Package 'gDRcore'

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Description This package contains core functions to process and analyze drug response data. The package provides tools for normalizing, averaging, and calculation of gDR metrics data. All core functions are wrapped into the pipeline function allowing analyzing the data in a straightforward way.

License Artistic-2.0

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`gDRcore-package` *gDRcore: Processing functions and interface to process and analyze drug dose-response data*

Description

This package contains core functions to process and analyze drug response data. The package provides tools for normalizing, averaging, and calculation of gDR metrics data. All core functions are wrapped into the pipeline function allowing analyzing the data in a straightforward way.

Value

package help page

Note

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

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See Also

Useful links:

- https://github.com/gdrplatform/gDRcore
- https://gdrplatform.github.io/gDRcore/
- Report bugs at https://github.com/gdrplatform/gDRcore/issues

---

.map_references *Map references*

Description

Map references

Usage

```
.map_references(
  mat_elem,
  rowData_colnames = c(gDRutils::get_env_identifiers("duration"), paste0(c("drug",
    "drug_name", "drug_moa"), "3"))
)
```

Arguments

mat_elem	input data frame
rowData_colnames	character vector of variables for the mapping of reference treatments

Details

Using the given rownames, map the treated and reference conditions.

Value

list

add_intermediate_data *add intermediate data (qs files) for given ma*

Description

add intermediate data (qs files) for given ma

Usage

```
add_intermediate_data(mae, data_dir, steps = get_pipeline_steps())
```

Arguments

mae	mae with dose-response data
data_dir	output directory
steps	character vector with pipeline steps for which intermediate data should be saved

Value

NULL

annotate_dt_with_cell_line *annotate_dt_with_cell_line*

Description

Annotate cell line data with the provided annotation table

Usage

```
annotate_dt_with_cell_line(data, cell_line_annotation, fill = "unknown")
```

Arguments

data	data.table with dose-response data
cell_line_annotation	data.table with cell line annotations
fill	string indicating how unknown cell lines should be filled in the DB

Value

data.table with annotated cell lines

Examples

```
data <- data.table::data.table(
  clid = c("CL1", "CL2", "CL3"),
  Gnumber = c("D1", "D2", "D3")
)
cell_line_annotation <- get_cell_line_annotation(data)
annotated_metadata <- annotate_dt_with_cell_line(data, cell_line_annotation)
```

annotate_dt_with_drug *annotate_dt_with_drug*

Description

Annotate drug data with the provided annotation table

Usage

```
annotate_dt_with_drug(data, drug_annotation, fill = "unknown")
```

Arguments

data	data.table with dose-response data
drug_annotation	data.table with drug annotations
fill	string indicating how unknown drugs should be filled in the DB

Value

data.table with annotated drugs

Examples

```
data <- data.table::data.table(
  clid = c("CL1", "CL2", "CL3"),
  Gnumber = c("D1", "D2", "D3")
)
drug_annotation <- get_drug_annotation(data)
annotated_metadata <- annotate_dt_with_drug(data, drug_annotation)
```

average_SE *Run drug response processing pipeline*

Description

Run different components of the gDR drug response processing pipeline. Either: create a SummarizedExperiment and normalize raw treated and control data (create_and_normalize_SE), average data (average_SE), or fit the processed data (fit_SE). See details for more in-depth explanations.

