

# Package ‘rCGH’

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**Type** Package

**Title** Comprehensive Pipeline for Analyzing and Visualizing Array-Based CGH Data

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**Maintainer** Frederic Commo <fredcommo@gmail.com>

**URL** <https://github.com/fredcommo/rCGH>

**Description** A comprehensive pipeline for analyzing and interactively visualizing genomic profiles generated through commercial or custom aCGH arrays. As inputs, rCGH supports Agilent dual-color Feature Extraction files (.txt), from 44 to 400K, Affymetrix SNP6.0 and cytoScanHD probeset.txt, cychp.txt, and cnchp.txt files exported from ChAS or Affymetrix Power Tools. rCGH also supports custom arrays, provided data complies with the expected format. This package takes over all the steps required for individual genomic profiles analysis, from reading files to profiles segmentation and gene annotations. This package also provides several visualization functions (static or interactive) which facilitate individual profiles interpretation.

Input files can be in compressed format, e.g. .bz2 or .gz.

**License** Artistic-2.0

**biocViews** aCGH,CopyNumberVariation,Preprocessing,FeatureExtraction

**Depends** R (>= 3.4),methods,stats,utils,graphics

**Imports** plyr,DNAcopy,lattice,ggplot2,grid,shiny (>= 0.11.1),  
limma,affy,mclust,TxDb.Hsapiens.UCSC.hg18.knownGene,  
TxDb.Hsapiens.UCSC.hg19.knownGene,TxDb.Hsapiens.UCSC.hg38.knownGene,  
org.Hs.eg.db,GenomicFeatures,GenomeInfoDb,GenomicRanges,AnnotationDbi,  
parallel,IRanges,grDevices,aCGH

**Suggests** BiocStyle, knitr, BiocGenerics, RUnit

**VignetteBuilder** knitr

**LazyData** true

**NeedsCompilation** no

**Author** Frederic Commo [aut, cre]

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rCGH-package	<i>Comprehensive Pipeline for Analyzing and Visualizing Array-Based CGH Data</i>
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### Description

A comprehensive pipeline for analyzing and interactively visualizing genomic profiles generated through commercial or custom aCGH arrays. As inputs, rCGH supports Agilent dual-color Feature Extraction files (.txt), from 44 to 400K, Affymetrix SNP6.0 and cytoScanHD probeset.txt, cychp.txt, and cnchp.txt files exported from ChAS or Affymetrix Power Tools.

rCGH also supports custom arrays, provided data is in a suitable format. This package takes over all the steps required for individual genomic profiles analysis, from reading files to segmenting and annotating genes. This package provides several visualization functions (static or interactive) which facilitate individual profiles interpretation. Input files can be in compressed format, e.g. .bz2 or .gz.

**Author(s)**

Frederic Commo <frederic.commo@gustaveroussy.fr>

**See Also**

[readAgilent](#), [readAffySNP6](#), [readAffyCytoScan](#), [readGeneric](#)

**Examples**

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")

cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)

# Static visualizations
plotDensity(cgh)
multiplot(cgh)

## Not run:
# Interactive visualizations
view(cgh)

## End(Not run)
```

---

adjustSignal

*Array-based CGH Preprocessing*

---

**Description**

This function performs several preprocessing steps: local regressions (loessFit) are used to correct cy3/cy5 and GC% bias, when Agilent dual-color hybridization are used only.

In case of Affymetrix cychp.txt (or cnchp.txt) data are used, these steps have been already done in ChAS or Affymetrix Power Tools.

**Usage**

```
## S4 method for signature 'rCGH'
adjustSignal(object, Scale=TRUE, Cy=TRUE, GC=TRUE, Ref="cy3",
  suppOutliers=TRUE, nCores=NULL, verbose=TRUE)
```

**Arguments**

**object** : An object of class "rCGH"

**Scale** : logical. If TRUE (default), Log2Ratios are standardized.

**Cy** : logical. If TRUE (default), cy3/cy5 bias is corrected using a local regression (loessFit). For Agilent dual-color hybridization only. Notice that, in case of Affymetrix files (cychp.txt or cnchp.txt), this argument is automatically set to FALSE, since this step is managed when files are exported from ChAS or APT.

- GC : logical. If TRUE (default), the GC% bias is corrected using a local regression (loessFit). For Agilent dual-color hybridization only. Notice that, in case of Affymetrix files (cychp.txt or cnchp.txt), this argument is automatically set to FALSE, since this step is managed when files are exported from ChAS or APT.
- Ref : string. Which cyanine was used as the reference. Possible values are "cy3" (default) and "cy5". For Agilent dual-color hybridization only.
- suppOutliers : logical. If TRUE (default), outliers are removed using an Expectation-Maximization algorithm (EM). See details below.
- nCores : numeric. The number of cores to use in order to speed up the computation. When NULL (default), half of the available cores are used. If a value greater than the number of available cores is passed, this latter will be used. See [detectCores](#).
- verbose : logical. When TRUE (default), progress is printed.

### Details

When `suppOutliers` is TRUE (default), the `Log2Ratios` are splitted with respect to chromosomes. The main regions within each chromosome are identified using EM. Within each region  $r_i$ ,  $x[r_i]$  values are redefined according to the corresponding model parameters. as:

$$x[r_i] \sim N(\mu_i, \sigma_i)$$

Notice that this step may substantially increase the computation time.

### Value

An object of class "[rCGH](#)"

### Author(s)

Frederic Commo

### See Also

[detectCores](#), [mclapply](#)

### Examples

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
getParam(cgh)
```

---

agilentDB

*aCGH Agilent Probes GC Fraction*

---

### Description

A dataset containing the Agilent probe Ids, and their GC content. These data allow [rCGH](#) to support Agilent aCGH arrays, from 44K to 400K. See the source section. This information is used to correct the GC% bias. For Agilent data only.

