

Package ‘gDRimport’

May 19, 2024

Type Package

Title Package for handling the import of dose-response data

Version 1.2.0

Date 2024-04-08

Description The package is a part of the gDR suite. It helps to prepare raw drug response data for downstream processing. It mainly contains helper functions for importing/loading/validating dose-response data provided in different file formats.

License Artistic-2.0

LazyLoad yes

Depends R (>= 4.2)

Imports assertthat, BumpyMatrix, checkmate, CoreGx, PharmacoGx, data.table, futile.logger, gDRutils (>= 1.1.5), magrittr, methods, MultiAssayExperiment, readxl, rio, S4Vectors, stats, stringi, SummarizedExperiment, tibble, tools, utils, XML, yaml, openxlsx

Suggests BiocStyle, gDRtestData (>= 1.1.7), gDRstyle (>= 1.1.3), knitr, purrr, qs, testthat

URL <https://github.com/gdrplatform/gDRimport>,
<https://gdrplatform.github.io/gDRimport/>

BugReports <https://github.com/gdrplatform/gDRimport/issues>

biocViews Software, Infrastructure, DataImport

VignetteBuilder knitr

ByteCompile TRUE

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

SwitchrLibrary gDRimport

DeploySubPath gDRimport

Encoding UTF-8

git_url <https://git.bioconductor.org/packages/gDRimport>

git_branch RELEASE_3_19

git_last_commit 473f4be

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-19

Author Arkadiusz Gladki [aut, cre] (<<https://orcid.org/0000-0002-7059-6378>>),

Bartosz Czech [aut] (<<https://orcid.org/0000-0002-9908-3007>>),

Marc Hafner [aut] (<<https://orcid.org/0000-0003-1337-7598>>),

Sergiu Mocanu [aut],

Dariusz Scigocki [aut],

Allison Vuong [aut],

Luca Gerosa [aut] (<<https://orcid.org/0000-0001-6805-9410>>),

Janina Smola [aut]

Maintainer Arkadiusz Gladki <gladki.arkadiusz@gmail.com>

Contents

gDRimport-package	4
.check_against_single_template_sheet	5
.check_file_structure	5
.createPseudoData	6
.extractDoseResponse	6
.extract_or_create_assay	6
.fill_empty_wells	7
.get_plate_size	7
.removeNegatives	8
.standardize_untreated_values	8
are_template_sheets_valid	9
check_metadata_against_spaces	9
check_metadata_field_names	10
check_metadata_headers	10
check_metadata_names	11
check_metadata_req_col_names	11
convert_MAE_to_PSet	12
convert_pset_to_df	13
correct_template_sheets	14
detect_file_format	14
enhance_raw_edited_EnVision_df	15
fix_typos_with_reference	15
gdr_test_data-class	16
getPSet	17
get_df_from_raw_edited_EnVision_df	18
get_df_from_raw_unedited_EnVision_df	19
get_EnVision_properties	19
get_excel_sheet_names	20
get_exception_data	20

get_expected_template_sheets	21
get_plate_info_from_template_xlsx	21
get_test_D300_data	22
get_test_data	22
get_test_EnVision_data	23
get_test_Tecan_data	23
get_test_tsv_data	24
get_xl_sheets	24
import_D300	25
is_readable_v	26
load_data	26
load_manifest	27
load_results	28
load_results_EnVision	28
load_results_Tecan	29
load_results_tsv	29
load_templates	30
load_templates_tsv	30
load_templates_xlsx	31
manifest_path	31
mgrepl	32
parse_D300_xml	32
read_EnVision_delim	33
read_EnVision_xlsx	33
read_excel_to_dt	34
read_in_EnVision_file	34
read_in_manifest_file	35
read_in_results_Tecan	35
read_in_result_files	36
read_in_template_sheet_xlsx	36
read_in_template_xlsx	37
read_in_tsv_template_files	37
read_ref_data	38
result_path	38
save_drug_info_per_well	39
setEnvForPSet	39
standardize_record_values	40
template_path	40
validate_template_xlsx	41

gDRimport-package

gDRimport: Package for handling the import of dose-response data

Description

The package is a part of the gDR suite. It helps to prepare raw drug response data for downstream processing. It mainly contains helper functions for importing/loading/validating dose-response data provided in different file formats.

