

# Package ‘PROsetta’

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**Type** Package

**Title** Linking Patient-Reported Outcomes Measures

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**Description** Perform scale linking to establish relationships between instruments that measure similar constructs according to the PROsetta Stone methodology, as in Choi, Schalet, Cook, & Cella (2014) <doi:10.1037/a0035768>.

**URL** <http://prosettastone.org>

**BugReports** <https://github.com/choi-phd/PROsetta/issues>

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|                |   |
|----------------|---|
| checkFrequency | <i>Check frequency table for unobserved response categories</i> |
|----------------|---|

---

### Description

[checkFrequency](#) is a descriptive function to check whether all response categories in a frequency table have a frequency of at least 1.

### Usage

```
checkFrequency(data)
```

### Arguments

data            a [PROsetta\\_data](#) object. See [loadData](#) for loading a dataset.

### Value

If all response categories have a frequency of at least 1, the value is TRUE.

Otherwise, the value is FALSE.

---

|               |                                   |
|---------------|-----------------------------------|
| compareScores | <i>Compare two sets of scores</i> |
|---------------|-----------------------------------|

---

### Description

`compareScores` is a helper function to compare two sets of scores.

### Usage

```
compareScores(left, right, type = c("corr", "mean", "sd", "rmsd", "mad"))
```

### Arguments

|                    |   |
|--------------------|---|
| <code>left</code>  | scores on the left side of comparison.  |
| <code>right</code> | scores on the right side of comparison. This is subtracted from 'left'.                     |
| <code>type</code>  | type of comparisons to include. Accepts 'corr', 'mean', 'sd', 'rmsd'. Defaults to all four. |

### Value

`compareScores` returns a `data.frame` containing the comparison results.

---

|             |                    |
|-------------|--------------------|
| dataset_asq | <i>ASQ dataset</i> |
|-------------|--------------------|

---

### Description

This dataset is associated with the following objects:

### Details

- `response_asq` a `data.frame` containing raw response data of 751 participants and 41 variables.
  - `prosettaid`. participant IDs.
  - `EDANX01 --MASQ11`. response to items.
- `itemmap_asq` a `data.frame` containing the item map, describing the items in each instrument.
  - `item_order` item numeric IDs. This column refers to the column `item_order` in anchor item attributes.
  - `instrument` the instrument ID that each item belongs to.
  - `item_id` item ID strings. This column refers to column names in raw response data, excluding the participant ID column.
  - `item_name` new item ID strings to be used in the combined scale.
  - `ncat` the number of response categories.

- `min_score` the minimum score of the item.
- `reverse` whether the item data has been reverse-scored. 1 indicates the item has been reverse-scored, and 0 indicates the item has not been reverse-scored.
- `scores` a comma-separated string representing all possible score values from the item.
- `anchor_asq` a `data.frame` containing anchor item parameters for 29 items.
  - `item_order` item numeric IDs.
  - `item_id` item ID strings. This column refers to column names in raw response data, excluding the participant ID column.
  - `a` the discrimination (slope) parameter for the graded response model.
  - `cb1 -cb4` the boundaries between each category-pair for the graded response model.
  - `ncat` the number of response categories.
- `data_asq` a `PROsetta_data` object containing the datasets above. See `loadData` for creating `PROsetta_data` objects.

## Examples

```
## load datasets into a PROsetta_data object
data_asq <- loadData(
  response = response_asq,
  itemmap  = itemmap_asq,
  anchor   = anchor_asq
)

## run descriptive statistics
runDescriptive(data_asq)

## run item parameter calibration on the response data, linking to the anchor item parameters
runLinking(data_asq, method = "FIXEDPAR")
```

---

dataset\_dep

*DEP dataset*

---

## Description

This dataset is associated with the following objects:

## Details

- `response_dep` a `data.frame` containing raw response data of 747 participants and 49 variables.
  - `prosettaid`. participant IDs.
  - `EDDEP04 --CESD20`. response to items.
- `itemmap_dep` a `data.frame` containing the item map, describing the items in each instrument.
  - `item_order` item numeric IDs. This column refers to the column `item_order` in anchor item parameters.

