

Package: metalite.sl (via r-universe)

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Title Subject-Level Analysis Using 'metalite'

Version 0.1.0

Description Analyzes subject-level data in clinical trials using the 'metalite' data structure. The package simplifies the workflow to create production-ready tables, listings, and figures discussed in the subject-level analysis chapters of ``R for Clinical Study Reports and Submission'' by Zhang et al. (2022) <<https://r4csr.org/>>.

Depends R (>= 4.1.0)

License GPL (>= 3)

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| | |
|------------------|---------------------------------|
| collect_baseline | <i>Count number of subjects</i> |
|------------------|---------------------------------|

Description

Count number of subjects

Usage

```
collect_baseline(
  meta,
  population,
  parameter,
  type = "Subjects",
  use_na = c("ifany", "no", "always"),
  display_total = TRUE
)
```

Arguments

| | |
|---------------|---|
| meta | A metadata object created by metalite. |
| population | A character value of population term name. The term name is used as key to link information. |
| parameter | A character value of parameter term name. The term name is used as key to link information. |
| type | A character value to control title name, e.g., Subjects or Records. |
| use_na | A character value for whether to include NA values in the table. See the useNA argument in <code>base::table()</code> for more details. |
| display_total | A logical value to display total column. |

Value

A list containing number of subjects

Examples

```
meta <- meta_sl_example()
meta |> collect_baseline(
  population = "apat",
  parameter = "age"
)
```

| | |
|-----------|-------------------------|
| defmt_pct | <i>Deformat percent</i> |
|-----------|-------------------------|

Description

Deformat percent

Usage

```
defmt_pct(pct)
```

Arguments

| | |
|-----|--------------------------------|
| pct | string eager to remove percent |
|-----|--------------------------------|

Value

Numeric value without percent

Examples

```
defmt_pct("10.0%")
defmt_pct(c("10.0%", "(11.2%)"))
```

extend_exp_duration *Add cumulative count and summary stats for categories for exposure duration analysis*

Description

Add cumulative count and summary stats for categories for exposure duration analysis

Usage

```
extend_exp_duration(
  outdata,
  category_section_label = NULL,
  duration_category_list = NULL,
  duration_category_labels = NULL
)
```

Arguments

`outdata` An outdata object created by [prepare_exp_duration\(\)](#).

`category_section_label`
A character value of section label. If NULL, the parameter label is used with "(cumulative)".

`duration_category_list`
A list of duration category ranges. Must be real numbers and may overlap or be mutually exclusive. A list should be in the form of `list(c(low1, high1), c(low2, high2), ...)`. If NA is included in the range, it is treated as `-Inf` or `Inf`. The range is defined as `low <= x < high` for each.

`duration_category_labels`
A character vector of internal labels. Labels to be displayed for the `duration_category_list` values. Must be the same length as `duration_category_list`.

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_exposure_example()
outdata <- meta |> prepare_exp_duration()
outdata |>
  extend_exp_duration(
    duration_category_list = list(c(1, NA), c(7, NA), c(21, NA)),
    duration_category_labels = c(">=1 day", ">=7 days", ">=21 days")
  )
```

| | |
|------------------|---|
| format_base_char | <i>Format Baseline Characteristics Analysis</i> |
|------------------|---|

Description

Format Baseline Characteristics Analysis

Usage

```
format_base_char(  
  outdata,  
  display_col = c("n", "prop", "total"),  
  digits_prop = 1,  
  display_stat = c("mean", "sd", "se", "median", "q1 to q3", "range")  
)
```

Arguments

| | |
|--------------|--|
| outdata | A metadata object created by prepare_sl_summary() . |
| display_col | Column wants to display on the table. The term could be selected from <code>c("n", "prop", "total")</code> . |
| digits_prop | Number of digits for proportion columns. |
| display_stat | A vector of statistics term name. The term name could be selected from <code>c("mean", "sd", "se", "median", "q1 to q3", "range", "q1", "q3", "min", "max")</code> . |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()  
  
meta |>  
  prepare_base_char(population = "apat", parameter = "age;gender") |>  
  format_base_char()
```

