Package ‘dataquieR’

March 29, 2024

Title Data Quality in Epidemiological Research

Version 2.1.0

Description Data quality assessments guided by a
‘data quality framework introduced by Schmidt and colleagues, 2021’
<doi:10.1186/s12874-021-01252-7> target the
data quality dimensions integrity, completeness, consistency, and
accuracy. The scope of applicable functions rests on the
availability of extensive metadata which can be provided in
spreadsheet tables. Either standardized (e.g. as 'html5' reports) or
individually tailored reports can be generated. For an introduction
into the specification of corresponding metadata, please refer to the
'package website'
<https://dataquality.qihs.uni-greifswald.de/Annotation_of_Metadata.html>.

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URL https://dataquality.qihs.uni-greifswald.de/

BugReports https://gitlab.com/libreumg/dataquier/-/issues

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lubridate, MASS, MultinomialCI, parallelMap, patchwork,
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scales, withr, lifecycle, units

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knitr, markdown, parallel, parallelly, rJava, rmarkdown,
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R topics documented:

acc_distributions .................................................. 6
acc_distributions_loc .............................................. 7
acc_distributions_loc_ecdf ..................................... 9
acc_distributions_only ........................................... 10
acc_distributions_only_ecdf ................................. 12
acc_distributions_prop ....................................... 13
acc_end_digits .................................................. 15
acc_loess ....................................................... 16
accMargins ...................................................... 18
acc_multivariate_outlier ................................. 20
acc_robust_univariate_outlier ....................... 22
acc_shape_or_scale ...................................... 24
acc_univariate_outlier .................................. 25
acc_varcomp .................................................. 27
as.data.frame.dataquieR_resultset .................... 29
as.list.dataquieR_resultset ............................. 30
ASSOCIATION_DIRECTION ..................................... 31
ASSOCIATION_FORM .......................................... 31
ASSOCIATION_METRIC ...................................... 32
ASSOCIATION_RANGE ...................................... 32
cause_label_df ............................................... 33
CHECK_ID ..................................................... 33
CHECK_LABEL ................................................ 34
check_table ................................................... 34
com_item_missingness ................................... 35
com_qualified_item_missingness ..................... 37
R topics documented:

com_qualified_segment_missingness ........................................ 38
com_segment_missingness .................................................. 39
com_unit_missingness ....................................................... 41
contradiction_functions_descriptions ..................................... 42
CONTRACTION_TERM ....................................................... 43
CONTRACTION_TYPE ....................................................... 43
con_contradictions ......................................................... 44
con_contradictions_redcap .................................................. 46
con_inadmissible_categorical ............................................. 49
con_limit_deviations ....................................................... 50
dataquieR_resultset ....................................................... 52
dataquieR_resultset_verify ............................................... 52
DATA_PREPARATION ....................................................... 53
DATA_TYPES ............................................................... 53
DATA_TYPES_OF_R_TYPE .................................................. 54
des_scatterplot_matrix ..................................................... 55
des_summary ............................................................... 56
DF_ELEMENT_COUNT ....................................................... 57
DF_ID_REF_TABLE ........................................................ 57
DF_ID_VARS ............................................................... 58
DF_NAME ................................................................. 58
DF_RECORD_CHECK ......................................................... 59
DF_RECORD_COUNT ........................................................ 59
DF_UNIQUE_ID ............................................................ 60
DF_UNIQUE_ROWS ........................................................ 60
dim.dataquieR_resultset2 ................................................. 61
dimensions ................................................................. 61
dimnames.dataquieR_resultset2 ......................................... 62
dims ...................................................................... 62
DISTRIBUTIONS ........................................................... 63
dq_report ................................................................. 63
dq_report2 ............................................................... 64
dq_report_by ............................................................. 66
GOLDSTANDARD .......................................................... 68
html_dependency_clipboard ............................................... 69
html_dependency_dataquieR ............................................... 69
html_dependency_report_dt ............................................... 70
html_dependency_tippy ..................................................... 70
html_dependency_vert_dt ................................................... 71
int_all_datastructure_dataframe ........................................ 71
int_all_datastructure_segment ......................................... 72
int_datatype_matrix ...................................................... 74
int_duplicate_content .................................................... 75
int_duplicate_ids ......................................................... 76
int_part_vars_structure .................................................. 77
int_sts_element_dataframe .............................................. 78
int_sts_element_segment ............................................... 78
int_unexp_elements ....................................................... 80
int_unexp_records_dataframe ........................................ 81
int_unexp_records_segment ......................................... 81
int_unexp_records_set ............................................... 83
meta_data .............................................................. 84
meta_data_cross ....................................................... 84
meta_data_dataframe ................................................ 84
meta_data_segment .................................................... 85
MULTIVARIATE_OUTLIER_CHECKTYPE .................................. 85
nres ................................................................. 86
N_RULES ............................................................... 86
pipeline_recursive_result ............................................ 87
pipeline_vectorized .................................................. 87
plot.dataquieR_summary .............................................. 88
prep_add_cause_label_df ............................................ 88
prep_add_data_frames ................................................ 89
prep_add_missing_codes ............................................. 90
prep_add_to_meta .................................................... 92
prep_apply_coding ................................................... 93
prep_check_for_dataquieR_updates ................................ 94
prep_check_meta_data_dataframe ................................... 94
prep_check_meta_data_segment ..................................... 95
prep_check_meta_names .............................................. 96
prep_clean_labels ................................................... 98
prep_combine_report_summaries ................................... 99
prep_create_meta .................................................... 100
prep_create_meta_data_file ........................................ 101
prep_datatype_from_data ........................................... 102
prep_deparse_assignments ......................................... 102
prep_dq_data_type_of .............................................. 103
prep_expand_codes .................................................. 104
prep_extract_cause_label_df ....................................... 105
prep_extract_classes_by_functions ................................ 105
prep_extract_summary ............................................... 106
prep_extract_summary.dataquieR_result .......................... 107
prep_extract_summary.dataquieR_resultset2 ..................... 107
prep_get_data_frame ................................................ 108
prep_get_labels ..................................................... 110
prep_get_user_name .................................................. 111
prep_link_escape ................................................... 111
prep_list_dataframes ............................................... 112
prep_load_folder_with_metadata .................................. 112
prep_load_report .................................................... 113
prep_load_workbook_like_file ..................................... 114
prep_map_labels ..................................................... 115
prep_merge_study_data .............................................. 116
prep_meta_data_v1_to_item_level_meta_data ....................... 116
prep_min_obs_level ................................................. 117
prep_pmap .......................................................... 118
R topics documented:

prep_prepare_dataframes .............................................. 119
prep_purge_data_frame_cache ........................................ 121
prep_render_pie_chart_from_summaryclasses_ggplot2 ............... 122
prep_render_pie_chart_from_summaryclasses_plotly ................ 123
prep_save_report .................................................... 123
prep_scalelevel_from_data_and_metadata ............................ 124
prep_study2meta ..................................................... 125
prep_summary_to_classes ............................................. 126
prep_title_escape ................................................. 126
prep_valuelabels_from_data ........................................ 127
print.dataquieR_result ............................................ 128
print.dataquieR_resultset ......................................... 128
print.dataquieR_resultset2 ....................................... 129
print.dataquieR_summary ........................................... 129
print.interval ...................................................... 130
print.ReportSummaryTable ........................................... 131
pro_applicability_matrix ........................................... 132
rbind.ReportSummaryTable .......................................... 133
REL_VAL ............................................................. 134
resnames ............................................................ 134
resnames.dataquieR_resultset2 ..................................... 135
SCALE_LEVELS ....................................................... 135
SEGMENT_ID_REF_TABLE ............................................. 136
SEGMENT_ID_TABLE .................................................. 136
SEGMENT_ID_VARS .................................................. 137
SEGMENT_MISS ....................................................... 137
SEGMENT_PART_VARS ................................................ 138
SEGMENT_RECORD_CHECK ........................................... 138
SEGMENT_RECORD_COUNT ......................................... 139
SEGMENT_UNIQUE_ROWS ........................................... 139
SPLIT_CHAR ........................................................ 140
study_data ......................................................... 140
summary.dataquieR_resultset .................................... 140
summary.dataquieR_resultset2 ................................... 141
UNITS ............................................................... 142
UNIT_IS_COUNT ...................................................... 142
UNIT_PREFIXES ....................................................... 142
UNITOURCES ......................................................... 143
UNIVARIATE_OUTLIER_CHECKTYPE ................................ 143
util_compute_kurtosis ............................................... 144
util_compute_SE_skewness .......................................... 144
util_compute_skewness .............................................. 145
util_first_row_to_colnames ....................................... 145
VARATT_REQUIRE_LEVELS .......................................... 146
VARIABLE_LIST ...................................................... 146
VARIABLE_ROLES .................................................... 147
WELL_KNOWN_META_VARIABLE_NAMES ................................ 147
[.dataquieR_resultset2 ........................................ 148
Description

Data quality indicator checks "Unexpected location" and "Unexpected proportion" with histograms and, if a grouping variable is included, plots of empirical cumulative distributions for the subgroups.

Indicator

Usage

```r
acc_distributions(
  resp_vars = NULL,
  group_vars = NULL,
  study_data,
  meta_data,
  label_col,
  check_param = c("any", "location", "proportion"),
  plot_ranges = TRUE,
  flip_mode = "noflip"
)
```

Arguments

- `resp_vars` variable list the names of the measurement variables
- `group_vars` variable list the name of the observer, device or reader variable
- `study_data` data.frame the data frame that contains the measurements
- `meta_data` data.frame the data frame that contains metadata attributes of study data
- `label_col` variable attribute the name of the column in the metadata with labels of variables
- `check_param` enum any | location | proportion. Which type of check should be conducted (if possible): a check on the location of the mean or median value of the study data, a check on proportions of categories, or either of them if the necessary metadata is available.
- `plot_ranges` logical Should the plot show ranges and results from the data quality checks? (default: TRUE)
- `flip_mode` enum default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this can be controlled by setting the `options(dataquieR.flip_mode = ...)`. If called from `dq_report`, you can also pass `flip_mode` to all function calls or set them specifically using `specific_args`. 

Value

A list with:

- **SummaryTable**: data.frame containing data quality checks for "Unexpected location" (FLG_acc_ud_loc) and "Unexpected proportion" (FLG_acc_ud_prop) for each response variable in resp_vars.
- **SummaryData**: a data.frame containing data quality checks for "Unexpected location" and / or "Unexpected proportion" for a report
- **SummaryPlotList**: list of ggplots for each response variable in resp_vars.

Algorithm of this implementation:

- If no response variable is defined, select all variables of type float or integer in the study data.
- Remove missing codes from the study data (if defined in the metadata).
- Remove measurements deviating from (hard) limits defined in the metadata (if defined).
- Exclude variables containing only NA or only one unique value (excluding NAs).
- Perform check for "Unexpected location" if defined in the metadata (needs a LOCATION_METRIC (mean or median) and LOCATION_RANGE (range of expected values for the mean and median, respectively)).
- Perform check for "Unexpected proportion" if defined in the metadata (needs PROPORTION_RANGE (range of expected values for the proportions of the categories)).
- Plot histogram(s).
- If group_vars is specified by the user, distributions within group-wise ecdf are presented.

See Also

Online Documentation

---

**acc_distributions_loc**  
Plots and checks for distributions – Location

Description

Data quality indicator checks "Unexpected location" and "Unexpected proportion" with histograms and, if a grouping variable is included, plots of empirical cumulative distributions for the subgroups.

Indicator

Usage

```r
cacc_distributions_loc(
  resp_vars = NULL,
  study_data,
  meta_data,
  label_col,
  check_param = "location",
  plot_ranges = TRUE,
  flip_mode = "noflip"
)
```
Arguments

- **resp_vars**: variable list the names of the measurement variables
- **study_data**: data.frame the data frame that contains the measurements
- **meta_data**: data.frame the data frame that contains metadata attributes of study data
- **label_col**: variable attribute the name of the column in the metadata with labels of variables
- **check_param**: enum any | location | proportion. Which type of check should be conducted (if possible): a check on the location of the mean or median value of the study data, a check on proportions of categories, or either of them if the necessary metadata is available.
- **plot_ranges**: logical Should the plot show ranges and results from the data quality checks? (default: TRUE)
- **flip_mode**: enum default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this can be controlled by setting the `options(dataquieR.flip_mode = ...)`. If called from `dq_report`, you can also pass `flip_mode` to all function calls or set them specifically using `specific_args`.

Value

A list with:

- **SummaryTable**: data.frame containing data quality checks for "Unexpected location" (FLG_acc_ud_loc) and "Unexpected proportion" (FLG_acc_ud_prop) for each response variable in `resp_vars`.
- **SummaryData**: a data.frame containing data quality checks for "Unexpected location" and / or "Unexpected proportion" for a report
- **SummaryPlotList**: list of ggplots for each response variable in `resp_vars`.

Algorithm of this implementation:

- If no response variable is defined, select all variables of type float or integer in the study data.
- Remove missing codes from the study data (if defined in the metadata).
- Remove measurements deviating from (hard) limits defined in the metadata (if defined).
- Exclude variables containing only NA or only one unique value (excluding NAs).
- Perform check for "Unexpected location" if defined in the metadata (needs a LOCATION_METRIC (mean or median) and LOCATION_RANGE (range of expected values for the mean and median, respectively)).
- Perform check for "Unexpected proportion" if defined in the metadata (needs PROPOR-TION_RANGE (range of expected values for the proportions of the categories)).
- Plot histogram(s).
- If group_vars is specified by the user, distributions within group-wise ecdf are presented.

See Also

- acc_distributions
- Online Documentation
acc_distributions_loc_ecdf

Plots and checks for distributions – Location, ECDF

Description

Data quality indicator checks "Unexpected location" and "Unexpected proportion" with histograms and, if a grouping variable is included, plots of empirical cumulative distributions for the subgroups.

Indicator

Usage

acc_distributions_loc_ecdf(
  resp_vars = NULL,
  group_vars = NULL,
  study_data,
  meta_data,
  label_col,
  check_param = "location",
  plot_ranges = TRUE,
  flip_mode = "noflip"
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>resp_vars</td>
<td>variable list the names of the measurement variables</td>
</tr>
<tr>
<td>group_vars</td>
<td>variable list the name of the observer, device or reader variable</td>
</tr>
<tr>
<td>study_data</td>
<td>data.frame the data frame that contains the measurements</td>
</tr>
<tr>
<td>meta_data</td>
<td>data.frame the data frame that contains metadata attributes of study data</td>
</tr>
<tr>
<td>label_col</td>
<td>variable attribute the name of the column in the metadata with labels of variables</td>
</tr>
<tr>
<td>check_param</td>
<td>enum any</td>
</tr>
<tr>
<td>plot_ranges</td>
<td>logical Should the plot show ranges and results from the data quality checks? (default: TRUE)</td>
</tr>
<tr>
<td>flip_mode</td>
<td>enum default</td>
</tr>
</tbody>
</table>
Value

A list with:

- **SummaryTable**: data.frame containing data quality checks for "Unexpected location" (FLG_acc_ud_loc) and "Unexpected proportion" (FLG_acc_ud_prop) for each response variable in resp_vars.
- **SummaryData**: a data.frame containing data quality checks for "Unexpected location" and / or "Unexpected proportion" for a report
- **SummaryPlotList**: list of ggplots for each response variable in resp_vars.

Algorithm of this implementation:

- If no response variable is defined, select all variables of type float or integer in the study data.
- Remove missing codes from the study data (if defined in the metadata).
- Remove measurements deviating from (hard) limits defined in the metadata (if defined).
- Exclude variables containing only NA or only one unique value (excluding NAs).
- Perform check for "Unexpected location" if defined in the metadata (needs a LOCATION_METRIC (mean or median) and LOCATION_RANGE (range of expected values for the mean and median, respectively)).
- Perform check for "Unexpected proportion" if defined in the metadata (needs PROPOR-
  TION_RANGE (range of expected values for the proportions of the categories)).
- Plot histogram(s).
- If group_vars is specified by the user, distributions within group-wise ecdf are presented.

See Also

- acc_distributions
- Online Documentation

---

**acc_distributions_only**

*Plots and checks for distributions – only*

---

**Description**

**Descriptor**

**Usage**

```r
acc_distributions_only(
  resp_vars = NULL,
  study_data,
  meta_data,
  label_col,
  flip_mode = "noflip"
)
```
acc_distributions_only

Arguments

- **resp_vars**: variable list the names of the measurement variables
- **study_data**: data.frame the data frame that contains the measurements
- **meta_data**: data.frame the data frame that contains metadata attributes of study data
- **label_col**: variable attribute the name of the column in the metadata with labels of variables
- **flip_mode**: enum default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this can be controlled by setting the `roptions(dataquieR.flip_mode = ...)`. If called from `dq_report`, you can also pass `flip_mode` to all function calls or set them specifically using `specific_args`.

Value

A list with:

- **SummaryTable**: data.frame containing data quality checks for "Unexpected location" (FLG_acc_ud_loc) and "Unexpected proportion" (FLG_acc_ud_prop) for each response variable in **resp_vars**.
- **SummaryData**: a data.frame containing data quality checks for "Unexpected location" and / or "Unexpected proportion" for a report
- **SummaryPlotList**: list of ggplots for each response variable in **resp_vars**.

Algorithm of this implementation:

- If no response variable is defined, select all variables of type float or integer in the study data.
- Remove missing codes from the study data (if defined in the metadata).
- Remove measurements deviating from (hard) limits defined in the metadata (if defined).
- Exclude variables containing only NA or only one unique value (excluding NAs).
- Perform check for "Unexpected location" if defined in the metadata (needs a LOCATION_METRIC (mean or median) and LOCATION_RANGE (range of expected values for the mean and median, respectively)).
- Perform check for "Unexpected proportion" if defined in the metadata (needs PROPORTION_RANGE (range of expected values for the proportions of the categories)).
- Plot histogram(s).
- If group_vars is specified by the user, distributions within group-wise ecdf are presented.

See Also

- acc_distributions
- Online Documentation
acc_distributions_only_ecdf

Plots and checks for distributions – only, but with ecdf

Description

Descriptor

Usage

acc_distributions_only_ecdf(
  resp_vars = NULL,
  study_data,
  group_vars = NULL,
  meta_data,
  label_col,
  flip_mode = "noflip"
)

Arguments

resp_vars  variable list the names of the measurement variables
study_data  data.frame the data frame that contains the measurements
group_vars  variable list the name of the observer, device or reader variable
meta_data   data.frame the data frame that contains metadata attributes of study data
label_col   variable attribute the name of the column in the metadata with labels of variables
flip_mode   enum default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this can be controlled by setting the roptions(dataquieR.flip_mode = ...). If called from dq_report, you can also pass flip_mode to all function calls or set them specifically using specific_args.

Value

A list with:

- SummaryTable: data.frame containing data quality checks for "Unexpected location" (FLG_acc_ud_loc) and "Unexpected proportion" (FLG_acc_ud_prop) for each response variable in resp_vars.
- SummaryData: a data.frame containing data quality checks for "Unexpected location" and / or "Unexpected proportion" for a report
- SummaryPlotList: list of ggplots for each response variable in resp_vars.
Algorithm of this implementation:

- If no response variable is defined, select all variables of type float or integer in the study data.
- Remove missing codes from the study data (if defined in the metadata).
- Remove measurements deviating from (hard) limits defined in the metadata (if defined).
- Exclude variables containing only NA or only one unique value (excluding NAs).
- Perform check for "Unexpected location" if defined in the metadata (needs a LOCATION_METRIC (mean or median) and LOCATION_RANGE (range of expected values for the mean and median, respectively)).
- Perform check for "Unexpected proportion" if defined in the metadata (needs PROPORTION_RANGE (range of expected values for the proportions of the categories)).
- Plot histogram(s).
- If group_vars is specified by the user, distributions within group-wise ecdf are presented.

See Also

- acc_distributions
- Online Documentation

---

**acc_distributions_prop**

*Plots and checks for distributions – Proportion*

**Description**

Data quality indicator checks "Unexpected location" and "Unexpected proportion" with histograms and, if a grouping variable is included, plots of empirical cumulative distributions for the subgroups.

**Indicator**

**Usage**

```r
acc_distributions_prop(
    resp_vars = NULL,
    study_data,
    meta_data,
    label_col,
    check_param = "proportion",
    plot_ranges = TRUE,
    flip_mode = "noflip"
)
```
acc_distributions_prop

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>resp_vars</td>
<td>variable list the names of the measurement variables</td>
</tr>
<tr>
<td>study_data</td>
<td>data.frame the data frame that contains the measurements</td>
</tr>
<tr>
<td>meta_data</td>
<td>data.frame the data frame that contains metadata attributes of study data</td>
</tr>
<tr>
<td>label_col</td>
<td>variable attribute the name of the column in the metadata with labels of variables</td>
</tr>
<tr>
<td>check_param</td>
<td>enum any</td>
</tr>
<tr>
<td>plot_ranges</td>
<td>logical Should the plot show ranges and results from the data quality checks? (default: TRUE)</td>
</tr>
<tr>
<td>flip_mode</td>
<td>enum default</td>
</tr>
</tbody>
</table>

Value

A list with:

- **SummaryTable**: data.frame containing data quality checks for "Unexpected location" (FLG_acc_ud_loc) and "Unexpected proportion" (FLG_acc_ud_prop) for each response variable in resp_vars.
- **SummaryData**: a data.frame containing data quality checks for "Unexpected location" and / or "Unexpected proportion" for a report
- **SummaryPlotList**: list of ggplots for each response variable in resp_vars.

Algorithm of this implementation:

- If no response variable is defined, select all variables of type float or integer in the study data.
- Remove missing codes from the study data (if defined in the metadata).
- Remove measurements deviating from (hard) limits defined in the metadata (if defined).
- Exclude variables containing only NA or only one unique value (excluding NAs).
- Perform check for "Unexpected location" if defined in the metadata (needs a LOCATION_METRIC (mean or median) and LOCATION_RANGE (range of expected values for the mean and median, respectively)).
- Perform check for "Unexpected proportion" if defined in the metadata (needs PROPORTION_RANGE (range of expected values for the proportions of the categories)).
- Plot histogram(s).
- If group_vars is specified by the user, distributions within group-wise ecdf are presented.

See Also

- acc_distributions
- Online Documentation
## Description

This implementation contrasts the empirical distribution of a measurement variables against assumed distributions. The approach is adapted from the idea of rootograms (Tukey (1977)) which is also applicable for count data (Kleiber and Zeileis (2016)).

**Indicator**

**Usage**

```r
acc_end_digits(resp_vars = NULL, study_data, meta_data, label_col = VAR_NAMES)
```

**Arguments**

- `resp_vars`: variable the names of the measurement variables, mandatory
- `study_data`: data.frame the data frame that contains the measurements
- `meta_data`: data.frame the data frame that contains metadata attributes of study data
- `label_col`: variable attribute the name of the column in the metadata with labels of variables

**Value**

- a list with:
  - `SummaryTable`: data frame underlying the plot
  - `SummaryPlot`: ggplot2 distribution plot comparing expected with observed distribution

**Algorithm of this implementation:**

- This implementation is restricted to data of type float or integer.
- Missing codes are removed from `resp_vars` (if defined in the metadata)
- The user must specify the column of the metadata containing probability distribution (currently only: normal, uniform, gamma)
- Parameters of each distribution can be estimated from the data or are specified by the user
- A histogram-like plot contrasts the empirical vs. the technical distribution

**See Also**

- [Online Documentation](#)
Description

The following R implementation executes calculations for quality indicator "Unexpected location" (see here. Local regression (LOESS) is a versatile statistical method to explore an averaged course of time series measurements (Cleveland, Devlin, and Grosse 1988). In context of epidemiological data, repeated measurements using the same measurement device or by the same examiner can be considered a time series. LOESS allows to explore changes in these measurements over time.

