crlmm

October 5, 2010

`CNSetLM-class` *CNSetLM class*

Description

Container for allele-specific copy number and linear model parameters

Objects from the Class

Objects from the class can be created by calls of the form `new("CNSetLM", CA=matrix(), CB=matrix(), alleleA=matrix(), alleleB=matrix(), call=matrix(), callProbability=`

Slots

`lM`: Object of class `"list_or_ffdf"`

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

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

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

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

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

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

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

Extends

Class `"CNSet"`, directly. Class `"SnpSuperSet"`, by class "CNSet", distance 2. Class `"AlleleSet"`, by class "CNSet", distance 3. Class `"SnpSet"`, by class "CNSet", distance 3. Class `"eSet"`, by class "CNSet", distance 4. Class `"VersionedBiobase"`, by class "CNSet", distance 5. Class `"Versioned"`, by class "CNSet", distance 6.

Methods

[`signature(x = "CNSetLM")`: subset `CNSetLM` objects

lM `signature(object = "CNSetLM")`: Extract list or ffdf object containing linear model parameters ##

lM<- `signature(object = "CNSetLM", value = "list_or_ffdf")`: ...

open `signature(con = "CNSetLM")`: opens file connects to ff objects for assayData elements and linear model parameters

show `signature(object = "CNSetLM")`: print method for the class

Author(s)

R. Scharpf

See Also

SnpSuperSet, CNSet

Examples

```
showClass("CNSetLM")
```

---

batch *Function to extract batch information.*

Description

Checks the phenoData and protocolData for a variable named batch and, if present, returns the vector.

Usage

```
batch(object)
```

Arguments

object	An object extending the eSet class.

Details

For copy number estimation, a batch variable must be specified. Currently, we suggest storing this variable in the protocolData.

Batch represents groups of samples that were processed (DNA preparation and collection, PCR amplification, scan date) at similar times. Often, the 96 well chemistry plate or scan date is a useful surrogate for batch.

Value

Vector indicating batch.

Author(s)

R. Scharpf

See Also

genotype, genotype2

celDates *Extract dates from the cel file header*

Description

Extract dates from the cel file header.

Usage

```
celDates(celfiles)
```

Arguments

celfiles	CEL file names. Must specify the complete path.

Value

date-time class POSIXt

Author(s)

R. Scharpf

See Also

read.celfile.header, *POSIXt*

crlmm-package *Genotype Calling via CRLMM Algorithm*

Description

Faster implementation of CRLMM specific to SNP 5.0 and 6.0 arrays.

Details

Index:

```
crlmm-package           New implementation of the CRLMM Algorithm.
crlmm                   Genotype SNP 5.0 or 6.0 samples.
calls                   Accessor for genotype calls.
confs                   Accessor for confidences.
```

The 'crlmm' package reimplements the CRLMM algorithm present in the 'oligo' package. This implementation primes for efficient genotyping of samples on SNP 5.0 and SNP 6.0 Affymetrix arrays.

To use this package, the user must have additional data packages: 'genomewidesnp5Crlmm' - SNP 5.0 arrays 'genomewidesnp6Crlmm' - SNP 6.0 arrays

Author(s)

Rafael A Irizarry Maintainer: Benilton S Carvalho <carvalho@bclab.org>

References

Carvalho BS, Louis TA, Irizarry RA. Quantifying uncertainty in genotype calls. Bioinformatics. 2010 Jan 15;26(2):242-9. Epub 2009 Nov 11.

`crlmm` *Genotype oligonucleotide arrays with CRLMM*

Description

This is a faster and more efficient implementation of the CRLMM algorithm, especially designed for Affymetrix SNP 5 and 6 arrays (to be soon extended to other platforms).

Usage

```
crlmm(filenames, row.names=TRUE, col.names=TRUE,
      probs=c(1/3, 1/3, 1/3), DF=6, SNRMin=5,
      gender=NULL, save.it=FALSE, load.it=FALSE,
      intensityFile, mixtureSampleSize=10^5,
      eps=0.1, verbose=TRUE, cdfName, sns, recallMin=10,
      recallRegMin=1000, returnParams=FALSE, badSNP=0.7)
crlmm2(filenames, row.names=TRUE, col.names=TRUE,
      probs=c(1/3, 1/3, 1/3), DF=6, SNRMin=5,
      gender=NULL, save.it=FALSE, load.it=FALSE,
      intensityFile, mixtureSampleSize=10^5,
      eps=0.1, verbose=TRUE, cdfName, sns, recallMin=10,
      recallRegMin=1000, returnParams=FALSE, badSNP=0.7)
```

