

# Package ‘gDRimport’

April 11, 2025

**Type** Package

**Title** Package for handling the import of dose-response data

**Version** 1.5.11

**Date** 2025-04-10

**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, PharmacGx, data.table, futile.logger, gDRutils (>= 1.3.17), magrittr, methods, MultiAssayExperiment, readxl, rio, S4Vectors, stats, stringi, SummarizedExperiment, tibble, tools, utils, XML, yaml, openxlsx

**Suggests** BiocStyle, gDRtestData (>= 1.3.3), gDRstyle (>= 1.3.3), knitr, purrr, qs, testthat

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

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

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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)**

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Authors:

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- 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.

---

|                                |                                                                         |
|--------------------------------|-------------------------------------------------------------------------|
| <code>.createPseudoData</code> | <i>Add in pseudo-data for duration and cell reference division time</i> |
|--------------------------------|-------------------------------------------------------------------------|

---

**Description**

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

**Usage**

```
.createPseudoData(dt)
```

**Value**

data.table

---

|                                   |                                                                       |
|-----------------------------------|-----------------------------------------------------------------------|
| <code>.extractDoseResponse</code> | <i>Get dose and viability readouts and melt into large data table</i> |
|-----------------------------------|-----------------------------------------------------------------------|

---

**Description**

Get dose and viability readouts and melt into large data table

**Usage**

```
.extractDoseResponse(pset)
```

**Value**

data.table with dose-response data

---

|                                       |                                                                                                       |
|---------------------------------------|-------------------------------------------------------------------------------------------------------|
| <code>.extract_or_create_assay</code> | <i>Extracts an assay from a SummarizedExperiment object or creates a new one if it does not exist</i> |
|---------------------------------------|-------------------------------------------------------------------------------------------------------|

---

**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

---

|                                |                                                            |
|--------------------------------|------------------------------------------------------------|
| <code>.fill_empty_wells</code> | <i>Correct plates with not fully filled readout values</i> |
|--------------------------------|------------------------------------------------------------|

---

**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

---

|                              |                       |
|------------------------------|-----------------------|
| <code>.get_plate_size</code> | <i>Get plate size</i> |
|------------------------------|-----------------------|

---

**Description**

Get plate size

**Usage**

```
.get_plate_size(df)
```

**Details**

All plate sizes assume 1.5x nrow = ncolumn.

**Value**

charvec with plate dims

---

|                  |                                    |
|------------------|------------------------------------|
| .removeNegatives | <i>Remove negative viabilities</i> |
|------------------|------------------------------------|

---

**Description**

Remove negative viabilities

**Usage**

.removeNegatives(dataset)

**Value**

data.table with positive values in column ReadoutValue

---

|                               |                                                     |
|-------------------------------|-----------------------------------------------------|
| .standardize_untreated_values | <i>Standardize untreated values to ignore cases</i> |
|-------------------------------|-----------------------------------------------------|

---

**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 | <i>Check metadata field names</i> |
|----------------------------|-----------------------------------|

---

**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 | <i>Check whether metadata headers are correct and make fixes if needed</i> |
|------------------------|----------------------------------------------------------------------------|

---

**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 | <i>check_metadata_names</i> |
|----------------------|-----------------------------|

---

**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 | <i>Check metadata for required column names</i> |
|------------------------------|-------------------------------------------------|

---

**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_LEVEL5_prism_to_gDR_input`

*Load, convert and process the level 5 PRISM data into a gDR input*

---

**Description**

Load, convert and process the level 5 PRISM data into a gDR input

**Usage**

```
convert_LEVEL5_prism_to_gDR_input(  
  prism_data_path,  
  meta_data_path,  
  readout_min = 1.03  
)
```

**Arguments**

|                              |                                                                                                                                    |
|------------------------------|------------------------------------------------------------------------------------------------------------------------------------|
| <code>prism_data_path</code> | path to PRISM LEVEL5 csv file with data                                                                                            |
| <code>meta_data_path</code>  | path to metadata file describing all cancer models/cell lines which are referenced by a dataset contained within the DepMap portal |
| <code>readout_min</code>     | minimum ReadoutValue                                                                                                               |

**Value**

`data.table` object with input data for gDR pipeline

**Examples**

```
prism_data <- system.file("testdata/prism_sa.csv", package = "gDRimport")  
prism_meta <- system.file("testdata/prism_model.csv", package = "gDRimport")  
convert_LEVEL5_prism_to_gDR_input(prism_data, prism_meta)
```

---

`convert_LEVEL6_prism_to_gDR_input`*Load, convert and process the level 6 PRISM data into a gDR input*