Descriptor

Usage

```r
acc_loess(
  resp_vars,
  group_vars = NULL,
  time_vars,
  co_vars = NULL,
  study_data,
  meta_data,
  label_col = NULL,
  min_obs_in_subgroup = 30,
  resolution = 80,
  comparison_lines = list(type = c("mean/sd", "quartiles"), color = "grey30", linetype = 2, sd_factor = 0.5),
  mark_time_points = getOption("dataquieR.acc_loess.mark_time_points", FALSE),
  plot_observations = getOption("dataquieR.acc_loess.plot_observations", TRUE),
  plot_format = "AUTO"
)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Type</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>resp_vars</td>
<td>variable</td>
<td>the name of the continuous measurement variable</td>
</tr>
<tr>
<td>group_vars</td>
<td>variable</td>
<td>the name of the observer, device or reader variable</td>
</tr>
<tr>
<td>time_vars</td>
<td>variable</td>
<td>the name of the variable giving the time of measurement</td>
</tr>
<tr>
<td>co_vars</td>
<td>variable list</td>
<td>a vector of covariables for adjustment, for example age and sex. Can be NULL (default) for no adjustment.</td>
</tr>
<tr>
<td>study_data</td>
<td>data.frame</td>
<td>the data frame that contains the measurements</td>
</tr>
<tr>
<td>meta_data</td>
<td>data.frame</td>
<td>the data frame that contains metadata attributes of study data</td>
</tr>
<tr>
<td>label_col</td>
<td>variable attribute</td>
<td>the name of the column in the metadata with labels of variables</td>
</tr>
<tr>
<td>min_obs_in_subgroup</td>
<td>integer</td>
<td>(optional argument) If group_vars is specified, this argument can be used to specify the minimum number of observations required for each of the subgroups. Subgroups with fewer observations are excluded. The default number is 30.</td>
</tr>
</tbody>
</table>
resolution numeric the maximum number of time points used for plotting the trend lines

comparison_lines list type and style of lines with which trend lines are to be compared. Can be mean +/- 0.5 standard deviation (the factor can be specified differently in sd_factor) or quartiles (Q1, Q2, and Q3). Arguments color and linetype are passed to `ggplot2::geom_line()`.

mark_time_points logical mark time points with observations (caution, there may be many marks)

plot_observations logical show observations as scatter plot in the background. If there are co_vars specified, the values of the observations in the plot will also be adjusted for the specified covariables.

plot_format enum AUTO | COMBINED | FACETS | BOTH. Return the plot as one combined plot for all groups or as facet plots (one figure per group). BOTH will return both variants, AUTO will decide based on the number of observers.

Details

If mark_time_points or plot_observations is selected, but would result in plotting more than 400 points, only a sample of the data will be displayed.

Limitations

The application of LOESS requires model fitting, i.e. the smoothness of a model is subject to a smoothing parameter (span). Particularly in the presence of interval-based missing data, high variability of measurements combined with a low number of observations in one level of the group_vars may distort the fit. Since our approach handles data without knowledge of such underlying characteristics, finding the best fit is complicated if computational costs should be minimal. The default of LOESS in R uses a span of 0.75, which provides in most cases reasonable fits. The function acc_loess adapts the span for each level of the group_vars (with at least as many observations as specified in min_obs_in_subgroup and with at least three time points) based on the respective number of observations. LOESS consumes a lot of memory for larger datasets. That is why acc_loess switches to a generalized additive model with integrated smoothness estimation (gam by mgcv) if there are 1000 observations or more for at least one level of the group_vars (similar to geom_smooth from ggplot2).

Value

a list with:

- SummaryPlotList: list with two plots if plot_format = "BOTH", otherwise one of the two figures described below:
  - Loess_fits_facets: The plot contains LOESS-smoothed curves for each level of the group_vars in a separate panel. Added trend lines represent mean and standard deviation or quartiles (specified in comparison_lines) for moving windows over the whole data.
  - Loess_fits_combined: This plot combines all curves into one panel. Given a low number of levels in the group_vars, this plot eases comparisons. However, if the number increases this plot may be too crowded and unclear.
See Also

Online Documentation

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**accMargins**

Estimate marginal means, see *emmeans::emmeans*

---

### Description

margins does calculations for quality indicator Unexpected distribution wrt location (link). Therefore we pursue a combined approach of descriptive and model-based statistics to investigate differences across the levels of an auxiliary variable.

CAT: Unexpected distribution w.r.t. location

Marginal means

Marginal means rests on model based results, i.e. a significantly different marginal mean depends on sample size. Particularly in large studies, small and irrelevant differences may become significant. The contrary holds if sample size is low.

### Indicator

### Usage

```r
accMargins(
  resp_vars = NULL,
  group_vars = NULL,
  co_vars = NULL,
  threshold_type = NULL,
  threshold_value,
  min_obs_in_subgroup = 5,
  study_data,
  meta_data,
  label_col
)
```

### Arguments

- **resp_vars**: variable the name of the continuous measurement variable
- **group_vars**: variable list len=1-1. the name of the observer, device or reader variable
- **co_vars**: variable list a vector of covariables, e.g. age and sex for adjustment
- **threshold_type**: enum empirical | user | none. In case empirical is chosen a multiplier of the scale measure is used, in case of user a value of the mean or probability (binary data) has to be defined see Implementation and use of thresholds. In case of none, no thresholds are displayed and no flagging of unusual group levels is applied.
- **threshold_value**: numeric a multiplier or absolute value see Implementation and use of thresholds
**acc_margins**

- **min_obs_in_subgroup**
  - integer from=0. optional argument if a "group_var" is used. This argument specifies the minimum no. of observations that is required to include a subgroup (level) of the "group_var" in the analysis. Subgroups with less observations are excluded. The default is 5.
- **study_data**
  - data.frame the data frame that contains the measurements
- **meta_data**
  - data.frame the data frame that contains metadata attributes of study data
- **label_col**
  - variable attribute the name of the column in the metadata with labels of variables

**Details**

Limitations

Selecting the appropriate distribution is complex. Dozens of continuous, discrete or mixed distributions are conceivable in the context of epidemiological data. Their exact exploration is beyond the scope of this data quality approach. The function above uses the help function `util_dist_selection` which discriminates four cases:

- continuous data
- binary data
- count data with <= 20 categories
- count data with > 20 categories

Nonetheless, only three different plot types are generated. The fourth case is treated as continuous data. This is in fact a coarsening of the original data but for the purpose of clarity this approach is chosen.

**Value**

a list with:

- SummaryTable: data frame underlying the plot
- SummaryData: data frame
- SummaryPlot: ggplot2 margins plot

**See Also**

Online Documentation

**Examples**

```
## Not run:
# runs spuriously slow on rhub
load(system.file("extdata/study_data.RData", package = "dataquieR"))
load(system.file("extdata/meta_data.RData", package = "dataquieR"))
acc_margins(resp_vars = "DBP_0",
            study_data = study_data,
            meta_data = meta_data,
            group_vars = "USR_BP_0",
            label_col = LABEL,
```
acc_multivariate_outlier

Calculate and plot Mahalanobis distances

Description

A standard tool to detect multivariate outliers is the Mahalanobis distance. This approach is very helpful for the interpretation of the plausibility of a measurement given the value of another. In this approach the Mahalanobis distance is used as a univariate measure itself. We apply the same rules for the identification of outliers as in univariate outliers:

- the classical approach from Tukey: $1.5 \times IQR$ from the 1st ($Q_{25}$) or 3rd ($Q_{75}$) quartile.
- the 3SD approach, i.e. any measurement of the Mahalanobis distance not in the interval of $\bar{x} \pm 3 \times \sigma$ is considered an outlier.
- the approach from Hubert for skewed distributions which is embedded in the R package robustbase
- a completely heuristic approach named $\sigma$-gap.

For further details, please see the vignette for univariate outlier.

Indicator

Usage

```r
acc_multivariate_outlier(
  variable_group = NULL,
  id_vars = NULL,
  label_col,
  n_rules = 4,
  max_non_outliers_plot = 10000,
  criteria = c("tukey", "3sd", "hubert", "sigmagap"),
  study_data,
  meta_data
)
```

Arguments

- `variable_group` numeric list the names of the continuous measurement variables building a group, for that multivariate outliers make sense.
- `id_vars` variable optional, an ID variable of the study data. If not specified row numbers are used.
- `label_col` variable attribute the name of the column in the metadata with labels of variables
- `n_rules` numeric from=1 to=4. the no. of rules that must be violated to classify as outlier
acc_multivariate_outlier

max_non_outliers_plot

integer from=0. Maximum number of non-outlier points to be plot. If more points exist, a subsample will be plotted only. Note, that sampling is not deterministic.

criteria

set tukey | 3SD | hubert | sigmagap. a vector with methods to be used for detecting outliers.

study_data

data.frame the data frame that contains the measurements

meta_data

data.frame the data frame that contains metadata attributes of study data

Value

a list with:

• SummaryTable: data.frame underlying the plot
• SummaryPlot: ggplot2 outlier plot
• FlaggedStudyData data.frame contains the original data frame with the additional columns tukey, 3SD, hubert, and sigmagap. Every observation is coded 0 if no outlier was detected in the respective column and 1 if an outlier was detected. This can be used to exclude observations with outliers.

ALGORITHM OF THIS IMPLEMENTATION:

• Implementation is restricted to variables of type float
• Remove missing codes from the study data (if defined in the metadata)
• The covariance matrix is estimated for all variables from variable_group
• The Mahalanobis distance of each observation is calculated $MD_i^2 = (x_i - \mu)^T \Sigma^{-1} (x_i - \mu)$
• The four rules mentioned above are applied on this distance for each observation in the study data
• An output data frame is generated that flags each outlier
• A parallel coordinate plot indicates respective outliers

List function.

See Also

Online Documentation
Identify univariate outliers by four different approaches

Description

A classical but still popular approach to detect univariate outlier is the boxplot method introduced by Tukey 1977. The boxplot is a simple graphical tool to display information about continuous univariate data (e.g., median, lower and upper quartile). Outliers are defined as values deviating more than $1.5 \times IQR$ from the 1st (Q25) or 3rd (Q75) quartile. The strength of Tukey’s method is that it makes no distributional assumptions and thus is also applicable to skewed or non mound-shaped data Marsh and Seo, 2006. Nevertheless, this method tends to identify frequent measurements which are falsely interpreted as true outliers.

A somewhat more conservative approach in terms of symmetric and/or normal distributions is the 3SD approach, i.e. any measurement not in the interval of $\text{mean}(x) + / - 3 \times \sigma$ is considered an outlier.

Both methods mentioned above are not ideally suited to skewed distributions. As many biomarkers such as laboratory measurements represent in skewed distributions the methods above may be insufficient. The approach of Hubert and Vandervieren 2008 adjusts the boxplot for the skewness of the distribution. This approach is implemented in several R packages such as \texttt{robustbase::mc} which is used in this implementation of \texttt{dataquieR}.

Another completely heuristic approach is also included to identify outliers. The approach is based on the assumption that the distances between measurements of the same underlying distribution should homogeneous. For comprehension of this approach:

- consider an ordered sequence of all measurements.
- between these measurements all distances are calculated.
- the occurrence of larger distances between two neighboring measurements may than indicate a distortion of the data. For the heuristic definition of a large distance $1 \times \sigma$ has been been chosen.

Note, that the plots are not deterministic, because they use \texttt{ggplot2::geom_jitter}.

Indicator

Usage

\begin{verbatim}
acc_robust_univariate_outlier(
    resp_vars = NULL,
    label_col,
    study_data,
    meta_data,
    exclude_roles,
    n_rules = length(unique(criteria)),
    max_non_outliers_plot = 10000,
    criteria = c("tukey", "3sd", "hubert", "sigmagap")
)
\end{verbatim}
Arguments

- **resp_vars**: variable list the name of the continuous measurement variable
- **label_col**: variable attribute the name of the column in the metadata with labels of variables
- **study_data**: data.frame the data frame that contains the measurements
- **meta_data**: data.frame the data frame that contains metadata attributes of study data
- **exclude_roles**: variable roles a character (vector) of variable roles not included
- **n_rules**: integer from 1 to 4. the no. rules that must be violated to flag a variable as containing outliers. The default is 4, i.e. all.
- **max_non_outliers_plot**: integer from=0. Maximum number of non-outlier points to be plot. If more points exist, a subsample will be plotted only. Note, that sampling is not deterministic.
- **criteria**: set tukey | 3SD | hubert | sigmagap. a vector with methods to be used for detecting outliers.

Details

**Hint**: The function is designed for unimodal data only.

Value

a list with:

- SummaryTable: data.frame with the columns Variables, Mean, SD, Median, Skewness, Tukey (N), 3SD (N), Hubert (N), Sigma-gap (N), NUM_acc_ud_outlu, Outliers, low (N), Outliers, high (N) Grading
  - SummaryData: data.frame with the columns Variables, Mean, SD, Median, Skewness, Tukey (N), 3SD (N), Hubert (N), Sigma-gap (N), Outliers (N), Outliers, low (N), Outliers, high (N) Grading
  - SummaryPlotList: ggplot univariate outlier plots

ALGORITHM OF THIS IMPLEMENTATION:

- Select all variables of type float in the study data
- Remove missing codes from the study data (if defined in the metadata)
- Remove measurements deviating from limits defined in the metadata
- Identify outliers according to the approaches of Tukey (Tukey 1977), 3SD (Saleem et al. 2021), Hubert (Hubert and Vandervieren 2008), and SigmaGap (heuristic)
- An output data frame is generated which indicates the no. possible outliers, the direction of deviations (Outliers, low; Outliers, high) for all methods and a summary score which sums up the deviations of the different rules
- A scatter plot is generated for all examined variables, flagging observations according to the no. violated rules (step 5).

See Also

acc_univariate_outlier
acc_shape_or_scale

Description

This implementation contrasts the empirical distribution of a measurement variables against assumed distributions. The approach is adapted from the idea of rootograms (Tukey 1977) which is also applicable for count data (Kleiber and Zeileis 2016).

Indicator

Usage

```r
acc_shape_or_scale(
  resp_vars,
  dist_col,
  guess,
  par1,
  par2,
  end_digits,
  label_col,
  study_data,
  meta_data,
  flip_mode = "noflip"
)
```

Arguments

- `resp_vars`: `variable` the name of the continuous measurement variable
- `dist_col`: `variable attribute` the name of the variable attribute in meta_data that provides the expected distribution of a study variable
- `guess`: `logical` estimate parameters
- `par1`: `numeric` first parameter of the distribution if applicable
- `par2`: `numeric` second parameter of the distribution if applicable
- `end_digits`: `logical` internal use. check for end digits preferences
- `label_col`: `variable attribute` the name of the column in the metadata with labels of variables
- `study_data`: `data.frame` the data frame that contains the measurements
- `meta_data`: `data.frame` the data frame that contains metadata attributes of study data
- `flip_mode`: `enum` default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this can be controlled by setting the roptions(dataquieR.flip_mode = ...). If called from dq_report, you can also pass flip_mode to all function calls or set them specifically using specific_args.
Value

a list with:

- SummaryData: data.frame underlying the plot
- SummaryPlot: ggplot2 probability distribution plot
- SummaryTable: data.frame with the columns Variables and FLG_acc_ud_shape

ALGORITHM OF THIS IMPLEMENTATION:

- This implementation is restricted to data of type float or integer.
- Missing codes are removed from resp_vars (if defined in the metadata)
- The user must specify the column of the metadata containing probability distribution (currently only: normal, uniform, gamma)
- Parameters of each distribution can be estimated from the data or are specified by the user
- A histogram-like plot contrasts the empirical vs. the technical distribution

See Also

Online Documentation

Identify univariate outliers by four different approaches

Description

A classical but still popular approach to detect univariate outliers is the boxplot method introduced by Tukey 1977. The boxplot is a simple graphical tool to display information about continuous univariate data (e.g., median, lower and upper quartile). Outliers are defined as values deviating more than $1.5 \times IQR$ from the 1st (Q25) or 3rd (Q75) quartile. The strength of Tukey’s method is that it makes no distributional assumptions and thus is also applicable to skewed or non mound-shaped data Marsh and Seo, 2006. Nevertheless, this method tends to identify frequent measurements which are falsely interpreted as true outliers.

A somewhat more conservative approach in terms of symmetric and/or normal distributions is the 3SD approach, i.e. any measurement not in the interval of $\mu \pm 3 \sigma$ is considered an outlier.

Both methods mentioned above are not ideally suited to skewed distributions. As many biomarkers such as laboratory measurements represent in skewed distributions the methods above may be insufficient. The approach of Hubert and Vandervieren 2008 adjusts the boxplot for the skewness of the distribution. This approach is implemented in several R packages such as robustbase::mc which is used in this implementation of dataquicR.

Another completely heuristic approach is also included to identify outliers. The approach is based on the assumption that the distances between measurements of the same underlying distribution should homogeneous. For comprehension of this approach:
consider an ordered sequence of all measurements.
- between these measurements all distances are calculated.
- the occurrence of larger distances between two neighboring measurements may than indicate a distortion of the data. For the heuristic definition of a large distance $1 \times \sigma$ has been chosen.

Note, that the plots are not deterministic, because they use `ggplot2::geom_jitter`.

**Usage**

```r
acc_univariate_outlier(
  resp_vars = NULL,
  label_col,
  study_data,
  meta_data,
  exclude_roles,
  n_rules = length(unique(criteria)),
  max_non_outliers_plot = 10000,
  criteria = c("tukey", "3sd", "hubert", "sigmagap")
)
```

**Arguments**

- **resp_vars** variable list the name of the continuous measurement variable
- **label_col** variable attribute the name of the column in the metadata with labels of variables
- **study_data** data.frame the data frame that contains the measurements
- **meta_data** data.frame the data frame that contains metadata attributes of study data
- **exclude_roles** variable roles a character (vector) of variable roles not included
- **n_rules** integer from=1 to=4. the no. rules that must be violated to flag a variable as containing outliers. The default is 4, i.e. all.
- **max_non_outliers_plot** integer from=0. Maximum number of non-outlier points to be plot. If more points exist, a subsample will be plotted only. Note, that sampling is not deterministic.
- **criteria** set tukey | 3SD | hubert | sigmagap. a vector with methods to be used for detecting outliers.

**Details**

**Hint:** The function is designed for unimodal data only.

**Value**

a list with:
• SummaryTable: data.frame with the columns Variables, Mean, SD, Median, Skewness, Tukey (N), 3SD (N), Hubert (N), Sigma-gap (N), NUM_acc_ud_outlu, Outliers, low (N), Outliers, high (N) Grading
  – SummaryData: data.frame with the columns Variables, Mean, SD, Median, Skewness, Tukey (N), 3SD (N), Hubert (N), Sigma-gap (N), Outliers (N), Outliers, low (N), Outliers, high (N) Grading
  – SummaryPlotList: ggplot univariate outlier plots

ALGORITHM OF THIS IMPLEMENTATION:

• Select all variables of type float in the study data
• Remove missing codes from the study data (if defined in the metadata)
• Remove measurements deviating from limits defined in the metadata
• Identify outliers according to the approaches of Tukey (Tukey 1977), 3SD (Saleem et al. 2021), Hubert (Hubert and Vandervieren 2008), and SigmaGap (heuristic)
• An output data frame is generated which indicates the no. possible outliers, the direction of deviations (Outliers, low; Outliers, high) for all methods and a summary score which sums up the deviations of the different rules
• A scatter plot is generated for all examined variables, flagging observations according to the no. violated rules (step 5).

See Also

• acc_robust_univariate_outlier
• Online Documentation

acc_varcomp

Estimates variance components

Description

Variance based models and intraclass correlations (ICC) are approaches to examine the impact of so-called process variables on the measurements. This implementation is model-based.

NB: The term ICC is frequently used to describe the agreement between different observers, examiners or even devices. In respective settings a good agreement is pursued. ICC-values can vary between [-1;1] and an ICC close to 1 is desired (Koo and Li 2016, Müller and Büttner 1994). However, in multi-level analysis the ICC is interpreted differently. Please see Snijders et al. (Sniders and Bosker 1999). In this context the proportion of variance explained by respective group levels indicate an influence of (at least one) level of the respective group_vars. An ICC close to 0 is desired.

Indicator
Usage

acc_varcomp(
    resp_vars = NULL,
    group_vars,
    co_vars = NULL,
    min_obs_in_subgroup = 30,
    min_subgroups = 5,
    label_col = NULL,
    threshold_value = 0.05,
    study_data,
    meta_data
)

Arguments

resp_vars         variable list the names of the continuous measurement variables
group_vars        variable list the names of the resp. observer, device or reader variables
co_vars           variable list a vector of covariables, e.g. age and sex for adjustment
min_obs_in_subgroup integer from=0. optional argument if a "group_var" is used. This argument specifies the minimum no. of observations that is required to include a subgroup (level) of the "group_var" in the analysis. Subgroups with fewer observations are excluded. The default is 30.
min_subgroups     integer from=0. optional argument if a "group_var" is used. This argument specifies the minimum no. of subgroups (levels) included "group_var". If the variable defined in "group_var" has fewer subgroups it is not used for analysis. The default is 5.
label_col         variable attribute the name of the column in the metadata with labels of variables
threshold_value   numeric from=0 to=1. a numerical value ranging from 0-1
study_data        data.frame the data frame that contains the measurements
meta_data         data.frame the data frame that contains metadata attributes of study data

Value

a list with:

- SummaryTable: data frame with ICCs per rvs
- SummaryData: data frame with ICCs per rvs
- ScalarValue_max_icc: maximum variance contribution value by group_vars
- ScalarValue_argmax_icc: variable with maximum variance contribution by group_vars
**ALGORITHM OF THIS IMPLEMENTATION:**

- This implementation is yet restricted to data of type float.
- Missing codes are removed from resp_vars (if defined in the metadata)
- Deviations from limits, as defined in the metadata, are removed
- A linear mixed-effects model is estimated for resp_vars using co_vars and group_vars for adjustment.
- An output data frame is generated for group_vars indicating the ICC.

**See Also**

Online Documentation

**Examples**

```r
## Not run:
# runs spuriously slow on rhub
load(system.file("extdata/study_data.RData", package = "dataquieR"))
load(system.file("extdata/meta_data.RData", package = "dataquieR"))
co_vars <- c("SEX_0", "AGE_0")
min_obs_in_subgroup <- 30
min_subgroups <- 3
label_col <- LABEL
rvs <- c("DBP_0", "SBP_0")
group_vars <- prep_map_labels(rvs, meta_data = meta_data, from = label_col,
  to = VAR_NAMES)
group_vars <- prep_map_labels(group_vars, meta_data = meta_data,
  to = GROUP_VAR_OBSERVER)
group_vars <- prep_map_labels(group_vars, meta_data = meta_data)
acc_varcomp(
  resp_vars = rvs, group_vars = group_vars, co_vars = co_vars,
  min_obs_in_subgroup = min_obs_in_subgroup,
  min_subgroups = min_subgroups, label_col = label_col,
  study_data = study_data, meta_data = meta_data)
)
## End(Not run)
```

---

**as.data.frame.dataquieR_resultset**

*Convert a full dataquieR report to a data.frame*

**Description**

Deprecated
Usage

```r
## S3 method for class 'dataquieR_resultset'
as.data.frame(x, ...)
```

Arguments

- `x` Deprecated
- `...` Deprecated

Value

Deprecated

---

```r
as.list.dataquieR_resultset
```

*Convert a full dataquieR report to a list*

---

Description

Deprecated

Usage

