Package ‘gmgm’

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Version 1.1.1
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dynamic Bayesian networks (their temporal extension) whose local probability
distributions are described by Gaussian mixture models. They are powerful
tools for graphically and quantitatively representing nonlinear dependencies
between continuous variables. This package provides a complete framework to
create, manipulate, learn the structure and the parameters, and perform
inference in these models. Most of the algorithms are described in the PhD

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## Description

This package provides a complete framework to deal with Gaussian mixture graphical models, which covers Bayesian networks and dynamic Bayesian networks (their temporal extension) whose local probability distributions are described by Gaussian mixture models. It includes a wide range of functions for:

- creating or modifying the structure of Gaussian mixture models (`add_var`, `gmm`, `merge_comp`, `remove_var`, `rename_var`, `reorder`, `split_comp`) or graphical models (`add_arcs`, `add_nodes`, `gmbn`, `gmdbn`, `relevant`, `remove_arcs`, `remove_nodes`, `rename_nodes`);
- describing or visualizing Gaussian mixture models (`conditional`, `ellipses`, `summary.gmm`) or graphical models (`network`, `structure`, `summary.gmbn`, `summary.gmdbn`);
- computing densities, expectations, or sampling Gaussian mixture models (`density`, `expectation`, `sampling`);
- computing scores of Gaussian mixture models (`AIC.gmm`, `BIC.gmm`, `logLik.gmm`) or graphical models (`AIC.gmbn`, `AIC.gmdbn`, `BIC.gmbn`, `BIC.gmdbn`, `logLik.gmbn`, `logLik.gmdbn`);
- learning the structure and/or the parameters of Gaussian mixture models (`em`, `smem`, `stepwise`) or graphical models (`param_em`, `param_learn`, `struct_em`, `struct_learn`);
- performing inference in Gaussian mixture graphical models (`aggregation`, `filtering`, `inference`, `particles`, `prediction`, `propagation`, `smoothing`).

Descriptions of these functions are provided in this manual with related references. Most of the algorithms are described in the PhD thesis of Roos (2018, in french). To better handle this package, two real-world datasets are provided (`data_air`, `data_body`) with examples of Gaussian mixture models and graphical models (`gmbn_body`, `gmdbn_air`, `gmm_body`).

### References


---

### add_arcs

**Add arcs to a Gaussian mixture graphical model**

This function adds arcs to a Gaussian mixture graphical model. For each added arc, a variable related to the start node is added to the Gaussian mixture model describing the local distribution over the end node and its parents, with mean 0 and variance 1 for each mixture component.
add_nodes

Usage

add_arcs(gmgm, arcs)

Arguments

gmgm An object of class gmbn or gmdbn.
arcs A data frame containing the added arcs. The column from describes the start
node, the column to the end node and the column lag the time lag between
them. Missing values in from or to are interpreted as "all possible nodes",
which allows to quickly define large set of arcs that share common attributes.
Missing values in lag are replaced by 0. If gmgm is a gmdbn object, the same
arcs are added to each of its gmbn elements. This constraint can be overcome by
passing a list of data frames named after some of these elements (b_1, ...) and
containing arcs specifically added to them. The arcs whose time lags exceed the
maximum temporal depth of their gmbn element are not taken into account.

Value

The gmbn or gmdbn object after adding the arcs.

See Also

add_nodes, relevant, remove_arcs, remove_nodes, rename_nodes

Examples

data(gmbn_body)
gmbn_1 <- add_arcs(gmbn_body,
data.frame(from = c("GENDER", "AGE"),
to = c("GLYCO", "WEIGHT")))

data(gmdbn_air)
gmdbn_1 <- add_arcs(gmdbn_air,
list(b_2 = data.frame(from = "WIND", to = "NO2", lag = 1),
b_13 = data.frame(from = c("NO2", "NO2"),
to = c("O3", "O3"), lag = c(0, 1))))

add_nodes Add nodes to a Gaussian mixture graphical model

Description

This function adds nodes to a Gaussian mixture graphical model. If this model is a dynamic
Bayesian network, the nodes are added to each of its transition models. For each added node, a
one-component univariate Gaussian mixture model is created with mean 0 and variance 1.
add_var

Usage

add_nodes(gmm, nodes)

Arguments

  gmm          An object of class gmbn or gmdbn. If NULL, a gmbn object is created with the
               added nodes.
  nodes        A character vector containing the added nodes.

Value

The gmbn or gmdbn object after adding the nodes.

See Also

  add_arcs, relevant, remove_arcs, remove_nodes, rename_nodes

Examples

data(gmbn_body)
gmbn_1 <- add_nodes(gmbn_body, c("CHOL", "TRIGLY"))

data(gmdbn_air)
gmdbn_1 <- add_nodes(gmdbn_air, "PM10")

add_var

Add variables to a Gaussian mixture model

Description

  This function adds variables to a Gaussian mixture model.

Usage

  add_var(gmm, var)

Arguments

  gmm          An object of class gmm. If NULL, a gmm object is created with the added variables
               and one mixture component.
  var          A character vector containing the added variables, or a data frame or numeric
               matrix whose columns are named after the added variables. In the first case, for
               each mixture component, the marginal mean vector of the added variables is 0
               and the marginal covariance matrix the identity matrix. In the second case, these
               mean vector and covariance matrix are computed from the data (after removing
               the rows that contain missing values).
aggregation

Value

The gmm object after adding the variables.

See Also

remove_var, rename_var

Examples

data(gmm_body, data_body)
gmm_1 <- add_var(gmm_body, "GENDER")
gmm_2 <- add_var(gmm_body, data_body[, "GENDER"])

aggregation

Aggregate particles to obtain inferred values

Description

This function aggregates particles to obtain inferred values. Assuming that the particles have been propagated to a given time slice \( t \), the weighted average of the samples is computed to estimate the state of the system at \( t \) or at previous time slices (Koller and Friedman, 2009).

Usage

aggregation(part, nodes, col_seq = NULL, col_weight = "weight", lag = 0)

Arguments

part A data frame containing the particles propagated to time slice \( t \), as obtained from function particles or propagation.

nodes A character vector containing the inferred nodes.

col_seq A character vector containing the column names of part that describe the observation sequence. If NULL (the default), all the particles belong to a single sequence.

col_weight A character string corresponding to the column name of part that describes the particle weight.

lag A non-negative integer vector containing the time lags \( l_1, l_2, \ldots \) such that the samples of time slices \( t - l_1, t - l_2, \ldots \) are aggregated.

Value

If lag has one element, a data frame (tibble) containing the aggregated values of the inferred nodes and their observation sequences (if col_seq is not NULL). If lag has two or more elements, a list of data frames (tibbles) containing these values for each time lag.
AIC

References


See Also

aggregation, particles

Examples

```r
library(dplyr)
set.seed(0)
data(gmdbn_air, data_air)
evid <- data_air %>%
  group_by(DATE) %>%
  slice(1:3) %>%
  ungroup()
evid$NO2[sample.int(150, 30)] <- NA
evid$O3[sample.int(150, 30)] <- NA
evid$TEMP[sample.int(150, 30)] <- NA
evid$WIND[sample.int(150, 30)] <- NA
aggreg <- particles(data.frame(DATE = unique(evid$DATE))) %>%
  propagation(gmdbn_air, evid, col_seq = "DATE", n_times = 3) %>%
  aggregation(c("NO2", "O3", "TEMP", "WIND"), col_seq = "DATE", lag = c(0, 1))
```

---

**AIC**

Compute the Akaike Information Criterion (AIC) of a Gaussian mixture model or graphical model

**Description**

This function computes the Akaike Information Criterion (AIC) of a Gaussian mixture model or graphical model:

\[
AIC = \log\text{Lik} - n_{\text{par}}
\]

where \(\log\text{Lik}\) is the log-likelihood and \(n_{\text{par}}\) the number of free parameters.

**Usage**

```r
# S3 method for class 'gmm'
AIC(object, data, y = NULL, regul = 0.01, ...)

# S3 method for class 'gmbn'
AIC(object, data, col_seq = NULL, ...)

# S3 method for class 'gmdbn'
AIC(object, data, col_seq = NULL, ...)
```
Arguments

- **object**: An object of class `gmm`, `gmbn` or `gmdbn`.
- **data**: A data frame containing the data used to compute the AIC. Its columns must explicitly be named after the variables (or nodes) of `object`. If `object` is a `gmm` object, a numeric matrix can be passed.
- **y**: A character vector containing the dependent variables if a conditional AIC is computed. If `NULL` (the default), the joint AIC is computed.
- **regul**: A positive numeric value corresponding to the regularization constant if a penalty term is added for Bayesian regularization. If `NULL` (the default), no penalty term is added. If a conditional AIC is computed, this argument is ignored.
- **...**: Unused arguments from the generic function.
- **col_seq**: A character vector containing the column names of `data` that describe the observation sequence. If `NULL` (the default), all the observations belong to a single sequence. If `object` is a temporal `gmbn` or `gmdbn` object, the observations of a same sequence must be ordered such that the $t$th one is related to time slice $t$ (note that the sequences can have different lengths). If `object` is a non-temporal `gmbn` object, this argument is ignored.

Value

- If `object` is a `gmm` object, a numeric value corresponding to the AIC.
- If `object` is a `gmbn` or `gmdbn` object, a list with elements:
  - **global**: A numeric value corresponding to the global AIC.
  - **local**: For a `gmbn` object, a numeric vector containing the local conditional AICs. For a `gmdbn` object, a list of numeric vectors containing these values for each `gmbn` element.

See Also

- `BIC`, `logLik`

Examples

```R
data(gmm_body, data_body)
aic_1 <- AIC(gmm_body, data_body)
aic_2 <- AIC(gmm_body, data_body, y = "WAIST")

data(gmbn_body, data_body)
aic_3 <- AIC(gmbn_body, data_body)

data(gmdbn_air, data_air)
aic_4 <- AIC(gmdbn_air, data_air, col_seq = "DATE")
```
**BIC**

*Compute the Bayesian Information Criterion (BIC) of a Gaussian mixture model or graphical model*

**Description**

This function computes the Bayesian Information Criterion (BIC) of a Gaussian mixture model or graphical model:

\[
BIC = \logLik - \frac{\log(n_{obs})}{2} n_{par}
\]

where \(\logLik\) is the log-likelihood, \(n_{obs}\) the number of observations in the data and \(n_{par}\) the number of free parameters.

**Usage**

```r
## S3 method for class 'gmm'
BIC(object, data, y = NULL, regul = 0.01, ...)

## S3 method for class 'gmbn'
BIC(object, data, col_seq = NULL, ...)

## S3 method for class 'gmdbn'
BIC(object, data, col_seq = NULL, ...)
```

**Arguments**

- `object`  
  An object of class `gmm`, `gmbn` or `gmdbn`.

- `data`  
  A data frame containing the data used to compute the BIC. Its columns must explicitly be named after the variables (or nodes) of `object`. If `object` is a `gmm` object, a numeric matrix can be passed.