Value

package help page

Note

To learn more about functions start with `help(package = "gDRimport")`

Author(s)

Maintainer: Arkadiusz Gladki <gladki.arkadiusz@gmail.com> ([ORCID](#))

Authors:

- Bartosz Czech ([ORCID](#))
- Marc Hafner ([ORCID](#))
- Sergiu Mocanu
- Dariusz Scigocki
- Allison Vuong
- Luca Gerosa ([ORCID](#))
- Janina Smola

See Also

Useful links:

- <https://github.com/gdrplatform/gDRimport>
- <https://gdrplatform.github.io/gDRimport/>
- Report bugs at <https://github.com/gdrplatform/gDRimport/issues>

`.check_against_single_template_sheet`

Evaluate if template file with single sheet is present, if the name of the sheet is correct and if it can be fixed

Description

get sheets for given set of XLS files

Usage

`.check_against_single_template_sheet(ts)`

Arguments

ts list with template sheets info

Value

logical flag

`.check_file_structure` *Check the structure of raw data*

Description

Check the structure of raw data

Usage

```
.check_file_structure(  
  df,  
  filename,  
  sheet_name,  
  readout_offset,  
  n_row,  
  n_col,  
  bcode_idx,  
  bcode_col  
)
```

Value

NULL invisibly.

`.createPseudoData` *Add in pseudo-data for duration and cell reference division time*

Description

Add in pseudo-data for duration and cell reference division time

Usage

```
.createPseudoData(dt)
```

Value

data.table

`.extractDoseResponse` *Get dose and viability readouts and melt into large data table*

Description

Get dose and viability readouts and melt into large data table

Usage

```
.extractDoseResponse(pset)
```

Value

data.table with dose-reponse data

`.extract_or_create_assay`
Extracts an assay from a SummarizedExperiment object or creates a new one if it does not exist

Description

This function takes a SummarizedExperiment object and an assay name as input. If the specified assay already exists in the SummarizedExperiment object, it is returned. Otherwise, a new assay with the specified name is created and added to the SummarizedExperiment object. The new assay is initialized with NA values. This is useful for when multiple Summarized Experiments in a given MAE do not have the same assays. And it is necessary to have the same assays in all Summarized Experiments in order to convert the MAE to a PSet.

Usage

```
.extract_or_create_assay(SE, assay_name)
```

Arguments

SE A SummarizedExperiment object
assay_name A character string specifying the name of the assay to extract or create

Value

A SummarizedExperiment object with the specified assay

`.fill_empty_wells` *Correct plates with not fully filled readout values*

Description

Correct plates with not fully filled readout values

Usage

```
.fill_empty_wells(  
  df,  
  plate_rows,  
  data_rows,  
  exp_row,  
  exp_col,  
  numeric_regex = "\\d+$"  
)
```

Value

data.table with corrected plates data

`.get_plate_size` *Get plate size*

Description

Get plate size

Usage

```
.get_plate_size(df)
```

Details

All plate sizes assume 1.5x nrows = ncolumns.

Value

charvec with plate dims

`.removeNegatives` *Remove negative viabilities*

Description

Remove negative viabilities

Usage

`.removeNegatives(dataset)`

Value

data.table with positive values in column ReadoutValue

`.standardize_untreated_values`
Standardize untreated values to ignore cases

Description

Standardize untreated values to ignore cases

Usage

`.standardize_untreated_values(df)`

Value

data.table with standardized untreated values

are_template_sheets_valid
are template sheet valid?

Description

are template sheet valid?

Usage

are_template_sheets_valid(ts)

Arguments

ts list with (per file) template sheets

Value

logical flag

See Also

get_xl_sheets

check_metadata_against_spaces
Check metadata against spaces

Description

Check metadata against spaces

Usage

check_metadata_against_spaces(corrected_names, df_name)

Arguments

corrected_names a charvec with corrected colnames of df
df_name a name of data.table (" by default)

Value

a charvec with corrected colnames of df

check_metadata_field_names

Check metadata field names

Description

Check metadata field names

Usage

```
check_metadata_field_names(corrected_names, df_name)
```

Arguments

corrected_names

a charvec with corrected colnames of df

df_name

a name of data.table (" " by default)

Value

a charvec with corrected colnames of df

check_metadata_headers

Check whether metadata headers are correct and make fixes if needed

Description

Check whether metadata headers are correct and make fixes if needed

Usage

```
check_metadata_headers(corrected_names, df_name)
```

Arguments

corrected_names

a charvec with corrected colnames of df

df_name

a name of data.table (" " by default)

Value

a charvec with corrected colnames of df

check_metadata_names *check_metadata_names*

Description

Check whether all metadata names are correct

Usage

```
check_metadata_names(col_df, df_name = "", df_type = NULL)
```

Arguments

col_df a character with colnames of df
df_name a name of data.table (" " by default)
df_type a type of a data.table (NULL by default)

