Package ‘STAN’

April 26, 2017

Version 2.4.0
Date 2016-05-30
Title The genomic STate ANnotation package
Author Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch
Maintainer Benedikt Zacher <zacher@genzentrum.lmu.de>
Imports GenomicRanges, IRanges, S4Vectors, BiocGenerics, GenomeInfoDb, Gviz, Rsolnp
Depends methods, poilog, parallel
VignetteBuilder knitr
Suggests BiocStyle, gplots, knitr
Description Genome segmentation with hidden Markov models has become a useful tool to annotate genomic elements, such as promoters and enhancers. STAN (genomic STate ANnotation) implements (bidirectional) hidden Markov models (HMMs) using a variety of different probability distributions, which can model a wide range of current genomic data (e.g. continuous, discrete, binary). STAN de novo learns and annotates the genome into a given number of 'genomic states'. The 'genomic states' may for instance reflect distinct genome-associated protein complexes (e.g. 'transcription states') or describe recurring patterns of chromatin features (referred to as 'chromatin states'). Unlike other tools, STAN also allows for the integration of strand-specific (e.g. RNA) and non-strand-specific data (e.g. ChIP).
License GPL (>= 2)
biocViews HiddenMarkovModel, GenomeAnnotation, Microarray, Sequencing, ChIPSeq, RNASeq, ChipOnChip, Transcription
LazyLoad yes
NeedsCompilation yes

R topics documented:

STAN-package .......................................................... 2
bdHMM ................................................................. 3
bdHMM-class .......................................................... 4
binarizeData .......................................................... 5
c2optimize ............................................................. 5
call_dpoilog .......................................................... 6
data2Gviz ............................................................. 6
DimNames .............................................................. 7
The genomic STate ANnotation package

Description

The genomic STate ANnotation package

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch

References

bdHMM

Create a bdHMM object

Description
This function creates a bdHMM function.

Usage
bdHMM(initProb = numeric(), transMat = matrix(numeric(), ncol = 0, nrow = 0), emission, nStates = numeric(), status = character(), stateNames = character(), dimNames = character(), transitionsOptim = "analytical", directedObs = integer(), dirScore = numeric())

Arguments
initProb Initial state probabilities.
transMat Transition probabilities.
emission Emission parameters as an HMMEmission object.
nStates Number of states.
status Status of the bdHMM. 'Initial' means that the model was not fitted yet. 'EM' means that the model was optimized using Expectation maximization.
stateNames Indicates directinality of states. States can be forward (F1, F2, ..., Fn), reverse (R1, R2, ..., Rn) or undirectional (U1, U2, ..., Um). Number of F and R states must be equal and twin states are indicated by integers in id (e.g. F1 and R1 and twins).
dimNames Names of data tracks.
transitionsOptim There are three methods to choose from for fitting the transitions. Bidirectional transition matrices (invariant under reversal of time and direction) can be fitted using c('rsolnp', 'analytical'). 'None' uses standard update formulas and the resulting matrix is not constrained to be bidirectional.
directedObs An integer indicating which dimensions are directed. Undirected dimensions are 0. Directed observations must be marked as unique integer pairs. For instance c(0,0,0,0,1,1,2,2,3,3) contains 5 undirected observations, and three pairs (one for each direction) of directed observations.
dirScore Directionality score of states of a fitted bdHMM.

See Also
HMMEmission

Examples
nStates = 5
stateNames = c('F1', 'F2', 'R1', 'R2', 'U1')
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4), as.matrix)
bdHMM-class

This class is a generic container for bidirectional Hidden Markov Models.

Slots

- initProb Initial state probabilities.
- transMat Transition probabilities
- emission Emission parameters as an HMMEmission object.
- nStates Number of states.
- status of the HMM. On of c('initial', 'EM').
- stateNames State names.
- dimNames Names of data tracks.
- LogLik Log likelihood of a fitted HMM.
- transitionsOptim There are three methods to choose from for fitting the transitions. Bidirectional transition matrices (invariant under reversal of time and direction) can be fitted using c('rsolnp', 'ipopt'). 'None' uses standard update formulas and the resulting matrix is not constrained to be bidirectional.
- directedObs An integer indicating which dimensions are directed. Undirected dimensions are 0. Directed observations must be marked as unique integer pairs. For instance c(0,0,0,0,1,1,2,2,3,3) contains 5 undirected observations, and three pairs (one for each direction) of directed observations.
- dirScore Directionality score of states of a fitted bdHMM.