```r
## S3 method for class 'dataquieR_resultset'
as.list(x, ...)
```

Arguments

- `x` Deprecated
- `...` Deprecated

Value

Deprecated
ASSOCIATION_DIRECTION

Cross-item level metadata attribute name

Description
The allowable direction of an association. The input is a string that can be either "positive" or "negative".

Usage
ASSOCIATION_DIRECTION

Format
An object of class character of length 1.

See Also
meta_data_cross
Other meta_data_cross: ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()

ASSOCIATION_FORM

Cross-item level metadata attribute name

Description
The allowable form of association. The string specifies the form based on a selected list.

Usage
ASSOCIATION_FORM

Format
An object of class character of length 1.

See Also
meta_data_cross
Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()
**ASSOCIATION_METRIC**

Cross-item level metadata attribute name

**Description**

The metric underlying the association in `ASSOCIATION_RANGE`. The input is a string that specifies the analysis algorithm to be used.

**Usage**

`ASSOCIATION_METRIC`

**Format**

An object of class `character` of length 1.

**See Also**

meta_data_cross

Other meta_data_cross: `ASSOCIATION_DIRECTION`, `ASSOCIATION_FORM`, `ASSOCIATION_RANGE`, `CHECK_ID`, `CHECK_LABEL`, `CONTRADICTION_TERM`, `CONTRADICTION_TYPE`, `DATA_PREPARATION`, `GOLDSTANDARD`, `MULTIVARIATE_OUTLIER_CHECKTYPE`, `N_RULES`, `REL_VAL`, `VARIABLE_LIST`, `util_normalize_cross_item()`

---

**ASSOCIATION_RANGE**

Cross-item level metadata attribute name

**Description**

Specifies the allowable range of an association. The inclusion of the endpoints follows standard mathematical notation using round brackets for open intervals and square brackets for closed intervals. Values must be separated by a semicolon.

**Usage**

`ASSOCIATION_RANGE`

**Format**

An object of class `character` of length 1.

**See Also**

meta_data_cross

Other meta_data_cross: `ASSOCIATION_DIRECTION`, `ASSOCIATION_FORM`, `ASSOCIATION_METRIC`, `CHECK_ID`, `CHECK_LABEL`, `CONTRADICTION_TERM`, `CONTRADICTION_TYPE`, `DATA_PREPARATION`, `GOLDSTANDARD`, `MULTIVARIATE_OUTLIER_CHECKTYPE`, `N_RULES`, `REL_VAL`, `VARIABLE_LIST`, `util_normalize_cross_item()`
cause_label_df

Data frame with labels for missing- and jump-codes

Description

data.frame with the following columns:

- CODE_VALUE: numeric | DATETIME Missing code (the number or date representing a missing)
- CODE_LABEL: character a label for the missing code
- CODE_CLASS: enum JUMP | MISSING. Class of the missing code.
- CODE_INTERPRET enum I | P | PL | R | BO | NC | O | UH | UO | NE. Class of the missing code according to AAPOR.
- resp_vars: character optional, if a missing code is specific for some variables, it is listed for each such variable with one entry in resp_vars. If NA, the code is assumed shared among all variables. For v1.0 metadata, you need to refer to VAR_NAMES here.

See Also

Online

CHECK_ID

Cross-item level metadata attribute name

Description

Specifies the unique IDs for cross-item level metadata records

Usage

CHECK_ID

Format

An object of class character of length 1.

Details

if missing, dataquieR will create such IDs

See Also

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()
**CHECK_LABEL**  
*Cross-item level metadata attribute name*

### Description

Specifies the unique labels for cross-item level metadata records

### Usage

CHECK_LABEL

### Format

An object of class character of length 1.

### Details

if missing, dataquieR will create such labels

### See Also

meta_data_cross  

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECK, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()

---

**check_table**  
*Data frame with contradiction rules*

### Description

Two versions exist, the newer one is used by con_contradictions_redcap and is described here, the older one used by con_contradictions is described here.

### See Also

meta_data_cross
Item-Missingness (also referred to as item nonresponse (De Leeuw et al. 2003)) describes the missingness of single values, e.g. blanks or empty data cells in a data set. Item-Missingness occurs for example in case a respondent does not provide information for a certain question, a question is overlooked by accident, a programming failure occurs or a provided answer were missed while entering the data.

Indicator

Usage

```r
com_item_missingness(
  study_data,       # data.frame the data frame that contains the measurements
  meta_data,        # data.frame the data frame that contains metadata attributes of study data
  resp_vars = NULL, # variable list the name of the measurement variables
  label_col,        # variable attribute the name of the column in the metadata with labels of variables
  show_causes = TRUE,# logical if TRUE, then the distribution of missing codes is shown
  cause_label_df,   # data.frame missing code table. If missing codes have labels the respective data frame can be specified here or in the metadata as assignments, see cause_label_df
  include_sysmiss = TRUE, # logical Optional, if TRUE system missingness (NAs) is evaluated in the summary plot
  threshold_value,  # numeric from=0 to=100. a numerical value ranging from 0-100
  suppressWarnings = FALSE, # logical
  assume_consistent_codes = TRUE, # logical
  expand_codes = assume_consistent_codes, # logical
  drop_levels = TRUE, # logical
  expected_observations = c("HIERARCHY", "ALL", "SEGMENT"), # char vector
  pretty_print = lifecycle::deprecated() # logical
)
```

Arguments

- **study_data**: data frame the data frame that contains the measurements
- **meta_data**: data frame the data frame that contains metadata attributes of study data
- **resp_vars**: variable list the name of the measurement variables
- **label_col**: variable attribute the name of the column in the metadata with labels of variables
- **show_causes**: logical if TRUE, then the distribution of missing codes is shown
- **cause_label_df**: data frame missing code table. If missing codes have labels the respective data frame can be specified here or in the metadata as assignments
- **include_sysmiss**: logical Optional, if TRUE system missingness (NAs) is evaluated in the summary plot
- **threshold_value**: numeric from=0 to=100. a numerical value ranging from 0-100
suppressWarnings logical warn about consistency issues with missing and jump lists
assume_consistent_codes logical if TRUE and no labels are given and the same missing/jump code is used for more than one variable, the labels assigned for this code are treated as being be the same for all variables.
expand_codes logical if TRUE, code labels are copied from other variables, if the code is the same and the label is set somewhere
drop_levels logical if TRUE, do not display unused missing codes in the figure legend.
expected_observations enum HIERARCHY | ALL | SEGMENT. If ALL, all observations are expected to comprise all study segments. If SEGMENT, the PART_VAR is expected to point to a variable with values of 0 and 1, indicating whether the variable was expected to be observed for each data row. If HIERARCHY, this is also checked recursively, so, if a variable points to such a participation variable, and that other variable does has also a PART_VAR entry pointing to a variable, the observation of the initial variable is only expected, if both segment variables are 1.
pretty_print logical deprecated. If you want to have a human readable output, use SummaryData instead of SummaryTable

Value

a list with:

- SummaryTable: data frame about item missingness per response variable
- SummaryData: data frame about item missingness per response variable formatted for user
- SummaryPlot: ggplot2 heatmap plot, if show_uses was TRUE
- ReportSummaryTable: data frame underlying SummaryPlot

ALGORITHM OF THIS IMPLEMENTATION:

- Lists of missing codes and, if applicable, jump codes are selected from the metadata
- The no. of system missings (NA) in each variable is calculated
- The no. of used missing codes is calculated for each variable
- The no. of used jump codes is calculated for each variable
- Two result dataframes (1: on the level of observations, 2: a summary for each variable) are generated
- OPTIONAL: if show_uses is selected, one summary plot for all resp_vars is provided

See Also

Online Documentation
com_qualified_item_missingness

Compute Indicators for Qualified Item Missingness

Description

Indicator

Usage

com_qualified_item_missingness(
  resp_vars,
  study_data,
  meta_data,
  label_col = NULL,
  expected_observations = c("HIERARCHY", "ALL", "SEGMENT")
)

Arguments

resp_vars variable list the name of the measurement variables
study_data data.frame the data frame that contains the measurements
meta_data data.frame the data frame that contains metadata attributes of study data
label_col variable attribute the name of the column in the metadata with labels of variables
expected_observations enum HIERARCHY | ALL | SEGMENT. Report the number of observations expected using the old PART_VAR concept. See com_item_missingness for an explanation.

Value

list list with entries:

Examples

## Not run:
prep_load_workbook_like_file("inst/extdata/Metadata_example_v3-6.xlsx")
clean <- prep_get_data_frame("item_level")
clean <- subset(clean, `Metadata name` == "Example" &
  !dataquieR:::util_empty(VAR_NAMES))
clean$`Metadata name` <- NULL
clean[, "MISSING_LIST_TABLE"] <- "missing_matchtable1"
prep_add_data_frames(item_level = clean)
clean <- prep_get_data_frame("missing_matchtable1")
clean <- clean[!clean$`Metadata name` == "Example", , FALSE]
clean <-
clean[suppressWarnings(as.character(as.integer(clean$CODE_VALUE)) ==

---
com_qualified_segment_missingness

**Description**

**Indicator**

**Usage**

```r
com_qualified_segment_missingness(
  study_data, 
  meta_data, 
  label_col = NULL, 
  meta_data_segment, 
  expected_observations = c("HIERARCHY", "ALL", "SEGMENT")
)
```
Arguments

- **study_data**: data.frame the data frame that contains the measurements
- **meta_data**: data.frame the data frame that contains metadata attributes of study data
- **label_col**: variable attribute the name of the column in the metadata with labels of variables
- **meta_data_segment**: data.frame Segment level metadata
- **expected_observations**: enum HIERARCHY | ALL | SEGMENT. Report the number of observations expected using the old PART_VAR concept. See com_item_missingness for an explanation.

Value

- list list with entries:

<table>
<thead>
<tr>
<th>com_segment_missingness</th>
</tr>
</thead>
<tbody>
<tr>
<td>Summarizes missingness for individuals in specific segments</td>
</tr>
</tbody>
</table>

Description

This implementation can be applied in two use cases:

1. participation in study segments is not recorded by respective variables, e.g. a participant’s refusal to attend a specific examination is not recorded.
2. participation in study segments is recorded by respective variables.

Use case (1) will be common in smaller studies. For the calculation of segment missingness it is assumed that study variables are nested in respective segments. This structure must be specified in the static metadata. The R-function identifies all variables within each segment and returns TRUE if all variables within a segment are missing, otherwise FALSE.

Use case (2) assumes a more complex structure of study data and metadata. The study data comprise so-called intro-variables (either TRUE/FALSE or codes for non-participation). The column PART_VAR in the metadata is filled by variable-IDs indicating for each variable the respective intro-variable. This structure has the benefit that subsequent calculation of item missingness obtains correct denominators for the calculation of missingness rates.

Descriptor

Usage

```r
com_segment_missingness(
  study_data,
  meta_data,
  group_vars = NULL,
  meta_data_segment,
  strata_vars = NULL,
)```

label_col,
threshold_value,
direction,
color_gradient_direction,
expected_observations = c("HIERARCHY", "ALL", "SEGMENT"),
exclude_roles = c(VARIABLE_ROLES$PROCESS)
)

Arguments

study_data data.frame the data frame that contains the measurements
meta_data data.frame the data frame that contains metadata attributes of study data
group_vars variable the name of a variable used for grouping, defaults to NULL for not grouping output
meta_data_segment data.frame Segment level metadata. Optional.
strata_vars variable the name of a variable used for stratification, defaults to NULL for not grouping output
label_col variable attribute the name of the column in the metadata with labels of variables
threshold_value numeric from=0 to=100. a numerical value ranging from 0-100
direction enum low | high. "high" or "low", i.e. are deviations above/below the threshold critical. This argument is deprecated and replaced by color_gradient_direction.
color_gradient_direction enum above | below. "above" or "below", i.e. are deviations above or below the threshold critical? (default: above)
expected_observations enum HIERARCHY | ALL | SEGMENT. If ALL, all observations are expected to comprise all study segments. If SEGMENT, the PART_VAR is expected to point to a variable with values of 0 and 1, indicating whether the variable was expected to be observed for each data row. If HIERARCHY, this is also checked recursively, so, if a variable points to such a participation variable, and that other variable does has also a PART_VAR entry pointing to a variable, the observation of the initial variable is only expected, if both segment variables are 1.
exclude_roles variable roles a character (vector) of variable roles not included

Details

Implementation and use of thresholds:
This implementation uses one threshold to discriminate critical from non-critical values. If direction is above than all values below the threshold_value are normal (displayed in dark blue in the plot and flagged with GRADING = 0 in the dataframe). All values above the threshold_value are considered critical. The more they deviate from the threshold the displayed color shifts to dark red. All critical values are highlighted with GRADING = 1 in the summary data frame. By default, highest values are always shown in dark red irrespective of the absolute deviation.
If direction is below than all values above the threshold_value are normal (displayed in dark blue, GRADING = 0).
**Hint:**
This function does not support a `resp_vars` argument but `exclude_roles` to specify variables not relevant for detecting a missing segment.
List function.

**Value**
a list with:

- `SummaryData`: data frame about segment missingness
- `SummaryPlot`: ggplot2 heatmap plot: a heatmap-like graphic that highlights critical values depending on the respective threshold_value and direction.

**See Also**
[Online Documentation](#)

---

**Description**
This implementation examines a crude version of unit missingness or unit-nonresponse (Kalton and Kasprzyk 1986), i.e. if all measurement variables in the study data are missing for an observation it has unit missingness.

The function can be applied on stratified data. In this case `strata_vars` must be specified.

**Descriptor**

**Usage**

```r
com_unit_missingness(  
  study_data,  
  meta_data,  
  id_vars = NULL,  
  strata_vars = NULL,  
  label_col  
)
```

**Arguments**

- `study_data`: data.frame the data frame that contains the measurements
- `meta_data`: data.frame the data frame that contains metadata attributes of study data
- `id_vars`: variable list optional, a (vectorized) call of ID-variables that should not be considered in the calculation of unit- missingness
- `strata_vars`: variable optional, a string or integer variable used for stratification
- `label_col`: variable attribute the name of the column in the metadata with labels of variables
Details

This implementation calculates a crude rate of unit-missingness. This type of missingness may have several causes and is an important research outcome. For example, unit-nonresponse may be selective regarding the targeted study population or technical reasons such as record-linkage may cause unit-missingness.

It has to be discriminated from segment and item missingness, since different causes and mechanisms may be the reason for unit-missingness.

Hint:
This function does not support a `resp_vars` argument but an `id_vars`, which have a roughly inverse logic behind: `id_vars` with values do not prevent a row from being considered missing, because an ID is the only hint for a unit that otherwise would not occur in the data at all.
List function.

Value

A list with:

- `FlaggedStudyData`: `data.frame` with id-only-rows flagged in a column `Unit_missing`
- `SummaryData`: `data.frame` with numbers and percentages of unit missingness

See Also

Online Documentation

contradiction_functions_descriptions

Description

description of the contradiction functions

Usage

contradiction_functions_descriptions

Format

An object of class list of length 11.
Description

Specifies a contradiction rule. Use REDCap like syntax, see online vignette

Usage

CONTRADICTION_TERM

Format

An object of class character of length 1.

See Also

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()

Description

Specifies the type of a contradiction. According to the data quality concept, there are logical and empirical contradictions, see online vignette

Usage

CONTRADICTION_TYPE

Format

An object of class character of length 1.

See Also

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, REL_VAL, VARIABLE_LIST, util Normalize_cross_item()
Description

This approach considers a contradiction if impossible combinations of data are observed in one participant. For example, if age of a participant is recorded repeatedly the value of age is (unfortunately) not able to decline. Most cases of contradictions rest on comparison of two variables.

Important to note, each value that is used for comparison may represent a possible characteristic but the combination of these two values is considered to be impossible. The approach does not consider implausible or inadmissible values.

Descriptor

Usage

```r
con_contractions(
    resp_vars = NULL,
    study_data,
    meta_data,
    label_col,
    threshold_value,
    check_table,
    summarize_categories = FALSE
)
```

Arguments

- `resp_vars` variable list the name of the measurement variables
- `study_data` data.frame the data frame that contains the measurements
- `meta_data` data.frame the data frame that contains metadata attributes of study data
- `label_col` variable attribute the name of the column in the metadata with labels of variables
- `threshold_value` numeric from=0 to=100. a numerical value ranging from 0-100
- `check_table` data.frame contradiction rules table. Table defining contradictions. See details for its required structure.
- `summarize_categories` logical Needs a column 'tag' in the check_table. If set, a summary output is generated for the defined categories plus one plot per category.

Details

**Algorithm of this implementation:::**

- Select all variables in the data with defined contradiction rules (static metadata column CONTRACTIONS)
• Remove missing codes from the study data (if defined in the metadata)
• Remove measurements deviating from limits defined in the metadata
• Assign label to levels of categorical variables (if applicable)
• Apply contradiction checks on predefined sets of variables
• Identification of measurements fulfilling contradiction rules. Therefore two output data frames are generated:
  – on the level of observation to flag each contradictory value combination, and
  – a summary table for each contradiction check.
• A summary plot illustrating the number of contradictions is generated.

List function.

Value

If `summarize_categories` is FALSE: A list with:

• `FlaggedStudyData`: The first output of the contradiction function is a data frame of similar dimension regarding the number of observations in the study data. In addition, for each applied check on the variables an additional column is added which flags observations with a contradiction given the applied check.
• `SummaryTable`: The second output summarizes this information into one data frame. This output can be used to provide an executive overview on the amount of contradictions. This output is meant for automatic digestion within pipelines.
• `SummaryData`: The third output is the same as `SummaryTable` but for human readers.
• `SummaryPlot`: The fourth output visualizes summarized information of `SummaryData`.

if `summarize_categories` is TRUE, other objects are returned: one per category named by that category (e.g. "Empirical") containing a result for contradictions within that category only. Additionally, in the slot `all_checks` a result as it would have been returned with `summarize_categories` set to FALSE. Finally, a slot `SummaryData` is returned containing sums per Category and an according `ggplot` in `SummaryPlot`.

See Also

Online Documentation

Examples

```r
# Not run:
load(system.file("extdata", "meta_data.RData", package = "dataquieR"))
load(system.file("extdata", "study_data.RData", package = "dataquieR"))
check_table <- read.csv(system.file("extdata",
  "contradiction_checks.csv",
  package = "dataquieR"
),
header = TRUE, sep = "#"
)
check_table[, "tag"] <- "Logical"
check_table[, "Label"] <- "Becomes younger"
```
Description

This approach considers a contradiction if impossible combinations of data are observed in one participant. For example, if age of a participant is recorded repeatedly the value of age is (unfortunately) not able to decline. Most cases of contradictions rest on comparison of two variables.

Important to note, each value that is used for comparison may represent a possible characteristic but the combination of these two values is considered to be impossible. The approach does not consider implausible or inadmissible values.
**con_contractions_redcap**

**Indicator**

**Usage**

```r
con_contractions_redcap(
  study_data,
  meta_data,
  label_col,
  threshold_value,
  meta_data_cross_item = "cross-item_level",
  use_value_labels,
  summarize_categories = FALSE
)
```

**Arguments**

- **study_data** `data.frame` the data frame that contains the measurements
- **meta_data** `data.frame` the data frame that contains metadata attributes of study data
- **label_col** variable attribute the name of the column in the metadata with labels of variables
- **threshold_value** numeric from=0 to=100. a numerical value ranging from 0-100
- **meta_data_cross_item** `data.frame` contradiction rules table. Table defining contradictions. See details for its required structure.
- **use_value_labels** `logical` Deprecated in favor of DATA_PREPARATION. If set to TRUE, labels can be used in the REDCap syntax to specify contraction checks for categorical variables. If set to FALSE, contractions have to be specified using the coded values. In case that this argument is not set in the function call, it will be set to TRUE if the metadata contains a column VALUE_LABELS which is not empty.
- **summarize_categories** `logical` Needs a column 'CONTRADICTION_TYPE' in the meta_data_cross_item. If set, a summary output is generated for the defined categories plus one plot per category. TODO: Not yet controllable by metadata.

**Details**

**Algorithm of this implementation::**

- Remove missing codes from the study data (if defined in the metadata)
- Remove measurements deviating from limits defined in the metadata
- Assign label to levels of categorical variables (if applicable)
- Apply contraction checks (given as REDCap-like rules in a separate metadata table)
- Identification of measurements fulfilling contradiction rules. Therefore two output data frames are generated:
  - on the level of observation to flag each contradictory value combination, and
  - a summary table for each contraction check.
- A summary plot illustrating the number of contradictions is generated.

List function.

Value

If `summarize_categories` is `FALSE`: A list with:

- `FlaggedStudyData`: The first output of the contradiction function is a data frame of similar dimension regarding the number of observations in the study data. In addition, for each applied check on the variables an additional column is added which flags observations with a contradiction given the applied check.
- `SummaryData`: The second output summarizes this information into one data frame. This output can be used to provide an executive overview on the amount of contradictions.
- `VariableGroupTable`: A subset of `SummaryData` used within the pipeline.
- `SummaryPlot`: The third output visualizes summarized information of `SummaryData`.

If `summarize_categories` is `TRUE`, other objects are returned: One per category named by that category (e.g. "Empirical") containing a result for contradiction checks within that category only. Additionally, in the slot `all_checks`, a result as it would have been returned with `summarize_categories` set to `FALSE`. Finally, a slot `SummaryData` is returned containing sums per Category and an according `ggplot` in `SummaryPlot`.

See Also

**Online Documentation**

Examples

```r
## Not run: # slow
load(system.file("extdata", "meta_data.RData", package = "dataquieR"))
load(system.file("extdata", "study_data.RData", package = "dataquieR"))
meta_data_cross_item <- prep_get_data_frame("meta_data_v2\cross-item_level")
label_col <- "LABEL"
threshold_value <- 1
con_contradictions_redcap(
  study_data = study_data, meta_data = meta_data, label_col = label_col,
  threshold_value = threshold_value, meta_data_cross_item = meta_data_cross_item
)
con_contradictions_redcap(
  study_data = study_data, meta_data = meta_data, label_col = label_col,
  threshold_value = threshold_value, meta_data_cross_item = meta_data_cross_item,
  summarize_categories = TRUE
)
## End(Not run)
```
con_inadmissible_categorical

*Detects variable levels not specified in metadata*

**Description**

For each categorical variable, value lists should be defined in the metadata. This implementation will examine, if all observed levels in the study data are valid.

**Indicator**

**Usage**

```r
con_inadmissible_categorical(
  resp_vars = NULL,
  study_data,
  meta_data,
  label_col,
  threshold_value = 0
)
```

**Arguments**

- `resp_vars`: variable list the name of the measurement variables
- `study_data`: data.frame the data frame that contains the measurements
- `meta_data`: data.frame the data frame that contains metadata attributes of study data
- `label_col`: variable attribute the name of the column in the metadata with labels of variables
- `threshold_value`: numeric from=0 to=100. a numerical value ranging from 0-100.

**Details**

**Algorithm of this implementation::**

- Remove missing codes from the study data (if defined in the metadata)
- Interpretation of variable specific VALUE_LABELS as supplied in the metadata.
- Identification of measurements not corresponding to the expected categories. Therefore two output data frames are generated:
  - on the level of observation to flag each undefined category, and
  - a summary table for each variable.
- Values not corresponding to defined categories are removed in a data frame of modified study data
con_limit_deviations

Value

a list with:

- `SummaryData`: data frame summarizing inadmissible categories with the columns:
  - `Variables`: variable name/label
  - `OBSERVED_CATEGORIES`: the categories observed in the study data
  - `DEFINED_CATEGORIES`: the categories defined in the metadata
  - `NON_MATCHING`: the categories observed but not defined
  - `NON_MATCHING_N`: the number of observations with categories not defined
  - `NON_MATCHING_N_PERCATEGORY`: the number of observations for each of the unexpected categories
  - `GRADING`: indicator TRUE/FALSE if inadmissible categorical values were observed (more than indicated by the `threshold_value`)
- `SummaryTable`: data frame for the `dataquieR` pipeline reporting the number and percentage of inadmissible categorical values
- `ModifiedStudyData`: study data having inadmissible categories removed
- `FlaggedStudyData`: study data having cases with inadmissible categories flagged

See Also

Online Documentation

---

con_limit_deviations  Detects variable values exceeding limits defined in metadata

Description

Inadmissible numerical values can be of type integer or float. This implementation requires the definition of intervals in the metadata to examine the admissibility of numerical study data. This helps identify inadmissible measurements according to hard limits (for multiple variables).

