Package ‘chromstaR’

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Type Package

Title Combinatorial and Differential Chromatin State Analysis for ChIP-Seq Data

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Author Aaron Taudt, Maria Colome Tatche, Matthias Heinig, Minh Anh Nguyen

Maintainer Aaron Taudt <aaron.taudt@gmail.com>

Description This package implements functions for combinatorial and differential analysis of ChIP-seq data. It includes uni- and multivariate peak-calling, export to genome browser viewable files, and functions for enrichment analyses.

Depends R (>= 3.3), GenomicRanges, ggplot2, chromstaRData

Imports methods, utils, grDevices, graphics, stats, foreach, doParallel, BiocGenerics (>= 0.31.6), S4Vectors, GenomeInfoDb, IRanges, reshape2, Rsamtools, GenomicAlignments, bamsignals, mvtnorm

Suggests knitr, BiocStyle, testthat, biomaRt

URL https://github.com/ataudt/chromstaR

BugReports https://github.com/ataudt/chromstaR/issues

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Description

This package implements functions for the combinatorial and differential analysis of ChIP-seq data. It was developed for histone modifications with a broad profile but is also suitable for the analysis of transcription factor binding data. A Hidden Markov Model with a mixture of Negative Binomials as emission densities is used to call peaks. Please refer to our manuscript at http://dx.doi.org/10.1101/038612 for a detailed description of the method.

Details

The main function of this package is Chromstar. For a detailed introduction type browseVignettes("chromstaR") and read the vignette. Here is an overview of all plotting functions.

Author(s)

Aaron Taudt, Maria Colome-Tatche, Matthias Heinig, Minh Anh Nguyen
**binned.data**  
* Binned read counts

**Description**

A GRanges-class object which contains binned read counts as meta data column counts. It is output of the binReads function.

**binReads**  
* Convert aligned reads from various file formats into read counts in equidistant bins

**Description**

Convert aligned reads in .bam or .bed(.gz) format into read counts in equidistant windows.

**Usage**

```r
binReads(
  file,
  experiment.table = NULL,
  ID = NULL,
  assembly,
  bamindex = file,
  chromosomes = NULL,
  pairedEndReads = FALSE,
  min.mapq = 10,
  remove.duplicate.reads = TRUE,
  max.fragment.width = 1000,
  blacklist = NULL,
  binsizes = 1000,
  stepsizes = binsizes/2,
  reads.per.bin = NULL,
  bins = NULL,
  variable.width.reference = NULL,
  use.bamsignals = TRUE,
  format = NULL
)
```

**Arguments**

- **file**  
  A file with aligned reads. Alternatively a GRanges-class with aligned reads.

- **experiment.table**  
  An experiment.table containing the supplied file. This is necessary to uniquely identify the file in later steps of the workflow. Set to NULL if you don’t have it (not recommended).
**binReads**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ID</td>
<td>Optional ID to select a row from the experiment table. Only necessary if the experiment table contains the same file in multiple positions in column 'file'.</td>
</tr>
<tr>
<td>assembly</td>
<td>Please see <code>getChromInfoFromUCSC</code> for available assemblies. Only necessary when importing BED files. BAM files are handled automatically. Alternatively a data.frame with columns 'chromosome' and 'length'.</td>
</tr>
<tr>
<td>bamindex</td>
<td>BAM index file. Can be specified without the .bai ending. If the index file does not exist it will be created and a warning is issued.</td>
</tr>
<tr>
<td>chromosomes</td>
<td>If only a subset of the chromosomes should be binned, specify them here.</td>
</tr>
<tr>
<td>pairedEndReads</td>
<td>Set to TRUE if you have paired-end reads in your BAM files (not implemented for BED files).</td>
</tr>
<tr>
<td>min.mapq</td>
<td>Minimum mapping quality when importing from BAM files. Set min.mapq=0 to keep all reads.</td>
</tr>
<tr>
<td>remove.duplicate.reads</td>
<td>A logical indicating whether or not duplicate reads should be removed.</td>
</tr>
<tr>
<td>max.fragment.width</td>
<td>Maximum allowed fragment length. This is to filter out erroneously wrong fragments due to mapping errors of paired end reads.</td>
</tr>
<tr>
<td>blacklist</td>
<td>A <code>GRanges-class</code> or a bed(.gz) file with blacklisted regions. Reads falling into those regions will be discarded.</td>
</tr>
<tr>
<td>binsizes</td>
<td>An integer vector specifying the bin sizes to use.</td>
</tr>
<tr>
<td>stepsizes</td>
<td>An integer vector specifying the step size. One number can be given for each element in <code>binsizes</code>, <code>reads.per.bin</code> and <code>bins</code> (in that order).</td>
</tr>
<tr>
<td>reads.per.bin</td>
<td>Approximate number of desired reads per bin. The bin size will be selected accordingly.</td>
</tr>
<tr>
<td>bins</td>
<td>A <code>GRanges-class</code> or a named list() with <code>GRanges-class</code> containing precalculated bins produced by <code>fixedWidthBins</code> or <code>variableWidthBins</code>. Names of the list must correspond to the binsize. If the list is unnamed, an attempt is made to automatically determine the binsize.</td>
</tr>
<tr>
<td>variable.width.reference</td>
<td>A BAM file that is used as reference to produce variable width bins. See <code>variableWidthBins</code> for details.</td>
</tr>
<tr>
<td>use.bamsignals</td>
<td>If TRUE the <code>bamsignals</code> package is used for parsing of BAM files. This gives tremendous speed advantage for only one binsize but linearly increases for multiple binsizes, while use.bamsignals=FALSE has a binsize dependent runtime and might be faster if many binsizes are calculated.</td>
</tr>
<tr>
<td>format</td>
<td>One of c('bed','bam','GRanges',NULL). With NULL the format is determined automatically from the file ending.</td>
</tr>
</tbody>
</table>

**Details**

Convert aligned reads from .bam or .bed(.gz) files into read counts in equidistant windows (bins). This function uses GenomicRanges::countOverlaps to calculate the read counts, or alternatively bamsignals::bamProfile if option use.bamsignals is set (only effective for .bam files).
callPeaksMultivariate

Fit a Hidden Markov Model to multiple ChIP-seq samples

Description

Fit a HMM to multiple ChIP-seq samples to determine the combinatorial state of genomic regions. Input is a list of uniHMMs generated by callPeaksUnivariate.

Usage

```r
callPeaksMultivariate(
  hmms,
  use.states,
  max.states = NULL,
  per.chrom = TRUE,
  chromosomes = NULL,
  eps = 0.01,
  keep.posteriors = FALSE,
  num.threads = 1,
  max.time = NULL,
  max.iter = NULL,
  keep.densities = FALSE,
  verbosity = 1,
  temp.savedir = NULL
)
```
callPeaksMultivariate

Arguments

- **hmm**s: A list of uniHMMs generated by callPeaksUnivariate, e.g. list(hmm1, hmm2, ...), or a vector of files that contain such objects, e.g. c("file1", "file2", ...).

- **use.states**: A data.frame with combinatorial states which are used in the multivariate HMM, generated by function stateBrewer. If both use.states and max.states are NULL, the maximum possible number of combinatorial states will be used.

- **max.states**: Maximum number of combinatorial states to use in the multivariate HMM. The states are ordered by occurrence as determined from the combination of univariate state calls.

- **per.chrom**: If per.chrom=TRUE chromosomes will be treated separately. This tremendously speeds up the calculation but results might be noisier as compared to per.chrom=FALSE, where all chromosomes are concatenated for the HMM.

- **chromosomes**: A vector specifying the chromosomes to use from the models in hmm. The default (NULL) uses all available chromosomes.

- **eps**: Convergence threshold for the Baum-Welch algorithm.

- **keep.posteriors**: If set to TRUE, posteriors will be available in the output. This can be useful to change the posterior cutoff later, but increases the necessary disk space to store the result immensely.

- **num.threads**: Number of threads to use. Setting this to >1 may give increased performance.

- **max.time**: The maximum running time in seconds for the Baum-Welch algorithm. If this time is reached, the Baum-Welch will terminate after the current iteration finishes. The default NULL is no limit.

- **max.iter**: The maximum number of iterations for the Baum-Welch algorithm. The default NULL is no limit.

- **keep.densities**: If set to TRUE (default=FALSE), densities will be available in the output. This should only be needed debugging.

- **verbosity**: Verbosity level for the fitting procedure. 0 - No output, 1 - Iterations are printed.

- **temp.savedir**: A directory where to store intermediate results if per.chrom=TRUE.

Details

Emission distributions from the univariate HMMs are used with a Gaussian copula to generate a multivariate emission distribution for each combinatorial state. This multivariate distribution is then kept fixed and the transition probabilities are fitted with a Baum-Welch. Please refer to our manuscript at [http://dx.doi.org/10.1101/038612](http://dx.doi.org/10.1101/038612) for a detailed description of the method.

Value

A multiHMM object.

Author(s)

Aaron Taudt, Maria Colome Tatche
callPeaksReplicates

Fit a multivariate Hidden Markov Model to multiple ChIP-seq replicates

Description

Fit an HMM to multiple ChIP-seq replicates and derive correlation measures. Input is a list of uniHMMs generated by callPeaksUnivariate.

Usage

callPeaksReplicates(
  hmm.list,
  max.states = 32,
  force.equal = FALSE,
  eps = 0.01,
)
callPeaksReplicates

max.iter = NULL,
max.time = NULL,
keep.posteriors = TRUE,
num.threads = 1,
max.distance = 0.2,
per.chrom = TRUE
)

Arguments

hmm.list  A list of uniHMMs generated by callPeaksUnivariate, e.g. list(hmm1,hmm2,...) or c("file1","file2",...). Alternatively, this parameter also accepts a multiHMM and will check if the distance between replicates is greater than max.distance.

max.states  The maximum number of combinatorial states to consider. The default (32) is sufficient to treat up to 5 replicates exactly and more than 5 replicates approximately.

force.equal  The default (FALSE) allows replicates to differ in their peak-calls, although the majority will usually be identical. If force.equal=TRUE, all peaks will be identical among all replicates.

eps  Convergence threshold for the Baum-Welch algorithm.

max.iter  The maximum number of iterations for the Baum-Welch algorithm. The default NULL is no limit.

max.time  The maximum running time in seconds for the Baum-Welch algorithm. If this time is reached, the Baum-Welch will terminate after the current iteration finishes. The default NULL is no limit.

keep.posteriors  If set to TRUE, posteriors will be available in the output. This is useful to change the post.cutoff later, but increases the necessary disk space to store the result immensely.

num.threads  Number of threads to use. Setting this to >1 may give increased performance.

max.distance  This number is used as a cutoff to group replicates based on their distance matrix. The lower this number, the more similar replicates have to be to be grouped together.

per.chrom  If per.chrom=TRUE chromosomes will be treated separately. This tremendously speeds up the calculation but results might be noisier as compared to per.chrom=FALSE, where all chromosomes are concatenated for the HMM.

Value

Output is a multiHMM object with additional entry replicateInfo. If only one uniHMM was given as input, a simple list() with the replicateInfo is returned.

Author(s)

Aaron Taudt
callPeaksUnivariate

Fit a Hidden Markov Model to a ChIP-seq sample.

Description

Fit a HMM to a ChIP-seq sample to determine the modification state of genomic regions, e.g. call peaks in the sample.

