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 (>= 1.7.1), gDRimport (>= 1.7.1), gDRutils (>= 1.7.1)

Suggests BiocStyle, BumpyMatrix, futile.logger, gDRstyle (>= 1.7.1), gDRtestData (>= 1.7.1), 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

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Author Allison Vuong [aut],
Bartosz Czech [aut] (ORCID: <https://orcid.org/0000-0002-9908-3007>),
Arkadiusz Gladki [cre, aut] (ORCID:
<https://orcid.org/0000-0002-7059-6378>),
Marc Hafner [aut] (ORCID: <https://orcid.org/0000-0003-1337-7598>),
Dariusz Scigocki [aut],
Janina Smola [aut],
Sergiu Mocanu [aut]

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

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`gDR-package` *gDR: Umbrella package for R packages in the gDR suite*

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)

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

Authors:

- Allison Vuong <vuong.allison@gene.com>
- Bartosz Czech (ORCID)
- 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*

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))
```

---

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

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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