`format_base_char_subgroup`*Prepare data for Subgroup Analysis for Baseline Characteristic*

Description

Prepare data for Subgroup Analysis for Baseline Characteristic

Usage

```
format_base_char_subgroup(  
  outdata,  
  display = c("n", "prop", "total"),  
  display_stat = c("mean", "sd", "median", "range")  
)
```

Arguments

| | |
|---------------------------|--|
| <code>outdata</code> | A metadata object created by <code>prepare_base_char_subgroup()</code> . |
| <code>display</code> | Column wants to display on the table. The term could be selected from <code>c("n", "prop", "total")</code> . |
| <code>display_stat</code> | A vector of statistics term name. The term name could be selected from <code>c("mean", "sd", "se", "median", "q1 to q3", "range", "q1", "q3", "min", "max")</code> . |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()  
  
outdata <- prepare_base_char_subgroup(  
  meta,  
  population = "apat",  
  parameter = "age",  
  subgroup_var = "TRTA",  
  subgroup_header = c("SEX", "TRTA"),  
  display_subgroup_total = TRUE  
)  
  
outdata |> format_base_char_subgroup()
```

format_disposition *Format Disposition Analysis*

Description

Format Disposition Analysis

Usage

```
format_disposition(  
  outdata,  
  display_col = c("n", "prop", "total"),  
  digits_prop = 1,  
  display_stat = c("mean", "sd", "se", "median", "q1 to q3", "range")  
)
```

Arguments

| | |
|--------------|--|
| outdata | A metadata object created by prepare_sl_summary() . |
| display_col | Column wants to display on the table. The term could be selected from <code>c("n", "prop", "total")</code> . |
| digits_prop | Number of digits for proportion columns. |
| display_stat | A vector of statistics term name. The term name could be selected from <code>c("mean", "sd", "se", "median", "q1 to q3", "range", "q1", "q3", "min", "max")</code> . |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()  
  
meta |>  
  prepare_disposition(population = "apat", parameter = "disposition;medical-disposition") |>  
  format_disposition()
```

format_exp_duration *Format Exposure Duration Analysis*

Description

Format Exposure Duration Analysis

Usage

```
format_exp_duration(  
  outdata,  
  display_col = c("n", "prop", "n_cum", "prop_cum", "total"),  
  digits_prop = 1,  
  display_stat = c("mean", "sd", "se", "median", "q1 to q3", "range")  
)
```

Arguments

| | |
|--------------|--|
| outdata | A metadata object created by <code>prepare_sl_summary()</code> . |
| display_col | Column wants to display on the table. "n_cum", "prop_cum" can additionally be selected. <ul style="list-style-type: none">• n_cum: Number of subjects created by <code>extend_exp_duration()</code>.• prop_cum: Proportion of subjects created by <code>extend_exp_duration()</code>. |
| digits_prop | Number of digits for proportion columns. |
| display_stat | A vector of statistics term name. The term name could be selected from <code>c("mean", "sd", "se", "median", "q1 to q3", "range", "q1", "q3", "min", "max")</code> . |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_exposure_example()  
  
meta |>  
  prepare_exp_duration(population = "apat", parameter = "expdur") |>  
  format_exp_duration(display_col = c("n", "prop", "total"))
```

| | |
|-------------------|---|
| format_sl_summary | <i>Prepare data for baseline characteristic table</i> |
|-------------------|---|

Description

Prepare data for baseline characteristic table

Usage