### Usage

agilentDB

### Format

A data frame with 411056 rows and 2 columns:

- ProbeID: Official Agilent probe ids.
- GC: The GC content in each probe sequence, expressed as the GC fraction.

### Value

A dataset

### Note

Probe sequences are not used and have been removed after computing the GC fractions as  $GC = \text{sum}(G \text{ or } C) / \text{length}(\text{sequence})$ , for each sequence in file.

### Author(s)

Frederic Commo

### Source

These data derive from the official Agilent Sequence List, SurePrint\_G3\_Human\_CGH\_Microarray 2x400K\_021850\_D\_SequenceList\_20111015.txt, freely available at: [Agilent SureDesign](#)  
Access date: 3-2-2015  
Notice that a User ID and Password are required to sign in.

---

AllAccessors

"rCGH" Accessor Functions

---

## Description

Methods for extracting information from an object of class "rCGH".

Each of the below methods are simply convenience functions which extract the corresponding slots (as the name of each method suggests) from an object of class "rCGH".

## Usage

```
## S4 method for signature 'rCGH'
getInfo(object, item = NULL)
## S4 method for signature 'rCGH'
getCNset(object)
## S4 method for signature 'rCGH'
getParam(object)
## S4 method for signature 'rCGH'
getSegTable(object, minLen = NULL)
```

## Arguments

**object** : An object of class "rCGH"

**item** : character. Can be one, or a vector of items. When NULL, the full available information is returned. If `item` is specified, and exists, the corresponding value(s) only is(are) returned.

**minLen** : numeric. The minimal length for a segment, in Kb. When NULL (default), the segmentation table is exported, as it has been computed with [segmentCGH](#), segments shorter than the specified value are re-merged otherwise.

## Value

- `getInfo(object, item = NULL)`: character.
- `getCNset(object)`: a data frame.
- `getParam(object)`: a list of parameters.
- `getSegTable(object, minLen = NULL)`: a data frame.

## Methods

"rCGH"

- `getInfo(object, item = NULL)`: returns the values of the specified items, all the information otherwise.
- `getCNset(object)`: returns the full by-probe dataset.
- `getParam(object)`: returns the analysis parameters.
- `getSegTable(object, minLen = NULL)`: returns the segmentation table - one row per segment.

## Author(s)

Frederic Commo

**See Also**

[setInfo](#), [segmentCGH](#)

**Examples**

```
filePath <- system.file("extdata", "Agilent4x180K.txt.bz2", package = "rCGH")
cgh <- readAgilent(filePath, sampleName = "Agilent4x180K", labName = "myLab")

# Getting all the information
getInfo(cgh)

# Getting specific items
getInfo(cgh, c("sampleName", "labName"))
```

---

byGeneTable

*Converting a Segmentation Table Into a By-Genes Table*


---

**Description**

This function creates a by-gene table by listing all the genes contained in each of the segments in the segmentation table.

Gene annotations (symbol, location,...), segmented Log2Ratios, and segment length are reported in the final table.

A supplementary score is the `relativeLog`: the magnitude, in Log2, from the closest centromere.

**Usage**

```
byGeneTable(segTable, symbol = NULL,
            genome = c("hg19", "hg18", "hg38"), columns = NA, verbose = TRUE)
```

**Arguments**

<code>segTable</code>	: data frame. A segmentation table exported from an object of class <code>"rCGH"</code>
<code>symbol</code>	: character. A valid HUGO symbol. When NULL the full gene table is returned, the corresponding gene information only o/w.
<code>genome</code>	: string. The genome build to use. Supported genomes are hg18, hg19 (default), and hg38.
<code>columns</code>	: string. what supplementary genes annotations to export. Allowed annotations are those supported by the <a href="#">select</a> method from the <code>AnnotationDbi</code> bioconductor package. When NA (default), 'SYMBOL', 'ENTREZID', 'GENENAME' and 'MAP' are exported.
<code>verbose</code>	: logical. When TRUE progress is printed.

**Details**

For gene annotations, Hg19/GRCh37 annotations downloaded from *NCBI* are considered.

**Value**

An object of class "rCGH"

**Author(s)**

Frederic Commo

**See Also**

[getSegTable](#)

**Examples**

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)
st <- getSegTable(cgh)
bygene <- byGeneTable(st)
head(bygene)
```

---

EMnormalize

*Genomic Profile Centralization*


---

**Description**

This function analyses the Log2Ratios as a mixture of several gaussian populations, using an Expectation-Maximization algorithm (EM).

The peakThresh argument specifies what proportion of the main density peak is allowed for choosing a neutral 2-copies population. The mean of the chosen population is used for centralizing the profile.

See [Mclust](#).

**Usage**

```
## S4 method for signature 'rCGH'
EMnormalize(object, G = 2:6, priorScale = 5,
  peakThresh = 0.5, mergeVal = 0.1, Title = NA, verbose = TRUE)
```

**Arguments**

**object** : An object of class "rCGH"

**G** : numeric. The number of groups to test during the gaussian mixture estimation. Default is from 2 to 6.

**priorScale** : numeric. A scale value passed to [priorControl](#). Default is 5.

**peakThresh** : numeric. The proportion of the highest peak to consider as a peak selection threshold. Default is 0.5.



`mergeVal` : numeric. Populations with means closer than `mergeVal` will be pooled together, default is 0.1. Set `mergeVal` to zero to not pool closed sub-populations.

`Title` : character string. A title for the density plot. If NA (default), the sample name (when exists in object info) will be used.

`verbose` : logical. When TRUE (default), progress is printed.

## Details

Depending on `peakThresh`, the mean of the highest density, or a lower value, is chosen for centering the genomic profile. To do so, L2R are modeled for each segment `s_i`, with respect to `n_i` (the number of probes included in segment `i`), `mu_i` and `sd_i`. The mixture of L2Rs is then analysed as a mixture of gaussian populations.

When a `peakThresh` value is specified, heights of density peaks are compared: the lowest peak mean among the peaks respecting the criteria: `peakHeight > max(peaks)*peakThresh`, is chosen for centralizing the data. See References

## Value

An object of same class as the input.

## Author(s)

Frederic Commo

## References

Commo et al. Impact of centralization on aCGH-based genomic profiles for precision medicine in oncology. *Ann Oncol.* 2014

## See Also

[plotDensity](#), [mclust](#)

## Examples

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)
getParam(cgh)
```

---

hg18

*Hg18 Chromosome Lengths and Centromere Locations*

---

### Description

A data set containing lengths and centromere locations for each of the 24 chromosomes, according to Hg18.