Value

a charvec with corrected colnames of df

Examples

```
td <- get_test_data()
m_file <- manifest_path(td)
m_data <- read_excel_to_dt(m_file)
result <- check_metadata_names(col_df = colnames(m_data))
```

check_metadata_req_col_names

Check metadata for required column names

Description

Check metadata for required column names

Usage

```
check_metadata_req_col_names(col_df, df_name, df_type)
```

Arguments

col_df a charvec with corrected colnames of df
df_name a name of data.table (" " by default)
df_type a type of a data.table (NULL by default)

Value

NULL invisibly.

convert_MAE_to_PSet *Convert MultiAssayExperiment to TreatmentResponseExperiment*

Description

This function converts a `MultiAssayExperiment` generated by `gDR` into a `TreatmentResponseExperiment` for use in the `PharmacGx` package. The resulting `PharmacSet` can be used for pharmacogenomic analysis of drug response.

Usage

```
convert_MAE_to_PSet(mae, pset_name)
```

Arguments

`mae` A `MultiAssayExperiment` object generated by `gDR`.
`pset_name` A character string specifying the name of the resulting `PharmacSet` object.

Value

A `PharmacSet` object.

Examples

```
# Convert a MultiAssayExperiment object to a PharmacSet object
m <- 20
n <- 10
rnames <- LETTERS[1:m]
cnames <- letters[1:n]
ref_gr_value <- matrix(runif(m * n), nrow = m, ncol = n, dimnames = list(rnames, cnames))
se <- SummarizedExperiment::SummarizedExperiment(assays = list(RefGRvalue = ref_gr_value),
                                                  rowData = S4Vectors::DataFrame(rnames),
                                                  colData = S4Vectors::DataFrame(cnames))
mae <- MultiAssayExperiment::MultiAssayExperiment(experiments = list("single-agent" = se))
convert_MAE_to_PSet(mae, "my_pset")
```

convert_pset_to_df	<i>Convert a PharmacoSet to a data.table that is prepare for input into gDR pipeline</i>
--------------------	--

Description

Convert a PharmacoSet to a data.table that is prepare for input into gDR pipeline

Usage

```
convert_pset_to_df(pharmacoset, run_parallel = TRUE, workers = 2L)
```

Arguments

pharmacoset	PharmacoSet object
run_parallel	logical, TRUE (default) if to run functions in Parallel, FALSE to run in serial
workers	integer, number of workers defaults to 2L if run_parallel is TRUE

Value

data.table of PharmacoSet's dose response data with column names aligned with gDR standard

Author(s)

Jermiah Joseph – collaboration with BHKLab

Examples

```
pset <- suppressMessages(getPSet(  
  "Tavor_2020",  
  psetDir = system.file("extdata/pset", package = "gDRimport"),  
  use_local_PSets_list = TRUE  
))  
dt <- convert_pset_to_df(pset)  
gDRutils::reset_env_identifiers()
```

`correct_template_sheets`*Correct names of the template sheets (if required)*

Description

Correct names of the template sheets (if required)

Usage

```
correct_template_sheets(tfiles)
```

Arguments

tfiles charvec with paths to template files

Value

charvec with paths to corrected sheet names

`detect_file_format` *Detect format of results data*

Description

Detect format of results data

Usage

```
detect_file_format(results_file)
```

Arguments

results_file path to results data

Value

string of the detected file format

Examples

```
td2 <- get_test_Tecan_data()
detect_file_format(td2$r_files[1])
```

enhance_raw_edited_EnVision_df
Enhance raw edited EnVision data.table

Description

Enhance raw edited EnVision data.table

Usage

```
enhance_raw_edited_EnVision_df(df, barcode_col, headers)
```

Arguments

df	raw data.table
barcode_col	column number for barcode data
headers	list with the headersa

Value

data.table derived from EnVision data

fix_typos_with_reference
Fix typos using reference data

Description

Fix typos using reference data Evaluate given list of ids and try to update them

Usage

```
fix_typos_with_reference(  
  data,  
  ref,  
  method = c("exact", "grepl", "adist"),  
  fix_underscores = FALSE  
)
```

Arguments

data	list of charvec(s) or charvec with data
ref	charvec with reference data
method	charvec type of the method to be used 'exact' is used to find identical entries from 'ref' in the data (after corrections and uppercase'ing) 'grepl' is used to find entries from 'ref' that might be somehow pre- or post- fixed
fix_underscores	logical flag fix the issues with underscores in data identifiers?

