

Package: gDRtestData (via r-universe)

October 10, 2026

Title gDRtestData - R data package with testing dose response data

Version 1.11.10

Date 2026-10-08

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 qs2 files with MAE data processed by gDR.

Depends R (>= 4.2)

Imports checkmate, data.table

Suggests BiocStyle, gDRstyle (>= 1.7.1), knitr, qs2, reshape2, rmarkdown, SummarizedExperiment, testthat, yaml

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

BugReports <https://github.com/gdrplatform/gDRtestData/issues>

biocViews ExperimentData, TechnologyData

VignetteBuilder knitr

License Artistic-2.0

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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	<i>Add data replicates</i>
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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	<i>Add data with day 0</i>
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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()
df_merged <- prepareData(cell_lines[seq_len(2), ], drugs[seq_len(4), ])
df_merged$Duration <- 72
df_merged$ReadoutValue <- 0
add_day0_data(df_merged)
```

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()

DepMap_CRISPRGeneEffect
<i>CRISPR Gene Effect Scores</i>

Description

Genome-wide CRISPR/Cas9 knockout dependency scores.

Format

Matrix with cell lines as rows and genes as columns

Loading

data.table::fread(system.file("depmap_data/CRISPRGeneEffect.csv.gz", package = "gDRtestData"))

Description

- Rows: Cell line identifiers
- Columns: NCBI gene IDs (Entrez format)
- Values: Dependency scores (-1 to +1); lower = more essential
- NA indicates insufficient screen coverage

Source

DepMap Portal - Data

Details

Downloaded May 26, 2026 from DepMap Portal (version 24Q4).
Citation: 24Q4 DepMap Release, including CRISPR Screens, PRISM Drug Screens, Copy Number, Mutation, Expression, and Fusions DepMap, Broad (2024). DepMap 24Q4 Public. Figshare+. Dataset. <https://doi.org/10.25452/figshare.plus.27993248.v1>

DepMap_Model

*DepMap Models (Cell Line Metadata)***Description**

Cell line information from DepMap Public 24Q4.

Format

Table

Loading

```
data.table::fread(system.file("depmap_data/Model.csv.gz", package = "gDRtestData"))
```

Description

- Rows: Cell line identifiers
- Columns: Metadata columns (see below)
- Values: Cell line annotations and donor demographics

Columns:

ModelID Unique cell line identifier (ACH-XXXXXX format)

CCLename Cell line name from Cancer Cell Line Encyclopedia (CCLE)

CellLineName Common cell line name (e.g., "A375", "HCT-116")

DepmapModelType Abbreviated ID for model type. For cancer models, from Oncotree; for other disease types, generated by DepMap

OncotreeLineage Primary cancer lineage classification (from Oncotree for cancer models, generated by DepMap for others)

OncotreePrimaryDisease Primary disease of model (from Oncotree for cancer models, generated by DepMap for others)

OncotreeSubtype Subtype classification of model (from Oncotree for cancer models, generated by DepMap for others)

OncotreeCode Oncotree code for cancer models; left blank if no corresponding code exists

PrimaryOrMetastasis Site of tumor origin (Primary/Metastatic/Recurrence/Other/Unknown)

Age Age at time of tissue sampling

AgeCategory Age category at time of sampling (Adult/Pediatric/Fetus/Unknown)

Sex Sex at time of sampling (Female/Male/Unknown)

PatientRace Patient/clinical indicated race (not derived)

Source

[DepMap Portal - Data](#)

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DepMap_OmicsCNGene	<i>Copy Number Variation (CNV)</i>
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Description

Gene-level copy number estimates from SNP microarray or WES.

Format

Matrix with cell lines as rows and genes as columns

Loading