Usage

```
average_SE(
  se,
  data_type,
  series_identifiers = NULL,
  override_masked = FALSE,
  normalized_assay = "Normalized",
  averaged_assay = "Averaged"
)
```

```
create_SE(
  df_,
  data_type,
  readout = "ReadoutValue",
  nested_identifiers = NULL,
 nested_confounders = intersect(names(df_), gDRutils::get_env_identifiers("barcode")),
  override_untrt_controls = NULL
)

fit_SE(
  se,
  data_type = "single-agent",
  nested_identifiers = NULL,
  averaged_assay = "Averaged",
  metrics_assay = "Metrics",
  n_point_cutoff = 4,
  range_conc = c(0.005, 5),
  force_fit = FALSE,
  pcutoff = 0.05,
  cap = 0.1,
  curve_type = c("GR", "RV")
)

normalize_SE(
  se,
  data_type,
  nested_identifiers = NULL,
 nested_confounders = gDRutils::get_SE_identifiers(se, "barcode", simplify = TRUE),
  control_mean_fxn = function(x) {
     mean(x, trim = 0.25)
 },
  control_assay = "Controls",
  raw_treated_assay = "RawTreated",
  normalized_assay = "Normalized",
  ndigit_rounding = 4
)

create_and_normalize_SE(
  df_,
  data_type,
  readout = "ReadoutValue",
  control_mean_fxn = function(x) {
     mean(x, trim = 0.25)
 },
  nested_identifiers = NULL,
 nested_confounders = intersect(names(df_), gDRutils::get_env_identifiers("barcode")),
  override_untrt_controls = NULL,
  ndigit_rounding = 4,
  control_assay = "Controls",
  raw_treated_assay = "RawTreated",
  normalized_assay = "Normalized"
```

```
)

runDrugResponseProcessingPipeline(
  x,
  readout = "ReadoutValue",
  control_mean_fxn = function(x) {
     mean(x, trim = 0.25)
 },
  nested_identifiers_l = NULL,
  nested_confounders = gDRutils::get_env_identifiers("barcode"),
  override_untrt_controls = NULL,
  override_masked = FALSE,
  ndigit_rounding = 4,
  n_point_cutoff = 4,
  control_assay = "Controls",
  raw_treated_assay = "RawTreated",
  normalized_assay = "Normalized",
  averaged_assay = "Averaged",
  metrics_assay = "Metrics",
  split_data = TRUE,
  data_dir = NULL,
  partial_run = FALSE,
  start_from = get_pipeline_steps()[1],
  selected_experiments = NULL
)
```

Arguments

se	SummarizedExperiment object.
data_type	single-agent vs combination
series_identifiers	character vector of identifiers in measured or metric which define a unique data point.
override_masked	boolean indicating whether or not to override the masked wells in the averaging and include all wells. Defaults to FALSE.
normalized_assay	string of the assay name containing the normalized data. Defaults to "Normalized".
averaged_assay	string of the name of the averaged assay in the SummarizedExperiment. Defaults to "Averaged".
df_	data.table of raw drug response data containing both treated and untreated values. If a column called "BackgroundValue" exists in df_, it will be removed from the readout column.
readout	string of the name containing the cell viability readout values.
nested_identifiers	character vector with the nested_identifiers for the given SE with a given data_type
nested_confounders	Character vector of the nested_confounders for a given assay. nested_keys is character vector of column names to include in the data.tables in the assays of the resulting SummarizedExperiment object. Defaults to the nested_identifiers

and nested_confounders if passed through create_and_normalize_SE or runDrugResponseProcessingPipeline.

override_untrt_controls
named list containing defining factors in the treatments. Defaults to NULL.

metrics_assay string of the name of the metrics assay to output in the returned SummarizedExperiment Defaults to "Metrics".

n_point_cutoff integer of how many points should be considered the minimum required to try to fit a curve. Defaults to 4.

range_conc vector of concetrations range values.

force_fit boolean indicating whether or not to force the fit.

pcutoff numeric cutoff value.

cap numeric value representing the value to cap the highest allowed relative viability at.

curve_type vector of curve type values.

control_mean_fxn
function indicating how to average controls. Defaults to mean(x, trim = 0.25).

control_assay string containing the name of the assay representing the controls in the se. Defaults to "Controls".

raw_treated_assay
string containing the name of the assay representing the raw treated data in the se. Defaults to "RawTreated".

ndigit_rounding
integer indicating number of digits to round to in calculations. Defaults to 4.

x data.table of MAE with drug response data

nested_identifiers_l
list with the nested_identifiers(character v ectors) for single-agent and (optionally) for combination data

split_data boolean indicating whether data provided as the MultiAssayExperiment should be split again into appropriate data types

data_dir string with the path to the directory with intermediate data of experiments (qs files). If set to NULL (default) intermediate data is not saved/read in.

partial_run logical flag indicating if the pipeline should be run partially (from the step defined with start_from)

start_from string indicating the pipeline step from which partial run should be launched

selected_experiments
character vector with experiments for which pipeline should be run. This option works only for the pipeline being run partially (i.e. with partial_run flag set to TRUE)

Details

runDrugResponseProcessingPipeline is made up of 3 separate steps:

- "create_and_normalize_SE"
- "average_SE"
- "fit_SE"

For create_and_normalize_SE, this creates a SummarizedExperiment object from a data.table, where the data.table contains treatments on rows, and conditions on columns. A SummarizedExperiment object containing two asssays is created: treated readouts will live in an assay called "RawTreated", and reference readouts live in an assay called "Controls". Subsequently, the treated and control elements will be normalized to output two metrics:

For average_SE, take the normalized assay and average the nested DataFrames across uniquenested_identifiers.

For fit_SE, take the averaged assay and fit curves to obtain metrics, one set of metrics for each normalization type set.

