Package: longmixr (via r-universe)

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Title Longitudinal Consensus Clustering with 'flexmix'

Version 1.2.0

Description An adaption of the consensus clustering approach from 'ConsensusClusterPlus' for longitudinal data. The longitudinal data is clustered with flexible mixture models from 'flexmix', while the consensus matrices are hierarchically clustered as in 'ConsensusClusterPlus'. By using the flexibility from 'flexmix' and 'FactoMineR', one can use mixed data types for the clustering.

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BugReports https://github.com/cellmapslab/longmixr/issues

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Imports checkmate, ConsensusClusterPlus, ggplot2, graphics, grDevices, flexmix, StatMatch, stats, utils

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Contents

`crosssectional_consensus_cluster`
Cross-sectional clustering with categorical variables

Description

This function uses the `ConsensusClusterPlus` function from the package with the same name with defaults for clustering data with categorical variables. As the distance function, the Gower distance is used.

Usage

```
crosssectional_consensus_cluster(
  data,
  reps = 1000,
  finalLinkage = "ward.D2",
  innerLinkage = "ward.D2",
  ...
)
```

Arguments

`data`	a matrix or data.frame containing variables that should be used for computing the distance. This argument is passed to `StatMatch::gower.dist`
`reps`	number of repetitions, same as in `ConsensusClusterPlus`
`finalLinkage`	linkage method for final clustering, same as in `ConsensusClusterPlus`same as in `ConsensusClusterPlus`
`innerLinkage`	linkage method for clustering steps, same as in `ConsensusClusterPlus`
`...`	other arguments passed to `ConsensusClusterPlus`, attention: the `d` argument can **not** be set as it is directly computed by `crosssectional_consensus_cluster`

Details

`data` can take all input data types that `gower.dist` can handle, i.e. `numeric`, `character/factor`, `ordered` and `logical`.

Value

The output is produced by `ConsensusClusterPlus`

Examples

```
dc <- mtcars
# scale continuous variables
dc <- sapply(mtcars[, 1:7], scale)
# code factor variables
dc <- cbind(as.data.frame(dc),
            vs = as.factor(mtcars$vs),
            am = as.factor(mtcars$am),
            gear = as.factor(mtcars$gear),
            carb = as.factor(mtcars$carb))
cc <- crosssectional_consensus_cluster(
  data = dc,
  reps = 10,
  seed = 1
)
```

---

fake_questionnaire_data

Fake questionnaire data

Description

A simulated data set containing observations of 100 individuals at four time points. The data was simulated in two groups (50 individuals each) and contains two questionnaires with five items each, one questionnaire with five continuous variables and one additional cross-sectional continuous variable. In this data set the group variable from the simulation is included. You typically don't have this group variable in your data.

Usage

```
fake_questionnaire_data
```

Format

A data frame with 400 rows and 20 variables:

ID patient ID

visit time point of the observation

group to which simulated group the observation belongs to

age_visit_1 age of the patient at time point 1

single_continuous_variable a cross-sectional continuous variable, i.e. there is only one unique value per individual

questionnaire_A_1 the first item of questionnaire A with categories 1 to 5

questionnaire_A_2 the second item of questionnaire A with categories 1 to 5

questionnaire_A_3 the third item of questionnaire A with categories 1 to 5

questionnaire_A_4 the fourth item of questionnaire A with categories 1 to 5

questionnaire_A_5 the fifth item of questionnaire A with categories 1 to 5

questionnaire_B_1 the first item of questionnaire B with categories 1 to 5

questionnaire_B_2 the second item of questionnaire B with categories 1 to 5

questionnaire_B_3 the third item of questionnaire B with categories 1 to 5

questionnaire_B_4 the fourth item of questionnaire B with categories 1 to 5

questionnaire_B_5 the fifth item of questionnaire B with categories 1 to 5

questionnaire_C_1 the first continuous variable of questionnaire C

questionnaire_C_2 the second continuous variable of questionnaire C

questionnaire_C_3 the third continuous variable of questionnaire C

questionnaire_C_4 the fourth continuous variable of questionnaire C

questionnaire_C_5 the fifth continuous variable of questionnaire C

Source

simulated data

`get_clusters` *Extract the cluster assignments*

Description

This functions extracts the cluster assignments from an `lcc` object. One can specify which for which number of clusters the assignments should be returned.