- `y`  
  A character vector containing the dependent variables if a conditional BIC is computed. If `NULL` (the default), the joint BIC is computed.

- `regul`  
  A positive numeric value corresponding to the regularization constant if a penalty term is added for Bayesian regularization. If `NULL` (the default), no penalty term is added. If a conditional BIC is computed, this argument is ignored.

- `...`  
  Unused arguments from the generic function.

- `col_seq`  
  A character vector containing the column names of `data` that describe the observation sequence. If `NULL` (the default), all the observations belong to a single sequence. If `object` is a temporal `gmbn` or `gmdbn` object, the observations of a same sequence must be ordered such that the \(t\)th one is related to time slice \(t\) (note that the sequences can have different lengths). If `object` is a non-temporal `gmbn` object, this argument is ignored.
Value

If object is a \texttt{gmm} object, a numeric value corresponding to the BIC.

If object is a \texttt{gmbn} or \texttt{gmdbn} object, a list with elements:

- **global**: A numeric value corresponding to the global BIC.
- **local**: For a \texttt{gmbn} object, a numeric vector containing the local conditional BICs. For a \texttt{gmdbn} object, a list of numeric vectors containing these values for each \texttt{gmbn} element.

See Also

\texttt{AIC}, \texttt{logLik}

Examples

```r
data(gmm_body, data_body)
bic_1 <- BIC(gmm_body, data_body)
bic_2 <- BIC(gmm_body, data_body, y = \"WAIST\")

data(gmbn_body, data_body)
bic_3 <- BIC(gmbn_body, data_body)

data(gmdbn_air, data_air)
bic_4 <- BIC(gmdbn_air, data_air, col_seq = \"DATE\")
```

---

\texttt{conditional} \textit{Conditionalize a Gaussian mixture model}

Description

This function conditionalizes a Gaussian mixture model (Sun et al., 2006).

Usage

\texttt{conditional(gmm, y = rownames(gmm$mu)[1])}

Arguments

- **gmm**: An object of class \texttt{gmm}.
- **y**: A character vector containing the dependent variables (by default the first variable of \texttt{gmm}).
Value

A list with elements:

- **alpha**: A numeric vector containing the mixture proportions.
- **mu_x**: A numeric matrix containing the marginal mean vectors of the explanatory variables bound by column.
- **sigma_x**: A list containing the marginal covariance matrices of the explanatory variables.
- **coeff**: A list containing the regression coefficient matrices of the dependent variables on the explanatory variables.
- **sigma_c**: A list containing the conditional covariance matrices.

References


Examples

```r
data(gmm_body)
cond <- conditional(gmm_body)
```

---

**data_air**

*Beijing air quality dataset*

Description

This dataset includes hourly air pollutants and weather data measured at the Dongsi air quality monitoring site in Beijing (China) for 320 complete days of the year 2015. These data are taken from the Beijing Multi-Site Air Quality Dataset published in the UCI Machine Learning Repository: [https://archive.ics.uci.edu/ml/datasets/Beijing+Multi-Site+Air+Quality+Data](https://archive.ics.uci.edu/ml/datasets/Beijing+Multi-Site+Air+Quality+Data) (Zhang et al., 2017).

Usage

```r
data_air
```

Format

A data frame (tibble) with 7680 rows and 6 columns:

- **DATE**: day’s date;
- **HOUR**: hour of the day;
- **NO2**: nitrogen dioxide concentration (µg/m³);
- **O3**: ozone concentration (µg/m³);
- **TEMP**: temperature (°C);
- **WIND**: wind speed (m/s).
References


See Also

data_body, gmbn_body, gmdbn_air, gmm_body

data_body

NHANES body composition dataset

Description

This dataset includes body composition data measured in 2148 adults aged 20 to 59 years in the United States. These data are taken from the National Health and Nutrition Examination Survey (NHANES) 2017-2018: https://wwwn.cdc.gov/nchs/nhanes/continuousnhanes/default.aspx?BeginYear=2017 (Centers for Disease Control and Prevention, 2020).

Usage

data_body

Format

A data frame (tibble) with 2148 rows and 8 columns:

- ID: respondent identifier;
- GENDER: gender (0: male, 1: female);
- AGE: age (years);
- HEIGHT: height (cm);
- WEIGHT: weight (kg);
- FAT: body fat (%);
- WAIST: waist circumference (cm);
- GLYCO: glycohemoglobin (%).

References


See Also

data_air, gmbn_body, gmdbn_air, gmm_body
**density**

Compute densities of a Gaussian mixture model

**Description**

This function computes densities of a Gaussian mixture model.

**Usage**

\[
\text{density}(\text{gmm}, \text{data}, y = \text{NULL}, \text{log} = \text{FALSE})
\]

**Arguments**

- **gmm**: An object of class gmm.
- **data**: A data frame or numeric matrix containing the observations whose densities are computed. Its columns must explicitly be named after the variables of gmm.
- **y**: A character vector containing the dependent variables if conditional densities are computed. If NULL (the default), joint densities are computed.
- **log**: A logical value indicating whether the densities are returned as log-densities.

**Value**

A numeric vector containing the (log-)densities.

**See Also**

expectation, sampling

**Examples**

```r
data(gmm_body, data_body)
dens_1 <- density(gmm_body, data_body, log = TRUE)
dens_2 <- density(gmm_body, data_body, y = "WAIST", log = TRUE)
```

**ellipses**

Display the mixture components of a Gaussian mixture model

**Description**

This function displays the mixture components of a Gaussian mixture model. For each pair of variables, the covariance matrices are represented by confidence ellipses.
Usage

```r
ellipses(
  gmm,
  data = NULL,
  y = rownames(gmm$mu),
  x = rownames(gmm$mu),
  level = 0.95
)
```

Arguments

- **gmm** An object of class `gmm`.
- **data** A data frame or numeric matrix containing the data displayed with the mixture components. Its columns must explicitly be named after the variables of `gmm`. If `NULL` (the default), no data is displayed.
- **y** A character vector containing the variables displayed on the y-axis (by default all the variables of `gmm`).
- **x** A character vector containing the variables displayed on the x-axis (by default all the variables of `gmm`).
- **level** A numeric value in [0, 1] corresponding to the confidence level of the ellipses.

Value

A `ggplot` object displaying the mixture components (and the data if required).

Examples

```r
set.seed(0)
data(gmm_body)
ellipses(gmm_body, sampling(gmm_body, n = 500))
```

---

**em**

Estimate the parameters of a Gaussian mixture model

Description

This function estimates the parameters of a Gaussian mixture model using the expectation-maximization (EM) algorithm. Given an initial model, this algorithm iteratively updates the parameters, monotonically increasing the log-likelihood until convergence to a local maximum (Bilmes, 1998). A Bayesian regularization is applied by default to prevent that a mixture component comes down to a single point and leads to a zero covariance matrix (Ordonez and Tresp, 1996). Although the EM algorithm only applies to the joint model, good parameters can be found for a derived conditional model. However, care should be taken as the monotonic increase of the conditional log-likelihood is not guaranteed.
em

Usage

em(
  gmm,
  data,
  regul = 0.01,
  epsilon = 1e-06,
  max_iter_em = 100,
  verbose = FALSE
)

Arguments

  gmm  An initial object of class gmm.
  data  A data frame or numeric matrix containing the data used in the EM algorithm. Its columns must explicitly be named after the variables of gmm and must not contain missing values.
  regul  A positive numeric value corresponding to the regularization constant if a Bayesian regularization is applied. If NULL, no regularization is applied.
  epsilon  A positive numeric value corresponding to the convergence threshold for the increase in log-likelihood.
  max_iter_em  A non-negative integer corresponding to the maximum number of iterations.
  verbose  A logical value indicating whether iterations in progress are displayed.

Value

A list with elements:

  gmm  The final gmm object.
  posterior  A numeric matrix containing the posterior probabilities for each observation.
  seq_loglik  A numeric vector containing the sequence of log-likelihoods measured initially and after each iteration.

References


See Also

  smem, stepwise
Examples

data(data_body)
gmm_1 <- split_comp(add_var(NULL,
    data_body[, c("WAIST", "AGE", "FAT", "HEIGHT",
    "WEIGHT")]),
    n_sub = 3)
res_em <- em(gmm_1, data_body, verbose = TRUE)

elementation

Description

This function computes expectations of a Gaussian mixture model.

Usage

expectation(gmm, data_x = NULL)

Arguments

gmm | An object of class gmm.

data_x | A data frame or numeric matrix containing observations of the explanatory variables if conditional expectations are computed. Its columns must explicitly be named after the explanatory variables. If NULL (the default), the joint expectation is computed in a one-row matrix.

Value

A numeric matrix containing the expectations.

See Also

density, sampling

Examples

data(gmm_body, data_body)
expect_1 <- expectation(gmm_body)
expect_2 <- expectation(gmm_body,
    data_body[, c("WEIGHT", "FAT", "HEIGHT", "AGE")])
**filtering**

*Perform filtering inference in a Gaussian mixture dynamic Bayesian network*

**Description**

This function performs filtering inference in a Gaussian mixture dynamic Bayesian network. For a sequence of \( T \) time slices, this task consists in estimating the state of the system at each time slice \( t \) (for \( 1 \leq t \leq T \)) given all the data (the evidence) collected up to \( t \). This function is also designed to perform fixed-lag smoothing inference, which consists in defining a time lag \( l \) such that at each time slice \( t \) (for \( l + 1 \leq t \leq T \)), the state at \( t - l \) is estimated given the evidence collected up to \( t \) (Murphy, 2002). Filtering and fixed-lag smoothing inference are performed by sequential importance resampling, which is a particle-based approximate method (Koller and Friedman, 2009).

**Usage**

```r
filtering(
  gmdbn,
  evid,
  nodes = names(gmdbn$b_1),
  col_seq = NULL,
  lag = 0,
  n_part = 1000,
  max_part_sim = 1e+06,
  min_ess = 1,
  verbose = FALSE
)
```

**Arguments**

- `gmdbn`: An object of class gmdbn.
- `evid`: A data frame containing the evidence. Its columns must explicitly be named after nodes of gmdbn and can contain missing values (columns with no value can be removed).
- `nodes`: A character vector containing the inferred nodes (by default all the nodes of gmdbn).
- `col_seq`: A character vector containing the column names of evid that describe the observation sequence. If NULL (the default), all the observations belong to a single sequence. The observations of a same sequence must be ordered such that the \( t \)th one is related to time slice \( t \) (note that the sequences can have different lengths).
- `lag`: A non-negative integer vector containing the time lags for which fixed-lag smoothing inference is performed. If 0 (the default), filtering inference is performed.
- `n_part`: A positive integer corresponding to the number of particles generated for each observation sequence.
max_part_sim  An integer greater than or equal to n_part corresponding to the maximum number of particles that can be processed simultaneously. This argument is used to prevent memory overflow, dividing evid into smaller subsets that are handled sequentially.

min_ess  A numeric value in [0, 1] corresponding to the minimum ESS (expressed as a proportion of n_part) under which the renewal step of sequential importance resampling is performed. If 1 (the default), this step is performed at each time slice.

verbose  A logical value indicating whether subsets of evid and time slices in progress are displayed.