Indicator

Usage

```r
con_limit_deviations(
  resp_vars = NULL,
  label_col,
  study_data,
  meta_data,
  limits = NULL,
  flip_mode = "noflip",
  return_flagged_study_data = FALSE
)
```
**Arguments**

- **resp_vars**  
  variable list the name of the measurement variables

- **label_col**  
  variable attribute the name of the column in the metadata with labels of variables

- **study_data**  
  data.frame the data frame that contains the measurements

- **meta_data**  
  data.frame the data frame that contains metadata attributes of study data

- **limits**  
  enum HARD_LIMITS | SOFT_LIMITS | DETECTION_LIMITS. what limits from metadata to check for

- **flip_mode**  
  enum default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this can be controlled by setting the \texttt{options(dataquieR.flip_mode = \ldots)}. If called from \texttt{dq_report}, you can also pass \texttt{flip_mode} to all function calls or set them specifically using \texttt{specific_args}.

- **return_flagged_study_data**  
  logical return FlaggedStudyData in the result

**Details**

Algorithm of this implementation::

- Remove missing codes from the study data (if defined in the metadata)
- Interpretation of variable specific intervals as supplied in the metadata.
- Identification of measurements outside defined limits. Therefore two output data frames are generated:
  - on the level of observation to flag each deviation, and
  - a summary table for each variable.
- A list of plots is generated for each variable examined for limit deviations. The histogram-like plots indicate respective limits as well as deviations.
- Values exceeding limits are removed in a data frame of modified study data

**Value**

a list with:

- FlaggedStudyData data.frame related to the study data by a 1:1 relationship, i.e. for each observation is checked whether the value is below or above the limits. Optional, see \texttt{return_flagged_study_data}.

- SummaryTable data.frame summarizes limit deviations for each variable.

- SummaryPlotList list of \texttt{ggplots} The plots for each variable are either a histogram (continuous) or a barplot (discrete).

- ReportSummaryTable: heatmap-like data frame about limit violations

**See Also**

- Online Documentation
dataquieR_resultset

**Internal constructor for the internal class** dataquieR_resultset.

**Description**

creates an object of the class dataquieR_resultset.

**Usage**

dataquieR_resultset(...)

**Arguments**

... properties stored in the object

**Details**

The class features the following methods:

- as.data.frame.dataquieR_resultset
- as.list.dataquieR_resultset
- print.dataquieR_resultset
- summary.dataquieR_resultset

**Value**

an object of the class dataquieR_resultset.

**See Also**

dq_report

dataquieR_resultset_verify

**Verify an object of class** dataquieR_resultset

**Description**

Deprecated

**Usage**

dataquieR_resultset_verify(...)

**Arguments**

... Deprecated

**Value**

Deprecated
**DATA_PREPARATION**

Cross-item level metadata attribute name

**Description**

For contradiction rules, the required pre-processing steps that can be given. TODO JM: MISSING_LABEL will not work for non-factor variables

**Usage**

DATA_PREPARATION

**Format**

An object of class character of length 1.

**Details**

LABEL MISSING LIMITS MISSING_LABEL MISSING_INTERPRET

**See Also**

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()

---

**DATA_TYPES**

Data Types

**Description**

Data Types of Study Data:

In the metadata, the following entries are allowed for the variable attribute DATA_TYPE:

**Usage**

DATA_TYPES

**Format**

An object of class list of length 4.
Details

- integer for integer numbers
- string for text/string/character data
- float for decimal/floating point numbers
- datetime for timepoints

Data Types of Function Arguments:
As function arguments, dataquieR uses additional type specifications:

- numeric is a numerical value (float or integer), but it is not an allowed DATA_TYPE in the metadata. However, some functions may accept float or integer for specific function arguments. This is, where we use the term numeric.
- enum allows one element out of a set of allowed options similar to match.arg
- set allows a subset out of a set of allowed options similar to match.arg with several.ok = TRUE.
- variable Function arguments of this type expect a character scalar that specifies one variable using the variable identifier given in the metadata attribute VAR_NAMES or, if label_col is set, given in the metadata attribute given in that argument. Labels can easily be translated using prep_map_labels
- variable list Function arguments of this type expect a character vector that specifies variables using the variable identifiers given in the metadata attribute VAR_NAMES or, if label_col is set, given in the metadata attribute given in that argument. Labels can easily be translated using prep_map_labels

See Also

- integer
- string

DATA_TYPES_OF_R_TYPE  All available data types, mapped from their respective R types

Description

All available data types, mapped from their respective R types

Usage

DATA_TYPES_OF_R_TYPE

Format

An object of class list of length 14.

See Also

- prep_dq_data_type_of
des_scatterplot_matrix

Compute Pairwise Correlations

Description

works on variable groups (cross-item_level), which are expected to show a Pearson correlation

Usage

des_scatterplot_matrix(
  study_data,
  meta_data,
  label_col = LABEL,
  meta_data_cross_item = "cross-item_level"
)

Arguments

study_data data.frame the data frame that contains the measurements
meta_data data.frame the data frame that contains metadata attributes of study data
label_col variable attribute the name of the column in the metadata with labels of variables
meta_data_cross_item meta_data_cross

Details

Descriptor # TODO: This can be an indicator

Value

a list with the slots:

• SummaryPlotList: for each variable group a ggplot object with pairwise correlation plots
• SummaryData: table with columns VARIABLE_LIST, cors, max_cor, min_cor
• SummaryTable: like SummaryData, but machine readable and with stable column names.

Examples

## Not run:
devtools::load_all()
prep_load_workbook_like_file("meta_data_v2")
des_scatterplot_matrix("study_data")

## End(Not run)
Compute Descriptive Statistics

des_summary

Description

generates a descriptive overview on the variables in resp_vars.

Descriptor

Usage

des_summary(
  study_data,
  resp_vars = NULL,
  meta_data = "item_level",
  label_col = LABEL
)

Arguments

  study_data  data.frame the data frame that contains the measurements
  resp_vars   variable the name of the continuous measurement variable
  meta_data   data.frame the data frame that contains metadata attributes of study data
  label_col   variable attribute the name of the column in the metadata with labels of variables

Details

  TODO

Value

  a list with:
  • SummaryTable: data frame
  • SummaryData: data frame

See Also

  Online Documentation

Examples

  ## Not run:
  prep_load_workbook_like_file("meta_data_v2")
  xx <- des_summary("study_data", meta_data =
                       prep_get_data_frame("item_level"))
  util_html_table(xx$SummaryData)
  util_html_table(des_summary(study_data = prep_get_data_frame("study_data"),


**DF_ELEMENT_COUNT**

Data frame level metadata attribute name

---

### Description

Number of expected data elements in a data frame. numeric. Check only conducted if number entered.

### Usage

```r
DF_ELEMENT_COUNT
```

### Format

An object of class character of length 1.

### See Also

meta_data_dataframe

---

**DF_ID_REF_TABLE**

Data frame level metadata attribute name

---

### Description

The name of the data frame containing the reference IDs to be compared with the IDs in the study data set.

### Usage

```r
DF_ID_REF_TABLE
```

### Format

An object of class character of length 1.

### See Also

meta_data_dataframe
<table>
<thead>
<tr>
<th>Attribute</th>
<th>Description</th>
<th>Usage</th>
<th>Format</th>
<th>See Also</th>
</tr>
</thead>
<tbody>
<tr>
<td>DF_ID_VARS</td>
<td>All variables that are to be used as one single ID variable (combined key) in a data frame.</td>
<td>DF_ID_VARS</td>
<td>An object of class character of length 1.</td>
<td>meta_data_dataframe</td>
</tr>
<tr>
<td>DF_NAME</td>
<td>Name of the data frame</td>
<td>DF_NAME</td>
<td>An object of class character of length 1.</td>
<td>meta_data_dataframe</td>
</tr>
</tbody>
</table>
**DF_RECORD_CHECK**

Data frame level metadata attribute name

**Description**

The type of check to be conducted when comparing the reference ID table with the IDs delivered in the study data files.

**Usage**

DF_RECORD_CHECK

**Format**

An object of class character of length 1.

**See Also**

meta_data_dataframe

---

**DF_RECORD_COUNT**

Data frame level metadata attribute name

**Description**

Number of expected data records in a data frame. numeric. Check only conducted if number entered

**Usage**

DF_RECORD_COUNT

**Format**

An object of class character of length 1.

**See Also**

meta_data_dataframe
### DF_UNIQUE_ID

**Data frame level metadata attribute name**

**Description**

Defines expectancies on the uniqueness of the IDs across the rows of a data frame, or the number of times some ID can be repeated.

**Usage**

DF_UNIQUE_ID

**Format**

An object of class character of length 1.

**See Also**

meta_data_dataframe

### DF_UNIQUE_ROWS

**Data frame level metadata attribute name**

**Description**

Specifies whether identical data is permitted across rows in a data frame (excluding ID variables)

**Usage**

DF_UNIQUE_ROWS

**Format**

An object of class character of length 1.

**See Also**

meta_data_dataframe
**dim.dataquieR_resultset2**

*Get the dimensions of a dq_report2 result*

### Description

Get the dimensions of a dq_report2 result

### Usage

```r
## S3 method for class 'dataquieR_resultset2'
dim(x)
```

### Arguments

- `x` a `dataquieR_resultset2` result

### Value

- `dimensions` a vector of data quality dimensions. The supported dimensions are Completeness, Consistency and Accuracy.

### Description

- `dimensions` an object of class `character` of length 3.

### Format

- An object of class `character` of length 3.

### Value

- `dimensions` Only a definition, not a function, so no return value

### See Also

- [Data Quality Concept](#)
dimnames.dataquieR_resultset2

*Names of a dataquieR report object (v2.0)*

### Description

Names of a dataquieR report object (v2.0)

### Usage

```r
## S3 method for class 'dataquieR_resultset2'
dimnames(x)
```

### Arguments

- `x` the result object

### Value

the names

---

dims

*Dimension Titles for Prefixes*

### Description

order does matter, because it defines the order in the dq_report2.

### Usage

dims

### Format

An object of class character of length 5.

### See Also

- `util_html_for_var()`
- `util_html_for_dims()`
DISTRIBUTIONS

All available probability distributions for acc_shape_or_scale

Description

- **uniform** For uniform distribution
- **normal** For Gaussian distribution
- **GAMMA** For a gamma distribution

Usage

DISTRIBUTIONS

Format

An object of class list of length 3.

dq_report

*Generate a full DQ report*

Description

Deprecated

Usage

dq_report(...)

Arguments

... Deprecated

Value

Deprecated
dq_report2

Generate a full DQ report, v2

Description

Generate a full DQ report, v2

Usage

dq_report2(
  study_data,
  meta_data = "item_level",
  label_col = LABEL,
  meta_data_segment = "segment_level",
  meta_data_dataframe = "dataframe_level",
  meta_data_cross_item = "cross-item_level",
  meta_data_v2,
  ...
  dimensions = c("Completeness", "Consistency"),
  cores = list(mode = "socket", logging = FALSE, cpus = util_detect_cores(),
    load.balancing = TRUE),
  specific_args = list(),
  advanced_options = list(),
  author = prep_get_user_name(),
  title = "Data quality report",
  subtitle = as.character(Sys.Date()),
  user_info = NULL,
  debug_parallel = FALSE,
  resp_vars = character(0),
  filter_indicator_functions = character(0),
  filter_result_slots = c("^Summary", "^Segment", "^DataTypePlotList",
    "^ReportSummaryTable", "^Dataframe", "^Result", "^VariableGroup"),
  mode = c("default", "futures", "queue", "parallel"),
  mode_args = list(),
  notes_from_wrapper = list()
)

Arguments

study_data  data.frame the data frame that contains the measurements
meta_data  data.frame the data frame that contains metadata attributes of study data
label_col  variable attribute the name of the column in the metadata with labels of variables
meta_data_segment  data.frame – optional: Segment level metadata
meta_data_dataframe  data.frame – optional: Data frame level metadata
meta_data_cross_item
  data.frame – optional: Cross-item level metadata

meta_data_v2
  character path to workbook like metadata file, see prep_load_workbook_like_file for details. ALL LOADED DATAFRAMES WILL BE PURGED, using prep_purge_data_frame_cache, if you specify meta_data_v2.

... arguments to be passed to all called indicator functions if applicable.

dimensions
  dimensions Vector of dimensions to address in the report. Allowed values in the vector are Completeness, Consistency, and Accuracy. The generated report will only cover the listed data quality dimensions. Accuracy is computational expensive, so this dimension is not enabled by default. Completeness should be included, if Consistency is included, and Consistency should be included, if Accuracy is included to avoid misleading detections of e.g. missing codes as outliers, please refer to the data quality concept for more details. Integrity is always included.

cores
  integer number of cpu cores to use or a named list with arguments for parallelMap::parallelStart or NULL, if parallel has already been started by the caller. Can also be a cluster.

specific_args
  list named list of arguments specifically for one of the called functions, the of the list elements correspond to the indicator functions whose calls should be modified. The elements are lists of arguments.

advanced_options
  list options to set during report computation, see options()

author
  character author for the report documents.

title
  character optional argument to specify the title for the data quality report

subtitle
  character optional argument to specify a subtitle for the data quality report

user_info
  list additional info stored with the report, e.g., comments, title, ...

debug_parallel
  logical print blocks currently evaluated in parallel

resp_vars
  variable list the name of the measurement variables for the report. If missing, all variables will be used. Only item level indicator functions are filtered, so far.

filter_indicator_functions
  character regular expressions, only if an indicator function’s name matches one of these, it’ll be used for the report. If of length zero, no filtering is performed.

filter_result_slots
  character regular expressions, only if an indicator function’s result’s name matches one of these, it’ll be used for the report. If of length zero, no filtering is performed.

mode
  character work mode for parallel execution. default is "default", the values mean: - default: use queue except cores has been set explicitly - futures: use the future package - queue: use a queue as described in the examples from the callr package by Csárdi and Chang and start sub-processes as workers that evaluate the queue. - parallel: use the cluster from cores to evaluate all calls of indicator functions using the classic R parallel back-ends

mode_args
  list of arguments for the selected mode. As of writing this manual, only for the mode queue the argument step is supported, which gives the number of
dq_report_by

Generate a stratified full DQ report

Description

Generate a stratified full DQ report

function calls that are run by one worker at a time. The default is 15, which gives on most of the tested systems a good balance between synchronization overhead and idling workers.

Notes from wrapper

- list a list containing notes about changed labels by dq_report_by (otherwise NULL)

Details

See dq_report_by for a way to generate stratified or splitted reports easily.

Value

- a dataquieR_resultset2 that can be printed creating a HTML-report.

See Also

- as.data.frame.dataquieR_resultset
- as.list.dataquieR_resultset
- print.dataquieR_resultset
- summary.dataquieR_resultset
- dq_report_by

Examples

```r
## Not run:
prep_load_workbook_like_file("inst/extdata/meta_data_v2.xlsx")
meta_data <- prep_get_data_frame("item_level")
meta_data_cross <- prep_get_data_frame("cross-item_level")
x <- dq_report2("study_data", dimensions = NULL, label_col = "LABEL")
xx <- pbapply::pblapply(x, util_eval_to_dataquieR_result, env = environment())
xx <- pbapply::pblapply(tail(x), util_eval_to_dataquieR_result, env = environment())
xx <- parallel
  cat(vapply(x, deparse1, FUN.VALUE = character(1)), sep = "\n", file = "all_calls.txt")
  rstudioapi::navigateToFile("all_calls.txt")
  eval(x$`acc_multivariate_outlier.Blood pressure checks`)  
## End(Not run)
```
dq_report_by

Usage

dq_report_by(
    study_data,
    meta_data = "item_level",
    meta_data_segment = "segment_level",
    meta_data_dataframe = "dataframe_level",
    meta_data_cross_item = "cross-item_level",
    label_col,
    meta_data_v2,
    meta_data_split = STUDY_SEGMENT,
    study_data_split,
    ...,
    output_dir = NULL,
    also_print = FALSE,
    disable_plotly = FALSE
)

Arguments

study_data data.frame the data frame that contains the measurements
meta_data data.frame the data frame that contains metadata attributes of study data
meta_data_segment data.frame – optional: Segment level metadata
meta_data_dataframe data.frame – optional: Data frame level metadata
meta_data_cross_item data.frame – optional: Cross-item level metadata
label_col variable attribute the name of the column in the metadata with labels of variables
meta_data_v2 character path to workbook like metadata file, see prep_load_workbook_like_file for details. ALL LOADED DATAFRAMES WILL BE PURGED, using prep_purge_data_frame_cache, if you specify meta_data_v2.
meta_data_split variable attribute name of a metadata attribute to split the report in sections of variables, e.g. all blood-pressure. By default, reports are split by STUDY_SEGMENT if available.
study_data_split variable Name of a study variable to stratify the report by, e.g. the study centers.
... arguments to be passed through to dq_report or dq_report2
output_dir character if given, the output is not returned but
also_print logical if output_dir is not NULL, also create HTML output for each segment using print.dataquieR_resultset2(), written to the path output_dir
disable_plotly logical do not use plotly, even if installed

Value

named list of named lists of dq_report2 reports or, if output_dir has been specified, invisible(NULL)
See Also

dq_report

Examples

```r
## Not run: # really long-running example.
prep_load_workbook_like_file("meta_data_v2")
rep <- dq_report_by("study_data", label_col = LABEL, study_data_split = "CENTER_0")
rep <- dq_report_by("study_data",
  label_col = LABEL, study_data_split = "CENTER_0",
  meta_data_split = NULL
)
unlink("/tmp/testRep/", force = TRUE, recursive = TRUE)
dq_report_by("study_data",
  label_col = LABEL, study_data_split = "CENTER_0",
  meta_data_split = STUDY_SEGMENT, output_dir = "/tmp/testRep"
)
unlink("/tmp/testRep/", force = TRUE, recursive = TRUE)
dq_report_by("study_data",
  label_col = LABEL, study_data_split = "CENTER_0",
  meta_data_split = NULL, output_dir = "/tmp/testRep"
)
dq_report_by("study_data",
  label_col = LABEL,
  meta_data_split = STUDY_SEGMENT, output_dir = "/tmp/testRep"
)
dq_report_by("study_data",
  label_col = LABEL,
  meta_data_split = STUDY_SEGMENT, output_dir = "/tmp/testRep",
  also_print = TRUE
)
dq_report_by(study_data = "study_data", meta_data_v2 = "meta_data_v2",
  advanced_options = list(dataquieR.study_data_cache_max = 0,
    dataquieR.study_data_cache_metrics = TRUE,
    dataquieR.study_data_cache_metrics_env = environment()),
  cores = NULL, dimensions = "int")
dq_report_by(study_data = "study_data", meta_data_v2 = "meta_data_v2",
  advanced_options = list(dataquieR.study_data_cache_max = 0),
  cores = NULL, dimensions = "int")
## End(Not run)
```

<table>
<thead>
<tr>
<th>GOLDSTANDARD</th>
<th>Cross-item level metadata attribute name</th>
</tr>
</thead>
</table>

Description

Defines the measurement variable to be used as a known gold standard. Only one variable can be defined as the gold standard.
Usage

GOLDSTANDARD

Format

An object of class character of length 1.

See Also

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, MULTIVARIATE_OUTLIER_CHECK, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()

html_dependency_clipboard

HTML Dependency for report headers in clipboard

Description

HTML Dependency for report headers in clipboard

Usage

html_dependency_clipboard()

Value

the dependency

html_dependency_dataquieR

HTML Dependency for dataquieR

Description

generate all dependencies used in static dataquieR reports

Usage

html_dependency_dataquieR(iframe = FALSE)

Arguments

iframe logical(1) if TRUE, create the dependency used in figure iframes.
### html_dependency_report_dt

**HTML Dependency for report headers in DT::datatable**

**Description**

HTML Dependency for report headers in DT::datatable

**Usage**

html_dependency_report_dt()

**Value**

the dependency

### html_dependency_tippy

**HTML Dependency for tippy**

**Description**

HTML Dependency for tippy

**Usage**

html_dependency_tippy()

**Value**

the dependency
**html_dependency_vert_dt**

*HTML Dependency for vertical headers in DT::datatable*

### Description

HTML Dependency for vertical headers in DT::datatable

### Usage

```r
html_dependency_vert_dt()
```

### Value

the dependency

---

**int_all_datastructure_dataframe**

*Wrapper function to check for studies data structure*

### Description

This function tests for unexpected elements and records, as well as duplicated identifiers and content. The unexpected element record check can be conducted by providing the number of expected records or an additional table with the expected records. It is possible to conduct the checks by study segments or to consider only selected segments.

### Usage

```r
int_all_datastructure_dataframe(
    meta_data_dataframe = "dataframe_level",
    meta_data = "item_level"
)
```

### Arguments

- **meta_data_dataframe**
  - `data.frame` the data frame that contains the metadata for the data frame level, mandatory

- **meta_data**
  - `data.frame` the data frame that contains metadata attributes of the study data, mandatory. The metadata data frame is assumed to contain the information from all the studies. This is needed to know the VAR_NAMES, i.e., the column names used in data frames and known from the metadata.
Value

- DataframeTable: data frame with selected check results, used for the data quality report.

Examples

```r
## Not run:
out_dataframe <- int_all_datastructure_dataframe(
  meta_data_dataframe = "meta_data_dataframe",
  meta_data = "ship_meta"
)
md0 <- prep_get_data_frame("ship_meta")
md0
md0$VAR_NAMES
md0$VAR_NAMES[[1]] <- "Id" # is this mismatch reported -- is the data frame also reported, if nothing is wrong with it
out_dataframe <- int_all_datastructure_dataframe(
  meta_data_dataframe = "meta_data_dataframe",
  meta_data = md0
)

# This is the "normal" procedure for inside pipeline
# but outside this function checktype is exact by default
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "subset_u")
lapply(setNames(nm = prep_get_data_frame("meta_data_dataframe")$DF_NAME),
  int_sts_element_dataframe, meta_data = md0)
md0$VAR_NAMES[[1]] <- "id" # is this mismatch reported -- is the data frame also reported,
  # if nothing is wrong with it
lapply(setNames(nm = prep_get_data_frame("meta_data_dataframe")$DF_NAME),
  int_sts_element_dataframe, meta_data = md0)
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "exact")

## End(Not run)
```

---

**int_all_datastructure_segment**

*Wrapper function to check for segment data structure*

**Description**

This function tests for unexpected elements and records, as well as duplicated identifiers and content. The unexpected element record check can be conducted by providing the number of expected records or an additional table with the expected records. It is possible to conduct the checks by study segments or to consider only selected segments.

**Indicator**
int_all_datastructure_segment

Usage

int_all_datastructure_segment(
  meta_data_segment = "segment_level",
  study_data,
  meta_data = "item_level"
)

Arguments

meta_data_segment  
data.frame the data frame that contains the metadata for the segment level, mandatory.

study_data  
data.frame the data frame that contains the measurements, mandatory.

meta_data  
data.frame the data frame that contains metadata attributes of the study data, mandatory.

Value

a list with

• SegmentTable: data frame with selected check results, used for the data quality report.

