Package ‘waveTiling’

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Title Wavelet-Based Models for Tiling Array Transcriptome Analysis
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Depends oligo, oligoClasses, Biobase, Biostrings, GenomeGraphs
Imports methods, affy, preprocessCore, GenomicRanges, wavedim, IRanges
Suggests BSgenome, BSgenome.Athaliana.TAIR9, waveTilingData, pd.atdschip.tiling, TxDb.Athaliana.BioMart.plantsmart22
Description This package is designed to conduct transcriptome analysis for tiling arrays based on fast wavelet-based functional models.
URL https://r-forge.r-project.org/projects/wavetiling/
LazyLoad yes
LazyData
biocViews Microarray, DifferentialExpression, TimeCourse, GeneExpression
NeedsCompilation yes

R topics documented:

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**addPheno**

Add phenotypic info to WaveTilingFeatureSet

**Description**

Function to add phenotypic information such as sample names or group names to a WaveTilingFeatureSet-class object

**Usage**

```r
addPheno(object, noGroups, groupNames, replics, ...)
```

**Arguments**

- **object**: object of class WaveTilingFeatureSet
- **noGroups**: Number of groups in the tiling array experiment
- **groupNames**: Vector containing the group or sample names in the tiling array experiment. The vector length should be equal to the indicated number of groups.
- **replics**: Numeric vector containing the number of replicates for each group. The vector length should be equal to the indicated number of groups.
- ... other arguments

**Value**

object of class WaveTilingFeatureSet annotated with the phenotypic data
Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

```r
## Not run:
data(leafdev)
leafdev <- as(leafdev,"WaveTilingFeatureSet")
leafdev <- addPheno(leafdev,noGroups=6,groupNames=c("day8","day9","day10","day11","day12","day13"),replics=rep(3,6))
leafdev
## End(Not run)
```

---

### Description

Function to perform background correction and quantile normalization of tiling arrays

### Usage

```r
bgCorrQn(object, useMapFilter=NULL)
```

### Arguments

- **object**: object of class `WaveTilingFeatureSet`
- **useMapFilter**: NULL or object of class `mapFilterProbe` indicating the probes to use for background correction and quantile normalization

### Value

object of class `WaveTilingFeatureSet` containing the background-corrected and quantile-normalized intensity signals

### Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

### Examples

```r
## Not run:
data(leafdev)
leafdev <- as(leafdev,"WaveTilingFeatureSet")
data(leafdevMapAndFilterTAIR9)
leafdevBQ <- bgCorrQn(leafdev,useMapFilter=leafdevMapAndFilterTAIR9)
## End(Not run)
```
cel2TilingFeatureSet  \hspace{1cm} \textit{Read CEL-files to TilingFeatureSet}

\textbf{Description}

Wrapper function to read in CEL-files and output their content as a TilingFeatureSet-class object.

\textbf{Usage}

\begin{verbatim}
cel2TilingFeatureSet(dataPath, annotationPackage)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{dataPath} character indicating the data path where the CEL-files to read in are stored
  \item \texttt{annotationPackage} name of the package containing the array probe and annotation information, as produces by the pdInfoBuilder-package
\end{itemize}

\textbf{Details}

Uses the \texttt{list.celfiles} and \texttt{read.celfiles} functions of the \texttt{oligo}-package.

\textbf{Value}

object of class TilingFeatureSet

\textbf{Author(s)}

Kristof De Beuf <kristof.debeuf@ugent.be>

\textbf{Examples}

\begin{verbatim}
## No example
\end{verbatim}

\hline

filterOverlap  \hspace{1cm} \textit{function to filter probe sequence overlaps and remap probes}

\textbf{Description}

This function remaps the probe sequence to a reference sequence and filters probe sequence overlaps between PM and MM probes and/or between probes on the forward and reverse strand.

\textbf{Usage}

\begin{verbatim}
filterOverlap(object, remap = TRUE, BSgenomeObject, chrId, strand = c("forward","reverse","both"),
\end{verbatim}
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>object of class WaveTilingFeatureSet</td>
</tr>
<tr>
<td>remap</td>
<td>logical to determine whether the tiling array probe sequences have to be remapped to a more recent reference DNA sequence</td>
</tr>
<tr>
<td>BSgenomeObject</td>
<td>object of class BSgenome containing the genome sequence of the species for which the probes need to be filtered and remapped</td>
</tr>
<tr>
<td>chrId</td>
<td>vector of numerics identifying the chromosomes for which the probes have to be filtered and/or remapped</td>
</tr>
<tr>
<td>strand</td>
<td>character indicating the strands for which the probes have to be filtered and/or remapped (forward, reverse or both)</td>
</tr>
<tr>
<td>MM</td>
<td>logical to indicate whether the tiling array contains MM probes or not</td>
</tr>
<tr>
<td>...</td>
<td>other arguments</td>
</tr>
</tbody>
</table>

Value

An object of class mapFilterProbe is returned containing the indices of the filtered probes.