---

**Description**

Load, convert and process the level 6 PRISM data into a gDR input

**Usage**

```
convert_LEVEL6_prism_to_gDR_input(  
  prism_data_path,  
  cell_line_data_path,  
  treatment_data_path,  
  meta_data_path,  
  readout_min = 1.03  
)
```

**Arguments**

|                                  |                                                                                                                                    |
|----------------------------------|------------------------------------------------------------------------------------------------------------------------------------|
| <code>prism_data_path</code>     | path to PRISM LEVEL6 csv file with collapsed log fold change data                                                                  |
| <code>cell_line_data_path</code> | path to cell line info data                                                                                                        |
| <code>treatment_data_path</code> | path to collapsed treatment info data                                                                                              |
| <code>meta_data_path</code>      | path to metadata file describing all cancer models/cell lines which are referenced by a dataset contained within the DepMap portal |
| <code>readout_min</code>         | minimum ReadoutValue                                                                                                               |

**Value**

`data.table` object with input data for gDR pipeline

**Examples**

```
prism_data_path <- system.file("testdata/prism_collapsed_LOGFC.csv", package = "gDRimport")  
cell_line_data_path <- system.file("testdata/prism_cell_lines.csv", package = "gDRimport")  
treatment_data_path <- system.file("testdata/prism_treatment.csv", package = "gDRimport")  
prism_meta <- system.file("testdata/prism_model.csv", package = "gDRimport")  
convert_LEVEL6_prism_to_gDR_input(prism_data_path, cell_line_data_path, treatment_data_path, prism_meta)
```

---

|                     |                                                                    |
|---------------------|--------------------------------------------------------------------|
| convert_MAE_to_PSet | <i>Convert MultiAssayExperiment to TreatmentResponseExperiment</i> |
|---------------------|--------------------------------------------------------------------|

---

### 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 PharmacSet to a data.table that is prepare for input into gDR pipeline</i> |
|--------------------|-----------------------------------------------------------------------------------------|

---

### Description

Convert a PharmacSet 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 headers

**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

*Get PharmacoSet*


---

**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**

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

**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**

|             |                                |
|-------------|--------------------------------|
| df          | raw data.table                 |
| n_row       | number of rows                 |
| n_col       | number of columns              |
| barcode_col | 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**

|              |                         |
|--------------|-------------------------|
| results.list | list with EnVision data |
| fname        | name of the input file  |

**Value**

list with EnVision propertiesa

---

|                       |                                                                                   |
|-----------------------|-----------------------------------------------------------------------------------|
| get_excel_sheet_names | <i>get Excel sheets names for a charvec of files for non-Excel files return 0</i> |
|-----------------------|-----------------------------------------------------------------------------------|

---

**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 | <i>get exception data</i> |
|--------------------|---------------------------|

---

**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                              |
| <i>Get names of the sheets expected in templates xlsx</i> |

---

**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        |
| <i>Get plate info from template xlsx</i> |

---

**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 | <i>get test D300 data</i> |
|--------------------|---------------------------|

---

**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 | <i>get primary test data</i> |
|---------------|------------------------------|

---

**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 | <i>get test tsv data</i> |
|-------------------|--------------------------|

---

**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 | <i>Get Excel sheets</i> |
|---------------|-------------------------|

---

**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 functions 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 | <i>Load tecan results from xlsx</i> |
|--------------------|-------------------------------------|

---

**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 | <i>Load results from tsv</i> |
|------------------|------------------------------|

---

**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 | <i>Read EnVision delimited text files</i> |
|---------------------|-------------------------------------------|

---

**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 | <i>Read in single xlsx data from EnVision</i> |
|--------------------|-----------------------------------------------|

---

**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 | <i>Read excel file and transform it into data.table object</i> |
|------------------|----------------------------------------------------------------|

---

**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 | <i>Read EnVision file</i> |
|-----------------------|---------------------------|

---

**Description**

This function reads file from the EnVision Workstation

**Usage**

```
read_in_EnVision_file(file, nrow, seps)
```

**Arguments**

|      |                                              |
|------|----------------------------------------------|
| file | input file from EnVision                     |
| nrow | 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

|                  |                          |
|------------------|--------------------------|
| trt_info         | list with treatment info |
| trt_gnumber_conc | list with treatment data |
| wb               | pointer to xlsx workbook |
| idfs             | 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        |
| <i>standardize_record_values</i> |

---

**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 | <i>Method template_path</i> |
|---------------|-----------------------------|

---

**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.

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