

# Package: CHMM (via r-universe)

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**Type** Package

**Title** Coupled Hidden Markov Models

**Version** 0.1.1

**Description** An exact and a variational inference for coupled Hidden Markov Models applied to the joint detection of copy number variations.

**Depends** R (>= 3.1.0)

**Imports** mclust

**License** GPL-2

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**URL** <http://github.com/julieaubert/CHMM>

**BugReports** <http://github.com/julieaubert/CHMM/issues>

**Repository** <https://julieaubert.r-universe.dev>

**RemoteUrl** <https://github.com/julieaubert/chmm>

**RemoteRef** HEAD

**RemoteSha** cf283a7e25c6af8ce6f972c630b46a7da310e386

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CHMM\_EM

*Perform exact inference of coupled hidden markov models.***Description**

Perform exact inference of coupled hidden markov models.

**Usage**

```
CHMM_EM(X, nb.states, S, omega, meth.init = "mclust", var.equal = TRUE,
        itmax = 500, threshold = 1e-07)
```

**Arguments**

|           |   |
|-----------|---|
| X         | a data matrix of observations. Columns correspond to individuals.                                     |
| nb.states | a integer specifying the numbers of states.   |
| S         | a matrix of similarity between individuals.   |
| omega     | a value of omega.   |
| meth.init | a string specifying the initialization method ("mclust" or "kmeans"). The default method is "mclust". |
| var.equal | a logical variable indicating whether to treat the variances as being equal.                          |
| itmax     | an integer specifying the maximal number of iterations for the EM algorithm.                          |
| threshold | a value for the threshold used for the stopping criteria.   |

**Value**

a list of 10 components

- postPr a list containing for each series the posterior probabilities.
- initGb a numeric specifying the initial state probabilities.
- transGb a matrix of the state transition probabilities.
- emisGb a list containing for each series the emission probabilities.
- esAvg a numeric of the estimated mean for each state.
- esVar a numeric of the estimated variance for each state.
- ID.K a matrix containing all combination of possible state for nbI series.
- loglik a numeric with the value of the loglikelihood.
- RSS a numeric corresponding to the Residuals Sum of Squares.
- iterstop an integer corresponding to the total number of iterations.

**References**

Wang, X., Lebarbier, E., Aubert, J. and Robin, S., Variational inference for coupled Hidden Markov Models applied to the joint detection of copy number variations.

CHMM\_VEM

*Perform variational inference of coupled Hidden Markov Models.***Description**

Perform variational inference of coupled Hidden Markov Models.

**Usage**

```
CHMM_VEM(X, nb.states, S = NULL, omega = 0.7, meth.init = "mclust",
          var.equal = TRUE, itmax = 500, threshold = 1e-07)
```

**Arguments**

|           |   |
|-----------|---|
| X         | a data matrix of observations. Columns correspond to individuals.                                     |
| nb.states | a integer specifying the numbers of states.   |
| S         | a matrix of similarity between individuals.   |
| omega     | a value of omega.   |
| meth.init | a string specifying the initialization method ("mclust" or "kmeans"). The default method is "mclust". |
| var.equal | a logical variable indicating whether to treat the variances as being equal.                          |
| itmax     | an integer specifying the maximal number of iterations for the EM algorithm.                          |
| threshold | a value for the threshold used for the stopping criteria.   |

**Value**

a list of 9 components

postPr a list containing for each series the posterior probabilities.

initPr a numeric specifying the initial state probabilities.

transPr a matrix of the state transition probabilities.

esAvg a numeric of the estimated mean for each state.

esVar a numeric of the estimated variance for each state.

emisPr a list containing for each series the emission probabilities.

emisPrW a list containing for each series the emission probabilities taking into account for the dependency structure.

RSS a numeric corresponding to the Residuals Sum of Squares.

iterstop an integer corresponding to the total number of iterations.

**References**

Wang, X., Lebarbier, E., Aubert, J. and Robin, S., Variational inference for coupled Hidden Markov Models applied to the joint detection of copy number variations.

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|------------|--|
| clusterseg | <i>Summarize the results of the coupled HMM.</i> |
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**Description**

Summarize the results of the coupled HMM.

**Usage**

```
clusterseg(x)
```

**Arguments**

x a matrix of status. Columns corresponds to series (individuals).

**Value**

a data.frame with 4 columns

sample name of the sample (series).

posbegin beginning position.

posend ending position.

status status.

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|------------|---|
| coupledHMM | <i>Perform inference of coupled hidden markov models.</i> |
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**Description**

Perform inference of coupled hidden markov models.

