

# Package ‘dexter’

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**Type** Package

**Title** Data Management and Analysis of Tests

**Version** 1.1.4

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**Description** A system for the management, assessment, and psychometric analysis of data from educational and psychological tests.

**License** GPL-3

**URL** <https://dexter-psychometrics.github.io/dexter/>

**BugReports** <https://github.com/dexter-psychometrics/dexter/issues>

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dexter-package	3
ability	4
add_booklet	6
add_item_properties	8
add_person_properties	9
close_project	9
coef.p2pass	10
coef.prms	10
design_info	11
DIF	12
distractor_plot	13
fit_domains	14
fit_enorm	15
fit_inter	16
get_booklets	17
get_design	17
get_items	18
get_persons	19
get_responses	19
get_resp_data	20
get_rules	22
get_testscores	22
get_variables	23
individual_differences	23
information	24
keys_to_rules	26
latent_cor	27
open_project	28
plausible_scores	28
plausible_values	29
plot.DIF_stats	31
plot.p2pass	32
plot.prms	32
plot.rim	33
probability_to_pass	34
profile_plot	35
profile_tables	37
ratedData	38
ratedDataProperties	38
ratedDataRules	39
read_oplm_par	39
r_score_IM	40
standards_3dc	40
standards_db	42
start_new_project	43
start_new_project_from_oplm	44

<i>dexter-package</i>	3
tia_tables . . . . .	45
touch_rules . . . . .	46
verbAggrData . . . . .	47
verbAggrProperties . . . . .	47
verbAggrRules . . . . .	48
<b>Index</b>	<b>49</b>

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dexter-package	<i>Dexter: data analyses for educational and psychological tests.</i>
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## Description

Dexter provides a comprehensive solution for managing and analyzing educational test data.

## Details

The main features are:

- project databases providing a structure for storing data about persons, items, responses and booklets.
- methods to assess data quality using Classical test theory and plots.
- CML calibration of the extended nominal response model and interaction model.

To learn more about dexter, start with the vignettes: ‘browseVignettes(package="dexter")‘

## Author(s)

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Authors:

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- Timo Bechger
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## See Also

Useful links:

- <https://dexter-psychometrics.github.io/dexter/>
- Report bugs at <https://github.com/dexter-psychometrics/dexter/issues>

---

ability

*Estimate abilities*


---

### Description

Computes estimates of ability for persons or for booklet scores

### Usage

```
ability(
  dataSrc,
  parms,
  predicate = NULL,
  method = c("MLE", "EAP", "WLE"),
  prior = c("normal", "Jeffreys"),
  use_draw = NULL,
  npv = 500,
  mu = 0,
  sigma = 4,
  standard_errors = FALSE,
  merge_within_persons = FALSE
)
```

```
ability_tables(
  parms,
  design = NULL,
  method = c("MLE", "EAP", "WLE"),
  prior = c("normal", "Jeffreys"),
  use_draw = NULL,
  npv = 500,
  mu = 0,
  sigma = 4,
  standard_errors = TRUE
)
```

### Arguments

dataSrc	a connection to a dexter database, a matrix, or a data.frame with columns: person_id, item_id, item_score
parms	object produced by <code>fit_enorm</code> or a data.frame with columns item_id, item_score and, depending on parametrization, a column named either beta/delta, eta or b
predicate	An optional expression to subset data, if NULL all data is used
method	Maximum Likelihood (MLE), Expected A posteriori (EAP) or Weighted Likelihood (WLE)
prior	If an EAP estimate is produced one can choose a normal prior or Jeffreys prior; i.e., a prior proportional to the square root of test information.

use_draw	When parms is Bayesian, use_draw is the index of the posterior sample of the item parameters that will be used for generating plausible values. If use_draw=NULL, a posterior mean is used. If outside range, the last iteration will be used.
npv	Number of plausible values sampled to calculate EAP with normal prior
mu	Mean of the normal prior
sigma	Standard deviation of the normal prior
standard_errors	If true standard-errors are produced
merge_within_persons	for persons who were administered multiple booklets, whether to provide just one ability value (TRUE) or one per booklet(FALSE)
design	A data.frame with columns item_id and optionally booklet_id. If the column booklet_id is not included, the score transformation table will be based on all items found in the design. If design is NULL and parms is an enorm fit object the score transformation table will be computed based on the test design that was used to fit the items.

### Details

MLE estimates of ability will produce an NA for the minimum (=0) or the maximum score on a booklet. If this is undesirable, we advise to use WLE. The WLE was proposed by Warm (1989) to reduce bias in the MLE and is also known as the Warm estimator.

### Value

**ability** a data.frame with columns: booklet\_id, person\_id, booklet\_score, theta and optionally se (standard error)

**ability\_tables** a data.frame with columns: booklet\_id, booklet\_score, theta and optionally se (standard error)

### References

Warm, T. A. (1989). Weighted likelihood estimation of ability in item response theory. *Psychometrika*, 54(3), 427-450.

### Examples

```
## Not run:
db = start_new_project(verbAggrRules, "verbAggression.db")
add_booklet(db, verbAggrData, "agg")
f = fit_enorm(db)
aa = ability_tables(f,method="MLE",standard_errors=FALSE)
bb = ability_tables(f,method="EAP",standard_errors=FALSE)
cc = ability_tables(f,method="EAP",prior="Jeffreys", standard_errors=FALSE)
plot(bb$booklet_score, bb$theta, xlab="test-score", ylab="ability est.", pch=19, cex=0.7)
points(aa$booklet_score, aa$theta, col="red", pch=19, cex=0.7)
points(aa$booklet_score, cc$theta, col="green", pch=19, cex=0.7)
legend("topleft", legend = c("EAP normal prior", "EAP Jeffreys prior", "MLE"), bty = "n",
```

```

    lwd = 1, cex = 0.7, col = c("black", "green", "red"), lty=c(0,0,0), pch = c(19,19,19))
close_project(db)

## End(Not run)

```

---

add_booklet	<i>Add response data to a project</i>
-------------	---------------------------------------

---

### Description

Add item response data in long or wide format

### Usage

```

add_booklet(db, x, booklet_id, auto_add_unknown_rules = FALSE)

add_response_data(
  db,
  data,
  auto_add_unknown_rules = FALSE,
  missing_value = "NA"
)

```

### Arguments

db	a connection to a dexter database, i.e. the output of <code>start_new_project</code> or <code>open_project</code>
x	A data frame containing the responses and, optionally, <code>person_properties</code> . The data.frame should have one row per respondent and the column names should correspond to the <code>item_id</code> 's in the rules or the names of the <code>person_properties</code> . See details.
booklet_id	A (short) string identifying the test form (booklet)
auto_add_unknown_rules	If FALSE (the default), an error will be generated if one or more responses do not appear in the scoring rules. If TRUE, unknown responses will be assumed to have a score of 0.
data	response data in normalized (long) format. Must contain columns <code>person_id</code> , <code>booklet_id</code> , <code>item_id</code> and <code>response</code> and optionally <code>item_position</code> (useful if your data contains new booklets, see details)
missing_value	value to use for responses in missing rows in your data, see details

## Details

It is a common practice to keep response data in tables where each row contains the responses from a single person. `add_booklet` is provided to input data in that form, one booklet at a time.

If the dataframe `x` contains a variable named `person_id` this variable will be used to identify unique persons. It is assumed that a single person will only make a single booklet once, otherwise an error will be generated.

If a `person_id` is not supplied, `dexter` will generate unique `person_id`'s for each row of data.

Any column whose name has an exact match in the scoring rules inputted with function `start_new_project` will be treated as an item; any column whose name has an exact match in the `person_properties` will be treated as a person property. If a name matches both a `person_property` and an `item_id`, the item takes precedence. Columns other than items, person properties and `person_id` will be ignored.

`add_response_data` can be used to add data that is already 'normalized'. This function takes a `data.frame` in long format with columns `person_id`, `booklet_id`, `item_id` and `response` such as can usually be found in databases for example. The first time a new booklet is encountered, the design (i.e. which items are contained in each booklet at each position) is derived from data. In this case it is useful if you specify an extra column named `item_position`, otherwise `dexter` will generate the `item_positions` automatically in some way that may not reflect your actual design (of course, if the item positions in your tests are randomized, that is not a problem).