- instrument the instrument ID that each item belongs to.
- item\_id item ID strings. This column refers to column names in raw response data, excluding the participant ID column.
- item\_name new item ID strings to be used in the combined scale.
- ncat the number of response categories.
- min\_score the minimum score of the item.
- reverse whether the item data has been reverse-scored. 1 indicates the item has been reverse-scored, and 0 indicates the item has not been reverse-scored.
- scores a comma-separated string representing all possible score values from the item.
- [anchor\\_dep](#) a `data.frame` containing anchor item parameters for 28 items.
  - item\_order item numeric IDs.
  - item\_id item ID strings. This column refers to column names in raw response data, excluding the participant ID column.
  - a the discrimination (slope) parameter for the graded response model.
  - cb1 -cb4 the boundaries between each category-pair for the graded response model.
  - ncat the number of response categories.
- [data\\_dep](#) a `PROsetta_data` object containing the datasets above. See [loadData](#) for creating `PROsetta_data` objects.

## Examples

```
## load datasets into a PROsetta_data object
data_dep <- loadData(
  response = response_dep,
  itemmap  = itemmap_dep,
  anchor   = anchor_dep
)

## run descriptive statistics
runDescriptive(data_dep)

## run item parameter calibration on the response data, linking to the anchor item parameters
runLinking(data_dep, method = "FIXEDPAR")
```

---

|                              |                          |
|------------------------------|--------------------------|
| <code>getCompleteData</code> | <i>Get complete data</i> |
|------------------------------|--------------------------|

---

## Description

`getCompleteData` is a helper function to perform casewise deletion of missing values.

## Usage

```
getCompleteData(data, scale = NULL)
```

**Arguments**

|       |   |
|-------|---|
| data  | a <a href="#">PROsetta_data</a> object.   |
| scale | the index of the scale to perform casewise deletion. Leave empty or set to "combined" to perform on all scales. |

---

|           |   |
|-----------|---|
| getEscore | <i>Calculate expected scores at theta</i> |
|-----------|---|

---

**Description**

[getEscore](#) is a helper function to calculate expected scores at supplied thetas.

**Usage**

```
getEscore(ipar, model, theta, is_minscore_0)
```

**Arguments**

|               |   |
|---------------|---|
| ipar          | item parameters.                              |
| model         | item model to use.                            |
| theta         | theta values.                                 |
| is_minscore_0 | if TRUE the score begins from 0 instead of 1. |

**Value**

[getEscore](#) returns a vector of expected scores.

---

|             |  |
|-------------|--|
| getScaleSum | <i>Calculate raw sum scores of a scale</i> |
|-------------|--|

---

**Description**

[getScaleSum](#) is a helper function to calculate raw sum scores of a scale.

**Usage**

```
getScaleSum(data, scale_idx)
```

**Arguments**

|           |  |
|-----------|--|
| data      | a <a href="#">PROsetta_data</a> object.              |
| scale_idx | the index of the scale to obtain the raw sum scores. |

---

|          |                             |
|----------|-----------------------------|
| getTheta | <i>Obtain EAP estimates</i> |
|----------|-----------------------------|

---

## Description

`getTheta` is a helper function to calculate EAP estimates.

## Usage

```
getTheta(  
  data,  
  ipar,  
  scale = "combined",  
  model = "grm",  
  theta_grid = seq(-4, 4, 0.1),  
  prior_dist = "normal",  
  prior_mean = 0,  
  prior_sd = 1  
)
```

## Arguments

|                         |   |
|-------------------------|---|
| <code>data</code>       | a <code>PROsetta_data</code> object.  |
| <code>ipar</code>       | a <code>data.frame</code> containing item parameters.                       |
| <code>scale</code>      | the index of the scale to use. Set to 'combined' to use the combined scale. |
| <code>model</code>      | the item model to use. Accepts 'grm' or 'gpcm'.                             |
| <code>theta_grid</code> | the theta grid to use in calculating EAP estimates.                         |
| <code>prior_dist</code> | the type of prior distribution. Accepts 'normal' or 'logistic'.             |
| <code>prior_mean</code> | mean of the prior distribution.   |
| <code>prior_sd</code>   | SD of the prior distribution.   |

## Value

`getTheta` returns a `list` containing EAP estimates.