Arguments

`filenames`	'character' vector with CEL files to be genotyped.
`row.names`	'logical'. Use rownames - SNP names?
`col.names`	'logical'. Use colnames - Sample names?
`probs`	'numeric' vector with priors for AA, AB and BB.
`DF`	'integer' with number of degrees of freedom to use with t-distribution.
`SNRMin`	'numeric' scalar defining the minimum SNR used to filter out samples.
`gender`	'integer' vector, with same length as 'filenames', defining sex. (1 - male; 2 - female)
`save.it`	'logical'. Save preprocessed data?
`load.it`	'logical'. Load preprocessed data to speed up analysis?
`intensityFile`	'character' with filename to be saved/loaded - preprocessed data.
`mixtureSampleSize`	Number of SNP's to be used with the mixture model.
`eps`	Minimum change for mixture model.

verbose	'logical'.
cdfName	'character' defining the CDF name to use ('GenomeWideSnp5', 'GenomeWideSnp6')
sns	'character' vector with sample names to be used.
recallMin	Minimum number of samples for recalibration.
recallRegMin	Minimum number of SNP's for regression.
returnParams	'logical'. Return recalibrated parameters.
badSNP	'numeric'. Threshold to flag as bad SNP (affects batchQC)

Details

'crlmm2' allows one to genotype very large datasets (via ff package) and also permits the use of clusters or multiple cores (via snow package) to speed up genotyping.

Value

A SnpSet object.

calls	Genotype calls (1 - AA, 2 - AB, 3 - BB)
confs	Confidence scores 'round(-1000*log2(1-p))'
SNPQC	SNP Quality Scores
batchQC	Batch Quality Score
params	Recalibrated parameters

References

Carvalho B, Bengtsson H, Speed TP, Irizarry RA. Exploration, normalization, and genotype calls of high-density oligonucleotide SNP array data. Biostatistics. 2007 Apr;8(2):485-99. Epub 2006 Dec 22. PMID: 17189563.

Carvalho BS, Louis TA, Irizarry RA. Quantifying uncertainty in genotype calls. Bioinformatics. 2010 Jan 15;26(2):242-9.

Examples

```
## this can be slow
if (require(genomewidesnp6Crlmm) & require(hapmapsnp6)){
  path <- system.file("celFiles", package="hapmapsnp6")

  ## the filenames with full path...
  ## very useful when genotyping samples not in the working directory
  cels <- list.celfiles(path, full.names=TRUE)
  (crlmmOutput <- crlmm(cels))
}

## Not run:
## HPC Example
library(ff)
library(snow)
library(crlmm)
## genotype 50K SNPs at a time
ocProbesets(50000)
## setup cluster - 8 cores on the machine
setCluster(8, "SOCK")
```

```
path <- system.file("celFiles", package="hapmapsnp6")
cels <- list.celfiles(path, full.names=TRUE)
crlmmOutput <- crlmm2(cels)


## End(Not run)
```

`crlmmCopynumber` *Locus- and allele-specific estimation of copy number*

Description

Locus- and allele-specific estimation of copy number.

Usage

```
crlmmCopynumber(object, chromosome = 1:23, which.batches, MIN.SAMPLES
= 10, SNRMin = 5, MIN.OBS = 3, DF.PRIOR = 50, bias.adj = FALSE,
prior.prob = rep(1/4, 4), seed = 1, verbose = TRUE, GT.CONF.THR =
0.99, PHI.THR = 2^6, nHOM.THR = 5, MIN.NU = 2^3, MIN.PHI = 2^3,
THR.NU.PHI = TRUE, thresholdCopynumber = TRUE)

crlmmCopynumber2(object, which.batches, MIN.SAMPLES = 10, SNRMin = 5,
MIN.OBS = 1, DF.PRIOR = 50, bias.adj = FALSE, prior.prob = rep(1/4,
4), seed = 1, verbose = TRUE, GT.CONF.THR = 0.99, PHI.THR = 2^6,
nHOM.THR = 5, MIN.NU = 2^3, MIN.PHI = 2^3, THR.NU.PHI = TRUE,
thresholdCopynumber = TRUE)
```