Value

list or charvec with corrected data

gdr_test_data-class *gDR Test Data object*

Description

Object class gdr_test_data is build by function [get_test_data\(\)](#)

Value

object class gdr_test_data with primary test data

Slots

manifest_path character, path to manifest file
 result_path character, path(s) to results file
 template_path character, path(s) to data.table with template data
 ref_m_df character, data.table with manifest data
 ref_r1_r2 character, path to reference file with raw data for treated & untreated
 ref_r1 character, path to reference file with raw data for treated
 ref_t1_t2 character, path to reference template file with treated & untreated data
 ref_t1 character, path to reference template file with treated data

getPSet	<i>Get PharmacoSet</i>
---------	------------------------

Description

Get PharmacoSet

Usage

```
getPSet(  
  pset_name,  
  psetDir = getwd(),  
  canonical = FALSE,  
  timeout = 600,  
  use_local_PSets_list = FALSE  
)
```

Arguments

pset_name	string with the name of the PharmacoSet
psetDir	string with the temporary directory for the PharmacoSet
canonical	logical flag indicating if the PSet canonical
timeout	maximum number of seconds allowed for PSet download
use_local_PSets_list	logical flag if PSets list should be used from local. If FALSE PSets list will be taken from web.

Value

PharmacoSet object

Examples

```
suppressMessages(getPSet(  
  "Tavor_2020",  
  psetDir = system.file("extdata/pset", package = "gDRimport"),  
  use_local_PSets_list = TRUE  
))
```

`get_df_from_raw_edited_EnVision_df`*Get final results (as a data.table) from raw edited EnVision data.table*

Description

Get final results (as a data.table) from raw edited EnVision data.table

Usage

```
get_df_from_raw_edited_EnVision_df(  
  df,  
  barcode_idx,  
  barcode_col,  
  n_row,  
  n_col,  
  fname,  
  sheet_name,  
  headers  
)
```

Arguments

<code>df</code>	raw data.table
<code>barcode_idx</code>	numeric vector with barcode indices
<code>barcode_col</code>	column number for barcode data
<code>n_row</code>	number of rows
<code>n_col</code>	number of columns
<code>fname</code>	file name
<code>sheet_name</code>	name of the Excel sheet
<code>headers</code>	list with the headers

Value

data.table derived from EnVision data

`get_df_from_raw_unedited_EnVision_df`

Get final results (as a data.table) from raw unedited EnVision data.table

Description

Get final results (as a data.table) from raw unedited EnVision data.table

Usage

`get_df_from_raw_unedited_EnVision_df(df, n_row, n_col, barcode_col)`

Arguments

<code>df</code>	raw data.table
<code>n_row</code>	number of rows
<code>n_col</code>	number of columns
<code>barcode_col</code>	column number for barcode data

Value

data.table derived from EnVision data

`get_EnVision_properties`

Get properties of EnVision data

Description

This function return properties of EnVision data

Usage

`get_EnVision_properties(results.list, fname)`

Arguments

<code>results.list</code>	list with EnVision data
<code>fname</code>	name of the input file

Value

list with EnVision propertiesa

get_excel_sheet_names *get Excel sheets names for a charvec of files for non-Excel files return 0*

Description

get Excel sheets names for a charvec of files for non-Excel files return 0

Usage

get_excel_sheet_names(fls)

Arguments

fls charvec with file pathsa

Value

list with one element per file with sheet names or 0 (for non-Excel file)

get_exception_data *get exception data*

Description

get exception data

Usage

get_exception_data(status_code = NULL)

Arguments

status_code A numeric value

Value

A data.table row with exception data or all exceptions

Examples

```
get_exception_data(1)
get_exception_data()
```

`get_expected_template_sheets`

Get names of the sheets expected in templates.xlsx

Description

Get names of the sheets expected in templates.xlsx

Usage

```
get_expected_template_sheets(type = c("all", "core", "optional"))
```

Arguments

`type` charvec type of the sheets

Value

string with type of the sheets

`get_plate_info_from_template.xlsx`

Get plate info from template.xlsx

Description

Get plate info from template.xlsx

Usage

```
get_plate_info_from_template.xlsx(template_file, Gnumber_idx, idx)
```

Arguments

`template_file` character, file path(s) to template(s)

`Gnumber_idx` index with Gnumber data

`idx` template file index

Value

list with plate info

get_test_D300_data *get test D300 data*

Description

get test D300 data

Usage

get_test_D300_data()

Value

list with with input data (manifest/template/result paths) and related reference data (qs file paths)

Examples

get_test_D300_data()

get_test_data *get primary test data*

Description

get primary test data

Usage

get_test_data()

Value

object class "gdr_test_data" with with input data (manifest/template/result paths) and related reference data (qs file paths)