If there are missing rows (e.g. there are only 9 rows for a person-booklet where the booklet should contain 10 items) `missing_value` will be used for the omitted responses. This can lead to an error in case `missing_value` is not defined in your rules and `auto_add_unknown_rules` is set to `FALSE` (the default). Please also note that the `booklet_design` for any specific booklet is derived from the distinct combination of `booklet_id` and `item_id` in data the first time that booklet is encountered. If subsequent calls to `add_response_data` contain data with more or different items for this same booklet, this will cause an error.

Note that responses are always treated as strings (in both functions), and NA values are transformed to the string "NA".

## Value

A list with information about the recent import.

## Examples

```
db = start_new_project(verbAggrRules, ":memory:",
                      person_properties=list(gender="unknown"))
head(verbAggrData)
add_booklet(db, verbAggrData, "agg")

close_project(db)
```

---

add\_item\_properties    *Add item properties to a project*

---

### Description

Add, change or define item properties in a dexter project

### Usage

```
add_item_properties(db, item_properties = NULL, default_values = NULL)
```

### Arguments

**db**                    a connection to a dexter database, e.g. the output of `start_new_project` or `open_project`

**item\_properties**        A data frame containing a column `item_id` (matching `item_id`'s already defined in the project) and 1 or more other columns with item properties (e.g. `item_type`, `subject`)

**default\_values**        a list where the names are `item_properties` and the values are defaults. The defaults will be used wherever the item property is unknown.

### Details

When entering response data in the form of a rectangular person x item table, it is easy to provide person properties but practically impossible to provide item properties. This function provides a possibility to do so.

Note that it is not possible to add new items with this function, use [touch\\_rules](#) if you want to add new items to your project.

### Value

nothing

### See Also

[fit\\_domains](#), [profile\\_plot](#) for possible uses of `item_properties`

### Examples

```
## Not run: \donttest{
db = start_new_project(verbAggrRules, "verbAggression.db")
head(verbAggrProperties)
add_item_properties(db, verbAggrProperties)
get_items(db)

close_project(db)
}
```

```
## End(Not run)
```

---

```
add_person_properties Add person properties to a project
```

---

### Description

Add, change or define person properties in a dexter project. Person properties defined here will also be automatically imported with [add\\_booklet](#)

### Usage

```
add_person_properties(db, person_properties = NULL, default_values = NULL)
```

### Arguments

`db` a connection to a dexter database, e.g. the output of `start_new_project` or `open_project`

`person_properties` A data frame containing a column `person_id` and 1 or more other columns with person properties (e.g. `education_type`, `birthdate`)

`default_values` a list where the names are `person_properties` and the values are defaults. The defaults will be used wherever the person property is unknown.

### Details

Due to limitations in the sqlite database backend that we use, the default values for a person property can only be defined once for each `person_property`

### Value

nothing

---

```
close_project Close a project
```

---

### Description

This is just an alias for `DBI::dbDisconnect(db)`, included for completeness

### Usage

```
close_project(db)
```

### Arguments

`db` connection to a dexter database

---

coef.p2pass	<i>extract equating information</i>
-------------	-------------------------------------

---

**Description**

extract equating information

**Usage**

```
## S3 method for class 'p2pass'
coef(object, ...)
```

**Arguments**

object	an p2pass object, generated by <a href="#">probability_to_pass</a>
...	further arguments are currently ignored

**Value**

A data.frame with columns:

**booklet\_id** id of the target booklet

**score\_new** score on the target booklet

**probability\_to\_pass** probability to pass on the reference test given score\_new

**true\_positive** proportion that correctly passes

**sensitivity** The proportion of positives that are correctly identified as such

**specificity** The proportion of negatives that are correctly identified as such

**proportion** proportion in sample with score\_new

---

coef.prms	<i>extract enorm item parameters</i>
-----------	--------------------------------------

---

**Description**

extract enorm item parameters

**Usage**

```
## S3 method for class 'prms'
coef(object, hpd = 0.95, what = c("items", "var", "posterior"), ...)
```

**Arguments**

object	an enorm parameters object, generated by the function <code>fit_enorm</code>
hpd	width of Bayesian highest posterior density interval around mean_beta, value must be between 0 and 1, default is 0.95
what	which coefficients to return. Defaults to 'items' (the item parameters). Can also be 'var' for the variance-covariance matrix (CML only) or 'posterior' for all draws of the item parameters (Bayes only)
...	further arguments to coef are ignored

**Value**

Depends on the calibration method and the value of 'what'. For 'items' #'

**CML** a data.frame with columns: item\_id, item\_score, beta, SE\_beta

**Bayes** a data.frame with columns: item\_id, item\_score, mean\_beta, SD\_beta, <hpd\_b\_left>, <hpd\_b\_right>

The posterior distribution and variance covariance matrix are returned as matrices.

---

design_info	<i>Information about the design</i>
-------------	-------------------------------------

---

**Description**

This function is useful to inspect incomplete designs

**Usage**

```
design_info(dataSrc, predicate = NULL)
```

**Arguments**

dataSrc	a connection to a dexter database, a matrix, or a data.frame with columns: person_id, item_id, item_score
predicate	An optional expression to subset data, if NULL all data is used

**Value**

a list with the following components

**design** a data.frame with columns booklet\_id, item\_id, item\_position, n\_persons

**connected\_booklets** a data.frame with columns booklet\_id, group; booklets with the same 'group' are connected to each other.

**connected** TRUE/FALSE indicating whether the design is connected or not

**testlets** a data.frame with columns item\_id and testlet; items within the same testlet always occur together in a booklet

**adj\_matrix** list of two adjacency matrices: \*weighted\_by\_items\* and \*weighted\_by\_persons\*;  
These matrices can be useful in visually inspecting the design using a package like \*igraph\*

---

DIF

*Exploratory test for Differential Item Functioning*

---

### Description

Exploratory test for Differential Item Functioning

### Usage

```
DIF(dataSrc, person_property, predicate = NULL)
```

### Arguments

dataSrc	a connection to a dexter database or a data.frame with columns: person_id, item_id, item_score
person_property	Defines groups of persons to calculate DIF
predicate	An optional expression to subset data, if NULL all data is used

### Details

Tests for equality of relative item/category difficulties across groups. Supplements the confirmatory approach of the profile plot.

### Value

An object of class `DIF_stats` holding statistics for overall-DIF and a matrix of statistics for DIF in the relative position of item-category parameters in the beta-parameterization where they represent locations on the ability scale where adjacent categories are equally likely. If there is DIF, the function `'plot'` can be used to produce an image of the pairwise DIF statistics.

### References

Bechger, T. M. and Maris, G (2015); A Statistical Test for Differential Item Pair Functioning. *Psychometrika*. Vol. 80, no. 2, 317-340.

### See Also

A plot of the result is produced by the function [plot.DIF\\_stats](#)

### Examples

```
db = start_new_project(verbAggrRules, ":memory:", person_properties=list(gender='unknown'))
add_booklet(db, verbAggrData, "agg")
dd = DIF(db, person_property="gender")
print(dd)
plot(dd)
str(dd)
```

```
close_project(db)
```

---

distractor_plot	<i>Distractor plot</i>
-----------------	------------------------

---

## Description

Produce a diagnostic distractor plot for an item

## Usage

```
distractor_plot(
  dataSrc,
  item_id,
  predicate = NULL,
  legend = TRUE,
  curtains = 10,
  adjust = 1,
  col = NULL,
  ...
)
```

## Arguments

dataSrc	a connection to a dexter database or a data.frame with columns: person_id, item_id, response, item_score and optionally booklet_id
item_id	The ID of the item to plot. A separate plot will be produced for each booklet that contains the item, or an error message if the item_id is not known. Each plot contains a non-parametric regression of each possible response on the total score.
predicate	An optional expression to subset data, if NULL all data is used
legend	logical, whether to include the legend. default is TRUE
curtains	100*the tail probability of the sum scores to be shaded. Default is 10. Set to 0 to have no curtains shown at all.
adjust	factor to adjust the smoothing bandwidth respective to the default value
col	vector of colors to use for plotting
...	further arguments to plot.