Usage

callPeaksUnivariate(
  binned.data,
  control.data = NULL,
  prefit.on.chr = NULL,
  short = TRUE,
  eps = 0.1,
  init = "standard",
  max.time = NULL,
  max.iter = 5000,
)
callPeaksUnivariate

num.trials = 1,
eps.try = NULL,
num.threads = 1,
read.cutoff = TRUE,
read.cutoff.quantile = 1,
read.cutoff.absolute = 500,
max.mean = Inf,
post.cutoff = 0.5,
control = FALSE,
keep.posteriors = FALSE,
keep.densities = FALSE,
verbosity = 1
)

Arguments

binned.data A GRanges-class object with binned read counts or a file that contains such an object.
control.data Input control for the experiment. A GRanges-class object with binned read counts or a file that contains such an object.
prefit.on.chr A chromosome that is used to pre-fit the Hidden Markov Model. Set to NULL if you don’t want to prefit but use the whole genome instead.
short If TRUE, the second fitting step is only done with one iteration.
eps Convergence threshold for the Baum-Welch algorithm.
init One of the following initialization procedures:
standard The negative binomial of state ’unmodified’ will be initialized with
mean=mean(counts), var=var(counts) and the negative binomial of state
’modified’ with mean=mean(counts)+1, var=var(counts). This procedure usually gives the fastest convergence.
random Mean and variance of the negative binomials will be initialized with
random values (in certain boundaries, see source code). Try this if the ’standard’ procedure fails to produce a good fit.
empiric Yet another way to initialize the Baum-Welch. Try this if the other
two methods fail to produce a good fit.
max.time The maximum running time in seconds for the Baum-Welch algorithm. If this
time is reached, the Baum-Welch will terminate after the current iteration finishes. The default NULL is no limit.
max.iter The maximum number of iterations for the Baum-Welch algorithm. The default
NULL is no limit.
num.trials The number of trials to run the HMM. Each time, the HMM is seeded with
different random initial values. The HMM with the best likelihood is given as output.
eps.try If code num.trials is set to greater than 1, eps.try is used for the trial runs. If
unset, eps is used.
num.threads Number of threads to use. Setting this to >1 may give increased performance.
callPeaksUnivariate

read.cutoff

The default (TRUE) enables filtering of high read counts. Set read.cutoff=FALSE to disable this filtering.

read.cutoff.quantile

A quantile between 0 and 1. Should be near 1. Read counts above this quantile will be set to the read count specified by this quantile. Filtering very high read counts increases the performance of the Baum-Welch fitting procedure. However, if your data contains very few peaks they might be filtered out. If option read.cutoff.quantile is also specified, the minimum of the resulting cutoff values will be used. Set read.cutoff=FALSE to disable this filtering.

read.cutoff.absolute

Read counts above this value will be set to the read count specified by this value. Filtering very high read counts increases the performance of the Baum-Welch fitting procedure. However, if your data contains very few peaks they might be filtered out. If option read.cutoff.quantile is also specified, the minimum of the resulting cutoff values will be used. Set read.cutoff=FALSE to disable this filtering.

max.mean

If mean(counts)>max.mean, bins with low read counts will be set to 0. This is a workaround to obtain good fits in the case of large bin sizes.

post.cutoff

False discovery rate. codeNULL means that the state with maximum posterior probability will be chosen, irrespective of its absolute probability (default=codeNULL).

control

If set to TRUE, the binned data will be treated as control experiment. That means only state 'zero-inflation' and 'unmodified' will be used in the HMM.

keep.posteriors

If set to TRUE (default=FALSE), posteriors will be available in the output. This is useful to change the post.cutoff later, but increases the necessary disk space to store the result.

keep.densities

If set to TRUE (default=FALSE), densities will be available in the output. This should only be needed debugging.

verbosity

Verbosity level for the fitting procedure. 0 - No output, 1 - Iterations are printed.

Details

This function is similar to callPeaksUnivariateAllChr but allows to pre-fit on a single chromosome instead of the whole genome. This gives a significant performance increase and can help to converge into a better fit in case of unsteady quality for some chromosomes.

Value

A uniHMM object.

Author(s)

Aaron Taudt, Maria Colome Tatche

See Also

uniHMM, callPeaksMultivariate
Examples

```r
## Get an example BAM file with ChIP-seq reads
file <- system.file("extdata", "euratrans", "lv-H3K27me3-BN-male-bio2-tech1.bam", package="chromstaRData")
## Bin the BED file into bin size 1000bp
data(rn4_chrominfo)
data(experiment_table)
binned <- binReads(file, experiment.table=experiment_table, assembly=rn4_chrominfo, binsizes=1000, stepsizes=500, chromosomes='chr12')
## Fit the univariate Hidden Markov Model
hmm <- callPeaksUnivariate(binned, max.time=60, eps=1)
## Check if the fit is ok
plotHistogram(hmm)
```

### callPeaksUnivariateAllChr

*Fit a Hidden Markov Model to a ChIP-seq sample.*

**Description**

Fit a HMM to a ChIP-seq sample to determine the modification state of genomic regions, e.g. call peaks in the sample.

**Usage**

```r
callPeaksUnivariateAllChr(
  binned.data,  # Binned data
  control.data = NULL,  # Control data
  eps = 0.01,  # Epsilon for termination
  init = "standard",  # Initialization method
  max.time = NULL,  # Maximum time for fitting
  max.iter = NULL,  # Maximum number of iterations
  num.trials = 1,  # Number of trials
  eps.try = NULL,  # Epsilon for trial
  num.threads = 1,  # Number of threads
  read.cutoff = TRUE,  # Read cutoff
  read.cutoff.quantile = 1,  # Quantile for read cutoff
  read.cutoff.absolute = 500,  # Absolute read cutoff
  max.mean = Inf,  # Maximum mean
  post.cutoff = 0.5,  # Post-cutoff
  control = FALSE,  # Control
  keep.posteriors = FALSE,  # Keep posteriors
  keep.densities = FALSE,  # Keep densities
  verbosity = 1  # Verbosity
)
```
Arguments

**binned.data**  
A `GRanges-class` object with binned read counts or a file that contains such an object.

**control.data**  
Input control for the experiment. A `GRanges-class` object with binned read counts or a file that contains such an object.

**eps**  
Convergence threshold for the Baum-Welch algorithm.

**init**  
One of the following initialization procedures:

- **standard**  
The negative binomial of state 'unmodified' will be initialized with mean=mean(counts), var=var(counts) and the negative binomial of state 'modified' with mean=mean(counts)+1, var=var(counts). This procedure usually gives the fastest convergence.

- **random**  
Mean and variance of the negative binomials will be initialized with random values (in certain boundaries, see source code). Try this if the 'standard' procedure fails to produce a good fit.

- **empiric**  
Yet another way to initialize the Baum-Welch. Try this if the other two methods fail to produce a good fit.

**max.time**  
The maximum running time in seconds for the Baum-Welch algorithm. If this time is reached, the Baum-Welch will terminate after the current iteration finishes. The default `NULL` is no limit.

**max.iter**  
The maximum number of iterations for the Baum-Welch algorithm. The default `NULL` is no limit.

**num.trials**  
The number of trials to run the HMM. Each time, the HMM is seeded with different random initial values. The HMM with the best likelihood is given as output.

**eps.try**  
If code `num.trials` is set to greater than 1, `eps.try` is used for the trial runs. If unset, `eps` is used.

**num.threads**  
Number of threads to use. Setting this to >1 may give increased performance.

**read.cutoff**  
The default (TRUE) enables filtering of high read counts. Set `read.cutoff=FALSE` to disable this filtering.

**read.cutoff.quantile**  
A quantile between 0 and 1. Should be near 1. Read counts above this quantile will be set to the read count specified by this quantile. Filtering very high read counts increases the performance of the Baum-Welch fitting procedure. However, if your data contains very few peaks they might be filtered out. If option `read.cutoff.absolute` is also specified, the minimum of the resulting cutoff values will be used. Set `read.cutoff=FALSE` to disable this filtering.

**read.cutoff.absolute**  
Read counts above this value will be set to the read count specified by this value. Filtering very high read counts increases the performance of the Baum-Welch fitting procedure. However, if your data contains very few peaks they might be filtered out. If option `read.cutoff.quantile` is also specified, the minimum of the resulting cutoff values will be used. Set `read.cutoff=FALSE` to disable this filtering.
changeMaxPostCutoff

max.mean If mean(counts)>max.mean, bins with low read counts will be set to 0. This is a workaround to obtain good fits in the case of large bin sizes.

post.cutoff False discovery rate. codeNULL means that the state with maximum posterior probability will be chosen, irrespective of its absolute probability (default=codeNULL).

control If set to TRUE, the binned data will be treated as control experiment. That means only state ’zero-inflation’ and ’unmodified’ will be used in the HMM.

keep.posters If set to TRUE (default=FALSE), posteriors will be available in the output. This is useful to change the post.cutoff later, but increases the necessary disk space to store the result.

keep.densities If set to TRUE (default=FALSE), densities will be available in the output. This should only be needed debugging.

verbosity Verbosity level for the fitting procedure. 0 - No output, 1 - Iterations are printed.

Details

The Hidden Markov Model which is used to classify the bins uses 3 states: state ’zero-inflation’ with a delta function as emission density (only zero read counts), ‘unmodified’ and ‘modified’ with Negative Binomials as emission densities. A Baum-Welch algorithm is employed to estimate the parameters of the distributions. Please refer to our manuscript at http://dx.doi.org/10.1101/038612 for a detailed description of the method.

Value

A uniHMM object.

Author(s)

Aaron Taudt, Maria Coome Tatche

See Also

uniHMM, callPeaksMultivariate

changeMaxPostCutoff Adjust sensitivity of peak detection

Description

Adjusts the peak calls of a uniHMM, multiHMM or combinedMultiHMM object with a cutoff on the maximum-posterior within each peak. Higher values of maxPost.cutoff mean less sensitive and more precise peak calls. Remaining peaks are kept intact, as opposed to function changePostCutoff, where broad peaks are fragmented. This function was formerly called 'changeFDR' and is still available for backwards compatibility.
Usage

changeMaxPostCutoff(model, maxPost.cutoff = 0.99, invert = FALSE)

changeFDR(model, fdr = 0.01, invert = FALSE)

Arguments

model A uniHMM or multiHMM object with posteriors.

maxPost.cutoff A vector of values between 0 and 1 for each column in model$bins$posteriors. If only one value is given, it will be reused for all columns. Values close to 1 will yield more stringent peak calls with lower false positive but higher false negative rate (i.e. more precise but less sensitive).

invert Select peaks below (FALSE) or above (TRUE) the given maxPost.cutoff. This is useful to select low confidence peaks.

fdr Same as 1-maxPost.cutoff.

Details

Each peak has a maximum-posterior (maxPostInPeak, between 0 and 1) associated. The sensitivity is adjusted with a simple cutoff on maxPostInPeak, e.g. for maxPost.cutoff = 0.99 only peaks with maxPostInPeak >= 0.99 will be selected.

Value

The input object is returned with adjusted peak calls.

Functions

- changeFDR: This function was renamed to 'changeMaxPostCutoff' in chromstaR 1.5.1 but it still available for backwards compatibility.

Author(s)

Aaron Taudt

See Also

changePostCutoff

Examples

```r
# Get an example uniHMM
file <- system.file("data","H3K27me3-BN-rep1.RData", package="chromstaR")
model <- get(load(file))

# Compare fits with different fdrs
plotHistogram(model) + ylim(0,0.25) + ylim(0,0.3)
plotHistogram(changeMaxPostCutoff(model, maxPost.cutoff=0.99)) + ylim(0,0.3)
plotHistogram(changeMaxPostCutoff(model, maxPost.cutoff=1-1e-12)) + ylim(0,0.3)
```
changePostCutoff

## Get an example multiHMM ##

```r
file <- system.file("data", "multivariate_mode-combinatorial_condition-SHR.RData", package="chromstaR")
model <- get(load(file))
genomicFrequencies(model)
model.new <- changeMaxPostCutoff(model, maxPost.cutoff=0.9999, invert=FALSE)
genomicFrequencies(model.new)
```

## Get an example combinedMultiHMM ##

```r
file <- system.file("data", "combined_mode-differential.RData", package="chromstaR")
model <- get(load(file))
genomicFrequencies(model)
model.new <- changeMaxPostCutoff(model, maxPost.cutoff=0.9999, invert=FALSE)
genomicFrequencies(model.new)
```

---

### changePostCutoff

**Change the posterior cutoff of a Hidden Markov Model**

**Description**

Adjusts the peak calls of a uniHMM, multiHMM or combinedMultiHMM object with the given posterior cutoff.

**Usage**

```r
changePostCutoff(model, post.cutoff = 0.5)
```

**Arguments**

- `model`: A uniHMM or multiHMM object with posteriors.
- `post.cutoff`: A vector of posterior cutoff values between 0 and 1 the same length as `ncol(model$bins$posteriors)`. If only one value is given, it will be reused for all columns. Values close to 1 will yield more stringent peak calls with lower false positive but higher false negative rate.

**Details**

Posterior probabilities are between 0 and 1. Peaks are called if the posteriors for a state (univariate) or sample (multivariate) are `>= post.cutoff`.

**Value**

The input object is returned with adjusted peak calls.