Examples

get_test_data()

`get_test_EnVision_data`
get test EnVision data

Description

get test EnVision data

Usage

`get_test_EnVision_data()`

Value

list with with input data (manifest/template/result paths) and related reference data (.qs file paths)

Examples

`get_test_EnVision_data()`

`get_test_Tecan_data` *get test Tecan data*

Description

get test Tecan data

Usage

`get_test_Tecan_data()`

Value

list with with input data (manifest/template/result paths) and related reference data (qs file paths)

Examples

`get_test_Tecan_data()`

get_test_tsv_data *get test tsv data*

Description

get test tsv data

Usage

get_test_tsv_data()

Value

list with with input data (manifest/template/result paths) and related reference data (.qs file paths)

Examples

get_test_tsv_data()

get_xl_sheets *Get Excel sheets*

Description

get sheets for given set of XLS files

Usage

get_xl_sheets(files)

Arguments

files charvec with file paths

Value

named list where names are the excel filenames and the values are the sheets within each file

`import_D300`*Import D300*

Description

This function takes a D300 file and generates corresponding template files

Usage

```
import_D300(D300_file, metadata_file, destination_path)
```

Arguments

`D300_file` character, file path to D300 file
`metadata_file` character, file path to file with mapping from D300 names to Gnumbers
`destination_path`
character, path to folder where template files will be generated

Details

For example, wells treated with 2 drugs in combination will result in 4 sheets per plate.

- Sheet 1: Drug 1
- Sheet 2: Conc of Drug 1
- Sheet 3: Drug 2
- Sheet 4: Conc of Drug 2

Value

Create one Excel file per plate. Each sheet in each plate file describes the drugs and corresponding concentrations of what was tested in each well.

Examples

```
td3 <- get_test_D300_data()[["f_96w"]]  
o_path <- file.path(tempdir(), "td3")  
dir.create(o_path)  
import_D300(td3$d300, td3$Gnum, o_path)  
list.files(o_path)  
unlink(o_path, recursive = TRUE)
```

is_readable_v	<i>is_readable_v</i> Check if all paths in vector are readable
---------------	--

Description

is_readable_v Check if all paths in vector are readable

Usage

```
is_readable_v(paths)
```

Arguments

paths a character with path(s)

Value

NULL invisibly.

Examples

```
td2 <- get_test_Tecan_data()
is_readable_v(td2$r_files)
```

load_data	<i>Load data</i>
-----------	------------------

Description

This functions loads and checks the data file(s)

Usage

```
load_data(
  manifest_file,
  df_template_files,
  results_file,
  instrument = "EnVision"
)
```

Arguments

manifest_file character, file path(s) to manifest(s)
df_template_files data.table, with datapaths and names of results file(s) or character with file path of templates file(s)
results_file data.table, with datapaths and names of results file(s) or character with file path of results file(s)
instrument character

Value

a list with three data.tables for manifest/treatment and results

Examples

```
td <- get_test_data()
l_tbl <- load_data(manifest_path(td), template_path(td), result_path(td))
```

load_manifest	<i>Load manifest</i>
---------------	----------------------

Description

This functions loads and checks the manifest file(s)

Usage

```
load_manifest(manifest_file)
```

Arguments

manifest_file character, file path(s) to manifest(s)

Value

list with manifest data.table and headers

Examples

```
td <- get_test_data()
ml <- load_manifest(manifest_path(td))
```

load_results	<i>Load results</i>
--------------	---------------------

Description

This functions loads and checks the results file(s)

Usage

```
load_results(
  df_results_files,
  instrument = "EnVision",
  headers = gDRutils::get_env_identifiers()
)
```

Arguments

df_results_files	data.table, with datapaths and names of results file(s) or character with file path of results file(s)
instrument	character
headers	list of headers identified in the manifest file

Value

data.table with results' data

Examples

```
td <- get_test_data()
r_df <- load_results(result_path(td))
```

load_results_EnVision	<i>Load EnVision results from xlsx</i>
-----------------------	--

Description

This functions loads and checks the results file(s)

Usage

```
load_results_EnVision(results_file, headers = gDRutils::get_env_identifiers())
```

Arguments

results_file character vector containing file path(s) to results file(s)
 headers list of headers identified in the manifest

Value

data.table with results data

load_results_Tecan *Load tecan results from xlsx*

Description

This functions loads and checks the results file

Usage

```
load_results_Tecan(results_file, headers = gDRutils::get_env_identifiers())
```

Arguments

results_file string, file path to a result file
 headers list of headers identified in the manifest

