

Package ‘SMAP’

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Title A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling

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Description Functions and classes for DNA copy number profiling of array-CGH data

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LazyLoad true

Collate AllClasses.R AllGenerics.R methods-SMAPHMM.R
methods-SMAPObservations.R methods-SMAPProfile.R
methods-GaussParam.R methods-grad.R methods-eta.R

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R topics documented:

GBM	2
smap	3
SMAP-internal	5
SMAPHMM	6
SMAPHMM-class	7
SMAPObservations	8
SMAPObservations-class	9
SMAPProfile-class	10
SMAPProfiles-class	11

GBM*Glioblastoma multiforme array CGH data*

Description

Array CGH data measurements of glioblastoma multiforme sample G24460.

Usage

```
data(GBM)
```

Source

Genome wide array CGH data from Diaz de Stahl, T., et *al.* (2005).

References

Diaz de Stahl, T., et *al.* (2005) Chromosome 22 tiling-path array-CGH analysis identifies germ-line- and tumor-specific aberrations in patients with glioblastoma multiforme. *Genes Chromosomes Cancer* **44**(2), 161–169

See Also

[smap](#)

Examples

```
data(GBM)
observations <- SMAPObservations(value=as.numeric(GBM[,2]),
                                chromosome=as.character(GBM[,3]),
                                startPosition=as.numeric(GBM[,4]),
                                endPosition=as.numeric(GBM[,5]),
                                name="G24460",
                                reporterId=as.character(GBM[,1]))

plot(observations)
```

smap	<i>smap: A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling</i>
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Description

This function fits a Hidden Markov Model (HMM) to a set of observed microarray intensity ratios and outputs the most plausible state sequence in the HMM through segmental a posteriori maximization.

Briefly, given an HMM with initial parameter settings *lambda* and a set of observations *O*, the method alternates maximization of the joint posterior probability of the state sequence *Q* and *lambda* given *O*, $p(Q, \lambda | O)$, over *Q* (using a modified Viterbi algorithm) and *lambda* (using a gradient descent scheme with individual learning rate adaptation).

Usage

```
smap(x, Obs, sd.min=0.05, mean.sd=0.05,
     max.its=Inf, gd.max.its=Inf, tau=0.05,
     eta=0.01, e.change=0.5, e.same=1.2,
     e.min=0.0001, e.max=0.5, adaptive=TRUE,
     overlap=TRUE, distance=TRUE, chrom.wise=FALSE,
     verbose=1, L=5000000)
```

Arguments

<code>x</code>	An object of class <code>SMAPHMM-class</code> .
<code>Obs</code>	An object of class <code>SMAPObservations-class</code> .
<code>sd.min</code>	The minimum allowed standard deviation of state associated Gaussian distributions (numeric).
<code>mean.sd</code>	Prior standard deviation of state associated Gaussian means (numeric).
<code>max.its</code>	Maximum number of iterations in the SMAP algorithm (numeric).
<code>gd.max.its</code>	Maximum number of iterations in the gradient descent algorithm per SMAP iteration (numeric).
<code>tau</code>	Minimum log probability improvement required in the SMAP and gradient descent optimization (numeric).
<code>eta</code>	Initial learning rate in the gradient descent optimization (numeric).
<code>e.change</code>	Multiplier for individual learning rate adaptation if the sign of partial derivative changes (numeric). Only used if <code>adaptive == TRUE</code> .
<code>e.same</code>	Multiplier for individual learning rate adaptation if the sign of partial derivative stays the same (numeric). Only used if <code>adaptive == TRUE</code> .
<code>e.min</code>	Minimum allowed learning rate (numeric).
<code>e.max</code>	Maximum allowed learning rate (numeric).


```

                                endPosition=as.numeric(GBM[,5]),
                                name="G24460",
                                reporterId=as.character(GBM[,1]))

plot(observations, ylim=c(0,2))
## Initiate HMM
init.means <- c(0.4, 0.7, 1, 1.3, 1.6, 3)
init.sds <- rep(0.1, 6)
phi <- cbind(init.means, init.sds)
hmm <- SMAPHMM(6, phi, initTrans=0.02)
hmm
## RUN SMAP:
profile <- smap(hmm, observations, verbose=2)
## genome profile
plot(profile, ylim=c(0,2))
## chromosome 9 profile
ids <- which(chromosome(observations) == "9")
plot(profile[ids], ylim=c(0,2), main="chromosome 9")
## output results for chromosome 9
#cbind(reporterId(observations[ids]), Q(profile[ids]))

```

SMAP-internal

SMAP-internal

Description

Internal methods for the **SMAP** package.