## Details

Customization of title and subtitle can be done by using the arguments main and sub. These arguments can contain references to the variables item\_id, booklet\_id, item\_position(if available), pvalue, rit and rir. References are made by prefixing these variables with a dollar sign. Variable names may be postfixed with a sprintf style format string, e.g. distractor\_plot(db,main='item: \$item\_id',sub='Item rest correlation: \$rir:.2f')

**Value**

Silently, a data.frame of response categories and colors used. Potentially useful if you want to customize the legend or print it separately

---

fit_domains	<i>Estimate the Rasch and the Interaction model per domain</i>
-------------	--

---

**Description**

Estimate the parameters of the Rasch model and the Interaction model

**Usage**

```
fit_domains(dataSrc, item_property, predicate = NULL)
```

**Arguments**

dataSrc	a connection to a dexter database or a data.frame with columns: person_id, item_id, item_score
item_property	The item property defining the domains (subtests)
predicate	An optional expression to subset data, if NULL all data is used

**Details**

We have generalised the interaction model for items having more than two (potentially, a largish number) of response categories. This function represents scores on subtests as super-items and analyses these as normal items.

**Value**

An object of class imp holding results for the Rasch model and the interaction model.

**See Also**

[plot.rim](#), [fit\\_inter](#), [add\\_item\\_properties](#)

**Examples**

```
db = start_new_project(verbAggrRules, ":memory:")
add_booklet(db, verbAggrData, "agg")
add_item_properties(db, verbAggrProperties)
mSit = fit_domains(db, item_property= "situation")
plot(mSit)

close_project(db)
```

---

fit\_enorm

*Fit the extended nominal response model*


---

### Description

Fits an Extended NOMinal Response Model (ENORM) using conditional maximum likelihood (CML) or a Gibbs sampler for Bayesian estimation.

### Usage

```
fit_enorm(
  dataSrc,
  predicate = NULL,
  fixed_params = NULL,
  method = c("CML", "Bayes"),
  nDraws = 1000,
  merge_within_persons = FALSE
)
```

### Arguments

dataSrc	a connection to a dexter database, a matrix, or a data.frame with columns: person_id, item_id, item_score
predicate	An optional expression to subset data, if NULL all data is used
fixed_params	Optionally, a prms object from a previous analysis or a data.frame with parameters, see details.
method	If CML, the estimation method will be Conditional Maximum Likelihood; otherwise, a Gibbs sampler will be used to produce a sample from the posterior
nDraws	Number of Gibbs samples when estimation method is Bayes.
merge_within_persons	whether to merge different booklets administered to the same person, enabling linking over persons as well as booklets.

### Details

To support some flexibility in fixing parameters, fixed\_params can be a dexter prms object of a data.frame. If a data.frame, it should contain the columns item\_id, item\_score and a difficulty parameter. Three types of parameters are supported:

**delta/beta** thresholds between subsequent item categories

**eta** item-category parameters

**b** exp(-eta)

Each type corresponds to a different parametrization of the model.

**Value**

An object of type `prms`. The `prms` object can be cast to a `data.frame` of item parameters using function `'coef'` or used directly as input for other Dexter functions.

**References**

Maris, G., Bechger, T.M. and San-Martin, E. (2015) A Gibbs sampler for the (extended) marginal Rasch model. *Psychometrika*. 80(4), 859-879.

Koops, J. and Bechger, T.M. and Maris, G. (in press); Bayesian inference for multistage and other incomplete designs. In *Research for Practical Issues and Solutions in Computerized Multistage Testing*. Routledge, London.

**See Also**

functions that accept a `prms` object as input: [ability](#), [plausible\\_values](#), [plot.prms](#), and [plausible\\_scores](#)

---

fit\_inter

*Estimate the Interaction and the Rasch model*

---

**Description**

Estimate the parameters of the Interaction model and the Rasch model

**Usage**

```
fit_inter(dataSrc, predicate = NULL)
```

**Arguments**

<code>dataSrc</code>	a connection to a dexter database, a matrix, or a <code>data.frame</code> with columns: <code>person_id</code> , <code>item_id</code> , <code>item_score</code>
<code>predicate</code>	An optional expression to subset data, if <code>NULL</code> all data is used

**Details**

Unlike the Rasch model, the interaction model cannot be computed concurrently for a whole design of test forms. This function therefore fits the Rasch model and the interaction model on complete data. This typically consist of responses to items in one booklet but can also consist of the intersection (common items) in two or more booklets. If the intersection is empty (no common items for all persons), the function will exit with an error message.

**Value**

An object of class `rim` holding results for the Rasch model and the interaction model.

**See Also**

[plot.rim](#), [fit\\_domains](#)

**Examples**

```

db = start_new_project(verbAggrRules, ":memory:")
add_booklet(db, verbAggrData, "agg")

m = fit_inter(db, booklet_id=='agg')
plot(m, "S1DoScold", show.observed=TRUE)

close_project(db)

```

---

get_booklets	<i>Booklets entered in a project</i>
--------------	--------------------------------------

---

**Description**

Retrieve information about the booklets entered in the db so far

**Usage**

```
get_booklets(db)
```

**Arguments**

db	a connection to a dexter database, i.e. the output of start_new_project or open_project
----	---

**Value**

A data frame with columns: booklet\_id, n\_persons, n\_items and booklet\_max\_score. booklet\_max\_score gives the maximum theoretically possible score according to the scoring rules

---

get_design	<i>Test design</i>
------------	--------------------

---

**Description**

Retrieve all items that have been entered in the db so far by booklet and position in the booklet

**Usage**

```

get_design(
  dataSrc,
  format = c("long", "wide"),
  rows = c("booklet_id", "item_id", "item_position"),
  columns = c("item_id", "booklet_id", "item_position"),
  fill = NA
)

```

**Arguments**

dataSrc	a dexter database or any object form which a design can be inferred
format	return format, see below
rows	variable that defines the rows, ignored if format='long'
columns	variable that defines the columns, ignored if format='long'
fill	If set, missing values will be replaced with this value, ignored if format='long'

**Value**

A data.frame with the design. The contents depend on the rows, columns and format parameters if format is 'long' a data.frame with columns: booklet\_id, item\_id, item\_position (if available) if format is 'wide' a data.frame with the rows defined by the rows parameter and the columns by the columns parameter, with the remaining variable (i.e. item\_id, booklet\_id or item\_position) making up the cells

---

get\_items

*Items in a project*

---

**Description**

Retrieve all items that have been entered in the db so far together with the item properties

**Usage**

```
get_items(db)
```

**Arguments**

db	a connection to a dexter database, e.g. the output of start_new_project or open_project
----	---

**Value**

A data frame with column item\_id and a column for each item property

---

get_persons	<i>Persons in a project</i>
-------------	-----------------------------

---

**Description**

Retrieve all persons/respondents that have been entered in the db so far together with their properties

**Usage**

```
get_persons(db)
```

**Arguments**

db	a connection to a dexter database, e.g. the output of <code>start_new_project</code> or <code>open_project</code>
----	---

**Value**

A data frame with columns `person_id` and columns for each `person_property`

---

get_responses	<i>Selecting data</i>
---------------	-----------------------

---

**Description**

Extract data from a dexter database

**Usage**

```
get_responses(
  dataSrc,
  predicate = NULL,
  columns = c("person_id", "item_id", "item_score")
)
```

**Arguments**

dataSrc	a connection to a dexter database, a matrix, or a data.frame with columns: <code>person_id</code> , <code>item_id</code> , <code>item_score</code>
predicate	an expression to select data on
columns	the columns you wish to select, can include any column in the project, see: <a href="#">get_variables</a>

## Details

Many functions in Dexter accept a data source and a predicate. Predicates are extremely flexible but they have a few limitations because they work on the individual response level. It is therefore not possible for example, to remove complete person cases from an analysis based on responses to a single item by using just a predicate expression.

For such cases, Dexter supports selecting the data and manipulating it before passing it back to a Dexter function or possibly doing something else with it. The following example will hopefully clarify this.

