

Package: mighty.metadata (via r-universe)

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Title Manage 'CDISC' 'ADaM' Dataset Specifications in 'YAML' Format

Version 0.1.0

Description Load, validate, and manipulate Clinical Data Interchange Standards Consortium ('CDISC') Analysis Data Model ('ADaM') dataset metadata stored as 'YAML' files. Metadata files are validated against a JSON schema. Provides functions to inspect and modify columns, parameters, and row-level operations within and across 'ADaM' domains. Designed for use with the 'mighty' framework.

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URL <https://novonordisk-opensource.github.io/mighty.metadata/>,
<https://github.com/NovoNordisk-OpenSource/mighty.metadata>

BugReports <https://github.com/NovoNordisk-OpenSource/mighty.metadata/issues>

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columns	<i>Update columns in your metadata</i>
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Description

Functions to list, select, remove, add, update, and move columns in your `mighty_domain()` objects.

Usage

```
list_columns(x)

remove_columns(x, id)

add_column(x, id, ..., .pos = length(x[["columns"]]) + 1L)

move_column(x, id, .pos = length(x[["columns"]]))

select_column(x, id)

update_column(x, id, ...)
```

Arguments

x	<code>mighty_domain()</code> Object to manipulate.
id	<code>character()</code> Id of the column(s) to remove, add, or move.
...	Additional properties to add/update for the column, e.g. a <code>label = "my label"</code> .
.pos	<code>integer(1)</code> Position to put or move the column to. Default places the column as the last.

Value

```
invisible(x)
```

Examples

```
# Load example configuration
x <- mighty_domain(
  file = system.file("examples", "adv.s.yml", package = "mighty.metadata")
)

# List all columns defined
list_columns(x)

# Remove the STUDYID and USUBJID columns
x |>
  remove_columns(c("STUDYID", "USUBJID")) |>
  list_columns()

# Add a new column
x |>
  add_column(id = "NEW") |>
  list_columns()

# Add new column with label and as the first column
y <- x |>
  add_column(id = "NEW", label = "My label", .pos = 1)

list_columns(y)

y[["columns"]][[1]] |>
  str()

# Move the STUDYID column to the 3rd position
x |>
  move_column(id = "STUDYID", .pos = 3) |>
  list_columns()

# Update an existing column
x |>
  update_column(id = "STUDYID", label = "Updated Label") |>
  select_column(id = "STUDYID") |>
  str()

# Select a specific column
select_column(x, id = "STUDYID") |>
  str()
```

create_md_col

Create Metadata Column Table

Description

Converts a [mighty_study](#) or [mighty_domain](#) object into a flat dataframe of column definitions.

Usage

```
create_md_col(x)
```

Arguments

x A [mighty_study](#) or [mighty_domain](#) object.

Value

A tibble with one row per column containing:

table_id Table identifier

table_label Table label/description

order Column order within table

id Column name

label Column label

origin Origin type (e.g., "Predecessor", "Derived")

key Logical, whether column is a key

is_core Logical, whether column is a core variable

core String, whether a column is Req, Cond or Perm

method Derivation method

codelist Codelist reference

format_type Data type ("C" or "N")

format_length Maximum length

format_display Display format

comment Comment

See Also

[mighty_study](#), [populate_sparse\(\)](#), [populate_core\(\)](#)

Examples

```
study <- mighty_study(  
  path = system.file("examples", package = "mighty.metadata")  
)  
mdcol <- create_md_col(study)
```

 mighty.metadata-options

Options for mighty.metadata

Description

verbosity_level:

Verbosity level for functions in mighty.metadata. See [zephyr::verbosity_level](#) for details.

- Default: NA_character_
 - Option: mighty.metadata.verbosity_level
 - Environment: R_MIGHTY.METADATA_VERBOSITY_LEVEL
-

mighty_domain

Mighty Domain

Description

mighty_domain() provides a robust way of working with ADaM metadata in the {mighty} framework.

A new object is initialized by supplying an existing yaml metadata file. This package provides helpers to update column, parameter, and row entries. See the references below for help:

- help("columns")
- help("parameters")
- help("rows")

mighty_domain() inherits from `S7schema::S7schema()` and the yaml file is automatically validated when loaded. The helper functions above also always validates the new configuration before returning.

You can at anytime validate an object by calling `validate()` and use `write_config()` to save it as a yaml file again.