```
data.table::fread(system.file("depmap_data/OmicsCNGene.csv.gz", package = "gDRtestData"))
```

Description

- Rows: Cell line identifiers
- Columns: NCBI gene IDs
- Values: Log2 ratio relative to diploid reference
- Typical range: -2 (deletion) to +3 (amplification)
- 0 = diploid (2 copies)

Source

[DepMap Portal - Data](#)

Details

Downloaded May 26, 2026 from DepMap Portal (version 24Q4).
Citation: 24Q4 DepMap Release, including CRISPR Screens, PRISM Drug Screens, Copy Number, Mutation, Expression, and Fusions DepMap, Broad (2024). DepMap 24Q4 Public. Figshare+. Dataset. <https://doi.org/10.25452/figshare.plus.27993248.v1>

DepMap_OmicsExpressionProteinCodingGenesTPMLogp1
<i>Gene Expression (Log2 TPM)</i>

Description

RNA-seq based gene expression for protein-coding genes.

Format

Matrix with cell lines as rows and genes as columns

Loading

```
data.table::fread( system.file("depmap_data/OmicsExpressionProteinCodingGenesTPMLogp1.csv.gz", package = "gDRtestData"))
```

Description

- Rows: Cell line identifiers
- Columns: NCBI gene IDs (Entrez format)
- Values: Log2(TPM + 1) transformed expression
- Only protein-coding genes included

Source

DepMap Portal - Data

Details

Downloaded May 26, 2026 from DepMap Portal (version 24Q4).
Citation: 24Q4 DepMap Release, including CRISPR Screens, PRISM Drug Screens, Copy Number, Mutation, Expression, and Fusions DepMap, Broad (2024). DepMap 24Q4 Public. Figshare+. Dataset. <https://doi.org/10.25452/figshare.plus.27993248.v1>

DepMap_OmicsSomaticMutationsMatrixDamaging
Somatic Mutations (Damaging)

Description

Binary matrix of damaging mutations (frame-shift, stop-gain, splice-site).

Format

Matrix with cell lines as rows and genes as columns

Loading

```
data.table::fread(system.file("depmap_data/OmicsSomaticMutationsMatrixDamaging.csv.gz", package = "gDRtestData"))
```

Description

- Rows: Cell line identifiers
- Columns: NCBI gene IDs
- Values: Binary (0 = no mutation, 1 = damaging mutation)
- High-confidence loss-of-function mutations

Source

[DepMap Portal - Data](#)

Details

Downloaded May 26, 2026 from DepMap Portal (version 24Q4).

Citation: 24Q4 DepMap Release, including CRISPR Screens, PRISM Drug Screens, Copy Number, Mutation, Expression, and Fusions DepMap, Broad (2024). DepMap 24Q4 Public. Figshare+. Dataset. <https://doi.org/10.25452/figshare.plus.27993248.v1>

DepMap_OmicsSomaticMutationsMatrixHotspot
Somatic Mutations (Hotspot)

Description

Binary matrix of known hotspot mutations from whole exome sequencing.

Format

Matrix with cell lines as rows and genes as columns

Loading

```
data.table::fread(system.file("depmap_data/OmicsSomaticMutationsMatrixHotspot.csv.gz", package = "gDRtestData"))
```

Description

- Rows: Cell line identifiers
- Columns: NCBI gene IDs
- Values: Binary (0 = no mutation, 1 = hotspot mutation)
- Hotspots defined by COSMIC and OncoKB

Source

[DepMap Portal - Data](#)

Details

Downloaded May 26, 2026 from DepMap Portal (version 24Q4).

Citation: 24Q4 DepMap Release, including CRISPR Screens, PRISM Drug Screens, Copy Number, Mutation, Expression, and Fusions DepMap, Broad (2024). DepMap 24Q4 Public. Figshare+. Dataset. <https://doi.org/10.25452/figshare.plus.27993248.v1>

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_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_hill_coef	<i>Generate hill coefficient</i>
--------------------	----------------------------------

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	<i>Generate response data</i>
------------------------	-------------------------------

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()
df_layout <- prepareData(cell_lines[seq_len(2), ], drugs[seq_len(4), ])
generate_response_data(df_layout)
```

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 qs2 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)
```

```
prepareCodilutionData  prepareCodilutionData
```

Description

Create data.table with input co-dilution data containing noise for testing purposes

Usage