```
format_sl_summary(  
  outdata,  
  display_col = c("n", "prop", "total"),  
  digits_prop = 1,  
  display_stat = c("mean", "sd", "se", "median", "q1 to q3", "range")  
)
```

Arguments

| | |
|--------------|--|
| outdata | A metadata object created by prepare_sl_summary() . |
| display_col | Column wants to display on the table. The term could be selected from <code>c("n", "prop", "total")</code> . |
| digits_prop | Number of digits for proportion columns. |
| display_stat | A vector of statistics term name. The term name could be selected from <code>c("mean", "sd", "se", "median", "q1 to q3", "range", "q1", "q3", "min", "max")</code> . |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()  
  
meta |>  
  prepare_sl_summary(population = "apat", analysis = "base_char", parameter = "age;gender") |>  
  format_sl_summary()
```

format_trt_compliance *Format Treatment Compliance Analysis*

Description

Format Treatment Compliance Analysis

Format Treatment Compliance Analysis

Usage

```
format_trt_compliance(
  outdata,
  display_col = c("n", "prop", "total"),
  digits_prop = 1,
  display_stat = c("mean", "sd", "se", "median", "q1 to q3", "range")
)
```

```
format_trt_compliance(
  outdata,
  display_col = c("n", "prop", "total"),
  digits_prop = 1,
  display_stat = c("mean", "sd", "se", "median", "q1 to q3", "range")
)
```

Arguments

| | |
|--------------|--|
| outdata | A metadata object created by prepare_sl_summary() . |
| display_col | Column wants to display on the table. The term could be selected from <code>c("n", "prop", "total")</code> . |
| digits_prop | Number of digits for proportion columns. |
| display_stat | A vector of statistics term name. The term name could be selected from <code>c("mean", "sd", "se", "median", "q1 to q3", "range", "q1", "q3", "min", "max")</code> . |

Value

A list of analysis raw datasets.

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()

meta |>
  prepare_trt_compliance(parameter = "comp8;comp16") |>
  format_trt_compliance()
meta <- meta_sl_example()
```

```
meta |>
  prepare_trt_compliance(population = "apat", parameter = "comp8;comp16") |>
  format_trt_compliance()
```

 meta_sl

Create metadata for subject-level analysis table

Description

Create metadata for subject-level analysis table

Usage

```
meta_sl(
  dataset_population,
  dataset_observation = NULL,
  population_term,
  observation_term = NULL,
  parameter_term = "age;race;gender",
  parameter_var = "AGE^AGEGR1;RACE;SEX",
  parameter_labels = NULL,
  analysis_term = "base_char",
  analysis_title = "Participant Baseline Characteristics by Treatment Group",
  population_subset = SAFFL == "Y",
  observation_subset = NULL,
  population_label = "All Participants as Treated",
  treatment_group = "TRT01A"
)
```

Arguments

`dataset_population` Source dataset of population.

`dataset_observation` Source dataset of observation

`population_term` A character value of population term name.

`observation_term` A character value of observation term name.

`parameter_term` A character value of parameter term name. If there are multiple terms, they are separated by the semicolon (;).

`parameter_var` A character value of parameter variable name. If there are multiple variables, they are separated by the semicolon (;). A group variable can be specified followed by a variable and the hat symbol (^).

parameter_labels A character vector of parameter label name. The length of vector should be the same as the number of parameter terms. A label from an input data is used if NA for a variable is specified.

analysis_term A character value of analysis term name.

analysis_title A character value of analysis title name.

population_subset An unquoted condition for selecting the populations from dataset of population.

observation_subset An unquoted condition for selecting the populations from dataset of observation

population_label A character value of population label.

treatment_group A character value of treatment group name.

Value

A metalite object.

Examples

```
meta_sl(
  dataset_population = r2rtf::r2rtf_adsl,
  population_term = "apat",
  parameter_term = "age;race",
  parameter_var = "AGE^AGEGR1;RACE"
)
```

meta_sl_example

Create an example meta_sl_example object

Description

This function is only for illustration purpose. r2rtf is required.

Usage

```
meta_sl_example()
```

Value

A metadata object.

Examples

```
meta_sl_example()
```

`meta_sl_exposure_example`*Create an example meta_sl_exposure_example object*

Description

This function is only for illustration purpose. r2rtf is required.

Usage