Usage

```
mighty_domain(file)
```

Arguments

file character(1) path to a yaml file defining an ADaM dataset.

Value

A mighty_domain S7 object extending [S7schema::S7schema](#). The underlying list contains the parsed and validated YAML metadata including id, label, class, keys, columns, parameters, and rows.

Examples

```
x <- mighty_domain(
  file = system.file("examples", "adv.s.yml", package = "mighty.metadata")
)

# Custom print method gives a small overview
print(x)

# Underlying object is a `list`
str(x)
```

mighty_study

Mighty Study

Description

Creates a `mighty_study` object by loading all YAML metadata files from a directory. Each YAML file (except `_mighty.yml` and `_study.yml`) is parsed as a `mighty_domain` object. The optional `_study.yml` file provides study-level properties and the optional `_mighty.yml` file provides mighty framework configuration.

Usage

```
mighty_study(path, populate = FALSE)
```

Arguments

<code>path</code>	character(1) path to a directory containing YAML metadata files.
<code>populate</code>	logical(1) if TRUE, calls <code>populate_core()</code> then <code>populate_sparse()</code> before returning. Default is FALSE.

Details

The function scans the directory for files matching `*.yaml` or `*.yml`:

- Files named `_study.yml` or `_study.yaml` are treated as study properties
- Files named `_mighty.yml` or `_mighty.yaml` are treated as mighty framework config
- All other YAML files are loaded as `mighty_domain` objects
- Only one `_mighty.yml` and one `_study.yml` file is allowed per directory

Value

A mighty_study S7 object extending list:

List elements [mighty_domain](#) objects, named by their id field. Access via e.g. study\$ads1.

@study Study-level properties from _study.yml, or empty list if no properties file exists.

@mighty Mighty framework configuration from _mighty.yml, or empty list if no configuration file exists.

@path The source directory path as character(1).

Write Study Metadata

Use write_config() to serialize a mighty_study() object back to YAML files. Each domain is written as a separate file, plus _mighty.yml and _study.yml when non-empty.

If path is NULL (default), files are written to x@path.

See Also

[mighty_domain](#), [write_config\(\)](#), [populate_sparse\(\)](#), [populate_core\(\)](#), [create_md_col\(\)](#)

Examples

```
# Load example study
study <- mighty_study(
  path = system.file("examples", package = "mighty.metadata")
)

# List tables with metadata
names(study)

# Access ADVS
study$ADVS

# Access study-level properties
study@study

# Access mighty framework configuration
study@mighty

# Load and populate in one step
study <- mighty_study(
  path = system.file("examples", package = "mighty.metadata"),
  populate = TRUE
)

# Write study back to YAML
tmp <- tempdir()
write_config(study, path = tmp)
```

 parameters

Update parameters in your metadata

Description

Functions to list, select, remove, add, update, and move parameters in your `mighty_domain()` objects.

Usage

```
list_parameters(x)
```

```
remove_parameters(x, id)
```

```
add_parameter(
  x,
  id,
  label,
  columns,
  ...,
  .pos = length(x[["parameters"]]) + 1L
)
```

```
move_parameter(x, id, .pos = length(x[["parameters"]]))
```

```
update_parameter(x, id, ...)
```

```
select_parameter(x, id)
```

Arguments

<code>x</code>	<code>mighty_domain()</code> Object to manipulate.
<code>id</code>	<code>character()</code> Id of the parameter(s) to remove, add, or move.
<code>label</code>	<code>character(1)</code> Parameter label.
<code>columns</code>	<code>list()</code> Columns to set for the parameter.
<code>...</code>	Additional properties to add for the parameter, e.g. a component reference.
<code>.pos</code>	<code>integer(1)</code> Position to put or move the parameter to. Default places the parameter as the last.

Value

```
invisible(x)
```

Examples

```
# Load example configuration
x <- mighty_domain(
  file = system.file("examples", "adv.s.yml", package = "mighty.metadata")
)

# List all parameters defined
list_parameters(x)

# Remove the BMIGRP parameter
x |>
  remove_parameters("BMIGRP") |>
  list_parameters()

# Add a new parameter
x |>
  add_parameter(
    id = "NEW",
    label = "My new parameter",
    columns = list(list(id = "AVAL"))
  ) |>
  list_parameters()

# Move the BMIGRP parameter to the 1st position
x |>
  move_parameter(id = "BMIGRP", .pos = 1) |>
  list_parameters()

# Update an existing parameter
x |>
  update_parameter(id = "BMI", label = "Updated BMI Label") |>
  select_parameter(id = "BMI") |>
  str()

# Select a specific parameter
select_parameter(x, id = "BMI") |>
  str()
```

populate_core

Populate Core Variables

Description

Adds core variables from supplier datasets as predecessor columns to datasets that use them (marked with `usecore = TRUE`).