### Usage

hg18

### Format

A data set with 24 rows and 5 columns:

- chrom: chromosome number.
- length: chromosome length.
- centromerStart: centromere start position.
- centromerEnd: centromere start position.
- cumlen: cumulative length (where the previous chromosome ends).

### Value

a data set.

### Author(s)

Frederic Commo

### Source

These data derived from the Hg18 gap UCSC table, freely available at: [UCSC](#)  
Access date: 10-10-2015  
Within the browser, select:  
group: All Tables  
database: hg18  
table: gap

### Examples

```
# For users convenience, we provide a prebuilt dataset
# containing the Hg18 chr lengths, and centromeres location.
hg18

# The same dataset can be obtained as follow:
## Not run:
library(BSgenome)
library(rtracklayer)

getChrLength <- function(genome){
  genome <- sprintf("BSgenome.Hsapiens.UCSC.
```

```

g <- getBSgenome(genome, masked=FALSE)
data.frame(chrom=1:24, length=seqlengths(g)[1:24])
}
.chrAsNum <- function(tbl){
  tbl$chrom <- gsub("chr", "", tbl$chrom)
  tbl$chrom[tbl$chrom=="X"] <- 23
  tbl$chrom[tbl$chrom=="Y"] <- 24
  tbl$chrom <- as.numeric(tbl$chrom)
  tbl[order(tbl$chrom),]
}
getCentromeres <- function(genome){
  mySession <- try(browserSession("UCSC"), silent=TRUE)
  # In case it fails, use another mirror
  if(inherits(mySession, "try-error"))
    mySession <- browserSession("UCSC",
                                url="http://genome-euro.ucsc.edu/cgi-bin/")
  genome(mySession) <- genome
  obj <- ucscTableQuery(mySession, table="gap")
  tbl <- getTable(obj)
  tbl <- tbl[tbl$type=="centromere", c("chrom", "chromStart", "chromEnd")]
  colnames(tbl)[2:3] <- c("centromerStart", "centromerEnd")
  .chrAsNum(tbl)
}
makeHg <- function(genome){
  chrL <- getChrLength(genome)
  ctm <- getCentromeres(genome)
  tbl <- merge(chrL, ctm, by="chrom")
  cumlen <- c(0, cumsum(as.numeric(tbl$length))[-nrow(tbl)])
  cbind.data.frame(tbl, cumlen=cumlen)
}
hg18 <- makeHg("hg18")
hg18

## End(Not run)

```

---

hg19

*Hg19 Chromosome Lengths and Centromere Locations*


---

### Description

A data set containing lengths and centromere locations for each of the 24 chromosomes, according to Hg19.

### Usage

```
hg19
```

### Format

A data set with 24 rows and 5 columns:

- chrom: chromosome number.
- length: chromosome length.
- centromerStart: centromere start position.

- centromerEnd: centromere start position.
- cumlen: cumulative length (where the previous chromosome ends).

### Value

a data set.

### Author(s)

Frederic Commo

### Source

These data derived from the Hg19 gap UCSC table, freely available at: [UCSC](#)

Access date: 1-31-2014

Within the browser, select:

group: All Tables

database: hg19

table: gap

### Examples

```
# For users convenience, we provide a prebuilt dataset
# containing the Hg19 chr lengths, and centromeres location.
hg19

# The same dataset can be obtained as follow:
## Not run:
library(BSgenome)
library(rtracklayer)

getChrLength <- function(genome = "BSgenome.Hsapiens.UCSC.hg19"){
  g <- getBSgenome(genome, masked=FALSE)
  data.frame(chrom=1:24, length=seqlengths(g)[1:24])
}

.chrAsNum <- function(tbl){
  tbl$chrom <- gsub("chr", "", tbl$chrom)
  tbl$chrom[tbl$chrom=="X"] <- 23
  tbl$chrom[tbl$chrom=="Y"] <- 24
  tbl$chrom <- as.numeric(tbl$chrom)
  tbl[order(tbl$chrom),]
}

getCentromeres <- function( genome="hg19" ){
  mySession <- try(browserSession("UCSC"), silent=TRUE)
  # In case of failure, try another mirror
  if(inherits(mySession, "try-error"))
    mySession <- browserSession("UCSC",
                                url="http://genome-euro.ucsc.edu/cgi-bin/")

  genome(mySession) <- genome
  obj <- ucscTableQuery(mySession, table="gap")
  tbl <- getTable(obj)
  tbl <- tbl[tbl$type=="centromere", c("chrom", "chromStart", "chromEnd")]
  colnames(tbl)[2:3] <- c("centromerStart", "centromerEnd")
  .chrAsNum(tbl)
}

makeHg19 <- function(){
```

```
tbl <- merge(getChrLength(), getCentromeres(), by="chrom")
cumlen <- c(0, cumsum(as.numeric(tbl$length))[-nrow(tbl)])
cbind.data.frame(tbl, cumlen=cumlen)
}
hg19 <- makeHg19()
hg19

## End(Not run)
```

---

hg38

*Hg38 Chromosome Lengths and Centromere Locations*

---

### Description

A data set containing lengths and centromere locations for each of the 24 chromosomes, according to Hg38.

### Usage

```
hg38
```

### Format

A data set with 24 rows and 5 columns:

- chrom: chromosome number.
- length: chromosome length.
- centromerStart: centromere start position.
- centromerEnd: centromere start position.
- cumlen: cumulative length (where the previous chromosome ends).