```
meta_sl_exposure_example()
```

Value

A metadata object.

Examples

```
meta_sl_exposure_example()
```

`plotly_exp_duration` *Create an interactive plot for exposure duration*

Description

Create an interactive plot for exposure duration

Usage

```
plotly_exp_duration(  
  outdata,  
  color = NULL,  
  display = c("n", "prop"),  
  display_total = TRUE,  
  plot_group_label = "Treatment group",  
  plot_category_label = "Exposure duration",  
  hover_summary_var = c("n", "median", "sd", "se", "median", "min", "max", "q1 to q3",  
    "range"),  
  width = 1000,  
  height = 400  
)
```

Arguments

| | |
|---------------------|---|
| outdata | An outdata object created from prepare_exp_duration(). extend_exp_duration() can also be applied. |
| color | Color for a histogram. |
| display | A character vector of display type. n or prop can be selected. |
| display_total | A logical value to display total. |
| plot_group_label | A label for grouping. |
| plot_category_label | A label for category. |
| hover_summary_var | A character vector of statistics to be displayed on hover label of bar. |
| width | Width of the plot. |
| height | Height of the plot. |

Value

Interactive plot for exposure duration.

Examples

```
# Only run this example in interactive R sessions
if (interactive()) {
  meta <- meta_sl_exposure_example()
  outdata <- meta |>
    prepare_exp_duration() |>
    extend_exp_duration(
      duration_category_list = list(c(1, 7), c(7, 21), c(21, 84)),
      duration_category_labels = c("1-7 days", "7-21 days", "21-84 days")
    )

  outdata |> plotly_exposure_duration()
}
```

| | |
|-------------------|---|
| prepare_base_char | <i>Prepare data for baseline characteristic table</i> |
|-------------------|---|

Description

Prepare data for baseline characteristic table

Usage

```
prepare_base_char(
  meta,
  analysis = "base_char",
  population = meta$plan[meta$plan$analysis == analysis, ]$population,
  parameter = paste(meta$plan[meta$plan$analysis == analysis, ]$parameter, collapse =
    ";")
)
```

Arguments

| | |
|------------|--|
| meta | A metadata object created by metalite. |
| analysis | A character value of analysis term name. The term name is used as key to link information. |
| population | A character value of population term name. The term name is used as key to link information. |
| parameter | A character value of parameter term name. The term name is used as key to link information. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()
meta |> prepare_base_char()
```

```
prepare_base_char_subgroup
```

Prepare data for treatment compliance table

Description

Prepare data for treatment compliance table

Usage

```
prepare_base_char_subgroup(
  meta,
  population,
  analysis = "base_char_subgroup",
  parameter,
  subgroup_var,
  subgroup_header = c(meta$population[[population]]$group, subgroup_var),
  display_subgroup_total = TRUE
)
```

Arguments

| | |
|------------------------|--|
| meta | A metadata object created by metalite. |
| population | A character value of population term name. The term name is used as key to link information. |
| analysis | A character value of analysis term name. The term name is used as key to link information. |
| parameter | A character value of parameter term name. The term name is used as key to link information. |
| subgroup_var | A character value of subgroup variable name in observation data saved in meta\$data_observation. |
| subgroup_header | A character vector for column header hierarchy. The first element will be the first level header and the second element will be second level header. |
| display_subgroup_total | A logic value of displaying the total group. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()
outdata <- prepare_base_char_subgroup(
  meta,
  population = "apat",
  parameter = "age",
  subgroup_var = "TRTA",
  subgroup_header = c("SEX", "TRTA"),
  display_subgroup_total = TRUE
)
```

prepare_disposition *Prepare data for treatment compliance table*

Description

Prepare data for treatment compliance table

Usage