Note: Currently only accepts core variables from ADSL.

Usage

```
populate_core(x, ...)
```

Arguments

x A [mighty_study](#) or [mighty_domain](#) object.
... Additional arguments passed to methods.

Value

A modified [mighty_study](#) or [mighty_domain](#) with core variables added as predecessor columns.

See Also

[mighty_study](#), [populate_sparse\(\)](#), [create_md_col\(\)](#)

Examples

```
study <- mighty_study(  
  path = system.file("examples", package = "mighty.metadata")  
)  
study <- populate_core(study)
```

populate_sparse

Populate Predecessor Metadata

Description

Populates column metadata from predecessor references. Columns with a method in the format `domain.column` (e.g., `ADSL.USUBJID`) inherit metadata from the referenced predecessor.

Usage

```
populate_sparse(x, ...)
```

Arguments

x A [mighty_study](#) or [mighty_domain](#) object.
... Additional arguments passed to methods.

Value

A modified [mighty_study](#) or [mighty_domain](#) with predecessor column metadata populated.

See Also

[mighty_study](#), [populate_core\(\)](#), [create_md_col\(\)](#)

Examples

```
study <- mighty_study(  
  path = system.file("examples", package = "mighty.metadata")  
)  
study <- populate_sparse(study)
```

resolve_includes	<i>Resolve conditional metadata items</i>
------------------	---

Description

Evaluates include fields on metadata items (domains, columns, rows, parameters) and removes items where the condition evaluates to FALSE.

Usage

```
resolve_includes(x, info = list())
```

Arguments

x	A mighty_study or mighty_domain object.
info	list() Named list of values used to evaluate include expressions. For mighty_study , merged into x@study.

Details

Include conditions are R expressions with {glue} syntax for variable substitution and evaluation. The info list provides the values used to do this.

Value

The input object with conditional items resolved.

Examples

```
study <- mighty_study(  
  path = system.file("examples", package = "mighty.metadata")  
)  
  
# Add a conditional column  
study$ADVS <- update_column(  
  study$ADVS,  
  id = "STUDYID",  
  include = "{study_id == 'my_study'}"  
)  
  
# Condition TRUE: column kept (study_id is "my_study" in @study)  
study |>
```

```

resolve_includes() |>
getElement("ADVS") |>
list_columns()

# Condition FALSE: column removed
study |>
  resolve_includes(info = list(study_id = "other")) |>
  getElement("ADVS") |>
  list_columns()

```

rows

Update rows in your metadata

Description

Functions to list, select, remove, add, update, and move row operations in your `mighty_domain()` objects.

Usage

```

list_rows(x)

remove_rows(x, id)

add_row(x, id, ..., .pos = length(x[["rows"]]) + 1L)

move_row(x, id, .pos = length(x[["rows"]]))

update_row(x, id, ...)

select_row(x, id)

```

Arguments

<code>x</code>	<code>mighty_domain()</code> Object to manipulate.
<code>id</code>	<code>character()</code> Id of the row(s) to remove, add, or move.
<code>...</code>	Additional properties to add for the row, e.g. a <code>label = "my row"</code> .
<code>.pos</code>	<code>integer(1)</code> Position to put or move the row to. Default places the row as the last.

Value

```
invisible(x)
```

Examples

```
# Load example configuration
x <- mighty_domain(
  file = system.file("examples", "adv.s.yml", package = "mighty.metadata")
)

# List all rows defined
list_rows(x)

# Add a new row
y <- x |>
  add_row(id = "NEW")

list_rows(y)

# Remove the new row again
y |>
  remove_rows("NEW") |>
  list_rows()

# Update an existing row
x |>
  update_row(id = "BASELINE", method = "Updated method") |>
  select_row(id = "BASELINE") |>
  str()

# Select a specific row
select_row(x, id = "BASELINE") |>
  str()
```

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