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

```r
## Not run:
data(leafdev)
as(leafdev,"WaveTilingFeatureSet")
library(BSgenome.Athaliana.TAIR.TAIR9)
leafdevMapAndFilterTAIR9 <- filterOverlap(leafdev,remap=TRUE,BSgenomeObject=Athaliana,chrId=1:7,strand="both")
## End(Not run)
```

Description

class to store the genomic info from a WfmFit-class object

Objects from the Class

Objects can be created by calls of the form new("GenomeInfo", chromosome, strand, minPos, maxPos).

Slots

<table>
<thead>
<tr>
<th>Slot</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chromosome</td>
<td>Object of class &quot;vector&quot;</td>
</tr>
<tr>
<td>strand</td>
<td>Object of class &quot;character&quot;</td>
</tr>
<tr>
<td>minPos</td>
<td>Object of class &quot;numeric&quot;</td>
</tr>
<tr>
<td>maxPos</td>
<td>Object of class &quot;numeric&quot;</td>
</tr>
</tbody>
</table>
getNonAnnotatedRegions

Methods

initialize signature(.Object = "GenomeInfo"): ...
show signature(.Object = "GenomeInfo"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

showClass("GenomeInfo")

getNonAnnotatedRegions

Get non-annotated regions

Description

Extract the significant regions found in the wavelet-based transcriptome analysis that don’t show any overlap with the existing annotation.

Usage

getNonAnnotatedRegions(fit, inf, biomartObj)

Arguments

fit object of class WfmFit
inf object of class WfmInf
biomartObj object of class TxDb representing an annotation database generated from BioMart.

Value

GRangesList object with the non-annotated regions. The first element gives the regions with no annotation overlap on the strand used in the analysis, the second element gives the regions with no annotation overlap on both strands.

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

library(waveTilingData)
library(TxDb.Athaliana.BioMart.plantsmart22)
data(leafdevFit)
data(leafdevInfCompare)
nonAnnoCompare <- getNonAnnotatedRegions(fit=leafdevFit, inf=leafdevInfCompare, biomartObj=TxDb.Athaliana.BioMart.plantsmart22)
nonAnnoCompare
### getSigGenes

**Get significant genes**

**Description**

Extract the annotated regions (often genes) that overlap with the significant regions found in the wavelet-based transcriptome analysis.

**Usage**

```r
getSigGenes(fit, inf, biomartObj)
```

**Arguments**

- **fit**: object of class WfmFit
- **inf**: object of class WfmInf
- **biomartObj**: object of class TxDb representing an annotation database generated from BioMart.

**Value**

GRangesList object. In the elementMetadata of the GRanges elements percOverGene gives the percentage of basepair overlap of the annotated regions by the detected significant region in the analysis; percOverReg gives the percentage of basepair overlap of the detected significant region in the analysis with the annotated region; totPercOverGene gives per annotated region the total percentage of basepair overlap by all detected significant regions in the analysis that map to that annotated region.

**Author(s)**

Kristof De Beuf <kristof.debeuf@ugent.be>

**Examples**

```r
library(waveTilingData)
library(TxDb.Athaliana.BioMart.plantsmart22)
data(leafdevFit)
data(leafdevInfCompare)
sigGenesCompare <- getSigGenes(fit=leafdevFit, inf=leafdevInfCompare, biomartObj=TxDb.Athaliana.BioMart.plantsmart22)
head(sigGenesCompare[[2]])
```

### makeContrasts

**Construct contrast matrix**

**Description**

Helper function to construct a contrast matrix to be used in the inference procedure of the wavelet-based transcriptome analysis when conducting a pairwise comparison analysis.

**Usage**

```r
makeContrasts(contrasts, nlevels)
```
makeDesign

Arguments

contrasts compare: contrasts for pairwise comparison analysis.
nlevels Number of groups for pairwise comparison analysis.

Value

numeric matrix

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

makeContrasts(contrasts="compare",nlevels=6)

makeDesign  Construct design matrix

Description

Helper function to construct a design matrix to be used in the wavelet-based transcriptome analysis.

Usage

makeDesign(design=c("time","circadian","group","factorial"), replics, noGroups, factor.levels=NULL)

Arguments

design character indicating the design of the tiling array experiment. Currently, the following designs are implemented: time for a time-course design based on polynomial contrasts; circadian for circadian rhythm analysis; group for unordered one-factor designs; factorial for two-factor designs
replics Numeric vector containing the number of replicates for each group. The vector length should be equal to the indicated number of groups.
noGroups Number of groups in the tiling array experiment
factor.levels Factor levels to use if applying two-factor design

Value

numeric matrix

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

makeDesign(design="time",replics=rep(3,6),noGroups=6)
MapFilterProbe-class  Class "MapFilterProbe"

Description

class to store probe information after remapping and/or filtering of probes.

