

# Package ‘metalite’

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**Title** ADaM Metadata Structure

**Version** 0.1.4

**Description** A metadata structure for clinical data analysis and reporting based on Analysis Data Model (ADaM) datasets. The package simplifies clinical analysis and reporting tool development by defining standardized inputs, outputs, and workflow. The package can be used to create analysis and reporting planning grid, mock table, and validated analysis and reporting results based on consistent inputs.

**License** GPL-3

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---

adam_mapping	<i>Construct ADaM mappings</i>
--------------	--------------------------------

---

### Description

ADaM mappings describe how variables and meta information in the ADaM data are mapped to standardized term.

### Usage

```
adam_mapping(  
  name,  
  id = NULL,  
  group = NULL,  
  var = NULL,  
  subset = NULL,  
  label = NULL,  
  ...  
)
```

### Arguments

name	A character value of term name. The term name is used as key to link information.
id	A character value of subject identifier variable name in an ADaM dataset.
group	A character vector of group variable names in an ADaM dataset.
var	A character vector of useful variable names in an ADaM dataset.
subset	An expression to identify analysis records. See <code>base::subset()</code> .
label	A character value of analysis label.
...	Additional variables.

### Details

The design is inspired by `ggplot2::aes()`.

### Value

A list with class `adam_mapping`. Components of the list are either quosures or constants.

### Examples

```
adam_mapping(  
  name = "apat",  
  id = "USUBJID",  
  group = "TRT01A",  
  subset = TRTFL == "Y",  
  label = "All Participants as Treated"  
)
```

---

add_plan	<i>Add additional analysis plan</i>
----------	-------------------------------------

---

## Description

Add additional analysis plan

## Usage

```
add_plan(plan, analysis, population, observation, parameter, ...)
```

## Arguments

plan	A meta_plan object.
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.
observation	A character value of observation 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.
...	Additional arguments.

## Value

A data frame containing analysis plans with new plans added.

## Examples

```
plan("ae_summary",
  population = "apat",
  observation = c("wk12", "wk24"), parameter = "any;rel"
) |>
  add_plan("ae_specific",
    population = "apat",
    observation = c("wk12", "wk24"), parameter = c("any", "rel")
  )
```

---

`assign_label`*A function to assign labels to a data frame*

---

**Description**

A function to assign labels to a data frame

**Usage**

```
assign_label(data, var = names(data), label = names(data))
```

**Arguments**

<code>data</code>	A data frame.
<code>var</code>	The variables to assign labels.
<code>label</code>	The labels to be assigned.

**Details**

- Case 1: If the variable's label is already define in the original data frame but not redefined in `assign_label(...)`, its original labels will be kept.
- Case 2: If the variable's label is already define in the original data frame but re-defined by `assign_label(...)`, its labels will be re-defined.
- Case 3: If the variable's label is not define in the original data frame but it is defined by `assign_label(...)`, its labels will added.
- Case 4: If the variable's label is not define in the original data frame, neither was it defined by `assign_label(...)`, its labels will be the variable name itself.

**Value**

A data frame with labels updated.

**Examples**

```
assign_label(r2rtf::r2rtf_adae) |> head()
assign_label(
  r2rtf::r2rtf_adae,
  var = "USUBJID",
  label = "Unique subject identifier"
) |> head()
```

collect\_adam\_mapping *Collect adam\_mapping from meta\_adam by name*

---

**Description**

Collect adam\_mapping from meta\_adam by name

**Usage**

```
collect_adam_mapping(meta, name)
```

**Arguments**

meta            A meta\_adam object.  
name            A keyword value.

**Value**

An adam\_mapping class object containing the definition of the search variable in name.

**Examples**

```
meta <- meta_example()  
collect_adam_mapping(meta, "apat")
```

---

collect\_dataname        *Collect specification for dataset name*

---

**Description**

Collect specification for dataset name

**Usage**

```
collect_dataname(meta)
```

**Arguments**

meta            A meta\_adam object.

**Value**

A vector of character strings containing the name of the population/observation.

