Package 'beadarraySNP'

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Type Package

Title Normalization and reporting of Illumina SNP bead arrays

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Depends methods, Biobase (>= 2.14), quantsmooth

Suggests aCGH, affy, limma, snapCGH, beadarray, DNAcopy

Description Importing data from Illumina SNP experiments and performing copy number calculations and reports.

License GPL-2

biocViews CopyNumberVariation, SNP, GeneticVariability, TwoChannel, Preprocessing, DataImport

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R topics documented:

`alterCN` *alterCN*

Description

Changes one of the levels of a cn.sum data structure

Usage

```
alterCN(cn.sum, opa, value, updown)
```

Arguments

cn.sum	cn.sum structure to change
opa	opa panel within the structure
value	the predicted value to change
updown	the value has a higher (TRUE) or lower (FALSE) cn value

Details

The state in the cn.sum structure that has a predicted value of value will have it's associated associated inferred copy number increased (updown is TRUE) or decreased (updown is FALSE). The function makes sure that the copynumber values within a OPA panel have the same order as the predicted values.

Value

a new cn.sum data structure

Author(s)

Jan Oosting

See Also

interactiveCNselect, createCNSummary, setRealCN

---

backgroundCorrect.SNP *Background correction*

Description

Perform background correction on Illumina Golden Gate bead arrays

Usage

```
backgroundCorrect.SNP(object,method=c("none", "subtract", "half", "minimum",
                      "edwards", "normexp", "rma"),offset = 0)
```

Arguments

object	SnpSetIllumina object
method	character, method of correction
offset	numeric, constant to add after correction

Details

Code has been ported from the limma package. The matrices Gb and Rb should be available in the arrayData slot of the object.

Value

This function returns an SnpSetIllumina object with background corrected values in the G and R.

Author(s)

Jan Oosting, based on limma package by G. Smyth

See Also

SnpSetIllumina-class, backgroundCorrect,

backgroundEstimate, normalizeBetweenAlleles.SNP, normalizeWithinArrays.SNP

Examples

```
## Not run: data.bg<-backgroundCorrect.SNP(data.raw,"subtract")
```

---

backgroundEstimate *Estimate background intensities from foreground intensity*

Description

Background intensity from Illumina Golden Gate bead arrays are estimated based on several data models

Usage

```
backgroundEstimate(object,method=c("minimum", "mode","intmin",
"anglemode"), maxmode=3000, bincount=40, maxangle=0.3, subsample="OPA")
```

Arguments

object	SnpSetIllumina object
method	chracter, data model to use
maxmode	numeric, maximum intensity for mode for method="mode"
bincount	numeric, for method="intmin" , see details
maxangle	numeric in radians, maximum theta for mode for method="anglemode"
subsample	factor or column name in featureData slot

Details

The Illumina software does not provide background values in the output. Some models can be used to estimate background from the raw data intensities.
`minimum`: The allele specific minimum intensity is used.
`mode`: This model assumes that the first mode of the density of the intensities is determined by the zero-allele in the data, see ref. The signal intensity of the zero-allele should be zero, therefore this is considered the background value.
`intmin`: This model assumes there is crosstalk between the alleles, and background increases with the intensity of the other allele. The range between 0 and the maximum of the other allele is divided in `bincount` bins, and the minimum for this allele is determined for probes where the other allele falls in a bin. A linear fit is determined though the minimum values to obtain a gradually increasing value.
`anglemode`: This model finds the density modes closest to 0 and $\frac{\pi}{2}$ for polar transformed intensities, and uses this to determine background.

Value

This function returns an `SnpSetIllumina` object. The `Rb` and `Gb` matrices in the `assayData` slot contain estimated background values.

Author(s)

Jan Oosting

See Also

`SnpSetIllumina-class`, `backgroundCorrect.SNP`

`BeadstudioQC` *Quality control of Beadstudio report files*

Description

When data has been imported using a Beadstudio samplesheet and reportfile, these functions can be used to generate quality measures

Usage

```
BeadstudioQC(object, QClist = list(), arrayType = "Sentrix96")
pdfBeadstudioQC(QClist, basename = "beadstudio", by = 10)
```

Arguments

`object`	`SnpSetIllumina` object.
`QClist`	list, result of previous call to `BeadstudioQC`
`arrayType`	character, type of array

basename	character, prefix for PDF files. This name will be added before the Barcode of the chip
by	integer, number of samples in barplot, see reportSamplePanelQC

Value

The BeadstudioQC function generates a list of QCIllumina objects The pdfBeadstudioQC function generates a pdf-file for each QCIllumina object in the list

Author(s)

J. Oosting

See Also

pdfQC,calculateQCarray

---

calculateLOH *Determine LOH in experiment*

Description

Using pairings of normal and tumor samples the LOH pattern is determined

Usage

```
calculateLOH(object, grouping, NorTum = "NorTum", ...)
calculateLair(object, grouping = NULL, NorTum = "NorTum", min.intensity = NULL,
    use.homozygous.avg = FALSE)
```

Arguments

object	SnpSetIllumina object
grouping	Factor to show which samples belong together (are of the same individual)
NorTum	character vector or factor. Elements containing "N" are considered to be the normal sample
min.intensity	numeric
use.homozygous.avg	logical
...	extra arguments for link{heterozygousSNPs}

Details

The heterozygous SNPs of the normal sample are inspected for changes. SNPs where the genotype of the test sample are homozygous are set to TRUE

Value

For calculateLOH a SnpSetIllumina object with `loh` and `nor.gt` matrices in assayData. `loh` is a logical matrix, and `nor.gt` is a character matrix containing the genotypes of the corresponding normal sample For calculateLair a SnpSetIllumina object with `lair` matrix in assayData. lair is the lesser allele intensity ratio. If a corresponding normal sample is found, it is taken as reference. Else the genotypes of normal samples are taken as a reference

Author(s)

Jan Oosting

See Also

`SnpSetIllumina-class`

`calculateQCarray` *Retrieve QC information from a SnpSetIllumina object*

Description

Retrieves QC and identifying information of Illumina Sentrix arrays.