```
prepare_disposition(
  meta,
  analysis = "disp",
  population = meta$plan[meta$plan$analysis == analysis, ]$population,
  parameter = paste(meta$plan[meta$plan$analysis == analysis, ]$parameter, collapse =
    ";")
)
```


Arguments

| | |
|------------|--|
| meta | A metadata object created by metalite. |
| analysis | A character value of analysis term name. The term name is used as key to link information. |
| population | A character value of population term name. The term name is used as key to link information. |
| parameter | A character value of parameter term name. The term name is used as key to link information. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()
meta |> prepare_base_char()
```

prepare_exp_duration *Prepare data for exposure duration table*

Description

Prepare data for exposure duration table

Usage

```
prepare_exp_duration(
  meta,
  analysis = "exp_dur",
  population = meta$plan[meta$plan$analysis == analysis, ]$population,
  parameter = paste(meta$plan[meta$plan$analysis == analysis, ]$parameter, collapse =
    ";")
)
```

Arguments

| | |
|------------|--|
| meta | A metadata object created by metalite. |
| analysis | A character value of analysis term name. The term name is used as key to link information. |
| population | A character value of population term name. The term name is used as key to link information. |
| parameter | A character value of parameter term name. The term name is used as key to link information. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_exposure_example()
meta |> prepare_exp_duration()
```

```
prepare_sl_summary      Prepare data for baseline characteristic table
```

Description

Prepare data for baseline characteristic table

Usage

```
prepare_sl_summary(
  meta,
  population,
  analysis,
  parameter = paste(names(meta$parameter), collapse = ";")
)
```

Arguments

| | |
|------------|--|
| meta | A metadata object created by metalite. |
| population | A character value of population term name. The term name is used as key to link information. |
| analysis | A character value of analysis term name. The term name is used as key to link information. |
| parameter | A character value of parameter term name. The term name is used as key to link information. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()
meta |> prepare_sl_summary(population = "apat", analysis = "base_char")
```

`prepare_trt_compliance`*Prepare data for treatment compliance table*

Description

Prepare data for treatment compliance table

Usage

```
prepare_trt_compliance(  
  meta,  
  analysis = "trt_compliance",  
  population = meta$plan[meta$plan$analysis == analysis, ]$population,  
  parameter = paste(meta$plan[meta$plan$analysis == analysis, ]$parameter, collapse =  
    ";")  
)
```

Arguments

| | |
|-------------------------|--|
| <code>meta</code> | A metadata object created by <code>metalite</code> . |
| <code>analysis</code> | A character value of analysis term name. The term name is used as key to link information. |
| <code>population</code> | A character value of population term name. The term name is used as key to link information. |
| <code>parameter</code> | A character value of parameter term name. The term name is used as key to link information. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()  
meta |> prepare_trt_compliance()
```

| | |
|-----------------|---|
| react_base_char | <i>Display interactive baseline characteristic tables with AE subgroup analysis</i> |
|-----------------|---|

Description

Display interactive baseline characteristic tables with AE subgroup analysis

Usage

```
react_base_char(
  metadata_sl,
  metadata_ae,
  population = "apat",
  observation = "wk12",
  display_total = TRUE,
  sl_parameter = "age;gender;race",
  ae_subgroup = c("gender", "race"),
  ae_specific = "rel",
  width = 1200
)
```

Arguments

| | |
|---------------|---|
| metadata_sl | A metadata created by metalite, which builds the baseline characteristic table |
| metadata_ae | A metadata created by metalite, which builds the AE subgroup specific table |
| population | A character value of population term name. The term name is used as key to link information. |
| observation | A character value of observation term name. The term name is used as key to link information. |
| display_total | Display total column or not. |
| sl_parameter | A character value of parameter term name for the baseline characteristic table. The term name is used as key to link information. |
| ae_subgroup | A vector of strubf to specify the subgroups in the AE subgroup specific table. |
| ae_specific | A string specifying the AE specific category. |
| width | A numeric value of width of the table in pixels. |

Value

An reactable combing both baseline characteristic table and AE subgroup specific tables.

Examples