Methods

- [ get elements from the bdHMM

See Also

HMMEmission
Examples

nStates = 5
stateNames = c('F1', 'F2', 'R1', 'R2', 'U1')
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
myEmission = list(d1=HMMEmision(type='Gaussian', parameters=list(mu=means, cov=Sigma), nStates=length(means)))

bdhmm = bdHMM(initProb=initProb, transMat=transMat, emission=myEmission, nStates=nStates, status='initial',
               stateNames=stateNames, transitionsOptim='none', directedObs=as.integer(0))

binarizeData

Binarize Sequencing data with the default ChromHMM binarization

Description

Binarize Sequencing data with the default ChromHMM binarization

Usage

binarizeData(obs)

Arguments

obs The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).

Value

Binarized observation sequences as a list.

Examples

data(trainRegions)
binData = binarizeData(trainRegions)

c2optimize

Optimize transitions

Description

The function is called from C++ to optimize transitions.

Usage

c2optimize(pars)
Arguments
par  Parameters for optimization.

Value
optimized transitions

call_dpoilog  Calculate density of the Poisson-Log-Normal distribution.

Description
Calculate density of the Poisson-Log-Normal distribution.

Usage
call_dpoilog(x)

Arguments
x  A vector c(n, mu, sigma), where n is the number of observed counts, mu the mean of the Log-Normal distribution and sigma its variance.

Value
Density of the Poisson-Log-Normal distribution.

Examples
call_dpoilog(c(5, 2, 1))

data2Gviz  Convert data for plotting with Gviz

Description
Convert data for plotting with Gviz

Usage
data2Gviz(obs, regions, binSize, gen, col = "black")

Arguments
obs  The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
regions  GRanges object of the regions (e.g. chromosomes) stored in the viterbi path.
binSize  The bin size of the viterbi path.
gen  The geome id, e.g. hg19, hg38 for human.
col  The color of the data tracks.
**DimNames**

**Description**
This function returns the names of dimensions (data tracks).

**Usage**
DimNames(hmm)

**Arguments**
- **hmm**: An object of class HMM or bdHMM.

**Value**
A character vector

**Examples**
```r
nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
hmm = HMM(dimNames="1", initProb=initProb, transMat=transMat, emission=HMMEmision(type='Gaussian', parameters=list(mu=means, cov=Sigma), nStates=length(means)), nStates=nStates, status="initial")
DimNames(hmm)
```

**DirScore**

**Description**
This function returns the directionality score of a bdHMM.

**Usage**
DirScore(bdhmm)

**Arguments**
- **bdhmm**: An object of class bdHMM.

**Value**
Directionality score of the bdHMM after model fitting.
Examples

data(example)
bdhmm_ex = initBdHMM(observations, nStates=3, method="Gaussian", directedObs=0)

# without flags
bdhmm_fitted_noFlags = fitHMM(observations, bdhmm_ex)
DirScore(bdhmm_fitted_noFlags)

# with flags
bdhmm_fitted_flags = fitHMM(observations, bdhmm_ex, dirFlags=flags)
DirScore(bdhmm_fitted_flags)

---

Emission: Get Emission functions of a (bd)HMM

Description

This function returns the Emission functions of a (bd)HMM.

Usage

Emission(hmm)

Arguments

hmm: An object of class HMM or bdHMM.

Value

An object of class HMMEmission

See Also

HMMEmission

Examples

nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
hmm = HMM(initProb=initProb, transMat=transMat, emission=HMMEmission(type='Gaussian', parameters=list(mu=means, cov=Sigma), nStates=length(means)), nStates=nStates, status='initial')
Emission(hmm)
EmissionParams

Get Emission parameters of a (bd)HMM.

Description

This function returns the parameters of emission functions of a (bd)HMM object.

Usage

EmissionParams(hmm)

Arguments

hmm

An object of class (bd)HMM.

Value

A list containing the parameters of the Emission functions.