---

|          |                                       |
|----------|---------------------------------------|
| loadData | <i>Load data from supplied config</i> |
|----------|---------------------------------------|

---

### Description

`loadData` is a data loading function to create a `PROsetta_data` object, for scale linking/equating with 'PROsetta' package.

### Usage

```
loadData(  
  response,  
  itemmap,  
  anchor,  
  item_id = NULL,  
  person_id = NULL,  
  scale_id = NULL,  
  input_dir = getwd()  
)
```

### Arguments

|                        |  |
|------------------------|--|
| <code>response</code>  | response data containing case IDs and item responses. This can be a <code>.csv</code> filename or a <code>data.frame</code> object.    |
| <code>itemmap</code>   | an item map containing item IDs and scale IDs. This can be a <code>.csv</code> filename or a <code>data.frame</code> object.           |
| <code>anchor</code>    | anchor data containing item parameters for anchor items. This can be a <code>.csv</code> filename or a <code>data.frame</code> object. |
| <code>item_id</code>   | the column name to look for item IDs. Automatically determined if not specified.   |
| <code>person_id</code> | the column name to look for case IDs. Automatically determined if not specified.   |
| <code>scale_id</code>  | the column name to look for scale IDs. Automatically determined if not specified.  |
| <code>input_dir</code> | the directory to look for the files.   |

### Value

`loadData` returns a `PROsetta_data` object containing the loaded data.



---

plot,PROsetta\_data,ANY-method  
*Plot frequency distribution*

---

## Description

This is an extension of [plot](#) to visualize frequency distribution from [PROsetta\\_data](#) object.

## Usage

```
## S4 method for signature 'PROsetta_data,ANY'  
plot(  
  x,  
  y,  
  scale_id = "combined",  
  filename = NULL,  
  title = NULL,  
  xlim = NULL,  
  color = "blue",  
  nbar = 20,  
  rug = FALSE,  
  filetype = "pdf",  
  savefile = FALSE,  
  bg = "white",  
  width = 6,  
  height = 6,  
  pointsize = 12  
)
```

## Arguments

|          |   |
|----------|---|
| x        | a <a href="#">PROsetta_data</a> object.   |
| y        | unused argument, exists for compatibility with <a href="#">plot</a> in the base R package.          |
| scale_id | scale ID to plot. combined (default) represents the combined scale.                                 |
| filename | filename to write if 'savefile' argument is TRUE.   |
| title    | the title of the figure.  |
| xlim     | the range of scores to plot.  |
| color    | the color to fill the histogram.  |
| nbar     | the number of histogram bars.   |
| rug      | if TRUE, display the actual distribution of scores below each bar.                                  |
| filetype | the type of file to write if 'savefile' argument is TRUE. Accepts 'pdf', 'jpeg', 'png', and 'tiff'. |
| savefile | if TRUE, save the figure as a file.   |
| bg       | the background color of the plot.   |

width            the width of the plot.  
 height         the height of the plot.  
 pointsize      point size to pass onto file writing functions.

### Examples

```
plot(data_asq)
plot(data_asq, scale_id = 1)
plot(data_asq, scale_id = 2)
```

---

plotInfo                      *Plot scale information*

---

### Description

[plotInfo](#) is a plotting function to visualize scale-level information.