**Author(s)**

Aaron Taudt
Chromstar

Wrapper function for the chromstaR package

Description

This function performs binning, univariate peak calling and multivariate peak calling from a list of input files.
Chromstar

Usage

Chromstar(
  inputfolder,
  experiment.table,
  outputfolder,
  configfile = NULL,
  numCPU = 1,
  binsize = 1000,
  stepsize = binsize/2,
  assembly = NULL,
  chromosomes = NULL,
  remove.duplicate.reads = TRUE,
  min.mapq = 10,
  format = NULL,
  prefit.on.chr = NULL,
  eps.univariate = 0.1,
  max.time = NULL,
  max.iter = 5000,
  read.cutoff.absolute = 500,
  keep.posterior = TRUE,
  mode = "differential",
  max.states = 128,
  per.chrom = TRUE,
  eps.multivariate = 0.01,
  exclusive.table = NULL
)

Arguments

inputfolder  Folder with either BAM or BED-6 (see readBedFileAsGRanges files.
experiment.table
  A data.frame or tab-separated text file with the structure of the experiment. See experiment.table for an example.
outputfolder  Folder where the results and intermediate files will be written to.
configfile   A file specifying the parameters of this function (without inputfolder, outputfolder and configfile). Having the parameters in a file can be handy if many samples with the same parameter settings are to be run. If a configfile is specified, it will take priority over the command line parameters.
numCPU       Number of threads to use for the analysis. Beware that more CPUs also means more memory is needed. If you experience crashes of R with higher numbers of this parameter, leave it at numCPU=1.
binsize      An integer specifying the bin size that is used for the analysis.
stepsize     An integer specifying the step size for analysis.
assembly     A data.frame or tab-separated file with columns 'chromosome' and 'length'. Alternatively a character specifying the assembly, see getChromInfoFromUCSC for available assemblies. Specifying an assembly is only necessary when importing BED files. BAM files are handled automatically.
chromosomes

If only a subset of the chromosomes should be imported, specify them here.

remove.duplicate.reads

A logical indicating whether or not duplicate reads should be removed.

min.mapq

Minimum mapping quality when importing from BAM files. Set min.mapq=0 to keep all reads.

format

One of c('bed','bam',NULL). With NULL the format is determined automatically from the file ending.

prefit.on.chr

A chromosome that is used to pre-fit the Hidden Markov Model. Set to NULL if you don’t want to prefit but use the whole genome instead.

eps.univariate

Convergence threshold for the univariate Baum-Welch algorithm.

max.time

The maximum running time in seconds for the Baum-Welch algorithm. If this time is reached, the Baum-Welch will terminate after the current iteration finishes. The default NULL is no limit.

max.iter

The maximum number of iterations for the Baum-Welch algorithm. The default NULL is no limit.

read.cutoff.absolute

Read counts above this value will be set to the read count specified by this value. Filtering very high read counts increases the performance of the Baum-Welch fitting procedure. However, if your data contains very few peaks they might be filtered out. If option read.cutoff.quantile is also specified, the minimum of the resulting cutoff values will be used. Set read.cutoff=FALSE to disable this filtering.

keep.posteriors

If set to TRUE (default=FALSE), posteriors will be available in the output. This is useful to change the post.cutoff later, but increases the necessary disk space to store the result.

mode

One of c('differential','combinatorial','full'). The modes determine how the multivariate part is run. Here is some advice which mode to use:

combinatorial Each condition is analyzed separately with all marks combined. Choose this mode if you have more than ~7 conditions or you want to have a high sensitivity for detecting combinational states. Differences between conditions will be more noisy (more false positives) than in mode 'differential' but combinational states are more precise.

differential Each mark is analyzed separately with all conditions combined. Choose this mode if you are interested in accurate differences. Combinatorial states will be more noisy (more false positives) than in mode 'combinatorial' but differences are more precise.

full Full analysis of all marks and conditions combined. Best of both, but:

Choose this mode only if (number of conditions * number of marks ≤ 8), otherwise it might be too slow or crash due to memory limitations.

separate Only replicates are analyzed multivariately. Combinatorial states are constructed by a simple post-hoc combination of peak calls.

max.states

The maximum number of states to use in the multivariate part. If set to NULL, the maximum number of theoretically possible states is used. CAUTION: This
can be very slow or crash if you have too many states. chromstaR has a built in mechanism to select the best states in case that less states than theoretically possible are specified.

per.chrom If set to TRUE chromosomes will be treated separately in the multivariate part. This tremendously speeds up the calculation but results might be noisier as compared to per.chrom=FALSE, where all chromosomes are concatenated for the HMM.

eps.multivariate Convergence threshold for the multivariate Baum-Welch algorithm.

exclusive.table A data.frame or tab-separated file with columns 'mark' and 'group'. Histone marks with the same group will be treated as mutually exclusive.

Value

NULL

Examples

```r
## Prepare the file paths. Exchange this with your input and output directories.
inputfolder <- system.file("extdata","euratrans", package="chromstaRData")
outputfolder <- file.path(tempdir(), 'SHR-example')

## Define experiment structure
data(experiment_table_SHR)

## Define assembly
# This is only necessary if you have BED files, BAM files are handled automatically.
# For common assemblies you can also specify them as 'hg19' for example.
data(rn4_chrominfo)

## Run ChromstaR
Chromstar(inputfolder, experiment.table=experiment_table_SHR,
          outputfolder=outputfolder, numCPU=4, binsize=1000, assembly=rn4_chrominfo,
          prefit.on.chr='chr12', chromosomes='chr12', mode='combinatorial', eps.univariate=1,
          eps.multivariate=1)
```

chromstaR-objects chromstaR objects

Description

chromstaR defines several objects.

- uniHMM: Returned by callPeaksUnivariate.
- multiHMM: Returned by callPeaksMultivariate and callPeaksReplicates.
- combinedMultiHMM: Returned by combineMultivariates.
### collapseBins

**Collapse consecutive bins**

**Description**

The function will collapse consecutive bins which have, for example, the same combinatorial state.

**Usage**

```r
collapseBins(
  data,
  column2collapseBy = NULL,
  columns2sumUp = NULL,
  columns2average = NULL,
  columns2getMax = NULL,
  columns2drop = NULL
)
```

**Arguments**

- **data**
  A data.frame containing the genomic coordinates in the first three columns.

- **column2collapseBy**
  The number of the column which will be used to collapse all other inputs. If a set of consecutive bins has the same value in this column, they will be aggregated into one bin with adjusted genomic coordinates.

- **columns2sumUp**
  Column numbers that will be summed during the aggregation process.

- **columns2average**
  Column numbers that will be averaged during the aggregation process.

- **columns2getMax**
  Column numbers where the maximum will be chosen during the aggregation process.

- **columns2drop**
  Column numbers that will be dropped after the aggregation process.

**Details**

The following tables illustrate the principle of the collapsing:

**Input data:**

<table>
<thead>
<tr>
<th>seqnames</th>
<th>start</th>
<th>end</th>
<th>column2collapseBy</th>
<th>moreColumns</th>
<th>columns2sumUp</th>
</tr>
</thead>
<tbody>
<tr>
<td>chr1</td>
<td>0</td>
<td>199</td>
<td>2</td>
<td>1 10</td>
<td>1 3</td>
</tr>
<tr>
<td>chr1</td>
<td>200</td>
<td>399</td>
<td>2</td>
<td>2 11</td>
<td>0 3</td>
</tr>
<tr>
<td>chr1</td>
<td>400</td>
<td>599</td>
<td>2</td>
<td>3 12</td>
<td>1 3</td>
</tr>
<tr>
<td>chr1</td>
<td>600</td>
<td>799</td>
<td>1</td>
<td>4 13</td>
<td>0 3</td>
</tr>
<tr>
<td>chr1</td>
<td>800</td>
<td>999</td>
<td>1</td>
<td>5 14</td>
<td>1 3</td>
</tr>
</tbody>
</table>

**Output data:**

<table>
<thead>
<tr>
<th>seqnames</th>
<th>start</th>
<th>end</th>
<th>column2collapseBy</th>
<th>moreColumns</th>
<th>columns2sumUp</th>
</tr>
</thead>
</table>
**combinatorialStates**

```r
seqnames start end column2collapseBy moreColumns columns2sumUp
chr1 0 599 2 1 10 2 9
chr1 600 999 1 4 13 1 6
```

**Value**

A data.frame.

**Author(s)**

Aaron Taudt

**Examples**

```r
## Load example data
## Get an example multiHMM
file <- system.file("data","multivariate_mode-combinatorial_condition-SHR.RData",
                   package="chromstaR")
model <- get(load(file))
shortdf <- collapseBins(df, column2collapseBy='state', columns2sumUp='width', columns2average=6:9)
```

---

**combinatorialStates**  
*Get the (decimal) combinatorial states of a list of univariate HMM models*

**Description**

Get the combinatorial states of a list of models generated by `callPeaksUnivariate`. The function returns the decimal combinatorial states for each bin (see details for an explanation of combinatorial state).

**Usage**

```r
combinatorialStates(hmm.list, binary = FALSE)
```

**Arguments**

- `hmm.list` A list of models generated by `callPeaksUnivariate`, e.g. `list(model1,model2,...)`.
- `binary` If TRUE, a matrix of binary instead of decimal states will be returned.
Details

For a given model, each genomic bin can be either called 'unmodified' or 'modified', depending on the posterior probabilities estimated by the Baum-Welch. Thus, a list of models defines a binary combinatorial state for each bin. This binary combinatorial state can be expressed as a decimal number. Example: We have 4 histone modifications, and we run the univariate HMM for each of them. Then we use a false discovery rate of 0.5 to call each bin either 'unmodified' or 'modified'. The resulting binary combinatorial states can then be converted to decimal representation. The following table illustrates this:

<table>
<thead>
<tr>
<th>bin</th>
<th>modification state</th>
<th>decimal state</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0 0 1 0</td>
<td>2</td>
</tr>
<tr>
<td>2</td>
<td>0 0 0 0</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>0 1 1 0</td>
<td>6</td>
</tr>
<tr>
<td>4</td>
<td>0 1 1 1</td>
<td>7</td>
</tr>
</tbody>
</table>

Value

Output is a vector of integers representing the combinatorial state of each bin.

Author(s)

Aaron Taudt

See Also

dec2bin, bin2dec

Examples

```r
# Get example BAM files for 3 different marks in hypertensive rat (SHR)
file.path <- system.file("extdata","euratrans", package='chromstaRData')
files <- list.files(file.path, full.names=TRUE, pattern='SHR.*bam$')[c(1,4,6)]

# Bin the data
data(rn4_chrominfo)
binned.data <- list()
for (file in files) {
  binned.data[[basename(file)]] <- binReads(file, binsizes=1000, stepsizes=500, assembly=rn4_chrominfo, chromosomes='chr12')
}

# Obtain the univariate fits
models <- list()
for (i1 in 1:length(binned.data)) {
  models[[i1]] <- callPeaksUnivariate(binned.data[[i1]], max.time=60, eps=1)
}

## Get the decimal representation of the combinatorial state of this combination of models
states <- chromstaR:::combinatorialStates(models, binary=FALSE)
## Show number of each state
table(states)
```
**combinedMultiHMM**

**Combined multivariate HMM object**

**Description**

The combined multivariate HMM object is output of the function `combineMultivariates` and is a `list()` with various entries. The `class()` attribute of this list was set to "combinedMultiHMM". For a given hmm, the entries can be accessed with the list operators 'hmm[[]]' or 'hmm$'.

**Value**

A `list()` with the following entries:

- `info`: Experiment table for this object.
- `bins`: A `GRanges-class` object containing genomic bin coordinates and human readable combinations for the combined `multiHMM` objects.
- `segments`: Same as bins, but consecutive bins with the same state are collapsed into segments.
- `segments.per.condition`: A `list()` with segments for each condition separately.
- `peaks`: A `list()` with `GRanges-class` containing peak coordinates for each ID in `info`.
- `frequencies`: Genomic frequencies of combinations.
- `mode`: Mode of analysis.

**See Also**

`combineMultivariates, uniHMM, multiHMM`

**combineMultivariates**

**Combine combinatorial states from several Multivariates**

**Description**

Combine combinatorial states from several `multiHMM` objects. Combinatorial states can be combined for objects containing multiple marks (mode='combinatorial') or multiple conditions (mode='differential').