Usage

```
calculateQCarray(object, QCobject = NULL, arrayType="Sentrix96")
```

Arguments

`object`	`SnpSetIllumina` object. Should contain information of a single Sentrix array and a single type of OPA panel
`QCobject`	`QCIllumina-class` object: If set the information in the object is amended with data from the SnpSetIllumina object
`arrayType`	character, see `arrayType`

Details

Sample summary values are mapped to the physical layout of the Sentrix array using the `Row` and `Col` columns of the `phenoData` slot. These will be available when `read.SnpSetIllumina` is used to create `SnpSetIllumina` objects.
Use successive calls to `calculateQCarray` to process Sentrix arrays with multiple probe panels.

If data is read using a samplesheet that defines manifest files it is possible to handle data with multiple manifests and/or multiple Sentrix arrays

Value

A `QCIllumina` object, when multiple arrays were combined a list of `QCIllumina` objects

Author(s)

Jan Oosting

See Also

link{QCIllumina-class}, link{reportSamplePanelQC}, link{plotQC}

Examples

```
## Not run: QC<-calculateQCarray(data.raw1)
## Not run: QC<-calculateQCarray(data.raw2,QC)
```

---

compareGenotypes *Compare genotypes*

Description

Pairwise comparison of genotypes between unaffected and affected tissue from the same subject

Usage

```
compareGenotypes(genotypeT, genotypeN)
```

Arguments

genotypeT	character or logical vector, genotypes of affected tissue
genotypeN	character or logical vector with same length as genotypeT, genotypes of unaffected, normal tissue

Details

Heterozygous probes have one the following values. TRUE, 'H' or 'AB'. All other values are considered homozygous. The primary purpose of the method is to find probes with loss of heterozygosity (LOH), where the unaffected probe is heterozygous and the affected is called homozygous.

Value

A vector with the same length as the arguments where each element can have one of four values

'u'	Uninformative: both affected and normal are homozygous
'i'	Informative: both affected and unaffected heterozygous
'l'	Loss: unaffected heterozygous, affected homozygous
'a'	Artefact: unaffected homozygous, affected heterozygous

Author(s)

Jan Oosting

See Also

heterozygousSNPs

Examples

```
data(chr17.260)
compareGenotypes(exprs(chr17.260)[,"514TV"],exprs(chr17.260)[,"514NP"])
```

---

copynumberConversion *Conversion to Copynumber analysis objects*

Description

SnpSetIllumina objects are converted to other objects for numerical analysis

Usage

```
convert2aCGH(object,normalizedTo=2,doLog=TRUE,organism="hsa")
convert2SegList(object,normalizedTo=2,doLog=TRUE,organism="hsa")
```

Arguments

object	SnpSetIllumina object
normalizedTo	numeric, 'normal' copynumber datavalue for object
doLog	logical, perform logarithmic transformation (log2)
organism	character, organism used in object. Currently 'hsa' and 'mmu' are recognized. Used to convert sex chromosomes to their proper numerical representation

Details

These functions produce objects that can be used by the analysis functions in the aCGH or snapCGH packages. The SnpSetIllumina intensity values are stored in a linear scale. Both types of objects assume a logarithmic scale, so by default the values are transformed to a log2 scale centered around 0.

Value

convert2aCGH returns a aCGH object as used in the aCGH package. convert2SegList returns a SegList object as used in the snapCGH package.

Author(s)

Jan Oosting

See Also

SnpSetIllumina-class, aCGH-class, SegList-class

createCNSummary *Summarization of Copy number states*

Description

Create a summary object of the genomic copy number states in a sample of segmented data

Usage

```
createCNSummary(object, sample, dnaIndex=1, subsample = "OPA")
```

Arguments

object	SNPSetIllumina object after segmentation segmentate
sample	SampleName or index of the sample for which to create the summary
dnaIndex	Measured DNA index of the sample
subsample	factor or column name in featureData slot

Details

The segments within a sample are assigned a copy number value. When the inferred slot in assayData is empty, all segments will be set to 2. Otherwise the values are recovered from the inferred slot. Gender is taken into account for the sex chromosomes.

Value

list with the following elements

dnaIndex	same as parameter dnaIndex
CN.total.nrm	Total expected copynumber for a 'normal' specimen ~ 2*featurecount
states	data.frame with columns opa, count ,intensity, copynumber

This list can be used as the cn.sum argument for plotGoldenGate4OPA, alterCN, getDNAindex and setRealCN

Author(s)

Jan Oosting

See Also

segmentate, alterCN, plotGoldenGate4OPA

dist.GT *dist.GT*

Description

Calculate distance matrix based of differences in genotype calls

Usage

```
dist.GT(object)
```

Arguments

object	SnpSetIllumina object

Details

Calculates distances between samples as percentage of differences in genotype

Value

'dist.GT' returns an object of class 'dist'

Author(s)

Jan Oosting

See Also

dist, hclust

Examples

```
data(chr17.260)
plot(hclust(dist.GT(chr17.260)))
```

GenomicReports *Genomic reports*

Description

Create reports for all samples in a dataset.

Usage

```
reportChromosomesSmoothCopyNumber(snpdata, grouping, normalizedTo=2,
  smooth.lambda=2, ridge.kappa=0, plotLOH=c("none", "marker", "line", "NorTum"),
  sample.colors = NULL, ideo.bleach=0.25, ...)
reportSamplesSmoothCopyNumber(snpdata, grouping, normalizedTo=2,
  smooth.lambda=2, ridge.kappa=0, plotLOH=c("none", "marker", "line", "NorTum"),
  sample.colors=NULL, ...)
reportGenomeGainLossLOH(snpdata, grouping, plotSampleNames=FALSE, sizeSampleNames=4,
 distance.min, upcolor="red", downcolor="blue", lohcolor="grey", hetcolor="lightgrey",
  lohwidth=1, segment=101, orientation=c("V","H"), ...)
reportChromosomeGainLossLOH(snpdata, grouping, plotSampleNames=FALSE, distance.min,
 upcolor="red", downcolor="blue", lohcolor="grey", hetcolor="lightgrey", proportion=0.2,
  plotLOH=TRUE, segment=101, ...)
reportGenomeIntensityPlot(snpdata, normalizedTo=NULL, subsample=NULL, smoothing=c("mean", "quant"),
  dot.col="black", smooth.col="red", ...)
```