Arguments

`object`	object of class `SnpSuperSet`.
`which.batches`	Character vector with length equal to the number of samples. Used to adjust for batch effects. Chemistry plate or date often work well. See examples. Ignored in crlmmCopynumber2.
`chromosome`	Numeric vector indicating which chromosomes to process (length <= 23). For chromosome X, use 23. A copy number method for chromosome Y is not yet available.
`MIN.SAMPLES`	'Integer'. The minimum number of samples in a batch. Bathes with fewer than MIN.SAMPLES are skipped. Therefore, samples in batches with fewer than MIN.SAMPLES have NA's for the allele-specific copy number and NA's for the linear model parameters.
`SNRMin`	Samples with low signal to noise ratios are excluded.
`MIN.OBS`	For genotypes with fewer than `MIN.OBS`, the within-genotype median is imputed from the observed genotypes. For example, assume at at a given SNP genotypes AA and AB were observed and BB is an unobserved genotype. For SNPs in which all 3 genotypes were observed, we fit the model E(mean_BB)

= beta0 + beta1*mean_AA + beta2*mean_AB, obtaining estimates; of beta0, beta1, and beta2. The imputed mean at the SNP with unobserved BB is then beta0hat + beta1hat * mean_AA of beta2hat * mean_AB.

`DF.PRIOR` The 2 x 2 covariance matrix of the background and signal variances is estimated from the data at each locus. This matrix is then smoothed towards a common matrix estimated from all of the loci. DF.PRIOR controls the amount of smoothing towards the common matrix, with higher values corresponding to greater smoothing. Currently, DF.PRIOR is not estimated from the data. Future versions may estimate DF.PRIOR empirically.

`bias.adj` If `TRUE`, initial estimates of the linear model are updated after excluding samples that have a low posterior probability of normal copy number. Excluding samples that have a low posterior probability can be helpful at loci in which a substantial fraction of the samples have a copy number alteration. For additional information, see Scharpf et al., 2009.

This argument is ignored in crlmmCopynumber2.

`prior.prob` A numerical vector providing prior probabilities for copy number states corresponding to homozygous deletion, hemizygous deletion, normal copy number, and amplification, respectively.

`seed` Seed for random number generation.

`verbose` Logical.

`GT.CONF.THR` Confidence threshold for genotype calls (0, 1). Calls with confidence scores below this theshold are not used to estimate the within-genotype medians.

`PHI.THR` SNPs with slopes (phi values) below this value are flagged. Flagged SNPs are not used in a regression to impute background and slope coefficients at nonpolymorphic loci.

`nHOM.THR` If fewer than `nHOM.THR` homozygous genotypes (AA or BB) are observed, the SNPs is flagged. Flagged SNPs are not used in a regression to impute background and slope coefficients at nonpolymorphic loci.

`MIN.NU` numeric. Minimum threshold for background. Ignored if `THR.NU.PHI` is `FALSE`.

`MIN.PHI` numeric. Minimum threshold for slope. Ignored if `THR.NU.PHI` is `FALSE`.

`THR.NU.PHI` If `THR.NU.PHI` is `FALSE`, `MIN.NU` and `MIN.PHI` are ignored.

`thresholdCopynumber`
If `TRUE`, allele-specific number estimates are truncated. Values less than 0.05 are assigned the value 0.05; values exceeding 5 are assigned the value 5.

Ignored in crlmmCopynumber2. Extreme values are automatically truncated.

Details

The function crlmmCopynumber uses matrices instead of ff objects if the ff library is not loaded.

The function crlmmCopynumber2 allows parallel processing via and requires large data support via the ff package.

We plan to phase out crlmmCopynumber and replace this function by crlmmCopynumber2.

Author(s)

R. Scharpf

Examples

```
## data(example.callSet)
## cnSet <- crlmmCopynumber2(example.callSet)
## total copy number
## cn <- copyNumber(cnSet)
## allele-specific copy number
## ca <- CA(cnSet)/100 ## A dosage
## cb <- CB(cnSet)/100 ## B dosage
```

`crlmmIllumina` *Genotype Illumina Infinium II BeadChip data with CRLMM*

Description

Implementation of the CRLMM algorithm for data from Illumina's Infinium II BeadChips.