**Examples**

```
meta <- meta_example()  
collect_dataname(meta)
```

---

collect_n_subject	<i>Collect number of subjects and its subset condition</i>
-------------------	--

---

## Description

Collect number of subjects and its subset condition

## Usage

```
collect_n_subject(  
  meta,  
  population,  
  parameter,  
  listing = FALSE,  
  histogram = FALSE,  
  var_listing = NULL,  
  remove_blank_group = FALSE,  
  type = "Subjects",  
  use_na = c("ifany", "no", "always"),  
  display_total = TRUE  
)
```

## Arguments

meta	A meta_adam object.
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.
listing	A logical value to display drill down listing per row.
histogram	A logical value to display histogram by group.
var_listing	A character vector of additional variables included in the listing.
remove_blank_group	A logical value to remove a group with all missing value of a parameter.
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 <a href="#">base::table()</a> for more details.
display_total	A logical value to display total column.

## Value

A list containing number of subjects and its subset condition.

**Examples**

```
suppressWarnings(  
  meta <- meta_example() |>  
  define_parameter(name = "sex", var = "SEX", label = "Sex")  
)  
collect_n_subject(meta, "apat", "sex")
```

---

`collect_observation_index`*Collect observation record index from observation dataset*

---

**Description**

Collect observation record index from observation dataset

**Usage**

```
collect_observation_index(meta, population, observation, parameter)
```

**Arguments**

<code>meta</code>	A <code>meta_adam</code> object.
<code>population</code>	A character value of population term name. The term name is used as key to link information.
<code>observation</code>	A character value of observation 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 vector of patient index within the observation group.

**Examples**

```
meta <- meta_example()  
collect_observation_index(meta, "apat", "wk12", "ser")
```



---

`collect_observation_record`*Collect observation record from observation dataset*

---

**Description**

The key variables used in `id`, `group`, and `subset` are displayed by default.

**Usage**

```
collect_observation_record(  
  meta,  
  population,  
  observation,  
  parameter,  
  var = NULL  
)
```

**Arguments**

<code>meta</code>	A <code>meta_adam</code> object.
<code>population</code>	A character value of population term name. The term name is used as key to link information.
<code>observation</code>	A character value of observation 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.
<code>var</code>	A character vector of additional variables to be displayed in the output.

**Value**

A data frame of the observation dataset.

**Examples**

```
meta <- meta_example()  
collect_observation_record(meta, "apat", "wk12", "ser")  
collect_observation_record(meta, "apat", "wk12", "ser", var = "AEDECOD")
```

---

collect\_population     *Collect specification for population definition*

---

### Description

Collect specification for population definition

### Usage

```
collect_population(meta, population, observation = NULL, parameter = NULL)
```

### Arguments

meta	A meta_adam object.
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.
parameter	A character value of parameter term name. The term name is used as key to link information.

### Value

A list covering the filter of population, observation (if given) and parameter (if given).

### Examples

```
meta <- meta_example()
collect_population(meta, "apat")
collect_population(meta, "apat", "wk12")
collect_population(meta, "apat", "wk12", "ser")
```

---

collect\_population\_id     *Collect subject identifier information from population dataset*

---

### Description

Collect subject identifier information from population dataset

### Usage

```
collect_population_id(meta, population)
```

**Arguments**

meta	A meta_adam object.
population	A character value of population term name. The term name is used as key to link information.

**Value**

A vector of patient ID within the population group.

**Examples**

```
meta <- meta_example()
head(collect_population_id(meta, "apat"))
```

---

collect\_population\_index

*Collect population record index from population dataset*

---

**Description**

Collect population record index from population dataset

**Usage**

```
collect_population_index(meta, population)
```

**Arguments**

meta	A meta_adam object.
population	A character value of population term name. The term name is used as key to link information.

**Value**

A vector of patient index within the population group.

**Examples**

```
meta <- meta_example()
head(collect_population_index(meta, "apat"))
```

---

```
collect_population_record
```

*Collect population record from population dataset*

---

### Description

The key variables used in id, group, and subset are displayed by default.

### Usage

```
collect_population_record(meta, population, var = NULL)
```

### Arguments

meta	A meta_adam object.
population	A character value of population term name. The term name is used as key to link information.
var	A character vector of additional variables to be displayed in the output.

### Value

A data frame containing the variables in the population dataset.