### Usage

```
plotInfo(
  object,
  data,
  theta = seq(-4, 4, 0.1),
  t_score = FALSE,
  scale_label = c(1, 2, "Combined"),
  color = c("red", "blue", "black"),
  lty = c(3, 2, 1)
)

## S4 method for signature 'SingleGroupClass'
plotInfo(
  object,
  data,
  theta = seq(-4, 4, 0.1),
  t_score = FALSE,
  scale_label = c(1, 2, "Combined"),
  color = c("red", "blue", "black"),
  lty = c(3, 2, 1)
)
```

### Arguments

object            a [SingleGroupClass](#) object from [runCalibration](#).  
 data             a [PROsetta\\_data](#) object.  
 theta            theta values to plot on the x-axis.

|             |  |
|-------------|--|
| t_score     | set to TRUE to convert thetas into T-scores. |
| scale_label | names of each scale.                         |
| color       | line colors to plot.                         |
| lty         | line types to plot.                          |

### Examples

```
out_calib = runCalibration(data_asq, technical = list(NCYCLES = 1000))
plotInfo(out_calib, data_asq)
```

---

PROsetta

*PROsetta*

---

### Description

[PROsetta](#) is a caller function to launch a Shiny app locally.

### Usage

```
PROsetta()
```

```
guiPROsetta()
```

### Examples

```
if (interactive()) {
  PROsetta()
}
```

---

runCalibration

*Run Calibration*

---

### Description

[runCalibration](#) is a function to perform item calibration on the response data.

### Usage

```
runCalibration(data, fixedpar = FALSE, ignore_nonconv = FALSE, ...)
```

**Arguments**

**data** a [PROsetta\\_data](#) object. See [loadData](#) for loading a dataset.  
**fixedpar** if TRUE (default), perform fixed parameter calibration using anchor data.  
**ignore\_nonconv** if TRUE, return results even when calibration did not converge. Defaults to FALSE.  
**...** additional arguments to pass onto [mirt](#) in ['mirt'](#) package.

**Value**

[runCalibration](#) returns a [SingleGroupClass](#) object containing item calibration results.  
 This object can be used in [coef](#), [itemfit](#), [itemplot](#) in ['mirt'](#) package to extract wanted information.

**Examples**

```

## Not run:
out_calib <- runCalibration(data_asq) # errors

## End(Not run)

out_calib <- runCalibration(data_asq, technical = list(NCYCLES = 1000))

mirt::coef(out_calib, IRTpars = TRUE, simplify = TRUE)
mirt::itemfit(out_calib, empirical.plot = 1)
mirt::itemplot(out_calib, item = 1, type = "info")
mirt::itemfit(out_calib, "S_X2", na.rm = TRUE)
  
```

---

runCFA

*Run a confirmatory factor analysis*


---

**Description**

[runCFA](#) is a function to perform a one-factor confirmatory factor analysis (CFA) to test unidimensionality.

**Usage**

```
runCFA(data, estimator = "WLSMV", std.lv = TRUE, scalewise = FALSE, ...)
```

**Arguments**

**data** a [PROsetta\\_data](#) object. See [loadData](#) for loading a dataset.  
**estimator** the estimator to be used. Passed onto [cfa](#) in ['lavaan'](#) package.  
**std.lv** if TRUE, the metric of the latent variable is determined by fixing their (residual) variances to 1.0. If FALSE, the metric of each latent variable is determined by fixing the factor loading of the first indicator to 1.0. Passed onto [cfa](#).

scalewise if TRUE, run analysis for each scale as well as for the combined scale. If FALSE (default), run analysis only for the combined scale.

... additional arguments to pass onto [cfa](#).

### Value

[runCFA](#) returns a list containing the CFA results.

### Examples

```
out_cfa <- runCFA(data_asq, scalewise = TRUE)
lavaan::summary(out_cfa$`1` , fit.measures = TRUE, standardized = TRUE, estimates = FALSE)
lavaan::summary(out_cfa$`2` , fit.measures = TRUE, standardized = TRUE, estimates = FALSE)
lavaan::summary(out_cfa$`combined`, fit.measures = TRUE, standardized = TRUE, estimates = FALSE)
```

---

runClassical

*Run CTT-based reliability analysis*

---

### Description

[runClassical](#) is a function to perform Classical Test Theory (CTT) based reliability analysis.