Value

If lag has one element, a data frame (tibble) with a structure similar to evid containing the estimated values of the inferred nodes and their observation sequences (if col_seq is not NULL). If lag has two or more elements, a list of data frames (tibbles) containing these values for each time lag.

References


See Also

inference, prediction, smoothing

Examples

set.seed(0)
data(gmdbn_air, data_air)
evid <- data_air
evid$NO2[sample.int(7680, 1536)] <- NA
evid$SO3[sample.int(7680, 1536)] <- NA
evid$TEMP[sample.int(7680, 1536)] <- NA
evid$WIND[sample.int(7680, 1536)] <- NA
filt <- filtering(gmdbn_air, evid, col_seq = "DATE", lag = c(0, 1), verbose = TRUE)
**gmbn**

Create a Gaussian mixture Bayesian network

**Description**

This function creates a Gaussian mixture Bayesian network as an object of S3 class gmbn. A Bayesian network is a probabilistic graphical model that represents the conditional dependencies and independencies between random variables by a directed acyclic graph. It encodes a global joint distribution over the nodes, which decomposes into a product of local conditional distributions:

\[
p(X_1, \ldots, X_n) = \prod_{i=1}^{n} p(X_i|Pa(X_i))
\]

where \( Pa(X_i) \) is the set of parents of \( X_i \) in the graph. In a Gaussian mixture Bayesian network, each local joint distribution over a node and its parents is described by a Gaussian mixture model, which means that the global distribution is a product of local conditional Gaussian mixture models (Davies and Moore, 2000). The gmbn class can be extended to the time factor by regarding the nodes as the state of the system at a given time slice \( t \) (denoted by \( X^{(t)} \)) and allowing them to have parents at previous time slices. This makes it possible to create a \((k+1)\)-slice temporal Bayesian network that encodes the transition distribution \( p(X^{(t)}|X^{(t-1)}, \ldots, X^{(t-k)}) \) (Hulst, 2006). Finally, note that a Gaussian mixture Bayesian network can be created with functions add_nodes (by passing NULL as argument gmm) and add_arcs, which allows to quickly initialize a gmbn object that can be passed to a learning function.

**Usage**

\[ gmbn(\ldots) \]

**Arguments**

\[ \ldots \]

Objects of class gmm describing the local joint distributions over the nodes and their parents. Each gmm object must be named after the node whose distribution it describes and contain variables named after this node and its parents. Two types of parents are accepted: other nodes (whose gmm objects must be defined) and instantiations of nodes at previous time slices (if the created gmbn object is a temporal Bayesian network). In the second case, the time lag must be added at the end of the variable name after a period . (e.g. the instantiation of a node \( X \) at time slice \( t-1 \) is represented by the variable \( X.1 \)).

**Value**

A list of class gmbn containing the gmm objects passed as arguments.

**References**


**See Also**

`gmdbn`, `gmm`

**Examples**

```r
data(data_body)
gmbn_1 <- gmbn(
  AGE = split_comp(add_var(NULL, data_body[, "AGE"]), n_sub = 3),
  FAT = split_comp(add_var(NULL,
    data_body[, c("FAT", "GENDER", "HEIGHT", "WEIGHT")]),
    n_sub = 2),
  GENDER = split_comp(add_var(NULL, data_body[, "GENDER"]), n_sub = 2),
  GLYCO = split_comp(add_var(NULL, data_body[, c("GLYCO", "AGE", "WAIST")]),
    n_sub = 2),
  HEIGHT = split_comp(add_var(NULL, data_body[, c("HEIGHT", "GENDER")]),
  WAIST = split_comp(add_var(NULL,
    data_body[, c("WAIST", "AGE", "FAT", "HEIGHT",
      "WEIGHT")]),
    n_sub = 3),
  WEIGHT = split_comp(add_var(NULL, data_body[, c("WEIGHT", "HEIGHT")]),
    n_sub = 2)
)

library(dplyr)
data(data_air)
data <- data_air %>%
group_by(DATE) %>%
  mutate(NO2.1 = lag(NO2), O3.1 = lag(O3), TEMP.1 = lag(TEMP),
    WIND.1 = lag(WIND)) %>%
  ungroup()
gmbn_2 <- gmbn(
  NO2 = split_comp(add_var(NULL, data[, c("NO2", "NO2.1", "WIND")]), n_sub = 3),
  O3 = split_comp(add_var(NULL,
    data[, c("O3", "NO2", "NO2.1", "O3.1", "TEMP",
      "TEMP.1")]),
    n_sub = 3),
  TEMP = split_comp(add_var(NULL, data[, c("TEMP", "TEMP.1")]), n_sub = 3),
  WIND = split_comp(add_var(NULL, data[, c("WIND", "WIND.1")]), n_sub = 3)
)
```

---

Gaussian mixture Bayesian network learned from the NHANES body composition dataset
Description

This Gaussian mixture dynamic Bayesian network is learned from the NHANES body composition dataset, following the example provided in the documentation page of function `struct_learn`.

Usage

`gmdbn_body`

Format

A `gmdbn` object.

See Also

`data_air`, `data_body`, `gmdbn_air`, `gmm_body`

---

`gmdbn`  
Create a Gaussian mixture dynamic Bayesian network

Description

This function creates a Gaussian mixture dynamic Bayesian network as an object of S3 class `gmdbn`. Assuming that the system evolves over time (possibly non-stationary) and denoting by $X^{(t)}$ its state at time slice $t$, a dynamic Bayesian network is a probabilistic graphical model that encodes the joint distribution over any finite time sequence:

$$p(X^{(1)}, \ldots, X^{(T)}) = p(X^{(1)}) \prod_{t=2}^{T} p(X^{(t)}|X^{(t-1)}, \ldots, X^{(1)})$$

It is defined by a sequence of transition models $B_1, B_2, \ldots, B_N$ associated with transition time slices $t_1 < t_2 < \ldots < t_N$, where:

- $B_1$ is a Bayesian network that encodes the distribution $p(X^{(t)})$ for $1 \leq t \leq t_2 - 1$, assuming that the states at these time slices do not depend on previous states;
- for each $i \geq 2$, $B_i$ is a $(k_i + 1)$-slice temporal Bayesian network (where $k_i < t_i$) that encodes the transition distribution $p(X^{(t)}|X^{(t-1)}, \ldots, X^{(t-k_i)})$ for $t_i \leq t \leq t_{i+1} - 1$ (or $t \geq t_i$ if $i = N$), assuming that the states at these time slices only depend on the $k_i$ previous states (Hourbracq et al., 2017).

In a Gaussian mixture dynamic Bayesian network, these transition models are Gaussian mixture Bayesian networks (Roos et al., 2017).

Usage

`gmdbn(...)`
Arguments

Objects of class gmbn corresponding to the transition models. Each gmbn object must be named with the prefix b_ followed by its associated transition time slice (e.g. a transition model whose transition time slice is 8 is represented by the gmbn object b_8). If the first gmbn object (chronologically) is associated with a transition time slice $t \geq 2$ (i.e. b_1 is not specified), it is duplicated to create transition models associated with 1, ..., $t - 1$ (removing the arcs whose time lags exceed the maximum temporal depths of these models).

Value

A list of class gmbn containing the gmbn objects passed as arguments.

References


See Also

- gmbn, gmm

Examples

```r
library(dplyr)
data(data_air)
data <- data_air %>%
group_by(DATE) %>%
mutate(NO2.1 = lag(NO2), O3.1 = lag(O3), TEMP.1 = lag(TEMP),
      WIND.1 = lag(WIND)) %>%
ungroup()
gmdbn_1 <- gmdbn(
  b_2 = gmbn(
    NO2 = split_comp(add_var(NULL, data[, c("NO2", "NO2.1", "WIND")]),
              n_sub = 3),
    O3 = split_comp(add_var(NULL, data[, c("O3", "NO2", "NO2.1", "O3.1", "TEMP",
                 "TEMP.1")]),
              n_sub = 3),
    TEMP = split_comp(add_var(NULL, data[, c("TEMP", "TEMP.1")]), n_sub = 3),
    WIND = split_comp(add_var(NULL, data[, c("WIND", "WIND.1")]), n_sub = 3)
  ),
  b_13 = gmbn(
    NO2 = split_comp(add_var(NULL, data[, c("NO2", "NO2.1", "WIND")]),
                   n_sub = 3),
    O3 = split_comp(add_var(NULL, data[, c("O3", "NO2", "NO2.1", "O3.1", "TEMP",
                   "TEMP.1")]),
                   n_sub = 3)
  ),
  b_14 = gmbn(
    NO2 = split_comp(add_var(NULL, data[, c("NO2", "NO2.1", "WIND")]),
                   n_sub = 3)
  )
```
gmdbn_air

```r
data[, c("O3", "O3.1", "TEMP", "TEMP.1", "WIND")],
n_sub = 3),
TEMP = split_comp(add_var(NULL, data[, c("TEMP", "TEMP.1")]), n_sub = 3),
WIND = split_comp(add_var(NULL, data[, c("WIND", "WIND.1")]), n_sub = 3)
)
```

---

**gmdbn_air**

*Gaussian mixture dynamic Bayesian network learned from the Beijing air quality dataset*

**Description**

This Gaussian mixture dynamic Bayesian network is learned from the Beijing air quality dataset, following the example provided in the documentation page of function `struct_learn`.

**Usage**

`gmdbn_air`

**Format**

A `gmdbn` object.

**See Also**

`data_air`, `data_body`, `gmbn_body`, `gmm_body`

---

**gmm**

*Create a Gaussian mixture model*

**Description**

This function creates a Gaussian mixture model as an object of S3 class `gmm`. A Gaussian mixture model is a weighted sum of multivariate Gaussian distributions:

\[ p(x) = \sum_{i=1}^{M} \alpha_i \mathcal{N}(x | \mu_i, \Sigma_i) \]

where \( \alpha_i \) is the \( i \)th mixture proportion such that \( \alpha_i > 0 \) and \( \sum_{i=1}^{M} \alpha_i = 1 \), \( \mu_i \) the mean vector and \( \Sigma_i \) the covariance matrix of the \( i \)th mixture component (Bilmes, 1998). Since conditional distributions can be derived from joint distributions, the `gmm` class is also used to work with conditional Gaussian mixture models (see function `conditional` to explicit their parameters). Finally, note that a one-component Gaussian mixture model can be created with function `add_var` (by passing `NULL` as argument `gmm`), which allows to quickly initialize a `gmm` object that can be passed to a learning function.
Usage

gmm(alpha, mu, sigma, var = rownames(mu))

Arguments

alpha  A positive numeric vector containing the mixture proportions. If the sum of these proportions is not 1, a normalization is performed by dividing them by this sum.
mu     A numeric matrix containing the mean vectors bound by column.
sigma  A list containing the covariance matrices.
var    A character vector containing the variable names (by default the row names of mu).

