

# Package: prcr (via r-universe)

September 15, 2024

**Type** Package

**Title** Person-Centered Analysis

**Version** 0.2.1

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**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-Khoury (1999) <[DOI:10.1002/\(SICI\)1521-4036\(199910\)41:6%3C753::AID-BIMJ753%3E3.0.CO;2-K](https://doi.org/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.

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**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)

**Repository** <https://jrosen48.r-universe.dev>

**RemoteUrl** <https://github.com/jrosen48/prcr>

**RemoteRef** HEAD

**RemoteSha** 95db5c839ddfc1f440a78e7776bb5e63c6abf9b5

## Contents

create_profiles_cluster . . . . .	2
detect_outliers . . . . .	3

estimate_r_squared . . . . .	4
pisaUSA15 . . . . .	5
plot_profiles . . . . .	5
print.prcr . . . . .	6
summary.prcr . . . . .	6

<b>Index</b>	<b>7</b>
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create\_profiles\_cluster

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

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## 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)
```

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

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<code>estimate_r_squared</code>	<i>Estimates R<sup>2</sup> (r-squared) values for a range of number of profiles</i>
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### Description

Estimates R<sup>2</sup> (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

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

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

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

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

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

## \* datasets

pisaUSA15, [5](#)

create\_profiles\_cluster, [2](#)

detect\_outliers, [3](#)

estimate\_r\_squared, [4](#)

pisaUSA15, [5](#)

plot\_profiles, [5](#)

print.prcr, [6](#)

summary.prcr, [6](#)