Arguments

snpdata	SnpSetIllumina object.
grouping	factor, elements with same value are plotted together. Defaults to groups of 4 in order of the samples in the object.
normalizedTo	numeric, a horizontal line is drawn at this position.
smooth.lambda	smoothing parameter for quantsmooth.
ridge.kappa	smoothing parameter for quantsmooth.
plotLOH	indicate regions or probes with LOH, see details.
sample.colors	vector of color.
plotSampleNames	logical.
sizeSampleNames	numeric, margin size for sample names.
distance.min	numerical.
upcolor	color.
downcolor	color.
lohcolor	color.
hetcolor	color.

lohwidth	numerical, relative width of the LOH part of the sample
segment	integer.
orientation	["V","H"], vertical or horizontal orientation of plot.
proportion	numerical, proportion of the plot to use for idiogram annotation
subsample	character, or factor of length of features
smoothing	Type of smoothing per chromosome.
dot.col	color.
smooth.col	color.
ideo.bleach	numeric [0,1]
...	arguments are forwarded to plot or getChangedRegions.

Details

The first function creates plots for each group and each chromosome in the dataset. The second function creates full genome plot for each group in the dataset. Beware that a lot of plots can be created, and usually you should prepare for that, by redirecting the plots to pdf or functions that create picture files like jpg, png, bmp.

Value

These functions are executed for their side effects

Author(s)

Jan Oosting

See Also

quantsmooth,prepareGenomePlot, pdfChromosomesSmoothCopyNumber, pdfSamplesSmoothCopyNumber

Examples

```
data(chr17.260)
chr17nrm <- standardNormalization(chr17.260)
par(mfrow = c(4,2), mar = c(2,4,2,1))
reportChromosomesSmoothCopyNumber(chr17nrm, grouping=pData(chr17.260)$Group,smooth.lambda = 4)
```

GetBeadStudioSampleNames *Extract samplenames from a report file*

Description

Extract the samplenames from a report file that was created as a final report from Illumina Beadstudio

Usage

```
GetBeadStudioSampleNames(reportfile)
```

Arguments

reportfile	character, name of report file

Details

This function will read the report file, and extract the sample names from the `Sample ID` column

Value

character vector

Author(s)

Jan Oosting

See Also

`read.SnpSetIllumina`

---

getDNAindex *Calculate the DNA index based on assigned copy number values to probes*

Description

Calculate the DNA index based on assigned copy number values to probes

Usage

```
getDNAindex(cn.sum)
```

Arguments

cn.sum	list with elements dnaIndex, CN.total.nrm, states, see createCNSummary

Value

scalar. DNA index of an unaffected sample is 1

Author(s)

Jan Oosting

See Also

createCNSummary, plotGoldenGate4OPA

---

heterozygosity *Find regions of homozygous SNPs*

Description

Analyze affected material without corresponding unaffected material in order to find regions that contain stretches of homozygous SNPs as an indication of loss of heterozygosity (LOH)

Usage

```
heterozygosity(genotype, decay = 0.8, threshold = 0.1)
```

Arguments

genotype	character or logical vector, genotypes of affected tissue
decay	numeric in range (0,1)
threshold	numeric in range (0,1)

Details

The method calculates how long the stretch of homozygous SNPs is for each element delay and threshold can be set to skip individual heterozygous probes in a longer stretch of homozygous probes. The default setting tolerate 1 erroneous heterozygous SNP every 10 homozygous SNPs. Set threshold at 1 to stop discarding hetrozygous SNPs

Value

A numeric vector with the same length as genotype is returned. Higher values, of 15 and higher, indicate regions of LOH

Author(s)

Jan Oosting

See Also

compareGenotypes, heterozygousSNPs

Examples

```
data(chr17.260)
plot(heterozygosity(exprs(chr17.260)[,"514TV"]))
```

---

heterozygousSNPs *Retrieve heterozygous SNPs*

Description

Heterozygous SNPs are determined based on quality score criteria

Usage

```
heterozygousSNPs(object, threshold=0.9, useQuality=TRUE, relative=TRUE,
                 percentile=FALSE)
```

Arguments

object	class SnpSetIllumina
threshold	numeric (0:1) minimum quality score to be called heterozygous
useQuality	logical, use quality score
relative	logical, use quality score relative to GTS, see details
percentile	logical, use percentage of probes above threshold

Details

This function presumes that the specificity for determining heterozygity is more important than the sensitivity, and will therefore only call probes heterozygous if that can be done with high certainty. The Illumina genotyping software calculates two quality measures: gen train score (GTS) and gen call score (GCS). The GTS is a measure for how well clusters can be recognized in a training set. This value is probe specific, and the same for all samples in an experiment. The GCS is a probe-specific, sample specific value that measures how close a probe in a sample is to the clusters determined in the training step. This value is always lower than the GTS for a probe.
`read.SnpSetIllumina` will put GCS into the `callProbability` element of the `assaydata` slot and the GTS into the `featureData` slot. The function uses these locations to retrieve the necessary information.
If `relative` is `FALSE` then the raw GCS values are compared to the `threshold`. In this case a `threshold` of around 0.5 should be used. If `relative` is `TRUE` then GCS/GTS is compared to the `threshold` and `threshold` should be around 0.9.
With `percentile=TRUE` the `threshold` quantile is calculated for each sample, and only probes with higher scores can be called heterozygous. A `threshold` of around 0.2 seems to work fine usually.

Value

This function returns a `logical matrix` with same dimensions as `object`.

Note

The purpose of the function is to separate heterozygous probes from non-heterozygous probes. In tumor samples the determination of the genotype can be difficult, because of aneuploidy and the fact that a sample is often a mixture of normal and tumor cells.