See Also

HMMEmission, HMM, bdHMM

Examples

nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
hmm = HMM(initProb=initProb, transMat=transMat, emission=HMMEmission(type='Gaussian', parameters=list(mu=means, cov=Sigma)), nStates=nStates, status='initial')
EmissionParams(hmm)

Example

The data for the bdHMM example in the vignette and examples in the manual

Description

The data for the bdHMM example in the vignette and examples in the manual

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch
fitHMM

Fit a Hidden Markov Model

Description

The function is used to fit (bidirectional) Hidden Markov Models, given one or more observation sequence.

Usage

fitHMM(obs=list(), hmm, convergence=1e-6, maxIters=1000, dirFlags=list(), emissionProbs=list(), effectiveZero=0, verbose=FALSE, nCores=1, incrementalEM=FALSE, updateTransMat=TRUE, sizeFactors=matrix(1, nrow=length(obs), ncol=ncol(obs[[1]])))

Arguments

obs The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
hmm The initial Hidden Markov Model. This is a HMM.
convergence Convergence cutoff for EM-algorithm (default: 1e-6).
maxIters Maximum number of iterations.
dirFlags The flag sequence is needed when a bdHMM is fitted on undirected data (e.g.) ChIP only. It is a list of character vectors indication for each position its known directionality. U allows all states. F allows undirected states and states in forward direction. R allows undirected states and states in reverse direction.
emissionProbs List of precalculated emission probabilities of emission function is of type 'null'.
effectiveZero Transitions below this cutoff are analytically set to 0 to speed up computations.
verbose logical for printing algorithm status or not.
nCores Number of cores to use for computations.
incrementalEM When TRUE, the incremental EM is used to fit the model, where parameters are updated after each iteration over a single observation sequence.
updateTransMat Wether transitions should be updated during model learning. default: TRUE.
sizeFactors Library size factors for Emissions PoissonLogNormal or NegativeBinomial as a length(obs) x ncol(obs[[1]]) matrix.

Value

A list containing the trace of the log-likelihood during EM learning and the fitted HMM model.

See Also

HMM

Examples

data(example)
hmm_ex = initHMM(observations, nStates=3, method="Gaussian")
hmm_fitted = fitHMM(observations, hmm_ex)
Pre-computed flag sequence for the 'example' data.

Description
Pre-computed flag sequence for the 'example' data.

Author(s)
Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch

getAvgSignal
Compute average signal in state segmentation

Description
Compute average signal in state segmentation

Usage
getAvgSignal(viterbi, obs, fct=mean)

Arguments
viterbi A list containing the viterbi paths as factors. The output from getViterbi.
obs The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
fct The averaging function, default: mean.

Value
A state x data track matrix containing the average signal.

Examples
data(yeastTF_databychrom_ex)
nStates = 6
dirobs = as.integer(c(rep(0,10), 1, 1))
bdhmm_gauss = initBdHMM(yeastTF_databychrom_ex, nStates, "Gaussian", directedObs=dirobs)
bdhmm_fitted_gauss = fitHMM(yeastTF_databychrom_ex, bdhmm_gauss)
viterbi_bdhmm_gauss = getViterbi(bdhmm_fitted_gauss, yeastTF_databychrom_ex)
avg_signal = getAvgSignal(viterbi_bdhmm_gauss, yeastTF_databychrom_ex)
getLogLik

Calculate log likelihood state distribution.

Description

The function calculates log likelihood for one or more observation sequence.

Usage

getLogLik(hmm, obs = list(), emissionProbs = list(), dirFlags = list(), verbose = FALSE, nCores = 1, sizeFactors=matrix(1, nrow=length(obs), ncol=ncol(obs[[1]])))

Arguments

hmm The Hidden Markov Model.
obs The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
emissionProbs List of precalculated emission probabilities of emission function is of type 'null'.
dirFlags The flag sequence is needed when a bdHMM is fitted on undirected data (e.g.) ChIP only. It is a list of character vectors indication for each position its known directionality. U allows all states. F allows undirected states and states in forward direction. R allows undirected states and states in reverse direction.
verbose logical for printing algorithm status or not.
nCores Number of cores to use for computations.
sizeFactors Library size factors for Emissions PoissonLogNormal or NegativeBinomial as a length(obs) x ncol(obs[[1]]) matrix.

Value

The log likelihood of the observations sequences, given the model.