**Usage**

`combineMultivariates(hmms, mode)`

**Arguments**

- `hmms`: A `list()` with `multiHMM` objects. Alternatively a character vector with filenames that contain `multiHMM` objects.
- `mode`: Mode of combination. See `Chromstar` for a description of the mode parameter.
Value

A `combinedMultivar` object with combinatorial states for each condition.

Author(s)

Aaron Taudt

Examples

### Multivariate peak calling for spontaneous hypertensive rat (SHR) ###

```r
# Get example BAM files for 2 different marks in hypertensive rat (SHR)
file.path <- system.file("extdata", "euratrans", package="chromstaRData")
files <- list.files(file.path, full.names=TRUE, pattern='SHR.*bam')[c(1:2,4:5)]
# Construct experiment structure
exp <- data.frame(file=files, mark=c("H3K27me3","H3K27me3","H3K4me3","H3K4me3"),
                  condition=rep("SHR",4), replicate=c(1:2,1:2), pairedEndReads=FALSE,
                  controlFiles=NA)
states <- stateBrewer(exp, mode='combinatorial')
# Bin the data
data(rn4_chrominfo)
binned.data <- list()
for (file in files) {
  binned.data[[basename(file)]] <- binReads(file, binsizes=1000, stepsizes=500,
                                          experiment.table=exp,
                                          assembly=rn4_chrominfo, chromosomes='chr12')
}
# Obtain the univariate fits
models <- list()
for (i1 in 1:length(binned.data)) {
  models[[i1]] <- callPeaksUnivariate(binned.data[[i1]], max.time=60, eps=1)
}
# Call multivariate peaks
multimodel.SHR <- callPeaksMultivariate(models, use.states=states, eps=1, max.time=60)
```

### Multivariate peak calling for brown norway rat (BN) ###

```r
# Get example BAM files for 2 different marks in brown norway rat
file.path <- system.file("extdata", "euratrans", package="chromstaRData")
files <- list.files(file.path, full.names=TRUE, pattern='BN.*bam')[c(1:2,3:4)]
# Construct experiment structure
exp <- data.frame(file=files, mark=c("H3K27me3","H3K27me3","H3K4me3","H3K4me3"),
                  condition=rep("BN",4), replicate=c(1:2,1:2), pairedEndReads=FALSE,
                  controlFiles=NA)
states <- stateBrewer(exp, mode='combinatorial')
# Bin the data
data(rn4_chrominfo)
binned.data <- list()
for (file in files) {
  binned.data[[basename(file)]] <- binReads(file, binsizes=1000, stepsizes=500,
                                          experiment.table=exp,
                                          assembly=rn4_chrominfo, chromosomes='chr12')
}
# Obtain the univariate fits
```
models <- list()
for (i1 in 1:length(binned.data)) {
  models[[i1]] <- callPeaksUnivariate(binned.data[[i1]], max.time=60, eps=1)
}
# Call multivariate peaks
multimodel.BN <- callPeaksMultivariate(models, use.states=states, eps=1, max.time=60)

### Combine multivariates ###
hmms <- list(multimodel.SHR, multimodel.BN)
comb.model <- combineMultivariates(hmms, mode='combinatorial')

---

### Conversion of decimal and binary states ###

**Description**

Convert combinatorial states in decimal representation to combinatorial states in binary representation and vice versa.

**Usage**

- `dec2bin(dec, colnames = NULL, ndigits = NULL)`
- `bin2dec(bin)`

**Arguments**

- `dec` : A vector with whole numbers.
- `colnames` : The column names for the returned matrix. If specified, `ndigits` will be the length of `colnames`.
- `ndigits` : The number of digits that the binary representation should have. If unspecified, the shortest possible representation will be chosen.
- `bin` : A matrix with only 0 and 1 (or TRUE and FALSE) as entries. One combinatorial state per row.

**Details**

`chromstaR` uses decimal numbers to represent combinatorial states of peaks. These functions serve as a convenient way to get from the efficient decimal representation to a more human-readable binary representation.

**Value**

A vector of integers for `bin2dec` and a matrix of logicals with one state per row for `dec2bin.`
Functions

- **dec2bin**: Decimal to binary conversion.
- **bin2dec**: Binary to decimal conversion.

Author(s)

Aaron Taudt

Examples

```r
decimal.states <- c(0:31)
binary.states <- dec2bin(decimal.states, colnames=paste0('mark',1:5))
control.decimal.states <- bin2dec(binary.states)
```

---

**enrichmentAtAnnotation**

*Enrichment of (combinatorial) states for genomic annotations*

Description

The function calculates the enrichment of a genomic feature with peaks or combinatorial states. Input is a `multiHMM` object (containing the peak calls and combinatorial states) and a `GRanges-class` object containing the annotation of interest (e.g. transcription start sites or genes).

Usage

```r
enrichmentAtAnnotation(
  bins,
  info,
  annotation,
  bp.around.annotation = 10000,
  region = c("start", "inside", "end"),
  what = "combinations",
  num.intervals = 21,
  statistic = "fold"
)
```

Arguments

- **bins**: The `$bins` entry from a `multiHMM` or `combinedMultiHMM` object.
- **info**: The `$info` entry from a `multiHMM` or `combinedMultiHMM` object.
- **annotation**: A `GRanges-class` object with the annotation of interest.
- **bp.around.annotation**: An integer specifying the number of basepairs up- and downstream of the annotation for which the enrichment will be calculated.
region
  A combination of c('start','inside','end') specifying the region of the annotation for which the enrichment will be calculated. Select 'start' if you have a point-sized annotation like transcription start sites. Select c('start','inside','end') if you have long annotations like genes.

what
  One of c('combinations','peaks','counts') specifying on which feature the statistic is calculated.

num.intervals
  Number of intervals for enrichment 'inside' of annotation.

statistic
  The statistic to calculate. Either 'fold' for fold enrichments or 'fraction' for fraction of bins falling into the annotation.

Value
  A list() containing data.frame()s for enrichment of combinatorial states and binary states at the start, end and inside of the annotation.

Author(s)
  Aaron Taudt

Description
  Plotting functions for enrichment analysis of multiHMM or combinedMultiHMM objects with any annotation of interest, specified as a GRanges-class object.

Usage

```r
plotFoldEnrichHeatmap(
  hmm,
  annotations,
  what = "combinations",
  combinations = NULL,
  marks = NULL,
  plot = TRUE,
  logscale = TRUE
)
```

```r
plotEnrichCountHeatmap(
  hmm,
  annotation,
  bp.around.annotation = 10000,
  max.rows = 1000,
  combinations = NULL,
  colorByCombinations = sortByCombinations,
)```
sortByCombinations = is.null(sortByColumns),
sortByColumns = NULL
)

plotEnrichment(
    hmm,
    annotation,
    bp.around.annotation = 10000,
    region = c("start", "inside", "end"),
    num.intervals = 20,
    what = "combinations",
    combinations = NULL,
    marks = NULL,
    statistic = "fold",
    logscale = TRUE
)

Arguments

hmm A combinedMultiHMM or multiHMM object or a file that contains such an object.
annotations A list() with GRanges-class objects containing coordinates of multiple annotations The names of the list entries will be used to name the return values.
what One of c('combinations','peaks','counts','transitions') specifying on which feature the statistic is calculated.
combinations A vector with combinations for which the enrichment will be calculated, e.g. combinations = c('[H3K4me3]', '[H3K4me3+H3K27me3]'). If NULL all combinations will be considered.
marks A vector with marks for which the enrichment is plotted. If NULL all marks will be considered.
plot A logical indicating whether the plot or an array with the fold enrichment values is returned.
logscale Set to TRUE to plot fold enrichment on log-scale. Ignored if statistic = 'fraction'.
annotation A GRanges-class object with the annotation of interest.
bp.around.annotation An integer specifying the number of basepairs up- and downstream of the annotation for which the enrichment will be calculated.
max.rows An integer specifying the number of randomly subsampled rows that are plotted from the annotation object. This is necessary to avoid crashing for heatmaps with too many rows.
colorByCombinations A logical indicating whether or not to color the heatmap by combinations.
sortByCombinations A logical indicating whether or not to sort the heatmap by combinations.
sortByColumns An integer vector specifying the column numbers by which to sort the rows. If sortByColumns is specified, will force sortByCombinations=FALSE.
region  A combination of c('start', 'inside', 'end') specifying the region of the annotation for which the enrichment will be calculated. Select 'start' if you have a point-sized annotation like transcription start sites. Select c('start', 'inside', 'end') if you have long annotations like genes.

num.intervals  Number of intervals for enrichment 'inside' of annotation.

statistic  The statistic to calculate. Either 'fold' for fold enrichments or 'fraction' for fraction of bins falling into the annotation.

Value
A ggplot object containing the plot or a list() with ggplot objects if several plots are returned. For plotFoldEnrichHeatmap a named array with fold enrichments if plot=FALSE.

Functions
- plotFoldEnrichHeatmap: Compute the fold enrichment of combinatorial states for multiple annotations.
- plotEnrichCountHeatmap: Plot read counts around annotation as heatmap.
- plotEnrichment: Plot fold enrichment of combinatorial states around and inside of annotation.

Author(s)
Aaron Taudt

See Also
plotting

Examples
### Get an example multiHMM ###
file <- system.file("data","multivariate_mode-combinatorial_condition-SHR.RData", package="chromstaR")
model <- get(load(file))

### Obtain gene coordinates for rat from biomaRt ###
library(biomaRt)
ensembl <- useEnsembl(biomart='ENSEMBL_MART_ENSEMBL', dataset='rnorvegicus_gene_ensembl')
genes <- getBM(attributes=c('ensembl_gene_id', 'chromosome_name', 'start_position', 'end_position', 'strand', 'external_gene_name', 'gene_biotype'),
       mart=ensembl)
# Transform to GRanges for easier handling
genes <- GRanges(seqnames=paste0('chr',genes$chromosome_name), ranges=IRanges(start=genes$start, end=genes$end),
               strand=genes$strand,
               name=genes$external_gene_name, biotype=genes$gene_biotype)
# Rename chrMT to chrM
seqlevels(genes)[seqlevels(genes)=='chrMT'] <- 'chrM'
print(genes)

### Make the enrichment plots ###
# We expect promoter [H3K4me3] and bivalent-promoter signatures [H3K4me3+H3K27me3]
# to be enriched at transcription start sites.
plotEnrichment(hmm = model, annotation = genes, bp.around.annotation = 15000) +
  ggtitle('Fold enrichment around genes') +
  xlab('distance from gene body')

# Plot enrichment only at TSS. We make use of the fact that TSS is the start of a gene.
plotEnrichment(model, genes, region = 'start') +
  ggtitle('Fold enrichment around TSS') +
  xlab('distance from TSS in [bp]')
# Note: If you want to facet the plot because you have many combinatorial states you
# can do that with
plotEnrichment(model, genes, region = 'start') +
  facet_wrap(~ combination)

# Another form of visualization that shows every TSS in a heatmap
# If transparency is not supported try to plot to pdf() instead.
tss <- resize(genes, width = 3, fix = 'start')
plotEnrichCountHeatmap(model, tss) +
  theme(strip.text.x = element_text(size=6))

# Fold enrichment with different biotypes, showing that protein coding genes are
# enriched with (bivalent) promoter combinations [H3K4me3] and [H3K4me3+H3K27me3],
# while rRNA is enriched with the empty [] and repressive combinations [H3K27me3].
tss <- resize(genes, width = 3, fix = 'start')
biotypes <- split(tss, tss$biotype)
plotFoldEnrichHeatmap(model, annotations=biotypes) + coord_flip()
exportFiles  

Export genome browser uploadable files

Description

These functions allow to export \texttt{chromstaR-objects} as files which can be uploaded to a genome browser. Peak calls are exported in BED format (.bed.gz), read counts in wiggle format (.wig.gz) as RPKM values, and combinatorial states are exported in BED format (.bed.gz).

Usage

\begin{verbatim}
exportPeaks(
  model,
  filename,
  header = TRUE,
  separate.files = TRUE,
  trackname = NULL
)
\end{verbatim}

\begin{verbatim}
expo**rtCounts(
  model,
  filename,
  header = TRUE,
  separate.files = TRUE,
  trackname = NULL
)
\end{verbatim}

\begin{verbatim}
expo**rtCombinations(
  model,
  filename,
  header = TRUE,
  separate.files = TRUE,
  trackname = NULL,
  exclude.states = "[]",
  include.states = NULL
)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{model} \hspace{1cm} A \texttt{chromstaR-objects}.
  \item \texttt{filename} \hspace{1cm} The name of the file that will be written. The appropriate ending will be appended, either ".peaks.bed.gz" for peak-calls or ".counts.wig.gz" for read counts or ".combinations.bed.gz" for combinatorial states. Any existing file will be overwritten.
  \item \texttt{header} \hspace{1cm} A logical indicating whether the output file will have a heading track line (\texttt{TRUE}) or not (\texttt{FALSE}).
\end{itemize}
**exportGRangesAsBedFile**

Export genome browser viewable files

**Description**

Export GRanges as genome browser viewable file

**Usage**