Examples

## Not run:
out_segment <- int_all_datastructure_segment(
  meta_data_segment = "meta_data_segment",
  study_data = "ship",
  meta_data = "ship_meta"
)

study_data <- cars
meta_data <- dataquieR::prep_create_meta(VAR_NAMES = c("speedx", "distx"),
DATA_TYPE = c("integer", "integer"), MISSING_LIST = "|", JUMP_LIST = "|",
STUDY_SEGMENT = c("Intro", "Ex"))

out_segment <- int_all_datastructure_segment(
  meta_data_segment = "meta_data_segment",
  study_data = study_data,
  meta_data = meta_data
)

## End(Not run)
int_datatype_matrix  Check declared data types of metadata in study data

Description

Checks data types of the study data and for the data type declared in the metadata

Indicator

Usage

int_datatype_matrix(
  resp_vars = NULL,
  study_data,
  meta_data,
  split_segments = FALSE,
  label_col,
  max_vars_per_plot = 20,
  threshold_value = 0
)

Arguments

resp_vars  variable the names of the measurement variables, if missing or NULL, all variables will be checked
study_data  data.frame the data frame that contains the measurements
meta_data  data.frame the data frame that contains metadata attributes of study data
split_segments  logical return one matrix per study segment
label_col  variable attribute the name of the column in the metadata with labels of variables
max_vars_per_plot  integer from=0. The maximum number of variables per single plot.
threshold_value  numeric from=0 to=100. percentage failing conversions allowed to still classify a study variable convertible.

Details

This is a preparatory support function that compares study data with associated metadata. A prerequisite of this function is that the no. of columns in the study data complies with the no. of rows in the metadata.

For each study variable, the function searches for its data type declared in static metadata and returns a heatmap like matrix indicating data type mismatches in the study data.

List function.
**int_duplicate_content**

**Value**

a list with:

- **SummaryTable**: data frame about the applicability of each indicator function (each function in a column). Its integer values can be one of the following four categories: 0. Non-matching datatype, 1. Matching datatype,
- **SummaryPlot**: `ggplot2` heatmap plot, graphical representation of `SummaryTable`
- **DataTypePlotList**: list of plots per (maybe artificial) segment
- **ReportSummaryTable**: data frame underlying `SummaryPlot`

**Examples**

```r
## Not run:
load(system.file("extdata/meta_data.RData", package = "dataquieR"), envir = environment())
load(system.file("extdata/study_data.RData", package = "dataquieR"), envir = environment())
study_data$v00000 <- as.character(study_data$v00000)
study_data$v00002 <- as.character(study_data$v00002)
study_data$v00002[3] <- ""
appmatrix <- int_datatype_matrix(study_data = study_data,
                                 meta_data = meta_data,
                                 label_col = LABEL)
study_data$v00002[5] <- "X"
appmatrix <- int_datatype_matrix(study_data = study_data,
                                 meta_data = meta_data,
                                 label_col = LABEL)
appmatrix$ReportSummaryTable
## End(Not run)
```

**Description**

This function tests for duplicates entries in the data set. It is possible to check duplicated entries by study segments or to consider only selected segments.

**Indicator**

**Usage**

```r
int_duplicate_content(level = c("dataframe", "segment"), ...)
```
int_duplicate_ids

Arguments

level character a character vector indicating whether the assessment should be conducted at the study level (level = "dataframe") or at the segment level (level = "segment").

... Depending on level, passed to either util_int_duplicate_content_segment or util_int_duplicate_content_dataframe

Value

a list. Depending on level, see util_int_duplicate_content_segment or util_int_duplicate_content_dataframe for a description of the outputs.

Description

This function tests for duplicates entries in identifiers. It is possible to check duplicated identifiers by study segments or to consider only selected segments.

Indicator

Usage

int_duplicate_ids(level = c("dataframe", "segment"), ...)

Arguments

level character a character vector indicating whether the assessment should be conducted at the study level (level = "dataframe") or at the segment level (level = "segment").

... Depending on level, passed to either util_int_duplicate_ids_segment or util_int_duplicate_ids_dataframe

Value

a list. Depending on level, see util_int_duplicate_ids_segment or util_int_duplicate_ids_dataframe for a description of the outputs.
**int_part_vars_structure**

*Detect Expected Observations*

**Description**

For each participant, check, if an observation was expected, given the PART_VARS from item-level metadata.

**Usage**

```r
int_part_vars_structure(
  study_data,
  meta_data,
  label_col = LABEL,
  expected_observations = c("HIERARCHY", "SEGMENT"),
  disclose_problem_part_var_data = FALSE
)
```

**Arguments**

- **study_data**: study_data must have all relevant PART_VARS to avoid false-positives on PART_VARS missing from study_data.
- **meta_data**: meta_data must be complete to avoid false positives on non-existing PART_VARS.
- **label_col**: character mapping attribute colnames(study_data) vs. meta_data[label_col].
- **expected_observations**: enum HIERARCHY | SEGMENT. How should PART_VARS be handled: - SEGMENT: if PART_VAR is 1, an observation is expected - HIERARCHY: the default, if the PART_VAR is 1 for this variable and also for all PART_VARS of PART_VARS up in the hierarchy, an observation is expected.
- **disclose_problem_part_var_data**: logical show the problematic data (PART_VAR only).

**Details**

- **Descriptor**

**Value**

empty list, so far – the function only warns.
int_sts_element_dataframe

_Determine missing and/or superfluous data elements_

**Description**

Depends on dataquieR.ELEMENT_MISSMATCH_CHECKTYPE option, see there – # TODO: Rind out, how to document and link it here using Roxygen.

**Usage**

`int_sts_element_dataframe(study_data, meta_data = "item_level")`

**Arguments**

- `study_data` _data.frame_ the data frame that contains the measurements
- `meta_data` _data.frame_ the data frame that contains metadata attributes of study data

**Details**

- **Indicator**

**Value**

A list with names lots:

- `DataframeData`: data frame with the unexpected elements check results.
- `DataframeTable`: _data.frame_ table with all errors, used for the data quality report: - `MISSING`: meta_data or study_data: where is the element missing - `PCT_int_sts_element`: Percentage of element mismatches - `NUM_int_sts_element`: Number of element mismatches - `resp_vars`: affected element names

---

int_sts_element_segment

_Checks for element set_

**Description**

Depends on dataquieR.ELEMENT_MISSMATCH_CHECKTYPE option, see there – # TODO: Rind out, how to document and link it here using Roxygen.

**Usage**

`int_sts_element_segment(study_data, meta_data = "item_level")`
int_sts_element_segment

Arguments

study_data  data.frame the data frame that contains the measurements, mandatory.
meta_data  data.frame the data frame that contains metadata attributes of the study data, mandatory.

Details

Indicator

Value

a list with

- SegmentData: data frame with the unexpected elements check results. - Segment: name of the corresponding segment, if applicable, ALL otherwise
- SegmentTable: data frame with the unexpected elements check results, used for the data quality report. - Segment: name of the corresponding segment, if applicable, ALL otherwise

Examples

```r
## Not run:
study_data <- cars
meta_data <- dataquieR::prep_create_meta(VAR_NAMES = c("speedx", "distx"),
DATA_TYPE = c("integer", "integer"), MISSING_LIST = "|", JUMP_LIST = "|",
STUDY_SEGMENT = c("Intro", "Ex"))
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "none")
int_sts_element_segment(study_data, meta_data)
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "exact")
int_sts_element_segment(study_data, meta_data)
study_data <- cars
meta_data <- dataquieR::prep_create_meta(VAR_NAMES = c("speedx", "distx"),
DATA_TYPE = c("integer", "integer"), MISSING_LIST = "|", JUMP_LIST = "|",
STUDY_SEGMENT = c("Intro", "Intro"))
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "none")
int_sts_element_segment(study_data, meta_data)
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "exact")
int_sts_element_segment(study_data, meta_data)
study_data <- cars
meta_data <- dataquieR::prep_create_meta(VAR_NAMES = c("speed", "distx"),
DATA_TYPE = c("integer", "integer"), MISSING_LIST = "|", JUMP_LIST = "|",
STUDY_SEGMENT = c("Intro", "Intro"))
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "none")
int_sts_element_segment(study_data, meta_data)
options(dataquieR.ELEMENT_MISSMATCH_CHECKTYPE = "exact")
int_sts_element_segment(study_data, meta_data)

## End(Not run)
```
**int_unexp_elements**

*Check for unexpected data element count*

**Description**
This function contrasts the expected element number in each study in the metadata with the actual element number in each study data frame.

**Indicator**

**Usage**

```r
int_unexp_elements(identifier_name_list, data_element_count)
```

**Arguments**

- **identifier_name_list**
  - character a character vector indicating the name of each study data frame, mandatory.
- **data_element_count**
  - integer an integer vector with the number of expected data elements, mandatory.

**Value**

a list with

- **DataframeData**: data frame with the results of the quality check for unexpected data elements
- **DataframeTable**: data frame with selected unexpected data elements check results, used for the data quality report.

**Examples**

```r
## Not run:
study_tables <- list("sd1" = readRDS(system.file("extdata", "ship_subset1.RDS", package = "dataquieR")),
                     "sd2" = readRDS(system.file("extdata", "ship_subset2.RDS", package = "dataquieR")))

prep_add_data_frames(data_frame_list = study_tables)

int_unexp_elements(
  identifier_name_list = c("sd1", "sd2"),
  data_element_count = c(30, 29)
)

## End(Not run)
```
**int_unexp_records_dataframe**

*Check for unexpected data record count at the data frame level*

**Description**

This function contrasts the expected record number in each study in the metadata with the actual record number in each study data frame.

**Indicator**

**Usage**

```r
int_unexp_records_dataframe(identifier_name_list, data_record_count)
```

**Arguments**

- `identifier_name_list` character a character vector indicating the name of each study data frame, mandatory.
- `data_record_count` integer an integer vector with the number of expected data records per study data frame, mandatory.

**Value**

a list with

- `DataframeData`: data frame with the results of the quality check for unexpected data elements
- `DataframeTable`: data frame with selected unexpected data elements check results, used for the data quality report.

**int_unexp_records_segment**

*Check for unexpected data record count within segments*

**Description**

This function contrasts the expected record number in each study segment in the metadata with the actual record number in each segment data frame.

**Indicator**
Usage

```r
int_unexp_records_segment(
    study_segment,
    data_record_count,
    study_data,
    meta_data
)
```

Arguments

- **study_segment**  character a character vector indicating the name of each study data frame, mandatory.
- **data_record_count**  integer an integer vector with the number of expected data records, mandatory.
- **study_data**  data.frame the data frame that contains the measurements, mandatory.
- **meta_data**  data.frame the data frame that contains metadata attributes of the study data, mandatory.

Details

The current implementation does not take into account jump or missing codes, the function is rather based on checking whether NAs are present in the study data

Value

a list with

- SegmentData: data frame with the results of the quality check for unexpected data elements
- SegmentTable: data frame with selected unexpected data elements check results, used for the data quality report.

Examples

```r
## Not run:
study_data <- readRDS(system.file("extdata", "ship.RDS", package = "dataquieR"))
meta_data <- readRDS(system.file("extdata", "ship_meta.RDS", package = "dataquieR"))

int_unexp_records_segment(
    study_segment = c("PART_STUDY", "PART_INTERVIEW"),
    data_record_count = c(3000, 1100),
    study_data = study_data,
    meta_data = meta_data
)
## End(Not run)
```
**int_unexp_records_set**  
*Check for unexpected data record set*

**Description**

This function tests that the identifiers match a provided record set. It is possible to check for unexpected data record sets by study segments or to consider only selected segments.

**Indicator**

**Usage**

```r
int_unexp_records_set(level = c("dataframe", "segment"), ...)
```

**Arguments**

- `level` character a character vector indicating whether the assessment should be conducted at the study level (level = "dataframe") or at the segment level (level = "segment").
- `...` Depending on `level`, passed to either `util_int_unexp_records_set_segment` or `util_int_unexp_records_set_dataframe`

**Value**

a list. Depending on `level`, see `util_int_unexp_records_set_segment` or `util_int_unexp_records_set_dataframe` for a description of the outputs.

**Examples**

```r
## Not run:
study_data <- readRDS(system.file("extdata", "ship.RDS",  
  package = "dataquieR")
)  
meta_data <- readRDS(system.file("extdata", "ship_meta.RDS",  
  package = "dataquieR")
)  
md1_segment <- readRDS(system.file("extdata", "meta_data_segment.RDS",  
  package = "dataquieR")
)  
ids_segment <- readRDS(system.file("extdata", "meta_data_ids_segment.RDS",  
  package = "dataquieR")
)

# TODO: update examples
int_unexp_records_set(  
  level = "segment",  
  identifier_name_list = c("INTERVIEW", "LABORATORY"),  
  valid_id_table_list = ids_segment,  
  meta_data_record_check = md1_segment[
```


data.frame with metadata about the study data on variable level

Description

Variable level metadata.

See Also

further details on variable level metadata.

meta_data_segment

meta_data_dataframe

Well known columns on the meta_data_cross-item sheet

Description

Metadata describing groups of variables, e.g., for their multivariate distribution or for defining contradiction rules.

See Also

check_table

Well known columns on the meta_data_dataframe sheet

Description

Metadata describing data delivered on one data frame/table sheet, e.g., a full questionnaire, not its items.
**meta_data_segment**

---

**meta_data_segment**   *Well known columns on the meta_data_segment sheet*

---

**Description**

Metadata describing study segments, e.g., a full questionnaire, not its items.

---

**MULTIVARIATE_OUTLIER_CHECKTYPE**

*Cross-item level metadata attribute name*

---

**Description**

Select, which outlier criteria to compute, see `acc_multivariate_outlier`.

**Usage**

MULTIVARIATE_OUTLIER_CHECKTYPE

**Format**

An object of class character of length 1.

**Details**

You can leave the cell empty, then, all checks will apply. If you enter a set of methods, the maximum for N_RULES changes. See also `UNIVARIATE_OUTLIER_CHECKTYPE`.

**See Also**

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, GOLDSTANDARD, N_RULES, REL_VAL, VARIABLE_LIST, util_normalize_cross_item()
\textit{nres} \hspace{1cm} \textit{return the number of result slots in a report}

**Description**
return the number of result slots in a report

**Usage**
nres(x)

**Arguments**
x \hspace{1cm} \text{the dataquieR report (v2.0)}

**Value**
the number of used result slots

\textbf{N\_RULES} \hspace{1cm} \textit{Cross-item and item level metadata attribute name}

**Description**
Select, how many violated outlier criteria make an observation an outlier, see \texttt{acc\_multivariate\_outlier}.

**Usage**
N\_RULES

**Format**
An object of class \texttt{character} of length 1.

**Details**
You can leave the cell empty, then, all applied checks must deem an observation an outlier to have it flagged. See \texttt{UNIVARIATE\_OUTLIER\_CHECKTYPE} and \texttt{MULTIVARIATE\_OUTLIER\_CHECKTYPE} for the selected outlier criteria.

**See Also**
meta\_data\_cross
meta\_data
Other \texttt{meta\_data\_cross}: \texttt{ASSOCIATION\_DIRECTION, ASSOCIATION\_FORM, ASSOCIATION\_METRIC, ASSOCIATION\_RANGE, CHECK\_ID, CHECK\_LABEL, CONTRADICTION\_TERM, CONTRADICTION\_TYPE, DATA\_PREPARATION, GOLDSTANDARD, MULTIVARIATE\_OUTLIER\_CHECKTYPE, REL\_VAL, VARIABLE\_LIST, util\_normalize\_cross\_item()}
pipeline_recursive_result

Convert a pipeline result data frame to named encapsulated lists

Description

Deprecated

Usage

pipeline_recursive_result(...)

Arguments

...  Deprecated

Value

Deprecated

pipeline_vectorized

Call (nearly) one "Accuracy" function with many parameterizations at once automatically

Description

Deprecated

Usage

pipeline_vectorized(...)

Arguments

...  Deprecated

Value

Deprecated
plot.dataquieR_summary

Plot a dataquieR summary

Description
Plot a dataquieR summary

Usage
## S3 method for class 'dataquieR_summary'
plot(x, y, ..., filter, dont_plot = FALSE, stratify_by)

Arguments
x the dataquieR summary, see summary() and dq_report2()
y not yet used
... not yet used
filter if given, this filters the summary, e.g., filter = call_names == "com_qualified_item_missingness"
dont_plot suppress the actual plotting, just return a printable object derived from x
stratify_by column to stratify the summary, may be one string.

Value
invisible html object

prep_add_cause_label_df

Convert missing codes in metadata format v1.0 and a missing-cause-table to v2.0 missing list / jump list assignments

Description
The function has to working modes. If replace_meta_data is TRUE, by default, if cause_label_df contains a column named resp_vars, then the missing/jump codes in meta_data[, c(MISSING_CODES, JUMP_CODES)] will be overwritten, otherwise, it will be labeled using the cause_label_df.

Usage
prep_add_cause_label_df(
    meta_data = "item_level",
    cause_label_df,
    label_col = VAR_NAMES,
    assume_consistent_codes = TRUE,
    replace_meta_data = ("resp_vars" %in% colnames(cause_label_df))
)
prep_add_data_frames

Arguments

- **meta_data** *data.frame* the data frame that contains metadata attributes of study data.
- **cause_label_df** *data.frame* missing code table. If missing codes have labels the respective data frame can be specified here, see `cause_label_df`
- **label_col** *variable attribute* the name of the column in the metadata with labels of variables
- **assume_consistent_codes** *logical* if TRUE and no labels are given and the same missing/jump code is used for more than one variable, the labels assigned for this code will be the same for all variables.
- **replace_meta_data** *logical* if TRUE, ignore existing missing codes and jump codes and replace them with data from the `cause_label_df`. Otherwise, copy the labels from `cause_label_df` to the existing code columns.

Details

If a column `resp_vars` exists, then rows with a value in `resp_vars` will only be used for the corresponding variable.

Value

*data.frame* updated metadata including all the code labels in missing/jump lists

See Also

- `prep_extract_cause_label_df`

Description

These can be referred to by their names, then, wherever dataquieR expects a `data.frame` – just pass a character instead. If this character is not found, dataquieR would additionally look for files with the name and for URLs. You can also refer to specific sheets of a workbook or specific object from an RData by appending a pipe symbol and its name. A second pipe symbol allows to extract certain columns from such sheets (but they will remain data frames).

Usage

`prep_add_data_frames(..., data_frame_list = list())`
prod_add_missing_codes

Arguments

... data frames, if passed with names, these will be the names of these tables in the
data frame environment. If not, then the names in the calling environment will
be used.

data_frame_list a named list with data frames. Also these will be added and names will be
handled as for the ... argument.

Value

data.frame invisible(the cache environment)

See Also

prep_load_workbook_like_file
prep_get_data_frame

Other data-frame-cache: prep_get_data_frame(), prep_list_dataframes(), prep_load_folder_with_metadata(),
prep_load_workbook_like_file(), prep_purge_data_frame_cache()
prep_add_missing_codes

label_col  variable attribute the name of the column in the metadata with labels of variables
rules  data.frame with the columns:
  • resp_vars: Variable, whose NA-values should be replaced by jump codes
  • CODE_CLASS: Either MISSING or JUMP: Is the currently described case an expected missing value (JUMP) or not (MISSING)
  • CODE_VALUE: The jump code or missing code
  • CODE_LABEL: A label describing the reason for the missing value
  • RULE: A rule in REDcap style (see, e.g., REDcap help, REDcap how-to), and REDcap branching logic that describes cases for the missing

use_value_labels  logical In rules for factors, use the value labels, not the codes. Defaults to TRUE, if any VALUE_LABELS are given in the metadata.
overwrite  logical Also insert missing codes, if the values are not NA

Value

a list with the entries:
  • ModifiedStudyData: Study data with NAs replaced by the CODE_VALUE
  • ModifiedMetaData: Metadata having the new codes amended in the columns JUMP_LIST or MISSING_LIST, respectively

Examples

## Not run:
load(system.file("extdata", "study_data.RData", package = "dataquieR"))
load(system.file("extdata", "meta_data.RData", package = "dataquieR"))
vn <- subset(r$ModifiedMetaData, LABEL == "PREGNANT_0", VAR_NAMES)[[1]]
rules <- tibble::tribble(  ~resp_vars, ~CODE_CLASS, ~CODE_LABEL, ~CODE_VALUE, ~RULE,
                        "PREGNANT_0", "JUMP", "No pregnancies in males", "9999", '/quotesingle.Var[SEX_0]=1',

r <- prep_add_missing_codes(NA, study_data, meta_data,
                           label_col = "LABEL", rules, use_value_labels = FALSE)
subset(r$ModifiedMetaData, LABEL == "PREGNANT_0", JUMP_LIST)
subset(meta_data, LABEL == "PREGNANT_0", JUMP_LIST)
table(study_data[[vn]])
table(r$ModifiedStudyData[[vn]])
r <- prep_add_missing_codes(NA, study_data, meta_data,
                           label_col = "LABEL", rules, use_value_labels = FALSE, overwrite = TRUE)
table(study_data[[vn]])
table(r$ModifiedStudyData[[vn]])
	rules <- tibble::tribble(  ~resp_vars, ~CODE_CLASS, ~CODE_LABEL, ~CODE_VALUE, ~RULE,
                        "PREGNANT_0", "JUMP", "No pregnancies in males", "9999", '[SEX_0]="males"',

r <- prep_add_missing_codes(NA, study_data, meta_data,
                           label_col = "LABEL", rules, use_value_labels = TRUE, overwrite = FALSE)
prep_add_to_meta

Support function to augment metadata during data quality reporting

Description

adds an annotation to static metadata

Usage

prep_add_to_meta(
  VAR_NAMES,  
data_type,  
  Label,  
  VALUE_LABELS,  
  meta_data = "item_level",  
  ...  
)

Arguments

VAR_NAMES character Names of the Variables to add
DATA_TYPE character Data type for the added variables
LABEL character Labels for these variables
prep_apply_coding

**VALUE_LABELS** character Value labels for the values of the variables as usually pipe separated and assigned with `=`: `1 = male | 2 = female`

**meta_data** data.frame the metadata to extend

... Further defined variable attributes, see prep_create_meta

**Details**

Add metadata e.g. of transformed/new variable This function is not yet considered stable, but we already export it, because it could help. Therefore, we have some inconsistencies in the formals still.

**Value**

a data frame with amended metadata.