### Examples

```
meta <- meta_example()
head(collect_population_record(meta, "apat"))
head(collect_population_record(meta, "apat", var = "AGE"))
```

---

```
collect_title
```

*Collect specification for title*

---

### Description

Collect specification for title

### Usage

```
collect_title(
  meta,
  population,
  observation,
  parameter,
  analysis,
  title_order = c("analysis", "observation", "population")
)
```

**Arguments**

meta	A meta_adam object.
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.
parameter	A character value of parameter 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.
title_order	A character vector to define the order of title from each component.

**Value**

A vector of strings to compose the table captions.

**Examples**

```
meta <- meta_example()
collect_title(meta, "apat", "wk12", "ser", "ae_summary")
collect_title(meta, "apat", "wk12", "ser", "ae_specific")
```

---

default_apply	<i>Apply default values to ADaM mappings</i>
---------------	--

---

**Description**

Apply default values to ADaM mappings

**Usage**

```
default_apply(x)
```

**Arguments**

x	An adam_mapping object.
---	-------------------------

**Value**

Similar to the input, but with the missing values updated to the default values.

**Examples**

```
default_apply(adam_mapping(name = "apat"))
```

---

define_analysis	<i>Define analysis function meta information for ADaM dataset</i>
-----------------	---

---

## Description

Define analysis function meta information for ADaM dataset

## Usage

```
define_analysis(meta, name, ...)
```

## Arguments

meta	A meta_adam object.
name	A character value of term name. The term name is used as key to link information.
...	Additional variables.

## Value

A metadata object with analysis details defined.

## Examples

```
plan <- plan(  
  analysis = "ae_summary", population = "apat",  
  observation = c("wk12", "wk24"), parameter = "any;rel;ser"  
)  
  
meta_adam(  
  population = r2rtf::r2rtf_adsl,  
  observation = r2rtf::r2rtf_adae  
) |>  
  define_plan(plan = plan) |>  
  define_analysis(  
    name = "ae_summary",  
    title = "Summary of Adverse Events"  
  )
```

---

define_observation	<i>Define analysis observation meta information for ADaM dataset</i>
--------------------	--

---

## Description

Define analysis observation meta information for ADaM dataset

## Usage

```
define_observation(  
  meta,  
  name,  
  id = "USUBJID",  
  group = NULL,  
  var = NULL,  
  subset = NULL,  
  label = NULL,  
  ...  
)
```

## Arguments

meta	A meta_adam object.
name	A character value of term name. The term name is used as key to link information.
id	A character value of subject identifier variable name in an ADaM dataset.
group	A character vector of group variable names in an ADaM dataset.
var	A character vector of useful variable names in an ADaM dataset.
subset	An expression to identify analysis records. See <code>base::subset()</code> .
label	A character value of analysis label.
...	Additional variables.

## Value

A metadata object with observation defined.

## Examples

```
plan <- plan(  
  analysis = "ae_summary", population = "apat",  
  observation = c("wk12", "wk24"), parameter = "any;rel;ser"  
)  
  
meta_adam(  
  population = r2rtf::r2rtf_adsl,  
  observation = r2rtf::r2rtf_adae
```

```

) |>
  define_plan(plan = plan) |>
  define_observation(
    name = "wk12",
    group = "TRTA",
    subset = SAFFL == "Y",
    label = "Weeks 0 to 12"
  )

```

---

define\_parameter      *Define analysis parameter meta information for ADaM dataset*

---

## Description

Define analysis parameter meta information for ADaM dataset

## Usage

```
define_parameter(meta, name, subset = NULL, ...)
```

## Arguments

meta	A meta_adam object.
name	A character value of term name. The term name is used as key to link information.
subset	An expression to identify analysis records. See <a href="#">base::subset()</a> .
...	Additional variables.

## Value

A metadata object with parameters defined.

## Examples

```

plan <- plan(
  analysis = "ae_summary", population = "apat",
  observation = c("wk12", "wk24"), parameter = "any;rel;ser"
)

meta_adam(
  population = r2rtf::r2rtf_adsl,
  observation = r2rtf::r2rtf_adae
) |>
  define_plan(plan = plan) |>
  define_parameter(
    name = "rel",
    subset = AEREL %in% c("POSSIBLE", "PROBABLE")
  )

```



---

define_plan	<i>Define analysis plan meta information for ADaM dataset</i>
-------------	---

---

**Description**

Define analysis plan meta information for ADaM dataset

**Usage**

```
define_plan(meta, plan)
```

**Arguments**

meta	A meta_adam object.
plan	A data frame for analysis plan.