See Also

HMM

Examples

data(example)
hmm_ex = initHMM(observations, nStates=3, method="Gaussian")
hmm_fitted = fitHMM(observations, hmm_ex)
loglik = getLogLik(hmm_fitted, observations)
loglik
getPosterior

**Description**

The function calculates posterior state probabilities for one or more observation sequence.

**Usage**

```
getPosterior(hmm, obs=list(), emissionProbs=list(), dirFlags=list(), verbose=FALSE, nCores=1, sizeFactors=matrix(1, nrow=length(obs), ncol=ncol(obs[[1]])))
```

**Arguments**

- `hmm` The Hidden Markov Model.
- `obs` The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
- `emissionProbs` List of precalculated emission probabilities of emission function is of type ‘null’.
- `dirFlags` The flag sequence is needed when a bdHMM is fitted on undirected data (e.g.) ChIP only. It is a list of character vectors indication for each position its known directionality. U allows all states. F allows undirected states and states in forward direction. R allows undirected states and states in reverse direction.
- `verbose` logical for printing algorithm status or not.
- `nCores` Number of cores to use for computations.
- `sizeFactors` Library size factors for Emissions PoissonLogNormal or NegativeBinomial as a length(obs) x ncol(obs[[1]]) matrix.

**Value**

A list containing for the observation sequences the posterior state (col) distribution at each position (row).

**Examples**

```r
data(example)
hmm_ex = initHMM(observations, nStates=3, method="Gaussian")
hmm_fitted = fitHMM(observations, hmm_ex)
posterior = getPosterior(hmm_fitted, observations)
```
**getDescription**
Compute size factors

**Usage**

`getSizeFactors(obs, celltypes)`

**Arguments**

- `obs` The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
- `celltypes` Indicates the cell type/tissue for each entry in `obs`.

**Value**

A celltype/tissue x data tracks matrix containing the size factors.

**Examples**

```r
data(trainRegions)
celltypes = list("E123"=grep("E123", names(trainRegions)),
                "E116"=grep("E116", names(trainRegions)))
sizeFactors = getSizeFactors(trainRegions, celltypes)
sizeFactors
```

**getViterbi**
Calculate the most likely state path

**Description**
Given a Hidden Markov Model, the function calculates the most likely state path (viterbi) for one or more observation sequence.

**Usage**

`getViterbi(hmm, obs=list(), NAtol=5, emissionProbs=list(), verbose=FALSE, sizeFactors=matrix(1, nrow=length(obs), ncol=ncol(obs[[1]])))`
Arguments

- **hmm**
  The initial Hidden Markov Model.

- **obs**
  The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).

- **NAtol**
  Successive positions having NAs longer than this threshold are masked in the viterbi path.

- **emissionProbs**
  List of precalculated emission probabilities of emission function is of type 'null'.

- **verbose**
  logical for printing algorithm status or not.

- **sizeFactors**
  Library size factors for Emissions PoissonLogNormal or NegativeBinomial as a length(obs) x ncol(obs[[1]]) matrix.

Value

A list containint the vterbi paths.

Examples

```r
data(example)
hmm_ex = initHMM(observations, nStates=3, method="Gaussian")
hmm_fitted = fitHMM(observations, hmm_ex)
viterbi = getViterbi(hmm_fitted, observations)
```

---

**HMM**

Create a HMM object

Description

This function creates a HMM object.

Usage

```r
HMM(initProb = numeric(), transMat = matrix(numeric(), ncol = 1, nrow = 1),
    emission, nStates = numeric(), status = character(),
    stateNames = character(), dimNames = character(), LogLik = numeric())
```

Arguments

- **initProb**
  Initial state probabilities.

- **transMat**
  Transition probabilities

- **emission**
  Emission parameters as an HMMEmmission object.

- **nStates**
  Number of states.

- **status**
  of the HMM. On of c('initial', 'EM').

- **stateNames**
  State names.

- **dimNames**
  Names of data tracks.

- **LogLik**
  Log likelihood of a fitted HMM.
HMM-class

This class is a generic container for Hidden Markov Models.

Description

This class is a generic container for Hidden Markov Models.

Slots

- `initProb` Initial state probabilities.
- `transMat` Transition probabilities.
- `emission` Emission parameters as an HMM-Emission object.
- `nStates` Number of states.
- `status` of the HMM. One of c('initial', 'EM').
- `stateNames` State names.
- `dimNames` Names of data tracks.
- `LogLik` Log likelihood of a fitted HMM.

