Package ‘longmixr’

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Title Longitudinal Consensus Clustering with 'flexmix'

Version 1.0.0

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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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

URL `https://cellmapslab.github.io/longmixr/`

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

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`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, ...)
```

Arguments

`x`	`lcc` object (output from `longitudinal_consensus_cluster`)
`color_palette`	optional character vector of colors for consensus matrix
`...`	additional parameters for plotting; currently not used

Value

Plots the following plots:

`consensus matrix legend`	the legend for the following consensus matrix plots
`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
`Delta area`	elbow plot of the difference in the CDFs between the different numbers of clusters
`tracking plot`	cluster assignment of the subjects throughout the different cluster solutions
`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

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`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
```

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