Author(s)

Jan Oosting

See Also

`SnpSetIllumina-class`

Examples

```
data(chr17.260)
plot(heterozygosity(heterozygousSNPs(chr17.260[,"514TV"])),col="red",pch="x")
points(heterozygosity(exprs(chr17.260)[,"514TV"]))
```

`Illumina Genomic data` *Illumina example data*

Description

These datasets are subsets of an experiment to test the applicability of paraffin embedded material in Illumina SNP arrays

Usage

```
data(chr17.260)
data(QC.260)
```

Format

`chr17.260` is a `SnpSetIllumina` object with data from chromosome 17 of 24 samples. `QC.260` is a `QCIllumina` object with summary data of 96 samples of a single SAM array

`interactiveCNselect` *Interactive assignment of copynumbers to genomic segments*

Description

This function plots the genomic view of a sample, and allows the assignment of a discrete copy number to each segment

Usage

```
interactiveCNselect(object, sample = 1, dnaIndex)
```

Arguments

`object`	class `SnpSetIllumina` after segmentation
`sample`	Sample identifier within `object`
`dnaIndex`	numeric, measured DNA index of the sample (1=normal)

Details

The user can interactively assign discrete, integer copy number values to each segment. This is done by either clicking in the lower part of a panel to decrease the copy number, or in the higher part of a panel to increase the copy number. The order of copy number values is always maintained; a segment with a lower raw value can not get a higher copy number assigned then a segment with a higher raw copy number value.

Value

list, see `createCNSummary`

Author(s)

Jan Oosting

See Also

`segmentate`, `alterCN`, `plotGoldenGate4OPA` `createCNSummary`

normalizeBetweenAlleles.SNP
between Allele normalization

Description

Perform between Allele normalization on Illumina Golden Gate bead arrays

Usage

```
normalizeBetweenAlleles.SNP(object,method=c("quantile"),subsample="OPA")
```

Arguments

object	class SnpSetIllumina
method	char, type of normalization
subsample	factor with length number of features in object or char,column name in featureData slot

Details

This function performs a quantile normalization between the Red and Green channels for each sample. The rationale for this procedure stems from the fact that the allele frequencies within each channel are always very similar, even in the presence of genomic abnormalities.

Value

This function returns an SnpSetIllumina object.

Author(s)

Jan Oosting

See Also

SnpSetIllumina-class,normalizeWithinArrays.SNP, backgroundCorrect.SNP

Examples

```
data(chr17.260)
data.nrm<-normalizeBetweenAlleles.SNP(chr17.260)
```

normalizeBetweenSubsamples.SNP *Normalization between subsamples*

Description

Quantile normalization between subsamples within a single SnpSetIllumina object

Usage

```
normalizeBetweenSubsamples.SNP(object, subsample = "OPA")
```

Arguments

object	class SnpSetIllumina
subsample	factor with length number of features in object or char,column name in featureData slot

Details

Perform quantile normalization of the red and green channel between subsamples. This can be used in situations where multiple different assays that cover the same genomic regions (or whole genome) have been done on the same biological specimen. This function was introduced for version 5 Golden Gate Linkage analysis that consist of 4 assays of ~ 1500 probes. Where previous versions of this assay each targeted a number of chromosomes, in version 5 each assay covers the whole genome.

Value

This function returns an SnpSetIllumina object.

Author(s)

Jan Oosting

See Also

SnpSetIllumina-class,normalizeBetweenAlleles.SNP, normalizeWithinArrays.SNP,backgroundCorrect.SNP

Examples

```
data(chr17.260)
data.nrm<-normalizeBetweenSubsamples.SNP(chr17.260)
```

normalizeLoci.SNP *locus normalization*

Description

Perform locus normalization on Illumina Golden Gate bead arrays

Usage

```
normalizeLoci.SNP(object, method=c("normals","paired","alleles"), NorTum="NorTum",
                  Gender="Gender", Subject="Subject", normalizeTo=2, trig=FALSE)
```

Arguments

object	object class SnpSetIllumina
method	character. If "normals" then all normal samples in the dataset are used as the invariant set. If "paired" then affected samples are normalized to their paired normal samples. "alleles" fits a linear model between the B-allele ratio and the signal intensity and normalizes for that
NorTum	logical or character vector or name of column in pData slot. depicts the normal, unaffected samples in the dataset. In a character vector these should have the value "N"
Gender	logical or character vector or name of column in pData slot. depicts the female samples in the dataset and is used to normalize the sex chromosomes. In a character vector these should have value "F"
Subject	factor or name of or column in pData slot. This factor is used to pair the samples when method is "paired"
normalizeTo	normalizeTo numeric. The average copy number of the sample.
trig	Logical, use geometric distance of intensity. Otherwise use addition of intensities

Details

This function is usually performed in the last step of normalization in order to obtain calculated copy numbers.

Value

This function returns an SnpSetIllumina object.

Author(s)

Jan Oosting

See Also

SnpSetIllumina,normalizeWithinArrays.SNP, normalizeBetweenAlleles.SNP

Examples

```
data(chr17.260)
data.nrm<-normalizeLoci.SNP(chr17.260)
```

`normalizeWithinArrays.SNP` *Within Array normalization*

Description

Perform within array normalization on Illumina Golden Gate bead arrays.

Usage

```
normalizeWithinArrays.SNP(object, callscore=0.5, normprob=0.5, quantilepersample=FALSE,
                  relative=FALSE, fixed=FALSE, useAll=FALSE, subsample="OPA",
                          Q.scores="callProbability")
```

Arguments

`object`	class SnpSetIllumina.
`callscore`	numeric with range 0:1, threshold for probe inclusion.
`normprob`	numeric with range 0:1, target quantile for normalization. The default is to divide the sample intensities by the median of the selected subset.
`quantilepersample`	logical. If `TRUE` then the threshold is determined for each sample, else it is experiment wide. This is only relevant when `fixed` is `FALSE`.
`relative`	logical. If `TRUE` then the ratio of GCS and GTS is used, else only the GCS is used as the quality score.
`fixed`	logical. If `TRUE` then `callscore` is the fixed threshold for the quality score, else the probes above the quantile `callscore` are used.
`useAll`	logical. If `TRUE` then all probes in the dataset are eligible as the invariant set, else only the heterozygous SNPs.
`subsample`	factor or column name in `featureData` slot, the levels of the factor are treated separately.
`Q.scores`	name of assayData() element, or numeric matrix of appropriate size. Quality scores to select high quality SNPs

Details

The function uses high quality heterozygous SNPs as an invariant set with the assumption that these have the highest probability of coming from unaffected regions of the genome. Most of the arguments are used to determine the quality of the call.