Usage

```
crlmmIllumina(RG, XY, stripNorm=TRUE,
      useTarget=TRUE, row.names=TRUE, col.names=TRUE,
      probs=c(1/3, 1/3, 1/3), DF=6, SNRMin=5,
      gender=NULL, seed=1, save.it=FALSE, load.it=FALSE,
      snpFile, cnFile, mixtureSampleSize=10^5,
      eps=0.1, verbose=TRUE, cdfName, sns, recallMin=10,
      recallRegMin=1000, returnParams=FALSE, badSNP=0.7)
```

Arguments

`RG`	`NChannelSet` containing R and G bead intensities
`XY`	`NChannelSet` containing X and Y bead intensities
`stripNorm`	'logical'. Should the data be strip-level normalized?
`useTarget`	'logical' (only used when `stripNorm=TRUE`). Should the reference HapMap intensities be used in strip-level normalization?
`row.names`	'logical'. Use rownames - SNP names?
`col.names`	'logical'. Use colnames - Sample names?
`probs`	'numeric' vector with priors for AA, AB and BB.
`DF`	'integer' with number of degrees of freedom to use with t-distribution.
`SNRMin`	'numeric' scalar defining the minimum SNR used to filter out samples.
`gender`	'integer' vector, with same length as 'filenames', defining sex. (1 - male; 2 - female)
`seed`	'integer' scalar for random number generator (used to sample `mixtureSampleSize` SNPs for mixture model.
`save.it`	'logical'. Save preprocessed SNP and copy number data?
`load.it`	'logical'. Load preprocessed SNP data to speed up analysis?
`snpFile`	'character' with filename of preprocessed SNP data to be saved/loaded.
`cnFile`	'character' with filename of preprocessed copy number data to be saved.

`mixtureSampleSize`
: 'integer'. The number of SNP's to be used when fitting the mixture model.

`eps`
: Minimum change for mixture model.

`verbose`
: 'logical'.

`cdfName`
: 'character' defining the chip annotation (manifest) to use ('human370v1c', human550v3b', 'human650v3a', 'human1mv1c', 'human370quadv3c', 'human610quadv1b', 'human660quadv1a', 'human1mduov3b', 'humanomni1quadv1b')

`sns`
: 'character' vector with sample names to be used.

`recallMin`
: 'integer'. Minimum number of samples for recalibration.

`recallRegMin`
: 'integer'. Minimum number of SNP's for regression.

`returnParams`
: 'logical'. Return recalibrated parameters.

`badSNP`
: 'numeric'. Threshold to flag as bad SNP (affects batchQC)

Details

Note: The user should specify either the `RG` or `XY` intensities, not both. Alternatively if `crlmmIllumina` has been run already with `save.it=TRUE`, the preprocessed data can be loaded from file by specifying `load.it=TRUE` and `intensityFile` (`RG` or `XY` are not needed in this case).

Value

A `SnpSet` object which contains

`calls`
: Genotype calls (1 - AA, 2 - AB, 3 - BB)

`callProbability`
: confidence scores 'round(-1000*log2(1-p))'

in the `assayData` slot and

`SNPQC`
: SNP Quality Scores

`batchQC`
: Batch Quality Scores

along with center and scale parameters when `returnParams=TRUE` in the `featureData` slot.

Author(s)

Matt Ritchie

References

Ritchie ME, Carvalho BS, Hetrick KN, Tavar\'e S, Irizarry RA. R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. Bioinformatics. 2009 Oct 1;25(19):2621-3.

Carvalho B, Bengtsson H, Speed TP, Irizarry RA. Exploration, normalization, and genotype calls of high-density oligonucleotide SNP array data. Biostatistics. 2007 Apr;8(2):485-99. Epub 2006 Dec 22. PMID: 17189563.

Carvalho BS, Louis TA, Irizarry RA. Quantifying uncertainty in genotype calls. Bioinformatics. 2010 Jan 15;26(2):242-9.

Examples

```
## crlmmOut = crlmmIllumina(RG)
```

genotype *Preprocessing and genotyping of Affymetrix arrays.*

Description

Preprocessing and genotyping of Affymetrix arrays.