Usage

```
get_clusters(cluster_solution, number_clusters = NULL)
```

Arguments

`cluster_solution`
: an `lcc` object

`number_clusters`
: default is `NULL` to return all assignments. Otherwise specify a numeric vector with the number of clusters for which the assignments should be returned, e.g. `2:4`

Value

a data.frame with an ID column (the name of the ID column was specified by the user when calling the longitudinal_consensus_cluster) function and one column with cluster assignments for every specified number of clusters. Only the assignments included in number_clusters are returned in the form of columns with the names assignment_num_clus_x

Examples

```
# not run
set.seed(5)
test_data <- data.frame(patient_id = rep(1:10, each = 4),
visit = rep(1:4, 10),
var_1 = c(rnorm(20, -1), rnorm(20, 3)) +
rep(seq(from = 0, to = 1.5, length.out = 4), 10),
var_2 = c(rnorm(20, 0.5, 1.5), rnorm(20, -2, 0.3)) +
rep(seq(from = 1.5, to = 0, length.out = 4), 10))
model_list <- list(flexmix::FLXMRmgcv(as.formula("var_1 ~ .")),
flexmix::FLXMRmgcv(as.formula("var_2 ~ .")))
clustering <- longitudinal_consensus_cluster(
data = test_data,
id_column = "patient_id",
max_k = 2,
reps = 3,
model_list = model_list,
flexmix_formula = as.formula("~s(visit, k = 4) | patient_id"))
cluster_assignments <- get_clusters(clustering, number_clusters = 2)
# end not run
```

---

longitudinal_consensus_cluster

Longitudinal consensus clustering with flexmix

Description

This function performs longitudinal clustering with flexmix. To get robust results, the data is subsampled and the clustering is performed on this subsample. The results are combined in a consensus matrix and a final hierarchical clustering step performed on this matrix. In this, it follows the approach from the ConsensusClusterPlus package.

Usage

```
longitudinal_consensus_cluster(
  data = NULL,
  id_column = NULL,
  max_k = 3,
  reps = 10,
  p_item = 0.8,
  model_list = NULL,
```

```
  flexmix_formula = as.formula("~s(visit, k = 4) | patient_id"),
  title = "untitled_consensus_cluster",
 final_linkage = c("average", "ward.D", "ward.D2", "single", "complete", "mcquitty",
    "median", "centroid"),
  seed = 3794,
  verbose = FALSE
)
```

Arguments

data	a data.frame with one or several observations per subject. It needs to contain one column that specifies to which subject the entry (row) belongs to. This ID column is specified in id_column. Otherwise, there are no restrictions on the column names, as the model is specified in flexmix_formula.
id_column	name (character vector) of the ID column in data to identify all observations of one subject
max_k	maximum number of clusters, default is 3
reps	number of repetitions, default is 10
p_item	fraction of samples contained in subsampled sample, default is 0.8
model_list	either one flexmix driver or a list of flexmix drivers of class FLXMR
flexmix_formula	a formula object that describes the flexmix model relative to the formula in the flexmix drivers (the dot in the flexmix drivers is replaced, see the example). That means that you usually only specify the right-hand side of the formula here. However, this is not enforced or checked to give you more flexibility over the flexmix interface
title	name of the clustering; used if writeTable = TRUE
final_linkage	linkage used for the last hierarchical clustering step on the consensus matrix; has to be average, ward.D, ward.D2, single, complete, mcquitty, median or centroid. The default is average
seed	seed for reproducibility
verbose	boolean if status messages should be displayed. Default is FALSE

Details

The data types longitudinal_consensus_cluster can handle depends on how the flexmix models are set up, in principle all data types are supported for which there is a flexmix driver with the desired outcome variable.

If you follow the dimension reduction approach outlined in vignette("Example clustering analysis", package = "longmixr"), the input data types depend on what FAMD from the FactoMineR package can handle. FAMD accepts numeric variables and treats all other variables as factor variables which it can handle as well.