## Value

a data.frame of responses

## Examples

```
## Not run:
# goal: fit the extended nominal response model using only persons
# without any missing responses
library(dplyr)

# the following would not work since it will omit only the missing
# responses, not the persons; which is not what we want in this case
wrong = fit_enorm(db, response != 'NA')

# to select on an aggregate level, we need to gather the data and
# manipulate it ourselves
data = get_responses(db,
  columns=c('person_id', 'item_id', 'item_score', 'response')) %>%
  group_by(person_id) %>%
  mutate(any_missing = any(response=='NA')) %>%
  filter(!any_missing)

correct = fit_enorm(data)

## End(Not run)
```

## Description

These functions are meant for people who want to develop their own models based on the data management structure of dexter. Very little input checking is performed, the benefit is some extra speed over using ‘get\_responses’. Regular users are advised not to use these functions as incorrect use can easily crash your R-session or lead to unexpected results.

**Usage**

```

get_resp_data(
  dataSrc,
  qtpredicate = NULL,
  extra_columns = NULL,
  summarised = FALSE,
  env = NULL,
  protect_x = TRUE,
  retain_person_id = TRUE,
  merge_within_persons = FALSE,
  parms_check = NULL
)

get_resp_matrix(dataSrc, qtpredicate = NULL, env = NULL)

```

**Arguments**

dataSrc	data.frame, integer matrix, dexter database or 'dx_resp_data' object
qtpredicate	quoted predicate
extra_columns	to be returned in addition to person_id, booklet_id, item_score, item_id
summarised	if TRUE, no item scores are returned, just booklet scores
env	environment for evaluation of qtpredicate, defaults to caller environment
protect_x	best set TRUE (default)
retain_person_id	whether to retain the original person_id levels or just use arbitrary integers
merge_within_persons	merge different booklets for the same person together
parms_check	data.frame of item_id, item_score to check for coverage of data

**Value**

**get\_resp\_data** returns a list with class 'dx\_resp\_data' with elements

- x** when summarised is FALSE, a tibble(person\_id, booklet\_id, item\_id, item\_score, booklet\_score [, extra\_columns>]), sorted in such a way that all rows pertaining to the same person-booklet are together
- when summarised is TRUE, a tibble(person\_id, booklet\_id, booklet\_score [, extra\_columns])
- design** tibble(booklet\_id, item\_id), sorted

**get\_resp\_matrix** returns a matrix of item scores as commonly used in other IRT packages, facilitating easy connection of your own package to the data management capabilities of dexter

---

get_rules	<i>Get scoring rules</i>
-----------	--------------------------

---

**Description**

Retrieve the scoring rules currently present in the dexter project db

**Usage**

```
get_rules(db)
```

**Arguments**

db                    a connection to a Dexter database

**Value**

data.frame of scoring rules containing columns: item\_id, response, item\_score

---

get_testscores	<i>Provide test scores</i>
----------------	----------------------------

---

**Description**

Supplies the sum of item scores for each person selected.

**Usage**

```
get_testscores(dataSrc, predicate = NULL)
```

**Arguments**

dataSrc              a connection to a dexter database, a matrix, or a data.frame with columns: person\_id, item\_id, item\_score

predicate            An optional expression to filter data, if NULL all data is used

**Value**

A tibble with columns person\_id, item\_id, booklet\_score

---

get_variables	<i>Variables that are defined in the project</i>
---------------	--

---

**Description**

Inspect the variables defined in your dexter project and their datatypes

**Usage**

```
get_variables(db)
```

**Arguments**

db	a dexter project database
----	---------------------------

**Details**

The variables in Dexter consist of the item properties and person properties you specified and a number of reserved variables that are automatically defined like `response` and `booklet_id`.

Variables in Dexter are most useful when used in predicate expressions. A number of functions can take a `dataSrc` argument and an optional predicate. Predicates are a concise and flexible way to filter data for the different psychometric functions in Dexter.

The variables can also be used to retrieve data in [get\\_responses](#)

**Value**

a `data.frame` with name and type of the variables defined in your dexter project

---

individual_differences	<i>Test individual differences</i>
------------------------	------------------------------------

---

**Description**

Test individual differences

**Usage**

```
individual_differences(dataSrc, predicate = NULL)
```

**Arguments**

dataSrc	a connection to a dexter database, a matrix, or a <code>data.frame</code> with columns: <code>person_id</code> , <code>item_id</code> , <code>item_score</code>
predicate	An optional expression to subset data, if <code>NULL</code> all data are used.

**Details**

This function uses a score distribution to test whether there are individual differences in ability. First, it estimates ability based on the score distribution. Then, the observed distribution is compared to the one expected from the single estimated ability. The data are typically from one booklet but can also consist of the intersection (i.e., the common items) of two or more booklets. If the intersection is empty (i.e., no common items for all persons), the function will exit with an error message.

**Value**

An object of type `tind`. Printing the object will show test results. Plotting it will produce a plot of expected and observed score frequencies. The former under the hypothesis that there are no individual differences.

**Examples**

```
## Not run:
db = start_new_project(verbAggrRules, "verbAggression.db")
add_booklet(db, verbAggrData, "agg")
dd = individual_differences(db)
print(dd)
plot(dd)

close_project(db)

## End(Not run)
```

---

 information

*Functions of theta*


---

**Description**

returns information function, expected score function, score simulation function, or score distribution for a single item, an arbitrary group of items or all items

**Usage**

```
information(parms, items = NULL, booklet_id = NULL, which.draw = NULL)
```

```
expected_score(parms, items = NULL, booklet_id = NULL, which.draw = NULL)
```

```
r_score(parms, items = NULL, booklet_id = NULL, which.draw = NULL)
```

```
p_score(parms, items = NULL, booklet_id = NULL, which.draw = NULL)
```

**Arguments**

<code>parms</code>	object produced by <code>fit_enorm</code> or a data.frame with columns <code>item_id</code> , <code>item_score</code> and, depending on parametrization, a column named either <code>beta/delta</code> , <code>eta</code> or <code>b</code>
<code>items</code>	vector of one or more <code>item_id</code> 's. If NULL and <code>booklet_id</code> is also NULL, all items in <code>parms</code> are used
<code>booklet_id</code>	id of a single booklet (e.g. the test information function), if <code>items</code> is not NULL this is ignored
<code>which.draw</code>	the number of the random draw (only applicable if calibration method was Bayes). If NULL, the mean beta parameter will be used

**Value**

Each function returns a new function which accepts a vector of `theta`'s. These return the following values:

**information** an equal length vector with the information estimate at each value of `theta`.

**expected\_score** an equal length vector with the expected score at each value of `theta`

**r\_score** a matrix with `length(theta)` rows and one column for each item containing simulated scores based on `theta`. To obtain test scores, use `rowSums` on this matrix

**p\_score** a matrix with `length(theta)` rows and one column for each possible sumscore containing the probability of the score given `theta`

**Examples**

```
db = start_new_project(verbAggrRules, ':memory:')
add_booklet(db, verbAggrData, "agg")
p = fit_enorm(db)

# plot information function for single item
ifun = information(p, "S1DoScold")

plot(ifun, from=-4, to=4)

# compare test information function to the population ability distribution
ifun = information(p, booklet="agg")

pv = plausible_values(db, p)

op = par(no.readonly=TRUE)
par(mar = c(5,4,2,4))

plot(ifun, from=-4, to=4, xlab='theta', ylab='test information')

par(new=TRUE)

plot(density(pv$PV1), col='green', axes=FALSE, xlab=NA, ylab=NA, main=NA)
```

```
axis(side=4)
mtext(side = 4, line = 2.5, 'population density (green)')

par(op)
close_project(db)
```

---

keys\_to\_rules                      *Derive scoring rules from keys*

---

### Description

For multiple choice items that will be scored as 0/1, derive the scoring rules from the keys to the correct responses

### Usage

```
keys_to_rules(keys, include_NA_rule = FALSE)
```

### Arguments

keys                      A data frame containing columns `item_id`, `noptions`, and `key` See details.

include\_NA\_rule                      whether to add an option 'NA' (which is scored 0) to each item

### Details

This function might be useful in setting up the scoring rules when all items are multiple-choice and scored as 0/1.