Value

This function returns a SnpSetIllumina object.

Author(s)

Jan Oosting

See Also

SnpSetIllumina,normalizeLoci.SNP, backgroundCorrect.SNP,normalizeBetweenAlleles.SNP

Examples

```
data(chr17.260)
data.nrm <- normalizeWithinArrays.SNP(chr17.260)
```

---

pdfChromosomesSmoothCopyNumber

reportWrappers

Description

Functions that help create pdf reports

Usage

```
pdfChromosomesSmoothCopyNumber(object, filename, ...)
pdfSamplesSmoothCopyNumber(object, filename, ...)
pdfChromosomeGainLossLOH(object, filename, ...)
```

Arguments

object	SnpSetIllumina object
filename	filename of output pdf file
...	arguments for report functions

Details

These functions set up and perfom reporting to pdf files.

Value

This function is used for its side effects

Author(s)

Jan Oosting

See Also

reportChromosomesSmoothCopyNumber, reportSamplesSmoothCopyNumber, reportChromosomeGainLossLOH

Examples

```
 ## Not run: data(chr17.260)
 ## Not run: data.nrm<-standardNormalization(chr17.260)
## Not run: pdfChromosomesSmoothCopyNumber(data.nrm, "Chr17.pdf", grouping=pData(data.nrm)$Group,smooth.lambda=
```

---

pdfQC *QCreport*

Description

Create PDF file with experimental quality control plots

Usage

```
pdfQC(object, filename = "arrayQC.pdf", by = 10)
```

Arguments

object	QCIllumina object, or list of QCIllumina objects
filename	character, output pdf filename
by	number of samples in barplot, see reportSamplePanelQC

Details

This function creates a pdf file with QC information. The first page contains 8 plotQC panels showing the spatial distribution of intensities on a SAM plate. The following page(s) contain the output of reportSamplePanelQC

Value

A PDF file is produced

Author(s)

Jan Oosting

See Also

plotQC, reportSamplePanelQC, QCIllumina-class

plotGoldenGate4OPA *Plot Golden Gate genomic view*

Description

Plots a full genome view based on 4 subsamples of Illumina Golden Gate data

Usage

```
plotGoldenGate4OPA(object, cn.sum = NULL, sample = 1, plotRaw = FALSE, main = NULL, interact = FALSE, ...
plotGenomePanels(object, cn.sum = NULL, sample = 1, plotRaw = FALSE, main = NULL, interact = FALSE, allLa
```

Arguments

object	class SnpSetIllumina
cn.sum	list containing genomic states, see createCNSummary
sample	identifier to select the sample within the object
plotRaw	logical, plot raw data points
main	character, Title of plot
interact	logical, plot should be usable for interactive copy number determination interactiveCNselect
allLair	logical, TRUE: plot all LAIR values, FALSE: only plot LAIR values from probes that are heterozygous in the paired normal sample
panels	list, vectors of chromosomes for each panel
...	extra arguments are formwarded to plot

Details

prepare interactive selection

Value

list, see createCNSummary

Author(s)

Jan Oosting

See Also

segmentate, alterCN, interactiveCNselect createCNSummary

plotQC *Spatial plots of array QC information*

Description

Plots array wide summary information using the layout of the physical medium

Usage

```
plotQC(object, type)
```

Arguments

object	object that contains QC information. e.g. QCIllumina-class
type	character, the type of information to plot, currently the following types are supported: "intensityMed","greenMed","redMed", "validn","annotation" and "samples"

Value

The function is used for its side effects

Author(s)

Jan Oosting

See Also

pdfQC, reportSamplePanelQC

Examples

```
data(QC.260)
plotQC(QC.260,"greenMed")
```

PolarTransforms *Polar transformations*

Description

Perform polar transforms on Illumina Golden Gate bead arrays

Usage

```
RG2polar(object,trig=FALSE)
polar2RG(object,trig=FALSE)
```

Arguments

object	SnpSetIllumina object
trig	Logical, use geometric distance intensity. Otherwise use addition of intensities

Details

RG2polar transforms the R and G matrices to theta and intensity matrices. Note that the intensity value is the sum of R and G and not the geometric distance to the origin.

polar2RG performs the reverse transformation

Value

This function returns an SnpSetIllumina object.

Author(s)

Jan Oosting

See Also

SnpSetIllumina-class

Examples

```
data(chr17.260)
data.polar<-RG2polar(chr17.260)
plot(assayData(data.polar)$theta,assayData(data.polar)$intensity)
```

QCaccessors *Accessor methods for QC objects*

Description

These generic functions set and retrieve properties of quality control objects like QCIllumina-class

Usage

```
arrayType(object)
arrayType(object)<- value
arrayID(object)
arrayID(object)<- value
```

Arguments

object	Object, possibly derived from class QCIllumina-class.
value	character.

Details

Currently the following types of arrays are supported

"Sentrix96": Sentrix array, 12 columns, 8 rows

"Sentrix16": Sentrix array, 2 columns, 8 rows

"Slide12" : Slide with 12 samples

Value

`arrayType` and `arrayID` return a `character` value

Author(s)

Jan Oosting

QCIllumina-class *Class "QCIllumina"*

Description

Container of QC information on arrays that contain multiple samples.

Objects from the Class

Objects can be created by calls of the form `new("QCIllumina", arrayType, arrayID, intensityMed, greenMed, redMed, intensityMode, greenMode, redMode, validn, annotation, samples)`, but are usually created by `calculateQCarray`.