---

**prep_apply_coding** Re-Code labels with their respective codes according to the meta_data

**Description**

Re-Code labels with their respective codes according to the meta_data

**Usage**

prep_apply_coding(study_data, meta_data = "item_level")

**Arguments**

study_data data.frame the data frame that contains the measurements

meta_data data.frame the data frame that contains metadata attributes of study data

**Value**

data.frame modified study data with labels replaced by the codes
prep_check_for_dataquieR_updates

*Check for package updates*

**Description**

Check for package updates

**Usage**

```r
prep_check_for_dataquieR_updates(beta = FALSE, deps = TRUE)
```

**Arguments**

- `beta` *logical* check for beta version too
- `deps` *logical* check for missing (optional) dependencies

**Value**

```r
invisible(NULL)
```

prep_check_meta_data_dataframe

*Verify and normalize metadata on data frame level*

**Description**

if possible, mismatching data types are converted ("true" becomes TRUE)

**Usage**

```r
prep_check_meta_data_dataframe(meta_data_dataframe = "dataframe_level")
```

**Arguments**

- `meta_data_dataframe` *data.frame* data frame or path/url of a metadata sheet for the data frame level

**Details**

missing columns are added, filled with NA, if this is valid, i.e., n.a. for DF_NAME as the key column

**Value**

standardized metadata sheet as data frame
Examples

```r
# Not run:
mds <- prep_check_meta_data_dataframe("ship_meta_dataframe|dataframe_level")  # also converts
print(mds)
prep_check_meta_data_dataframe(mds)
mds1 <- mds
mds1$DF_RECORD_COUNT <- NULL
print(prep_check_meta_data_dataframe(mds1))  # fixes the missing column by NAs
mds1$DF_UNIQUE_ROWS[[2]] <- "xxx"  # not convertible
# print(prep_check_meta_data_dataframe(mds1))  # fail
mds1 <- mds
mds1$DF_UNIQUE_ID[[2]] <- 12  # not yet supported
# print(prep_check_meta_data_dataframe(mds1))  # fail

# End(Not run)
```

---

**prep_check_meta_data_segment**

*Verify and normalize metadata on segment level*

**Description**

if possible, mismatching data types are converted ("true" becomes TRUE)

**Usage**

```r
prep_check_meta_data_segment(meta_data_segment = "segment_level")
```

**Arguments**

- **meta_data_segment**
  
  *data.frame* data frame or path/url of a metadata sheet for the segment level

**Details**

missing columns are added, filled with NA, if this is valid, i.e., n.a. for STUDY_SEGMENT as the key column

**Value**

standardized metadata sheet as data frame
Examples

```r
## Not run:
mds <- prep_check_meta_data_segment("ship_meta_v2|segment_level") # also converts
print(mds)
prep_check_meta_data_segment(mds)
mds1 <- mds
mds1$SEGMENT_RECORD_COUNT <- NULL
print(prep_check_meta_data_segment(mds1)) # fixes the missing column by NAs
mds1 <- mds
mds1$SEGMENT_UNIQUE_ROWS[[2]] <- "xxx" # not convertible
# print(prep_check_meta_data_segment(mds1)) # fail

## End(Not run)
```

---

`prep_check_meta_names`  Checks the validity of metadata w.r.t. the provided column names

Description

This function verifies, if a data frame complies to metadata conventions and provides a given richness of meta information as specified by level.

Usage

```r
prep_check_meta_names(meta_data = "item_level", level, character.only = FALSE)
```

Arguments

- `meta_data`  `data.frame` the data frame that contains metadata attributes of study data
- `level`  `enum` level of requirement (see also `VARATT_REQUIRE_LEVELS`). set to NULL to deactivate the check of richness.
- `character.only`  `logical` a logical indicating whether level can be assumed to be character strings.

Details

Note, that only the given level is checked despite, levels are somehow hierarchical.

Value

a logical with:

- invisible(TRUE). In case of problems with the metadata, a condition is raised (`stop()`).  

Examples

## Not run:
prep_check_meta_names(data.frame(VAR_NAMES = 1, DATA_TYPE = 2, MISSING_LIST = 3))

prep_check_meta_names(data.frame(
), RECOMMENDED)

prep_check_meta_names(data.frame(
), OPTIONAL)

# Next one will fail
prep_clean_labels

Support function to scan variable labels for applicability

Description

Adjust labels in meta_data to be valid variable names in formulas for diverse r functions, such as glm or lme4::lmer.

Usage

prep_clean_labels(label_col, meta_data = "item_level", no_dups = FALSE)

Arguments

label_col character label attribute to adjust or character vector to adjust, depending on meta_data argument is given or missing.

meta_data data.frame metadata data frame: If label_col is a label attribute to adjust, this is the metadata table to process on. If missing, label_col must be a character vector with values to adjust.

no_dups logical disallow duplicates in input or output vectors of the function, then, prep_clean_labels would call stop() on duplicated labels.

Details

Currently, labels as given by label_col arguments in the most functions are directly used in formula, so that they become natural part of the outputs, but different models expect differently strict syntax for such formulas, especially for valid variable names. prep_clean_labels removes all potentially inadmissible characters from variable names (no guarantee, that some exotic model still rejects the names, but minimizing the number of exotic characters). However, variable names are modified, may become unreadable or indistinguishable from other variable names. For the latter case, a stop call is possible, controlled by the no_dups argument.

A warning is emitted, if modifications were necessary.

Value

a data.frame with:

- if meta_data is set, a list with:
  - modified meta_data[, label_col] column

- if meta_data is not set, adjusted labels that then were directly given in label_col
prep_combine_report_summaries

Examples

## Not run:
meta_data1 <- data.frame(
  LABEL =
    c("syst. Blood pressure (mmHg) 1",
      "1st heart frequency in MHz",
      "body surface (\u33A1)"
  )
)  
print(meta_data1)
print(prep_clean_labels(meta_data1$LABEL))
meta_data1 <- prep_clean_labels("LABEL", meta_data1)
print(meta_data1)

## End(Not run)

prep_combine_report_summaries

Combine two report summaries

Description

Combine two report summaries

Usage

prep_combine_report_summaries(..., summaries_list, amend_segment_names = FALSE)

Arguments

... objects returned by prep_extract_summary
summaries_list if given, list of objects returned by prep_extract_summary
amend_segment_names logical use names of the summaries_list and argument names as segment pre-
fixes

Value

combined summaries
combined summaries
prep_create_meta

Support function to create data.frames of metadata

Description

Create a metadata data frame and map names. Generally, this function only creates a data.frame, but using this constructor instead of calling data.frame(..., stringsAsFactors = FALSE), it becomes possible to adapt the metadata data.frame in later developments, e.g. if we decide to use classes for the metadata, or if certain standard names of variable attributes change. Also, a validity check is possible to implement here.

Usage

prep_create_meta(..., stringsAsFactors = FALSE, level, character.only = FALSE)

Arguments

... named column vectors, names will be mapped using WELL_KNOWN_META_VARIABLE_NAMES, if included in WELL_KNOWN_META_VARIABLE_NAMES can also be a data frame, then its column names will be mapped using WELL_KNOWN_META_VARIABLE_NAMES

stringsAsFactors logical if the argument is a list of vectors, a data frame will be created. In this case, stringsAsFactors controls, whether characters will be auto-converted to Factors, which defaults here always to false independent from the default.stringsAsFactors.

level enum level of requirement (see also VARATT_REQUIRE_LEVELS) set to NULL, if not a complete metadata frame is created.

character.only logical a logical indicating whether level can be assumed to be character strings.
prep_create_meta_data_file

Details
For now, this calls `data.frame`, but it already renames variable attributes, if they have a different name assigned in `WELL_KNOWN_META_VARIABLE_NAMES`, e.g. `WELL_KNOWN_META_VARIABLE_NAMES$RECODE` maps to `recode` in lower case.

NB: `dataquieR` exports all names from `WELL_KNOWN_META_VARIABLE_NAME` as symbols, so `RECODE` also contains "recode".

Value
a data frame with:

- metadata attribute names mapped and
- metadata checked using `prep_check_meta_names` and do some more verification about conventions, such as check for valid intervals in limits)

See Also
`WELL_KNOWN_META_VARIABLE_NAMES`

Description
Instantiate a new metadata file

Usage
```
prep_create_meta_data_file(
  file_name,  # character file path to write to
  study_data, # data.frame optional, study data to guess metadata from
  open = TRUE, # logical open the file after creation
  overwrite = FALSE
)
```

Arguments

- `file_name` character file path to write to
- `study_data` `data.frame` optional, study data to guess metadata from
- `open` logical open the file after creation
- `overwrite` logical overwrite file, if exists

Value
`invisible(NULL)`
prep_datatype_from_data

Get data types from data

Description

Get data types from data

Usage

prep_datatype_from_data(
  resp_vars = colnames(study_data),
  study_data,
  .dont_cast_off_cols = FALSE
)

Arguments

resp_vars  variable names of the variables to fetch the data type from the data
study_data  data.frame the data frame that contains the measurements Hint: Only data frames supported, no URL or file names.
.dont_cast_off_cols  logical internal use, only

Value

vector of data types

Examples

## Not run:
dataquieR::prep_datatype_from_data(cars)

## End(Not run)

prep_deparse_assignments

Convert two vectors from a code-value-table to a key-value list

Description

Convert two vectors from a code-value-table to a key-value list
Usage

prep_deparse_assignments(
  codes,
  labels,
  split_char = SPLIT_CHAR,
  mode = c("numeric_codes", "string_codes")
)

Arguments

codes codes, numeric or dates (as default, but string codes can be enabled using the option 'mode', see below)
labels character labels, same length as codes
split_char character split character character to split code assignments
mode character one of two options to insist on numeric or datetime codes (default) or to allow for string codes

Value

a vector with assignment strings for each row of cbind(codes, labels)

prep_dq_data_type_of Get the dataquieR DATA_TYPE of x

Description

Get the dataquieR DATA_TYPE of x

Usage

prep_dq_data_type_of(x)

Arguments

x object to define the dataquieR data type of

Value

the dataquieR data type as listed in DATA_TYPES

See Also

DATA_TYPES_OF_R_TYPE
prep_expand_codes  

Expand code labels across variables

Description

Code labels are copied from other variables, if the code is the same and the label is set only for some variables.

Usage

prep_expand_codes(
  meta_data = "item_level",
  suppressWarnings = FALSE,
  mix_jumps_and_missings = FALSE
)

Arguments

- **meta_data**: data.frame, the data frame that contains metadata attributes of study data.
- **suppressWarnings**: logical, show warnings, if labels are expanded.
- **mix_jumps_and_missings**: logical, ignore the class of the codes for label expansion, i.e., use missing code labels as jump code labels, if the values are the same.

Value

data.frame, an updated metadata data frame.

Examples

```r
## Not run:
load(system.file("extdata", "meta_data.RData", package = "dataquieR"))
meta_data$JUMP_LIST[meta_data$VAR_NAMES == "v00003"] <- "99980 = NOOP"
md <- prep_expand_codes(meta_data)
md$JUMP_LIST
md$MISSING_LIST
md <- prep_expand_codes(meta_data, mix_jumps_and_missings = TRUE)
md$JUMP_LIST
md$MISSING_LIST
load(system.file("extdata", "meta_data.RData", package = "dataquieR"))
meta_data$MISSING_LIST[meta_data$VAR_NAMES == "v00003"] <- "99980 = NOOP"
md <- prep_expand_codes(meta_data)
md$JUMP_LIST
md$MISSING_LIST

## End(Not run)
```
prep_extract_cause_label_df

Extract all missing/jump codes from metadata and export a cause-label-data-frame

Description

Extract all missing/jump codes from metadata and export a cause-label-data-frame

Usage

prep_extract_cause_label_df(meta_data = "item_level", label_col = VAR_NAMES)

Arguments

meta_data: data.frame the data frame that contains metadata attributes of study data
label_col: variable attribute the name of the column in the metadata with labels of variables

Value

list with the entries

- meta_data: data.frame a data frame that contains updated metadata
- cause_label_df: data.frame missing code table. If missing codes have labels the respective data frame are specified here, see cause_label_df

See Also

prep_add_cause_label_df

prep_extract_classes_by_functions

Extract old function based summary from data quality results

Description

Extract old function based summary from data quality results

Usage

prep_extract_classes_by_functions(r)

Arguments

r: dq_report2
Value
data.frame long format, compatible with prep_summary_to_classes()

See Also
Other summary_functions: prep_combine_report_summaries(), prep_extract_summary(), prep_extract_summary.dataquieR_result(), prep_extract_summary.dataquieR_resultset2(), prep_render_pie_chart_from_summaryclasses_ggplot2(), prep_render_pie_chart_from_summaryclasses_plotly(), prep_summary_to_classes(), util_as_cat(), util_extract_indicator_metrics(), util_get_category_for_result(), util_get_colors(), util_get_html_cell_for_result(), util_get_labels_grading_class(), util_get_message_for_result(), util_get_rule_sets(), util_get_ruleset_formats(), util_get_thresholds(), util_html_table(), util_melt_summary(), util_sort_by_order()

prep_extract_summary  Extract summary from data quality results

Description
Generic function, currently supports dq_report2 and dataquieR_result

Usage
prep_extract_summary(r, ...)

Arguments
r  dq_report2 or dataquieR_result object
...  further arguments, maybe needed for some implementations

Value
list with two slots Data and Table with data.frames featuring all metrics columns from the report or result in x, the STUDY_SEGMENT and the VAR_NAMES. In case of Data, the columns are formatted nicely but still with the standardized column names – use util_translate_indicator_metrics() to rename them nicely. In case of Table, just as they are.

See Also
Other summary_functions: prep_combine_report_summaries(), prep_extract_classes_by_functions(), prep_extract_summary.dataquieR_result(), prep_extract_summary.dataquieR_resultset2(), prep_render_pie_chart_from_summaryclasses_ggplot2(), prep_render_pie_chart_from_summaryclasses_plotly(), prep_summary_to_classes(), util_as_cat(), util_extract_indicator_metrics(), util_get_category_for_result(), util_get_colors(), util_get_html_cell_for_result(), util_get_labels_grading_class(), util_get_message_for_result(), util_get_rule_sets(), util_get_ruleset_formats(), util_get_thresholds(), util_html_table(), util_melt_summary(), util_sort_by_order()
**Description**

Extract report summary from reports

**Usage**

```r
## S3 method for class 'dataquieR_result'
prep_extract_summary(r, ...) 
```

**Arguments**

- `r` *dataquieR_result* a result from `adq_report2` report
- `...` not used

**Value**

`list` with two slots `Data` and `Table` with `data.frames` featuring all metrics columns from the report `r`, the `STUDY_SEGMENT` and the `VAR_NAMES`. In case of `Data`, the columns are formatted nicely but still with the standardized column names – use `util_translate_indicator_metrics()` to rename them nicely. In case of `Table`, just as they are.

**See Also**

`prep_combine_report_summaries()`

Other summary functions: `prep_combine_report_summaries()`, `prep_extract_classes_by_functions()`, `prep_extract_summary()`, `prep_extract_summary.dataquieR_resultset2()`, `prep_render_pie_chart_from_summaryclasses_plotly()`, `prep_summary_to_classes()`, `util_as_cat()`, `util_extract_indicator_metrics()`, `util_get_category_for_result()`, `util_get_colors()`, `util_get_html_cell_for_result()`, `util_get_labels_grading_class()`, `util_get_message_for_result()`, `util_get_rule_sets()`, `util_get_ruleset_formats()`, `util_get_thresholds()`, `util_html_table()`, `util_melt_summary()`, `util_sort_by_order()`
## S3 method for class 'dataquieR_resultset2'
prep_extract_summary(r, ...)

### Arguments

- **r**: a `dq_report2` report
- **...**: not used

### Value

A `list` with two slots: `Data` and `Table`, containing `data.frames` featuring all metrics columns from the report `r`, the `STUDY_SEGMENT` and the `VAR_NAMES`. In case of `Data`, the columns are formatted nicely but still with the standardized column names – use `util_translate_indicator_metrics()` to rename them nicely. In case of `Table`, just as they are.

### See Also

- `prep_combine_report_summaries()`
- `prep_combine_report_summaries()`, `prep_extract_classes_by_functions()`, `prep_extract_summary.dataquieR_result()`, `prep_render_pie_chart_from_summaryclasses_ggplot2()`, `prep_render_pie_chart_from_summaryclasses_plotly()`, `prep_summary_to_classes()`, `util_as_cat()`, `util_extract_indicator_metrics()`, `util_get_category_for_result()`, `util_get_colors()`, `util_get_html_cell_for_result()`, `util_get_labels_grading_class()`, `util_get_message_for_result()`, `util_get_rule_sets()`, `util_get_ruleset_formats()`, `util_get_thresholds()`, `util_html_table()`, `util_melt_summary()`, `util_sort_by_order()`

### Description

data_frame_name can be a file path or an URL you can append a pipe and a sheet name for Excel files or object name e.g. for RData files. Numbers may also work. All file formats supported by your rio installation will work.

### Usage

```r
prep_get_data_frame(
  data_frame_name,
  .data_frame_list = .dataframe_environment,
  keep_types = FALSE
)
```
Arguments

- **data_frame_name**
  - character name of the data frame to read, see details
- **.data_frame_list**
  - environment cache for loaded data frames
- **keep_types**
  - logical keep types as possibly defined in a file, if the data frame is loaded from one. set TRUE for study data.

Details

The data frames will be cached automatically, you can define an alternative environment for this using the argument `.data_frame_list`, and you can purge the cache using `prep_purge_data_frame_cache`. Use `prep_add_data_frames` to manually add data frames to the cache, e.g., if you have loaded them from more complex sources, before.

Value

- **data.frame** a data frame

See Also

- `prep_add_data_frames`
- `prep_load_workbook_like_file`

Other data-frame-cache: `prep_add_data_frames()`, `prep_list_dataframes()`, `prep_load_folder_with_metadata()`, `prep_load_workbook_like_file()`, `prep_purge_data_frame_cache()`

Examples

```r
## Not run:
bl <- as.factor(prep_get_data_frame(
  paste0("https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus",
  "/Projekte_RKI/COVID-19_Todesfaelle.xlsx?__blob=",
  "publicationFile|COVID_Todesfaelle_BL|Bundesland")[[1]]))

n <- as.numeric(prep_get_data_frame(paste0(
  "https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus",
  "/Projekte_RKI/COVID-19_Todesfaelle.xlsx?__blob=",
  "publicationFile|COVID_Todesfaelle_BL|Anzahl verstorbene",
  " COVID-19 Fälle")[[1]]))
plot(bl, n)
# Working names would be to date (2022-10-21), e.g.:
#
## https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/ 
## Projekte_RKI/COVID-19_Todesfaelle.xlsx?__blob=publicationFile 
## https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/ 
## Projekte_RKI/COVID-19_Todesfaelle.xlsx?__blob=publicationFile|2 
## https://www.rki.de/DE/Content/InfAZ/N/Neuartiges_Coronavirus/ 
## Projekte_RKI/COVID-19_Todesfaelle.xlsx?__blob=publicationFile|name 
## study_data
```
prep_get_labels

Fetch a label for a variable based on its purpose

Description
Fetch a label for a variable based on its purpose

Usage
prep_get_labels(
  resp_vars,
  meta_data = "item_level",
  label_col,
  max_len = MAX_LABEL_LEN,
  label_class = c("SHORT", "LONG"),
  label_lang = "",
  resp_vars_are_var_names_only = FALSE
)

Arguments
resp_vars \(\text{variable list}\) the variable names to fetch for
meta_data \(\text{meta_data}\) the metadata, item-level
label_col \(\text{variable attribute}\) the name of the column in the metadata with labels of variables
max_len \(\text{integer}\) the maximum label length to return, if not possible w/o causing ambiguous labels, the labels may still be longer
label_class \(\text{enum}\) SHORT | LONG. which sort of label according to the metadata model should be returned
label_lang \(\text{character}\) optional language suffix, if available in the metadata
resp_vars_are_var_names_only \(\text{logical}\) If TRUE, do not use other labels than VAR_NAMES for finding resp_vars in meta_data
Value

character suitable labels for each resp_vars, names of this vector are VAR_NAMES

Examples

## Not run:
prep_load_workbook_like_file("meta_data_v2")
prep_get_labels("SEX_0", label_class = "SHORT", max_len = 2)

## End(Not run)

prep_get_user_name  Return the logged-in User's Full Name

Description

If whoami is not installed, the user name from Sys.info() is returned.

Usage

prep_get_user_name()

Details

Can be overridden by options or environment:

options(FULLNAME = "Stephan Struckmann")
Sys.setenv(FULLNAME = "Stephan Struckmann")

Value

character the user’s name

prep_link_escape  Prepare a label as part of a link for RMD files

Description

Prepare a label as part of a link for RMD files

Usage

prep_link_escape(s, html = FALSE)
Arguments

s the label
html prepare the label for direct HTML output instead of RMD

Value

the escaped label

prep_list_dataframes List Loaded Data Frames

Description

List Loaded Data Frames

Usage

prep_list_dataframes()

Value

names of all loaded data frames

See Also

Other data-frame-cache: prep_add_data_frames(), prep_get_data_frame(), prep_load_folder_with_metadata(), prep_load_workbook_like_file(), prep_purge_data_frame_cache()

prep_load_folder_with_metadata Pre-load a folder with named (usually more than) one table(s)

Description

These can thereafter be referred to by their names only. Such files are, e.g., spreadsheet-workbooks or RData-files.

Usage

prep_load_folder_with_metadata(folder, keep_types = FALSE, ...)

Arguments

cfolder the folder name to load.
keep_types logical keep types as possibly defined in the file. set TRUE for study data.
... arguments passed to []
prep_load_report

Details

Note, that this function in contrast to prep_get_data_frame does neither support selecting specific sheets/columns from a file.

Value

invisible(the cache environment)

See Also

prep_add_data_frames
prep_get_data_frame

Other data-frame-cache: prep_add_data_frames(), prep_get_data_frame(), prep_list_dataframes(), prep_load_workbook_like_file(), prep_purge_data_frame_cache()

Examples

## Not run:
folder_name <-
  system.file("extdata", package = "dataquieR")
prep_load_folder_with_metadata(folder_name)
prep_get_data_frame(
  "dataframe_level") # dataframe_level is a sheet in the file

## End(Not run)

---

prep_load_report  Load a dq_report2

Description

Load a dq_report2

Usage

prep_load_report(file)

Arguments

file  character the file name to load from

Value

dataquieR_resultset2 the report
prep_load_workbook_like_file

Pre-load a file with named (usually more than) one table(s)

Description

These can thereafter be referred to by their names only. Such files are, e.g., spreadsheet-workbooks or RData-files.

Usage

prep_load_workbook_like_file(file, keep_types = FALSE)

Arguments

file the file name to load.
keep_types logical keep types as possibly defined in the file. set TRUE for study data.

Details

Note, that this function in contrast to prep_get_data_frame does neither support selecting specific sheets/columns from a file.

Value

invisible(the cache environment)

See Also

prep_add_data_frames
prep_get_data_frame

Other data-frame-cache: prep_add_data_frames(), prep_get_data_frame(), prep_list_dataframes(), prep_load_folder_with_metadata(), prep_purge_data_frame_cache()

Examples

## Not run:
file_name <-
  system.file("extdata", "meta_data_extended.xlsx", package = "dataquieR")
pref_load_workbook_like_file(file_name)
pref_get_data_frame(
  "dataframe_level") # dataframe_level is a sheet in the file

## End(Not run)
**prep_map_labels**  
*Support function to allocate labels to variables*

**Description**
Map variables to certain attributes, e.g. by default their labels.

**Usage**
```
prep_map_labels(  
  x,  
  meta_data = "item_level",  
  to = LABEL,  
  from = VAR_NAMES,  
  ifnotfound,  
  warn_ambiguous = FALSE  
)
```

**Arguments**
- **x**: character variable names, character vector, see parameter from
- **meta_data**: data.frame metadata data frame, if, as a dataquieR developer, you do not have item-level-metadata, you should use `util_map_labels` instead to avoid consistency checks on for item-level `meta_data`.
- **to**: character variable attribute to map to
- **from**: character variable identifier to map from
- **ifnotfound**: list A list of values to be used if the item is not found: it will be coerced to a list if necessary.
- **warn_ambiguous**: logical print a warning if mapping variables from `from` to `to` produces ambiguous identifiers.

**Details**
This function basically calls `colnames(study_data) <- meta_data$LABEL`, ensuring correct merging/joining of study data columns to the corresponding metadata rows, even if the orders differ. If a variable/study_data-column name is not found in `meta_data[[from]]` (default `from = VAR_NAMES`), either stop is called or, if `ifnotfound` has been assigned a value, that value is returned. See `mget`, which is internally used by this function.

The function not only maps to the `LABEL` column, but to can be any metadata variable attribute, so the function can also be used, to get, e.g. all `HARD_LIMITS` from the metadata.