Usage

```
genotype(filenames, cdfName, batch, mixtureSampleSize = 10^5, eps =
0.1, verbose = TRUE, seed = 1, sns, copynumber = FALSE, probs =
rep(1/3, 3), DF = 6, SNRMin = 5, recallMin = 10, recallRegMin = 1000,
gender = NULL, returnParams = TRUE, badSNP = 0.7)

genotype2(filenames, cdfName, batch, mixtureSampleSize = 10^5, eps = 0.1, verbos
```

Arguments

filenames	complete path to CEL files
cdfName	annotation package (see also validCdfNames)
batch	batch variable. See details.
mixtureSampleSize	Sample size to be use when fitting the mixture model.
eps	Stop criteria.
verbose	Logical. Whether to print descriptive messages during processing.
seed	Seed to be used when sampling. Useful for reproducibility
sns	The sample identifiers. If missing, the default sample names are basename(filenames)
copynumber	Whether to quantile normalize the nonpolymorphic probes. If TRUE, the quantile normalized intensities for nonpolymorphic markers are included in the 'A' matrix.
probs	'numeric' vector with priors for AA, AB and BB.
DF	'integer' with number of degrees of freedom to use with t-distribution.
SNRMin	'numeric' scalar defining the minimum SNR used to filter out samples.
recallMin	Minimum number of samples for recalibration.
recallRegMin	Minimum number of SNP's for regression.
gender	integer vector (male = 1, female =2) or missing, with same length as filenames. If missing, the gender is predicted.
returnParams	'logical'. Return recalibrated parameters from crlmm.
badSNP	'numeric'. Threshold to flag as bad SNP (affects batchQC)

Details

For large datasets it is important to utilize the large data support by installing and loading the ff package before calling the genotype or genotype2 function.

Currently, two functions are provided for preprocessing and genotyping Affymetrix platforms: genotype and genotype2. For small datasets, genotype and genotype2 are identical. For large datasets, genotype2 provides large data support (via ff) and permits the use of clusters or multiple cores (via snow package) to speed up genotyping (similar to crlmm2). The genotype function will be phased out in the future and replaced by genotype2.

Value

A SnpSuperSet instance.

Note

For large datasets, load the 'ff' package prior to genotyping – this will greatly reduce the RAM required for big jobs. See ldPath and ocSamples.

Author(s)

R. Scharpf

References

Carvalho B, Bengtsson H, Speed TP, Irizarry RA. Exploration, normalization, and genotype calls of high-density oligonucleotide SNP array data. Biostatistics. 2007 Apr;8(2):485-99. Epub 2006 Dec 22. PMID: 17189563.

Carvalho BS, Louis TA, Irizarry RA. Quantifying uncertainty in genotype calls. Bioinformatics. 2010 Jan 15;26(2):242-9.

See Also

snprma, crlmm, ocSamples, ldOpts, batch, crlmmCopynumber

Examples

```
if (require(ff) & require(genomewidesnp6Crlmm) & require(hapmapsnp6)){

  path <- system.file("celFiles", package="hapmapsnp6")
  ## the filenames with full path...
  ## very useful when genotyping samples not in the working directory
  cels <- list.celfiles(path, full.names=TRUE)

  ## To use less RAM, specify a smaller argument to ocProbesets
  ocProbesets(50e3)
  (cnSet <- genotype2(cels, cdfName="genomewidesnp6",
  copynumber=TRUE))

  dim(cnSet)
  table(isSnp(cnSet))

## The above is a trivial example.  Typically you may have a large
##    number of cel files, many of which were processed at different
##    times. For such datasets, it is important to set a batch
##    variable.  If not specified, the scan date of the file is used
##    as the batch variable.
      batch(cnSet)
      protocolData(cnSet)$ScanDate
}
```

misc *Miscellaneous classes*

Description

Added to avoid problems with R CMD check. See the ff package for documentation of the ffdf class.

readIdatFiles *Reads Idat Files from Infinium II Illumina BeadChips*

Description

Reads intensity information for each bead type from .idat files of Infinium II genotyping BeadChips

Usage

```
readIdatFiles(sampleSheet=NULL, arrayNames=NULL, ids=NULL, path="",
              arrayInfoColNames=list(barcode="SentrixBarcode_A",
                                     position="SentrixPosition_A"),
              highDensity=FALSE, sep="_",
              fileExt=list(green="Grn.idat", red="Red.idat"),
              saveDate=FALSE)
```

Arguments

sampleSheet	data.frame containing Illumina sample sheet information (for required columns, refer to BeadStudio Genotyping guide - Appendix A).
arrayNames	character vector containing names of arrays to be read in. If NULL, all arrays that can be found in the specified working directory will be read in.
ids	vector containing ids of probes to be read in. If NULL all probes found on the first array are read in.
path	character string specifying the location of files to be read by the function
arrayInfoColNames	(used when sampleSheet is specified) list containing elements 'barcode' which indicates column names in the sampleSheet which contains the arrayNumber/barcode number and 'position' which indicates the strip number. In older style sample sheets, this information is combined (usually in a column named 'SentrixPosition') and this should be specified as list(barcode=NULL, position="SentrixPosition")
highDensity	logical (used when sampleSheet is specified). If TRUE, array extensions '_A', '_B' in sampleSheet are replaced with 'R01C01', 'R01C02' etc.
sep	character string specifying separator used in .idat file names.
fileExt	list containing elements 'Green' and 'Red' which specify the .idat file extension for the Cy3 and Cy5 channels.
saveDate	logical. Should the dates from each .idat be saved with sample information?