The input data frame must contain the exact id of each item, the number of options, and the key. If the keys are all integers, it will be assumed that responses are coded as 1 through `noptions`. If they are all letters, it is assumed that responses are coded as A,B,C,... All other cases result in an error.

### Value

A data frame that can be used as input to `start_new_project`

---

latent_cor	<i>Latent correlations</i>
------------	----------------------------

---

### Description

Estimates correlations between latent traits. Use an `item_property` to distinguish the different scales. This function uses plausible values so results may differ slightly between calls. Note: this is a new and slightly experimental function and therefore still a bit slow. It will probably become faster in future versions of dexter.

### Usage

```
latent_cor(  
  dataSrc,  
  item_property,  
  predicate = NULL,  
  nDraws = 500,  
  hpd = 0.95,  
  use = "complete.obs"  
)
```

### Arguments

<code>dataSrc</code>	A connection to a dexter database or a <code>data.frame</code> with columns: <code>person_id</code> , <code>item_id</code> , <code>item_score</code> and the <code>item_property</code>
<code>item_property</code>	The name of the item property used to define the domains. If <code>dataSrc</code> is a dexter db then the <code>item_property</code> must match a known item property. If <code>datasrc</code> is a <code>data.frame</code> , <code>item_property</code> must be equal to one of its column names.
<code>predicate</code>	An optional expression to subset data, if <code>NULL</code> all data is used
<code>nDraws</code>	Number of draws for plausible values
<code>hpd</code>	width of Bayesian highest posterior density interval around the correlations, value must be between 0 and 1.
<code>use</code>	Only <code>complete.obs</code> at this time. Respondents who don't have a score for one or more scales are removed.

### Value

List containing a estimated correlation matrix, the corresponding standard deviations, and the lower and upper limits of the highest posterior density interval

---

open_project	<i>Open an existing project</i>
--------------	---------------------------------

---

**Description**

Opens a database created by function start\_new\_project

**Usage**

```
open_project(db_name = "dexter.db")
```

**Arguments**

db_name	The name of the database to be opened.
---------	--

**Value**

a database connection object

---

plausible_scores	<i>Generate plausible test scores</i>
------------------	---------------------------------------

---

**Description**

Generate plausible i.e., posterior predictive sumscores on a set of items. A typical use of this function is to generate plausible scores on a complete item bank when data is collected using an incomplete design

**Usage**

```
plausible_scores(  
  dataSrc,  
  parms = NULL,  
  predicate = NULL,  
  items = NULL,  
  covariates = NULL,  
  keep.observed = TRUE,  
  nPS = 1,  
  merge_within_persons = FALSE  
)
```

**Arguments**

dataSrc	a connection to a dexter database, a matrix, or a data.frame with columns: person_id, item_id, item_score
parms	An object returned by function fit_enorm and containing parameter estimates. If parms is given the function provides plausible scores conditional on the item parameters. These are considered known. If parms is NULL, Bayesian parameters are calculated from the datasrc
predicate	an expression to filter data. If missing, the function will use all data in dataSrc
items	vector of item_id's, this specifies the itemset to generate the testscores for. If items is NULL all items occurring in dataSrc are used.
covariates	name or a vector of names of the variables to group the population, used to update the prior. A covariate must be a discrete person covariate (e.g. not a float) that indicates nominal categories, e.g. gender or school. If dataSrc is a data.frame, it must contain the covariate.
keep.observed	If responses to one or more of the items have been observed, the user can choose to keep these observations or generate new ones.
nPS	Number of plausible testscores to generate per person.
merge_within_persons	If a person took multiple booklets, this indicates whether plausible scores are generated per person (TRUE) or per booklet (FALSE)

**Value**

A data.frame with columns booklet\_id, person\_id, booklet\_score and nPS plausible scores named PS1...PSn.

---

plausible_values	<i>Draw plausible values</i>
------------------	------------------------------

---

**Description**

Draws plausible values based on test scores

**Usage**

```
plausible_values(
  dataSrc,
  parms = NULL,
  predicate = NULL,
  covariates = NULL,
  nPV = 1,
  use_draw = NULL,
  prior.dist = c("normal", "mixture"),
  merge_within_persons = FALSE
)
```

**Arguments**

<code>dataSrc</code>	a connection to a dexter database, a matrix, or a data.frame with columns: <code>person_id</code> , <code>item_id</code> , <code>item_score</code>
<code>parms</code>	An object returned by function <code>fit_enorm</code> containing parameter estimates. If <code>parms</code> are provided, item parameters are considered known. If <code>parms = NULL</code> , plausible values are marginalized over the posterior distribution of the item parameters and uncertainty of the item parameters is taken into account.
<code>predicate</code>	an expression to filter data. If missing, the function will use all data in <code>dataSrc</code>
<code>covariates</code>	name or a vector of names of the variables to group the populations used to improve the prior. A covariate must be a discrete person property (e.g. not a float) that indicates nominal categories, e.g. <code>gender</code> or <code>school</code> . If <code>dataSrc</code> is a data.frame, it must contain the covariate.
<code>nPV</code>	Number of plausible values to draw per person.
<code>use_draw</code>	When the ENORM was fitted with a Gibbs sampler, this specifies the use of a particular sample of item parameters used to generate the plausible value(s). If <code>NULL</code> , the posterior means are used. If outside range, the last iteration will be used.
<code>prior.dist</code>	use a normal prior or a mixture of two normals recognised automatically),
<code>merge_within_persons</code>	If a person took multiple booklets, this indicates whether plausible values are generated per person ( <code>TRUE</code> ) or per booklet ( <code>FALSE</code> )

**Value**

A data.frame with columns `booklet_id`, `person_id`, `booklet_score` and `nPV` plausible values named `PV1...PVn`.

**References**

Marsman, M., Maris, G., Bechger, T. M., and Glas, C.A.C. (2016) What can we learn from plausible values? *Psychometrika*. 2016; 81: 274-289. See also the vignette.

**Examples**

```
db = start_new_project(verbAggrRules, ":memory:",
  person_properties=list(gender="<unknown>"))
add_booklet(db, verbAggrData, "agg")
add_item_properties(db, verbAggrProperties)

f=fit_enorm(db)
pv_M=plausible_values(db,f,(mode=="Do")&(gender=="Male"))
pv_F=plausible_values(db,f,(mode=="Do")&(gender=="Female"))

par(mfrow=c(1,2))

plot(ecdf(pv_M$PV1),
  main="Do: males versus females", xlab="Ability", col="red")
lines(ecdf(pv_F$PV1), col="green")
```

```

legend(-2.2,0.9, c("female", "male") ,
      lty=1, col=c('green', 'red'), bty='n', cex=.75)

pv_M=plausible_values(db,f,(mode=="Want")&(gender=="Male"))
pv_F=plausible_values(db,f,(mode=="Want")&(gender=="Female"))

plot(ecdf(pv_M$PV1),
     main="Want: males versus females", xlab=" Ability", col="red")
lines(ecdf(pv_F$PV1),col="green")
legend(-2.2,0.9, c("female", "male") ,
      lty=1, col=c('green', 'red'), bty='n', cex=.75)

close_project(db)

```

---

plot.DIF\_stats

*plot method for pairwise DIF statistics*


---

## Description

plot method for pairwise DIF statistics

## Usage

```

## S3 method for class 'DIF_stats'
plot(x, items = NULL, itemsX = items, itemsY = items, alpha = 0.05, ...)

```

## Arguments

x	object produced by <a href="#">DIF</a>
items	character vector of item id's for a subset of the plot. Useful if you have many items. If NULL all items are plotted.
itemsX	character vector of item id's for the X axis
itemsY	character vector of item id's for the Y axis
alpha	significance level used to color the plot (two sided)
...	further arguments to plot

## Details

Plotting produces an image of the matrix of pairwise DIF statistics. The statistics are standard normal deviates and colored to distinguish significant from non-significant values. If there is no DIF, a proportion alpha will be significant be change.