Value

An object (list) of class `lcc` with length `maxk`. The first entry `general_information` contains the entries:

`consensus_matrices`	a list of all consensus matrices (for all specified clusters)
`cluster_assignments`	a `data.frame` with an ID column named after `id_column` and a column for every specified number
`call`	the call/all arguments how `longitudinal_consensus_cluster` was called

The other entries correspond to the number of specified clusters (e.g. the second entry corresponds to 2 specified clusters) and each contains a list with the following entries:

`consensus_matrix`	the consensus matrix
`consensus_tree`	the result of the hierarchical clustering on the consensus matrix
`consensus_class`	the resulting class for every observation
`found_flexmix_clusters`	a vector of the actual found number of clusters by `flexmix` (which can deviate from the specifie

Examples

```
set.seed(5)
test_data <- data.frame(patient_id = rep(1:10, each = 4),
visit = rep(1:4, 10),
var_1 = c(rnorm(20, -1), rnorm(20, 3)) +
rep(seq(from = 0, to = 1.5, length.out = 4), 10),
var_2 = c(rnorm(20, 0.5, 1.5), rnorm(20, -2, 0.3)) +
rep(seq(from = 1.5, to = 0, length.out = 4), 10))
model_list <- list(flexmix::FLXMRmgcv(as.formula("var_1 ~ .")),
flexmix::FLXMRmgcv(as.formula("var_2 ~ .")))
clustering <- longitudinal_consensus_cluster(
data = test_data,
id_column = "patient_id",
max_k = 2,
reps = 3,
model_list = model_list,
flexmix_formula = as.formula("~s(visit, k = 4) | patient_id"))
# not run
# plot(clustering)
# end not run
```

`plot.lcc` *Plot a longitudinal consensus clustering*

Description

Plot a longitudinal consensus clustering

Usage

```
## S3 method for class 'lcc'
plot(x, color_palette = NULL, which_plots = "all", n_item_consensus = 3, ...)
```

Arguments

x	lcc object (output from longitudinal_consensus_cluster)
color_palette	optional character vector of colors for consensus matrix
which_plots	determine which plots should be plotted; the default is "all". Alternatively, a combination of the following values can be specified to plot only some of the below mentioned plots: "consensusmatrix_legend", "consensusmatrix_x" where x is replaced by the corresponding number of clusters, "CDF", "delta", "cluster_tracking", "item_consensus" or "cluster_consensus". When you want to plot all consensus matrices and the legend, you can just use "consensusmatrix".
n_item_consensus	determines how many item consensus plots are plotted together in one plot before a new plot is used; the default is 3.
...	additional parameters for plotting; currently not used

Value

Plots the following plots (when selected):

consensus matrix legend	the legend for the following consensus matrix plots (select with "consensusmatrix_legend")
consensus matrix plot	for every specified number of clusters, a heatmap of the consensus matrix and the result of the fi
consensus CDF	a line plot of the CDFs for all different specified numbers of clusters (select with "CDF")
Delta area	elbow plot of the difference in the CDFs between the different numbers of clusters (select with "
tracking plot	cluster assignment of the subjects throughout the different cluster solutions (select with "cluste
item-consensus	for every item (subject), calculate the average consensus value with all items that are assigned to
cluster-consensus	every bar represents the average pair-wise item-consensus within one consensus cluster (select w

---

plot_alluvial *Alluvial plot for longmixr clusterings*

Description

A helper function to plot alluvial plots of a categorical variable separated by the clusters found by longmixr. You need to have ggalluvial installed to use this function.

Usage

```
plot_alluvial(
  model,
  data,
  variable_name,
  time_variable,
  number_of_clusters = 2
)
```

Arguments

model	model lcc object (output from longitudinal_consensus_cluster)
data	a data.frame that contains the variables to be plotted and the time and ID variable used in the longmixr clustering; typically the data used for the clustering
variable_name	name of the categorical variable to be plotted as character
time_variable	the name of the variable that depicts the time point of the measurements
number_of_clusters	the number of clusters that should be plotted, the default is 2

Value

a ggplot object that is plotted

Examples

```
library(ggalluvial)
set.seed(5)
test_data <- data.frame(patient_id = rep(1:10, each = 4),
visit = rep(1:4, 10),
var_1 = c(rnorm(20, -1), rnorm(20, 3)) +
rep(seq(from = 0, to = 1.5, length.out = 4), 10),
var_2 = c(rnorm(20, 0.5, 1.5), rnorm(20, -2, 0.3)) +
rep(seq(from = 1.5, to = 0, length.out = 4), 10))
model_list <- list(flexmix::FLXMRmgcv(as.formula("var_1 ~ .")),
flexmix::FLXMRmgcv(as.formula("var_2 ~ .")))
clustering <- longitudinal_consensus_cluster(
data = test_data,
id_column = "patient_id",
max_k = 2,
reps = 3,
model_list = model_list,
flexmix_formula = as.formula("~s(visit, k = 4) | patient_id"))

# add categorical variable for test plotting
test_data$cat <- sample(LETTERS[1:3], 40, replace = TRUE)

plot_alluvial(
  model = clustering,
  data = test_data,
  variable_name = "cat",
```

```
  time_variable = "visit"
)
```

`plot_spaghetti` *Spaghetti plot for longmixr clusterings*

Description

A helper function to plot spaghetti plots of continuous variables separated by the clusters found by `longmixr`.