**Value**

A metadata object with plans defined.

**Examples**

```
plan <- plan(  
  analysis = "ae_summary", population = "apat",  
  observation = c("wk12", "wk24"), parameter = "any;rel;ser"  
)  
  
meta_adam(  
  population = r2rtf::r2rtf_adsl,  
  observation = r2rtf::r2rtf_adae  
) |>  
  define_plan(plan)
```

---

define_population	<i>Define analysis population meta information for ADaM dataset</i>
-------------------	---

---

**Description**

Define analysis population meta information for ADaM dataset

**Usage**

```
define_population(
  meta,
  name,
  id = "USUBJID",
  group = NULL,
  var = NULL,
  subset = NULL,
  label = NULL,
  ...
)
```

**Arguments**

meta	A meta_adam object.
name	A character value of term name. The term name is used as key to link information.
id	A character value of subject identifier variable name in an ADaM dataset.
group	A character vector of group variable names in an ADaM dataset.
var	A character vector of useful variable names in an ADaM dataset.
subset	An expression to identify analysis records. See <a href="#">base::subset()</a> .
label	A character value of analysis label.
...	Additional variables.

**Value**

A metadata object with population defined.

**Examples**

```
plan <- plan(
  analysis = "ae_summary", population = "apat",
  observation = c("wk12", "wk24"), parameter = "any;rel;ser"
)

meta_adam(
  population = r2rtf::r2rtf_ads1,
  observation = r2rtf::r2rtf_adae
) |>
  define_plan(plan) |>
  define_population(name = "apat")
```

---

get_label	<i>A function to get the labels of data frame columns</i>
-----------	---

---

**Description**

A function to get the labels of data frame columns

**Usage**

```
get_label(data)
```

**Arguments**

data            A data frame.

**Value**

Labels of the input data frame.

**Examples**

```
get_label(r2rtf::r2rtf_adae)
```

---

meta_adam	<i>Create a metadata representation for ADaM data analysis</i>
-----------	--

---

**Description**

Create a metadata representation for ADaM data analysis

**Usage**

```
meta_adam(observation, population = observation)
```

**Arguments**

observation    A data frame for observation level data.  
population     A data frame for population level data. Default is the same as observation.

**Value**

An initialized metadata object with observation and population defined.

**Examples**

```
meta_adam(observation = r2rtf::r2rtf_adae, population = r2rtf::r2rtf_adae)
```

---

meta_add_total	<i>Add duplicate data to enable a total group</i>
----------------	---

---

**Description**

Add duplicate data to enable a total group

**Usage**

```
meta_add_total(meta, total = "Total")
```

**Arguments**

meta	A metalite object.
total	A character value of total group name.

**Value**

A metadata object with a total group added.

**Examples**

```
x <- meta_add_total(meta_example())  
# A `Total` group is added  
table(x$data_population$TRTA)
```

---

meta_build	<i>Build complete meta information</i>
------------	--

---

**Description**

Build complete meta information

**Usage**

```
meta_build(meta)
```

**Arguments**

meta	A meta_adam object.
------	---------------------

**Value**

A composed metadata object.

## Examples

```
meta_adam(  
  observation = r2rtf::r2rtf_adae,  
  population = r2rtf::r2rtf_adsl  
) |>  
# define analysis plan  
define_plan(  
  plan(  
    analysis = "ae_summary",  
    population = "apat",  
    observation = c("wk12"),  
    parameter = "any;rel"  
  )  
) |>  
# define population  
define_population(  
  name = "apat",  
  group = "TRT01A",  
  subset = SAFFL == "Y"  
) |>  
# define observation  
define_observation(  
  name = "wk12",  
  group = "TRTA",  
  subset = SAFFL == "Y",  
  label = "Weeks 0 to 12"  
) |>  
# define parameter - rel  
define_parameter(  
  name = "rel",  
  subset = AEREL %in% c("POSSIBLE", "PROBABLE")  
) |>  
# define analysis  
define_parameter(  
  name = "rel",  
  subset = AEREL %in% c("POSSIBLE", "PROBABLE")  
) |>  
meta_build()
```

---

meta\_example

*Create an example meta\_adam object*

---

## Description

This function is only for illustration purposes. The r2rtf package is required.

## Usage

```
meta_example()
```

**Value**

A metadata object.