Slots

`arrayType`: character, Type of array. See `arrayType`

`arrayID`: character, Array ID

`intensityMed`: numeric matrix, Median of intensity of samples

`greenMed`: numeric matrix, Median of green values

`redMed`: numeric matrix, Median of red values

`callrate`: numeric matrix, callrate of genotyping

`hetPerc`: numeric matrix, Percentage of heterozygotes

`ptpdiff`: numeric matrix, point-to-point difference, local estimate of variability

`validn`: numeric matrix, Number of valid probe values in samples

`annotation`: character matrix, Annotation of samples

`samples`: character matrix, Sample IDs

Methods

arrayID `signature(object = "QCIllumina")`: Returns type of array

arrayID<- `signature(object = "QCIllumina")`: Sets type of array. Currently only `"Sentrix"` is supported

arrayType `signature(object = "QCIllumina")`: Returns ID of array

arrayType<- `signature(object = "QCIllumina")`: Sets ID/Barcode of array

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

plotQC `signature(object = "QCIllumina")character`: plots spatial overview of QC information, `type` is one of `c("intensityMed", "greenMed","redMed","validn","annotation","samples")`

Author(s)

Jan Oosting

See Also

`calculateQCarray`

---

read.SnpSetIllumina *Read Experimental Data, Featuredata and Phenodata into an 'SnpSetIllumina' Object*

Description

A SnpSetIllumina object is created from the textfiles created by the Illumina GenCall or BeadStudio software.

Usage

```
read.SnpSetIllumina(samplesheet, manifestpath=NULL, reportpath=NULL,
  rawdatapath=NULL, reportfile=NULL, briefOPAinfo=TRUE, readTIF=FALSE,
  nochecks=FALSE, sepreport="\t", essentialOnly=FALSE, ...)
```

Arguments

`samplesheet`	a data.frame or filename, contains the sample sheet
`manifestpath`	a character string for the path containing the manifests / OPA definition files, defaults to path of samplesheet
`reportpath`	a character string for the path containing the report files, defaults to path of samplesheet
`rawdatapath`	a character string for the path containing the intensity data files, defaults to path of samplesheet
`reportfile`	a character string for the name of BeadStudio reportfile

briefOPAinfo	logical, if TRUE then only the SNP name, Illumi code, chromosome and basepair position are put into the featureData slot of the result, else all information from the OPA file is put into the featureData slot
readTIF	logical, uses beadarray package and raw TIF files to read data
nochecks	logical, limited validity checks on beadstudio report files. See details
sepreport	character, field separator character for beadstudio report files
essentialOnly	logical, if TRUE then only the essential columns from a reportfile are included into the result. See details
...	arguments are forwarded to readIllumina and can be used to perform bead-level normalization

Details

The text files from Illumina software are imported to a SnpSetIllumina object. Both result files from GenCall and BeadStudio can be used. In both cases the sample sheets from the experiments are used to select the proper data from the report or data files. The following columns from the sample sheet file are used for this purpose: 'Sample_Name', 'Sentrix_Position', and 'Pool_ID'. The values in columns 'Sample_Plate', 'Pool_ID', and 'Sentrix_ID' should be the same for all samples in the file, as this is the case for processed experiments. The contents of the sample sheet are put into the phenoData slot.

Zero values in the raw data signals are set to NA

Ideally the OPA manifest file containing SNP annotation should be available, these files are provided by Illumina. Columns 'IllCode', 'CHR', and 'MapInfo' are put into the featureData slot.

GenCall Data

In order to process experiments that were genotyped using the GenCall software, the arrays should be scanned with the setting <SaveTextFiles>true</SaveTextFiles> in the Illumina configuration file Settings.XML. 3 Types of files need to be present in the same folder: The sample sheet, .csv files containing signal intensity data, and the report file that contains the genotype information. For each sample in the sample sheet there should be a .csv file with the following file mask: [sam_id]_R00[yy]_C00[xx].csv, where sam_id is the Illumina ID for the SAM, and xx and yy are the column and row number respectively. From the report files the file with mask [Pool_ID]_LocusByDNA[_ExpName].csv is used. 'Pool_ID' is the OPA panel used, and '_ExpName' is optional.

BeadStudio Data

To process experiments that were processed with BeadStudio, only two files are needed. The sample sheet and the Final Report file. The sample sheet must contain the same columns as for GenCall, the report file should contain the following columns: 'SNP Name', 'Sample ID', 'GC Score', 'Allele1 - AB', 'Allele2 - AB', 'GT Score', 'X Raw', and 'Y Raw'. 'SNP Name' and 'Sample ID' are used to form rows and columns in the experimental data, 'GC Score' is put in the callProbability matrix, 'Allele1 - AB' and 'Allele2 - AB' are combined into the call matrix, 'GT Score' is added to the featureData slot, 'X Raw' is put in the R matrix and 'Y Raw' in the G matrix. Other columns in the report file are added as matrices in the assayData slot, or columns in the featureData slot if values are identical for all samples in the reportfile. When nochecks is TRUE then only the 'SNP Name' and 'Sample ID' columns are required. The resulting object is now of class MultiSet

Sample sheets

To help generate a sample sheet for BeadStudio data a `Sample_Map.txt` file can be converted to a sample sheet with the `Sample_Map2Samplesheet` function. For Beadstudio reportfiles it is also possible to set samplesheet=`NULL`. In this case the `phenoData` slot will be fabricated from the sample names in the reportfile.

Manifest/OPA/annotation files

For BeadStudio reportfiles it is not necessary to have a Manifest file if the columns '`Chr`' and '`Position`' are available in the report file. Currently this is the only way to import data from Infinium arrays, because Illumina does not supply Manifest files for these arrays.

Value

This function returns an `SnpSetIllumina` object, or a `MultiSet` object when `nochecks` is `TRUE`.

Author(s)

Jan Oosting

See Also

`SnpSetIllumina-class`, `Sample_Map2Samplesheet`, `readIllumina`

Examples

```
# read a SnpSetIllumina object using example textfiles in data directory
datadir <- system.file("testdata", package="beadarraySNP")
SNPdata <- read.SnpSetIllumina(paste(datadir,"4samples_opa4.csv",sep="/"),datadir)
```

`removeLowQualityProbes`

Quality control of SnpSetIllumina objects

Description

Remove probes form a SnpSetIllumina object that show a low quality throughout the experiment

Usage

```
removeLowQualityProbes(object, cutoff = 0.25)
```

Arguments

`object`	SnpSetIllumina object
`cutoff`	numeric

Details

Probes that have a median value below `cutoff` * median value for the whole experiment are deleted from the object.