```
prepareCodilutionData(  
  cell_lines,  
  drugs,  
  drugsIdx2 = 1,  
  conc = 10^(seq(-3, 1, 0.5)),  
  noise = 0.1  
)
```

Arguments

cell_lines	data.table with cell line info
drugs	data.table with drug info
drugsIdx2	numeric vector of ids for secondary drug (in drugs data.table)
conc	vector of doses
noise	number indicating level of noise

Value

data.table with input data for testing

Examples

```
prepareCodilutionData(create_synthetic_cell_lines()[seq_len(2), ],  
                       create_synthetic_drugs()[seq_len(4), ])
```

```
prepareComboMergedData  
  prepareComboMergedData
```

Description

Create data.table with input combination data containing noise for testing purposes

Usage

```
prepareComboMergedData(
  cell_lines,
  drugs,
  drugsIdx1 = 2:4,
  drugsIdx2 = c(26, 26, 26),
  concentration = c(0, 0.2, 1),
  noise = 0.1,
  modifyDf2 = FALSE
)
```

Arguments

cell_lines	data.table with cell line info
drugs	data.table with drug info
drugsIdx1	numeric vector of ids for primary drug
drugsIdx2	numeric vector of ids for secondary drug
concentration	numeric vector of doses
noise	number indicating level of noise
modifyDf2	Boolean indicating if the table should be modified to keep reverse single agent data

Value

data.table with input data for testing

Examples

```
prepareComboMergedData(create_synthetic_cell_lines(), create_synthetic_drugs())
```

prepareData	<i>prepareData</i>
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Description

Create data.table with input data for testing purposes

Usage

```
prepareData(cell_lines, drugs, conc = 10^(seq(-3, 1, 0.5)))
```

Arguments

cell_lines	data.table with cell line info
drugs	data.table with drug info
conc	vector of doses

Value

data.table with input data for testing

Examples

```
prepareData(create_synthetic_cell_lines(), create_synthetic_drugs())
```

prepareMergedData	<i>prepareMergedData</i>
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Description

Create data.table with input data containing noise for testing purposes

Usage

```
prepareMergedData(cell_lines, drugs, noise = 0.1)
```

Arguments

- cell_lines data.table with cell line info
- drugs data.table with drug info
- noise number indicating level of noise

Value

data.table with input data for testing

Examples

```
prepareMergedData(create_synthetic_cell_lines(), create_synthetic_drugs())
```

PRISMBroadScreen_Hagenbeek_NatComm_2026

PRISM Broad Screen Cancer Cell Line Viability Dataset

Description

The single-agent screening data from the PRISM platform - with one drug and 774 cell lines.

Format

A `MultiAssayExperiment` object containing a single-agent experiment with 5 assays.

Loading

```
gDRutils::get_synthetic_data("prism")
```

Description

Assays:

Experimental data matrices tracking cell line viability across processing stages:

RawTreated Raw intensity values for treated cell line pools.

Controls Raw intensity values for DMSO and killing controls.

Normalized Viability scores relative to controls.

Averaged Replicate-averaged viability scores.

Metrics Dose-response curve parameters (e.g., IC50, AUC).

Column Metadata (colData):

Feature metadata describing the cell lines (models) across assays:

clid Unique Broad Institute cell line identifier.

CellLineName Publicly recognized cancer cell line name.

Tissue Primary tissue of origin.

parental_identifier Identifier for the parental cell line.

subtype Histological or molecular subtype.

ReferenceDivisionTime Estimated doubling time in hours.

Row Metadata (rowData):

Feature metadata describing the treatment compounds across assays:

Gnumber Genentech compound identifier.

DrugName Public or commercial name of the tested compound.

drug_moa Mechanism of action / biological target of the drug.

Duration Exposure time of the cell lines to the compound (e.g., 72h).

Source

Hagenbeek, T.J., Zbieg, J., Smith, R. et al. Covalent pan-TEAD inhibitors block YAP activity and demonstrate brain penetrance in a Hippo-dependent cancer model. Nat Commun (2026). <https://doi.org/10.1038/s41467-026-74722-5>

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