**Examples**

```
meta_example()
```

---

```
meta_example_exploration
```

*Create a data exploration meta\_adam object*

---

**Description**

Create a data exploration meta\_adam object

**Usage**

```
meta_example_exploration(  
  data,  
  group,  
  name = "ase",  
  subset = NULL,  
  label = "All Subjects Enrolled"  
)
```

**Arguments**

data	A data frame.
group	A character vector of group variable names in an ADaM dataset.
name	A character value of term name. The term name is used as key to link information.
subset	An expression to identify analysis records. See <a href="#">base::subset()</a> .
label	A character value of analysis label.

**Value**

A metadata object.

**Examples**

```
meta <- meta_example_exploration(r2rtf::r2rtf_adsl, group = "TRT01A")  
collect_n_subject(meta, "ase", "AGE")  
collect_n_subject(meta, "ase", "SEX")
```

---

meta_inherit	<i>Inherit meta information by keywords</i>
--------------	---

---

**Description**

Inherit meta information by keywords

**Usage**

```
meta_inherit(meta, inherit, name, overwrite = FALSE)
```

**Arguments**

meta	A meta_adam object.
inherit	A meta_adam object to be inherit.
name	A vector of keywords from meta_inherit to meta_adam.
overwrite	A logical value to force mapping update.

**Value**

A metadata object with population defined.

**Examples**

```
meta_adam(
  population = r2rtf::r2rtf_adsl,
  observation = r2rtf::r2rtf_adae
) |>
  meta_inherit(meta_example(), c("apat", "wk12", "ae_summary"))
```

---

meta_run	<i>Execute analysis based on the analysis plan</i>
----------	--

---

**Description**

Execute analysis based on the analysis plan

**Usage**

```
meta_run(meta, i = NULL, ...)
```

**Arguments**

meta	A meta_adam object.
i	A vector of integers to indicate i-th analysis in meta\$plan.
...	Additional arguments passed to [spec_call_program()].

**Value**

Executed analysis based on the analysis plan.

**Examples**

```
if (interactive()) {  
  meta <- meta_example()  
  ae_summary <- function(...) {  
    "results of ae_summary"  
  }  
  ae_specific <- function(...) {  
    "results of ae_specific"  
  }  
  meta_run(meta)  
  meta_run(meta, i = 2)  
}
```

---

meta\_split

*Split metadata into groups*

---

**Description**

Split metadata into groups

**Usage**

```
meta_split(meta, by)
```

**Arguments**

meta	A meta_adam object.
by	A character variable name both in population level and observation level data of a metadata object.

**Value**

A metadata object split by the input variable.

**Examples**

```
meta_example() |> meta_split("RACE")
```



---

n_subject	<i>Count number of unique subjects</i>
-----------	--

---

### Description

Count number of unique subjects

### Usage

```
n_subject(
  id,
  group,
  par = NULL,
  na = "Missing",
  use_na = c("ifany", "no", "always")
)
```

### Arguments

id	A character vector of subject identifier.
group	A factor vector of group name.
par	A character vector of parameter name.
na	A character string used to label missing values. Defaults to "Missing".
use_na	A character value for whether to include NA values in the table. See the useNA argument in <a href="#">base::table()</a> for more details.

### Value

A data frame summarizing the number of unique subjects in different arms.

### Examples

```
library(r2rtf)

r2rtf_adae$TRTA <- factor(r2rtf_adae$TRTA)
r2rtf_adae$SEX[1:5] <- NA

n_subject(r2rtf_adae$USUBJID, r2rtf_adae$TRTA)
n_subject(r2rtf_adae$USUBJID, r2rtf_adae$TRTA, r2rtf_adae$SEX)
n_subject(r2rtf_adae$USUBJID, r2rtf_adae$TRTA, r2rtf_adae$SEX, use_na = "always")
n_subject(r2rtf_adae$USUBJID, r2rtf_adae$TRTA, r2rtf_adae$SEX, na = "Null")
```

---

outdata	<i>Construct outdata class</i>
---------	--------------------------------

---

### Description

The outdata class defines a standard output format for analysis and reporting.

