

# Package ‘beadarraySNP’

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**Type** Package

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**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** CopyNumberVariants, SNP, GeneticVariability, TwoChannel,Preprocessing, DataImport

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alterCN	<i>alterCN</i>
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## 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	character, 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 through 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 <a href="#">reportSamplePanelQC</a>

**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](#)

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calculateLOH	<i>Determine LOH in experiment</i>
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### 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	<i>Retrieve QC information from a SnpSetIllumina object</i>
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### 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 <a href="#">arrayType</a>

### 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	<i>Compare genotypes</i>
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### 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 data value 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 <a href="#">segmentate</a>
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](#)

---

<code>dist.GT</code>	<i>dist.GT</i>
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---

**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	SnpsSetIllumina 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 <a href="#">quantsmooth</a> .
ridge.kappa	smoothing parameter for <a href="#">quantsmooth</a> .
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](#), [plotGoldenGate40PA](#)

---

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 decay 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 heterozygous 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](#), [plotGoldenGate40PA](#) [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**

<code>object</code>	class <code>SnpSetIllumina</code>
<code>subsample</code>	factor with length number of features in object or char,column name in <code>featureData</code> 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	<i>locus normalization</i>
-------------------	----------------------------

---

**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**

<code>object</code>	<code>SnpSetIllumina</code> object
<code>filename</code>	filename of output pdf file
<code>...</code>	arguments for report functions

**Details**

These functions set up and perform 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.lambdas=
```

---

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 <a href="#">reportSamplePanelQC</a>

**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, panels = NULL, ...)
```

### Arguments

object	class SnpSetIllumina
cn.sum	list containing genomic states, see <a href="#">createCNSummary</a>
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 <a href="#">interactiveCNselect</a>
panels	list, vectors of chromosomes for each panel
...	extra arguments are forwarded 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 <a href="#">QCillumina-class</a> .
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)` 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 <a href="#">readIllumina</a> 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', 'Sentry\_Position', and 'Pool\_ID'. The values in columns 'Sample\_Plate', 'Pool\_ID', and 'Sentry\_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 from 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  $\text{cutoff} * \text{median value for the whole experiment}$  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	<a href="#">SnpSetIllumina-class</a> 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	<i>Change the linkage panel in a dataset</i>
-----------	--

---

**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	<i>plot genomic view</i>
----------------------------	--------------------------

---

**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 forwarded 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 <code>convert2seglist</code>
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 <code>createCNSummary</code>
subsample	"OPA"

**Value**

SnpSetIllumina object with inferred element of AssayData slot set

**Author(s)**

Jan Oosting

**See Also**

[segmentate](#), [alterCN](#), [plotGoldenGate40PA](#) [createCNSummary](#)

---

smoothed.intensity      *Smooth intensity data*

---

**Description**

Create a table of smoothed 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 = [
```

SnpSetIllumina instances are usually created through `new("SnpSetIllumina", ...)`. Arguments to `new` include `call` (a matrix of genotypic 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, annotat`

### 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, quanti`  
`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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