Value

data.table derived from Tecan data

load_results_tsv *Load results from tsv*

Description

This functions loads and checks the results file(s)

Usage

```
load_results_tsv(results_file, headers)
```

Arguments

results_file character, file path(s) to template(s)
 headers list of headers identified in the manifest

Value

data.table with results data

load_templates	<i>Load templates</i>
----------------	-----------------------

Description

This functions loads and checks the template file(s)

Usage

```
load_templates(df_template_files)
```

Arguments

df_template_files
data.table, with datapaths and names of results file(s) or character with file path of templates file(s)

Value

data.table with templates data

Examples

```
td <- get_test_data()
t_df <- load_templates(template_path(td))
```

load_templates_tsv	<i>Load templates from tsv</i>
--------------------	--------------------------------

Description

This functions loads and checks the template file(s)

Usage

```
load_templates_tsv(template_file, template_filename = NULL)
```

Arguments

template_file character, file path(s) to template(s)
template_filename
character, file name(s)

Value

data.table with template data

load_templates_xlsx	<i>Load templates from xlsx</i>
---------------------	---------------------------------

Description

This functions loads and checks the template file(s)

Usage

```
load_templates_xlsx(template_file, template_filename = NULL)
```

Arguments

```
template_file  character, file path(s) to template(s)
template_filename
                character, file name(s)
```

Value

data.table with templates data

manifest_path	<i>Method manifest_path</i>
---------------	-----------------------------

Description

Method for object gdr_test_data - access to slot manifest_path

Usage

```
manifest_path(x)

## S4 method for signature 'gdr_test_data'
manifest_path(x)
```

Arguments

```
x                object class gdr_test_data
```

Value

value of slot manifest_path

Examples

```
td <- get_test_data()
manifest_file_path <- manifest_path(td)
```

mgrepl	<i>grep wrapper to support multiple patterns</i>
--------	--

Description

grep wrapper to support multiple patterns

Usage

```
mgrepl(patterns, x, do_unlist = TRUE, ...)
```

Arguments

patterns	charvec with patterns to be checked
x	charvec with data
do_unlist	logical_flag unlist the final results?
...	additional argument

Value

list of charvec with grep output

parse_D300_xml	<i>Parse D300</i>
----------------	-------------------

Description

This function parses a D300 *.tdd file (XML format) into a data.table

Usage

```
parse_D300_xml(D300_file)
```

Arguments

D300_file	string, file path to D300 .tdd file
-----------	-------------------------------------

Value

data.table representing input D300_file.

Examples

```
td3 <- get_test_D300_data()
fs <- td3[["f_96w"]]
dose_df <- parse_D300_xml(fs[["d300"]])
```

read_EnVision_delim *Read EnVision delimited text files*

Description

This function reads file from the EnVision Workstation

Usage

```
read_EnVision_delim(file, nrows = 10000, seps = c(",", "\t"))
```

Arguments

file	string to path of input file from EnVision scanner
nrows	maximum number of file rows to be processed
seps	potential field separators of the input file

Value

a list containing the data table, n_col, n_row, and if is edited

read_EnVision_xlsx *Read in single xlsx data from EnVision*

Description

Read in single xlsx data from EnVision

Usage

```
read_EnVision_xlsx(results_file, results_sheet)
```

Arguments

results_file	character, file path(s) to results file(s)
results_sheet	results sheet names

Value

data.table with results data

read_excel_to_dt *Read excel file and transform it into data.table object*

Description

Read excel file and transform it into data.table object

Usage

```
read_excel_to_dt(path, ...)
```

Arguments

path	path to excel file
...	other arguments that should be passed into readxl::read_excel

Value

data.table object with read excel file

Examples

```
datasets <- readxl::readxl_example("datasets.xlsx")
read_excel_to_dt(datasets)
```

read_in_EnVision_file *Read EnVision file*

Description

This function reads file from the EnVision Workstation

Usage

```
read_in_EnVision_file(file, nrows, seps)
```

Arguments

file	input file from EnVision
nrows	maximum number of file rows to be processed
seps	potential field separators of the input file

Value

list with one element per EnVisoin input file

`read_in_manifest_file` *read manifest files*

Description

read manifest files

Usage

`read_in_manifest_file(manifest_file, available_formats)`

Arguments

`manifest_file` character, file path(s) to manifest(s)
`available_formats`
charvec with available file formats

Value

a data.table with manifest data

`read_in_results_Tecan` *read in Tecan data*

Description

read in Tecan data

Usage

`read_in_results_Tecan(results_file, results_sheets, headers)`

Arguments

`results_file` string, file path to a result file
`results_sheets` template sheet names
`headers` list of headers identified in the manifest