Usage

## Accessors

getChromosome(object)
getFilteredIndices(object)
ggetPosition(object)
getStrand(object)

Arguments

object An instance of MapFilterProbe-class.

Objects from the Class

Objects can be created by calls of the form `new("mapFilterProbe", filteredIndices, chromosome, position, strand)`.

Slots

filteredIndices: Object of class "vector" ~
chromosome: Object of class "vector" ~
position: Object of class "vector" ~
strand: Object of class "vector" ~

Methods

getChromosome signature(object = "MapFilterProbe"): ...
getFilteredIndices signature(object = "MapFilterProbe"): ...
getPosition signature(object = "MapFilterProbe"): ...
getStrand signature(object = "MapFilterProbe"): ...
initialize signature(.Object = "MapFilterProbe"): ...
selectProbesFromFilterOverlap signature(object = "MapFilterProbe"): ...
show signature(object = "MapFilterProbe"): ...

Accessors

In the following code snippets, x is a MapFilterProbe object.

getChromosome(x): Extract the chromosome identifiers.
getFilteredIndices(x): Extract the filtered probe indices.
ggetPosition(x): Extract the genomic position of the filtered probes.
getStrand(x): Extract the strand orientation info for the filtered probes.
Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

```r
showClass("MapFilterProbe")

library(waveTilingData)
data(leafdevMapAndFilterTAIR9)
tt1 <- getChromosome(leafdevMapAndFilterTAIR9)
tt2 <- getFilteredIndices(leafdevMapAndFilterTAIR9)
tt3 <- getPosition(leafdevMapAndFilterTAIR9)
tt4 <- getStrand(leafdevMapAndFilterTAIR9)
```

Description

Plot function to visualize the results of the wavelet-based transcriptome analysis. Both the model fit and the significant genomic regions can be plotted and compared with the annotation.

Usage

```r
plotWfm(fit, inf, biomartObj, minPos, maxPos, trackFeature="exon", two.strand=TRUE, plotData=TRUE, plotMean=TRUE, tracks=0)
```

Arguments

- `fit` object of class `WfmFit`
- `inf` object of class `WfmInf`
- `biomartObj` object of class `TxDb` representing an annotation database generated from BioMart.
- `minPos` minimum genomic position to plot
- `maxPos` maximum genomic position to plot
- `trackFeature` track feature. See `GenomeGraphs`-package. Default is `exon`.
- `two.strand` logical indicating whether to plot two strands or not
- `plotData` logical indicating whether to plot the raw data or not
- `plotMean` logical indicating whether to plot the fitted overall mean function or not
- `tracks` vector of integers containing the track numbers to plot. Track numbers correspond with the order of the elements in the list output from the `getGenomicRegions`-function.

Details

The plot utilities of the `GenomeGraphs`-package constitute the backbone of the `plotWfm` function.

Value

nothing returned
selectProbesFromFilterOverlap

selectProbesFromFilterOverlap

select probes from MapFilterProbe object

Description

Extract the probe indices from a MapFilterProbe object that map to a region between two specified genomic positions

Usage

selectProbesFromFilterOverlap(object, chromosome, strand=c("forward","reverse"), minPos=min(getPosition(object)), maxPos=max(getPosition(object)))

Arguments

- object: object of class MapFilterProbe
- chromosome: chromosome
- strand: strand
- minPos: minimum genomic position
- maxPos: maximum genomic position

Value

A list of 2 elements is returned. The first element "selection" gives the probe indices in the filtered MapFilterProbe object; the second element "selectionInit" gives the probe indices in the original WaveTilingFeatureSet object.

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>
Examples

```r
library(waveTilingData)
data(leafdevMapAndFilterTAIR9)
tt <- selectProbesFromFilterOverlap(leafdevMapAndFilterTAIR9, chromosome=1, strand="forward", minPos=10000, maxPos=15000)
sel <- tt$selection
length(sel)
head(sel)
selfil <- tt$selectionFiltered
length(selfil)
head(selfil)
```

selectProbesFromTilingFeatureSet

select probes from WaveTilingFeatureSet object

Description

Extract the probe indices from a WaveTilingFeatureSet object that map to a region between two specified genomic positions

Usage

```r
selectProbesFromTilingFeatureSet(object, chromosome, strand=c("forward","reverse"), minPos, maxPos)
```

Arguments

- `object`: object of class WaveTilingFeatureSet
- `chromosome`: chromosome
- `strand`: strand
- `minPos`: minimum genomic position
- `maxPos`: maximum genomic position

Value

vector of integers indicating the probe indices

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

```r
### Not run:
data(leafdevBQ)
tt <- selectProbesFromTilingFeatureSet(leafdevBQ, chromosome=1, strand="forward", minPos=22000, maxPos=26000)
length(tt)
head(tt)
### End(Not run)
```
Description

Class to store expression and phenotypic data from a tiling array experiment, used as input for the wavelet-based transcriptome analysis.

Usage

## Accessors

groupNames(object)
getNoGroups(object)
getReplics(object)

Arguments

object An instance of WaveTilingFeatureSet-class.