**Value**
a character vector with:
- mapped values
Examples

```r
## Not run:
meta_data <- prep_create_meta(
  VAR_NAMES = c("ID", "SEX", "AGE", "DOE"),
  LABEL = c("Pseudo-ID", "Gender", "Age", "Examination Date"),
  DATA_TYPE = c(DATA_TYPES$INTEGER, DATA_TYPES$INTEGER, DATA_TYPES$INTEGER,
                DATA_TYPES$DATETIME),
  MISSING_LIST = ""
)
stopifnot(all(prep_map_labels(c("AGE", "DOE"), meta_data) == c("Age",
                                                 "Examination Date")))
## End(Not run)
```

---

**prep_merge_study_data**  
Merge a list of study data frames to one (sparse) study data frame

**Description**

Merge a list of study data frames to one (sparse) study data frame

**Usage**

```r
prep_merge_study_data(study_data_list)
```

**Arguments**

- `study_data_list`
  
  *list the list*

**Value**

*data.frame study_data*

---

**prep_meta_data_v1_to_item_level_meta_data**  
Convert item-level metadata from v1.0 to v2.0

**Description**

This function is idempotent.
Usage

prep_meta_data_v1_to_item_level_meta_data(
    meta_data = "item_level",
    verbose = TRUE,
    label_col = LABEL,
    cause_label_df
)

Arguments

- **meta_data**: data.frame the old item-level-metadata
- **verbose**: logical display all estimated decisions, defaults to TRUE, except if called in a dq_report2 pipeline.
- **label_col**: variable attribute the name of the column in the metadata with labels of variables
- **cause_label_df**: data.frame missing code table, see cause_label_df. Optional. If this argument is given, you can add missing code tables.

Details

The `options("dataquieR.force_item_specific_missing_codes")` (default FALSE) tells the system, to always fill in res_vars columns to the MISSING_LIST_TABLE, even, if the column already exists, but is empty.

Value

- data.frame the updated metadata

**prep_min_obs_level**  
Support function to identify the levels of a process variable with minimum number of observations

Description

utility function to subset data based on minimum number of observation per level

Usage

prep_min_obs_level(study_data, group_vars, min_obs_in_subgroup)

Arguments

- **study_data**: data.frame the data frame that contains the measurements
- **group_vars**: variable list the name grouping variable
- **min_obs_in_subgroup**: integer optional argument if a "group_var" is used. This argument specifies the minimum no. of observations that is required to include a subgroup (level) of the "group_var" in the analysis. Subgroups with less observations are excluded. The default is 30.
Details

This function removes observations having less than \texttt{min\_obs\_in\_subgroup} distinct values in a group variable, e.g. blood pressure measurements performed by an examiner having less than e.g. 50 measurements done. It displays a warning, if samples/rows are removed and returns the modified study data frame.

Value

a data frame with:

- a subsample of original data

---

\texttt{prep\_pmap} \quad \textit{Support function for a parallel \texttt{pmap}}

Description

parallel version of \texttt{purrr::pmap}

Usage

\texttt{prep\_pmap(.l, .f, ..., cores = 0)}

Arguments

\begin{verbatim}
  .l       data.frame with one call per line and one function argument per column
  .f       function to call with the arguments from .l
  ...      additional, static arguments for calling .f
  cores    number of cpu cores to use or a (named) list with arguments for \texttt{parallelMap::parallelStart}
            or NULL, if parallel has already been started by the caller. Set to 0 to run without parallelization.
\end{verbatim}

Value

\texttt{list} of results of the function calls

Author(s)

Aurèle

S Struckmann

See Also

\texttt{purrr::pmap}

Stack Overflow post
prep_prepare_dataframes

Prepare and verify study data with metadata

Description

This function ensures, that a data frame ds1 with suitable variable names study_data and meta_data exist as base data.frames.

Usage

prep_prepare_dataframes(
  .study_data,
  .meta_data,
  .label_col,
  .replace_hard_limits,
  .replace_missings,
  .sm_code = NULL,
  .allow_empty = FALSE,
  .adjust_data_type = TRUE,
  .amend_scale_level = TRUE,
  .internal = rlang::env_inherits(rlang::caller_env(), parent.env(environment()))
)

Arguments

.study_data if provided, use this data set as study_data
.meta_data if provided, use this data set as meta_data
.label_col if provided, use this as label_col
.replace_hard_limits replace HARD_LIMIT violations by NA, defaults to FALSE.
.replace_missings replace missing codes, defaults to TRUE
.sm_code missing code for NAs, if they have been re-coded by util_combine_missing_lists
.allow_empty allow ds1 to be empty, i.e., 0 rows and/or 0 columns
.adjust_data_type ensure that the data type of variables in the study data corresponds to their data type specified in the metadata
.amend_scale_level ensure that SCALE_LEVEL is available in the item-level meta_data. internally used to prevent recursion, if called from prep_scalelevel_from_data_and_metadata()
.internal logical internally called, modify caller’s environment.
**Details**

This function defines ds1 and modifies study_data and meta_data in the environment of its caller (see eval.parent). It also defines or modifies the object label_col in the calling environment. Almost all functions exported by dataquieR call this function initially, so that aspects common to all functions live here, e.g. testing. If an argument meta_data has been given and features really a data.frame. It verifies the existence of required metadata attributes (VARATT_REQUIRE_LEVELS). It can also replace missing codes by NAs, and calls prep_study2meta to generate a minimum set of metadata from the study data on the fly (should be amended, so on-the-fly-calling is not recommended for an instructive use of dataquieR).

The function also detects tibbles, which are then converted to base-R data.frames, which are expected by dataquieR.

Different from the other utility function that work in the caller’s environment, so it modifies objects in the calling function. It defines a new object ds1, it modifies study_data and/or meta_data and label_col, if .internal is TRUE.

**Value**

ds1 the study data with mapped column names

**See Also**

accMargins

**Examples**

```r
## Not run:
acc_test1 <- function(resp_variable, aux_variable, 
  time_variable, co_variables, 
  group_vars, study_data, meta_data) {
  prep_prepare_dataframes()
  invisible(ds1)
}
acc_test2 <- function(resp_variable, aux_variable, 
  time_variable, co_variables, 
  group_vars, study_data, meta_data, label_col) {
  ds1 <- prep_prepare_dataframes(study_data, meta_data)
  invisible(ds1)
}
environment(acc_test1) <- asNamespace("dataquieR")
# perform this inside the package (not needed for functions that have been
# integrated with the package already)
environment(acc_test2) <- asNamespace("dataquieR")
# perform this inside the package (not needed for functions that have been
# integrated with the package already)
acc_test3 <- function(resp_variable, aux_variable, time_variable, 
  co_variables, group_vars, study_data, meta_data, 
  label_col) {
  prep_prepare_dataframes()
  invisible(ds1)
}
```
prep_purge_data_frame_cache

Clear data frame cache

Description
Clear data frame cache

Usage
prep_purge_data_frame_cache()

Value
nothing
See Also

Other data-frame-cache: prep_add_data_frames(), prep_get_data_frame(), prep_list_dataframes(), prep_load_folder_with_metadata(), prep_load_workbook_like_file()

prep_render_pie_chart_from_summaryclasses_ggplot2

Create a ggplot2 pie chart

Description

Create a ggplot2 pie chart

Usage

prep_render_pie_chart_from_summaryclasses_ggplot2(
  data,
  meta_data = "item_level"
)

Arguments

data data as returned by prep_summary_to_classes but summarized by one column (currently, we support indicator_metric, STUDY_SEGMENT, and VAR_NAMES)

meta_data meta_data

Value

a ggplot2 plot

See Also

Other summary_functions: prep_combine_report_summaries(), prep_extract_classes_by_functions(), prep_extract_summary(), prep_extract_summary.dataquieR_result(), prep_extract_summary.dataquieR_resultset2(), prep_render_pie_chart_from_summaryclasses_plotly(), prep_summary_to_classes(), util_as_cat(), util_extract_indicator_metrics(), util_get_category_for_result(), util_get_colors(), util_get_html_cell_for_result(), util_get_labels_grading_class(), util_get_message_for_result(), util_get_rule_sets(), util_get_ruleset_formats(), util_get_thresholds(), util_html_table(), util_melt_summary(), util_sort_by_order()
Create a plotly pie chart

Usage

```r
prep_render_pie_chart_from_summaryclasses_plotly(
  data,
  meta_data = "item_level"
)
```

Arguments

data: data as returned by `prep_summary_to_classes` but summarized by one column (currently, we support `indicator_metric`, `call_names`, `STUDY_SEGMENT`, and `VAR_NAMES`)

meta_data: meta_data

Value

a `htmltools` compatible object

See Also

Other summary functions: `prep_combine_report_summaries()`, `prep_extract_classes_by_functions()`, `prep_extract_summary()`

```r
prep_render_pie_chart_from_summaryclasses_ggplot2()
prep_summary_to_classes()
util_as_cat()
util_extract_indicator_metrics()
util_get_category_for_result()
util_get_colors()
util_get_html_cell_for_result()
util_get_labels_grading_class()
util_get_message_for_result()
util_get_rule_sets()
util_get_ruleset_formats()
util_get_thresholds()
util_html_table()
util_melt_summary()
util_sort_by_order()
```
Arguments

- **report**: `dataquieR_resultset2` the report
- **file**: `character` the file name to write to
- **compression_level**: `integer` from=0 to=9. Compression level. 9 is very slow.

Value

`invisible(NULL)`

---

**prep_scalelevel_from_data_and_metadata**

*Heuristics to amend a SCALE_LEVEL column and a UNIT column in the metadata*

Description

...if missing

Usage

```
prep_scalelevel_from_data_and_metadata(
  resp_vars = NULL,
  study_data,
  meta_data = "item_level",
  label_col = LABEL
)
```

Arguments

- **resp_vars**: `variable list` the names of the measurement variables
- **study_data**: `data.frame` the data frame that contains the measurements
- **meta_data**: `data.frame` the data frame that contains metadata attributes of study data
- **label_col**: `variable attribute` the name of the column in the metadata with labels of variables

Value

`data.frame` modified metadata

Examples

```r
## Not run:
prep_load_workbook_like_file("meta_data_v2")
prep_scalelevel_from_data_and_metadata(study_data = "study_data")
## End(Not run)
```
**prep_study2meta**

Guess a metadata data frame from study data.

**Description**

Guess a minimum metadata data frame from study data. Minimum required variable attributes are:

**Usage**

```r
prep_study2meta(
  study_data,
  level = c(VARATT_REQUIRE_LEVELS$REQUIRED, VARATT_REQUIRE_LEVELS$RECOMMENDED),
  cumulative = TRUE,
  convert_factors = FALSE
)
```

**Arguments**

- `study_data` *data.frame* the data frame that contains the measurements
- `level` *enum* levels to provide (see also `VARATT_REQUIRE_LEVELS`)
- `cumulative` *logical* include attributes of all levels up to level
- `convert_factors` *logical* convert factor columns to coded integers. If selected, then also the study data will be updated and returned.

**Details**

```r
dataquieR:::util_get_var_att_names_of_level(VARATT_REQUIRE_LEVELS$REQUIRED)
#> VAR_NAMES   DATA_TYPE    MISSING_LIST_TABLE
#> "VAR_NAMES" "DATA_TYPE" "MISSING_LIST_TABLE"
```

The function also tries to detect missing codes.

**Value**

A `meta_data` data frame or a list with study data and metadata, if `convert_factors == TRUE`.

**Examples**

```r
## Not run:
dataquieR::prep_study2meta(Orange, convert_factors = FALSE)
## End(Not run)
```
prep_summary_to_classes

Classify metrics from a report summary table

Description

Classify metrics from a report summary table

Usage

prep_summary_to_classes(report_summary)

Arguments

- report_summary: list() as returned by prep_extract_summary()

Value

data.frame classes for the report summary table, long format

See Also

Other summary_functions: prep_combine_report_summaries(), prep_extract_classes_by_functions(), prep_extract_summary(), prep_extract_summary.dataquieR_result(), prep_extract_summary.dataquieR_resultset2(), prep_render_pie_chart_from_summaryclasses_ggplot2(), prep_render_pie_chart_from_summaryclasses_plotly(), util_as_cat(), util_extract_indicator_metrics(), util_get_category_for_result(), util_get_colors(), util_get_html_cell_for_result(), util_get_labels_grading_class(), util_get_message_for_result(), util_get_rule_sets(), util_get_ruleset_formats(), util_get_thresholds(), util_html_table(), util_melt_summary(), util_sort_by_order()

prep_title_escape

Prepare a label as part of a title text for RMD files

Description

Prepare a label as part of a title text for RMD files

Usage

prep_title_escape(s, html = FALSE)

Arguments

- s: the label
- html: prepare the label for direct HTML output instead of RMD
prep_valuelabels_from_data

Value

the escaped label

Description

Detects factors and converts them to compatible metadata/study data.

Usage

prep_valuelabels_from_data(resp_vars = colnames(study_data), study_data)

Arguments

resp_vars variable names of the variables to fetch the value labels from the data
study_data data.frame the data frame that contains the measurements

Value

a list with:

- VALUE_LABELS: vector of value labels and modified study data
- ModifiedStudyData: study data with factors as integers

Examples

## Not run:
dataquieR::prep_datatype_from_data(iris)

## End(Not run)
print.dataquieR_result

Print a dataquieR result returned by dq_report2

Description

Print a dataquieR result returned by dq_report2

Usage

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

Arguments

x

list a dataquieR result from dq_report2 or util_eval_to_dataquieR_result

... passed to print. Additionally, the argument slot may be passed to print only specific sub-results.

Value

see print

See Also

util_pretty_print()

print.dataquieR_resultset

Generate a RMarkdown-based report from a dataquieR report

Description

Generate a RMarkdown-based report from a dataquieR report

Usage

## S3 method for class 'dataquieR_resultset'
print(...)

Arguments

... deprecated

Value

deprecated
**print.dataquieR_resultset2**

*Generate a HTML-based report from a dataquieR report*

**Description**

Generate a HTML-based report from a dataquieR report

**Usage**

```r
## S3 method for class 'dataquieR_resultset2'
print(x, dir, view = TRUE, disable_plotly = FALSE, block_load_factor = 4, ...)
```

**Arguments**

- `x` : dataquieR report v2.
- `dir` : character directory to store the rendered report’s files, a temporary one, if omitted. Directory will be created, if missing, files may be overwritten inside that directory.
- `view` : logical display the report.
- `disable_plotly` : logical do not use plotly, even if installed.
- `block_load_factor` : numeric multiply size of parallel compute blocks by this factor.
- `...` : additional arguments.

**Value**

file names of the generated report’s HTML files

---

**print.dataquieR_summary**

*Print a dataquieR summary*

**Description**

Print a dataquieR summary

**Usage**

```r
## S3 method for class 'dataquieR_summary'
print(
  x,
  ...,
  grouped_by = c("call_names", "indicator_metric"),
  dont_print = FALSE
)
```
print.interval

Arguments

x: the dataquiR summary, see `summary()` and `dq_report2()`

...: not yet used

grouped_by: define the columns of the resulting matrix. It can be either "call_names", one column per function, or "indicator_metric", one column per indicator or both c("call_names", "indicator_metric"). The last combination is the default
dont_print: suppress the actual printing, just return a printable object derived from x

Value

invisible html object

print.interval
print.implementation for the class interval

Description

such objects, for now, only occur in RECCap rules, so this function is meant for internal use, mostly – for now.

Usage

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

Arguments

x: interval objects to print

...: not used yet

Value

the printed object

See Also

base::print
print.ReportSummaryTable

print implementation for the class ReportSummaryTable

Description

Use this function to print results objects of the class ReportSummaryTable.

Usage

```r
## S3 method for class 'ReportSummaryTable'
print(
x, relative, dt = FALSE, fillContainer = FALSE, displayValues = FALSE, view = TRUE, ...
flip_mode = "auto"
)
```

Arguments

- `x` ReportSummaryTable objects to print
- `relative` logical normalize the values in each column by division by the N column.
- `dt` logical use DT::datatables, if installed
- `fillContainer` logical if `dt` is `TRUE`, control table size, see DT::datatables.
- `displayValues` logical if `dt` is `TRUE`, also display the actual values
- `view` logical if `view` is `FALSE`, do not print but return the output, only
- `...` not used, yet
- `flip_mode` enum default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this can be controlled by setting the roptions(dataquieR.flip_mode = ...). If called from dq_report, you can also pass flip_mode to all function calls or set them specifically using specific_args.

Value

the printed object

See Also

base::print
pro_applicability_matrix

\textit{Check applicability of DQ functions on study data}

\subsection*{Description}
Checks applicability of DQ functions based on study data and metadata characteristics

\subsection*{Usage}

\begin{verbatim}
pro_applicability_matrix(
    study_data,
    meta_data,
    split_segments = FALSE,
    label_col,
    max_vars_per_plot = 20,
    meta_data_segment,
    meta_data_dataframe,
    flip_mode = "noflip"
)
\end{verbatim}

\subsection*{Arguments}

\begin{description}
\item[study_data] \texttt{data.frame} the data frame that contains the measurements
\item[meta_data] \texttt{data.frame} the data frame that contains metadata attributes of study data
\item[split_segments] \texttt{logical} return one matrix per study segment
\item[label_col] \texttt{variable attribute} the name of the column in the metadata with labels of variables
\item[max_vars_per_plot] \texttt{integer} from=0. The maximum number of variables per single plot.
\item[meta_data_segment] \texttt{data.frame} – optional: Segment level metadata
\item[meta_data_dataframe] \texttt{data.frame} – optional: Data frame level metadata
\item[flip_mode] \texttt{enum} default | flip | noflip | auto. Should the plot be in default orientation, flipped, not flipped or auto-flipped. Not all options are always supported. In general, this con be controlled by setting the \texttt{roptions(dataquieR.flip_mode = ...)}. If called from dq_report, you can also pass \texttt{flip_mode} to all function calls or set them specifically using specific_args.
\end{description}

\subsection*{Details}
This is a preparatory support function that compares study data with associated metadata. A prerequisite of this function is that the no. of columns in the study data complies with the no. of rows in the metadata.
For each existing R-implementation, the function searches for necessary static metadata and returns a heatmap like matrix indicating the applicability of each data quality implementation. In addition, the data type defined in the metadata is compared with the observed data type in the study data.

Value

a list with:

- **SummaryTable**: data frame about the applicability of each indicator function (each function in a column). Its integer values can be one of the following four categories: 0. Non-matching datatype + Incomplete metadata, 1. Non-matching datatype + complete metadata, 2. Matching datatype + Incomplete metadata, 3. Matching datatype + complete metadata, 4. Not applicable according to data type
- **ApplicabilityPlot**: ggplot2 heatmap plot, graphical representation of SummaryTable
- **ApplicabilityPlotList**: list of plots per (maybe artificial) segment
- **ReportSummaryTable**: data frame underlying ApplicabilityPlot

Examples

```r
## Not run:
load(system.file("extdata/meta_data.RData", package = "dataquieR"), envir = environment())
load(system.file("extdata/study_data.RData", package = "dataquieR"), envir = environment())
appmatrix <- pro_applicability_matrix(study_data = study_data,
                                      meta_data = meta_data,
                                      label_col = LABEL)
## End(Not run)
```

---

**rbind.ReportSummaryTable**

*Combine ReportSummaryTable outputs*

**Description**

Using this `rbind` implementation, you can combine different heatmap-like results of the class `ReportSummaryTable`.

**Usage**

```r
## S3 method for class 'ReportSummaryTable'
rbind(...)  
```

**Arguments**

... *ReportSummaryTable objects to combine.*
See Also

base::rbind.data.frame

---

REL_VAL

_Cross-item level metadata attribute name_

**Description**

Specifies the type of reliability or validity analysis. The string specifies the analysis algorithm to be used, and can be either "inter-class" or "intra-class".

**Usage**

REL_VAL

**Format**

An object of class character of length 1.

**See Also**

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, VARIABLE_LIST, util_normalize_cross_item()

---

resnames

_Return names of result slots (e.g., 3rd dimension of dataquieR results)_

**Description**

Return names of result slots (e.g., 3rd dimension of dataquieR results)

**Usage**

resnames(x)

**Arguments**

- x: the objects

**Value**

character vector with names
resnames.dataquieR_resultset2

Return names of result slots (e.g., 3rd dimension of dataquieR results)

Description

Return names of result slots (e.g., 3rd dimension of dataquieR results)

Usage

```r
## S3 method for class 'dataquieR_resultset2'
resnames(x)
```

Arguments

- `x`: the objects

Value

character vector with names

SCALE_LEVELS

<table>
<thead>
<tr>
<th>Scale Levels</th>
</tr>
</thead>
<tbody>
<tr>
<td>nominal</td>
</tr>
<tr>
<td>ordinal</td>
</tr>
<tr>
<td>interval</td>
</tr>
<tr>
<td>ratio</td>
</tr>
<tr>
<td>na</td>
</tr>
</tbody>
</table>

Description

**Scale Levels of Study Data according to Stevens’s Typology:**

In the metadata, the following entries are allowed for the variable attribute `SCALE_LEVEL`:

Usage

```r
SCALE_LEVELS
```

Format

An object of class `list` of length 5.

Details

- nominal for categorical variables
- ordinal for ordinal variables (i.e., comparison of values is possible)
- interval for interval scales, i.e., distances are meaningful
- ratio for ratio scales, i.e., ratios are meaningful
- na for variables, that contain e.g. unstructured texts, json, xml, ... to distinguish them from variables, that still need to have the SCALE_LEVEL estimated by `prep_scalelevel_from_data_and_metadata()`
**Examples:**
- sex, eye color – nominal
- income group, education level – ordinal
- temperature in degree Celsius – interval
- body weight, temperature in Kelvin – ratio

**See Also**
- Wikipedia

---

**SEGMENT_ID_REF_TABLE**  
*Segment level metadata attribute name*

**Description**

The name of the data frame containing the reference IDs to be compared with the IDs in the targeted segment.

**Usage**

SEGMENT_ID_REF_TABLE

**Format**

An object of class character of length 1.

**See Also**

meta_data_segment

---

**SEGMENT_ID_TABLE**  
*Deprecated segment level metadata attribute name*

**Description**

The name of the data frame containing the reference IDs to be compared with the IDs in the targeted segment.

**Usage**

SEGMENT_ID_TABLE

**Format**

An object of class character of length 1.

**Details**

Please use SEGMENT_ID_REF_TABLE
**SEGMENT_ID_VARS**

*Segment level metadata attribute name*

**Description**

All variables that are to be used as one single ID variable (combined key) in a segment.

**Usage**

SEGMENT_ID_VARS

**Format**

An object of class character of length 1.

**See Also**

meta_data_segment

---

**SEGMENT_MISS**

*Segment level metadata attribute name*

**Description**

true or false to suppress crude segment missingness output (Completeness/Misg. Segments in the report). Defaults to compute the output, if more than one segment is available in the item-level metadata.

**Usage**

SEGMENT_MISS

**Format**

An object of class character of length 1.

**See Also**

meta_data_segment
**SEGMENT_PART_VARS**  
*Segment level metadata attribute name*

**Description**

The name of the segment participation status variable

**Usage**

`SEGMENT_PART_VARS`

**Format**

An object of class `character` of length 1.

**See Also**

`meta_data_segment`

---

**SEGMENT_RECORD_CHECK**  
*Segment level metadata attribute name*

**Description**

The type of check to be conducted when comparing the reference ID table with the IDs in a segment.

**Usage**

`SEGMENT_RECORD_CHECK`

**Format**

An object of class `character` of length 1.

**See Also**

`meta_data_segment`
SEGMENT_RECORD_COUNT  Segment level metadata attribute name

**Description**

Number of expected data records in each segment. **numeric**. Check only conducted if number entered

**Usage**

SEGMENT_RECORD_COUNT

**Format**

An object of class character of length 1.

**See Also**

meta_data_segment

SEGMENT_UNIQUE_ROWS  Segment level metadata attribute name

**Description**

Specifies whether identical data is permitted across rows in a segment (excluding ID variables)

**Usage**

SEGMENT_UNIQUE_ROWS

**Format**

An object of class character of length 1.

**See Also**

meta_data_segment
SPLIT_CHAR

Character used by default as a separator in metadata such as missing codes.