Value

A list of class gmm containing the elements alpha, mu and sigma passed as arguments (completed with the variable names passed as argument var).

References


See Also

gmbn, gmdbn

Examples

gmm_1 <- gmm(alpha = c(0.2, 0.5, 0.3),
             mu = matrix(c(109, 91, 44, 160, 41, 99, 87, 27, 173, 40, 86, 65,
                           35, 161, 40),
                         nrow = 5),
             sigma = list(matrix(c(208, 240, 32, 17, -6, 240, 378, 40, 55, -38,
                                     32, 40, 15, -2, 1, 17, 55, -2, -13, -6,
                                     -38, 1, -13, 127),
                                  nrow = 5),
                         matrix(c(242, 270, 82, 10, 49, 270, 363, 83, 44, 19,
                                     82, 83, 38, -2, 15, 10, 44, -2, 45, -7, 49,
                                     19, 15, -7, 137),
                                  nrow = 5),
                         matrix(c(109, 102, 41, 11, 29, 102, 128, 34, 38, 10,
                                     41, 34, 36, -9, 16, 11, 38, -9, 56, -5, 29,
                                     10, 16, -5, 138),
                                  nrow = 5)),
             var = c("WAIST", "WEIGHT", "FAT", "HEIGHT", "AGE"))
This Gaussian mixture model is learned from the NHANES body composition dataset, following the example provided in the documentation page of function `stepwise`.

Usage

```r
gmm_body
```

Format

A `gmm` object.

See Also

`data_air, data_body, gmbn_body, gmdbn_air`

This function performs inference in a (non-temporal) Gaussian mixture Bayesian network. This task consists in estimating the state of the system given partial observations of it (the evidence). Inference is performed by likelihood weighting, which is a particle-based approximate method (Koller and Friedman, 2009).

Usage

```r
inference(
  gmbn,
  evid,
  nodes = names(gmbn),
  n_part = 1000,
  max_part_sim = 1e+06,
  verbose = FALSE
)
```
**Arguments**

- **gmbn**: A (non-temporal) object of class `gmbn`.
- **evid**: A data frame containing the evidence. Its columns must explicitly be named after nodes of `gmbn` and can contain missing values (columns with no value can be removed).
- **nodes**: A character vector containing the inferred nodes (by default all the nodes of `gmbn`).
- **n_part**: A positive integer corresponding to the number of particles generated for each observation.
- **max_part_sim**: An integer greater than or equal to `n_part` corresponding to the maximum number of particles that can be processed simultaneously. This argument is used to prevent memory overflow, dividing `evid` into smaller subsets that are handled sequentially.
- **verbose**: A logical value indicating whether subsets of `evid` in progress are displayed.

**Value**

A data frame (tibble) with a structure similar to `evid` containing the estimated values of the inferred nodes.

**References**


**See Also**

`filtering`, `prediction`, `smoothing`

**Examples**

```r
set.seed(0)
data(gmbn_body, data_body)
evid <- data_body
evid$GENDER[sample.int(2148, 430)] <- NA
evid$AGE[sample.int(2148, 430)] <- NA
evid$HEIGHT[sample.int(2148, 430)] <- NA
evid$WEIGHT[sample.int(2148, 430)] <- NA
evid$FAT[sample.int(2148, 430)] <- NA
evid$WAIST[sample.int(2148, 430)] <- NA
evid$GLYCO[sample.int(2148, 430)] <- NA
evid$GLYCO[sample.int(2148, 430)] <- NA
infer <- inference(gmbn_body, evid, verbose = TRUE)
```
**logLik**

*Compute the log-likelihood of a Gaussian mixture model or graphical model*

**Description**

This function computes the log-likelihood of a Gaussian mixture model or graphical model.

**Usage**

```r
## S3 method for class 'gmm'
logLik(object, data, y = NULL, regul = 0.01, ...)

## S3 method for class 'gmbn'
logLik(object, data, col_seq = NULL, ...)

## S3 method for class 'gmdbn'
logLik(object, data, col_seq = NULL, ...)
```

**Arguments**

- `object`: An object of class `gmm`, `gmbn` or `gmdbn`.
- `data`: A data frame containing the data used to compute the log-likelihood. Its columns must explicitly be named after the variables (or nodes) of `object`. If `object` is a `gmm` object, a numeric matrix can be passed.
- `y`: A character vector containing the dependent variables if a conditional log-likelihood is computed. If `NULL` (the default), the joint log-likelihood is computed.
- `regul`: A positive numeric value corresponding to the regularization constant if a penalty term is added for Bayesian regularization. If `NULL`, no penalty term is added. If a conditional log-likelihood is computed, this argument is ignored.
- `...`: Unused arguments from the generic function.
- `col_seq`: A character vector containing the column names of `data` that describe the observation sequence. If `NULL` (the default), all the observations belong to a single sequence. If `object` is a temporal `gmbn` or `gmdbn` object, the observations of a same sequence must be ordered such that the t^th one is related to time slice t (note that the sequences can have different lengths). If `object` is a non-temporal `gmbn` object, this argument is ignored.

**Value**

- If `object` is a `gmm` object, a numeric value corresponding to the log-likelihood.
- If `object` is a `gmbn` or `gmdbn` object, a list with elements:
  - `global`: A numeric value corresponding to the global log-likelihood.
  - `local`: For a `gmbn` object, a numeric vector containing the local conditional log-likelihoods.
    - For a `gmdbn` object, a list of numeric vectors containing these values for each `gmbn` element.
merge_comp

See Also

AIC, BIC

Examples

data(gmm_body, data_body)
loglik_1 <- logLik(gmm_body, data_body)
loglik_2 <- logLik(gmm_body, data_body, y = "WAIST")
data(gmbn_body, data_body)
loglik_3 <- logLik(gmbn_body, data_body)
data(gmdbn_air, data_air)
loglik_4 <- logLik(gmdbn_air, data_air, col_seq = "DATE")

merge_comp

Merge mixture components of a Gaussian mixture model

Description

This function merges mixture components of a Gaussian mixture model (Zhang et al., 2003).

Usage

merge_comp(gmm, comp = seq_along(gmm$alpha))

Arguments

gmm An object of class gmm.
comp An integer vector containing the indexes of the merged mixture components (by
default all the components of gmm).

Value

The gmm object after merging the mixture components.

References


See Also

split_comp
network

Examples

```r
data(gmm_body)
gmm_1 <- merge_comp(gmm_body, c(1, 2))
```

network

Display the graphical structure of a Gaussian mixture Bayesian network.

Description

This function displays the graphical structure of a Gaussian mixture Bayesian network.

Usage

```r
network(gmbn)
```

Arguments

- `gmbn` An object of class gmbn.

Value

A visNetwork object displaying the graphical structure.

Examples

```r
data(gmbn_body)
network(gmbn_body)

data(gmdbn_air)
network(gmdbn_air$b_2)
```

param_em

Learn the parameters of a Gaussian mixture graphical model with incomplete data

Description

This function learns the parameters of a Gaussian mixture graphical model with incomplete data using the parametric EM algorithm. At each iteration, inference (smoothing inference for a dynamic Bayesian network) is performed to complete the data given the current estimate of the parameters (E step). The completed data are then used to update the parameters (M step), and so on. Each iteration is guaranteed to increase the log-likelihood until convergence to a local maximum (Koller and Friedman, 2009). In practice, due to the sampling process inherent in particle-based inference, it may happen that the monotonic increase no longer occurs when approaching the local maximum, resulting in an earlier termination of the algorithm.
Usage

```r
param_em(
  gmgm,
  data,
  nodes = structure(gmgm)$nodes,
  col_seq = NULL,
  n_part = 1000,
  max_part_sim = 1e+06,
  min_ess = 1,
  max_iter_pem = 5,
  verbose = FALSE,
  ...
)
```

Arguments

- `gmgm` An object of class `gmbn` (non-temporal) or `gmdbn`.
- `data` A data frame containing the data used for learning. Its columns must explicitly be named after nodes of `gmgm` and can contain missing values (columns with no value can be removed).
- `nodes` A character vector containing the nodes whose local conditional models are learned (by default all the nodes of `gmgm`). If `gmgm` is a `gmdbn` object, the same nodes are learned for each of its `gmbn` elements. This constraint can be overcome by passing a list of character vectors named after some of these elements (`b_1`, …) and containing learned nodes specific to them.
- `col_seq` A character vector containing the column names of `data` that describe the observation sequence. If `NULL` (the default), all the observations belong to a single sequence. If `gmgm` is a `gmdbn` object, the observations of a same sequence must be ordered such that the `t`th one is related to time slice `t` (note that the sequences can have different lengths). If `gmgm` is a `gmbn` object, this argument is ignored.
- `n_part` A positive integer corresponding to the number of particles generated for each observation (if `gmgm` is a `gmdbn` object) or observation sequence (if `gmgm` is a `gmdbn` object) during inference.
- `max_part_sim` An integer greater than or equal to `n_part` corresponding to the maximum number of particles that can be processed simultaneously during inference. This argument is used to prevent memory overflow, dividing `data` into smaller subsets that are handle sequentially.
- `min_ess` A numeric value in [0, 1] corresponding to the minimum ESS (expressed as a proportion of `n_part`) under which the renewal step of sequential importance resampling is performed. If 1 (the default), this step is performed at each time slice. If `gmgm` is a `gmbn` object, this argument is ignored.
- `max_iter_pem` A non-negative integer corresponding to the maximum number of iterations.
- `verbose` A logical value indicating whether iterations in progress are displayed.
- `...` Additional arguments passed to function `em`. 
Value

A list with elements:

gmbn
The final gmbn or gmdbn object (with the highest log-likelihood).
data
A data frame (tibble) containing the complete data used to learn the final gmbn or gmdbn object.
seq_loglik
A numeric matrix containing the sequence of log-likelihoods measured after the E and M steps of each iteration.