## References

Feskens, R., Fox, J. P., & Zwitser, R. (2019). Differential item functioning in PISA due to mode effects. In *Theoretical and Practical Advances in Computer-based Educational Measurement* (pp. 231-247). Springer, Cham.

---

plot.p2pass

*A plot method for probability\_to\_pass*


---

### Description

Plot equating information from probability\_to\_pass

### Usage

```
## S3 method for class 'p2pass'
plot(
  x,
  what = c("all", "equating", "sens/spec", "roc"),
  booklet_id = NULL,
  ...
)
```

### Arguments

x	An object produced by function <a href="#">probability_to_pass</a>
what	information to plot, 'equating', 'sens/spec', 'roc', or 'all'
booklet_id	vector of booklet_id's to plot, if NULL all booklets are plotted
...	Any additional plotting parameters; e.g., cex = 0.7.

---

plot.prms

*Plot for the extended nominal Response model*


---

### Description

The plot shows 'fit' by comparing the expected score based on the model (grey line) with the average scores based on the data (black line with dots) for groups of students with similar estimated ability.

### Usage

```
## S3 method for class 'prms'
plot(
  x,
  item_id = NULL,
  dataSrc = NULL,
  predicate = NULL,
  nbins = 5,
  ci = 0.95,
  ...
)
```

**Arguments**

x	object produced by fit_enorm
item_id	which item to plot, if NULL, one plot for each item is made
dataSrc	data source, see details
predicate	an expression to subset data in dataSrc
nbins	number of ability groups
ci	confidence interval for the error bars, between 0 and 1. Use 0 to suppress the error bars. Default = 0.95 for a 95% confidence interval
...	further arguments to plot

**Details**

The standard plot shows the fit against the sample on which the parameters were fitted. If dataSrc is provided, the fit is shown against the observed data in dataSrc. This may be useful for plotting the fit in different subgroups as a visual test for item level DIF. The confidence intervals denote the uncertainty about the predicted pvalues within the ability groups for the sample size in dataSrc (if not NULL) or the original data on which the model was fit.

**Value**

Silently, a data.frame with observed and expected values possibly useful to create a numerical fit measure.

---

plot.rim	<i>A plot method for the interaction model</i>
----------	--

---

**Description**

Plot the item-total regressions fit by the interaction (or Rasch) model

**Usage**

```
## S3 method for class 'rim'
plot(
  x,
  items = NULL,
  summate = TRUE,
  overlay = FALSE,
  curtains = 10,
  show.observed = TRUE,
  ...
)
```

**Arguments**

x	An object produced by function <code>fit_inter</code>
items	The items to plot (item_id's). If NULL, all items will be plotted
summate	If FALSE, regressions for polytomous items will be shown for each response option separately; default is TRUE.
overlay	If TRUE and more than one item is specified, there will be two plots, one for the Rasch model and the other for the interaction model, with all items overlaid; otherwise, one plot for each item with the two models overlaid. Ignored if summate is FALSE. Default is FALSE
curtains	100*the tail probability of the sum scores to be shaded. Default is 10. Set to 0 to have no curtains shown at all.
show.observed	If TRUE, the observed proportion correct at each sum score will be shown as dots. Default is FALSE.
...	Any additional plotting parameters.

**Details**

Customization of title and subtitle can be done by using the arguments `main` and `sub`. These arguments can contain references to the variables `item_id` (if `overlay=FALSE`) or `model` (if `overlay=TRUE`) by prefixing them with a dollar sign, e.g. `plot(m, main='item: $item_id')`

---

`probability_to_pass`     *The probability to pass on a reference test given a score on a new booklet*

---

**Description**

Given response data that form a connected design, compute the probability to pass on the reference set conditional on each score on one or more target tests.

**Usage**

```
probability_to_pass(
  dataSrc,
  parms,
  ref_items,
  pass_fail,
  predicate = NULL,
  target_booklets = NULL,
  nDraws = 1000
)
```

**Arguments**

dataSrc	a connection to a dexter database, a matrix, or a data.frame with columns: person_id, item_id, item_score
parms	parameters returned from fit_enorm. If uncertainty about parameter estimation should be included in the computations, use 'method='Bayes'' and nDraws equal or larger than nDraws in probability_to_pass
ref_items	vector with id's of items in the reference set, they must all occur in dataSrc
pass_fail	pass-fail score on the reference set, the lowest score with which one passes
predicate	An optional expression to subset data in dataSrc, if NULL all data is used
target_booklets	The target test booklet(s). A data.frame with columns booklet_id (if multiple booklets) and item_id, if NULL (default) this will be derived from the dataSrc and the probability to pass will be computed for each test score for each booklet in your data.
nDraws	The function uses an Markov-Chain Monte-Carlo method to calculate the probability to pass and this is the number of Monte-Carlo samples used.

**Details**

Note that this function is computationally intensive and can take some time to run, especially when computing the probability to pass for multiple target booklets. Further technical details can be found in a vignette.

**Value**

An object of type p2pass. Use coef() to extract the probability to pass for each booklet and score. Use plot() to plot the probabilities, sensitivity and specificity or a ROC-curve.

**See Also**

The function used to plot the results: [plot.p2pass](#)

---

profile\_plot

*Profile plot*

---

**Description**

Profile plot

**Usage**

```
profile_plot(
  dataSrc,
  item_property,
  covariate,
  predicate = NULL,
  model = c("IM", "RM"),
  x = NULL,
  col = NULL,
  ...
)
```

**Arguments**

dataSrc	a connection to a dexter database or a data.frame with columns: person_id, item_id, item_score and the item_property and the covariate of interest.
item_property	The name of the item property defining the domains. The item property should have exactly two distinct values in your data
covariate	name of the person property used to create the groups. There will be one line for each distinct value.
predicate	An optional expression to filter data, if NULL all data is used
model	"IM" (default) or "RM" where "IM" is the interaction model and "RM" the Rasch model. The interaction model is the default as it fits the data better or at least as good as the Rasch model.
x	Which value of the item_property to draw on the x axis, if NULL, one is chosen automatically
col	vector of colors to use for plotting
...	further arguments to plot

**Details**

Profile plots can be used to investigate whether two (or more) groups of respondents attain the same test score in the same way. The user must provide a (meaningful) classification of the items in two non-overlapping subsets such that the test score is the sum of the scores on the subsets. The plot shows the probabilities to obtain any combinations of subset scores with thin gray lines indicating the combinations that give the same test score. The thick lines connect the most likely combination for each test score in each group. When applied to educational test data, the plots can be used to detect differences in the relative difficulty of (sets of) items for respondents that belong to different groups and are matched on the test score. This provides a content-driven way to investigate differential item functioning.

**Examples**

```
db = start_new_project(verbAggrRules, ":memory:",
                      person_properties=list(gender="unknown"))
add_booklet(db, verbAggrData, "agg")
add_item_properties(db, verbAggrProperties)
```

```
profile_plot(db, item_property='mode', covariate='gender')
close_project(db)
```

---

profile_tables	<i>Profile analysis</i>
----------------	-------------------------

---

### Description

Expected and observed domain scores, conditional on the test score, per person or test score. Domains are specified as categories of items using `item_properties`.

### Usage

```
profile_tables(parms, domains, item_property, design = NULL)

profiles(
  dataSrc,
  parms,
  item_property,
  predicate = NULL,
  merge_within_persons = FALSE
)
```

### Arguments

<code>parms</code>	An object returned by <code>fit_enorm</code> or a data.frame of item parameters
<code>domains</code>	data.frame with column <code>item_id</code> and a column with name equal to <code>item_property</code>
<code>item_property</code>	the name of the item property used to define the domains. If <code>dataSrc</code> is a dexter db then the <code>item_property</code> must match a known item property. If <code>dataSrc</code> is a data.frame, <code>item_property</code> must be equal to one of its column names. For <code>profile_tables</code> <code>item_property</code> must match a column name in <code>domains</code> .
<code>design</code>	data.frame with columns <code>item_id</code> and optionally <code>booklet_id</code>
<code>dataSrc</code>	a connection to a dexter database or a data.frame with columns: <code>person_id</code> , <code>item_id</code> , <code>item_score</code> , an arbitrarily named column containing an item property and optionally <code>booklet_id</code>
<code>predicate</code>	An optional expression to subset data in <code>dataSrc</code> , if NULL all data is used
<code>merge_within_persons</code>	whether to merge different booklets administered to the same person.