Author(s)

Robin Andersson, <robin.andersson@lcb.uu.se>

References

Andersson, R., Bruder, C. E. G., Piotrowski, A., Menzel, U., Nord, H., Sandgren, J., Hvidsten, T. R., Diaz de Stahl, T., Dumanski, J. P., Komorowski, J., A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling, submitted

See Also

[smap](#)

SMAPHMM

*Constructor for "SMAPHMM" objects***Description**

A constructor for [SMAPHMM-class](#) objects.

Usage

```
SMAPHMM(noStates, Phi, A=NULL,
        Pi=rep(1/noStates,noStates),
        initTrans=0.2/(noStates - 1))
```

Arguments

<code>noStates</code>	The number of hidden states in the HMM (numeric).
<code>Phi</code>	A Gaussian distribution parameter matrix (numeric).
<code>A</code>	A <code>noStates * noStates</code> matrix of transition probabilities between the hidden states (numeric).
<code>Pi</code>	A vector of initial probabilities of starting in a certain state (numeric).
<code>initTrans</code>	Specifies the transition probability between non-equal states (numeric).

Details

`Phi` is a `noStates * 2` matrix that specifies the parameters of Gaussian distributions associated with each hidden state. The first column specifies standard deviations, the second specifies means.

If `A == NULL`, `initTrans` specifies the transition probability between states `i` and `j` in `1:noStates`, such that `i != j`. Only used if `A == NULL`. `initTrans * noStates` must be smaller than (or equal to) 1.

Value

An object of class [SMAPHMM-class](#).

Author(s)

Robin Andersson, <robin.andersson@lcb.uu.se>

References

Andersson, R., Bruder, C. E. G., Piotrowski, A., Menzel, U., Nord, H., Sandgren, J., Hvidsten, T. R., Diaz de Stahl, T., Dumanski, J. P., Komorowski, J., A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling, submitted

See Also

[smap](#), [SMAPHMM-class](#), [SMAPObservations-class](#)

SMAPHMM-class	<i>Class "SMAPHMM": A class to manage HMMs for the SMAP package</i>
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Description

Holds parameters for a Hidden Markov Model (HMM) used in the **SMAP** package.

Objects from the Class

Objects should not be created directly but via the constructor function [SMAPHMM](#).

Slots

A: Object of class "matrix" The transition probability matrix between states.
Pi: Object of class "numeric" The initial probabilities of starting in a certain state.
Phi: Object of class "matrix" A matrix that specifies the parameters of Gaussian distributions associated with each hidden state. The first column specifies standard deviations, the second specifies means.
noStates: Object of class "numeric" The number of hidden states in the HMM.
Z: Object of class "matrix" Matrix of transition probabilities.
Y: Object of class "numeric" Vector of initial probabilities.
eta: Object of class "ANY". Internal slot.
grad: Object of class "ANY". Internal slot.

Methods

A signature(object = "SMAPHMM"): Returns the transition matrix.
Pi signature(object = "SMAPHMM"): Returns the initial probabilities.
Phi signature(object = "SMAPHMM"): Returns the distribution parameter matrix.
noStates signature(object = "SMAPHMM"): Returns the number of hidden states in the HMM.

Author(s)

Robin Andersson, <robin.andersson@lcb.uu.se>

References

Andersson, R., Bruder, C. E. G., Piotrowski, A., Menzel, U., Nord, H., Sandgren, J., Hvidsten, T. R., Diaz de Stahl, T., Dumanski, J. P., Komorowski, J., A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling, submitted

See Also

[smap](#), [SMAPHMM](#)

SMAPObservations	<i>Constructor for "SMAPObservations" objects</i>
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Description

A constructor for [SMAPObservations-class](#) objects.

Usage

```
SMAPObservations(value, chromosome, startPosition, endPosition,  
                 name=character(0),  
                 reporterId=as.character(1:length(value)))
```

Arguments

value	A vector of microarray intensity ratios (numeric).
chromosome	A vector of chromosome annotations (character).
startPosition	A vector of start positions (numeric).
endPosition	A vector of end positions (numeric).
name	The name of the observation set (character).
reporterId	A vector of observation identifiers, e.g., probe ids (character).

Details

The vectors value, chromosome, startPosition, endPosition, and reporterId must be of equal length.

Value

An object of class [SMAPObservations-class](#).

Author(s)

Robin Andersson, <robin.andersson@lcb.uu.se>

References

Andersson, R., Bruder, C. E. G., Piotrowski, A., Menzel, U., Nord, H., Sandgren, J., Hvidsten, T. R., Diaz de Stahl, T., Dumanski, J. P., Komorowski, J., A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling, submitted

See Also

[smap](#), [SMAPObservations-class](#), [SMAPHMM-class](#)

Examples

```
## Load Glioblastoma multiforme data
data(GBM)
observations <- SMAPObservations(value=as.numeric(GBM[,2]),
                                chromosome=as.character(GBM[,3]),
                                startPosition=as.numeric(GBM[,4]),
                                endPosition=as.numeric(GBM[,5]),
                                name="G24460",
                                reporterId=as.character(GBM[,1]))

## plot observations
plot(observations, ylim=c(0,2))
## plot subset of observations (chromosome 9)
ids <- which(chromosome(observations) == "9")
plot(observations[ids])
```

SMAPObservations-class

Class "SMAPObservations": A class to manage microarray observations for the SMAP package

Description

Holds observed microarray intensity ratios and clone annotations for the **SMAP** package.