References


See Also

param_learn, struct_em, struct_learn

Examples

```r
set.seed(0)
data(data_body)
data_1 <- data_body
data_1$GENDER[sample.int(2148, 430)] <- NA
data_1$AGE[sample.int(2148, 430)] <- NA
data_1$HEIGHT[sample.int(2148, 430)] <- NA
data_1$WEIGHT[sample.int(2148, 430)] <- NA
data_1$FAT[sample.int(2148, 430)] <- NA
data_1$WAIST[sample.int(2148, 430)] <- NA
data_1$GLYCO[sample.int(2148, 430)] <- NA
gmbn_1 <- gmbn(
  AGE = split_comp(add_var(NULL, data_1[, "AGE"], n_sub = 3),
  FAT = split_comp(add_var(NULL,
    data_1[, c("FAT", "GENDER", "HEIGHT", "WEIGHT")],
    n_sub = 2),
  GENDER = split_comp(add_var(NULL, data_1[, "GENDER"], n_sub = 2),
  GLYCO = split_comp(add_var(NULL, data_1[, c("GLYCO", "AGE", "WAIST")],
    n_sub = 2),
  HEIGHT = split_comp(add_var(NULL, data_1[, c("HEIGHT", "GENDER")]),
  WAIST = split_comp(add_var(NULL,
    data_1[, c("WAIST", "AGE", "FAT", "HEIGHT",
    "WEIGHT")],
    n_sub = 3),
  WEIGHT = split_comp(add_var(NULL, data_1[, c("WEIGHT", "HEIGHT")], n_sub = 2))
)
res_learn_1 <- param_em(gmbn_1, data_1, verbose = TRUE)
library(dplyr)
set.seed(0)
data(data_air)
```
data_2 <- data_air
data_2$NO2[sample.int(7680, 1536)] <- NA
data_2$O3[sample.int(7680, 1536)] <- NA
data_2$TEMP[sample.int(7680, 1536)] <- NA
data_2$WIND[sample.int(7680, 1536)] <- NA
data_3 <- data_2 %>%
group_by(DATE) %>%
mutate(NO2.1 = lag(NO2), O3.1 = lag(O3), TEMP.1 = lag(TEMP),
       WIND.1 = lag(WIND)) %>%
ungroup()
gmdbn_1 <- gmdbn(
  b_2 = gmbn(
    NO2 = split_comp(add_var(NULL, data_3[, c("NO2", "NO2.1", "WIND")]),
      n_sub = 3),
    O3 = split_comp(add_var(NULL, data_3[, c("O3", "NO2", "NO2.1", "O3.1", "TEMP",
                                                         "TEMP.1")]),
      n_sub = 3),
    TEMP = split_comp(add_var(NULL, data_3[, c("TEMP", "TEMP.1")]), n_sub = 3),
    WIND = split_comp(add_var(NULL, data_3[, c("WIND", "WIND.1")]), n_sub = 3)
  ),
  b_13 = gmbn(
    NO2 = split_comp(add_var(NULL, data_3[, c("NO2", "NO2.1", "WIND")]),
      n_sub = 3),
    O3 = split_comp(add_var(NULL, data_3[, c("O3", "O3.1", "TEMP", "TEMP.1",
                                                     "WIND")]),
      n_sub = 3),
    TEMP = split_comp(add_var(NULL, data_3[, c("TEMP", "TEMP.1")]), n_sub = 3),
    WIND = split_comp(add_var(NULL, data_3[, c("WIND", "WIND.1")]), n_sub = 3)
  )
)
res_learn_2 <- param_em(gmdbn_1, data_2, col_seq = "DATE", verbose = TRUE)

---

**param_learn**

*Learn the parameters of a Gaussian mixture graphical model*

**Description**

This function learns the parameters of a Gaussian mixture graphical model. Using the local decomposability of the log-likelihood, this task consists in learning each local conditional model independently with the EM algorithm (Koller and Friedman, 2009).

**Usage**

```r
param_learn(
  gmgm,
  data,
  nodes = structure(gmgm)$nodes,
)```

Arguments

- `gmgm`: An initial object of class `gmbn` or `gmdbn`.
- `data`: A data frame containing the data used for learning. Its columns must explicitly be named after the nodes of `gmgm` and must not contain missing values.
- `nodes`: A character vector containing the nodes whose local conditional models are learned (by default all the nodes of `gmgm`). If `gmgm` is a `gmdbn` object, the same nodes are learned for each of its `gmbn` elements. This constraint can be overcome by passing a list of character vectors named after some of these elements (b_1, ...) and containing learned nodes specific to them.
- `col_seq`: A character vector containing the column names of `data` that describe the observation sequence. If NULL (the default), all the observations belong to a single sequence. If `gmgm` is a temporal `gmbn` or `gmdbn` object, the observations of a same sequence must be ordered such that the tth one is related to time slice t (note that the sequences can have different lengths). If `gmgm` is a non-temporal `gmbn` object, this argument is ignored.
- `verbose`: A logical value indicating whether learned nodes in progress are displayed.
- `...`: Additional arguments passed to function `em`.

Value

A list with elements:

- `gmgm`: The final `gmbn` or `gmdbn` object.
- `evol_loglik`: A list with elements:
  - `global`: A numeric vector containing the global log-likelihood before and after learning.
  - `local`: For a `gmbn` object, a numeric matrix containing the local conditional log-likelihoods before and after learning. For a `gmdbn` object, a list of numeric matrices containing these values for each `gmbn` element.

References


See Also

`param_em`, `struct_em`, `struct_learn`
Examples

data(data_body)
gmbn_1 <- gmbn(
    AGE = split_comp(add_var(NULL, data_body[, "AGE"]), n_sub = 3),
    FAT = split_comp(add_var(NULL,
        data_body[, c("FAT", "GENDER", "HEIGHT", "WEIGHT")]),
        n_sub = 2),
    GENDER = split_comp(add_var(NULL, data_body[, "GENDER"], n_sub = 2),
    GLYCO = split_comp(add_var(NULL, data_body[, c("GLYCO", "AGE", "WAIST")]),
        n_sub = 2),
    HEIGHT = split_comp(add_var(NULL, data_body[, c("HEIGHT", "GENDER")]),
    WAIST = split_comp(add_var(NULL,
        data_body[, c("WAIST", "AGE", "FAT", "HEIGHT", "WEIGHT")]),
        n_sub = 3),
    WEIGHT = split_comp(add_var(NULL, data_body[, c("WEIGHT", "HEIGHT")]),
        n_sub = 2)
)
res_learn_1 <- param_learn(gmbn_1, data_body, verbose = TRUE)

library(dplyr)
data(data_air)
data <- data_air %>%
    group_by(DATE) %>%
    mutate(NO2.1 = lag(NO2), O3.1 = lag(O3), TEMP.1 = lag(TEMP),
    WIND.1 = lag(WIND)) %>%
    ungroup()
gmdbn_1 <- gmdbn(
    b_2 = gmbn(
        NO2 = split_comp(add_var(NULL, data[, c("NO2", "NO2.1", "WIND")]),
            n_sub = 3),
        O3 = split_comp(add_var(NULL,
            data[, c("O3", "NO2", "NO2.1", "O3.1", "TEMP", "TEMP.1")]),
            n_sub = 3),
        TEMP = split_comp(add_var(NULL, data[, c("TEMP", "TEMP.1")]), n_sub = 3),
        WIND = split_comp(add_var(NULL, data[, c("WIND", "WIND.1")]), n_sub = 3)
    ),
    b_13 = gmbn(
        NO2 = split_comp(add_var(NULL, data[, c("NO2", "NO2.1", "WIND")]),
            n_sub = 3),
        O3 = split_comp(add_var(NULL,
            data[, c("O3", "O3.1", "TEMP", "TEMP.1", "WIND")]),
            n_sub = 3),
        TEMP = split_comp(add_var(NULL, data[, c("TEMP", "TEMP.1")]), n_sub = 3),
        WIND = split_comp(add_var(NULL, data[, c("WIND", "WIND.1")]), n_sub = 3)
    )
)
res_learn_2 <- param_learn(gmdbn_1, data_air, col_seq = "DATE", verbose = TRUE)
**particles**

*Initialize particles to perform inference in a Gaussian mixture graphical model*

---

**Description**

This function initializes particles to perform (approximate) inference in a Gaussian mixture graphical model. Particles consist in weighted sample sequences propagated forward in time by sampling the model and aggregated to obtain the inferred values (Koller and Friedman, 2009).

**Usage**

```r
particles(seq = NULL, col_weight = "weight", n_part = 1000)
```

**Arguments**

- `seq`: A data frame containing the observation sequences for which particles are initialized. If `NULL` (the default), the initialization is performed for a single sequence.
- `col_weight`: A character string corresponding to the column name of the resulting data frame that describes the particle weight.
- `n_part`: A positive integer corresponding to the number of particles initialized for each observation sequence.

**Value**

A data frame (tibble) containing the initial particles.

**References**


**See Also**

`aggregation`, `propagation`

**Examples**

```r
data(data_air)
part <- particles(data.frame(DATE = unique(data_air$DATE)))
```
**prediction**

*Perform predictive inference in a Gaussian mixture dynamic Bayesian network*

**Description**

This function performs predictive inference in a Gaussian mixture dynamic Bayesian network. For a sequence of \( T \) time slices, this task consists in defining a time horizon \( h \) such that at each time slice \( t \) (for \( 0 \leq t \leq T - h \)), the state of the system at \( t + h \) is estimated given all the data (the evidence) collected up to \( t \). Although the states at \( t + 1, \ldots, t + h \) are observed in the future, some information about them can be known a priori (such as contextual information or features controlled by the user). This "predicted" evidence can be taken into account when propagating the particles from \( t \) to \( t + h \) in order to improve the predictions. Predictive inference is performed by sequential importance resampling, which is a particle-based approximate method (Koller and Friedman, 2009).

**Usage**

```r
prediction(
  gmdbn,     # An object of class gmdbn.
  evid,      # A data frame containing the evidence. Its columns must explicitly be named
  evid_pred = NULL, # after nodes of gmdbn and can contain missing values (columns with no value
  nodes = names(gmdbn$b_1), # can be removed).
  col_seq = NULL,       # A data frame containing the "predicted" evidence. Its columns must explicitly
  horizon = 1,         # be named after nodes of gmdbn and can contain missing values (columns with
  n_part = 1000,       # no value can be removed).
  max_part_sim = 1e+06, # A character vector containing the inferred nodes (by default all the nodes of
  min_ess = 1,         # gmdbn).
  verbose = FALSE      # A character vector containing the column names of evid and evid_pred that
)                   # describe the observation sequence. If NULL (the default), all the observations
```  

**Arguments**

- **gmdbn**: An object of class `gmdbn`.
- **evid**: A data frame containing the evidence. Its columns must explicitly be named after nodes of `gmdbn` and can contain missing values (columns with no value can be removed).
- **evid_pred**: A data frame containing the "predicted" evidence. Its columns must explicitly be named after nodes of `gmdbn` and can contain missing values (columns with no value can be removed).
- **nodes**: A character vector containing the inferred nodes (by default all the nodes of `gmdbn`).
- **col_seq**: A character vector containing the column names of `evid` and `evid_pred` that describe the observation sequence. If `NULL` (the default), all the observations belong to a single sequence. The observations of a same sequence must be ordered such that the \( t \)th one is related to time slice \( t \) (note that the sequences can have different lengths).
horizon A positive integer vector containing the time horizons for which predictive inference is performed.
n_part A positive integer corresponding to the number of particles generated for each observation sequence.
max_part_sim An integer greater than or equal to n_part corresponding to the maximum number of particles that can be processed simultaneously. This argument is used to prevent memory overflow, dividing evid into smaller subsets that are handled sequentially.
min_ess A numeric value in [0, 1] corresponding to the minimum ESS (expressed as a proportion of n_part) under which the renewal step of sequential importance resampling is performed. If 1 (the default), this step is performed at each time slice.
verbose A logical value indicating whether subsets of evid and time slices in progress are displayed.

Value

If horizon has one element, a data frame with a structure similar to evid containing the predicted values of the inferred nodes and their observation sequences (if col_seq is not NULL). If horizon has two or more elements, a list of data frames (tibbles) containing these values for each time horizon.

References


See Also

filtering, inference, smoothing

Examples

