

Package ‘prcr’

February 9, 2020

Type Package

Title Person-Centered Analysis

Version 0.2.1

Maintainer Joshua M Rosenberg <jmichaelrosenberg@gmail.com>

Description Provides an easy-to-use yet adaptable set of tools to conduct person-center analysis using a two-step clustering procedure. As described in Bergman and El-Khouri (1999) <DOI:10.1002/(SICI)1521-4036(199910)41:6%3C753::AID-BIMJ753%3E3.0.CO;2-K>, hierarchical clustering is performed to determine the initial partition for the subsequent k-means clustering procedure.

License MIT + file LICENSE

URL <https://github.com/jrosen48/prcr>

BugReports <https://github.com/jrosen48/prcr/issues>

LazyData TRUE

Imports dplyr, tidyr, ggplot2, tibble, irr, lpSolve, purrr, class, forcats, magrittr

Suggests rmarkdown, knitr, devtools

VignetteBuilder knitr

RoxygenNote 7.0.2

Depends R (>= 2.10)

NeedsCompilation no

Author Joshua M Rosenberg [aut, cre],
Jennifer A Schmidt [aut],
Patrick N Beymer [aut],
Rebecca R Steingut [ctb]

Repository CRAN

Date/Publication 2020-02-09 17:00:05 UTC

R topics documented:

create_profiles_cluster	2
detect_outliers	3
estimate_r_squared	4
pisaUSA15	5
plot_profiles	5
print.prcr	6
summary.prcr	6
Index	7

create_profiles_cluster
Create profiles of observed variables using two-step cluster analysis

Description

Create profiles of observed variables using two-step cluster analysis

Usage

```
create_profiles_cluster(
  df,
  ...,
  n_profiles,
  to_center = FALSE,
  to_scale = FALSE,
  distance_metric = "squared_euclidean",
  linkage = "complete"
)
```

Arguments

df	with two or more columns with continuous variables
...	unquoted variable names separated by commas
n_profiles	The specified number of profiles to be found for the clustering solution
to_center	Boolean (TRUE or FALSE) for whether to center the raw data with $M = 0$
to_scale	Boolean (TRUE or FALSE) for whether to scale the raw data with $SD = 1$
distance_metric	Distance metric to use for hierarchical clustering; "squared_euclidean" is default but more options are available (see ?hclust)
linkage	Linkage method to use for hierarchical clustering; "complete" is default but more options are available (see ?dist)

Details

Function to create a specified number of profiles of observed variables using a two-step (hierarchical and k-means) cluster analysis.

Value

A list containing the prepared data, the output from the hierarchical and k-means cluster analysis, the r-squared value, raw clustered data, processed clustered data of cluster centroids, and a ggplot object.

Examples

```
d <- pisaUSA15
m3 <- create_profiles_cluster(d,
                             broad_interest, enjoyment, instrumental_mot, self_efficacy,
                             n_profiles = 3)
summary(m3)
```

detect_outliers	<i>Identifies potential outliers</i>
-----------------	--------------------------------------

Description

Identifies potential outliers

Usage

```
detect_outliers(df, return_index = TRUE)
```

Arguments

df	data.frame (or tibble) with variables to be clustered; all variables must be complete cases
return_index	Boolean (TRUE or FALSE) for whether to return only the row indices of the possible multivariate outliers; if FALSE, then all of the output from the function (including the indices) is returned

Details

* add an argument to 'create_profiles_cluster()' to remove multivariate outliers based on Hadi's (1994) procedure

Value

either the row indices of possible multivariate outliers or all of the output from the function, depending on the value of return_index

estimate_r_squared	<i>Estimates R² (r-squared) values for a range of number of profiles</i>
--------------------	---

Description

Estimates R² (r-squared) values for a range of number of profiles

Usage

```
estimate_r_squared(
  df,
  ...,
  to_center = FALSE,
  to_scale = FALSE,
  distance_metric = "squared_euclidean",
  linkage = "complete",
  lower_bound = 2,
  upper_bound = 9,
  r_squared_table = TRUE
)
```

Arguments

df	with two or more columns with continuous variables
...	unquoted variable names separated by commas
to_center	(TRUE or FALSE) for whether to center the raw data with $M = 0$
to_scale	Boolean (TRUE or FALSE) for whether to scale the raw data with $SD = 1$
distance_metric	Distance metric to use for hierarchical clustering; "squared_euclidean" is default but more options are available (see ?hclust)
linkage	Linkage method to use for hierarchical clustering; "complete" is default but more options are available (see ?dist)
lower_bound	the smallest number of profiles in the range of number of profiles to explore; defaults to 2
upper_bound	the largest number of profiles in the range of number of profiles to explore; defaults to 9
r_squared_table	if TRUE (default), then a table, rather than a plot, is returned; defaults to FALSE

Details

Returns ggplot2 plot of cluster centroids

Value

A list containing a ggplot2 object and a tibble for the R² values

pisaUSA15	<i>student questionnaire data with four variables from the 2015 PISA for students in the United States</i>
-----------	--

Description

student questionnaire data with four variables from the 2015 PISA for students in the United States

Usage

```
pisaUSA15
```

Format

Data frame with columns #'

CNTSTUID international student ID

SCHID international school ID ...

Source

<http://www.oecd.org/pisa/data/>

plot_profiles	<i>Return plot of profile centroids</i>
---------------	---

Description

Return plot of profile centroids

Usage

```
plot_profiles(d, to_center = F, to_scale = F)
```

Arguments

d	summary data.frame output from create_profiles_cluster()
to_center	whether to center the data before plotting
to_scale	whether to scale the data before plotting

Details

Returns ggplot2 plot of cluster centroids

Value

A ggplot2 object

print.pcr	<i>Prints details of pcr cluster solution</i>
-----------	---

Description

Prints details of pcr cluster solution

Usage

```
## S3 method for class 'pcr'  
print(x, ...)
```

Arguments

x	A 'pcr' object
...	Additional arguments

Details

Prints details of of pcr cluster solution

summary.pcr	<i>Concise summary of pcr cluster solution</i>
-------------	--

Description

Concise summary of pcr cluster solution

Usage

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

Arguments

object	A 'pcr' object
...	Additional arguments

Details

Prints a concise summary of pcr cluster solution

Index

*Topic **datasets**

pisaUSA15, [5](#)

create_profiles_cluster, [2](#)

detect_outliers, [3](#)

estimate_r_squared, [4](#)

pisaUSA15, [5](#)

plot_profiles, [5](#)

print.pcr, [6](#)

summary.pcr, [6](#)