Description

This 1 character is according to our metadata concept "|".

Usage

SPLIT_CHAR

Format

An object of class character of length 1.

study_data

Data frame with the study data whose quality is being assessed.

Description

Study data is expected in wide format. If should contain all variables for all segments in one large table, even, if some variables are not measured for all observational units (study participants).

summary.dataquieR_resultset

Summarize a dataquieR report

Description

Deprecated

Usage

## S3 method for class 'dataquieR_resultset'
summary(...)

Arguments

... Deprecated

Value

Deprecated
Generate a report summary table

Description

Generate a report summary table

Usage

```r
## S3 method for class 'dataquieR_resultset2'
summary(
  object,
  aspect = c("applicability", "error", "anamat", "indicator_or_descriptor"),
  FUN,
  collapse = "\n<br />\n",
  ...
)
```

Arguments

- `object`: a square result set
- `aspect`: an aspect/problem category of results
- `FUN`: function to apply to the cells of the result table
- `collapse`: passed to `FUN`
- `...`: not used

Value

a summary of a dataquieR report

Examples

```r
## Not run:
util_html_table(summary(report),
  filter = "top", options = list(scrollCollapse = TRUE, scrollY = "75vh"),
  is_matrix_table = TRUE, rotate_headers = TRUE, output_format = "HTML"
)
## End(Not run)
```
## UNIT_PREFIXES

<table>
<thead>
<tr>
<th>UNITS</th>
<th>Valid unit symbols according to <code>units::valid_udunits()</code></th>
</tr>
</thead>
</table>

### Description

like m, g, N, ...

### See Also

Other UNITS: `UNIT_IS_COUNT, UNIT_PREFIXES, UNIT_SOURCES, WELL_KNOWN_META_VARIABLE_NAMES`

<table>
<thead>
<tr>
<th>UNIT_IS_COUNT</th>
<th>Is a unit a count according to <code>units::valid_udunits()</code></th>
</tr>
</thead>
</table>

### Description

see column def, therein

### Details

like %, ppt, ppm

### See Also

Other UNITS: `UNITS, UNIT_PREFIXES, UNIT_SOURCES, WELL_KNOWN_META_VARIABLE_NAMES`

<table>
<thead>
<tr>
<th>UNIT_PREFIXES</th>
<th>Valid unit prefixes according to <code>units::valid_udunits_prefixes()</code></th>
</tr>
</thead>
</table>

### Description

like k, m, M, c, ...

### See Also

Other UNITS: `UNITS, UNIT_IS_COUNT, UNIT_SOURCES, WELL_KNOWN_META_VARIABLE_NAMES`
UNIT_SOURCES

Maturity stage of a unit according to units::valid_udunits()

Description

see column source_xml therein, i.e., base, derived, accepted, or common

See Also

Other UNITS: UNITS, UNIT_IS_COUNT, UNIT_PREFIXES, WELL_KNOWN_META_VARIABLE_NAMES

UNIVARIATE_OUTLIER_CHECKTYPE

Item level metadata attribute name

Description

Select, which outlier criteria to compute, see acc_univariate_outlier.

Usage

UNIVARIATE_OUTLIER_CHECKTYPE

Format

An object of class character of length 1.

Details

You can leave the cell empty, then, all checks will apply. If you enter a set of methods, the maximum for N_RULES changes. See also MULTIVARIATE_OUTLIER_CHECKTYPE.

See Also

WELL_KNOWN_META_VARIABLE_NAMES
util_compute_kurtosis  \textit{Compute Kurtosis}

\textbf{Description}

Compute Kurtosis

\textbf{Usage}

\begin{verbatim}
util_compute_kurtosis(x)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} data
\end{itemize}

\textbf{Value}

the Kurtosis

---

util_compute_SE_skewness  \textit{Compute SE.Skewness}

\textbf{Description}

Compute SE.Skewness

\textbf{Usage}

\begin{verbatim}
util_compute_SE_skewness(x, skewness = util_compute_skewness(x))
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} \hspace{1cm} data
  \item \texttt{skewness} \hspace{1cm} if already known
\end{itemize}

\textbf{Value}

the standard error of skewness
util_compute_skewness  Compute the Skewness

Description

Compute the Skewness

Usage

util_compute_skewness(x)

Arguments

x  data

Value

the Skewness

util_first_row_to_colnames

Move the first row of a data frame to its column names

Description

Move the first row of a data frame to its column names

Usage

util_first_row_to_colnames(dfr)

Arguments

dfr  data.frame

Value

data.frame with first row as column names
**VARATT_REQUIRE_LEVELS**  
*Requirement levels of certain metadata columns*

**Description**

These levels are cumulatively used by the function `prep_create_meta` and related in the argument `level` therein.

**Usage**

`VARATT_REQUIRE_LEVELS`

**Format**

An object of class `list` of length 5.

**Details**

Currently available:

- 'COMPATIBILITY' = "compatibility"
- 'REQUIRED' = "required"
- 'RECOMMENDED' = "recommended"
- 'OPTIONAL' = "optional"
- 'TECHNICAL' = "technical"

**VARIABLE_LIST**  
*Cross-item level metadata attribute name*

**Description**

Specifies a group of variables for multivariate analyses. Separated by |, please use variable names from `VAR_NAMES` or a label as specified in `label_col`, usually `LABEL` or `LONG_LABEL`.

**Usage**

`VARIABLE_LIST`

**Format**

An object of class `character` of length 1.

**Details**

If missing, `dataquieR` will create such IDs from `CONTRADICTION_TERM`, if specified.
See Also

meta_data_cross

Other meta_data_cross: ASSOCIATION_DIRECTION, ASSOCIATION_FORM, ASSOCIATION_METRIC, ASSOCIATION_RANGE, CHECK_ID, CHECK_LABEL, CONTRADICTION_TERM, CONTRADICTION_TYPE, DATA_PREPARATION, GOLDSTANDARD, MULTIVARIATE_OUTLIER_CHECKTYPE, N_RULES, REL_VAL, util_normalize_cross_item()

VARIABLE_ROLES

Variable roles can be one of the following:

Description

• intro a variable holding consent-data
• primary a primary outcome variable
• secondary a secondary outcome variable
• process a variable describing the measurement process
• suppress a variable added on the fly computing sub-reports, i.e., by dq_report_by to have all referred variables available, even if they are not part of the currently processed segment. But they will only be fully assessed in their real segment’s report.

Usage

VARIABLE_ROLES

Format

An object of class list of length 5.

WELL_KNOWN_META_VARIABLE_NAMES

Well-known metadata column names, names of metadata columns

Description

names of the variable attributes in the metadata frame holding the names of the respective observers, devices, lower limits for plausible values, upper limits for plausible values, lower limits for allowed values, upper limits for allowed values, the variable name (column name, e.g. v0020349) used in the study data, the variable name used for processing (readable name, e.g. RR_DIAST_1) and in parameters of the QA-Functions, the variable label, variable long label, variable short label, variable data type (see also DATA_TYPES), re-code for definition of lists of event categories, missing lists and jump lists as CSV strings. For valid units see UNITS.

Usage

WELL_KNOWN_META_VARIABLE_NAMES
Format

An object of class `list` of length 53.

Details

all entries of this list will be mapped to the package’s exported NAMESPACE environment directly, i.e. they are available directly by their names too:


See Also

- `meta_data_segment` for `STUDY SEGMENT`
- Other UNITS: `UNITS`, `UNIT_IS_COUNT`, `UNIT_PREFIXES`, `UNIT_SOURCES`

Examples

```r
print(WELL_KNOWN_META_VARIABLE_NAMES$VAR_NAMES)
# print(VAR_NAMES) # should usually also work
```

Description

Get a subset of a dataquieR dq_report2 report

Usage

```r
## S3 method for class 'dataquieR_resultset2' 
x[row, col, res, drop = FALSE]
```
Arguments

- **x**: the report
- **row**: the variable names, must be unique
- **col**: the function-call-names, must be unique
- **res**: the result slot, must be unique
- **drop**: drop, if length is 1

Value

A list with results, depending on drop and the number of results, the list may contain all requested results in sub-lists. The order of the results follows the order of the row/column/result-names given...
Index

* **UNITS**
  - UNIT_IS_COUNT, 142
  - UNIT_PREFIXES, 142
  - UNIT_SOURCES, 143
  - UNITS, 142
  - WELL_KNOWN_META_VARIABLE_NAMES, 147
* **accuracy**
  - acc_margins, 18
* **data-frame-cache**
  - prep_add_data_frames, 89
  - prep_get_data_frame, 108
  - prep_list_dataframes, 112
  - prep_load_folder_with_metadata, 112
  - prep_load_workbook_like_file, 114
  - prep_purge_data_frame_cache, 121
* **datasets**
  - ASSOCIATION_DIRECTION, 31
  - ASSOCIATION_FORM, 31
  - ASSOCIATION_METRIC, 32
  - ASSOCIATION_RANGE, 32
  - CHECK_ID, 33
  - CHECK_LABEL, 34
  - contradiction_functions_descriptions, 42
  - CONTRADICTION_TERM, 43
  - CONTRADICTION_TYPE, 43
  - DATA_PREPARATION, 53
  - DATA_TYPES, 53
  - DATA_TYPES_OF_R_TYPE, 54
  - DF_ELEMENT_COUNT, 57
  - DF_ID_REF_TABLE, 57
  - DF_ID_VARS, 58
  - DF_NAME, 58
  - DF_RECORD_CHECK, 59
  - DF_RECORD_COUNT, 59
  - DF_UNIQUE_ID, 60
  - DF_UNIQUE_ROWS, 60
  - dimensions, 61
  - dims, 62
  - DISTRIBUTIONS, 63
  - GOLDSTANDARD, 68
  - MULTIVARIATE_OUTLIER_CHECKTYPE, 85
  - N_RULES, 86
  - REL_VAL, 134
  - SCALE_LEVELS, 135
  - SEGMENT_ID_REF_TABLE, 136
  - SEGMENT_ID_TABLE, 136
  - SEGMENT_ID_VARS, 137
  - SEGMENT_MISS, 137
  - SEGMENT_PART_VARS, 138
  - SEGMENT_RECORD_CHECK, 138
  - SEGMENT_RECORD_COUNT, 139
  - SEGMENT_UNIQUE_ROWS, 139
  - SPLIT_CHAR, 140
  - UNIVARIATE_OUTLIER_CHECKTYPE, 143
  - VARATT_REQUIRE_LEVELS, 146
  - VARIABLE_LIST, 146
  - VARIABLE_ROLES, 147
  - WELL_KNOWN_META_VARIABLE_NAMES, 147
* **meta_data_cross**
  - ASSOCIATION_DIRECTION, 31
  - ASSOCIATION_FORM, 31
  - ASSOCIATION_METRIC, 32
  - ASSOCIATION_RANGE, 32
  - CHECK_ID, 33
  - CHECK_LABEL, 34
  - CONTRADICTION_TERM, 43
  - CONTRADICTION_TYPE, 43
  - DATA_PREPARATION, 53
  - GOLDSTANDARD, 68
  - MULTIVARIATE_OUTLIER_CHECKTYPE, 85
  - N_RULES, 86
  - REL_VAL, 134
  - VARIABLE_LIST, 146
* **summary_functions**
INDEX

prep_combine_report_summaries, 99
prep_extract_classes_by_functions, 105
prep_extract_summary, 106
prep_extract_summary.dataquieR_result, 107
prep_extract_summary.dataquieR_resultset2, 107
prep_render_pie_chart_from_summaryclasses, 122
prep_render_pie_chart_from_summaryclasses, 123
prep_summary_to_classes, 126
[.dataquieR_resultset2, 148
acc_distributions, 6, 8, 10, 11, 13, 14
acc_distributions_loc, 7
acc_distributions_loc_ecdf, 9
acc_distributions_only, 10
acc_distributions_only_ecdf, 12
acc_distributions_prop, 13
acc_end_digits, 15
acc_loess, 16
accMargins, 18
acc_multivariate_outlier, 20, 85, 86
acc_robust_univariate_outlier, 22, 27
acc_shape_or_scale, 15, 24, 63
acc_univariate_outlier, 23, 25, 143
acc_varcomp, 27
as.data.frame.dataquieR_resultset, 29, 52, 66
as.list.dataquieR_resultset, 30, 52, 66
ASSOCIATION_DIRECTION, 31, 31, 32–34, 43, 53, 69, 85, 86, 134, 147
ASSOCIATION_FORM, 31, 31, 32–34, 43, 53, 69, 85, 86, 134, 147
ASSOCIATION_METRIC, 31, 31, 32, 32, 33, 34, 43, 53, 69, 85, 86, 134, 147
ASSOCIATION_RANGE, 31, 31, 32, 32, 33, 34, 43, 53, 69, 85, 86, 134, 147
base::rbind.data.frame, 134
cause_label_df, 33, 35, 89, 105, 117
CHECK_ID, 31, 32, 33, 34, 43, 53, 69, 85, 86, 134, 147
CHECK_LABEL, 31–33, 34, 43, 53, 69, 85, 86, 134, 147
check_table, 34
CO_VARS, 148
CO_VARS
(WELL_KNOWN_META_VARIABLE_NAMES), 147
CODE_CLASS (cause_label_df), 33
CODE_INTERPRET (cause_label_df), 33
CODE_LABEL (cause_label_df), 33
copolyUE (cause_label_df), 33
com_item_missingness, 35, 37, 39
com_item_missingness, 37
com_item_missingness, 38
com_segment_missingness, 39
com_unit_missingness, 41
COMPATIBILITY (VARATT_REQUIRE_LEVELS), 146
con_contractions, 34, 44
con_contractions_redcap, 34, 46
con_inadmissible_categorical, 49
con_limit_deviations, 50
contradiction_functions_descriptions, 42
CONTRADICTION_TERM, 31–34, 43, 53, 69, 85, 86, 134, 146, 147
CONTRADICTION_TYPE, 31–34, 43, 53, 69, 85, 86, 134, 147
CONTRACTIONS, 148
CONTRACTIONS
(WELL_KNOWN_META_VARIABLE_NAMES), 147
DATA_ENTRY_TYPE, 148
DATA_ENTRY_TYPE
(WELL_KNOWN_META_VARIABLE_NAMES), 147
DATA_PREPARATION, 31–34, 43, 47, 53, 69, 85, 86, 134, 147
DATA_TYPE, 53, 148
DATA_TYPE
(WELL_KNOWN_META_VARIABLE_NAMES), 147
INDEX

DATA_TYPES, 53, 147
DATA_TYPES_OF_R_TYPE, 54, 103
dataquieR, 22, 25, 54, 128, 129, 140
dataquieR report v2, 129
dataquieR_result, 106, 107
dataquieR_result
  (print.dataquieR_result), 128
dataquieR_resultset, 52, 52
dataquieR_resultset2, 66, 113, 124
dataquieR_resultset_verify, 52
DATETIME, 33
DATETIME (DATA_TYPES), 53
datetime (DATA_TYPES), 53
DECIMALS, 148
DECIMALS
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
default.stringsAsFactors, 100
des_scatterplot_matrix, 55
des_summary, 56
Descriptor, 10, 12, 16, 39, 41, 44, 55, 56, 77
DETECTION_LIMIT_LOW, 148
DETECTION_LIMIT_LOW
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
DETECTION_LIMIT_UP, 148
DETECTION_LIMIT_UP
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
DETECTION_LIMITS, 148
DETECTION_LIMITS
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
DF_ELEMENT_COUNT, 57
DF_ID_REF_TABLE, 57
DF_ID_VARS, 58
DF_NAME, 58
DF_RECORD_CHECK, 59
DF_RECORD_COUNT, 59
DF_UNIQUE_ID, 60
DF_UNIQUE_ROWS, 60
dim.dataquieR_resultset2, 61
dimensions, 61, 65
dimnames.dataquieR_resultset2, 62
dims, 62
DISTRIBUTION, 148
DISTRIBUTION
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
DISTRIBUTIONS, 63
dq_report, 52, 63, 67, 68
dq_report2, 64, 67, 105–108, 117, 128
dq_report2(), 88, 130
dq_report_by, 66, 66, 147
emmeans::emmeans, 18
END_DIGIT_CHECK, 148
END_DIGIT_CHECK
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
enum, 6, 8, 9, 11, 12, 14, 17, 18, 24, 33, 36, 37,
  39, 40, 51, 77, 96, 100, 110, 125,
  131, 132
enum (DATA_TYPES), 53
environment, 109
eval.parent, 120
FLOAT (DATA_TYPES), 53
float, 54
float (DATA_TYPES), 53
function, 118
ggplot, 7, 8, 10–12, 14, 23, 27, 45, 48, 51, 55
ggplot2, 21, 25, 75, 122, 133
ggplot2::geom_jitter, 22, 26
ggplot2::geom_line(), 17
glm, 98
GOLDSTANDARD, 31–34, 43, 53, 68, 85, 86, 134,
  147
GRADING_RULESET, 148
GRADING_RULESET
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
GROUP_VAR_DEVICE, 148
GROUP_VAR_DEVICE
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
GROUP_VAR_OBSERVER, 148
GROUP_VAR_OBSERVER
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
HARD_LIMIT_LOW, 148
HARD_LIMIT_LOW
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
HARD_LIMIT_UP, 148
INDEX

HARD_LIMIT_UP
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
HARD_LIMITS, 148
HARD_LIMITS
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
html_dependency_clipboard, 69
html_dependency_dataquieR, 69
html_dependency_report_dt, 70
html_dependency_tippy, 70
html_dependency_vert_dt, 71
INCL_HARD_LIMIT_LOW, 148
INCL_HARD_LIMIT_LOW
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
INCL_HARD_LIMIT_UP, 148
INCL_HARD_LIMIT_UP
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
INCL_LOCATION_LIMIT_LOW, 148
INCL_LOCATION_LIMIT_LOW
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
INCL_LOCATION_LIMIT_UP, 148
INCL_LOCATION_LIMIT_UP
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
INCL_PROPORTION_LIMIT_LOW, 148
INCL_PROPORTION_LIMIT_LOW
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
INCL_PROPORTION_LIMIT_UP, 148
INCL_PROPORTION_LIMIT_UP
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
INCL_SOFT_LIMIT_LOW, 148
INCL_SOFT_LIMIT_LOW
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
INCL_SOFT_LIMIT_UP, 148
INCL_SOFT_LIMIT_UP
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
Indicator, 6, 7, 9, 13, 15, 18, 20, 22, 24, 26,
   27, 33, 37, 38, 47, 49, 50, 71, 72,
   74–76, 78–81, 83
int_all_datastructure_dataframe, 71
int_all_datastructure_segment, 72
int_datatype_matrix, 74
int_duplicate_content, 75
int_duplicate_ids, 76
int_part_vars_structure, 77
int_sts_element_dataframe, 78
int_sts_element_segment, 78
int_unexp_elements, 80
int_unexp_records_dataframe, 81
int_unexp_records_segment, 81
int_unexp_records_set, 83
INTEGER (DATA_TYPES), 53
integer, 16, 19, 21, 23, 26, 28, 54, 65, 74, 75,
   80–82, 110, 117, 124, 132, 133
integer (DATA_TYPES), 53
JUMP_LIST, 148
JUMP_LIST
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
KEY_DATETIME, 148
KEY_DATETIME
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
KEY_DEVICE, 148
KEY_DEVICE
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
KEY_OBSERVER, 148
KEY_OBSERVER
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
KEY_STUDY_SEGMENT, 148
KEY_STUDY_SEGMENT
   (WELL_KNOWN_META_VARIABLE_NAMES), 147
LABEL, 146, 148
LABEL (WELL_KNOWN_META_VARIABLE_NAMES), 147
list, 7, 8, 10–12, 14, 15, 17, 37, 39, 45, 48,
   51, 65–67, 72, 73, 75, 76, 78–83, 99,
   105–108, 115, 116, 118, 127, 128,
   133
list(), 126
lme4::lmer, 98
LOCATION_LIMIT_LOW, 148
prep_load_folder_with_metadata, 90, 109, 112, 114, 122
prep_load_report, 113
prep_load_workbook_like_file, 65, 67, 90, 109, 112, 113, 114, 122
prep_map_labels, 54, 115
prep_merge_study_data, 116
prep_meta_data_v1_to_item_level_meta_data, 116
prep_min_obs_level, 117
prep_pmap, 118
prepPrepare_dataframes, 119
prep_purge_data_frame_cache, 65, 67, 90, 109, 112–114, 121
prep_render_pie_chart_from_summaryclasses_ggplot2, 100, 106–108, 122, 123, 126
prep_render_pie_chart_from_summaryclasses_plotly, 100, 106–108, 122, 123, 126
prep_save_report, 123
prep_scalelevel_from_data_and_metadata, 124
prep_scalelevel_from_data_and_metadata(), 119
prep_study2meta, 120, 125
prep_summary_to_classes, 100, 106–108, 122, 123, 126
prep_summary_to_classes(), 106
prep_title_escape, 126
prep_valuelabels_from_data, 127
print.dataquieR_result, 128
print.dataquieR_resultset, 52, 66, 128
print.dataquieR_resultset2, 129
print.dataquieR_resultset2(), 67
print.dataquieR_summary, 129
print.interval, 130
print.ReportSummaryTable, 131
printed, 66
pro_applicability_matrix, 132
PROPORTION_LIMIT_LOW, 148
PROPORTION_LIMIT_LOW
(WELL_KNOWN_META_VARIABLE_NAMES), 147
PROPORTION_LIMIT_UP, 148
PROPORTION_LIMIT_UP
(WELL_KNOWN_META_VARIABLE_NAMES), 147
PROPORTION_RANGE, 148
PROPORTION_RANGE
(WELL_KNOWN_META_VARIABLE_NAMES), 147
rbind.ReportSummaryTable, 133
RECODE, 148
RECODE
(WELL_KNOWN_META_VARIABLE_NAMES), 147
RECOMMENDED (VARATT_REQUIRE_LEVELS), 146
RELEVANCE (VARATT_REQUIRE_LEVELS), 146
resnames, 134
resnames.dataquieR_resultset2, 135
robustbase::mc, 22, 25
SCALE_LEVEL, 135, 148
SCALE_LEVEL
(WELL_KNOWN_META_VARIABLE_NAMES), 147
SCALE_LEVELS, 135
SEGMENT_ID_REF_TABLE, 136, 136
SEGMENT_ID_TABLE, 136
SEGMENT_ID_VARS, 137
SEGMENT_MISS, 137
SEGMENT_PART_VARS, 138
SEGMENT_RECORD_CHECK, 138
SEGMENT_RECORD_COUNT, 139
SEGMENT_UNIQUE_ROWS, 139
set, 21, 23, 26
set (DATA_TYPES), 53
SOFT_LIMIT_LOW, 148
SOFT_LIMIT_LOW
(WELL_KNOWN_META_VARIABLE_NAMES), 147
SOFT_LIMIT_UP, 148
SOFT_LIMIT_UP
(WELL_KNOWN_META_VARIABLE_NAMES), 147
SOFT_LIMITS, 148
SOFT_LIMITS
(WELL_KNOWN_META_VARIABLE_NAMES), 147
SPLIT_CHAR, 140
STRING (DATA_TYPES), 53
string, 54
string (DATA_TYPES), 53
study_data, 77, 116, 140
STUDY_SEGMENT, 67, 106–108, 148
variable roles, 23, 26, 40
variable roles (VARIABLE.Roles), 147
VARIABLE_LIST, 31–34, 43, 53, 69, 85, 86, 134, 146
VARIABLE_ORDER, 148
VARIABLE_ORDER
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
VARIABLE_ROLE, 148
VARIABLE_ROLE
  (WELL_KNOWN_META_VARIABLE_NAMES), 147
VARIABLE_ROLES, 147

WELL_KNOWN_META_VARIABLE_NAMES, 100, 101, 142, 143, 147