Objects from the Class

Objects can be created by calls of the form new("WaveTilingFeatureSet").

Slots

manufacturer: Object of class "character"
intensityFile: Object of class "character"
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

Methods

```r
addPheno signature(object = "WaveTilingFeatureSet"): ...
bgCorrQn signature(object = "WaveTilingFeatureSet"): ...
filterOverlap signature(object = "WaveTilingFeatureSet"): ...
getGroupNames signature(object = "WaveTilingFeatureSet"): ...
getNoGroups signature(object = "WaveTilingFeatureSet"): ...
getReplics signature(object = "WaveTilingFeatureSet"): ...
selectProbesFromTilingFeatureSet signature(object = "WaveTilingFeatureSet"): ...
wfm.fit signature(object = "WaveTilingFeatureSet"): ...
```

Accessors

In the following code snippets, `x` is a `WaveTilingFeatureSet` object. The described accessors are specific for `WaveTilingFeatureSet`-class objects. Other inherited accessors work as expected on this class.

- `getGroupNames(x)`: Extract the group or sample names in the tiling array experiment.
- `getNoGroups(x)`: Extract the number of groups or samples in the tiling array experiment.
- `getReplics(x)`: Extract the number of replicates in the tiling array experiment.

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

```r
showClass("WaveTilingFeatureSet")
library(waveTilingData)
data(leafdev)
leafdev <- as(leafdev,"WaveTilingFeatureSet")
leafdev <- addPheno(leafdev,noGroups=6,groupNames=c("day8","day9","day10","day11","day12","day13"),replics=rep(3,6))
tt1 <- getGroupNames(leafdev)
tt2 <- getNoGroups(leafdev)
tt3 <- getReplics(leafdev)
```

---

**wfm.fit**

Fit Wfm model to transcriptome data

Description

Main function to fit a wavelet-based functional model to the tiling array expression data.

Usage

```r
wfm.fit(object, filter.overlap=NULL, design=c("time","circadian","group","factorial","custom"), ...)```
Arguments

- **object**: object of class WaveTilingFeatureSet
- **filter.overlap**: object of class mapFilterProbe
- **design**: character indicating the design of tiling array experiment. Currently, the following designs are implemented: time for a time-course design based on polynomial contrasts; circadian for circadian rhythm analysis; group for unordered one-factor designs; factorial for two-factor designs; custom for other designs. When using design="custom" a specific design.matrix needs to be given.
- **n.levels**: number of levels in wavelet decomposition (integer)
- **factor.levels**: factor levels in case of two-factor analysis. Vector of integers with length the number of factors in the experiment, and with elements the number of levels for the respective factors.
- **chromosome**: numeric to indicate the chromosome associated with transcriptome data to fit
- **strand**: character to indicate the strand orientation associated with transcriptome data to fit. Either "forward" or "reverse".
- **minPos**: integer to indicate minimum genomic position
- **maxPos**: integer to indicate maximum genomic position
- **design.matrix**: custom design matrix to use
- **var.eps**: character indicating how to estimate residual variance. Either "margLik" for marginal maximum likelihood based estimation or "mad" for estimation based on the MAD (more info see references).
- **prior**: character indicating which prior distribution to put on effect functions. Either "normal" for a normally distributed prior, or "improper" for an improper prior (more info see references).
- **eqsmooth**: logical indicating whether to force equal amount of smooth for different effect functions or not
- **max.it**: integer giving the maximum number of iteration for estimation
- **wave.filt**: character indicating which wavelet filter to use. Default is "haar".
- **skiplevels**: integer indicating how many wavelet levels to put equal to 0
- **trace**: logical indicating whether to trace estimation
- **save.obs**: character to indicate which output to store in return object. Either "plot": all info needed to make the plots or "all": store all possible info.

Value

- object of class WfmFit

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

References


wfm.inference

Perform transcriptome analysis on fitted wavelet-based functional model

Description

Main function to perform transcriptome analysis on a fitted wavelet-based functional model of class WfmFit.

Usage

wfm.inference(object, contrast.matrix=NULL, contrasts=c("compare","means","effects","overallMean"), delta=NULL, two.sided=NULL, minRunPos=90, minRunProbe=1, alpha=0.05, nsim=1000, rescale=NULL)

Arguments

- **object**: object of class WfmFit
- **contrast.matrix**: custom contrasts matrix
- **contrasts**: character indicating the type of transcriptome analysis is to be applied. Currently the following types are implemented: compare for doing a pairwise differential expression analysis between any combination of two groups; effects, which corresponds to a circadian rhythm analysis if a circadian design is used for the fit, and to a time effects analysis (linear, quadratic,...) if a time-course design is used for the fit; means for doing a group-wise transcript discovery analysis.
- **delta**: threshold value to be used in the inference procedure. This should be a numeric vector with as first element the threshold for the overall mean transcript discovery and the other elements the threshold for the differential expression, the effects analysis or group-wise mean analysis. If the threshold should be equal for all comparisons, effects or group-wise means only a vector of length 2 is needed. Otherwise, the vector must be of length \( r+1 \) with \( r \) the number of pairwise comparisons, effects or group-wise means.
- **two.sided**: logical indicating if one-sided or two-sided tests are desired
- **minRunPos**: minrun by position. An integer to indicate the minimum number of basepairs a significant genomic region should contain.
- **minRunProbe**: minrun by probes. An integer to indicate the minimum number of probes the significant genomic region should map to.
- **alpha**: significance level
- **nsim**: number of simulations used when doing circadian rhythm inference
- **rescale**: rescale matrix

Value

object of class WfmFit
**WfmFit-class**

**Author(s)**

Kristof De Beuf <kristof.debeuf@ugent.be>

**References**


**Examples**