Value

data.table derived from Tecan data

read_in_result_files *Read in results files*

Description

Read in results files

Usage

```
read_in_result_files(results_file, results_filename, headers)
```

Arguments

results_file data.table, with datapaths and names of results file(s) or character with file path of results file(s)

results_filename charvect with file names

headers list of headers identified in the result files

Value

data.table with results data

read_in_template_sheet_xlsx
Read in data from xlsx template sheet

Description

Read in data from xlsx template sheet

Usage

```
read_in_template_sheet_xlsx(template_file, template_sheets, idx, plate_info)
```

Arguments

template_file character, file path(s) to template(s)

template_sheets template sheet names

idx template file index

plate_info list with plate info

Value

data.table with template data

read_in_template_xlsx *Read in xlsx template files*

Description

Read in xlsx template files

Usage

```
read_in_template_xlsx(template_file, template_filename, template_sheets)
```

Arguments

template_file character, file path(s) to template(s)
template_filename character, file name(s)
template_sheets template sheet names

Value

data.table with templates data

read_in_tsv_template_files
read in tsv template files

Description

read in tsv template files

Usage

```
read_in_tsv_template_files(template_file, template_filename, templates)
```

Arguments

template_file character, file path(s) to template(s)
template_filename character, file name(s)
templates list with templates data

Value

data.table with templates data

read_ref_data	<i>read_ref_data</i>
---------------	----------------------

Description

Read reference data

Usage

```
read_ref_data(inDir, prefix = "ref")
```

Arguments

inDir	a directory path of reference data
prefix	a prefix of reference file names ('ref' by default)

Value

a list of reference data

result_path	<i>Method result_path</i>
-------------	---------------------------

Description

Method for object gdr_test_data - access to slot result_path

Usage

```
result_path(x)

## S4 method for signature 'gdr_test_data'
result_path(x)
```

Arguments

x	object class gdr_test_data
---	----------------------------

Value

value of slot result_path

Examples

```
td <- get_test_data()
result_file_path <- result_path(td)
```

`save_drug_info_per_well`

for each drug create a Gnumber and Concentration information for each well

Description

for each drug create a Gnumber and Concentration information for each well

Usage

```
save_drug_info_per_well(trt_info, trt_gnumber_conc, wb, idfs)
```

Arguments

<code>trt_info</code>	list with treatment info
<code>trt_gnumber_conc</code>	list with treatment data
<code>wb</code>	pointer to xlsx workbook
<code>idfs</code>	charvec with identifiers

Value

NULL invisibly.

`setEnvForPSet`

Adjust environment variables to meet gDR standards

Description

Adjust environment variables to meet gDR standards

Usage

```
setEnvForPSet()
```

Value

NULL

Examples

```
setEnvForPSet()  
gDRutils::reset_env_identifiers()
```

standardize_record_values
standardize_record_values

Description

map values to a dictionary

Usage

```
standardize_record_values(x, dictionary = DICTIONARY)
```

Arguments

x a named array
dictionary a named array

Value

a named array with updated names

Examples

```
standardize_record_values(c("Vehicle", "vehcle"))
```

template_path *Method template_path*

Description

Method for object gdr_test_data - access to slot template_path

Usage

```
template_path(x)  
  
## S4 method for signature 'gdr_test_data'  
template_path(x)
```

Arguments

x object class gdr_test_data

Value

value of slot template_path

Examples

```
td <- get_test_data()
template_file_path <- template_path(td)
```

validate_template_xlsx

Validate template xlsx data

Description

Validate template xlsx data

Usage

```
validate_template_xlsx(template_file, template_filename, template_sheets, idx)
```

Arguments

template_file character, file path(s) to template(s)
template_filename character, file name(s)
template_sheets template sheet names
idx template file index

Value

NULL invisibly.