```

if (interactive()) {
  react_base_char(
    metadata_sl = meta_sl_example(),
    metadata_ae = metalite.ae::meta_ae_example(),
    population = "apat",
    observation = "wk12",
    display_total = TRUE,
    sl_parameter = "age;gender;race",
    ae_subgroup = c("age", "race", "gender"),
    ae_specific = "rel",
    width = 1200
  )
}

```

| | |
|-------------------|---|
| react_disposition | <i>Display interactive disposition tables with AE subgroup analysis</i> |
|-------------------|---|

Description

Display interactive disposition tables with AE subgroup analysis

Usage

```

react_disposition(
  metadata_sl,
  metadata_ae,
  analysis = "disp",
  population = metadata_sl$plan[metadata_sl$plan$analysis == analysis, ]$population,
  sl_parameter = paste(metadata_sl$plan[metadata_sl$plan$analysis == analysis,
    ]$parameter, collapse = ";"),
  display_total = TRUE,
  width = 1200
)

```

Arguments

| | |
|---------------|---|
| metadata_sl | A metadata created by metalite, which builds the baseline characteristic table |
| metadata_ae | A metadata created by metalite, which builds the AE subgroup specific table |
| analysis | The analysis label provided in metadata_sl. |
| population | A character value of population term name. The term name is used as key to link information. |
| sl_parameter | A character value of parameter term name for the baseline characteristic table. The term name is used as key to link information. |
| display_total | Display total column or not. |
| width | A numeric value of width of the table in pixels. |

Value

An rtable combining both baseline characteristic table and AE subgroup specific tables.

Examples

```
if (interactive()) {
  react_disposition(
    metadata_sl = meta_sl_example(),
    metadata_ae = metalite.ae::meta_ae_example(),
    width = 1200
  )
}
```

rtf_base_char

Baseline characteristic table

Description

Baseline characteristic table

Usage

```
rtf_base_char(
  outdata,
  source,
  col_rel_width = NULL,
  text_font_size = 9,
  orientation = "portrait",
  footnotes = NULL,
  title = NULL,
  path_outdata = NULL,
  path_outtable = NULL
)
```

Arguments

| | |
|----------------|--|
| outdata | An outdata object created by <code>prepare_sl_summary()</code> . |
| source | A character value of the data source. |
| col_rel_width | Column relative width in a vector e.g. <code>c(2,1,1)</code> refers to 2:1:1. Default is NULL for equal column width. |
| text_font_size | Text font size. To vary text font size by column, use numeric vector with length of vector equal to number of columns displayed e.g. <code>c(9,20,40)</code> . |
| orientation | Orientation in 'portrait' or 'landscape'. |
| footnotes | A character vector of table footnotes. |
| title | Term "analysis", "observation" and "population") for collecting title from metadata or a character vector of table titles. |
| path_outdata | A character string of the outdata path. |
| path_outtable | A character string of the outtable path. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()

meta |>
  prepare_base_char(
    population = "apat",
    analysis = "base_char",
    parameter = "age;gender"
  ) |>
  format_base_char() |>
  rtf_base_char(
    source = "Source: [CDISCpilot: adam-adsl]",
    path_outdata = tempfile(fileext = ".Rdata"),
    path_outtable = tempfile(fileext = ".rtf")
  )
```

rtf_base_char_subgroup

Subgroup Analysis for Baseline Characteristic

Description

Subgroup Analysis for Baseline Characteristic

Usage

```
rtf_base_char_subgroup(
  outdata,
  source,
  col_rel_width = NULL,
  text_font_size = 8,
  orientation = "landscape",
  footnotes = NULL,
  title = NULL,
  path_outdata = NULL,
  path_outtable = NULL
)
```

Arguments

| | |
|---------------|---|
| outdata | An outdata object created by prepare_base_char_subgroup() |
| source | A character value of the data source. |
| col_rel_width | Column relative width in a vector e.g. <code>c(2,1,1)</code> refers to 2:1:1. Default is NULL for equal column width. |

| | |
|----------------|--|
| text_font_size | Text font size. To vary text font size by column, use numeric vector with length of vector equal to number of columns displayed e.g. c(9,20,40). |
| orientation | Orientation in 'portrait' or 'landscape'. |
| footnotes | A character vector of table footnotes. |
| title | Term "analysis", "observation" and "population") for collecting title from meta-data or a character vector of table titles. |
| path_outdata | A character string of the outdata path. |
| path_outtable | A character string of the outtable path. |

Value

RTF file and source dataset for baseline characteristic table.