```r
library(waveTilingData)
data(leafdevFit)
delta <- log(1.2,2)
leafdevInfCompare <- wfm.inference(leafdevFit,contrasts="compare",delta=c("median",delta))
```

---

**WfmFit-class**

*Class “WfmFit”*

**Description**

Class to store model fits in the wavelet-based transcriptome analysis.

**Usage**

```r
## Accessors

getProbePosition(object)
getNoProbes(object)
getBetaWav(object)
getVarBetaWav(object)
getSmoothPar(object)
getVarEps(object)
getGenomeInfo(object)
getMinPos(object)
getMaxPos(object)
getNoLevels(object)
getDesignMatrix(object)
getPhenoInfo(object)
dataDataOrigSpace(object)
dataDataWaveletSpace(object)
getWaveletFilter(object)
getKj(object)
getPrior(object)
getF(object)
getVarF(object)
```
Arguments

object  An instance of WfmFit-class.

Objects from the Class

Objects can be created by calls of the form `new("WfmFit", betaWav, varbetaWav, smoothPar, varEps, dataOrigSpace, dataWaveletSpace, design.matrix, phenoData, genome.info, n.levels, probePosition, wave.filt, Kj, prior, F, varF, P, Z, noGroups, replics)`.

Slots

betaWav: Object of class "matrix" ~~
varbetaWav: Object of class "matrix" ~~
smoothPar: Object of class "matrix" ~~
varEps: Object of class "numeric" ~~
dataOrigSpace: Object of class "matrix" ~~
dataWaveletSpace: Object of class "matrix" ~~
design.matrix: Object of class "matrix" ~~
phenoData: Object of class "data.frame" ~~
genome.info: Object of class "genomeInfo" ~~
n.levels: Object of class "numeric" ~~
probePosition: Object of class "numeric" ~~
wave.filt: Object of class "character" ~~
Kj: Object of class "numeric" ~~
prior: Object of class "character" ~~
F: Object of class "matrix" ~~
varF: Object of class "matrix" ~~
P: Object of class "numeric" ~~
Z: Object of class "matrix" ~~
noGroups: Object of class "numeric" ~~
replics: Object of class "numeric" ~-

Methods

getBetaWav signature(object = "WfmFit"): ...
getChromosome signature(object = "WfmFit"): ...
getDataOrigSpace signature(object = "WfmFit"): ...
getDataWaveletSpace signature(object = "WfmFit"): ...
getDesignMatrix signature(object = "WfmFit"): ...
getF signature(object = "WfmFit"): ...
getGenomeInfo signature(object = "WfmFit"): ...
getKj signature(object = "WfmFit"): ...
getMaxPos signature(object = "WfmFit"): ...
getMinPos signature(object = "WfmFit"): ...
getNoLevels signature(object = "WfmFit"): ...
getNoProbes signature(object = "WfmFit"): ...
getPhenoInfo signature(object = "WfmFit"): ...
getPrior signature(object = "WfmFit"): ...
getProbePosition signature(object = "WfmFit"): ...
getSmoothPar signature(object = "WfmFit"): ...
getStrand signature(object = "WfmFit"): ...
getVarBetaWav signature(object = "WfmFit"): ...
getVarEps signature(object = "WfmFit"): ...
getVarF signature(object = "WfmFit"): ...
getWaveletFilter signature(object = "WfmFit"): ...
initialize signature(.Object = "WfmFit"): ...
show signature(object = "WfmFit"): ...
wfmi.inference signature(object = "WfmFit"): ...

Accessors

In the following code snippets, x is a WfmFit object.

getBetaWav(x): Extract the fitted effect functions in the wavelet space.
getChromosome(x): Extract the chromosome identifiers.
getDataOrigSpace(x): Extract the raw expression data in the original data space.
getDataWaveletSpace(x): Extract the raw data in the wavelet space, i.e. the wavelet coefficients.
getDesignMatrix(x): Extract the design matrix used in the wavelet-based analysis.
getF(x): Extract the fitted functional effects in the original data space.
getGenomeInfo(x): Extract the genomic information.
getKj(x): Extract the number of wavelet coefficients estimated per wavelet level.
getMaxPos(x): Extract the maximum genomic probe position.
getMinPos(x): Extract the minimum genomic probe position.
getNoLevels(x): Extract the number of levels in the wavelet decomposition when fitting the wavelet-based functional model.
getNoProbes(x): Extract the number of probes.
getPhenoInfo(x): Extract the phenotypic information for the tiling array experiment.
getPrior(x): Extract the prior imposed on the functional effects in the wavelet space.
getProbePosition(x): Extract probe position.
getSmoothPar(x): Extract the estimated smoothing parameters that control the regularization of the effect functions in the wavelet space.
getStrand(x): Extract the strand orientation info.
getVarBetaWav(x): Extract the variance of the fitted effect functions in the wavelet space.
getVarEps(x): Extract the estimated residual variance in the wavelet space. One variance parameter is estimated per wavelet level.
getVarF(x): Extract the variance of the fitted functional effects in the original data space.
getWaveletFilter(x): Extract the wavelet filter used to transform the data from the original space.

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>
Examples