```r
set.seed(0)
data(gmdbn_air, data_air)
evid <- data_air
evid$NO2[sample.int(7680, 1536)] <- NA
evid$O3[sample.int(7680, 1536)] <- NA
pred <- prediction(gmdbn_air, evid, evid[, c("DATE", "TEMP", "WIND")],
nodes = c("NO2", "O3"), col_seq = "DATE",
horizon = c(1, 2), verbose = TRUE)
```
propagation

Propagate particles forward in time

Description

This function propagates particles forward in time. Assuming that the particles have been propagated to a given time slice $t$, the aim is to propagate them to a later time slice $t + k$ according to the Gaussian mixture graphical model and to the evidence collected over time. At first, a renewal step is performed if the effective sample size (ESS) is below a given threshold (Doucet and Johansen, 2009). This step consists in randomly selecting new particles among the old ones proportionately to their current weights. Upon receiving the data (the evidence) of $t + 1$, each particle is used to generate samples for the unknown values. Its weight is then updated to the likelihood for the observed values. The higher this likelihood, the more likely the particle is selected at the next renewal step for propagation to $t + 2$, and so on (Koller and Friedman, 2009).

Usage

```r
propagation(
  part,  # A data frame containing the particles propagated to time slice $t$, as obtained from function particles or propagation.
  gmgm,  # An object of class gmbn or gmdbn. For a gmdbn object, the gmbn elements used for propagation are selected according to the temporal depth of the particles, assuming that the particles contain all the samples since the first time slice (this depth is thus considered as the current time slice).
  evid = NULL,  # A data frame containing the evidence of time slices $t + 1, \ldots, t + k$. Its columns must explicitly be named after nodes of gmgm and can contain missing values (columns with no value can be removed). If NULL (the default), no evidence is taken into account.
  col_seq = NULL,  # A character vector containing the column names of part and evid that describe the observation sequence. If NULL (the default), all the particles and observations belong to a single sequence. In evid, the observations of a same sequence must be ordered such that the $k$th one is related to time slice $t + k$ (note that the sequences can have different lengths).
  col_weight = "weight",  # A character string corresponding to the column name of part that describes the particle weight.
  n_times = 1,  # A data frame containing the particles propagated to time slice $t$, as obtained from function particles or propagation.
  min_ess = 1  # An object of class gmbn or gmdbn. For a gmdbn object, the gmbn elements used for propagation are selected according to the temporal depth of the particles, assuming that the particles contain all the samples since the first time slice (this depth is thus considered as the current time slice).
)
```

Arguments

- `part`: A data frame containing the particles propagated to time slice $t$, as obtained from function `particles` or `propagation`.
- `gmgm`: An object of class gmbn or gmdbn. For a gmdbn object, the gmbn elements used for propagation are selected according to the temporal depth of the particles, assuming that the particles contain all the samples since the first time slice (this depth is thus considered as the current time slice).
- `evid`: A data frame containing the evidence of time slices $t + 1, \ldots, t + k$. Its columns must explicitly be named after nodes of gmgm and can contain missing values (columns with no value can be removed). If NULL (the default), no evidence is taken into account.
- `col_seq`: A character vector containing the column names of part and evid that describe the observation sequence. If NULL (the default), all the particles and observations belong to a single sequence. In evid, the observations of a same sequence must be ordered such that the $k$th one is related to time slice $t + k$ (note that the sequences can have different lengths).
- `col_weight`: A character string corresponding to the column name of part that describes the particle weight.
- `n_times`: An integer indicating the number of times the propagation function is applied.
- `min_ess`: A numeric value indicating the minimum effective sample size (ESS) threshold for performing a renewal step.
relevant

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n_times A non-negative integer corresponding to the number of time slices \( k \) over which the particles are propagated.

min_ess A numeric value in \([0, 1]\) corresponding to the minimum ESS (expressed as a proportion of the number of particles) under which the renewal step is performed. If 1 (the default), this step is performed at each time slice.

Value

A data frame (tibble) containing the particles supplemented with the samples of time slices \( t + 1, \ldots, t + k \).

References


See Also

aggregate, particles

Examples

```r
library(dplyr)
set.seed(0)
data(gmdbn_air, data_air)
evid <- data_air %>%
  group_by(DATE) %>%
  slice(1:3) %>%
  ungroup()
evid$NO2[sample.int(150, 30)] <- NA
evid$O3[sample.int(150, 30)] <- NA
evid$TEMP[sample.int(150, 30)] <- NA
evid$WIND[sample.int(150, 30)] <- NA
part <- particles(data.frame(DATE = unique(evid$DATE))) %>%
  propagation(gmdbn_air, evid, col_seq = "DATE", n_times = 3)
```

---

relevant Extract the minimal sub-Gaussian mixture graphical model required to infer a subset of nodes

Description

This function extracts the minimal sub-Gaussian mixture graphical model required to infer a subset of nodes (i.e. the sub-model relevant to these nodes). The nodes that do not contribute to inference are removed, which includes those that are d-separated from the inferred ones by the nodes whose values are observed, as well as the barren nodes (Druzdzel and Suermondt, 1994).
remove_arcs

Usage

relevant(gmgbn, nodes, nodes_obs = NULL, nodes_miss = NULL)

Arguments

gmgbn An object of class gmgbn or gmdbn.
nodes A character vector containing the inferred nodes.
nodes_obs A character vector containing the nodes whose values are observed.
nodes_miss A character vector containing the nodes whose values are missing. Note that if a node is neither in nodes_obs nor in nodes_miss, its observability is considered uncertain or varying. Thus, it is not treated as an observed node, nor can it be removed as a barren node.

Value

The gmgbn or gmdbn object relevant to the subset of nodes.

References


See Also

add_arcs, add_nodes, remove_arcs, remove_nodes, rename_nodes

Examples

data(gmgbn_body)
gmgbn_1 <- relevant(gmgbn_body, "AGE",
                   nodes_obs = c("FAT", "HEIGHT", "WEIGHT"),
                   nodes_miss = "GLYCO")

data(gmdbn_air)
gmdbn_1 <- do.call("gmdbn", gmdbn_air[c("b_1", "b_2")])
gmdbn_2 <- relevant(gmdbn_1, "O3", nodes_obs = "NO2")

remove_arcs

Remove arcs from a Gaussian mixture graphical model

Description

This function removes arcs from a Gaussian mixture graphical model.
Usage

   remove_arcs(gmgm, arcs)

Arguments

   gmgm  An object of class gmbn or gmbn.
   arcs  A data frame containing the removed arcs. The column from describes the start
          node, the column to the end node and the column lag the time lag between
          them. Missing values in from or to are interpreted as "all possible nodes", which
          allows to quickly define large set of arcs that share common attributes. Missing
          values in lag are replaced by 0. If gmgm is a gmbn object, the same arcs are
          removed from each of its gmbn elements. This constraint can be overcome by
          passing a list of data frames named after some of these elements (b_1, ...) and
          containing arcs specifically removed from them.

Value

   The gmbn or gmbn object after removing the arcs.

See Also

   add_arcs, add_nodes, relevant, remove_nodes, rename_nodes

Examples

   data(gmbn_body)
   gmbn_1 <- remove_arcs(gmbn_body,
                        data.frame(from = c("HEIGHT", "AGE"),
                                   to = c("FAT", "WAIST")))

   data(gmdbn_air)
   gmdbn_1 <- remove_arcs(gmdbn_air,
                          list(b_2 = data.frame(from = c("NO2", "TEMP"),
                                          to = c("O3", "O3"),
                                          lag = c(1, 1)),
                               b_13 = data.frame(from = "TEMP", to = "O3",
                                              lag = 1)))

remove_nodes

Remove nodes from a Gaussian mixture graphical model

Description

   This function removes nodes from a Gaussian mixture graphical model. If this model is a dynamic
   Bayesian network, the nodes are removed from each of its transition models.

Usage

   remove_nodes(gmgm, nodes)
Arguments

- **gmm**: An object of class gmbn or gmdbn.
- **nodes**: A character vector containing the removed nodes.

Value

The gmbn or gmdbn object after removing the nodes.

See Also

- remove_arcs, add_nodes, relevant, remove_arcs, rename_nodes

Examples

```r
data(gmbn_body)
gmbn_1 <- remove_nodes(gmbn_body, c("FAT", "GLYCO"))

data(gmdbn_air)
gmdbn_1 <- remove_nodes(gmdbn_air, "TEMP")
```

---

**remove_var**  
Remove variables from a Gaussian mixture model

Description

This function removes variables from a Gaussian mixture model.

Usage

```r
remove_var(gmm, var)
```

Arguments

- **gmm**: An object of class gmm.
- **var**: A character vector containing the removed variables.

Value

The gmm object after removing the variables.

See Also

- add_var, rename_var

Examples

```r
data(gmm_body)
gmm_1 <- remove_var(gmm_body, "FAT")
```
rename_nodes

Rename nodes of a Gaussian mixture graphical model

Description
This function renames nodes of a Gaussian mixture graphical model. If this model is a dynamic Bayesian network, the nodes are renamed for each of its transition models.

Usage
rename_nodes(gmgm, nodes, names)

Arguments
- gmgm: An object of class gmbn or gmdbn.
- nodes: A character vector containing the renamed nodes.
- names: A character vector containing the respective new names of the nodes.

Value
The gmbn or gmdbn object after renaming the nodes.

See Also
add_arcs, add_nodes, relevant, remove_arcs, remove_nodes

Examples
```r
data(gmbn_body)
gmbn_1 <- rename_nodes(gmbn_body, c("FAT", "GLYCO"),
                          c("BODY_FAT", "GLYCOHEMOGLOBIN"))

data(gmdbn_air)
gmdbn_1 <- rename_nodes(gmdbn_air, "TEMP", "TEMPERATURE")
```

rename_var

Rename variables of a Gaussian mixture model

Description
This function renames variables of a Gaussian mixture model.

Usage
rename_var(gmm, var, names)
Arguments

- `gmm`: An object of class `gmm`.
- `var`: A character vector containing the renamed variables.
- `names`: A character vector containing the respective new names of the variables.

Value

The `gmm` object after renaming the variables.

See Also

- `add_var`, `remove_var`

Examples

```r
data(gmm_body)
gmm_1 <- rename_var(gmm_body, "FAT", "BODY_FAT")
```

Description

This function reorders the variables and the mixture components of a Gaussian mixture model.

Usage

```r
reorder(gmm, var = NULL, comp = NULL)
```

Arguments

- `gmm`: An object of class `gmm`.
- `var`: A character vector containing the variables in the desired order. If variables are not specified, they are added after the ordered ones. If `NULL` (the default), the variables are not reordered.
- `comp`: An integer vector containing the indexes of the mixture component in the desired order. If components are not specified, they are added after the ordered ones. If `NULL` (the default), the components are not reordered.

Value

The reordered `gmm` object.
Examples