Details

The summarised Cy3 (G) and Cy5 (R) intensities (on the orginal scale) are read in from the .idat files.

Where available, a `sampleSheet` data.frame, in the same format as used by BeadStudio (columns 'Sample_ID', 'SentrixBarcode_A' and 'SentrixPosition_A' are required) which keeps track of sample information can be specified.

Thanks to Keith Baggerly who provided the code to read in the binary .idat files.

Value

NChannelSet with intensity data (`R`, `G`), and indicator for SNPs with 0 beads (`zero`) for each bead type.

Author(s)

Matt Ritchie

References

Ritchie ME, Carvalho BS, Hetrick KN, Tavar\'e S, Irizarry RA. R/Bioconductor software for Illumina's Infinium whole-genome genotyping BeadChips. Bioinformatics. 2009 Oct 1;25(19):2621-3.

Examples

```
#RG = readIdatFiles()
```

`sample.CNSetLM` *Dataset of class 'CNSetLM'*

Description

The data for 2119 polymorphic and nonpolymorphic markers on chromosome 1 for the CEPH and Yoruban HapMap samples.

Usage

```
data(sample.CNSetLM)
```

Format

The data illustrates the `CNSetLM-class`, with `assayData` containing the quantile-normalized intensities for the A and B alleles, genotype calls and confidence scores (call and callProbability), and allele-specific copy number (CA and CB). The parameters from the linear model are stored in the lM slot.

Examples

```
data(sample.CNSetLM)
```

`snprma` *Preprocessing tool for SNP arrays.*

Description

SNPRMA will preprocess SNP chips. The preprocessing consists of quantile normalization to a known target distribution and summarization to the SNP-Allele level.

Usage

```
snprma(filenames, mixtureSampleSize = 10^5, fitMixture = FALSE, eps = 0.1, verbo
snprma2(filenames, mixtureSampleSize = 10^5, fitMixture = FALSE, eps = 0.1, verb
```

Arguments

`filenames`	'character' vector with file names.
`mixtureSampleSize`	Sample size to be use when fitting the mixture model.
`fitMixture`	'logical'. Fit the mixture model?
`eps`	Stop criteria.
`verbose`	'logical'.
`seed`	Seed to be used when sampling.
`cdfName`	cdfName: 'GenomeWideSnp_5', 'GenomeWideSnp_6'
`sns`	Sample names.

Details

'snprma2' allows one to genotype very large datasets (via ff package) and also permits the use of clusters or multiple cores (via snow package) to speed up preprocessing.

Value

`A`	Summarized intensities for Allele A
`B`	Summarized intensities for Allele B
`sns`	Sample names
`gns`	SNP names
`SNR`	Signal-to-noise ratio
`SKW`	Skewness
`mixtureParams`	Parameters from mixture model
`cdfName`	Name of the CDF

Examples

```
if (require(genomewidesnp6Crlmm) & require(hapmapsnp6) & require(oligoClasses)){
  path <- system.file("celFiles", package="hapmapsnp6")

  ## the filenames with full path...
  ## very useful when genotyping samples not in the working directory
  cels <- list.celfiles(path, full.names=TRUE)
  snprmaOutput <- snprma(cels)
  snprmaOutput[["A"]][1:10,]
  snprmaOutput[["B"]][1:10,]
}
## Not run:
## HPC Example
library(ff)
library(snow)
library(crlmm)
## genotype 50K SNPs at a time
ocProbesets(50000)
## setup cluster - 8 cores on the machine
setCluster(8, "SOCK")

path <- system.file("celFiles", package="hapmapsnp6")
cels <- list.celfiles(path, full.names=TRUE)
snprmaOutput <- snprma2(cels)


## End(Not run)
```

---

totalCopyNumber-methods

Method for computing total copy number from either ff

Description

calculates the sum of the allele-specific CN estimates

Methods

`signature(object = "CNSet")` an object of class `CNSet` or `CNSetLM`.

Index