**Details**

When using a unidimensional IRT Model like the extended nominal response model in dexter (see: [fit\\_enorm](#)), the model is as a rule to simple to catch all the relevant dimensions in a test. Nevertheless, a simple model is quite useful in practice. Profile analysis can complement the model in this case by indicating how a test-taker, conditional on her/his test score, performs on a number of pre-specified domains, e.g. in case of a mathematics test the domains could be numbers, algebra and geometry or in case of a digital test the domains could be animated versus non-animated items. This can be done by comparing the achieved score on a domain with the expected score, given the test score.

**Value**

**profiles** a data.frame with columns person\_id, booklet\_id, booklet\_score, <item\_property>, domain\_score, expected\_domain\_score

**profile\_tables** a data.frame with columns booklet\_id, booklet\_score, <item\_property>, expected\_domain\_score

**References**

Verhelst, N. D. (2012). Profile analysis: a closer look at the PISA 2000 reading data. *Scandinavian Journal of Educational Research*, 56 (3), 315-332.

---

ratedData

*Rated data*

---

**Description**

A data set with rated data. A number of student performances are rated twice on several aspects by independent judges. The ratings are binary and have been summed following the theory discussed by Maris and Bechger (2006, *Handbook of Statistics*). Data are a small subset of data collected on the State Exam Dutch as a second language for Speaking.

**Format**

A data set with 75 rows and 15 columns.

---

ratedDataProperties

*Item properties in the rated data*

---

**Description**

A data set of item properties related to the rated data. These are the aspects: IH = content, WZ = word choice and phrasing, and WK = vocabulary.

**Format**

A data set with 14 rows and 2 columns: item\_id and aspect

---

ratedDataRules	<i>Scoring rules for the rated data</i>
----------------	---

---

**Description**

A set of (trivial) scoring rules for the rated data set

**Format**

A data set with 42 rows and 3 columns (item\_id, response, item\_score).

---

read_oplm_par	<i>Read item parameters from oplm PAR or CML files</i>
---------------	--

---

**Description**

Read item parameters from oplm PAR or CML files

**Usage**

```
read_oplm_par(par_path)
```

**Arguments**

par_path	path to a file in the (binary) OPLM PAR format or the human readable CML format
----------	---

**Details**

It is very occasionally useful to calibrate new items on an existing scale. This function offers the possibility to read parameters from the proprietary oplm format so that they can be used to fix a new calibration in Dexter on an existing scale of items that were calibrated in oplm.

**Value**

depends on the input. For .PAR files a data.frame with columns: item\_id, item\_score, beta, nbr, for .CML files also several statistics columns that are outputted by OPLM as part of the calibration.

**Examples**

```
## Not run:
\donttest{
par = read_oplm_par('/parameters.PAR')
f = fit_enorm(db, fixed_params=par)
}
## End(Not run)
```

---

r_score_IM	<i>Simulation from the interaction model</i>
------------	--

---

**Description**

Simulate item scores conditional on test scores using the interaction model

**Usage**

```
r_score_IM(m, scores)
```

**Arguments**

m	an object produced by function <code>fit_inter</code>
scores	vector of test scores

**Value**

a matrix with item scores, one column per item and one row per test score. Row order equal to scores

---

standards_3dc	<i>Standard setting</i>
---------------	-------------------------

---

**Description**

Set performance standards on one or more test forms using the data driven direct consensus (3DC) method

**Usage**

```
standards_3dc(parms, design)

## S3 method for class 'sts_par'
coef(object, ...)

## S3 method for class 'sts_par'
plot(x, booklet_id = NULL, ...)
```

**Arguments**

parms	parameters object returned from fit_enorm
design	a data.frame with columns 'cluster_id', 'item_id' and optionally 'booklet_id'
object	an object containing parameters for the 3DC standard setting procedure
...	ignored Optionally you can include a column 'booklet_id' to specify multiple test forms for standard setting and/or columns 'cluster_nbr' and 'item_nbr' to specify ordering of clusters and items in the forms and application.
x	an object containing parameters for the 3DC standard setting procedure
booklet_id	which test form to plot

**Details**

The data driven direct consensus (3DC) method of standard setting was invented by Gunter Maris and described in Keuning et. al. (2017). To easily apply this procedure, we advise to use the free digital 3DC application. This application can be downloaded from the Cito website, see the [3DC application download page](#). If you want to apply the 3DC method using paper forms instead, you can use the function plot3DC to generate the forms from the 3DC database.

Although the 3DC method is used as explained in Keuning et. al., the method we use for computing the forms is a simple maximum likelihood scaling from an IRT model, described in Moe and Verhelst (2017)

**Value**

an object of type 'sts\_par'

**References**

Keuning J., Straat J.H., Feskens R.C.W. (2017) The Data-Driven Direct Consensus (3DC) Procedure: A New Approach to Standard Setting. In: Blomeke S., Gustafsson JE. (eds) Standard Setting in Education. Methodology of Educational Measurement and Assessment. Springer, Cham

Moe E., Verhelst N. (2017) Setting Standards for Multistage Tests of Norwegian for Adult Immigrants In: Blomeke S., Gustafsson JE. (eds) Standard Setting in Education. Methodology of Educational Measurement and Assessment. Springer, Cham

**See Also**

how to make a database for the 3DC standard setting application: [standards\\_db](#)

**Examples**

```
library(dplyr)
db = start_new_project(verbAggrRules, ":memory:")

add_booklet(db, verbAggrData, "agg")
add_item_properties(db, verbAggrProperties)
```

```

design = get_items(db) %>%
  rename(cluster_id='behavior')

f = fit_enorm(db)

sts_par = standards_3dc(f, design)

plot(sts_par)

# db_sts = standards_db(sts_par, 'test.db', c('mildly aggressive', 'dangerously aggressive'))

```

---

standards\_db

*Export a standard setting database for use by the free 3DC application*


---

### Description

This function creates an export (an sqlite database file) which can be used by the 3DC application. This is a free application with which a standard setting session can be facilitated through a LAN network using the Chrome browser. The 3DC application can be downloaded from [3DC application download page](#)

### Usage

```

standards_db(
  par.sts,
  file_name,
  standards,
  population = NULL,
  group_leader = "admin"
)

```

### Arguments

par.sts	an object containing parameters for the 3DC standard setting procedure produced by <a href="#">standards_3dc</a>
file_name	name of the exported database file
standards	vector of 1 or more standards. In case there are multiple test forms and they should use different performance standards, a list of such vectors. The names of this list should correspond to the names of the testforms
population	optional, a data.frame with three columns: 'booklet_id', 'booklet_score', 'n' (where n is a count)
group_leader	login name of the group leader. The login password will always be 'admin' but can be changed in the 3DC application

---

start_new_project	<i>Start a new project</i>
-------------------	----------------------------

---

### Description

Imports a complete set of scoring rules and starts a new project (data base)

### Usage

```
start_new_project(rules, db_name = "dexter.db", person_properties = NULL)
```

### Arguments

rules	A data frame with columns <code>item_id</code> , <code>response</code> , and <code>item_score</code> . The order is not important but spelling is. Any other columns will be ignored.
db_name	A connection to an existing sqlite database or a string specifying a filename for a new sqlite database to be created. If this name does not contain a path, the file will be created in the work directory. Any existing file with the same name will be overwritten. For an in-memory database you can use the string <code>":memory:"</code> .
person_properties	An optional list of person properties. Names should correspond to <code>person_properties</code> intended to be used in the project. Values are used as default (missing) values. The datatype will also be inferred from the values. Known <code>person_properties</code> will be automatically imported when adding response data with <a href="#">add_booklet</a> .

### Details

This package only works with closed items (e.g. likert, MC or possibly short answer) it does not score any open items. The first step to creating a project is to import an exhaustive list of all items and all admissible responses, along with the score that any of the latter will be given. Responses may be integers or strings but they will always be treated as strings. Scores must be integers, and the minimum score for an item must be 0. When inputting data, all responses not specified in the rules can optionally be treated as missing and ultimately scored 0, but it is good style to include the missing responses in the list. NA values will be treated as the string "NA".