```r
exportGRangesAsBedFile(
  gr,
  trackname,
  filename,
  namecol = "combination",
  scorecol = "score",
  colorcol = NULL,
  colors = NULL,
  header = TRUE,
  append = FALSE
)
```

**Value**

NULL

**Functions**

- **exportPeaks**: Export peak calls in BED format.
- **exportCounts**: Export read counts as RPKM values in wiggle format.
- **exportCombinations**: Export combinatorial states in BED format.

**Examples**

```r
## Get an example multiHMM
file <- system.file("data", "combined_mode-differential.RData",
package="chromstaR")
model <- get(load(file))
## Export peak calls and combinatorial states
exportPeaks(model, filename=tempfile())
exportCombinations(model, filename=tempfile())
```
**Arguments**

- `gr`: A `GRanges-class` object.
- `trackname`: The name that will be used as track name and description in the header.
- `filename`: The name of the file that will be written. The ending ".bed.gz". Any existing file will be overwritten.
- `namecol`: A character specifying the column that is used as name-column.
- `scorecol`: A character specifying the column that is used as score-column. The score should contain integers in the interval [0,1000] for compatibility with the UCSC genome browser convention.
- `colorcol`: A character specifying the column that is used for coloring the track. There will be one color for each unique element in `colorcol`.
- `colors`: A character vector with the colors that are used for the unique elements in `colorcol`.
- `header`: A logical indicating whether the output file will have a heading track line (TRUE) or not (FALSE).
- `append`: Whether or not to append to an existing file.

**Details**

Export regions from `GRanges-class` as a file which can be uploaded into a genome browser. Regions are exported in BED format (.bed.gz).

**Value**

`NULL`

**Author(s)**

Aaron Taudt

**See Also**

`exportPeaks`, `exportCounts`, `exportCombinations`

**Examples**

```r
### Export regions with read counts above 20 ###
# Get an example BAM file with ChIP-seq reads
file <- system.file("extdata", "euratrans",
                   "lv-H3K27me3-BN-male-bio2-tech1.bam",
                   package="chromstaRData")
# Bin the file into bin size 1000bp
data(rn4_chrominfo)
binned <- binReads(file, assembly=rn4_chrominfo, binsizes=1000,
                   stepsizes=500, chromosomes='chr12')
plotHistogram(binned)
# Export regions with read count above 20
exportGRangesAsBedFile(binned[binned$counts[,1] > 20], filename=tempfile()),
```
fixedWidthBins  

*Make fixed-width bins*

**Description**

Make fixed-width bins based on given bin size.

**Usage**

```r
fixedWidthBins(
  bamfile = NULL,
  assembly = NULL,
  chrom.lengths = NULL,
  chromosome.format,
  binsizes = 1e+06,
  chromosomes = NULL
)
```

**Arguments**

- `bamfile`: A BAM file from which the header is read to determine the chromosome lengths. If a bamfile is specified, option `assembly` is ignored.
- `assembly`: An assembly from which the chromosome lengths are determined. Please see `getChromInfoFromUCSC` for available assemblies. This option is ignored if `bamfile` is specified. Alternatively a data.frame generated by `getChromInfoFromUCSC`.
- `chrom.lengths`: A named character vector with chromosome lengths. Names correspond to chromosomes.
- `chromosome.format`: A character specifying the format of the chromosomes if `assembly` is specified. Either 'NCBI' for (1,2,3 ...) or 'UCSC' for (chr1,chr2,chr3 ...). If a bamfile or `chrom.lengths` is supplied, the format will be chosen automatically.
- `binsizes`: A vector of bin sizes in base pairs.
- `chromosomes`: A subset of chromosomes for which the bins are generated.

**Value**

A `list()` of `GRanges-class` objects with fixed-width bins.

**Author(s)**

Aaron Taudt
## Make fixed-width bins of size 500kb and 1Mb

```r
data(rn4_chrominfo)
chrom.lengths <- rn4_chrominfo$length
names(chrom.lengths) <- rn4_chrominfo$chromosome
bins <- fixedWidthBins(chrom.lengths=chrom.lengths, binsizes=c(5e5,1e6))
bins
```

## Make bins using NCBI server (requires internet connection)

```r
# bins <- fixedWidthBins(assembly='mm10', chromosome.format='NCBI', binsizes=c(5e5,1e6))
```

---

### genes_rn4

**Gene coordinates for rn4**

#### Description

A data.frame containing gene coordinates and biotypes of the rn4 assembly.

#### Format

A data.frame.

#### Examples

```r
data(genes_rn4)
head(genes_rn4)
```

---

### genomicFrequencies

**Frequencies of combinatorial states**

#### Description

Get the genomewide frequency of each combinatorial state.

#### Usage

```r
genomicFrequencies(multi.hmm, combinations = NULL, per.mark = FALSE)
```

#### Arguments

- **multi.hmm**: A `multiHMM` or `combinedMultiHMM` object or a file that contains such an object.
- **combinations**: A vector with combinations for which the frequency will be calculated. If NULL all combinations will be considered.
- **per.mark**: Set to TRUE if you want frequencies per mark instead of per combination.
getCombinations

Value
A table with frequencies of each combinatorial state.

Author(s)
Aaron Taudt

Examples
## Get an example multiHMM
file <- system.file("data", "multivariate_mode-combinatorial_condition-SHR.RData", package="chromstaR")
model <- get(load(file))
genomicFrequencies(model)

---

table of frequencies of each combinatorial state.

### Get combinations ###

#### Description ####
Get a DataFrame with combinations from a GRanges-class object.

#### Usage ####
getCombinations(gr)

#### Arguments ####
gr
A GRanges-class object from which the meta-data columns containing combinations will be extracted.

#### Value ####
A DataFrame.

#### Examples ####
## Get an example multiHMM ##
file <- system.file("data", "multivariate_mode-combinatorial_condition-SHR.RData", package="chromstaR")
model <- get(load(file))

### Get the combinations
bin.combs <- getCombinations(model$bins)
print(bin.combs)
seg.combs <- getCombinations(model$segments)
print(seg.combs)
**getDistinctColors**

*Get distinct colors*

**Description**

Get a set of distinct colors selected from `colors`.

**Usage**

```r
getDistinctColors(
  n,
  start.color = "blue4",
  exclude.colors = c("white", "black", "gray", "grey", "\yellow\", "yellow1", "lemonchiffon"),
  exclude.brightness.above = 1,
  exclude.rgb.above = 210
)
```

**Arguments**

- `n` Number of colors to select. If `n` is a character vector, `length(n)` will be taken as the number of colors and the colors will be named by `n`.
- `start.color` Color to start the selection process from.
- `exclude.colors` Character vector with colors that should not be used.
- `exclude.brightness.above` Exclude colors where the 'brightness' value in HSV space is above. This is useful to obtain a matt palette.
- `exclude.rgb.above` Exclude colors where all RGB values are above. This is useful to exclude whitish colors.

**Details**

The function computes the euclidian distance between all `colors` and iteratively selects those that have the furthest closes distance to the set of already selected colors.

**Value**

A character vector with colors.

**Author(s)**

Aaron Taudt
Examples

cols <- getDistinctColors(5)
pie(rep(1,5), labels=cols, col=cols)

---

getStateColors  Get state colors

Description

Get the colors that are used for plotting.

Usage

ggetStateColors(labels = NULL)

Arguments

labels  Any combination of c("zero-inflation","unmodified","modified","total","counts").

Value

A character vector with colors.

See Also

plotting

Examples

cols <- getStateColors()
pie(1:length(cols), col=cols, labels=names(cols))

---

heatmapCombinations  Plot a heatmap of combinatorial states

Description

Plot a heatmap that shows the binary presence/absence of marks for the different combinations.

Usage

heatmapCombinations(model = NULL, marks = NULL, emissionProbs = NULL)
Heatmap of read count correlations (see cor).

**Usage**

heatmapCountCorrelation(model, cluster = TRUE)

**Arguments**

- `model` A `multiHMM` or `combinedMultiHMM` object or file that contains such an object.
- `cluster` Logical indicating whether or not to cluster the heatmap.
Value

A `ggplot` object.

See Also

`plotting`

Examples

```r
## Get an example multiHMM ##
file <- system.file("data","multivariate_mode-combinatorial_condition-SHR.RData", package="chromstaR")
model <- get(load(file))
## Plot count correlations as heatmap
heatmapCountCorrelation(model)
```

```
heatmapTransitionProbs

Heatmap of transition probabilities

Description

Plot a heatmap of transition probabilities for a `multiHMM` model.

Usage

```r
heatmapTransitionProbs(
  model = NULL,
  reorder.states = TRUE,
  transitionProbs = NULL
)
```

Arguments

- **model**: A `multiHMM` object or file that contains such an object.
- **reorder.states**: Whether or not to reorder the states.
- **transitionProbs**: A matrix with transition probabilities where `dimnames(emissionProbs)` gives the state labels. This option is helpful to plot transition probabilities directly without needing a `chromstaR-objects`. If specified, `model` will be ignored.

Value

A `ggplot` object.
loadHmmsFromFiles

Load chromstaR objects from file

Description

Wrapper to load chromstaR objects from file and check the class of the loaded objects.

Usage

loadHmmsFromFiles(
  files,
  check.class = c("GRanges", "uniHMM", "multiHMM", "combinedMultiHMM")
)

Arguments

- **files**: A list of chromstaR-objects or a vector of files that contain such objects.
- **check.class**: Any combination of c('GRanges', 'uniHMM', 'multiHMM', 'combinedMultiHMM'). If any of the loaded objects does not belong to the specified class, an error is thrown.

Value

A list of chromstaR-object.

Examples

## Get an example multiHMM
file <- system.file("data", "multivariate_mode-combinatorial_condition-SHR.RData", package="chromstaR")
model <- get(load(file))
## Plot transition probabilites as heatmap
heatmapTransitionProbs(model, reorder.states=TRUE)

## Get an example BAM file
file <- system.file("extdata", "euratrans", "1v-H3K27me3-BN-male-bio2-tech1.bam", package="chromstaRData")
## Bin the file into bin size 1000bp
data(rn4_chrominfo)
binned <- binReads(file, assembly=rn4_chrominfo, binsizes=1000, stepsizes=500, chromosomes='chr12')
## Fit the univariate Hidden Markov Model

```r
hmm <- callPeaksUnivariate(binned, max.time=60, eps=1)
temp.file <- tempfile()
save(hmm, file=temp.file)
loaded.hmm <- loadHmmsFromFiles(temp.file)[[1]]
class(loaded.hmm)
```

---

### mergeChroms

- **Description**
  
  Merge several `multiHMM` objects into one object. This can be done to merge fits for separate chromosomes into one object for easier handling. Merging will only be done if all models have the same IDs.

- **Usage**
  
  ```r
  mergeChroms(multi.hmm.list, filename = NULL)
  ```

- **Arguments**
  
  - `multi.hmm.list`: A list of `multiHMM` objects or a character vector of files that contain such objects.
  - `filename`: The file name where the merged object will be stored. If `filename` is not specified, a `multiHMM` is returned.

- **Value**
  
  A `multiHMM` object or NULL, depending on option `filename`.

- **Author(s)**
  
  Aaron Taudt

---

### model.combined

- **Description**
  
  A `combinedMultiHMM` object for demonstration purposes in examples of package `chromstaR`.

- **Format**
  
  A `combinedMultiHMM` object.
Examples

## Get an example combinedMultiHMM
file <- system.file("data","combined_mode-differential.RData",
                      package="chromstaR")
model <- get(load(file))

model.multivariate  Multivariate HMM for demonstration purposes

Description

A multiHMM object for demonstration purposes in examples of package chromstaR.