### Usage

```
outdata(
  meta,
  population,
  observation,
  parameter,
  n,
  order,
  group,
  reference_group,
  ...
)
```

### 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.
observation	A character value of observation 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.
n	A data frame for number of subjects in each criteria.
order	A numeric vector of row display order.
group	A character vector of group variable names in an ADaM dataset.
reference_group	A numeric value to indicate reference group in levels of group.
...	Additional variables to save to outdata.

### Details

The design is inspired by `ggplot2::aes()`.

### Value

A list with class outdata. Components of the list are either quosures or constants.

**Examples**

```

outdata(
  meta = meta_example(),
  population = "apat",
  observation = "wk12",
  parameter = "rel",
  n = data.frame(
    TRTA = c("Placebo", "Xanomeline Low Dose", "Xanomeline High Dose"),
    n = c(86, 84, 84)
  ),
  group = "TRTA",
  reference_group = 1,
  order = 1:3
)

```

---

plan

---

*Create a analysis plan from all combination of variables*


---

**Description**

This function is a wrapper of `base::expand.grid()`.

**Usage**

```
plan(analysis, population, observation, parameter, mock = 1, ...)
```

**Arguments**

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.
observation	A character value of observation 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.
mock	A numeric value of mock table number.
...	Additional arguments.

**Value**

A data frame containing the analysis plan.

## Examples

```
# Example 1
# Create an analysis plan of AE summary
# with any AE, drug-related AE, and serious AE
plan(
  analysis = "ae_summary",
  population = "apat",
  observation = c("wk12", "wk24"),
  parameter = "any;rel;ser"
)

# Example 2
# Create an analysis plan of AE specific
# with any AE, drug-related AE, and serious AE
plan(
  analysis = "ae_specific",
  population = "apat",
  observation = c("wk12", "wk24"),
  parameter = c("any", "rel", "ser")
)
```

---

print.meta_adam	<i>Print a metadata object with its population, observation, and analysis plans</i>
-----------------	---

---

## Description

Print a metadata object with its population, observation, and analysis plans

## Usage

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

## Arguments

x	An object returned by <code>meta_adam()</code> .
...	Additional parameters for <code>print()</code> (not used).

## Value

A printed summary of the metadata.

## Examples

```
meta_adam(observation = r2rtf::r2rtf_adae, population = r2rtf::r2rtf_adae) |> print()
```

---

spec\_analysis\_population  
*Specification for population definition*

---

**Description**

Specification for population definition

**Usage**

```
spec_analysis_population(meta)
```

**Arguments**

meta            A meta\_adam object.

**Value**

A vector of character strings containing the populations used in the order of the analysis plans.

**Examples**

```
meta <- meta_example()
spec_analysis_population(meta)
```

---

spec\_call\_program        *Specification for analysis call program*

---

**Description**

Specification for analysis call program

**Usage**

```
spec_call_program(meta, ...)
```

**Arguments**

meta            A meta\_adam object.  
...             Additional arguments used in all call programs.

**Value**

A vector of character strings containing the call program in the order of the analysis plans.

**Examples**

```
meta <- meta_example()
spec_call_program(meta)
spec_call_program(meta, data_source = "[Study CDISCpilot: adam-adsl; adae]")
```

---

spec_filename	<i>Specification for analysis output filename</i>
---------------	---

---

**Description**

Specification for analysis output filename

**Usage**

```
spec_filename(meta)
```

**Arguments**

meta            A meta\_adam object.

**Value**

A vector of character strings containing the RTF file names.

**Examples**

```
meta <- meta_example()
spec_filename(meta)
```

---

spec_title	<i>Specification for analysis title</i>
------------	---

---

**Description**

Specification for analysis title

**Usage**

```
spec_title(meta)
```

**Arguments**

meta            A meta\_adam object.

**Value**

A vector of character strings containing the table captions in the order of the analysis plans.

**Examples**

```
meta <- meta_example()
spec_title(meta)
```

---

update\_adam\_mapping     *Update mapping rule in adam\_mapping*

---

**Description**

Update mapping rule in adam\_mapping

**Usage**

```
update_adam_mapping(meta, name, ...)
```

**Arguments**

meta	A meta_adam object.
name	A vector of keywords.
...	Additional variables to be added in the mapping rule among those keywords.

**Value**

A metadata object with the input updated.

**Examples**

```
meta <- meta_example()
meta <- update_adam_mapping(meta, names(meta$parameter), start_date = "ASTDT")
collect_adam_mapping(meta, "ser")
```

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