### Usage

```
runClassical(data, omega = FALSE, scalewise = TRUE, ...)
```

### Arguments

data a [PROsetta\\_data](#) object. See [loadData](#) for loading a dataset.

omega if TRUE, also obtain McDonald's omega using [omega](#) in [psych](#) package. (default = FALSE)

scalewise if TRUE, run analysis for each scale as well as for the combined scale. If FALSE, run analysis only for the combined scale. (default = TRUE)

... additional arguments to pass onto [omega](#).

### Value

[runClassical](#) returns a [list](#) containing reliability analysis results.

### Examples

```
out_alpha <- runClassical(data_asq)
out_omega <- runClassical(data_asq, omega = TRUE) # also obtain omega
```

---

|                |  |
|----------------|--|
| runDescriptive | <i>Obtain a descriptive statistics table</i> |
|----------------|--|

---

**Description**

`runDescriptive` is a descriptive function to obtain descriptive statistics for each item in the dataset.

**Usage**

```
runDescriptive(data = NULL)
```

**Arguments**

`data` a `PROsetta_data` object. See `loadData` for loading a dataset.

**Value**

`runDescriptive` returns a `data.frame` containing descriptive statistics (mean, standard deviation, median, ...) of the items in the dataset. These are calculated with `describe` in `'psych'` package.

**Examples**

```
out_desc <- runDescriptive(data_asq)
```

---

|                   |                          |
|-------------------|--------------------------|
| runEquateObserved | <i>Run Test Equating</i> |
|-------------------|--------------------------|

---

**Description**

`runEquateObserved` is a function to perform equipercntile test equating between two scales. A concordance table is produced, mapping the observed raw scores from one scale to the scores from another scale.

**Usage**

```
runEquateObserved(  
  data,  
  scale_from = 2,  
  scale_to = 1,  
  type_to = "raw",  
  rsss = NULL,  
  eq_type = "equipercntile",  
  smooth = "loglinear",  
  degrees = list(3, 1),  
  boot = TRUE,
```

```

    reps = 100,
    ...
  )

```

### Arguments

|            |   |
|------------|---|
| data       | a <a href="#">PROsetta_data</a> object. See <a href="#">loadData</a> for loading a dataset.   |
| scale_from | the scale ID of the input scale. References to <code>itemmap</code> in data argument.   |
| scale_to   | the scale ID of the target scale to equate to. References to <code>itemmap</code> in data argument.   |
| type_to    | the type of score to use in the target scale frequency table. Accepts <code>raw</code> , <code>tscore</code> , and <code>theta</code> . <code>tscore</code> and <code>theta</code> require argument <code>rsss</code> to be supplied. (default = <code>raw</code> ) |
| rsss       | the RSSS table to use to map each raw score level onto a t-score or a theta. See <a href="#">runRSSS</a> .  |
| eq_type    | the type of equating to be passed onto <a href="#">equate</a> in <code>'equate'</code> package.   |
| smooth     | the type of smoothing method to be passed onto <a href="#">presmoothing</a> in <code>'equate'</code> package.   |
| degrees    | the degrees of smoothing to be passed onto <a href="#">presmoothing</a> .   |
| boot       | performs bootstrapping if TRUE.   |
| reps       | the number of replications to perform in bootstrapping.   |
| ...        | other arguments to pass onto <a href="#">equate</a> .   |

### Value

[runEquateObserved](#) returns an [equate](#) object containing the test equating result.

The printed summary statistics indicate the distributional properties of the two supplied scales and the equated scale.

- `x` corresponds to `scale_from`.
- `y` corresponds to `scale_to`.
- `yx` corresponds to `scale_from` after equating to `scale_to`.

See [equate](#) for details.

The concordance table is stored in concordance slot.