### Value

a data set.

### Author(s)

Frederic Commo

### Source

These data derived from the Hg38 gap UCSC table, freely available at: [UCSC](#)  
Access date: 10-10-2015  
Within the browser, select:  
group: All Tables  
database: hg38  
table: gap

**Examples**

```

# For users convenience, we provide a prebuilt dataset
# containing the Hg38 chr lengths, and centromeres location.
hg38

# The same dataset can be obtained as follow:
## Not run:
library(BSgenome)
library(rtracklayer)

getChrLength <- function(genome){
  genome <- sprintf("BSgenome.Hsapiens.UCSC.
  g <- getBSgenome(genome, masked=FALSE)
  data.frame(chrom=1:24, length=seqlengths(g)[1:24])
}

.chrAsNum <- function(tbl){
  tbl$chrom <- gsub("chr", "", tbl$chrom)
  tbl$chrom[tbl$chrom=="X"] <- 23
  tbl$chrom[tbl$chrom=="Y"] <- 24
  tbl$chrom <- as.numeric(tbl$chrom)
  tbl[order(tbl$chrom),]
}

getCentromeres <- function(genome){
  mySession <- try(browserSession("UCSC"), silent=TRUE)
  # In case it fails, use another mirror
  if(inherits(mySession, "try-error"))
    mySession <- browserSession("UCSC",
                                url="http://genome-euro.ucsc.edu/cgi-bin/")

  genome(mySession) <- genome
  obj <- ucscTableQuery(mySession, table="gap")
  tbl <- getTable(obj)
  if(!"centromere"
    return(NULL)
  tbl <- tbl[tbl$type=="centromere", c("chrom", "chromStart", "chromEnd")]
  colnames(tbl)[2:3] <- c("centromerStart", "centromerEnd")
  .chrAsNum(tbl)
}

makeHg <- function(genome){
  chrL <- getChrLength(genome)
  ctm <- getCentromeres(genome)
  # Notice that, in case of Hg38, centromeres locations are in Hg19.
  if(is.null(ctm))
    ctm <- getCentromeres("hg19")
  tbl <- merge(chrL, ctm, by="chrom")
  cumlen <- c(0, cumsum(as.numeric(tbl$length))[-nrow(tbl)])
  cbind.data.frame(tbl, cumlen=cumlen)
}

hg38 <- makeHg("hg38")
hg38

## End(Not run)

```

**Description**

This function display a static view of the genomic profile and the allelic difference stored in an object of class "rCGH".

If no allelic difference is available, the genomic profile only is displayed.

**Usage**

```
## S4 method for signature 'rCGH'
multiplot(object, symbol=NULL, gain=.5,
          loss=(-.5), minLen=10, pCol = "grey50", GLcol = c("blue", "red3"),
          L=matrix(seq(1, 12)), p=c(1/2, 1/4, 1/4), Title=NULL, ylim=NULL)
```

**Arguments**

object	: An object of class "rCGH"
symbol	: character. A valid HUGO symbol (case insensitive).
gain	: numeric. A gain threshold value (in $\text{Log}_2(\text{Ratio})$ ). Segments greater, or equal to, this value will be colored, as specified by GLcol.
loss	: numeric. A loss threshold value (in $\text{Log}_2(\text{Ratio})$ ). Segments lower, or equal to, this value will be colored, as specified by GLcol.
minLen	: numeric. The minimal length for a segment, expressed in Kb. When NULL (default), segments are reported as they have been computed by <a href="#">segmentCGH</a> . Segments shorter than the specified value are re-merged otherwise.
pCol	: string. The probe points color. Default is "grey50".
GLcol	: vector. A vector of 2 colors: the gained and lost segments colors, respectively. Default is "blue" for gains and "red3" for losses.
L	: matrix. A matrix defining the layout. Default is 12 lines.
p	: numeric. The proportion of each plot within the plot window. Default is 1/2, 1/4, 1/4, which corresponds to 6-4-4 lines for the genomic profile in $\text{Log}_2R$ , in copy number, and the LOH plot, respectively, and given a 12-line layout.
Title	: character string. A title for the plot. If NULL (default), the sample name (when exists) is used.
ylim	: numeric. A vector of two values specifying the y-axis range. See <a href="#">plotProfile</a> .

**Value**

None.

**Note**

If no allelic difference is available, the genomic profile only is displayed.

**Author(s)**

Frederic Commo

**See Also**

[plotDensity](#), [plotProfile](#), [plotLOH](#), [view](#)

## Examples

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)

# Static visualizations
multiplot(cgh, symbol = "erbb2")
```

---

plotDensity

*Visualizing the Log2Ratios Density and Centralization Decision*

---

## Description

This function displays the distribution of the Log2Ratios, as well as how the "EMnormalize" step estimates the mixture of gaussian populations, and chooses a centralization value.

## Usage

```
## S4 method for signature 'rCGH'
plotDensity(object, breaks=NULL, Title=NULL,...)
```

## Arguments

**object** : An object of class "rCGH"

**breaks** : The number of breaks to use. See [hist](#). When NULL (default), breaks is arbitrarily defined from the number of values to draw.

**Title** : character string. A title for the density plot. If NULL (default), the sample name (when exists) will be used.

**...** : Other graphical parameters supported by [par](#).

## Value

None.

## Author(s)

Frederic Commo

## See Also

[plotProfile](#), [plotLOH](#), [multiplot](#), [view](#)



## Examples

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)
plotDensity(cgh)
```

---

plotLOH

*Allelic Differences Visualization*

---

## Description

This function display a static view of the allele differences, when available.

## Usage

```
## S4 method for signature 'rCGH'
plotLOH(object, Title=NULL)
```

## Arguments

**object** : An object of class "rCGH"  
**Title** : character string. A title for the density plot. If NULL (default), the sample name (when exists) is used.

