

Package: metalite.sl (via r-universe)

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Title Subject-Level Analysis Using 'metalite'

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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"
)
```

<code>meta_sl_example</code>	<i>Create an example meta_sl_example object</i>
------------------------------	---

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 combing 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

<code>outdata</code>	An outdata object created by <code>prepare_sl_summary()</code> .
<code>source</code>	A character value of the data source.
<code>col_rel_width</code>	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 meta-data 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

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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