**Usage**

```
coupledHMM(X, nb.states = 3, S = NULL, omega.list = c(0.3, 0.7, 0.9),  
var.equal = TRUE, exact = FALSE, meth.init = "mclust", viterbi = TRUE,  
itmax = 500, threshold = 1e-07)
```

**Arguments**

|                         |   |
|-------------------------|---|
| <code>X</code>          | a matrix of observations. Columns correspond to series (individuals).   |
| <code>nb.states</code>  | a integer specifying the numbers of states.   |
| <code>S</code>          | a matrix of similarity between individuals.   |
| <code>omega.list</code> | a vector of omega values.   |
| <code>var.equal</code>  | a logical variable indicating whether to treat the variances as being equal ( <code>var.equal = TRUE</code> ).  |
| <code>exact</code>      | a logical variable indicating whether to use VEM ( <code>exact = FALSE</code> ) or EM ( <code>exact = TRUE</code> ) algorithm for the inference of the model.                               |
| <code>meth.init</code>  | a string specifying the initialization method ("mclust" or "kmeans") for the (V)-EM algorithm. The default method is "mclust".  |
| <code>viterbi</code>    | a logical variable indicating whether to use Maximum A Posteriori method ( <code>FALSE</code> ) or Viterbi algorithm ( <code>TRUE</code> , by default) for recovering the most likely path. |
| <code>itmax</code>      | an integer specifying the maximal number of iterations for the CHMM_(V)EM algorithm.  |
| <code>threshold</code>  | a value for the threshold used for the stopping criteria for the CHMM_(V)EM algorithm.  |

**Value**

A list of 4 objets.

`omega` an integer corresponding to the selected value among the `omega.list`.

`model` a list corresponding to the output of the CHMM-EM or CHMM-VEM function for the selected model.

`status` a matrix with status associated to each series in column and each position in row.

`RSS.omega` a dataframe with omega values and the associated Residuals Sum of Squares.

**References**

Wang, X., Lebarbier, E., Aubert, J. and Robin, S., Variational inference for coupled Hidden Markov Models applied to the joint detection of copy number variations.

**See Also**

[CHMM\\_VEM](#), [CHMM\\_EM](#)

**Examples**

```
data(toyexample)
# Variational inference of a coupled hidden Markov Chains
resCHMM <- coupledHMM(X = toydata, nb.states = 3, S = cor(toystatus),
                      omega.list = c(0.3, 0.5, 0.7, 0.9))
# Breakpoints positions and status of segments
info <- clusterseg(resCHMM$status)
# head(info)
```

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init.EM                      *Initialization step of the CHMM\_EM function.*

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### Description

Initialization step of the CHMM\_EM function.

### Usage

```
init.EM(X, nb.states, meth.init, var.equal, nbI, nbT)
```

### Arguments

|           |  |
|-----------|--|
| X         | a matrix of observations. Columns correspond to series (individuals).  |
| nb.states | an integer specifying the numbers of states.   |
| meth.init | a string specifying the initialization method ("mclust" or "kmeans"). The default method is "mclust".                |
| var.equal | a logical variable indicating whether to treat the variances as being equal (TRUE, value by default) or not (FALSE). |
| nbI       | an integer specifying the number of series.  |
| nbT       | an integer specifying the length of one series.  |

### Details

By default, an initialization with the `meth.init="mclust"` is performed with homogeneous variances.

### Value

A list of 6 objects.

`esAvgGb` a matrix of  $nbK(nb.states^{nbI})$  rows and `nbI` columns of estimated mean.

`esVarGb` a matrix of  $nbK(nb.states^{nbI})$  rows and `nbI` columns of estimated variance.

`esAvg` a numeric of the estimated mean for each state.

`esVar` a numeric of the estimated variance for each state.

`transGb` a matrix of the state transition probabilities.

`initGb` a numeric specifying the initial state probabilities.

### See Also

[CHMM\\_EM](#)

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| init.VEM | <i>Initialization step of the CHMM_VEM function.</i> |
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**Description**

Initialization step of the CHMM\_VEM function.

**Usage**

```
init.VEM(X, nb.states, meth.init, var.equal, nbI, nbT)
```

**Arguments**

|           |  |
|-----------|--|
| X         | a matrix of observations. Columns correspond to series (individuals).  |
| nb.states | an integer specifying the numbers of states.   |
| meth.init | a string specifying the initialization method ("mclust" or "kmeans"). The default method is "mclust".                |
| var.equal | a logical variable indicating whether to treat the variances as being equal (TRUE, value by default) or not (FALSE). |
| nbI       | an integer specifying the number of series.  |
| nbT       | an integer specifying the length of one series.  |

**Value**

A list containing the parameters of the model

esAvg a numeric of the estimated mean for each state.

esVar a numeric of the estimated variance for each state.

transPr a matrix of the state transition probabilities

postPr a list containing for each series the posterior probabilities.

initPr a numeric specifying the initial state probabilities.

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|---------|---|
| toydata | <i>Toy example - observations for 5 correlated samples.</i> |
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**Description**

A matrix containing the observations for the 1,000 positions of 5 correlated samples.

**Format**

A simulated matrix with 1000 rows and 5 columns. Each column is a series

**Examples**

```
data(toyexample)
# Variational inference of a coupled hidden Markov Chains
resCHMM <- coupledHMM(X = toydata, nb.states = 3, S = cor(toystatus),
                      omega.list = c(0.3, 0.5, 0.7, 0.9))
# Breakpoints positions and status of segments
info <- clusterseg(resCHMM$status)
# head(info)
```

---

toystatus

*Toy example - status for 5 correlated samples.*

---

**Description**

A matrix containing the hidden status for the 1,000 positions of 5 correlated samples.

**Format**

A matrix of the hidden status corresponding to the toydata matrix.



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