Format

A multiHMM object.

Examples

## Get an example multiHMM
file <- system.file("data","multivariate_mode-combinatorial_condition-SHR.RData",
                      package="chromstaR")
model <- get(load(file))

model.univariate  Univariate HMM for demonstration purposes

Description

A uniHMM object for demonstration purposes in examples of package chromstaR.

Format

A uniHMM object.

Examples

## Get an example uniHMM
file <- system.file("data","H3K27me3-BN-rep1.RData", package="chromstaR")
model <- get(load(file))
**multiHMM**  
*Multivariate HMM object*

**Description**

The multivariate HMM object is output of the function `callPeaksMultivariate` and is a `list()` with various entries. The `class()` attribute of this list was set to "multiHMM". For a given `hmm`, the entries can be accessed with the list operators `hmm[[ ]]` or `hmm$`.

**Value**

A `list()` with the following entries:

- `info`: Experiment table for this object.
- `bincounts`: A `GRanges-class` object containing the genomic bin coordinates and original binned read count values for different offsets.
- `bins`: A `GRanges-class` object containing the genomic bin coordinates, their read count, (optional) posteriors and state classification.
- `segments`: Same as `bins`, but consecutive bins with the same state are collapsed into segments.
- `peaks`: A `list()` with `GRanges-class` containing peak coordinates for each ID in `info`.
- `mapping`: A named vector giving the mapping from decimal combinatorial states to human readable combinations.
- `weights`: Weight for each component. Same as `apply(hmm$posteriors,2,mean)`.
- `weights.univariate`: Weights of the univariate HMMs.
- `transitionProbs`: Matrix of transition probabilities from each state (row) into each state (column).
- `transitionProbs.initial`: Initial `transitionProbs` at the beginning of the Baum-Welch.
- `startProbs`: Probabilities for the first bin. Same as `hmm$posteriors[1,]`.
- `startProbs.initial`: Initial `startProbs` at the beginning of the Baum-Welch.
- `distributions`: Emission distributions used for this model.
- `convergenceInfo`: Contains information about the convergence of the Baum-Welch algorithm.
- `convergenceInfo$eps`: Convergence threshold for the Baum-Welch.
- `convergenceInfo$loglik`: Final loglikelihood after the last iteration.
- `convergenceInfo$loglik.delta`: Change in loglikelihood after the last iteration (should be smaller than `eps`).
multivariateSegmentation

convergenceInfo$num.iterations
    Number of iterations that the Baum-Welch needed to converge to the desired eps.

convergenceInfo$time.sec
    Time in seconds that the Baum-Welch needed to converge to the desired eps.

correlation.matrix
    Correlation matrix of transformed reads.

See Also

callPeaksMultivariate, uniHMM, combinedMultiHMM

Examples

```r
## Get an example multiHMM
file <- system.file("data","multivariate_mode-combinatorial_condition-SHR.RData",
    package="chromstaR")
model <- get(load(file))
```

**multivariateSegmentation**

*Multivariate segmentation*

Description

Make segmentation from bins for a **multiHMM** object.

Usage

```
multivariateSegmentation(bins, column2collapseBy = "state")
```

Arguments

- **bins**: A **GRanges-class** with binned read counts.
- **column2collapseBy**: The number of the column which will be used to collapse all other inputs. If a set of consecutive bins has the same value in this column, they will be aggregated into one bin with adjusted genomic coordinates.

Value

A **GRanges-class** with segmented regions.
plotExpression

Overlap with expression data

Description
Get the expression values that overlap with each combinatorial state.

Usage
plotExpression(hmm, expression, combinations = NULL, return.marks = FALSE)

Arguments
- hmm: A multihmm or combinedMultiHMM object or file that contains such an object.
- expression: A GRanges-class object with metadata column 'expression', containing the expression value for each range.
- combinations: A vector with combinations for which the expression overlap will be calculated. If NULL all combinations will be considered.
- return.marks: Set to TRUE if expression values for marks instead of combinations should be returned.

Value
A ggplot2 object if a multihmm was given or a named list with ggplot2 objects if a combinedMultiHMM was given.

Author(s)
Aaron Taudt

See Also
plotting

Examples
```r
## Load an example multiHMM
file <- system.file("data","multivariate_mode-combinatorial_condition-SHR.RData",
                   package="chromstaR")
model <- get(load(file))

## Obtain expression data
data(expression_lv)
head(expression_lv)

## We need to get coordinates for each of the genes
library(biomaRt)
ensembl <- useEnsembl(biomart='ENSEMBL_MART_ENSEMBL', dataset='rnorvegicus_gene_ensemble')
```
genes <- getBM(attributes=c('ensembl_gene_id', 'chromosome_name', 'start_position', 'end_position', 'strand', 'external_gene_name', 'gene_biotype'),
    mart=ensembl)
expr <- merge(genes, expression_lv, by='ensembl_gene_id')
# Transform to GRanges
expression.SHR <- GRanges(seqnames=paste0('chr', expr$chromosome_name),
    ranges=IRanges(start=expr$start, end=expr$end),
    strand=expr$strand, name=expr$external_gene_name,
    biotype=expr$gene_biotype,
    expression=expr$expression_SHR)
# We apply an asinh transformation to reduce the effect of outliers
expression.SHR$expression <- asinh(expression.SHR$expression)
## Plot
plotExpression(model, expression.SHR) +
  theme(axis.text.x=element_text(angle=0, hjust=0.5)) +
  ggtitle('Expression of genes overlapping combinatorial states')
plotExpression(model, expression.SHR, return.marks=TRUE) +
  ggtitle('Expression of marks overlapping combinatorial states')
# Plot a genome browser view

This is useful for scripted genome browser snapshots.  

## Example

```r
# Get an example multiHMM
# file <- system.file("data","multivariate_combinatorial_condition-SHR.RData", package="chromstaR")
# model <- get(load(file))
## Plot genome browser snapshot
# bins <- model$bins # bins$counts <- model$bins$counts.rpkms #
# plotGenomeBrowser(counts=bins, peaklist=model$peaks, #
# chr='chr12', start=1, end=1e6)
# plotGenomeBrowser2 <- function(counts, peaklist=NULL, chr, start, end, countcol='black',
# peakcols=NULL, style='peaks', peakTrackHeight=5) ## Select
# ranges to plot ranges2plot <- reduce(counts[counts@seqnames==chr & start(counts) >= start & start(counts) <= end]) ##
# Counts counts <- subsetByOverlaps(counts, ranges2plot) if (style == 'peaks')
# df <- data.frame(x=(start(counts)+end(counts))/2, counts=counts$counts) #
# ggpplt <- ggpplot(df) + geom_area(aes_string(x='x', y='counts')) +
# theme(panel.grid = element_blank(), panel.background = element_blank(), axis.title = element_blank(), axis.ticks.x = element_blank(), axis.line = element_blank()) maxcounts <- max(counts$counts) ggpplt <-
# ggpplt + scale_y_continuous(breaks=c(0, maxcounts)) else if (style == 'density')
# df <- data.frame(xmin=start(counts), xmax=end(counts), counts=counts$counts) ggpplt <-
# ggpplot(df) + geom_rect(aes_string(xmin='xmin', xmax='xmax', ymin=0, ymax=4, alpha='counts')) +
# theme(panel.grid = element_blank(), panel.background = element_blank(), axis.title = element_blank(), axis.ticks = element_blank(), axis.line = element_blank()) else stop("Unknown value ", style, ", for parameter 'style'.") # Peaks if (!is.null(peaklist)) if (is.null(peakcols)) peakcols <- getDistinctColors(length(peaklist)) for (i1 in 1:length(peaklist)) p <- peakTrackHeight peaks <-
# subsetByOverlaps(peaklist[[i1]], ranges2plot) if (length(peaks) > 0) df <- data.frame(start=start(peaks), end=end(peaks), ymin=-p*i1, ymax=-p*i1+0.9*p) ggpplt <-
# ggpplt + geom_rect(data=df, mapping=aes_string(xmin='start', xmax='end', ymin='ymin', ymax='ymax'), col=peakcols[i1], fill=peakcols[i1]) trackname <- names(peaklist)[i1] df <-
# data.frame(x=start(counts)[1], y=p*i1+0.5*p, label=trackname) ggpplt <-
# ggpplt + geom_text(data=df, mapping=aes_string(x='x', y='y', label='label'), vjust=0.5, hjust=0.5, col=peakcols[i1]) return(ggpplt)
```

Plot a genome browser view
Description

Plot a simple genome browser view of chromstaR-objects. This is useful for scripted genome browser snapshots.

Usage

plotGenomeBrowser(
  model,
  chr,
  start,
  end,
  style = "peaks",
  peakHeight = 0.2,
  peakColor = "blue",
  same.yaxis = TRUE
)

Arguments

model A uniHMM, multiHMM or combinedMultiHMM object or file that contains such an object.
chr, start, end Chromosome, start and end coordinates for the plot.
style One of c('peaks', 'density').
peakHeight Height of the peak track relative to the count track.
peakColor Color for the peak track.
same.yaxis Whether or not the plots for the same mark have the same y-axis.

Value

A list() of ggplot objects.

Examples

## Get an example uniHMM ##
file <- system.file("data","H3K27me3-BN-rep1.RData", package="chromstaR")
model <- get(load(file))
plotGenomeBrowser(model, chr='chr12', start=1, end=1e6, style='peaks',
  peakHeight=0.1)

## Get an example multiHMM ##
file <- system.file("data","multivariate_mode-combinatorial_condition-SHR.RData", package="chromstaR")
model <- get(load(file))
plotGenomeBrowser(model, chr='chr12', start=1, end=1e6, style='peaks',
  peakHeight=0.1)

## Get an example combinedMultiHMM ##
file <- system.file("data","combined_mode-differential.RData", package="chromstaR")
model <- get(load(file))
plotlist <- plotGenomeBrowser(model, chr='chr12', start=1, end=1e6, style='peaks',
                              peakHeight=0.1)

plotHistogram

Histogram of binned read counts with fitted mixture distribution

Description

Plot a histogram of binned read counts with fitted mixture distributions from a uniHMM object.

Usage

plotHistogram(
  model,
  state = NULL,
  chromosomes = NULL,
  start = NULL,
  end = NULL,
  linewidth = 1
)

Arguments

- **model**: A uniHMM object or file that contains such an object.
- **state**: Plot the histogram only for the specified state. One of c('unmodified','modified').
- **chromosomes, start, end**: Plot the histogram only for the specified chromosomes, start and end position.
- **linewidth**: Width of the distribution lines.

Value

A ggplot object.

See Also

plotting

Examples

```r
## Get an example BAM file with ChIP-seq reads
file <- system.file("extdata", "euratrans",
                    "lv-H3K27me3-BN-male-bio2-tech1.bam",
                    package="chromstaRData")
## Bin the BED file into bin size 1000bp
data(rn4_chrominfo)
data(experiment_table)
```
binned <- binReads(file, experiment.table=experiment_table, assembly=rn4_chrominfo, binsizes=1000, stepsizes=500, chromosomes='chr12')
plotHistogram(binned)
## Fit the univariate Hidden Markov Model
hmm <- callPeaksUnivariate(binned, max.time=60, eps=1)
## Check if the fit is ok
plotHistogram(hmm)

plotHistograms

Histograms of binned read counts with fitted mixture distribution

Description
Plot histograms of binned read counts with fitted mixture distributions from a multiHMM object.

Usage
plotHistograms(model, ...)

Arguments

model

A multiHMM object or file that contains such an object.

...

Additional arguments (see plotHistogram).

Value
A ggplot object.

See Also
plotting

plotting
chromstaR plotting functions

Description
This page provides an overview of all chromstaR plotting functions.
print.combinedMultiHMM

Details
Plotting functions that work on uniHMM objects:

plotHistogram  Read count histogram with fitted mixture distributions.

Plotting functions that work on multiHMM objects:

heatmapCountCorrelation  Heatmap of read count correlations.
heatmapTransitionProbs  Heatmap of transition probabilities of the Hidden Markov Model.
heatmapCombinations  Binary presence/absence pattern of combinatorial states.
plotExpression  Boxplot of expression values that overlap combinatorial states.