### Value

a database connection object.

### Examples

```
head(verbAggrRules)
db_name = tempfile(fileext='.db')
db = start_new_project(verbAggrRules, db_name,
                      person_properties = list(gender = "unknown"))
```

---

```
start_new_project_from_oplm
    Start a new project from oplm files
```

---

### Description

Creates a dexter project database and fills it with response data based on a .dat and .scr file

### Usage

```
start_new_project_from_oplm(
  dbname,
  scr_path,
  dat_path,
  booklet_position = NULL,
  responses_start = NULL,
  response_length = 1,
  person_id = NULL,
  missing_character = c(" ", "9"),
  use_discrim = FALSE,
  format = "compressed"
)
```

### Arguments

dbname	filename/path of new dexter project database (will be overwritten if already exists)
scr_path	path to the .scr file
dat_path	path to the .dat file
booklet_position	vector of start and end of booklet position in the dat file, e.g. c(1,4), all positions are counted from 1, start and end are both inclusive. If NULL, this is read from the scr file.
responses_start	start position of responses in the .dat file. If NULL, this is read from the scr file.
response_length	length of individual responses, default=1
person_id	optionally, a vector of start and end position of person_id in the .dat file. If NULL, person id's will be auto-generated.
missing_character	vector of character(s) used to indicate missing in .dat file, default is to use both a space and a 9 as missing characters.
use_discrim	if TRUE, the scores for the responses will be multiplied by the discrimination parameters of the items
format	not used, at the moment only the compressed format is supported.

## Details

start\_new\_project\_from\_oplm builds a complete dexter database from a .dat and .scr file in the proprietary oplm format. Three custom variables are added to the database: booklet\_on\_off, item\_local\_on\_off, item\_global\_on\_off. These are taken from the .scr file and can be used in predicates in the various dexter functions.

Booklet\_position and responses\_start are usually inferred from the scr file but since they are sometimes misspecified in the scr file they can be overridden. Response\_length is not inferred from the scr file since anything other than 1 is most often a mistake.

## Value

a database connection object.

## Examples

```
## Not run: \donttest{
db = start_new_project_from_oplm('test.db',
  'path_to_scr_file', 'path_to_dat_file',
  booklet_position=c(1,3), responses_start=101,
  person_id=c(50,62))

prms = fit_enorm(db,
  item_global_on_off==1 & item_local_on_off==1 & booklet_on_off==1)

}
## End(Not run)
```

---

tia\_tables

*Simple test-item analysis*

---

## Description

Show simple Classical Test Analysis statistics at item and test level

## Usage

```
tia_tables(
  dataSrc,
  predicate = NULL,
  type = c("raw", "averaged", "compared"),
  max_scores = c("observed", "theoretical")
)
```

**Arguments**

dataSrc	a connection to a dexter database, a matrix, or a data.frame with columns: person_id, item_id, item_score
predicate	An optional expression to subset data, if NULL all data is used
type	How to present the item level statistics: raw for each test booklet separately, averaged booklets are ignored, with the exception of rit and rir which are averaged over the test booklets, with the number of persons as weights, or compared, in which case the pvalues, correlations with the sum score (rit), and correlations with the rest score (rit) are shown in separate tables and compared across booklets
max_scores	use the observed maximum item score or the theoretical maximum item score according to the scoring rules in the database to compute pvalues and maximum scores

**Details**

The returned list also contains the elements 'testStats' and 'itemStats'. These contain the same information as 'booklets' and 'items' but using obsolete (mixed camelCase and snake\_case) variable names. These will be removed in the future and users are advised to not use these in newer code.

**Value**

A list containing:

booklets	a data.frame of statistics at booklet level
items	a data.frame (or list if type='compared') of statistics at item level

---

touch_rules	<i>Add or modify scoring rules</i>
-------------	------------------------------------

---

**Description**

It is occasionally necessary to alter or add a scoring rule, e.g. in case of a key error. This function offers the possibility to do so and also allows you to add new items to your project

**Usage**

```
touch_rules(db, rules)
```

**Arguments**

db	a connection to a dexter project database
rules	A data frame with columns item_id, response, and item_score. The order is not important but spelling is. Any other columns will be ignored. See details

**Details**

The rules should contain all rules that you want to change or add. This means that in case of a key error in a single multiple choice question, you typically have to change two rules.

**Value**

If the scoring rules pass a sanity check, a small summary of changes is printed and nothing is returned. Otherwise this function returns a data frame listing the problems found, with 4 columns:

**item\_id** id of the problematic item

**less\_than\_two\_scores** if TRUE, the item has only one distinct score

**duplicated\_responses** if TRUE, the item contains two or more identical response categories

**min\_score\_not\_zero** if TRUE, the minimum score of the item was not 0

**Examples**

```
## Not run: \donttest{
# given that in your dexter project there is an mc item with id 'itm_01',
# which currently has key 'A' but you want to change it to 'C'.

new_rules = data.frame(item_id='itm_01', response=c('A','C'), item_score=c(0,1))
touch_rules(db, new_rules)
}
## End(Not run)
```

---

 verbAggrData

*Verbal aggression data*


---

**Description**

A data set of self-reported verbal behaviour in different frustrating situations (Vansteelandt, 2000)

**Format**

A data set with 316 rows and 26 columns.

---

 verbAggrProperties

*Item properties in the verbal aggression data*


---

**Description**

A data set of item properties related to the verbal aggression data

**Format**

A data set with 24 rows and 5 columns.

---

verbAggrRules	<i>Scoring rules for the verbal aggression data</i>
---------------	---

---

**Description**

A set of (trivial) scoring rules for the verbal aggression data set

**Format**

A data set with 72 rows and 3 columns (item\_id, response, item\_score).

# Index

## \* datasets

- ratedData, 38
  - ratedDataProperties, 38
  - ratedDataRules, 39
  - verbAggrData, 47
  - verbAggrProperties, 47
  - verbAggrRules, 48
- ability, 4, 16
- ability\_tables (ability), 4
- add\_booklet, 6, 9, 43
- add\_item\_properties, 8, 14
- add\_person\_properties, 9
- add\_response\_data (add\_booklet), 6
- close\_project, 9
- coef.p2pass, 10
- coef.prms, 10
- coef.sts\_par (standards\_3dc), 40
- design\_info, 11
- dexter (dexter-package), 3
- dexter-package, 3
- DIF, 12, 31
- distractor\_plot, 13
- expected\_score (information), 24
- fit\_domains, 8, 14, 16
- fit\_enorm, 4, 11, 15, 25, 37, 38
- fit\_inter, 14, 16
- get\_booklets, 17
- get\_design, 17
- get\_items, 18
- get\_persons, 19
- get\_resp\_data, 20
- get\_resp\_matrix (get\_resp\_data), 20
- get\_responses, 19, 23
- get\_rules, 22
- get\_testscores, 22
- get\_variables, 19, 23
- individual\_differences, 23
- information, 24
- keys\_to\_rules, 26
- latent\_cor, 27
- open\_project, 28
- p\_score (information), 24
- plausible\_scores, 16, 28
- plausible\_values, 16, 29
- plot.DIF\_stats, 12, 31
- plot.p2pass, 32, 35
- plot.prms, 16, 32
- plot.rim, 14, 16, 33
- plot.sts\_par (standards\_3dc), 40
- probability\_to\_pass, 10, 32, 34
- profile\_plot, 8, 35
- profile\_tables, 37
- profiles (profile\_tables), 37
- r\_score (information), 24
- r\_score\_IM, 40
- ratedData, 38
- ratedDataProperties, 38
- ratedDataRules, 39
- read\_oplm\_par, 39
- standards\_3dc, 40, 42
- standards\_db, 41, 42
- start\_new\_project, 43
- start\_new\_project\_from\_oplm, 44
- tia\_tables, 45
- touch\_rules, 8, 46
- verbAggrData, 47
- verbAggrProperties, 47
- verbAggrRules, 48