Objects from the Class

Objects can be created by calls of the form `new("SMAPObservations", value, chromosome, startPosition, endPosition, name, reporterId)`. Values for internal slots (see below) are not intended to be passed upon construction. You can also use the convenience function [SMAPObservations](#).

Slots

value: Object of class "numeric" Microarray intensity ratios.
chromosome: Object of class "character" Associated chromosomes for the observations.
startPosition: Object of class "numeric" Associated start positions for the observations.
endPosition: Object of class "numeric" Associated end positions for the observations.
reporterId: Object of class "character" Identifiers of the observations, e.g., probe ids.
name: Object of class "character" An identifier of the observation set.
noObservations: Object of class "numeric" The number of observations in the set.
chrom.start: Object of class "numeric". Internal slot.
chroms: Object of class "character". Internal slot.
distance: Object of class "numeric". Internal slot.
noOverlaps: Object of class "numeric". Internal slot.
overlaps: Object of class "numeric". Internal slot.
overlapIds: Object of class "numeric". Internal slot.
startOverlaps: Object of class "numeric". Internal slot.

Methods

value signature(object = "SMAPObservations"): Returns the values of the observations.

chromosome signature(object = "SMAPObservations"): Returns the chromosome annotations of the observations.

startPosition signature(object = "SMAPObservations"): Returns the start positions of the observations.

endPosition signature(object = "SMAPObservations"): Returns the end positions of the observations.

reporterId signature(object = "SMAPObservations"): Returns the identifiers of the observations.

name signature(object = "SMAPObservations"): Returns the name of the observation set.

noObservations signature(object = "SMAPObservations"): Returns the number of observations in the set.

initialize signature(.Object = "SMAPObservations"): Creates an instance.

plot signature(x = "SMAPObservations", y = "missing"): A plot method for the observations.

[signature(x = "SMAPPObservations"): Creates a new object of class SMAPObservations with extracted elements as specified by the indices provided.

Author(s)

Robin Andersson, <robin.andersson@lcb.uu.se>

References

Andersson, R., Bruder, C. E. G., Piotrowski, A., Menzel, U., Nord, H., Sandgren, J., Hvidsten, T. R., Diaz de Stahl, T., Dumanski, J. P., Komorowski, J., A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling, submitted

See Also

[smap](#), [SMAPObservations](#)

SMAPProfile-class

Class "SMAPProfile"

Description

Holds results from running [smap](#).

Objects from the Class

Objects are not intended to be created directly but as a result from running [smap](#).

Slots

HMM: Object of class "SMAPHMM"

observations: Object of class "SMAPObservations"

P: Object of class "numeric" The log joint posterior probability of the state sequence Q and parameters of HMM given the observations.

Q: Object of class "numeric" The optimal state sequence (path) in the HMM.

name: Object of class "character" The name of the object.

Methods

P signature(object = "SMAPProfile"): Returns the log joint posterior probability.

Q signature(object = "SMAPProfile"): Returns the optimal state sequence.

HMM signature(object = "SMAPProfile"): Returns the optimized HMM.

name signature(object = "SMAPProfile"): Returns the name of the profile.

observations signature(object = "SMAPProfile"): Returns the observations.

plot signature(x = "SMAPProfile", y = "missing"): A plot method for the result profile.

[signature(x = "SMAPProfile"): Creates a new object of class SMAPProfile with extracted elements as specified by the indices provided.

Author(s)

Robin Andersson, <robin.andersson@lcb.uu.se>

References

Andersson, R., Bruder, C. E. G., Piotrowski, A., Menzel, U., Nord, H., Sandgren, J., Hvidsten, T. R., Diaz de Stahl, T., Dumanski, J. P., Komorowski, J., A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling, submitted

See Also

[smap](#), [SMAPProfiles-class](#)

SMAPProfiles-class	Class "SMAPProfiles"
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Description

Holds results from running [smap](#).

Objects from the Class

Objects are not intended to be created directly but as a result from running [smap](#).

Slots

.Data: Object of class "list" A list of objects of class [SMAPProfile-class](#).
name: Object of class "character" The name of the object.

Extends

Class "list", from data part. Class "vector", by class "list".

Methods

Q `signature(object = "SMAPProfiles")`: Returns the optimal state sequence of the list elements.

observations `signature(object = "SMAPProfiles")`: Returns the observations of the list elements.

name `signature(object = "SMAPProfiles")`: Returns the name of the profile.

plot `signature(x = "SMAPProfiles", y = "missing")`: A plot method for the result profiles.