Methods

- `[` get elements from the HMM

See Also

- `HMM-Emission`

Examples

```r
nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
HMM(initProb=initProb, transMat=transMat, emission=HMM-Emission(type='Gaussian', parameters=list(mu=means, cov=Sigma), nStates=length(means)), nStates=nStates, status='initial')
```
Create a HMMEmission object

**Description**

This function creates a HMMEmission object.

**Usage**

HMMEmission(type = character(), parameters = list(), nStates = numeric())

**Arguments**

- **type**
  The type of emission function `c('Gaussian')`
- **parameters**
  A list containing the parameters for each state.
- **nStates**
  The number of states.

**Examples**

```r
nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
HMMEmission(type='Gaussian', parameters=list(mu=means, cov=Sigma), nStates=length(means))
```

---

This class is a generic container for different emission functions of Hidden Markov Models.

**Description**

This class is a generic container for different emission functions of Hidden Markov Models.

**Slots**

- **type**
  The type of emission function `c('Gaussian')`
- **parameters**
  A list containing the parameters for each state.
- **dim**
  Number of dimensions.
- **nStates**
  The number of states.

**Examples**

```r
nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
HMMEmission(type='Gaussian', parameters=list(mu=means, cov=Sigma), nStates=length(means))
```
Initialization of bidirectional hidden Markov models

Usage

initBdHMM(obs, nStates, method, directedObs = rep(0, ncol(obs[[1]])), sizeFactors = matrix(1, nrow = length(obs), ncol = ncol(obs[[1]])), sharedCov = FALSE)

Arguments

obs The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
nStates The number of states.
directedObs Integer vector defining the directionality (or strand-specificity) of the data tracks. Undirected (non-strand-specific) data tracks (e.g. ChIP) are indicated indicated by ‘0’. Directed (strand-specific) data tracks are indicated by increasing pairs of integers. For instance c(0,0,0,1,1,2,2): The first three data tracks are undirected, followed by two pairs of directed measurements.
sizeFactors Library size factors for Emissions PoissonLogNormal or NegativeBinomial as a length(obs) x ncol(obs[[1]]) matrix.
sharedCov If TRUE, (co-)variance of (Independent)Gaussian is shared over states. Only applicable to ‘Gaussian’ or ‘IndependentGaussian’ emissions. Default: FALSE.

Value

A HMM object.

Examples

data(example)

hmm_ex = initHMM(observations, nStates=3, method="Gaussian")
initHMM

Initialization of hidden Markov models

Description

Initialization of hidden Markov models

Usage

\[
\text{initHMM}(\text{obs}, \text{nStates}, \text{method}, \text{sizeFactors} = \text{matrix}(1, \text{nrow} = \text{length(\text{obs})}, \text{ncol} = \text{ncol(\text{obs}[1])}), \text{sharedCov} = \text{FALSE})
\]

Arguments

- **obs**: The observations. A list of one or more entries containing the observation matrix (numeric) for the samples (e.g. chromosomes).
- **nStates**: The number of states.
- **method**: Emission distribution of the model. One out of c("NegativeBinomial", "PoissonLogNormal", "NegativeMultinomial", "ZINegativeBinomial", "Poisson", "Bernoulli", "Gaussian", "IndependentGaussian")
- **sizeFactors**: Library size factors for Emissions PoissonLogNormal or NegativeBinomial as a length(\text{obs}) x ncol(\text{obs}[1]) matrix.
- **sharedCov**: If TRUE, (co-)-variance of (Independent)Gaussian is shared over states. Only applicable to 'Gaussian' or 'IndependentGaussian' emissions. Default: FALSE.

Value

A HMM object.

Examples

\[
\text{data(example)}
\]
\[
\text{hmm\_ex} = \text{initHMM(observations, nStates=3, method="Gaussian")}
\]

InitProb

Get initial state probabilities of a (bd)HMM

Description

This function returns the initial state probabilities of a (bd)HMM.

Usage

InitProb(hmm)

Arguments

- **hmm**: An object of class HMM or bdHMM.
LogLik

Value

The initial state probabilities as a numeric vector.