Usage

```
plot_spaghetti(
  model,
  data,
  variable_names,
  time_variable,
  show_mean_sd_ribbon = TRUE,
  number_of_clusters = 2,
  scales = "fixed"
)
```

Arguments

`model`	`lcc` object (output from `longitudinal_consensus_cluster`)
`data`	a `data.frame` that contains the variables to be plotted and the time and ID variable used in the longmixr clustering; typically the data used for the clustering
`variable_names`	character vector of the continuous variables to be plotted
`time_variable`	the name of the variable that depicts the time point of the measurements
`show_mean_sd_ribbon`	`boolean` if the mean and SD per variable should be shown, the default is `TRUE`
`number_of_clusters`	the number of clusters that should be plotted, the default is `2`
`scales`	`scales` argument of `facet_wrap`, the default is `fixed`

Details

The spaghetti plot shows the longitudinal trajectory (defined by `time_variable`) of continuous variables separated by the clusters found by `longitudinal_consensus_cluster`. The provided `data.frame` for `data` can either be the same as used in the clustering with `longitudinal_consensus_cluster` or needs to contain the same `id_column` as in the clustering and a `time_variable`.

Value

a `ggplot` object that is plotted

Examples

```
set.seed(5)
test_data <- data.frame(patient_id = rep(1:10, each = 4),
visit = rep(1:4, 10),
var_1 = c(rnorm(20, -1), rnorm(20, 3)) +
rep(seq(from = 0, to = 1.5, length.out = 4), 10),
var_2 = c(rnorm(20, 0.5, 1.5), rnorm(20, -2, 0.3)) +
rep(seq(from = 1.5, to = 0, length.out = 4), 10))
model_list <- list(flexmix::FLXMRmgcv(as.formula("var_1 ~ .")),
flexmix::FLXMRmgcv(as.formula("var_2 ~ .")))
clustering <- longitudinal_consensus_cluster(
data = test_data,
id_column = "patient_id",
max_k = 2,
reps = 3,
model_list = model_list,
flexmix_formula = as.formula("~s(visit, k = 4) | patient_id"))

plot_spaghetti(
  model = clustering,
  data = test_data,
  variable_names = "var_1",
  time_variable = "visit"
)
```

---

test_clustering_methods

Try out different linkage methods

Description

In the final step, the consensus clustering performs a hierarchical clustering step on the consensus cluster. This function tries out different linkage methods and returns the corresponding clusterings. The outputs can be plotted like the results from `longitudinal_consensus_cluster`.

Usage

```
test_clustering_methods(
  results,
 use_methods = c("average", "ward.D", "ward.D2", "single", "complete", "mcquitty",
    "median", "centroid")
)
```

Arguments

`results`	clustering result of class `lcc`
`use_methods`	character vector of one or several items of `average`, `ward.D`, `ward.D2`, `single`, `complete`, `mcquitty`, `median` or `centroid`

Value

a list of elements, each element of class `lcc`. The entries are named after the used linkage method.

Examples

```
set.seed(5)
test_data <- data.frame(patient_id = rep(1:10, each = 4),
visit = rep(1:4, 10),
var_1 = c(rnorm(20, -1), rnorm(20, 3)) +
rep(seq(from = 0, to = 1.5, length.out = 4), 10),
var_2 = c(rnorm(20, 0.5, 1.5), rnorm(20, -2, 0.3)) +
rep(seq(from = 1.5, to = 0, length.out = 4), 10))
model_list <- list(flexmix::FLXMRmgcv(as.formula("var_1 ~ .")),
flexmix::FLXMRmgcv(as.formula("var_2 ~ .")))
clustering <- longitudinal_consensus_cluster(
data = test_data,
id_column = "patient_id",
max_k = 2,
reps = 3,
model_list = model_list,
flexmix_formula = as.formula("~s(visit, k = 4) | patient_id"))

clustering_linkage <- test_clustering_methods(results = clustering,
use_methods = c("average", "single"))
# not run
# plot(clustering_linkage[["single"]])
# end not run
```

Index