Plotting functions that work on multiHMM and combinedMultiHMM objects:

heatmapCountCorrelation  Heatmap of read count correlations.
plotEnrichCountHeatmap  Heatmap of read counts around annotation.
plotEnrichment  Enrichment of combinatorial states around annotation.
plotFoldEnrichHeatmap  Enrichment of combinatorial states at multiple annotations.
plotExpression  Boxplot of expression values that overlap combinatorial states.

Other plotting functions:

heatmapCombinations  Binary presence/absence pattern of combinatorial states.

---

print.combinedMultiHMM

Print combinedMultiHMM object

Description
Print combinedMultiHMM object

Usage

```r
## S3 method for class 'combinedMultiHMM'
print(x, ...)
```

Arguments

- `x`  An combinedMultiHMM object.
- `...`  Ignored.

Value

An invisible NULL.
print.multiHMM  
Print multiHMM object

Description
Print multiHMM object

Usage

```r
## S3 method for class 'multiHMM'
print(x, ...)
```

Arguments

- `x`: An `multiHMM` object.
- `...`: Ignored.

Value
An invisible `NULL`.

print.uniHMM  
Print uniHMM object

Description
Print uniHMM object

Usage

```r
## S3 method for class 'uniHMM'
print(x, ...)
```

Arguments

- `x`: An `uniHMM` object.
- `...`: Ignored.

Value
An invisible `NULL`. 
readBamFileAsGRanges  Import BAM file into GRanges

Description

Import aligned reads from a BAM file into a GRanges-class object.

Usage

readBamFileAsGRanges(
  bamfile,
  bamindex = bamfile,
  chromosomes = NULL,
  pairedEndReads = FALSE,
  remove.duplicate.reads = FALSE,
  min.mapq = 10,
  max.fragment.width = 1000,
  blacklist = NULL,
  what = "mapq"
)

Arguments

bamfile  A sorted BAM file.
bamindex  BAM index file. Can be specified without the .bai ending. If the index file does not exist it will be created and a warning is issued.
chromosomes  If only a subset of the chromosomes should be imported, specify them here.
pairedEndReads  Set to TRUE if you have paired-end reads in your BAM files (not implemented for BED files).
remove.duplicate.reads  A logical indicating whether or not duplicate reads should be removed.
min.mapq  Minimum mapping quality when importing from BAM files. Set min.mapq=0 to keep all reads.
max.fragment.width  Maximum allowed fragment length. This is to filter out erroneously wrong fragments due to mapping errors of paired end reads.
blacklist  A GRanges-class or a bed.gz file with blacklisted regions. Reads falling into those regions will be discarded.
what  A character vector of fields that are returned. Uses the Rsamtools::scanBamWhat function. See Rsamtools::ScanBamParam to see what is available.

Value

A GRanges-class object containing the reads.
readBedFileAsGRanges

Import BED file into GRanges

Description

Import aligned reads from a BED file into a GRanges-class object.

Usage

readBedFileAsGRanges(
  bedfile,
  assembly,
  chromosomes = NULL,
  remove.duplicate.reads = FALSE,
  min.mapq = 10,
  max.fragment.width = 1000,
  blacklist = NULL
)

Arguments

bedfile A file with aligned reads in BED-6 format. The columns have to be c('chromosome','start','end','description','mapq','strand').

assembly Please see getChromInfoFromUCSC for available assemblies. Only necessary when importing BED files. BAM files are handled automatically. Alternatively a data.frame with columns 'chromosome' and 'length'.

chromosomes If only a subset of the chromosomes should be imported, specify them here.

remove.duplicate.reads A logical indicating whether or not duplicate reads should be removed.

min.mapq Minimum mapping quality when importing from BAM files. Set min.mapq=0 to keep all reads.

max.fragment.width Maximum allowed fragment length. This is to filter out erroneously wrong fragments.

blacklist A GRanges-class or a bed(.gz) file with blacklisted regions. Reads falling into those regions will be discarded.

Examples

## Get an example BAM file with ChIP-seq reads
bamfile <- system.file("extdata", "euratrans", "lv-H3K4me3-BN-female-bio1-tech1.bam", package="chromstaRData")
## Read the file into a GRanges object
reads <- readBamFileAsGRanges(bamfile, chromosomes='chr12', pairedEndReads=FALSE, min.mapq=10, remove.duplicate.reads=TRUE)
print(reads)
## Value

A GRanges-class object containing the reads.

## Examples

```r
## Get an example BED file with single-cell-sequencing reads
bedfile <- system.file("extdata", "liver-H3K4me3-BN-male-bio2-tech1.bed.gz", 
  package="chromstaRData")

## Read the file into a GRanges object
data(rn4_chrominfo)
reads <- readBedFileAsGRanges(bedfile, assembly=rn4_chrominfo, chromosomes='chr12', 
  min.mapq=10, remove.duplicate.reads=TRUE)
print(reads)
```

## readConfig

### Read chromstaR configuration file

#### Description

Read a chromstaR configuration file into a list structure. The configuration file has to be specified in INI format. R expressions can be used and will be evaluated.

#### Usage

```r
readConfig(configfile)
```

#### Arguments

- **configfile** Path to the configuration file

#### Value

A list with one entry for each element in configFile.

#### Author(s)

Aaron Taudt
**readCustomBedFile**  
*Read bed-file into GRanges*

---

**Description**

This is a simple convenience function to read a bed(.gz)-file into a `GRanges-class` object. The bed-file is expected to have the following fields: chromosome, start, end, name, score, strand.

**Usage**

```r
def readCustomBedFile(
    bedfile,
    col.names = c("chromosome", "start", "end", "name", "score", "strand"),
    col.classes = NULL,
    skip = 0,
    chromosome.format = "NCBI",
    sep = ""
)
```

**Arguments**

- **bedfile**  
  Filename of the bed or bed.gz file.
- **col.names**  
  A character vector giving the names of the columns in the bedfile. Must contain at least c("chromosome","start","end").
- **col.classes**  
  A character vector giving the classes of the columns in bedfile. Speeds up the import.
- **skip**  
  Number of lines to skip at the beginning.
- **chromosome.format**  
  Desired format of the chromosomes. Either 'NCBI' for (1,2,3 ...) or 'UCSC' for (chr1,chr2,chr3 ...) or NULL to keep the original names.
- **sep**  
  Field separator from `read.table`.

**Value**

A `GRanges-class` object with the contents of the bed-file.

**Author(s)**

Aaron Taudt

**Examples**

```r
## Get an example BED file
bedfile <- system.file("extdata", "liver-H3K4me3-BN-male-bio2-tech1.bed.gz",
                     package="chromstaRData")
## Import the file and skip the first 10 lines
data <- readCustomBedFile(bedfile, skip=10)
```
removeCondition  Remove condition from model

Description
Remove a condition from a combinedMultiHMM object.

Usage
removeCondition(model, conditions)

Arguments
model  A combinedMultiHMM object or file which contains such an object.
conditions  A character vector with the condition(s) to be removed.

Value
The input combinedMultiHMM object with specified conditions removed.

Examples
## Get an example HMM
file <- system.file("data","combined_mode-differential.RData",
package="chromstaR")
model <- get(load(file))

## Print available conditions
print(unique(model$info$condition))

## Remove condition SHR
new.model <- removeCondition(model, conditions='SHR')

scanBinsizes  Find the best bin size for a given dataset

Description
Use simulations to find the best bin size among a set of input files. There is no guarantee that the bin size will be the best for your data, since it is only "best" in terms of fewest miscalls for simulated data. However, it can give you a hint what bin size to choose.
scanBinsizes

Usage

scanBinsizes(
  files.binned,
  outputfolder,
  chromosomes = "chr10",
  eps = 0.01,
  max.iter = 100,
  max.time = 300,
  repetitions = 3,
  plot.progress = FALSE
)

Arguments

files.binned A vector with files that contain binned.data in different bin sizes.
outputfolder Name of the folder where all files will be written to.
chromosomes A vector of chromosomes to use for the simulation.
eps Convergence threshold for the Baum-Welch algorithm.
max.iter The maximum number of iterations for the Baum-Welch algorithm. The default
  -1 is no limit.
max.time The maximum running time in seconds for the Baum-Welch algorithm. If this
  time is reached, the Baum-Welch will terminate after the current iteration finishes. The default -1 is no limit.
repetitions Number of repetitions for each simulation.
plot.progress If TRUE, the plot will be updated each time a simulation has finished. If FALSE,
  the plot will be returned only at the end.

Details

The function first runs callPeaksUnivariate on the given binned.data files. From the estimated
parameters it generates simulated data and calls the peaks on this simulated data. Because the data
is simulated, the fraction of miscalls can be precisely calculated.

Value

A ggplot object with a bar plot of the number of miscalls dependent on the bin size.

Author(s)

Aaron Taudt
scores

chromstaR scores

Description

Various scores used in chromstaR.

Usage

differentialScoreMax(mat, info, FUN = "-")
differentialScoreSum(mat, info, FUN = "-")

Arguments

mat A matrix with posterior probabilities, read counts or any other matrix with these dimensions. Column names must correspond to the ID entries in info.

info An experiment.table with additional column 'ID'.

FUN A function to compute the score with.

Value

A numeric vector.

Functions

- differentialScoreMax: Maximum differential score. Values are between 0 and 1. A value of 1 means that at least one mark is maximally different between conditions.

- differentialScoreSum: Additive differential score. Values are between 0 and N, where N is the number of marks. A value around 1 means that approximately 1 mark is different, a value of 2 means that 2 marks are different etc.

Author(s)

Aaron Taudt
simulateMultivariate  
Simulate multivariate data

Description
Simulate known states, read counts and read coordinates using a multivariate Hidden Markov Model.

Usage
simulateMultivariate(
  bins,
  transition,
  emissions,
  weights,
  correlationMatrices,
  combstates,
  IDs,
  fragLen = 50
)

Arguments
- **bins**: A `GRanges-class` object for which reads will be simulated.
- **transition**: A matrix with transition probabilities.
- **emissions**: A list() with data.frames with emission distributions (see `uniHMM` entry 'distributions').
- **weights**: A list() with weights for the three univariate states.
- **correlationMatrices**: A list with correlation matrices.
- **combstates**: A vector with combinatorial states.
- **IDs**: A character vector with IDs.
- **fragLen**: Length of the simulated read fragments.

Value
A list() with entries $bins containing the simulated states and read count, $reads with simulated read coordinates.
simulateReadsFromCounts

Simulate read coordinates

Description
Simulate read coordinates using read counts as input.

Usage
simulateReadsFromCounts(bins, fragLen = 50)

Arguments
- **bins**: A `GRanges-class` with read counts.
- **fragLen**: Length of the simulated read fragments.

Value
A `GRanges-class` with read coordinates.

simulateUnivariate

Simulate univariate data

Description
Simulate known states, read counts and read coordinates using a univariate Hidden Markov Model with three states ("zero-inflation", "unmodified" and "modified").

Usage
simulateUnivariate(bins, transition, emission, fragLen = 50)

Arguments
- **bins**: A `GRanges-class` object for which reads will be simulated.
- **transition**: A matrix with transition probabilities.
- **emission**: A data.frame with emission distributions (see `uniHMM` entry 'distributions').
- **fragLen**: Length of the simulated read fragments.

Value
A list with entries $bins containing the simulated states and read count, $reads with simulated read coordinates and $transition and $emission.
Obtain combinatorial states from specification

**Description**

This function returns all combinatorial (decimal) states that are consistent with a given abstract specification.

**Usage**

```r
state.brewer(
  replicates = NULL,
  differential.states = FALSE,
  min.diff = 1,
  common.states = FALSE,
  conditions = NULL,
  tracks2compare = NULL,
  sep = "+",
  statespec = NULL,
  diffstatespec = NULL,
  exclusive.table = NULL,
  binary.matrix = NULL
)
```

**Arguments**

- `replicates` A vector specifying the replicate structure. Similar entries will be treated as replicates.
- `differential.states` A logical specifying whether differential states shall be returned.
- `min.diff` The minimum number of differences between conditions.
- `common.states` A logical specifying whether common states shall be returned.
- `conditions` A vector with the same length as `replicates`. Similar entries will be treated as belonging to the same condition. Usually your tissue or cell types or time points.
- `tracks2compare` A vector with the same length as `replicates`. This vector defines the tracks between which conditions are compared. Usually your histone marks.
- `sep` Separator used to separate the tracknames in the combinations. The default '+' should not be changed because it is assumed in follow-up functions.
- `statespec` If this parameter is specified, `replicates` will be ignored. A vector composed of any combination of the following entries: '0.[ ]', '1.[ ]', 'x.[ ]', 'r.[ ]', where [] can be any string.
  - '0.A': sample A is 'unmodified'
  - '1.B': sample B is 'modified'
• 'x.C': sample C can be both 'unmodified' or 'modified'
• 'r.D': all samples in group D have to be in the same state
• 'r.[ ]': all samples in group [ ] have to be in the same state

**diffstatespec**

A vector composed of any combination of the following entries: 'x.[ ]', 'd.[ ]', where [ ] can be any string.

