Package ‘gDRtestData’

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Title gDRtestData - R data package with testing dose reponse data

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Description  R package with internal dose-response test data. Package provides functions to generate input testing data that can be used as the input for gDR pipeline. It also contains RDS files with MAE data processed by gDR.

Depends R (>= 4.2)

Imports checkmate

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gDRtestData-package  gDRtestData: gDRtestData - R data package with testing dose response data

Description

R package with internal dose-response test data. Package provides functions to generate input testing data that can be used as the input for gDR pipeline. It also contains RDS files with MAE data processed by gDR.

Value

package help page

Note

To learn more about functions start with help(package = "gDRtestData")
add_concentration

Author(s)

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Authors:

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- Bartosz Czech
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- Dariusz Scigocki
- Allison Young

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add_concentration    Add concentrations

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**Description**

Add concentrations

**Usage**

```r
add_concentration(df_layout, concentrations = 10^(seq(-3, 1, 0.5)))
```

**Arguments**

- `df_layout` data.table that should contains the cell line, drug, concentration, and replicate columns along with the annotations that needs to be propagated
- `concentrations` vector of numeric concentrations that will be added to `df_layout`

**Value**

data.table with concentrations

**Examples**

```r
cell_lines <- create_synthetic_cell_lines()
add_concentration(cell_lines)
```
### add_data_replicates
*Add data replicates*

**Description**
Add data replicates

**Usage**
```
add_data_replicates(df_layout)
```

**Arguments**
- `df_layout`: data.table that should contain the cell line, drug, concentration, and replicate columns along with the annotations that need to be propagated.

**Value**
data.table with replicates

**Examples**
```
cell_lines <- create_synthetic_cell_lines()
add_data_replicates(cell_lines)
```

### add_day0_data
*Add data with day 0*

**Description**
Add data with day 0

**Usage**
```
add_day0_data(df_merged, noise_level = 0.05)
```

**Arguments**
- `df_merged`: data.table with merged data
- `noise_level`: numeric scalar with the level of noise added to the data

**Value**
data.table with day0 data

**Examples**
```
cell_lines <- create_synthetic_cell_lines()
add_day0_data(cell_lines)
```
cell_lines

Examples

```r
cell_lines <- create_synthetic_cell_lines()
drugs <- create_synthetic_drugs()
data <- gDRtestData:::prepareData(cell_lines[seq_len(2), ], drugs[seq_len(4), ])
data$Duration <- 72
data$ReadoutValue <- 0
add_day0_data(data)
```

cell_lines | Cell lines
---|---

Description

Cell lines

Value

data.table

Examples

```r
path <- system.file("annotation_data", "cell_lines.csv", package = "gDRtestData")
data.table::fread(file = path)
```

create_synthetic_cell_lines

Create data.table with synthetic cell lines

Description

Create data.table with synthetic cell lines

Usage

`create_synthetic_cell_lines()`

Value

data.table with synthetic cell lines

Examples

`create_synthetic_cell_lines()`
create_synthetic_drugs

*Create data.table with synthetic drugs*

---

**Description**

Create data.table with synthetic drugs

**Usage**

`create_synthetic_drugs()`

**Value**

data.table with synthetic drugs

**Examples**

`create_synthetic_drugs()`

---

**Drugs**

---

**Description**

Drugs

**Value**

data.table

**Examples**

```r
path <- system.file("annotation_data", "drugs.csv", package = "gDRtestData")
data.table::fread(file = path)
```
**generate_ec50**

*Calculate EC50 metric*

**Description**

Calculate EC50 metric

**Usage**

```r
generate_ec50(drugs, cell_lines)
```

**Arguments**

- `drugs` data.table with drugs
- `cell_lines` data.table with cell lines

**Value**

matrix with random EC50

**Examples**

```r
generate_ec50(create_synthetic_drugs(), create_synthetic_cell_lines())
```

---

**generate_e_inf**

*Calculate E inf metric*

**Description**

Calculate E inf metric

**Usage**

```r
generate_e_inf(drugs, cell_lines)
```

**Arguments**

- `drugs` data.table with drugs
- `cell_lines` data.table with cell lines

**Value**

matrix with random E inf
generate_hill_coef  

Generate hill coefficient

Description

Generate hill coefficient

Usage

generate_hill_coef(drugs, cell_lines)

Arguments

drugs  
data.table with drugs
cell_lines  
data.table with cell lines

Value

matrix with random hill coefficient

Examples

generate_hill_coef(create_synthetic_drugs(), create_synthetic_cell_lines())

generate_response_data  

Generate response data

Description

Generate response data

Usage

generate_response_data(df_layout, noise_level = 0.1)

Arguments

df_layout  
data.table that should contains the cell line, drug, concentration, and replicate columns along with the annotations that needs to be propagated
noise_level  
numeric scalar with the level of noise added to the data
Value

data.table with response data

Examples

cell_lines <- create_synthetic_cell_lines()
drugs <- create_synthetic_drugs()
gDRtestData:::prepareData(cell_lines[seq_len(2), ], drugs[seq_len(4), ])

describe(get_test_dataset_paths)

describe(get_test_dataset_paths)

Description

Returns named vector of absolute paths to test datasets.

Usage

g_test_dataset_paths(datasets_dir = NULL, pattern = "finalMAE_")

Arguments

datasets_dir path to directory with datasets (default NULL). If NULL, then inst/testdata
directory from gDRtestData will be used.

pattern used to: (1) filter to qs files from the dataset_dir path and (2) prettify the labels
of the files

Value

named vector of absolute paths

Author(s)

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Examples

g_test_dataset_paths()

path <- system.file("testdata", package = "gDRtestData", mustWork = TRUE)
g_test_dataset_paths(path)
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