values <- regions(WiltingRegions)

# get the names of the samples
sampleNames(WiltingRegions)</pre>
```

cghSeg

Class to contain and describe segmented array comparative genomic

Description

Container for aCGH data and experimental metadata. cghSeg class is derived from eSet, and requires a matrix named copynumber as well as a matrix named segmented as assayData members of equal dimensions. Furthermore, columns named Chromosome, Start, and End are required as featureData members, containing feature position information.

Extends

Directly extends class eSet.

Creating Objects

```
new('cghSeg', phenoData = [AnnotatedDataFrame], experimentData = [MIAME],
annotation = [character], copynumber = [matrix], segmented = [matrix],
featureData = [AnnotatedDataFrame], ...)
```

An object of class cghSeg is generally obtained as output from segmentData.

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Slots

```
Inherited from eSet:
```

```
assayData: Contains matrices with equal dimensions, and with column number equal to nrow (phenoData).

assayData must contain matrices copynumber and segmented with rows representing array probes and columns representing samples. Additional matrices of identical size (e.g., representing measurement errors) may also be included in assayData. Class:AssayData-class

phenoData: See eSet

featureData: An AnnotatedDataFrame with columns Chromosome, Start, and End containing array element position data.

experimentData: See eSet

annotation: See eSet
```

Methods

Class-specific methods.

```
\label{lem:copynumber} \mbox{copynumber} \mbox{(cghSeg, matrix)} < - \mbox{ Access and set elements named copynumber} \mbox{ in the } \mbox{AssayData-class slot}.
```

segmented(cghSeg), segmented(cghSeg, matrix) <- Access and set elements named
segmented in the AssayData-class slot.</pre>

chromosomes, bpstart, bpend Access the chromosomal positions stored in featureData plot.cghSeg Create a plot containing log2ratios and segments ordered by chromosomal position

See eSet for derived methods.

Author(s)

Sjoerd Vosse

See Also

```
eSet-class, ExpressionSet-class, cghRaw-class, cghCall-class
```

```
# create an instance of cghSeg
new("cghSeg")

# load an instance of cghSeg
data(WiltingSeg)

# plot the first sample
# plot.cghSeg(WiltingSeg[,1])
# first three chromosomes
# plot.cghSeg(WiltingSeg[chromosomes(WiltingSeg)==1,1])

# get the copynumber values of the third and fourth sample
log2ratios <- copynumber(WiltingSeg[,3:4])

# get the names of the samples</pre>
```

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```
sampleNames(WiltingSeg)

# get the names of the array elements
featureNames(WiltingSeg)
```

copynumber

Retrieve copynumber data from cgh objects.

Description

These generic functions access the copynumber values of assay data stored in an object derived from the cghRaw-class, cghSeg-class or cghCall-class.

Usage

```
copynumber(object)
copynumber(object) <- value
segmented(object)
segmented(object) <- value
calls(object)
calls(object) <- value</pre>
```

Arguments

object Object derived from class cghRaw, cghSeg, or cghCall value Matrix with rows representing features and columns samples.

Value

copynumber returns a matrix of copynumber values;

Author(s)

Sjoerd Vosse

See Also

```
cghRaw-class, cghSeg-class, cghCall-class
```

```
data(WiltingCalled)
log2ratios <- copynumber(WiltingCalled)
segments <- segmented(WiltingCalled)
calls <- calls(WiltingCalled)</pre>
```

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frequencyPlot

Visualization of aCGH regions.

Description

This function creates a frequency plot for aCGH regions.

Usage

```
frequencyPlot(x, y, ...)
```

Arguments

x An object of class cghRegions.

Y This argument is not used and should be missing.

... Arguments plot.

Details

We find plotted on the x-axis the array probes sorted by chromosomal position. The vertical bars represent the frequency of gains and losses across your samples. The black bars represent gains, the gray bars represent losses.

Value

This function creates a plot.

Author(s)

Mark van de Wiel and Sjoerd Vosse

References

Mark A. van de Wiel and Wessel N. van Wieringen (2007). CGHregions: Dimension Reduction for Array CGH Data with Minimal Information Loss. *Cancer Informatics*, 2, 55-63.

```
## Not run:
data(WiltingRegions)
frequencyPlot(WiltingRegions)
## End(Not run)
```

plot.cghRaw 15

plot.cghRaw

Plot aCGH data.

Description

Please see the class descriptions for more details on the plot functions.

Usage

```
plot.cghRaw(x, y, ...)
plot.cghSeg(x, y, ...)
plot.cghCall(x, y, ...)
plot.cghRegions(x, y, ...)
```

Arguments

```
x An object of class cghRaw, cghSeg, cghCall, or cghSeg.
```

Y This argument is not used and should be missing.

... Arguments plot.

Author(s)

Sjoerd Vosse

See Also

```
cghRaw-class, cghSeg-class, cghCall-class, cghRegions-class
```

probloss

Retrieve call probabilities from a cghCall object.

Description

These generic functions access the call probabilities from assay data stored in a object derived from the cghCall-class.

Usage

```
probloss(object)
probloss(object) <- value
probnorm(object)
probnorm(object) <- value
probgain(object)
probgain(object) <- value
probamp(object)
probamp(object) <- value</pre>
```

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Arguments

object derived from class cghCall

value Matrix with rows representing features and columns samples.

Value

These functions return matrices of call probabilities.

Author(s)

Sjoerd Vosse

See Also

```
cghCall-class
```

regions

Retrieve regions data from cghRegions object.

Description

This function accesses the regions values of assay data stored in an object derived from the cghRegions-class.

Usage

```
regions(object)
regions(object) <- value</pre>
```

Arguments

object derived from class cghRegions

value Matrix with rows representing features and columns samples.

Value

regions returns a matrix of regions values;

Author(s)

Sjoerd Vosse

See Also

```
cghRegions-class
```

summaryPlot 17

summaryPlot

Visualization of aCGH profiles.

Description

This function creates a summary plot for aCGH profiles.

Usage

```
summaryPlot(x, y, ...)
```

Arguments

```
x An object of class cghCall.y This argument is not used and should be missing.
```

... Arguments plot.

Details

We find plotted on the x-axis the array probes sorted by chromosomal position. The vertical bars represent the average probability that the positions they cover are gained (green bars) or lost (red bars). The green bars represent gains, the red bars represent losses. When 4 levels have been used for calling, amplifications are indicated with a blue tickmark at the top of the plot.

Value

This function creates a plot.

Author(s)

Sjoerd Vosse & Mark van de Wiel

References

Mark A. van de Wiel, Kyung In Kim, Sjoerd J. Vosse, Wessel N. van Wieringen, Saskia M. Wilting and Bauke Ylstra. CGHcall: calling aberrations for array CGH tumor profiles. *Bioinformatics*, 23, 892-894.

```
## Not run:
   data(Wilting)
   rawcgh <- make_cghSeg(Wilting)
   normalized <- normalize(rawcgh)
   segmented <- segmentData(normalized)
   called <- CGHcall(segmented)
   summaryPlot(called)
## End(Not run)</pre>
```

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