

# Package ‘gDR’

December 17, 2024

**Type** Package

**Title** Umbrella package for R packages in the gDR suite

**Version** 1.5.1

**Date** 2024-11-05

**Description** Package is a part of the gDR suite. It reexports functions from other packages in the gDR suite that contain critical processing functions and utilities. The vignette walks through the full processing pipeline for drug response analyses that the gDR suite offers.

**License** Artistic-2.0

**Depends** R (>= 4.2), gDRcore (>= 1.1.19), gDRimport (>= 1.1.9), gDRutils (>= 1.1.12)

**Suggests** BiocStyle, BumpyMatrix, futile.logger, gDRstyle (>= 1.1.5), gDRtestData (>= 1.1.10), kableExtra, knitr, markdown, purrr, rmarkdown, SummarizedExperiment, testthat, yaml

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

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

**biocViews** Software, DataImport, ShinyApps

**VignetteBuilder** knitr

**ByteCompile** TRUE

**LazyLoad** yes

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**SwitchrLibrary** gDR

**DeploySubPath** gDR

**Encoding** UTF-8

**git\_url** <https://git.bioconductor.org/packages/gDR>

**git\_branch** devel

**git\_last\_commit** 8e0f13d

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**Repository** Bioconductor 3.21

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gDR-package	<i>gDR: Umbrella package for R packages in the gDR suite</i>
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## Description

Package is a part of the gDR suite. It reexports functions from other packages in the gDR suite that contain critical processing functions and utilities. The vignette walks through the full processing pipeline for drug response analyses that the gDR suite offers.

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## Value

package help page

package help page

## Note

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

**Author(s)**

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- Marc Hafner ([ORCID](#))
- Dariusz Scigocki
- Janina Smola
- Sergiu Mocanu

**See Also**

Useful links:

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

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import\_data

*Import raw data*

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**Description**

Import raw data

**Usage**

```
import_data(  
  manifest_file,  
  template_file,  
  results_file,  
  instrument = "EnVision"  
)
```

**Arguments**

manifest_file	character, file path(s) to manifest(s)
template_file	character, with datapaths and names of results file(s) or character with file path of templates file(s)
results_file	character, with datapaths and names of results file(s) or character with file path of results file(s)
instrument	string with type of instrument used

**Value**

a data.table

**Examples**

```
td <- get_test_data()
i_df <- import_data(manifest_path(td), template_path(td), result_path(td))
```

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small_combo_data	<i>Small data.table with raw combo data used for processing via gDR</i>
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**Description**

A dataset containing the ReadoutValues for combo experiments made-up of 3 drugs, 2 co-drugs, and 2 cell lines

**Usage**

```
data(small_combo_data)
```

**Format**

A data frame with 3600 rows and 16 variables:

**Barcode** barcode  
**clid** cell line id  
**CellLineName** cell line name  
**Tissue** cell line tissue  
**ReferenceDivisionTime** cell line division time  
**Gnumber** drug id  
**DrugName** drug name  
**drug\_moa** drug mode of action  
**Concentration** drug concentration  
**Gnumber\_2** co-drug id

**DrugName\_2** co-drug name  
**drug\_moa\_2** co-drug mode of action  
**Concentration\_2** co-drug concentration  
**ReadoutValue** readout value  
**BackgroundValue** background value  
**Duration** duration

**Value**

data.table

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small\_data

*Small data.table with raw data used for processing via gDR*

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**Description**

A dataset containing the ReadoutValues for single-agent experiments made-up of 10 drugs and 10 cell lines

**Usage**

data(small\_data)

**Format**

A data frame with 3300 rows and 12 variables:

**Barcode** barcode  
**clid** cell line id  
**CellLineName** cell line name  
**Tissue** cell line tissue  
**ReferenceDivisionTime** cell line division time  
**Gnumber** drug id  
**DrugName** drug name  
**drug\_moa** drug mode of action  
**Concentration** drug concentration  
**ReadoutValue** readout value  
**BackgroundValue** background value  
**Duration** duration

**Value**

data.table

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