Author(s)

Robin Andersson, <robin.andersson@lcb.uu.se>

References

Andersson, R., Bruder, C. E. G., Piotrowski, A., Menzel, U., Nord, H., Sandgren, J., Hvidsten, T. R., Diaz de Stahl, T., Dumanski, J. P., Komorowski, J., A Segmental Maximum A Posteriori Approach to Array-CGH Copy Number Profiling, submitted

See Also

[smap](#), [SMAPProfile-class](#)

Index

- * **classes**
 - SMAPHMM, 6
 - SMAPHMM-class, 7
 - SMAPObservations, 8
 - SMAPObservations-class, 9
 - SMAPProfile-class, 10
 - SMAPProfiles-class, 11
- * **datasets**
 - GBM, 2
- * **internal**
 - SMAP-internal, 5
- * **methods**
 - smap, 3
 - SMAP-internal, 5
 - [, SMAPObservations-method (SMAP-internal), 5
 - [, SMAPProfile-method (SMAP-internal), 5
 - [<-, SMAPProfiles-method (SMAP-internal), 5
 - A (SMAPHMM-class), 7
 - A, eta-method (SMAP-internal), 5
 - A, grad-method (SMAP-internal), 5
 - A, SMAPHMM-method (SMAP-internal), 5
 - chromosome (SMAPObservations-class), 9
 - chromosome, SMAPObservations-method (SMAP-internal), 5
 - endPosition (SMAPObservations-class), 9
 - endPosition, SMAPObservations-method (SMAP-internal), 5
 - GBM, 2
 - HMM (SMAPProfile-class), 10
 - HMM, SMAPProfile-method (SMAP-internal), 5
 - initialize, eta-method (SMAP-internal), 5
 - initialize, gaussparam-method (SMAP-internal), 5
 - initialize, grad-method (SMAP-internal), 5
 - initialize, SMAPHMM-method (SMAP-internal), 5
 - initialize, SMAPObservations-method (SMAP-internal), 5
 - initialize, SMAPProfile-method (SMAP-internal), 5
 - name (SMAPObservations-class), 9
 - name, SMAPObservations-method (SMAP-internal), 5
 - name, SMAPProfile-method (SMAP-internal), 5
 - name, SMAPProfiles-method (SMAP-internal), 5
 - noObservations (SMAPObservations-class), 9
 - noObservations, SMAPObservations-method (SMAP-internal), 5
 - noStates (SMAPHMM-class), 7
 - noStates, SMAPHMM-method (SMAP-internal), 5
 - observations (SMAPProfile-class), 10
 - observations, SMAPProfile-method (SMAP-internal), 5
 - observations, SMAPProfiles-method (SMAP-internal), 5
 - P (SMAPProfile-class), 10
 - P, SMAPProfile-method (SMAP-internal), 5
 - Phi (SMAPHMM-class), 7
 - Phi, eta-method (SMAP-internal), 5
 - Phi, grad-method (SMAP-internal), 5
 - Phi, SMAPHMM-method (SMAP-internal), 5
 - Pi (SMAPHMM-class), 7
 - Pi, eta-method (SMAP-internal), 5

Pi, grad-method (SMAP-internal), 5
Pi, SMAPHMM-method (SMAP-internal), 5
plot, SMAPObservations, missing-method
 (SMAPObservations-class), 9
plot, SMAPProfile, missing-method
 (SMAP-internal), 5
plot, SMAPProfiles, missing-method
 (SMAP-internal), 5

Q (SMAPProfile-class), 10
Q, SMAPProfile-method (SMAP-internal), 5
Q, SMAPProfiles-method (SMAP-internal), 5

reporterId (SMAPObservations-class), 9
reporterId, SMAPObservations-method
 (SMAP-internal), 5

show, SMAPHMM-method (SMAP-internal), 5
show, SMAPObservations-method
 (SMAP-internal), 5
show, SMAPProfile-method
 (SMAP-internal), 5
show, SMAPProfiles-method
 (SMAP-internal), 5
smap, 2, 3, 5–8, 10–12
smap, SMAPHMM, SMAPObservations-method
 (SMAP-internal), 5
SMAP-internal, 5
SMAPHMM, 4, 6, 7
SMAPHMM-class, 7
SMAPObservations, 4, 8, 9, 10
SMAPObservations-class, 9
SMAPProfile-class, 10
SMAPProfiles-class, 11
startPosition (SMAPObservations-class),
 9
startPosition, SMAPObservations-method
 (SMAP-internal), 5

value (SMAPObservations-class), 9
value, eta-method (SMAP-internal), 5
value, SMAPObservations-method
 (SMAP-internal), 5