Index

- * **D300**
 - import_D300, 25
 - parse_D300_xml, 32
 - save_drug_info_per_well, 39
- * **classes**
 - gdr_test_data-class, 16
- * **correction_exception**
 - .check_against_single_template_sheet, 5
 - are_template_sheets_valid, 9
 - check_metadata_against_spaces, 9
 - check_metadata_field_names, 10
 - check_metadata_headers, 10
 - check_metadata_names, 11
 - check_metadata_req_col_names, 11
 - correct_template_sheets, 14
 - fix_typos_with_reference, 15
 - get_exception_data, 20
 - get_expected_template_sheets, 21
 - get_xl_sheets, 24
 - mgrepl, 32
- * **internal**
 - .check_file_structure, 5
 - .createPseudoData, 6
 - .extractDoseResponse, 6
 - .fill_empty_wells, 7
 - .get_plate_size, 7
 - .removeNegatives, 8
 - .standardize_untreated_values, 8
 - gDRimport-package, 4
- * **load_files**
 - enhance_raw_edited_EnVision_df, 15
 - get_df_from_raw_edited_EnVision_df, 18
 - get_df_from_raw_unedited_EnVision_df, 19
 - get_EnVision_properties, 19
 - get_excel_sheet_names, 20
 - get_plate_info_from_template_xlsx, 21
 - load_data, 26
 - load_manifest, 27
 - load_results, 28
 - load_results_EnVision, 28
 - load_results_Tecan, 29
 - load_results_tsv, 29
 - load_templates, 30
 - load_templates_tsv, 30
 - load_templates_xlsx, 31
 - read_EnVision_delim, 33
 - read_EnVision_xlsx, 33
 - read_in_EnVision_file, 34
 - read_in_manifest_file, 35
 - read_in_result_files, 36
 - read_in_results_Tecan, 35
 - read_in_template_sheet_xlsx, 36
 - read_in_template_xlsx, 37
 - read_in_tsv_template_files, 37
 - validate_template_xlsx, 41
- * **methods**
 - manifest_path, 31
 - result_path, 38
 - template_path, 40
- * **pset**
 - .extract_or_create_assay, 6
 - convert_MAE_to_PSet, 12
 - convert_pset_to_df, 13
 - getPSet, 17
 - setEnvForPSet, 39
- * **test_data_class**
 - gdr_test_data-class, 16
 - get_test_data, 22
 - manifest_path, 31
 - result_path, 38
 - template_path, 40
- * **test_data**
 - get_test_D300_data, 22
 - get_test_EnVision_data, 23

- get_test_Tecan_data, 23
- get_test_tsv_data, 24
- * **utils**
 - detect_file_format, 14
 - is_readable_v, 26
 - read_excel_to_dt, 34
 - read_ref_data, 38
 - standardize_record_values, 40
- .check_against_single_template_sheet, 5
- .check_file_structure, 5
- .createPseudoData, 6
- .extractDoseResponse, 6
- .extract_or_create_assay, 6
- .fill_empty_wells, 7
- .get_plate_size, 7
- .removeNegatives, 8
- .standardize_untreated_values, 8
- are_template_sheets_valid, 9
- check_metadata_against_spaces, 9
- check_metadata_field_names, 10
- check_metadata_headers, 10
- check_metadata_names, 11
- check_metadata_req_col_names, 11
- convert_MAE_to_PSet, 12
- convert_pset_to_df, 13
- correct_template_sheets, 14
- detect_file_format, 14
- enhance_raw_edited_EnVision_df, 15
- fix_typos_with_reference, 15
- gdr_test_data-class, 16
- gDRimport (gDRimport-package), 4
- gDRimport-package, 4
- get_df_from_raw_edited_EnVision_df, 18
- get_df_from_raw_unedited_EnVision_df, 19
- get_EnVision_properties, 19
- get_excel_sheet_names, 20
- get_exception_data, 20
- get_expected_template_sheets, 21
- get_plate_info_from_template_xlsx, 21
- get_test_D300_data, 22
- get_test_data, 22
- get_test_data(), 16
- get_test_EnVision_data, 23
- get_test_Tecan_data, 23
- get_test_tsv_data, 24
- get_xl_sheets, 24
- getPSet, 17
- import_D300, 25
- is_readable_v, 26
- load_data, 26
- load_manifest, 27
- load_results, 28
- load_results_EnVision, 28
- load_results_Tecan, 29
- load_results_tsv, 29
- load_templates, 30
- load_templates_tsv, 30
- load_templates_xlsx, 31
- manifest_path, 31
- manifest_path, gdr_test_data-method (manifest_path), 31
- mgrepl, 32
- parse_D300_xml, 32
- read_EnVision_delim, 33
- read_EnVision_xlsx, 33
- read_excel_to_dt, 34
- read_in_EnVision_file, 34
- read_in_manifest_file, 35
- read_in_result_files, 36
- read_in_results_Tecan, 35
- read_in_template_sheet_xlsx, 36
- read_in_template_xlsx, 37
- read_in_tsv_template_files, 37
- read_ref_data, 38
- result_path, 38
- result_path, gdr_test_data-method (result_path), 38
- save_drug_info_per_well, 39
- setEnvForPSet, 39
- standardize_record_values, 40
- template_path, 40
- template_path, gdr_test_data-method (template_path), 40
- validate_template_xlsx, 41