## Value

None.

## Author(s)

Frederic Commo

## See Also

[plotDensity](#), [plotProfile](#), [multiplot](#), [view](#)

## Examples

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)

# Static visalizations
plotLOH(cgh)
```

---

plotProfile

*Static Genomic Profile Visualization*


---

### Description

This function display a static view of the genomic profile stored in an object of class "[rCGH](#)".

### Usage

```
## S4 method for signature 'rCGH'
plotProfile(object, showCopy=FALSE, symbol=NULL,
            gain=.5, loss=(-.5), minLen = 10, pCol = "grey50",
            GLcol = c("blue", "red3"), Title=NULL, ylim=NULL)
```

### Arguments

object	: An object of class " <a href="#">rCGH</a> "
showCopy	: logical. To show the estimated copy numbers instead of the Log2Ratios. default is FALSE.
symbol	: character. A valid HUGO symbol (case insensitive).
gain	: numeric. A gain threshold value (in $\text{Log}_2(\text{Ratio})$ ) from where gained segments will be shown, in blue.
loss	: numeric. A loss threshold value (in $\text{Log}_2(\text{Ratio})$ ) from where lossed segments will be shown, in red.
minLen	: numeric. The minimal length for a segment, in Kb. When NULL (default), segments are reported as they have been computed with <a href="#">segmentCGH</a> , segments shorter than the specified value are re-merged otherwise.
pCol	: string. The probe points color. DEfault is "grey50".
GLcol	: vector. A vector of 2 colors: the gained and lost segments colors, respectively. Default is "blue" for gains and "red3" for losses.
Title	: character string. A title for the density plot. If NULL (default), the sample name (when exists) is used.
ylim	: numeric. A vector of two values specifying a range for the y-axis. If NULL (default), the range of Log2Ratio is used.

### Value

None.

### Author(s)

Frederic Commo

### See Also

[plotDensity](#), [plotLOH](#), [multiplot](#), [view](#)

**Examples**

```

filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)

# Static visalization using Log2Ratios
plotProfile(cgh, symbol = "erbb2")

# Static visalization using estimated copy numbers
plotProfile(cgh, showCopy = TRUE, symbol = "erbb2")

```

---

rCGH-Agilent-class	Class "rCGH-Agilent"
--------------------	----------------------

---

**Description**

An instance of class "rCGH-Agilent", which inherits from the superclass "rCGH". Slots described below are used to store sample information, analysis parameters, and segmentation results. All are accessible through specific "Accessors" functions.

**Objects from the Class**

Objects can be created by calls of the form `new("rCGH-Agilent", ...)`.

**Slots**

**info:** Object of class "character": where sample information can be stored. See [getInfo](#) and [setInfo](#).

**cnSet:** Object of class "data.frame": the full data set. See [getCNset](#).

**param:** Object of class "list": the analysis parameters stored for traceability. [getParam](#).

**segTable:** Object of class "data.frame": the segmentation table. [getSegTable](#).

**Extends**

Class "rCGH", directly.

**Methods**

No methods defined with class "rCGH-Agilent" in the signature.

**Author(s)**

Frederic Commo

**See Also**

"rCGH", "rCGH-cytoScan", "rCGH-SNP6", "rCGH-generic"

**Examples**

```
showClass("rCGH-Agilent")
```

---

rCGH-class	<i>Class "rCGH"</i>
------------	---------------------

---

**Description**

Class `"rCGH"` is a superclass living on top of `"rCGH-Agilent"`, `"rCGH-SNP6"`, `"rCGH-cytoScan"`, `"rCGH-oncoScan"`, and `"rCGH-generic"`. These objects inherit most of the properties of the superclass, and allow specific parameterizations used during the analysis process.

Objects are created by platform-specific read functions: `"readAgilent"`, `"readAffySNP6"`, and `"readAffyCytoScan"`, each corresponding to their matched file format.

A supplementary `"readGeneric"` allows the user to create a `"rCGH"` object from custom arrays. Slots described below are used to store sample information and analysis parameters, as well as segmentation results. All are accessible through specific `"Accessors"` functions.

**Objects from the Class**

Objects can be created by calls of the form `new("rCGH", ...)`.

Slots content are updated at each different analysis step, and are accessible through specific get functions.

**Slots**

`info`: Object of class `"character"`: where sample information can be stored. See `"getInfo"` and `"setInfo"`.

`cnSet`: Object of class `"data.frame"`: the full data set. See `"getCNset"`.

`param`: Object of class `"list"`: the analysis parameters stored for traceability. See `"getParam"`.

`segTable`: Object of class `"data.frame"`: the segmentation table. See `"getSegTable"`.

**Methods**

`show` signature(object = "rCGH"): ...

**Author(s)**

Frederic Commo

**See Also**

`"rCGH-Agilent"`, `"rCGH-SNP6"`, `"rCGH-cytoScan"`, `"rCGH-generic"`

**Examples**

```
showClass("rCGH")
```

---

rCGH-cytoScan-class    *Class* "rCGH-cytoScan"

---

### Description

An instance of class "rCGH-cytoScan", which inherits from the superclass "rCGH". Slots described below are used to store sample information, analysis parameters, and segmentation results. All are accessible through specific "Accessors" functions.

### Objects from the Class

Objects can be created by calls of the form `new("rCGH-cytoScan", ...)`.

### Slots

`info`: Object of class "character": where sample information can be stored. See [getInfo](#) and [setInfo](#).

`cnSet`: Object of class "data.frame": the full data set. See [getCNset](#).

`param`: Object of class "list": the analysis parameters stored for traceability. [getParam](#).

`segTable`: Object of class "data.frame": the segmentation table. [getSegTable](#).

### Extends

Class "rCGH", directly.

### Methods

No methods defined with class "rCGH-cytoScan" in the signature.

### Author(s)

Frederic Commo

### See Also

["rCGH"](#), ["rCGH-Agilent"](#), ["rCGH-SNP6"](#), ["rCGH-generic"](#)

### Examples