```
showClass("WfmFit")
```

```
library(waveTilingData)
data(leafdevFit)
tt1 <- getBetaWav(leafdevFit)
tt2 <- getChromosome(leafdevFit)
tt3 <- getDataOrigSpace(leafdevFit)
tt4 <- getDataWaveletSpace(leafdevFit)
tt5 <- getDesignMatrix(leafdevFit)
tt6 <- getF(leafdevFit)
tt7 <- getGenomeInfo(leafdevFit)
tt8 <- getKj(leafdevFit)
tt9 <- getMaxPos(leafdevFit)
tt10 <- getMinPos(leafdevFit)
tt11 <- getNoLevels(leafdevFit)
tt12 <- getNoProbes(leafdevFit)
tt13 <- getPhenoInfo(leafdevFit)
tt14 <- getPrior(leafdevFit)
tt15 <- getProbePosition(leafdevFit)
tt16 <- getSmoothPar(leafdevFit)
tt17 <- getStrand(leafdevFit)
tt18 <- getVarBetaWav(leafdevFit)
tt19 <- getVarEps(leafdevFit)
tt20 <- getVarF(leafdevFit)
tt21 <- getWaveletFilter(leafdevFit)
```

---

**WfmFitCircadian-class**

Class “WfmFitCircadian”

Description

class to store model fits with a circadian rhythm design in the wavelet-based transcriptome analysis.

Objects from the Class

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

Slots

- `betaWav`: Object of class "matrix" ~~
- `varbetaWav`: Object of class "matrix" ~~
- `smoothPar`: Object of class "matrix" ~~
- `varEps`: Object of class "numeric" ~~
- `dataOrigSpace`: Object of class "matrix" ~~
- `dataWaveletSpace`: Object of class "matrix" ~~
- `design.matrix`: Object of class "matrix" ~~
- `phenoData`: Object of class "data.frame" ~~
- `genome.info`: Object of class "genomeInfo" ~~
- `n.levels`: Object of class "numeric" ~~
WfmFitCustom-class

probePosition: Object of class "numeric" ~~
wave.filt: Object of class "character" ~~
Kj: Object of class "numeric" ~~
prior: Object of class "character" ~~
F: Object of class "matrix" ~~
varF: Object of class "matrix" ~~
P: Object of class "numeric" ~~
Z: Object of class "matrix" ~~
noGroups: Object of class "numeric" ~~
replics: Object of class "numeric" ~~

Extends

Class "WfmFit", directly.

Methods

initialize signature(.Object = "WfmFitCircadian"): ...
show signature(object = "WfmFitCircadian"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

showClass("WfmFitCircadian")

WfmFitCustom-class  Class "WfmFitCustom"

Description

class to store model fits with custom design in the wavelet-based transcriptome analysis.

Objects from the Class

Objects can be created by calls of the form new("WfmFitCustom").

Slots

betaWav: Object of class "matrix" ~~
varbetaWav: Object of class "matrix" ~~
smoothPar: Object of class "matrix" ~~
varEps: Object of class "numeric" ~~
dataOrigSpace: Object of class "matrix" ~~
dataWaveletSpace: Object of class "matrix" ~
design.matrix: Object of class "matrix" ~
phenoData: Object of class "data.frame" ~
genome.info: Object of class "genomeInfo" ~
nlevels: Object of class "numeric" ~
probePosition: Object of class "numeric" ~
wave.filt: Object of class "character" ~
Kj: Object of class "numeric" ~
prior: Object of class "character" ~
F: Object of class "matrix" ~
varF: Object of class "matrix" ~
P: Object of class "numeric" ~
Z: Object of class "matrix" ~
noGroups: Object of class "numeric" ~
replics: Object of class "numeric" ~

Extends

Class "WfmFit", directly.

Methods

initialize signature(.Object = "WfmFitCustom"): ...
show signature(object = "WfmFitCustom"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

showClass("WfmFitCustom")

Description

class to store model fits with factorial design in the wavelet-based transcriptome analysis.

Objects from the Class

Objects can be created by calls of the form new("WfmFitFactor").
Slots

betaWav: Object of class "matrix" ~~
varbetaWav: Object of class "matrix" ~~
smoothPar: Object of class "matrix" ~~
varEps: Object of class "numeric" ~~
dataOrigSpace: Object of class "matrix" ~~
dataWaveletSpace: Object of class "matrix" ~~
design.matrix: Object of class "matrix" ~~
phenoData: Object of class "data.frame" ~~
genome.info: Object of class "genomeInfo" ~~
n.levels: Object of class "numeric" ~~
probePosition: Object of class "numeric" ~~
wave.filt: Object of class "character" ~~

Kj: Object of class "numeric" ~~
prior: Object of class "character" ~~

F: Object of class "matrix" ~~
varF: Object of class "matrix" ~~
P: Object of class "numeric" ~~
Z: Object of class "matrix" ~~
noGroups: Object of class "numeric" ~~
replics: Object of class "numeric" ~~

Extends

Class "WfmFit", directly.

Methods

initialize signature(.Object = "WfmFitFactor"): ...
show signature(object = "WfmFitFactor"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

showClass("WfmFitFactor")
Class "WfmFitTime"

Description

class to store model fits with a time-course design in the wavelet-based transcriptome analysis.

Objects from the Class

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

Slots

betaWav: Object of class "matrix" ~~
varbetaWav: Object of class "matrix" ~~
smoothPar: Object of class "matrix" ~~
varEps: Object of class "numeric" ~~
dataOrigSpace: Object of class "matrix" ~~
dataWaveletSpace: Object of class "matrix" ~~
design.matrix: Object of class "matrix" ~~
phenoData: Object of class "data.frame" ~~
genome.info: Object of class "genomeInfo" ~~
n.levels: Object of class "numeric" ~~
probePosition: Object of class "numeric" ~~
wave.filt: Object of class "character" ~~
Kj: Object of class "numeric" ~~
prior: Object of class "character" ~~
F: Object of class "matrix" ~~
varF: Object of class "matrix" ~~
P: Object of class "numeric" ~~
Z: Object of class "matrix" ~~
noGroups: Object of class "numeric" ~~
replics: Object of class "numeric" ~~

Extends

Class "WfmFit", directly.

Methods

initialize signature(.Object = "WfmFitTime"): ...

show signature(object = "WfmFitTime"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>
### WfmInf-class

**Examples**

