

Package ‘gDR’

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Type Package

Title Umbrella package for R packages in the gDR suite

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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.

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

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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")`

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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

Description

Import raw data

Usage

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

Arguments

<code>manifest_file</code>	character, file path(s) to manifest(s)
<code>template_file</code>	character, with datapaths and names of results file(s) or character with file path of templates file(s)
<code>results_file</code>	character, with datapaths and names of results file(s) or character with file path of results file(s)
<code>instrument</code>	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))
```

<code>small_combo_data</code>	<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 backgroud value
Duration duration

Value

data.table

small_data

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

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 backgroud value
Duration duration

Value

data.table

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