```
showClass("rCGH-cytoScan")
```

---

rCGH-generic-class      *Class "rCGH-generic"*

---

### Description

An instance of class "rCGH-generic", which inherits from the superclass "rCGH". Slots described below are used to store sample information, analysis parameters, and segmentation results. All are accessible through specific "Accessors" functions.

### Objects from the Class

Objects can be created by calls of the form `new("rCGH-generic", ...)`.

### Slots

`info`: Object of class "character": where sample information can be stored. See [getInfo](#) and [setInfo](#).

`cnSet`: Object of class "data.frame": the full data set. See [getCnSet](#).

`param`: Object of class "list": the analysis parameters stored for traceability. [getParam](#).

`segTable`: Object of class "data.frame": the segmentation table. [getSegTable](#).

### Extends

Class "rCGH", directly.

### Methods

No methods defined with class "rCGH-generic" in the signature.

### Author(s)

Frederic Commo

### See Also

["rCGH"](#), ["rCGH-Agilent"](#), ["rCGH-SNP6"](#), ["rCGH-cytoScan"](#)

### Examples

```
showClass("rCGH-generic")
```

---

rCGH-oncoScan-class    *Class* "rCGH-oncoScan"

---

### Description

An instance of class "rCGH-oncoScan", which inherits from the superclass "rCGH". Slots described below are used to store sample information, analysis parameters, and segmentation results. All are accessible through specific "Accessors" functions.

### Objects from the Class

Objects can be created by calls of the form `new("rCGH-oncoScan", ...)`.

### Slots

`info`: Object of class "character": where sample information can be stored. See [getInfo](#) and [setInfo](#).

`cnSet`: Object of class "data.frame": the full data set. See [getCnSet](#).

`param`: Object of class "list": the analysis parameters stored for traceability. [getParam](#).

`segTable`: Object of class "data.frame": the segmentation table. [getSegTable](#).

### Extends

Class "rCGH", directly.

### Methods

No methods defined with class "rCGH-oncoScan" in the signature.

### Author(s)

Frederic Commo

### See Also

["rCGH"](#), ["rCGH-Agilent"](#), ["rCGH-SNP6"](#), ["rCGH-cytoScan"](#), ["rCGH-generic"](#)

### Examples

```
showClass("rCGH-oncoScan")
```

---

rCGH-SNP6-class	Class "rCGH-SNP6"
-----------------	-------------------

---

### Description

An instance of class "rCGH-SNP6", which inherits from the superclass "rCGH". Slots described below are used to store sample information, analysis parameters, and segmentation results. All are accessible through specific "Accessors" functions.

### Objects from the Class

Objects can be created by calls of the form `new("rCGH-SNP6", ...)`.

### Slots

`info`: Object of class "character": where sample information can be stored. See [getInfo](#) and [setInfo](#).

`cnSet`: Object of class "data.frame": the full data set. See [getCnSet](#).

`param`: Object of class "list": the analysis parameters stored for traceability. [getParam](#).

`segTable`: Object of class "data.frame": the segmentation table. [getSegTable](#).

### Extends

Class "rCGH", directly.

### Methods

No methods defined with class "rCGH-SNP6" in the signature.

### Author(s)

Frederic Commo

### See Also

["rCGH"](#), ["rCGH-Agilent"](#), ["rCGH-cytoScan"](#)

### Examples

```
showClass("rCGH-SNP6")
```



---

readAffyCytoScan	<i>Affymetrix CytoScanHD "rCGH-cytoScan" Constructor</i>
------------------	--

---

### Description

A constructor function which takes an Affymetrix cytoScanHD cychp.txt (or cnchp.txt) file as input, possibly in a compressed format (.bz2 or .gz). These files are exported from Chromosome Analysis Suite (ChAS) or Affymetrix Power Tools (see References section).

### Usage

```
readAffyCytoScan(filePath, sampleName=NA, labName=NA,  
  useProbes=c("snp", "cn", "all"), genome = c("hg19", "hg18", "hg38"),  
  ploidy = 2, verbose=TRUE)
```

### Arguments

filePath	: string. A path to an Affymetrix cytoScanHD cychp.txt (or cnchp.txt) file.
sampleName	: string. A sample Id. Optional.
labName	: string. A lab Id. Optional.
useProbes	: character. What probes to consider. Possible choices are SNP probes only ("snp", default), CN probes only ("cn"), or all the probes ("all").
genome	: string. The genome build to use. Supported genomes are hg18, hg19 (default), and hg38.
ploidy	: numeric. A priori ploidy value, when known, to adjust the estimation of copy numbers. Default is 2.
verbose	: logical. When TRUE (default), progress is printed.

### Details

When available in the file preamble, several array information will be stored in `Object@info`: scanning date, grid version,... Any other useful item can be stored using [setInfo](#).

### Value

An object of class "rCGH"

### Author(s)

Frederic Commo

### References

[Affymetrix Power Tools](#)

### See Also

[readAgilent](#), [readAffySNP6](#), [readGeneric](#), [readAffyOncoScan](#), [setInfo](#), [getInfo](#)

**Examples**

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh
```

---

readAffyOncoScan      *Affymetrix OncoScan "rCGH-oncoScan" Constructor*

---

**Description**

A constructor function which takes an Affymetrix oncoScan tabulated file as input, possibly in a compressed format (.bz2 or .gz).

This can be either a 'ProbeSets, CopyNumber . tsv' alone, or merged with its corresponding 'ProbeSets, AllelicData' file. See the details section.

**Usage**

```
readAffyOncoScan(filePath, sampleName=NA, labName=NA,
  genome = c("hg19", "hg18", "hg38"),
  ploidy = 2, verbose=TRUE)
```

**Arguments**

filePath           : string. A path to an Affymetrix .tsv file. See details.

sampleName        : string. A sample Id. Optional.

labName           : string. A lab Id. Optional.

genome            : string. The genome build to use. Supported genomes are hg18, hg19 (default), and hg38.

ploidy            : numeric. A priori ploidy value, when known, to adjust the estimation of copy numbers. Default is 2.

verbose           : logical. When TRUE (default), progress is printed.