```r
demo(WfmInf)
```

### Description

Class "WfmInf"

class to store outputs from the inference in the wavelet-based transcriptome analysis.

### Usage

#### ## Accessors

- `getAlpha(object)`
- `getDelta(object)`
- `getTwoSided(object)`
- `getSigProbes(object)`
- `getRegions(object)`
- `getGenomicRegions(object)`
- `getFDR(object)`
- `getEff(object)`
- `getVarEff(object)`

#### Arguments

- `object`: An instance of WfmInf-class.

### Objects from the Class

Objects can be created by calls of the form `new("WfmInf", alpha, delta, two.sided, sigProbes, regions, GlocRegions, FDR, CI, eff, varEff)`.

### Slots

- `alpha`: Object of class "numeric"~
- `delta`: Object of class "numeric"~
- `two.sided`: Object of class "numeric"~
- `sigProbes`: Object of class "list"~
- `regions`: Object of class "list"~
- `GlocRegions`: Object of class "list"~
- `FDR`: Object of class "matrix"~
- `CI`: Object of class "array"~
- `eff`: Object of class "matrix"~
- `varEff`: Object of class "matrix"~
- `genome.info`: Object of class "genomeInfo"~
Methods

getAlpha signature(object = "WfmInf"): ...  
getDelta signature(object = "WfmInf"): ...  
getTwoSided signature(object = "WfmInf"): ...  
getSigProbes signature(object = "WfmInf"): ...  
getRegions signature(object = "WfmInf"): ...  
getGenomicRegions signature(object = "WfmInf"): ...  
getFDR signature(object = "WfmInf"): ...  
getEff signature(object = "WfmInf"): ...  
getVarEff signature(object = "WfmInf"): ...  
getGenomeInfo signature(object = "WfmFit"): ...  
initialize signature(.Object = "WfmInf"): ...  
show signature(object = "WfmInf"): ...  
plotWfm signature(fit = "WfmFit", inf = "WfmInf"): ...  
getSigGenes signature(fit = "WfmFit", inf = "WfmInf"): ...  
getNonAnnotatedRegions signature(fit = "WfmFit", inf = "WfmInf"): ...

Accessors

In the following code snippets, x is a WfmInf object.

getAlpha(x): Extract the alpha level of significance used in the wavelet-based analysis.
getDelta(x): Extract the threshold values used in the wavelet-based transcriptome analysis.
getTwoSided(x): Extract the direction of inference conducted in the wavelet-based transcriptome analysis.
getSigProbes(x): Extract the significant probe ids for the wavelet-based transcriptome analysis.
getRegions(x): Extract the significant regions from the wavelet-based transcriptome analysis. Regions are given in terms of the probe ids they map onto.
getGenomicRegions(x): Extract the significant genomic regions from the wavelet-based transcriptome analysis.
getFDR(x): Extract the FDR for each test in the wavelet-based transcriptome analysis.
getEff(x): Extract the estimated effects or contrasts of the wavelet-based transcriptome analysis.
getVarEff(x): Extract the estimated variances of the effects or contrasts in the wavelet-based transcriptome analysis.
getGenomeInfo(x): Extract the genomic information.

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

showClass("WfmInf")
library(waveTilingData)
data(leafdevInfCompare)
tt1 <- getAlpha(leafdevInfCompare)
tt2 <- getDelta(leafdevInfCompare)
tt3 <- getTwoSided(leafdevInfCompare)
tt4 <- getSigProbes(leafdevInfCompare)
tt5 <- getRegions(leafdevInfCompare)
WfmInfCompare-class

Description

class to store outputs from the inference for a pairwise comparison wavelet-based transcriptome analysis.

Objects from the Class

Objects can be created by calls of the form new("WfmInfCompare").

Slots

alpha: Object of class "numeric" ~~
delta: Object of class "numeric" ~~
two.sided: Object of class "numeric" ~~
sigProbes: Object of class "list" ~~
regions: Object of class "list" ~~