- 'x.A': sample A can be both 'unmodified' or 'modified'
- 'd.B': at least one sample in group B has to be different from the other samples in group A
- 'd[ ]': at least one sample in group [ ] has to be different from the other samples in group [ ]

**exclusive.table**

A data.frame or tab-separated text file with columns 'mark' and 'group'. Histone marks with the same group will be treated as mutually exclusive.

**binary.matrix**

A logical matrix produced by `dec2bin`. If this is specified, only states specified by the rows of this matrix will be considered. The number of columns must match `length(replicates)` or `length(statespec)`. Only for advanced use. No error handling for incorrect input.

### Details

The binary modification state (unmodified=0 or modified=1) of multiple ChIP-seq samples defines a (decimal) combinatorial state such as:

<table>
<thead>
<tr>
<th>sample1</th>
<th>sample2</th>
<th>sample3</th>
<th>sample4</th>
<th>sample5</th>
<th>combinatorial state</th>
</tr>
</thead>
<tbody>
<tr>
<td>bin1</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>bin2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>bin3</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>bin4</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>bin5</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

### Value

A data.frame with combinations and their corresponding (decimal) combinatorial states.

### Author(s)

Aaron Taudt, David Widmann

### Examples

```r
# Get all combinatorial states where sample1=0, sample2=1, sample3=(0 or 1),
# sample4=sample5
cchromstaR:::state.brewer(statespec=c('0.A','1.B','x.C','r.D','r.D'))

# Get all combinatorial states where sample1=sample2=sample3, sample4=sample5
cchromstaR:::state.brewer(statespec=c('r.A','r.A','r.A','r.B','r.B'))
```
stateBrewer

# Get all combinatorial states where sample1=sample5, sample2=sample3=1, # sample4=(0 or 1)
chromstaR:::state.brewer(statespec=c('r.A','1.B','1.C','x.D','r.A'))

stateBrewer

Obtain combinatorial states from experiment table

Description

This function computes combinatorial states from an experiment.table.

Usage

stateBrewer(
  experiment.table,
  mode,
  differential.states = FALSE,
  common.states = FALSE,
  exclusive.table = NULL,
  binary.matrix = NULL
)

Arguments

experiment.table
  A data.frame specifying the experiment structure. See experiment.table.
mode
  Mode of brewing. See Chromstar for a description of the parameter.
differential.states
  A logical specifying whether differential states shall be returned.
common.states
  A logical specifying whether common states shall be returned.
exclusive.table
  A data.frame or tab-separated text file with columns 'mark' and 'group'. Histone marks with the same group will be treated as mutually exclusive.
binary.matrix
  A logical matrix produced by dec2bin. If this is specified, only states specified by the rows of this matrix will be considered. The number of columns must match length(replicates) or length(statespec). Only for advanced use. No error handling for incorrect input.

Details

The binary modification state (unmodified=0 or modified=1) of multiple ChIP-seq samples defines a (decimal) combinatorial state such as:

<table>
<thead>
<tr>
<th>sample1</th>
<th>sample2</th>
<th>sample3</th>
<th>sample4</th>
<th>sample5</th>
<th>combinatorial state</th>
</tr>
</thead>
<tbody>
<tr>
<td>bin1</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

The binary modification state (unmodified=0 or modified=1) of multiple ChIP-seq samples defines a (decimal) combinatorial state such as:
subsample

## Normalize read counts

### Description

Normalize read counts to a given read depth. Reads counts are randomly removed from the input to match the specified read depth.

### Usage

```r
subsample(binned.data, sample.reads)
```

### Arguments

- **binned.data**: A GRanges-class object with meta data column 'reads' that contains the read count.
- **sample.reads**: The number of reads that will be retained.

### Examples

```r
## Construct an experiment table
data(experiment_table)
print(experiment_table)

## Construct combinatorial states
stateBrewer(experiment_table, mode='combinatorial')
stateBrewer(experiment_table, mode='differential')
stateBrewer(experiment_table, mode='full', common.states=TRUE)

## Exclude states with exclusive.table
excl <- data.frame(mark=c('H3K4me3', 'H3K27me3'),
                   group=c(1,1))
stateBrewer(experiment_table, mode='full', exclusive.table=excl)
```
transitionFrequencies

Value

   A GRanges-class object with downsampled read counts.

Author(s)

   Aaron Taudt

transitionFrequencies  Transition frequencies of combinatorial states

Description

   Get a table of transition frequencies between combinatorial states of different multiHMMs.

Usage

   transitionFrequencies(
       multi.hmms = NULL,
       combined.hmm = NULL,
       zero.states = "[]",
       combstates = NULL
   )

Arguments

   multi.hmms    A named list with multiHMM objects or a vector with filenames that contain such objects.
   combined.hmm  A combinedMultiHMM object. If specified, multi.hmms is ignored.
   zero.states   The string(s) which identifies the zero.states.
   combstates    Alternative input instead of multi.hmms: A named list of combinatorial state vectors instead of HMMs. Names must be of the form "combination.X", where X is an arbitrary string. If this is specified, multi.hmms and combined.hmm will be ignored.

Value

   A data.frame with transition frequencies.

Author(s)

   Aaron Taudt
Examples

```r
## Get an example combinedMultiHMM
file <- system.file("data","combined_mode-differential.RData", 
                  package="chromstaR")
model <- get(load(file))
freqs <- transitionFrequencies(combined.hmm=model)
freqs$table
```

uniHMM

*Univariate HMM object*

Description

The univariate HMM object is output of the function `callPeaksUnivariate` and is a list() with various entries. The `class()` attribute of this list was set to "uniHMM". For a given `hmm`, the entries can be accessed with the list operators 'hmm[[i]]' or 'hmm$'.

Value

A list() with the following entries:

- **info**
  Experiment table for this object.
- **bincounts**
  A `GRanges-class` object containing the genomic bin coordinates and original binned read count values for different offsets.
- **bins**
  A `GRanges-class` object containing the genomic bin coordinates, their read count, (optional) posteriors and state classification.
- **peaks**
  A list() with `GRanges-class` containing peak coordinates for each ID in `info`.
- **weights**
  Weight for each component. Same as `apply(hmm$posteriors,2,mean)`.
- **transitionProbs**
  Matrix of transition probabilities from each state (row) into each state (column).
- **transitionProbs.initial**
  Initial `transitionProbs` at the beginning of the Baum-Welch.
- **startProbs**
  Probabilities for the first bin. Same as `hmm$posteriors[1,]`.
- **startProbs.initial**
  Initial `startProbs` at the beginning of the Baum-Welch.
- **distributions**
  Estimated parameters of the emission distributions.
- **distributions.initial**
  Distribution parameters at the beginning of the Baum-Welch.
- **post.cutoff**
  Cutoff for posterior probabilities to call peaks.
- **convergenceInfo**
  Contains information about the convergence of the Baum-Welch algorithm.
unis2pseudomulti

Combine univariate HMMs to a multivariate HMM

Description

Combine multiple uniHMMs to a multiHMM without running callPeaksMultivariate. This should only be done for comparison purposes.

Usage

unis2pseudomulti(hmms)

Arguments

hmms A named list of uniHMM objects. Names will be used to generate the combinations.

Details

Use this function if you want to combine ChIP-seq samples without actually running a multivariate Hidden Markov Model. The resulting object will be of class multiHMM but will not be truly multivariate.

Value

A multiHMM object.
variableWidthBins

Make variable-width bins

Description

Make variable-width bins based on a reference BAM file. This can be a simulated file (produced by TODO: insert link and aligned with your favourite aligner) or a real reference.

Usage

variableWidthBins(reads, binsizes, chromosomes = NULL)

Arguments

reads A GRanges-class with reads. See readBamFileAsGRanges and readBedFileAsGRanges.
binsizes A vector with binsizes. Resulting bins will be close to the specified binsizes.
chromosomes A subset of chromosomes for which the bins are generated.
writeConfig

Details
Variable-width bins are produced by first binning the reference BAM file with fixed-width bins and selecting the desired number of reads per bin as the (non-zero) maximum of the histogram. A new set of bins is then generated such that every bin contains the desired number of reads.

Value
A list() of \texttt{GRanges-class} objects with variable-width bins.

Author(s)
Aaron Taudt

Examples
```r
## Get an example BAM file with ChIP-seq reads
bamfile <- system.file("extdata", "euratrans", "lv-H3K4me3-BN-female-bio1-tech1.bam", package="chromstaRData")
## Read the file into a GRanges object
reads <- readBamFileAsGRanges(bamfile, chromosomes='chr12', pairedEndReads=FALSE, min.mapq=10, remove.duplicate.reads=TRUE)
## Make variable-width bins of size 1000bp
bins <- variableWidthBins(reads, binsizes=1000)
## Plot the distribution of binsizes
hist(width(bins[['1000']]), breaks=50)
```

writeConfig

Write chromstaR configuration file

Description
Write a chromstaR configuration file from a list structure.

Usage
```r
writeConfig(conf, configfile)
```

Arguments
- `conf`: A list structure with parameter values. Each entry will be written in one line.
- `configfile`: Filename of the output file.

Value
NULL

Author(s)
Aaron Taudt
The Zero-inflated Negative Binomial Distribution

Description

Density, distribution function, quantile function and random generation for the zero-inflated negative binomial distribution with parameters \( w, \) \( \text{size} \) and \( \text{prob} \).

Usage

\[
dz\text{zinbinom}(x, w, \text{size}, \text{prob, mu})
\]

\[
pz\text{zinbinom}(q, w, \text{size, prob, mu, lower.tail = TRUE})
\]

\[
qz\text{zinbinom}(p, w, \text{size, prob, mu, lower.tail = TRUE})
\]

\[
rz\text{zinbinom}(n, w, \text{size, prob, mu})
\]

Arguments

- \( x \): Vector of (non-negative integer) quantiles.
- \( w \): Weight of the zero-inflation. \( 0 \leq w \leq 1 \).
- \( \text{size} \): Target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
- \( \text{prob} \): Probability of success in each trial. \( 0 < \text{prob} \leq 1 \).
- \( \text{mu} \): Alternative parametrization via mean: see ‘Details’.
- \( q \): Vector of quantiles.
- \( \text{lower.tail} \): logical; if TRUE (default), probabilities are \( P[X \leq x] \), otherwise, \( P[X > x] \).
- \( p \): Vector of probabilities.
- \( n \): number of observations. If \( \text{length}(n) > 1 \), the length is taken to be the number required.

Details

The zero-inflated negative binomial distribution with \( \text{size} = n \) and \( \text{prob} = p \) has density

\[
p(x) = w + (1 - w) \frac{\Gamma(x + n)}{\Gamma(n)x!} p^n (1 - p)^x
\]

for \( x = 0, n > 0, 0 < p \leq 1 \) and \( 0 \leq w \leq 1 \).

\[
p(x) = (1 - w) \frac{\Gamma(x + n)}{\Gamma(n)x!} p^n (1 - p)^x
\]

for \( x = 1, 2, \ldots, n > 0, 0 < p \leq 1 \) and \( 0 \leq w \leq 1 \).
Value
dzinbinom gives the density, pzbinom gives the distribution function, qzinbinom gives the quantile function, and rzbinom generates random deviates.

Functions

- dzinbinom: gives the density
- pzbinom: gives the cumulative distribution function
- qzinbinom: gives the quantile function
- rzinbinom: random number generation

Author(s)

Matthias Heinig, Aaron Taudt

See Also

Distributions for standard distributions, including dbinom for the binomial, dnbinom for the negative binomial, dpois for the Poisson and dgeom for the geometric distribution, which is a special case of the negative binomial.
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