**Details**

The Affymetrix Power Tools apt-copynumber-onco-ssa script produces 2 files: 'ProbeSets, CopyNumber . tsv' and 'ProbeSets, AllelicData . tsv'. Merging these 2 files may produce a unique file containing both probes Log2Ratio and AllelicDifference.

**Value**

An object of class "rCGH"

**Author(s)**

Frederic Commo

## References

[Affymetrix Power Tools](#)

## See Also

[readAgilent](#), [readAffySNP6](#), [readGeneric](#), [readAffyCytoScan](#), [setInfo](#), [getInfo](#)

## Examples

```
# Just a toy file
filePath <- system.file("extdata", "oncoscan.tsv.bz2", package = "rCGH")
cgh <- readAffyOncoScan(filePath, sampleName = "AffyOncoScan")
cgh
```

---

readAffySNP6

*Affymetrix SNP6 "rCGH-SNP6" Constructor*

---

## Description

A constructor function which takes an Affymetrix SNP6 cychp.txt (or cnchp.txt) file as input, possibly in a compressed format (.bz2 or .gz).

These files are exported from Chromosome Analysis Suite (ChAS) or Affymetrix Power Tools (APT) (see the References section).

## Usage

```
readAffySNP6(filePath, sampleName = NA, labName = NA,
  useProbes=c("snp", "cn", "all"), genome = c("hg19", "hg18", "hg38"),
  ploidy = 2, verbose = TRUE)
```

## Arguments

**filePath** : string. A path to an Affymetrix SNP6 cychp.txt (or cnchp.txt) file.

**sampleName** : string. A sample Id. Optional.

**labName** : string. A lab Id. Optional.

**useProbes** : character. What probes to consider. Possible choices are SNP probes only ("snp", default), CN probes only ("cn"), or all the probes ("all").

**genome** : string. The genome build to use. Supported genomes are hg18, hg19 (default), and hg38.

**ploidy** : numeric. A priori ploidy value, when known, to adjust the estimation of copy numbers. Default is 2.

**verbose** : logical. When TRUE (default), progress is printed.

## Details

When available in the file preamble, several array information will be stored in `Object@info`: scanning date, grid version,...

Any other useful item can be stored using [setInfo](#).

**Value**

An object of class "rCGH"

**Author(s)**

Frederic Commo

**References**

[Affymetrix Power Tools](#)

**See Also**

[readAgilent](#), [readAffyCytoScan](#), [readGeneric](#), [readAffyOncoScan](#), [setInfo](#), [getInfo](#)

**Examples**

```
filePath <- system.file("extdata", "Affy_snp6_cnchp.txt.bz2", package = "rCGH")
cgh <- readAffySNP6(filePath, sampleName = "AffySNP6")
cgh
```

---

readAgilent

*Agilent Dual-Color Hybridization "rCGH-Agilent" Constructor.*

---

**Description**

A constructor function taking as input an Agilent FE .txt file, exported from Feature Extraction, possibly in a compressed format (.bz2 or .gz). Agilent from 44 to 400K are supported.

**Usage**

```
readAgilent(filePath, sampleName = NA,
             labName = NA, supFlags = TRUE, genome = c("hg19", "hg18", "hg38"),
             ploidy = 2, verbose = TRUE)
```

**Arguments**

filePath	: string. A path to an Agilent FE (.txt) file.
sampleName	: string. A sample Id. Optional.
labName	: string. A lab Id. Optional.
supFlags	: should the flagged probes be suppressed. Default is TRUE.
genome	: string. The genome build to use. Supported genomes are hg18, hg19 (default), and hg38.
ploidy	: numeric. A priori ploidy value, when known, to adjust the estimation of copy numbers. Default is 2.
verbose	: logical. if TRUE (default), progress is printed.

**Details**

When available in the file preamble, several array information will be stored in `Object@info`: scanning date, grid version,...

Any other useful item can be stored using [setInfo](#).

**Value**

An object of class "`rCGH`"

**Author(s)**

Frederic Commo

**See Also**

[readAffyCytoScan](#), [readAffySNP6](#), [readGeneric](#), [readAffyOncoScan](#), [setInfo](#), [getInfo](#)

**Examples**

```
filePath <- system.file("extdata", "Agilent4x180K.txt.bz2", package = "rCGH")
cgh <- readAgilent(filePath, sampleName = "Agilent4x180K", labName = "myLab")
cgh
```

---

readGeneric

*Generic rCGH object "rCGH-generic" Constructor*

---

**Description**

A constructor function which takes a tabulated .txt file as input, possibly in a compressed format (.bz2 or .gz). Notice that precise column names are mandatory, see the details section.

**Usage**

```
readGeneric(filePath, sampleName=NA, labName=NA,
            genome = c("hg19", "hg18", "hg38"), ploidy = 2, verbose=TRUE)
```

**Arguments**

filePath	: string. A path to an Generic .txt file.
sampleName	: string. A sample Id. Optional.
labName	: string. A lab Id. Optional.
genome	: string. The genome build to use. Supported genomes are hg18, hg19 (default), and hg38.
ploidy	: numeric. A priori ploidy value, when known, to adjust the estimation of copy numbers. Default is 2.
verbose	: logical. When TRUE (default), progress is printed.

## Details

This generic constructor does not expect any preamble. Mandatory columns are:

**ProbeName:** Character strings. Typically the probe ids.

**ChrNum:** numeric. The chromosome numbers. In case Chr X and Y are used and named as "X" and "Y", these notations will be converted into 23 and 24, respectively.