See Also

HMM, bdHMM

Examples

nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
hmm = HMM(initProb=initProb, transMat=transMat, emission=HMMEmission(type='Gaussian', parameters=list(mu=means, sigma=Sigma)), nStates=length(means)), nStates=nStates
InitProb(hmm)

LogLik

Get stateNames of a (bd)HMM

Description

This function returns the Log-Likelihood of a (bd)HMM.

Usage

LogLik(hmm)

Arguments

hmm

An object of class HMM or bdHMM.

Value

Log likelihood during model fitting.

Examples

data(example)
hmm_ex = initHMM(observations, nStates=3, method="Gaussian")
hmm_fitted = fitHMM(observations, hmm_ex)
LogLik(hmm_fitted)
observations

Observation sequence for the 'example' data.

Description

Observation sequence for the 'example' data.

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch

pilot.hg19

Genomic positions of processed signal for the Roadmap Epigenomics data set. Regions from the ENCODE pilot phase.

Description

Genomic positions of processed signal for the Roadmap Epigenomics data set. Regions from the ENCODE pilot phase.

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch

runningMean

Smooth data with running mean

Description

Smooth data with running mean

Usage

runningMean(x, winHalfSize = 2)

Arguments

x A vector with the data.

winHalfSize The smoothing window half size.

Value

A vector containing the smoothed data.
Examples

```r
data(trainRegions)
celltypes = list("E123"=grep("E123", names(trainRegions)),
                 "E116"=grep("E116", names(trainRegions)))
sizeFactors = getSizeFactors(trainRegions, celltypes)
sizeFactors
```

---

**StateNames**

Get stateNames of a (bd)HMM

Description

This function returns the names of states.

Usage

```r
StateNames(hmm)
```

Arguments

- `hmm` An object of class HMM or bdHMM.

Value

A character vector

Examples

```r
nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
hmm = HMM(stateNames=as.character(1:5), initProb=initProb, transMat=transMat, emission=HMMEmission(type='Gaussian', parameters=list(mu=means, cov=Sigma), nStates=length(means)), nStates=nStates, status=initial)
StateNames(hmm)
```

---

**trainRegions**

Training regions for the Roadmap Epigenomics data set. Three ENCODE pilot regions with data from two cell lines.

Description

Training regions for the Roadmap Epigenomics data set. Three ENCODE pilot regions with data from two cell lines.

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch
Transitions

Get transitions of a (bd)HMM

Description

This function returns the transition matrix of a (bd)HMM.

Usage

Transitions(hmm)

Arguments

hmm An object of class HMM or bdHMM.

Value

The transitions as a nStates x nStates matrix.

See Also

HMM, bdHMM

Examples

nStates = 5
means = list(4,11,4,11,-1)
Sigma = lapply(list(4,4,4,4,4), as.matrix)
transMat = matrix(1/nStates, nrow=nStates, ncol=nStates)
initProb = rep(1/nStates, nStates)
hmm = HMM(initProb=initProb, transMat=transMat, emission=HMMEmission(type='Gaussian', parameters=list(mu=means, cov=Sigma)), nStates=nStates, status='initial')
Transitions(hmm)

ucscGenes

UCSC gene annotation for the Roadmap Epigenomics data set.

Description

UCSC gene annotation for the Roadmap Epigenomics data set.

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch
viterbi2GRanges  
*Convert the viterbi path to a GRanges object*

**Description**

Convert the viterbi path to a GRanges object

**Usage**

```r
viterbi2GRanges(viterbi, regions, binSize)
```

**Arguments**

- `viterbi`: A list containing the viterbi paths as factors. The output from `getViterbi`.
- `regions`: GRanges object of the regions (e.g. chromosomes) stored in the viterbi path.
- `binSize`: The bin size of the viterbi path.

**Value**

The viterbi path as GRanges object.