GlocRegions: Object of class "list" ~~
FDR: Object of class "matrix" ~~
CI: Object of class "array" ~~
eff: Object of class "matrix" ~~
varEff: Object of class "matrix" ~~

Extends

Class "WfmInf", directly.

Methods

initialize signature(.Object = "WfmInfCompare"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

showClass("WfmInfCompare")
Class “WfmInfCustom”

Description

Class "WfmInfCustom" to store outputs from the inference for a custom design fit in the wavelet-based transcriptome analysis.

Objects from the Class

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

Slots

- `alpha`: Object of class "numeric"
- `delta`: Object of class "numeric"
- `two.sided`: Object of class "numeric"
- `sigProbes`: Object of class "list"
- `regions`: Object of class "list"
- `GlocRegions`: Object of class "list"
- `FDR`: Object of class "matrix"
- `CI`: Object of class "array"
- `eff`: Object of class "matrix"
- `varEff`: Object of class "matrix"

Extends

Class "WfmInf", directly.

Methods

- `initialize` signature(.Object = "WfmInfCustom"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

`showClass("WfmInfCustom")`
Class "WfmInfEffects"

Description

class to store outputs from the inference on the effects in the wavelet-based transcriptome analysis.

Objects from the Class

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

Slots

- `alpha`: Object of class "numeric"
- `delta`: Object of class "numeric"
- `two.sided`: Object of class "numeric"
- `sigProbes`: Object of class "list"
- `regions`: Object of class "list"
- `GlocRegions`: Object of class "list"
- `FDR`: Object of class "matrix"
- `CI`: Object of class "array"
- `eff`: Object of class "matrix"
- `varEff`: Object of class "matrix"

Extends

Class "WfmInf", directly.

Methods

initialize signature(.Object = "WfmInfEffects"): ...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

showClass("WfmInfEffects")
Class "WfmInfMeans"

Description

class to store outputs from the inference on the group-wise means in the wavelet-based transcriptome analysis.

Objects from the Class

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

Slots

- `alpha`: Object of class "numeric"
- `delta`: Object of class "numeric"
- `two.sided`: Object of class "numeric"
- `sigProbes`: Object of class "list"
- `regions`: Object of class "list"
- `GlocRegions`: Object of class "list"
- `FDR`: Object of class "matrix"
- `CI`: Object of class "array"
- `eff`: Object of class "matrix"
- `varEff`: Object of class "matrix"

Extends

Class "WfmInf", directly.

Methods

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

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

`showClass("WfmInfMeans")`
Class "WfmInfOverallMean"

Description

class to store outputs from the inference on the overall mean expression in the wavelet-based transcriptome analysis.

Objects from the Class

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

Slots

- **alpha**: Object of class "numeric"
- **delta**: Object of class "numeric"
- **two.sided**: Object of class "numeric"
- **sigProbes**: Object of class "list"
- **regions**: Object of class "list"
- **GlocRegions**: Object of class "list"
- **FDR**: Object of class "matrix"
- **CI**: Object of class "array"
- **eff**: Object of class "matrix"
- **varEff**: Object of class "matrix"

Extends

Class "WfmInf", directly.

Methods

- `initialize` signature(.Object = "WfmInfOverallMean")...

Author(s)

Kristof De Beuf <kristof.debeuf@ugent.be>

Examples

`showClass("WfmInfOverallMean")`
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