```r
data(gmm_body)
gmm_1 <- reorder(gmm_body, var = c("WAIST", "AGE", "FAT", "HEIGHT", "WEIGHT"), 
                comp = c(2, 1, 3))
```

---

Sampling

Sample a Gaussian mixture model

Description

This function samples a Gaussian mixture model.

Usage

```r
sampling(gmm, data_x = NULL, n = 1)
```

Arguments

- `gmm`: An object of class `gmm`.
- `data_x`: A data frame or numeric matrix containing observations of the explanatory variables if conditional sampling is performed. Its columns must explicitly be named after the explanatory variables. If `NULL` (the default), joint sampling is performed.
- `n`: A non-negative integer corresponding to the number of samples. If conditional sampling is performed, this argument is ignored.

Value

A numeric matrix containing the samples.

See Also

density, expectation

Examples

```r
set.seed(0)
data(gmm_body, data_body)
samp1_1 <- sampling(gmm_body, n = 500)
samp1_2 <- sampling(gmm_body, 
                   data_body[, c("WEIGHT", "FAT", "HEIGHT", "AGE")])
```
smem

Select the number of mixture components and estimate the parameters of a Gaussian mixture model

Description

This function selects the number of mixture components and estimates the parameters of a Gaussian mixture model using a split-and-merge EM (SMEM) algorithm. At the first iteration, the classic EM algorithm is performed to update the parameters of the initial model. Then each following iteration consists in splitting a component into two or merging two components, before re-estimating the parameters with the EM algorithm. The selected split or merge operation is the one that maximizes a scoring function (after the re-estimation process). To avoid testing all possible operations, the split and merge candidates are initially ranked according to relevant criteria (Zhang et al., 2003). At first, the top-ranked split and top-ranked merge operations are tested. If neither of them increases the score, the second-ranked ones are considered, and so on. The SMEM algorithm stops if a given maximum rank is reached without improving the score.

Usage

smem(
  gmm,  
data, 
  y = NULL, 
  score = "bic", 
  split = TRUE, 
  merge = TRUE, 
  min_comp = 1, 
  max_comp = Inf, 
  space = 0.5, 
  max_rank = 1, 
  max_iter_smem = 10, 
  verbose = FALSE, 
... )

Arguments

- **gmm**: An initial object of class `gmm`.
- **data**: A data frame or numeric matrix containing the data used in the SMEM algorithm. Its columns must explicitly be named after the variables of `gmm` and must not contain missing values.
- **y**: A character vector containing the dependent variables if a conditional model is estimated (which involves maximizing a conditional score). If `NULL` (the default), the joint model is estimated.
- **score**: A character string ("aic", "bic" or "loglik") corresponding to the scoring function.
smem

split  A logical value indicating whether split operations are allowed (if FALSE, no mixture component can be split).
merge  A logical value indicating whether merge operations are allowed (if FALSE, no mixture component can be merged).
min_comp A positive integer corresponding to the minimum number of mixture components.
max_comp A positive integer corresponding to the maximum number of mixture components.
space  A numeric value in [0, 1] corresponding to the space between two subcomponents resulting from a split.
max_rank A positive integer corresponding to the maximum rank for testing the split and merge candidates.
max_iter_smem A non-negative integer corresponding to the maximum number of iterations.
verbose A logical value indicating whether iterations in progress are displayed.
...
Additional arguments passed to function em.

Value

A list with elements:
gmm The final gmm object.
posterior A numeric matrix containing the posterior probabilities for each observation.
seq_score A numeric vector containing the sequence of scores measured initially and after each iteration.
seq_oper A character vector containing the sequence of split and merge operations performed at each iteration.

References


See Also

data, stepwise

Examples

data(data_body)
gmm_1 <- add_var(NULL, c("WAIST", "AGE", "FAT", "HEIGHT", "WEIGHT"))
res_smem <- smem(gmm_1, data_body, max_comp = 3, verbose = TRUE)
smoothing

Perform smoothing inference in a Gaussian mixture dynamic Bayesian network

Description

This function performs smoothing inference in a Gaussian mixture dynamic Bayesian network. For a sequence of \( T \) time slices, this task consists in estimating the state of the system at each time slice \( t \) (for \( 1 \leq t \leq T \)) given all the data (the evidence) collected up to \( T \). Smoothing inference is performed by sequential importance resampling, which is a particle-based approximate method (Koller and Friedman, 2009).

Usage

```
smoothing(
  gmdbn,
  evid,
  nodes = names(gmdbn$b_1),
  col_seq = NULL,
  n_part = 1000,
  max_part_sim = 1e+06,
  min_ess = 1,
  verbose = FALSE
)
```

Arguments

- **gmdbn**: An object of class `gmdbn`.
- **evid**: A data frame containing the evidence. Its columns must explicitly be named after nodes of `gmdbn` and can contain missing values (columns with no value can be removed).
- **nodes**: A character vector containing the inferred nodes (by default all the nodes of `gmdbn`).
- **col_seq**: A character vector containing the column names of `evid` that describe the observation sequence. If `NULL` (the default), all the observations belong to a single sequence. The observations of a same sequence must be ordered such that the \( t \)th one is related to time slice \( t \) (note that the sequences can have different lengths).
- **n_part**: A positive integer corresponding to the number of particles generated for each observation sequence.
- **max_part_sim**: An integer greater than or equal to \( n_{\text{part}} \) corresponding to the maximum number of particles that can be processed simultaneously. This argument is used to prevent memory overflow, dividing `evid` into smaller subsets that are handled sequentially.
- **min_ess**: A numeric value in \([0, 1]\) corresponding to the minimum ESS (expressed as a proportion of \( n_{\text{part}} \)) under which the renewal step of sequential importance
resampling is performed. If 1 (the default), this step is performed at each time slice.

verbose  A logical value indicating whether subsets of evid and time slices in progress are displayed.

Value

A data frame (tibble) with a structure similar to evid containing the estimated values of the inferred nodes and their observation sequences (if col_seq is not NULL).

References


See Also

filtering, inference, prediction

Examples

```r
set.seed(0)
data(gmdbn_air, data_air)
evid <- data_air
evid$NO2[sample.int(7680, 1536)] <- NA
evid$O3[sample.int(7680, 1536)] <- NA
evid$TEMP[sample.int(7680, 1536)] <- NA
evid$WIND[sample.int(7680, 1536)] <- NA
smooth <- smoothing(gmdbn_air, evid, col_seq = "DATE", verbose = TRUE)
```

---

**split_comp**

*Split a mixture component of a Gaussian mixture model*

**Description**

This function splits a mixture component of a Gaussian mixture model using the singular value decomposition of the covariance matrix (Zhang et al., 2003).

**Usage**

```r
split_comp(gmm, comp = 1, n_sub = 2, space = 0.5)
```
Arguments

- `gmm`: An object of class `gmm`.
- `comp`: An integer corresponding to the index of the split mixture component.
- `n_sub`: A positive integer corresponding to the number of subcomponents.
- `space`: A numeric value in $[0, 1]$ corresponding to the space between the subcomponents.

Value

The `gmm` object after splitting the mixture component.

References


See Also

- `merge_comp`

Examples

```r
data(gmm_body)
gmm_1 <- split_comp(gmm_body, n_sub = 3)
```

stepwise

- `stepwise` Select the explanatory variables, the number of mixture components and estimate the parameters of a conditional Gaussian mixture model.

Description

This function selects the explanatory variables, the number of mixture components and estimates the parameters of a conditional Gaussian mixture model using a stepwise algorithm. At the first iteration, the SMEM algorithm is performed to update the number of components and the parameters of the initial model. Then each following iteration consists in adding or removing a candidate explanatory variable, before re-estimating the model with the SMEM algorithm. The selected add or remove operation is the one that maximizes a conditional scoring function (after the re-estimation process). The stepwise algorithm stops if none of the candidate operations improves the score.
stepwise

Usage

stepwise(
  gmm,
  data,
  y = rownames(gmm$mu)[1],
  x_cand = setdiff(colnames(data), y),
  score = "bic",
  add = TRUE,
  remove = TRUE,
  min_x = 0,
  max_x = Inf,
  max_iter_step = 10,
  verbose = FALSE,
  ...
)

Arguments

gmm  An initial object of class gmm.
data  A data frame or numeric matrix containing the data used in the stepwise algorithm. Its columns must explicitly be named after the variables of gmm and the candidate explanatory variables, and must not contain missing values.
y  A character vector containing the dependent variables (by default the first variable of gmm).
x_cand  A character vector containing the candidate explanatory variables for addition or removal (by default all the column names of data except y). If variables already in gmm are not candidates, they cannot be removed.
score  A character string ("aic", "bic" or "loglik") corresponding to the scoring function.
add  A logical value indicating whether add operations are allowed (if FALSE, no variable can be added).
remove  A logical value indicating whether remove operations are allowed (if FALSE, no variable can be removed).
min_x  A non-negative integer corresponding to the minimum number of explanatory variables.
max_x  A non-negative integer corresponding to the maximum number of explanatory variables.
max_iter_step  A non-negative integer corresponding to the maximum number of iterations.
verbose  A logical value indicating whether iterations in progress are displayed.
...  Additional arguments passed to function smem.

Value

A list with elements:

gmm  The final gmm object.
posterior A numeric matrix containing the posterior probabilities for each observation.
seq_score A numeric vector containing the sequence of scores measured initially and after each iteration.
seq_oper A character vector containing the sequence of add and remove operations performed at each iteration.

See Also
em, smem

Examples

data(data_body)
gmm_1 <- add_var(NULL, "WAIST")
res_step <- stepwise(gmm_1, data_body, verbose = TRUE, max_comp = 3)

structure
Provide the graphical structure of a Gaussian mixture graphical model

Description
This function provides the graphical structure of a Gaussian mixture graphical model.

Usage
structure(gmgm)

Arguments

   gmgm An object of class gmbn or gmdbn.

Value
A list with elements:
   nodes A character vector containing the nodes.
   arcs For a gmbn object, a data frame (tibble) containing the arcs. For a gmdbn object, a list of data frames (tibbles) containing the arcs of each gmbn element.

Examples

   data(gmbn_body)
   struct_1 <- structure(gmbn_body)

   data(gmdbn_air)
   struct_2 <- structure(gmdbn_air)
Learn the structure and the parameters of a Gaussian mixture graphical model with incomplete data

Description

This function learns the structure and the parameters of a Gaussian mixture graphical model with incomplete data using the structural EM algorithm. At each iteration, the parametric EM algorithm is performed to complete the data and update the parameters (E step). The completed data are then used to update the structure (M step), and so on. Each iteration is guaranteed to increase the scoring function until convergence to a local maximum (Koller and Friedman, 2009). In practice, due to the sampling process inherent in particle-based inference, it may happen that the monotonic increase no longer occurs when approaching the local maximum, resulting in an earlier termination of the algorithm.

Usage