Examples

```
meta <- meta_sl_example()

outdata <- prepare_base_char_subgroup(
  meta,
  population = "apat",
  parameter = "age",
  subgroup_var = "TRTA",
  subgroup_header = c("SEX", "TRTA"),
  display_subgroup_total = TRUE
)

outdata |>
  format_base_char_subgroup() |>
  rtf_base_char_subgroup(
    source = "Source: [CDISCpilot: adam-ads1]",
    path_outdata = tempfile(fileext = ".Rdata"),
    path_outtable = tempfile(fileext = ".rtf")
  )
```

rtf_disposition

Disposition table

Description

Disposition table

Usage

```
rtf_disposition(
  outdata,
  source,
  col_rel_width = NULL,
  text_font_size = 9,
  orientation = "portrait",
  footnotes = NULL,
  title = NULL,
  path_outdata = NULL,
  path_outtable = NULL
)
```

Arguments

| | |
|----------------|--|
| outdata | An outdata object created by <code>prepare_sl_summary()</code> . |
| source | A character value of the data source. |
| col_rel_width | Column relative width in a vector e.g. <code>c(2,1,1)</code> refers to 2:1:1. Default is NULL for equal column width. |
| text_font_size | Text font size. To vary text font size by column, use numeric vector with length of vector equal to number of columns displayed e.g. <code>c(9,20,40)</code> . |
| orientation | Orientation in 'portrait' or 'landscape'. |
| footnotes | A character vector of table footnotes. |
| title | Term "analysis", "observation" and "population") for collecting title from meta-data or a character vector of table titles. |
| path_outdata | A character string of the outdata path. |
| path_outtable | A character string of the outtable path. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()

meta |>
  prepare_disposition(population = "apat", parameter = "disposition;medical-disposition") |>
  format_disposition() |>
  rtf_disposition(
    source = "Source: [CDISCPilot: adam-adsl]",
    path_outdata = tempfile(fileext = ".Rdata"),
    path_outtable = tempfile(fileext = ".rtf")
  )
```

| | |
|------------------|--------------------------------|
| rtf_exp_duration | <i>Exposure duration table</i> |
|------------------|--------------------------------|

Description

Exposure duration table

Usage

```
rtf_exp_duration(
  outdata,
  source = "Source: [CDISCPilot: adam-adsl; adex]",
  col_rel_width = NULL,
  text_font_size = 9,
  orientation = "portrait",
  footnotes =
    c("Each participant is counted once on each applicable duration category row.",
      "Duration of Exposure is the time from the first dose date to the last dose date."),
  title = NULL,
  path_outdata = NULL,
  path_outtable = NULL
)
```

Arguments

| | |
|----------------|--|
| outdata | An outdata object created by prepare_sl_summary() . |
| source | A character value of the data source. |
| col_rel_width | Column relative width in a vector e.g. c(2,1,1) refers to 2:1:1. Default is NULL for equal column width. |
| text_font_size | Text font size. To vary text font size by column, use numeric vector with length of vector equal to number of columns displayed e.g. c(9,20,40). |
| orientation | Orientation in 'portrait' or 'landscape'. |
| footnotes | A character vector of table footnotes. |
| title | Term "analysis", "observation" and "population") for collecting title from meta-data or a character vector of table titles. |
| path_outdata | A character string of the outdata path. |
| path_outtable | A character string of the outtable path. |

Value

RTF file and source dataset for baseline characteristic table.

Examples

