

# 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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**Enhanced**

**biocViews** ExperimentData, TechnologyData

**VignetteBuilder** knitr

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gDRtestData-package	<i>gDRtestData: gDRtestData - R data package with testing dose response data</i>
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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.

### Value

package help page

### Note

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

**Author(s)**

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

Authors:

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- Bartosz Czech
- Marc Hafner
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- Sergiu Mocanu
- Natalia Potocka
- Dariusz Scigocki
- Allison Voung

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add_concentration	<i>Add concentrations</i>
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**Description**

Add concentrations

**Usage**

```
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**

```
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 contains the cell line, drug, concentration, and replicate columns along with the annotations that needs 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()
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	<i>Cell lines</i>
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---

**Description**

Cell lines

**Value**

data.table

**Examples**

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

---

create_synthetic_cell_lines	<i>Create data.table with synthetic cell lines</i>
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---

**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`*Drugs*

---

**Description**

Drugs

**Value**

data.table

**Examples**

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

---

generate_ec50	<i>Calculate EC50 metric</i>
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**Description**

Calculate EC50 metric

**Usage**

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

**Arguments**

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

**Value**

matrix with random EC50

**Examples**

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

---

generate_e_inf	<i>Calculate E inf metric</i>
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**Description**

Calculate E inf metric

**Usage**

```
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

**Examples**

```
generate_e_inf(create_synthetic_drugs(), create_synthetic_cell_lines())
```

---

```
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), ])
```

---

*get\_test\_dataset\_paths*  
*get\_test\_dataset\_paths*

---

**Description**

Returns named vector of absolute paths to test datasets.

**Usage**

```
get_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**

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

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