**Examples**

```r
library(GenomicRanges)
data(yeastTF_databychrom_ex)
nStates = 6
dirobs = as.integer(c(rep(0,10), 1, 1))
bdhmm_gauss = initBdHMM(yeastTF_databychrom_ex, nStates, "Gaussian", directedObs=dirobs)
bdhmm_fitted_gauss = fitHMM(yeastTF_databychrom_ex, bdhmm_gauss)
viterbi_bdhmm_gauss = getViterbi(bdhmm_fitted_gauss, yeastTF_databychrom_ex)
yeastGRanges = GRanges(IRanges(start=1214616, end=1225008), seqnames="chrIV")
names(viterbi_bdhmm_gauss) = "chrIV"
viterbi_bdhmm_gauss_gr = viterbi2GRanges(viterbi_bdhmm_gauss, yeastGRanges, 8)
```

---

viterbi2Gviz  
*Convert state segmentation for plotting with Gviz*

**Description**

Convert state segmentation for plotting with Gviz

**Usage**

```r
viterbi2Gviz(viterbi, chrom, gen, from, to, statecols)
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>viterbi</td>
<td>A list containing the viterbi paths as factors. The output from getViterbi.</td>
</tr>
<tr>
<td>chrom</td>
<td>The chromosome/sequence if to convert.</td>
</tr>
<tr>
<td>gen</td>
<td>The genome id, e.g. hg19, hg38 for human.</td>
</tr>
<tr>
<td>from</td>
<td>Genomic start position.</td>
</tr>
<tr>
<td>to</td>
<td>Genomic end position.</td>
</tr>
<tr>
<td>statecols</td>
<td>Named vector with state colors.</td>
</tr>
</tbody>
</table>

Value

A list containing the viterbi path converted to Gviz objects for plotting.

yeastTF_databasechrom_ex

Processed ChIP-on-chip data for yeast TF example

Description

Processed ChIP-on-chip data for yeast TF example

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch

yeastTF_SGDGenes

SGD annotation for the yeast TF example

Description

SGD annotation for the yeast TF example

Author(s)

Benedikt Zacher, Julia Ertl, Julien Gagneur, Achim Tresch
This function subsets a bdHMM object. Rows are interpreted as states, columns as dimensions of emissions.

**Usage**

```r
## S4 method for signature 'bdHMM,ANY,ANY'
x[i, j, ..., drop = "missing"]
```

**Arguments**

- **x**: A bidirectional hidden Markov model.
- **i**: State ids to extract.
- **j**: Emissions to extract.
- **...**: ...
- **drop**: ...

This function subsets an HMM object. Rows are interpreted as states, columns as dimensions of emissions.

**Usage**

```r
## S4 method for signature 'HMM,ANY,ANY'
x[i, j, ..., drop = "missing"]
```

**Arguments**

- **x**: A hidden Markov model.
- **i**: State ids to extract.
- **j**: Emissions to extract.
- **...**: ...
- **drop**: ...
Index

*Topic data
- data example, 9
- data flags, 11
- data observations, 21
- data pilot.hg19, 21
- data trainRegions, 22
- data ucscGenes, 23
- data yeastTF_data_bychrom_ex, 25
- data yeastTF_SGDGenes, 25

*Topic package
- package STAN-package, 2
- package .HMM (HMM-class), 16
- package .HMM.Emission (HMMEmission-class), 17
- package .bdHMM (bdHMM-class), 4
- package [],.HMM, ANY, ANY, ANY-method (HMM-class), 16
- package [],.HMM, ANY, ANY-method, 26
- package [],.bdHMM, ANY, ANY, ANY-method
  (bdHMM-class), 4
- package [],.bdHMM, ANY, ANY-method, 26
- package .bdHMM, 3, 9, 20, 23
- package .bdHMM-class, 4
- package binarizeData, 5
- package c2optimize, 5
- package call_dpoilog, 6
- package data2Gviz, 6
- package DimNames, 7
- package DirScore, 7
- package Emission, 8
- package EmissionParams, 9
- package example, 9
- package fitHMM, 10
- package flags, 11
- package getAvgSignal, 11
- package getLogLik, 12
- package getPosterior, 13
- package getSizeFactors, 14
- package getViterbi, 14
- package HMM, 9, 10, 12, 15, 20, 23
- package HMMEmission-class, 16
- package HMMEmission, 3, 4, 8, 9, 16, 17
- package initBdHMM, 18
- package initHMM, 19
- package InitProb, 19
- package LogLik, 20
- package observations, 21
- package pilot.hg19, 21
- package runningMean, 21
- package STAN-package, 2
- package StateNames, 22
- package trainRegions, 22
- package Transitions, 23
- package ucscGenes, 23
- package viterbi2GRanges, 24
- package viterbi2Gviz, 24
- package yeastTF_data_bychrom_ex, 25
- package yeastTF_SGDGenes, 25