**ChrStart:** numeric. The chromosomal probes locations.

**Log2Ratio:** numeric. The corresponding Log2Ratios.

## Value

An object of class "rCGH"

## Author(s)

Frederic Commo

## See Also

[readAgilent](#), [readAffySNP6](#), [readAffyCytoScan](#), [readAffyOncoScan](#), [setInfo](#), [getInfo](#)

## Examples

```
filePath <- system.file("extdata", "generic.txt.bz2", package = "rCGH")
cgh <- readGeneric(filePath, sampleName = "demo")
cgh
```

---

recenter<--methods      *Recentering a Genomic Profile*

---

## Description

This function allows the user to recenter a genomic profile stored in an object of class "rCGH". Peaks are indexed from 1 to k, from left to right, as they appear on the [plotDensity](#) after the [EMnormalize](#) step.

## Usage

```
## S4 replacement method for signature 'rCGH'
recenter(object) <- value
```

## Arguments

**object**               : An object of class "rCGH"  
**value**                : numeric. What peak number to choose to recenter the genomic profile.

## Value

An object of class "rCGH"

**Note**

When a profile is recentered, the stored workflow parameters are updated. see [getParam](#).

**Author(s)**

Frederic Commo

**See Also**

[EMnormalize](#), [plotDensity](#)

**Examples**

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)

# Default peak choice center the profile on the 1st peak
plotDensity(cgh)

# Recentering on the 2nd density peak
recenter(cgh) <- 2
plotDensity(cgh)
```

---

segmentCGH

*Genomic Profile Segmentation*


---

**Description**

A function for performing the Log2Ratio segmentation on an object of class "rCGH". See the details section below.

**Usage**

```
## S4 method for signature 'rCGH'
segmentCGH(object, Smooth=TRUE, UndoSD = NULL,
  minLen = 10, nCores=NULL, verbose = TRUE)
```

**Arguments**

object	: An object of class "rCGH"
Smooth	: logical. Should the LRR be smoothed before being segmented. See DNACopy for details.
UndoSD	: numeric. When not specified (default is NULL), the UndoSD value is estimated from the Log2Ratios. See DNACopy for details.
minLen	: numeric. The minimal length for a segment, in Kb. Shorter segments will be merged to the closest adjacent one. Default value is 10(Kb).

nCores : numeric. The number of cores to use in order to speed up the computation. When NULL (default), half of the available cores are used. See [mclapply](#).

verbose : logical. if TRUE (default), progress is printed.

### Details

This function is a wrapper for the DNACopy, [CNA](#) and [segment](#) functions, which allows parallelization and data-driven parameterization.

In addition to the usual DNACopy output, the segmentation table contains the probes Log2Ratio standard deviation for each segment, as well as there length, in Kb.

### Value

An object of class "[rCGH](#)"

### Author(s)

Frederic Commo

### References

Venkatraman ES1, Olshen AB. A faster circular binary segmentation algorithm for the analysis of array CGH data. *Bioinformatics*. 2007 Mar 15;23(6):657-63.

### See Also

[CNA](#), [segment](#), [mclapply](#)

### Examples

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
st <- getSegTable(cgh)
head(st)
```

---

setInfo<--methods      *Adding Information In An Object Of Class "rCGH"*

---

### Description

This function allows the user to store any type of supplementaty information in an object of class "[rCGH](#)".

### Usage

```
## S4 replacement method for signature 'rCGH'
setInfo(object, item = NULL) <- value
```



**Arguments**

object : An object of class "rCGH"  
item : character. An item name to store. Default is NULL.  
value : any. A value to store.

**Value**

An object of class "rCGH"

**Warning**

When either item or value is NULL, an error is returned.

**Author(s)**

Frederic Commo

**See Also**

[getInfo](#)

**Examples**

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")

# When supplementary information is added,
# numerical, logical, or strings are supported
setInfo(cgh, "someItem1") <- 35
setInfo(cgh, "someItem2") <- TRUE
setInfo(cgh, "someItem3") <- "someComment"
getInfo(cgh)

# or to get back specific items
getInfo(cgh, c("someItem1", "someItem3"))
```

---

show-methods

show "rCGH"

---

**Description**

A method for visualizing an object of class "rCGH"

**Methods**

signature(object = "rCGH")

**Author(s)**

Frederic Commo

---

view

*Interactive Genomic Profile Visualization*

---

### Description

This function is build on top of [shiny](#), and provides an interactive way for visualizing a genomic profile, and exploring the list of genes.

From a command panel, the user can interact with the graph in different ways. See [details](#).

### Usage

```
## S4 method for signature 'rCGH'  
view(object, browser = TRUE, ...)
```

### Arguments

`object` : An object of class "rCGH"  
`browser` : logical. When TRUE (default), the system's default web browser will be launched automatically.  
`...` : Optional parameters used by [runApp](#).

### Details

The left command panel allows the user several actions:

- displaying a specific gene by calling its HUGO symbol.
- showing all or one unique chromosome.
- merging segments shorter than a specified value, in Kb.
- recentering the entire profile.
- rescaling the y-axis.
- specifying the Log2Ratio cut offs for defining gains and losses.
- specifying a segment lenght cut off, in Mb.
- exporting the genomic plot.
- exporting the genes list.

Some actions, such as showing one unique chromosome or specifying cut offs (gain, loss, segment length), automatically update the gene table available in the "*Genes table*" tab.

### Value

None.

### Author(s)

Frederic Commo

### See Also

[plotProfile](#), [plotLOH](#), [multiplot](#), [runApp](#)

**Examples**

```
filePath <- system.file("extdata", "Affy_cytoScan.cyhd.CN5.CNCHP.txt.bz2",
  package = "rCGH")
cgh <- readAffyCytoScan(filePath, sampleName = "AffyScHD")
cgh <- adjustSignal(cgh, nCores=1)
cgh <- segmentCGH(cgh, nCores=1)
cgh <- EMnormalize(cgh)

## Not run:
# Interactive visualizations
view(cgh)

## End(Not run)
```

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