```
meta <- meta_sl_exposure_example()

meta |>
  prepare_exp_duration(population = "apat", parameter = "expdur") |>
  format_exp_duration(display_col = c("n", "prop", "total")) |>
  rtf_exp_duration(
    source = "Source: [CDISCpilot: adam-adsl; adex]",
    path_outdata = tempfile(fileext = ".Rdata"),
    path_outtable = tempfile(fileext = ".rtf")
  )
```

| | |
|----------------|--------------------------------------|
| rtf_sl_summary | <i>Baseline characteristic table</i> |
|----------------|--------------------------------------|

Description

Baseline characteristic table

Usage

```
rtf_sl_summary(
  outdata,
  source,
  col_rel_width = NULL,
  text_font_size = 9,
  orientation = "portrait",
  footnotes = NULL,
  title = NULL,
  path_outdata = NULL,
  path_outtable = NULL
)
```

Arguments

| | |
|----------------|--|
| outdata | An outdata object created by prepare_sl_summary() . |
| source | A character value of the data source. |
| col_rel_width | Column relative width in a vector e.g. <code>c(2,1,1)</code> refers to 2:1:1. Default is NULL for equal column width. |
| text_font_size | Text font size. To vary text font size by column, use numeric vector with length of vector equal to number of columns displayed e.g. <code>c(9,20,40)</code> . |
| orientation | Orientation in 'portrait' or 'landscape'. |
| footnotes | A character vector of table footnotes. |
| title | Term "analysis", "observation" and "population") for collecting title from meta-data or a character vector of table titles. |
| path_outdata | A character string of the outdata path. |
| path_outtable | A character string of the outtable path. |

Value

RTF file and source dataset for baseline characteristic table.

Examples

```
meta <- meta_sl_example()

meta |>
  prepare_sl_summary(
    population = "apat",
    analysis = "base_char",
    parameter = "age;gender"
  ) |>
  format_sl_summary() |>
  rtf_sl_summary(
    source = "Source: [CDISCpilot: adam-ads1]",
    path_outdata = tempfile(fileext = ".Rdata"),
    path_outtable = tempfile(fileext = ".rtf")
  )
```

| | |
|--------------------|-----------------------------------|
| rtf_trt_compliance | <i>Treatment compliance table</i> |
|--------------------|-----------------------------------|

Description

Treatment compliance table

Usage

```
rtf_trt_compliance(
  outdata,
  source,
  col_rel_width = NULL,
  text_font_size = 9,
  orientation = "portrait",
  footnotes = NULL,
  title = NULL,
  path_outdata = NULL,
  path_outtable = NULL
)
```

Arguments

| | |
|---------------|---|
| outdata | An outdata object created by <code>prepare_sl_summary()</code> . |
| source | A character value of the data source. |
| col_rel_width | Column relative width in a vector e.g. <code>c(2,1,1)</code> refers to 2:1:1. Default is NULL for equal column width. |

| | |
|-----------------------------|--|
| <code>text_font_size</code> | Text font size. To vary text font size by column, use numeric vector with length of vector equal to number of columns displayed e.g. <code>c(9,20,40)</code> . |
| <code>orientation</code> | Orientation in 'portrait' or 'landscape'. |
| <code>footnotes</code> | A character vector of table footnotes. |
| <code>title</code> | Term "analysis", "observation" and "population") for collecting title from metadata or a character vector of table titles. |
| <code>path_outdata</code> | A character string of the outdata path. |
| <code>path_outtable</code> | A character string of the outtable path. |

Value

A list of analysis raw datasets.

Examples

```
meta <- meta_sl_example()

meta |>
  prepare_trt_compliance(population = "apat", parameter = "comp8;comp16") |>
  format_trt_compliance() |>
  rtf_trt_compliance(
    source = "Source: [CDISCPilot: adam-adsl]",
    path_outdata = tempfile(fileext = ".Rdata"),
    path_outtable = tempfile(fileext = ".rtf")
  )
```

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