Value

SnpSetIllumina object

Author(s)

Jan Oosting

`removeLowQualitySamples`

Quality control of SnpSetIllumina objects

Description

Remove samples from a SnpSetIllumina object that show a low quality

Usage

```
removeLowQualitySamples(object, min.intensity = 1500, min.gt = 100, subsample = "OPA")
```

Arguments

`object`	`SnpSetIllumina-class` object
`min.intensity`	`numeric`. Samples that show a median intensity below this value in either Red or Green channel are removed
`min.gt`	`numeric`. Samples that have less than this amount of valid genotypes are removed
`subsample`	factor or column name in `featureData` slot of `object`

Value

This function returns an `SnpSetIllumina` object.

Author(s)

Jan Oosting

Examples

```
data(chr17.260)
chr17.260<-removeLowQualitySamples(chr17.260,min.gt=10)
```

renameOPA *Change the linkage panel in a dataset*

Description

Change the linkage panel in a dataset

Usage

```
renameOPA(snpdata, newOPA)
```

Arguments

snpdata	SnpSetIllumina object
newOPA	character, new linkage panel

Details

In order to combine different versions of the linkage panels, this function makes it possible to map the equivalent SNPs in both datasets.

Value

SnpSetIllumina object

Author(s)

Jan Oosting

reportGenotypeSegmentation *plot genomic view*

Description

Create a figure that can be used for interactive work

Usage

```
reportGenotypeSegmentation(object, plotRaw = TRUE, subsample = NULL, panels = 0, minProbes = 10, maxY =
```

Arguments

object	class SnpSetIllumina after segmentation
plotRaw	logical
subsample	factor
panels	number of panels on a page
minProbes	minimum number of probes for a chromosome within a panel
maxY	maximum value on vertical scale within panels
...	arguments are forwrded to plot

Value

this function is used for its side effects

Author(s)

Jan Oosting

---

reportSamplePanelQC-methods
reportSamplePanelQC

Description

Show raw intensity values for green and red channel for all samples in an experiment

Usage

```
reportSamplePanelQC(object, by=10, legend=TRUE, ...)
```

Arguments

object	QCIllumina object
by	numeric, number of samples in each plot
legend	logical, create a final plot with a common legend for the barplots
...	arguments are forwarded to barplot

Examples

```
data(QC.260)
par(mfrow=c(2,2))
reportSamplePanelQC(QC.260,by=8)
```

Sample_Map2Samplesheet *Convert Beadstudio Sample Map file to samplesheet*

Description

Create a samplesheet that can be used to import Illumina beadstudio data

Usage

```
Sample_Map2Samplesheet(samplemapfile, saveas = "")
```

Arguments

samplemapfile	character, name of the SampleMap file
saveas	character, optional, name of samplesheet file that can be used directly by read.SnpSetIllumina

Details

During the creation of a final reportfile from Beadstudio there is an option to create Map files. The Sample_Map.txt file can be used to create an initial samplesheet for use in the read.SnpSetIllumina function

Value

A data.frame with the samplesheet

Author(s)

J. Oosting

See Also

read.SnpSetIllumina

segmentate *Segmentation for SnpSetIllumina objects*

Description

Use snapCGH package to perform segmentation

Usage

```
segmentate(object, method = c("DNACopy", "HMM", "BioHMM", "GLAD"), normalizedTo = 2, doLog = TRUE,
           doMerge = FALSE, useLair = FALSE, subsample = "OPA", alpha = 0.01)
```

Arguments

object	class SnpSetIllumina
method	char, type of segmentation
normalizedTo	numeric
doLog	logical, perform transformation before segmentation, see convert2seglist
doMerge	logical, perform merging of close states
useLair	logical, Also segmentate on lair
subsample	factor
alpha	numeric, probability threshold to distinguish segments

Value

SnpSetIllumina object with elements observed, states and predicted set in the AssayData slot

Author(s)

Jan Oosting

---

setRealCN *Integrate state information into SNP object*

Description

Set calculated values of copy numbers in inferred element of AssayData slot

Usage

```
setRealCN(object, sample, cn.sum, subsample="OPA")
```

Arguments

object	class SnpSetIllumina
sample	sample identifier
cn.sum	list, see createCNSummary
subsample	"OPA"

Value

SnpSetIllumina object with inferred element of AssayData slot set

Author(s)

Jan Oosting

See Also

segmentate, alterCN, plotGoldenGate4OPA createCNSummary

smoothed.intensity *Smooth intensity data*

Description

Create a table of smoothe intensity values

Usage

```
smoothed.intensity(snpdata, smooth.lambda = 4, tau = 0.5)
```

Arguments

snpdata	SnpSetIllumina object
smooth.lambda	smoothing parameter
tau	quantile to smooth

Value

Numerical matrix with same dimensions as data

Author(s)

Jan Oosting

See Also

SnpSetIllumina-class

SnpSetIllumina *Class to Contain Objects Describing High-Throughput SNP Assays.*

Description

Container for high-throughput assays and experimental metadata. SnpSetIllumina class is derived from eSet, and requires matrices R, G, call, callProbability as assay data members.

It supports featureData. Several visualization methods use columns CHR and MapInfo. The CHR column is used to handle sex chromosomes in a specific way. The OPA column is the default way to specify subsamples.

Extends

Directly extends class eSet.

Creating Objects

new('SnpSetIllumina', phenoData = [AnnotatedDataFrame], experimentData = [MIAME], annotation = [character], call = [matrix], callProbability = [matrix], G = [matrix], R = [matrix], featureData = [data.frameOrNULL], ...)

SnpSetIllumina instances are usually created through new("SnpSetIllumina", ...). Arguments to new include call (a matrix of gentoypic calls, with features (SNPs) corresponding to rows and samples to columns), callProbability, G, R, phenoData, experimentData, and annotation. phenoData, experimentData, and annotation can be missing, in which case they are assigned default values.