### Examples

```

out_eq_raw <- runEquateObserved(data_asq,
  scale_to = 1, scale_from = 2,
  eq_type = "equipercntile", smooth = "loglinear"
)
out_eq_raw$concordance

out_link <- runLinking(data_asq, method = "FIXEDPAR")

```

```
out_rsss <- runRSSS(data_asq, out_link)
out_eq_tscore <- runEquateObserved(data_asq,
  scale_to = 1, scale_from = 2,
  type_to = "tscore", rsss = out_rsss,
  eq_type = "equipercentile", smooth = "loglinear"
)
out_eq_tscore$concordance
```

---

|              |                                 |
|--------------|---------------------------------|
| runFrequency | <i>Obtain a frequency table</i> |
|--------------|---------------------------------|

---

## Description

[runFrequency](#) is a descriptive function to obtain a frequency table from the dataset.

## Usage

```
runFrequency(data, check_frequency = TRUE)
```

## Arguments

**data** a [PROsetta\\_data](#) object. See [loadData](#) for loading a dataset.

**check\_frequency** Logical. If TRUE, check the frequency table for missing response categories, and display warning message if any is missing.

## Value

[runFrequency](#) returns a [data.frame](#) containing the frequency table.

## Examples

```
freq_asq <- runFrequency(data_asq)
freq_dep <- runFrequency(data_dep)
```



---

|            |                          |
|------------|--------------------------|
| runLinking | <i>Run Scale Linking</i> |
|------------|--------------------------|

---

## Description

`runLinking` is a function to obtain item parameters from the response data, and perform scale linking onto the metric of supplied anchor item parameters.

## Usage

```
runLinking(data, method, ...)
```

## Arguments

|        |   |
|--------|---|
| data   | a <code>PROsetta_data</code> object. See <code>loadData</code> for loading a dataset.   |
| method | the type of linking to perform. Accepts: <ul style="list-style-type: none"><li>• MM for mean-mean</li><li>• MS for mean-sigma</li><li>• HB for Haebara method</li><li>• SL for Stocking-Lord method</li><li>• FIXEDPAR for fixed parameter calibration</li></ul> Linear transformation methods are performed with <code>plink</code> in <code>'plink'</code> package. |
| ...    | additional arguments to pass onto <code>mirt</code> in <code>'mirt'</code> package.   |

## Value

`runLinking` returns a `list` containing the scale linking results.

- constants linear transformation constants. NA if method argument was FIXEDPAR.
- `ipar_linked` item parameters calibrated to the response data, and linked to the anchor item parameters.
- `ipar_anchor` anchor item parameters used in linking.

## Examples

```
out_link <- runLinking(data_asq, "SL", technical = list(NCYCLES = 1000))
out_link$constants # transformation constants
out_link$ipar_linked # item parameters linked to anchor
out_link <- runLinking(data_asq, "FIXEDPAR")
out_link$ipar_linked # item parameters linked to anchor
```

---

`runRSSS`*Run Crosswalk Table Generation*

---

**Description**

`runRSSS` is a function to generate raw-score to standard-score crosswalk tables from supplied calibrated item parameters.

**Usage**

```
runRSSS(  
  data,  
  ipar_linked,  
  prior_mean = 0,  
  prior_sd = 1,  
  min_theta = -4,  
  max_theta = 4,  
  inc = 0.01,  
  min_score = 1  
)
```

**Arguments**

|                          |   |
|--------------------------|---|
| <code>data</code>        | a <code>PROsetta_data</code> object. See <code>loadData</code> for loading a dataset. |
| <code>ipar_linked</code> | an object returned from <code>runLinking</code> or <code>runCalibration</code> .      |
| <code>prior_mean</code>  | prior mean.   |
| <code>prior_sd</code>    | prior standard deviation.   |
| <code>min_theta</code>   | the lower limit of theta grid.  |
| <code>max_theta</code>   | the upper limit of theta grid.  |
| <code>inc</code>         | the increment to use in theta grid.   |
| <code>min_score</code>   | minimum item score (0 or 1).  |

**Value**

`runRSSS` returns a `list` containing crosswalk tables.

**Examples**

```
out_link <- runLinking(data_asq, method = "FIXEDPAR")  
score_table <- runRSSS(data_asq, out_link)
```

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