```r
struct_em(
  gmgm, data,
  nodes = structure(gmgm)$nodes,
  arcs_cand = tibble(lag = 0),
  col_seq = NULL,
  score = "bic",
  n_part = 1000,
  max_part_sim = 1e+06,
  min_ess = 1,
  max_iter_sem = 5,
  max_iter_pem = 5,
  verbose = FALSE,
  ...
)
```

Arguments

- `gmgm`: An object of class `gmbn` (non-temporal) or `gmdbn`.
- `data`: A data frame containing the data used for learning. Its columns must explicitly be named after nodes of `gmgm` and can contain missing values (columns with no value can be removed).
- `nodes`: A character vector containing the nodes whose local conditional models are learned (by default all the nodes of `gmgm`). If `gmgm` is a `gmdbn` object, the same nodes are learned for each of its `gmbn` elements. This constraint can be overcome by passing a list of character vectors named after some of these elements (b_1, ...) and containing learned nodes specific to them.
- `arcs_cand`: A data frame containing the candidate arcs for addition or removal (by default all possible non-temporal arcs). The column `from` describes the start node, the
column to the end node and the column lag the time lag between them. Missing values in from or to are interpreted as "all possible nodes", which allows to quickly define large set of arcs that share common attributes. Missing values in lag are replaced by 0. If gmgm is a gmdbn object, the same candidate arcs are used for each of its gmbn elements. This constraint can be overcome by passing a list of data frames named after some of these elements (b_1, ...) and containing candidate arcs specific to them. If arcs already in gmgm are not candidates, they cannot be removed. Therefore, setting arcs_card to NULL is equivalent to learning only the mixture structure (and the parameters) of the model.

\textbf{col_seq} A character vector containing the column names of data that describe the observation sequence. If NULL (the default), all the observations belong to a single sequence. If gmgm is a gmdbn object, the observations of a same sequence must be ordered such that the \( t \)th one is related to time slice \( t \) (note that the sequences can have different lengths). If gmgm is a gmbn object, this argument is ignored.

\textbf{score} A character string ("aic", "bic" or "loglik") corresponding to the scoring function.

\textbf{n_part} A positive integer corresponding to the number of particles generated for each observation (if gmgm is a gmbn object) or observation sequence (if gmgm is a gmdbn object) during inference.

\textbf{max_part_sim} An integer greater than or equal to \( n \) part corresponding to the maximum number of particles that can be processed simultaneously during inference. This argument is used to prevent memory overflow, dividing data into smaller subsets that are handled sequentially.

\textbf{min_ess} A numeric value in [0, 1] corresponding to the minimum ESS (expressed as a proportion of \( n \) part) under which the renewal step of sequential importance resampling is performed. If 1 (the default), this step is performed at each time slice. If gmgm is a gmbn object, this argument is ignored.

\textbf{max_iter_sem} A non-negative integer corresponding to the maximum number of iterations.

\textbf{max_iter_pem} A non-negative integer corresponding to the maximum number of iterations of the parametric EM algorithm.

\textbf{verbose} A logical value indicating whether iterations in progress are displayed.

\textbf{...} Additional arguments passed to function \texttt{stepwise}.

\textbf{Value} A list with elements:

- \textbf{gmgm} The final gmbn or gmdbn object (with the highest score).
- \textbf{data} A data frame (tibble) containing the complete data used to learn the final gmbn or gmdbn object.
- \textbf{seq_score} A numeric matrix containing the sequence of scores measured after the E and M steps of each iteration.

\textbf{struct_learn}\  

Learn the structure and the parameters of a Gaussian mixture graphical model

\textbf{See Also}

\texttt{param_em, param_learn, struct_learn}

\textbf{Examples}

```r
set.seed(0)
data(data_body)
data_1 <- data_body
data_1$GENDER[sample.int(2148, 430)] <- NA
data_1$AGE[sample.int(2148, 430)] <- NA
data_1$HEIGHT[sample.int(2148, 430)] <- NA
data_1$WEIGHT[sample.int(2148, 430)] <- NA
data_1$FAT[sample.int(2148, 430)] <- NA
data_1$WAIST[sample.int(2148, 430)] <- NA
data_1$GLYCO[sample.int(2148, 430)] <- NA
gmbn_1 <- add_nodes(NULL, c("AGE", "FAT", "GENDER", "GLYCO", "HEIGHT", "WAIST", "WEIGHT"))
res_learn_1 <- struct_em(gmbn_1, data_1, arcs_cand = arcs_cand_1, verbose = TRUE, max_comp = 3)

set.seed(0)
data(data_air)
data_2 <- data_air
data_2$NO2[sample.int(7680, 1536)] <- NA
data_2$O3[sample.int(7680, 1536)] <- NA
data_2$TEMP[sample.int(7680, 1536)] <- NA
data_2$WIND[sample.int(7680, 1536)] <- NA

gmdbn_1 <- gmdbn(b_2 = add_nodes(NULL, c("NO2", "O3", "TEMP", "WIND")), b_13 = add_nodes(NULL, c("NO2", "O3", "TEMP", "WIND")))
arcs_cand_2 <- data.frame(from = c("NO2", "NO2", "NO2", "O3", "TEMP", "TEMP", "WIND", "WIND"),
to = c("NO2", "O3", "O3", NA, NA, NA, NA),
lag = c(1, 0, 1, 1, 0, 1, 0, 1))
res_learn_2 <- struct_em(gmdbn_1, data_2, arcs_cand = arcs_cand_2, col_seq = "DATE", verbose = TRUE, max_comp = 3)
```
Description

This function learns the (graphical and mixture) structure and the parameters of a Gaussian mixture graphical model. Using the local decomposability of the scoring function, this task consists in learning each local conditional model independently with the stepwise algorithm (Koller and Friedman, 2009). Note that some candidate arcs may be discarded to avoid that the global graphical structure contains cycles. To limit recourse to this action, the learning process is performed sequentially. The more arcs of a local model are likely to be part of cycles (considering the worst case where all the candidate arcs are selected), the later this local model is processed. By gradually taking into account the local structures learned over time, the number of possible cycles decreases and, with it, the number of candidate arcs to discard.

Usage

```r
struct_learn(
  gmgm,
  data,
  nodes = structure(gmgm)$nodes,
  arcs_cand = tibble(lag = 0),
  col_seq = NULL,
  score = "bic",
  verbose = FALSE,
  ...
)
```

Arguments

- **gmgm**: An initial object of class `gmbn` or `gmdbn`.
- **data**: A data frame containing the data used for learning. Its columns must explicitly be named after the nodes of `gmgm` and must not contain missing values.
- **nodes**: A character vector containing the nodes whose local conditional models are learned (by default all the nodes of `gmgm`). If `gmgm` is a `gmdbn` object, the same nodes are learned for each of its `gmbn` elements. This constraint can be overcome by passing a list of character vectors named after some of these elements (`b_1`, ...) and containing learned nodes specific to them.
- **arcs_cand**: A data frame containing the candidate arcs for addition or removal (by default all possible non-temporal arcs). The column from describes the start node, the column to the end node and the column lag the time lag between them. Missing values in from or to are interpreted as "all possible nodes", which allows to quickly define large set of arcs that share common attributes. Missing values in lag are replaced by 0. If `gmgm` is a `gmdbn` object, the same candidate arcs are used for each of its `gmbn` elements. This constraint can be overcome by passing a list of data frames named after some of these elements (`b_1`, ...) and containing candidate arcs specific to them. If arcs already in `gmgm` are not candidates, they cannot be removed. Therefore, setting `arcs_cand` to `NULL` is equivalent to learning only the mixture structure (and the parameters) of the model.
col_seq A character vector containing the column names of `data` that describe the observation sequence. If `NULL` (the default), all the observations belong to a single sequence. If `gmgm` is a temporal `gmbn` or `gmdbn` object, the observations of a same sequence must be ordered such that the \( t \)th one is related to time slice \( t \) (note that the sequences can have different lengths). If `gmgm` is a non-temporal `gmbn` object, this argument is ignored.

score A character string ("aic", "bic" or "loglik") corresponding to the scoring function.

verbose A logical value indicating whether learned nodes in progress are displayed.

Value

A list with elements:

- `gmgm` The final `gmbn` or `gmdbn` object.
- `evol_score` A list with elements:
  - `global` A numeric vector containing the global score before and after learning.
  - `local` For a `gmbn` object, a numeric matrix containing the local conditional scores before and after learning. For a `gmdbn` object, a list of numeric matrices containing these values for each `gmbn` element.

References


See Also

`param_em`, `param_learn`, `struct_em`

Examples

data(data_body)
gmbn_1 <- add_nodes(NULL,
c("AGE", "FAT", "GENDER", "GLYCO", "HEIGHT", "WAIST",
  "WEIGHT"))
arcs_cand_1 <- data.frame(from = c("AGE", "GENDER", "HEIGHT", "WEIGHT", NA,
  "AGE", "GENDER", "AGE", "FAT", "GENDER",
  "HEIGHT", "WEIGHT", "AGE", "GENDER",
  "HEIGHT"),
to = c("FAT", "FAT", "FAT", "FAT", "GLYCO", "HEIGHT",
  "HEIGHT", "WAIST", "WEIAT", "WAIST", "WAIST",
  "WAIST", "WEIGHT", "WEIGHT", "WEIGHT"))
res_learn_1 <- struct_learn(gmbn_1, data_body, arcs_cand = arcs_cand_1,
  verbose = TRUE, max_comp = 3)
data(data_air)
gmbn_1 <- gmbn(b_2 = add_nodes(NULL, c("NO2", "O3", "TEMP", "WIND")),
b_13 = add_nodes(NULL, c("NO2", "O3", "TEMP", "WIND")))

arcs_cand_2 <- data.frame(from = c("NO2", "NO2", "NO2", "O3", "TEMP", "TEMP",
                                  "WIND", "WIND"),
                           to = c("NO2", "O3", "O3", "O3", NA, NA, NA, NA),
                           lag = c(1, 0, 1, 1, 0, 1, 0, 1))

res_learn_2 <- struct_learn(gmbn_1, data_air, arcs_cand = arcs_cand_2,
                             col_seq = "DATE", verbose = TRUE, max_comp = 3)

summary

summarize a Gaussian mixture model or graphical model

Description

This function summarizes a Gaussian mixture model or graphical model.

Usage

## S3 method for class 'gmm'
summary(object, ...)

## S3 method for class 'gmbn'
summary(object, ...)

## S3 method for class 'gmdbn'
summary(object, ...)

Arguments

object An object of class gmm, gmbn or gmdbn.
...
Unused arguments from the generic function.

Value

If object is a gmm object, an integer vector containing the number of variables, mixture components and free parameters.

If object is a gmbn or gmdbn object, a list with elements:

global An integer vector containing the global number of nodes, arcs, mixture components and free parameters (for a gmdbn object, also the number of gmbn elements).

local For a gmbn object, an integer matrix containing the local numbers of arcs, mixture components and free parameters. For a gmdbn object, a list of integer matrices containing these statistics for each gmbn element.
Examples

```
data(gmm_body)
summ_1 <- summary(gmm_body)

data(gmbn_body)
summ_2 <- summary(gmbn_body)

data(gmdbn_air)
summ_3 <- summary(gmdbn_air)
```
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