Slots

Inherited from Biobase:eSet:

assayData: Contains matrices with equal dimensions, and with column number equal to nrow(phenoData). assayData must contain a matrix call with rows representing features (e.g., SNPs) and columns representing samples, a matrix callProbability describing the certainty of the call, and matrices R and G to describe allele specific intensities. The contents of these matrices are not enforced by the class. The assayData matrices Gb, Rb, intensity, theta are optional, but are either results or input for several methods of the class. Additional matrices of identical size may also be included in assayData. Class:AssayData.

phenoData: See eSet.

experimentData: See eSet.

annotation: See eSet.

featureData: annotation for SNPs, usually will contain a CHR and a MapInfo column for genomic localization.

Methods

Class-specific methods:

exprs(SnpSetIllumina), exprs(SnpSetIllumina,matrix)<- Access and set elements named call in the AssayData slot.

combine(SnpSetIllumina,SnpSetIllumina): performs union-like combination in both dimensions of SnpSetIllumina objects.

fData(SnpSetIllumina), fData(SnpSetIllumina,data.frame)<- Access and set the pData in the featureData slot.

calculateGSR(SnpSetIllumina) calculate ratio of Gentrain score and Gencall score. Creates GSR matrix in assayData. Should be performed before combining datasets.

calculateSmooth(object,smoothType) calculate smoothed data, creates smoothed matrix in assayData. smoothType can only be "quantsmooth" at the moment

sortGenomic(SnpSetIllumina) order the data by chromosome and position on the chromosome.

Derived from eSet:

sampleNames(SnpSetIllumina) **and** sampleNames(SnpSetIllumina)<-: See eSet.

`featureNames(SnpSetIllumina)`, `featureNames(SnpSetIllumina, value)<-`: See eSet.

`dims(SnpSetIllumina)`: See eSet.

`phenoData(SnpSetIllumina)`, `phenoData(SnpSetIllumina,value)<-`: See eSet.

`varLabels(SnpSetIllumina)`, `varLabels(SnpSetIllumina, value)<-`: See eSet.

`varMetadata(SnpSetIllumina)`, `varMetadata(SnpSetIllumina,value)<-`: See eSet.

`pData(SnpSetIllumina)`, `pData(SnpSetIllumina,value)<-`: See eSet.

`varMetadata(SnpSetIllumina)`, `varMetadata(SnpSetIllumina,value)` See eSet.

`experimentData(SnpSetIllumina)`,`experimentData(SnpSetIllumina,value)<-`: See eSet.

`pubMedIds(SnpSetIllumina)`, `pubMedIds(SnpSetIllumina,value)` See eSet.

`abstract(SnpSetIllumina)`: See eSet.

`annotation(SnpSetIllumina)`, `annotation(SnpSetIllumina,value)<-` See eSet.

`storageMode(eSet)`, `storageMode(eSet,character)<-`: See eSet.

`featureData(SnpSetIllumina)`, `featureData(SnpSetIllumina,AnnotatedDataFrame)<-` See eSet.

`object[(index)`: Conducts subsetting of matrices and phenoData and featureData components.

Standard generic methods:

`initialize(SnpSetIllumina)`: Object instantiation, used by `new`; not to be called directly by the user.

`validObject(SnpSetIllumina)`: Validity-checking method, ensuring that `call`, `callProbability`, `G`, and `R` are members of `assayData`. `checkValidity(SnpSetIllumina)` imposes this validity check, and the validity checks of `Biobase:class.eSet`.

`show(SnpSetIllumina)` See eSet.

`dim(SnpSetIllumina)`, `ncol` See eSet.

`SnpSetIllumina[(index)`: See eSet.

`SnpSetIllumina$`, `SnpSetIllumina$<-` See eSet.

Author(s)

J. Oosting, based on Biobase eSet class

See Also

eSet

SnpSetSegments-class *Class "SnpSetSegments"*

Description

The SnpSetSegments class is a direct descendant of the SnpSetIllumina class, with an extra slot to define the genomic segments in each sample.

Objects from the Class

Objects can be created by calls of the form `new("SnpSetSegments", assayData, phenoData, experimentData, annotation, protocolData, call, callProbability, G, R, cn.segments, featureData, extraData, ...)`.

Slots

`cn.segments`: Object of class `"list"`

`assayData`: Object of class `"AssayData"` see `"SnpSetIllumina"`

`phenoData`: Object of class `"AnnotatedDataFrame"` see `"SnpSetIllumina"`

`featureData`: Object of class `"AnnotatedDataFrame"` see `"SnpSetIllumina"`

`experimentData`: Object of class `"MIAME"` see `"SnpSetIllumina"`

`annotation`: Object of class `"character"` see `"SnpSetIllumina"`

`protocolData`: Object of class `"AnnotatedDataFrame"` see `"SnpSetIllumina"`

`.__classVersion__`: Object of class `"Versions"` `"VersionedBiobase"`

Extends

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

Methods

cn.segments `signature(object = "SnpSetSegments")`: ...

cn.segments<- `signature(object = "SnpSetSegments", value = "list")`: ...

initialize `signature(.Object = "SnpSetSegments")`: ...

Note

This class is under development, and not usable in the current form

Author(s)

Jan Oosting

References

Corver et.al. Can Res dec 2008

See Also

segmentate

Examples

```
showClass("SnpSetSegments")
```

---

standardNormalization *Default complete normalization*

Description

Performs all steps in normalization at best settings as determined in ref.

Usage

```
standardNormalization(snpdata)
```

Arguments

snpdata	SnpSetIllumina object with raw data

Details

The function performs in the following steps
`snpdata<-normalizeBetweenAlleles.SNP(snpdata)`
`snpdata<-normalizeWithinArrays.SNP(snpdata,callscore = 0.8, relative = TRUE, fixed = FALSE, quantilepersample = TRUE)`
`snpdata<-normalizeLoci.SNP(snpdata,normalizeTo = 2)`

Value

A `SnpSetIllumina` object with the `G`, `R` and `intensity` elements in assayData normalized to obtain values close to 2 on a linear scale for unaffected material.

Author(s)

Jan Oosting

See Also

normalizeBetweenAlleles.SNP,normalizeWithinArrays.SNP, normalizeLoci.SNP

Examples

```
data(chr17.260)
data.nrm<-standardNormalization(chr17.260)
```

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