Pipeline can be run partially with partial_run flag set to TRUE. The start_from string defines the step from which the pipeline will be launched. However, partial run of the pipeline is possible only if the whole pipeline was launched at least once with defined data_dir and intermediate data was saved as qs files into data_dir.

Pipeline can be run for the selected experiments by changing the default value of selected_experiments param. This scenario only works when partial_run is enabled.

Value

MAE object

Examples

```
d <- rep(seq(0.1, 0.9, 0.1), each = 4)
v <- rep(seq(0.1, 0.4, 0.1), 9)
df <- S4Vectors::DataFrame(
  Concentration = d,
  masked = rep(c(TRUE, TRUE, TRUE, FALSE), 9),
  normalization_type = rep(c("GR", "RV"), length(v) * 2),
  x = rep(v, 2)
)
normalized <- BumpyMatrix::splitAsBumpyMatrix(row = 1, column = 1, x = df)

keys <- list(Trt = "Concentration", "masked_tag" = "masked")
assays <- list("Normalized" = normalized)
se <- SummarizedExperiment::SummarizedExperiment(assays = assays)
se <- gDRutils::set_SE_keys(se, keys)
se <- gDRutils::set_SE_identifiers(se, gDRutils::get_env_identifiers())
se1 <- average_SE(
  se,
  data_type = "single-agent",
  override_masked = FALSE,
  normalized_assay = "Normalized",
  averaged_assay = "Averaged"
)


td <- gDRimport::get_test_data()
l_tbl <- gDRimport::load_data(
  manifest_file = gDRimport::manifest_path(td),
  df_template_files = gDRimport::template_path(td),
  results_file = gDRimport::result_path(td)
)
imported_data <- merge_data(
  l_tbl$manifest,
  l_tbl$treatments,
```

```
  l_tbl$data
)

se <- purrr::quietly(create_SE)(imported_data, data_type = "single-agent")


td <- gDRimport::get_test_data()
l_tbl <- gDRimport::load_data(
  manifest_file = gDRimport::manifest_path(td),
  df_template_files = gDRimport::template_path(td),
  results_file = gDRimport::result_path(td)
)
imported_data <- merge_data(
  l_tbl$manifest,
  l_tbl$treatments,
  l_tbl$data
)

inl <- prepare_input(imported_data)
se <- create_SE(
 inl$df_list[["single-agent"]],
 data_type = "single-agent",
 nested_confounders = inl$nested_confounders)

normalize_SE(se, data_type = "single-agent")
p_dir <- file.path(tempdir(), "pcheck")
dir.create(p_dir)
td <- gDRimport::get_test_data()
l_tbl <- gDRimport::load_data(
  manifest_file = gDRimport::manifest_path(td),
  df_template_files = gDRimport::template_path(td),
  results_file = gDRimport::result_path(td)
)
imported_data <- merge_data(
  l_tbl$manifest,
  l_tbl$treatments,
  l_tbl$data
)
runDrugResponseProcessingPipeline(
  imported_data,
  data_dir = p_dir
)
```

`calculate_excess` *Calculate the difference between values in two data.tables*

Description

Calculate the difference between values, likely representing the same metric, from two data.tables.

Usage

```
calculate_excess(
```

```
  metric,
  measured,
  series_identifiers,
  metric_col,
  measured_col
)
```

Arguments

metric	data.table often representing readouts derived by calculating some metric. Examples of this could include hsa or bliss calculations from single-agent data.
measured	data.table often representing measured data from an experiment.
series_identifiers	character vector of identifiers in measured or metric which define a unique data point.
metric_col	string of the column in metric to use in excess calculation.
measured_col	string of the column in measured to use in excess calculation.

Value

data.table of measured, now with an additional column named excess (positive values for synergy/benefit).

Examples

```
metric <- data.table::data.table(
  Concentration = c(1, 2, 3, 1, 2, 3),
  Concentration_2 = c(1, 1, 1, 2, 2, 2),
  GRvalue = c(100, 200, 300, 400, 500, 600)
)
measured <- data.table::data.table(
  Concentration = c(3, 1, 2, 2, 1, 3),
  Concentration_2 = c(1, 1, 1, 2, 2, 2),
  testvalue = c(200, 0, 100, 400, 300, 500)
)
series_identifiers <- c("Concentration", "Concentration_2")
metric_col <- "GRvalue"
measured_col <- "testvalue"
calculate_excess(
  metric,
  measured,
  series_identifiers,
  metric_col,
  measured_col
)
```

`calculate_GR_value` *Calculate a GR value.*

Description

Calculate a GR value for a given set of dose response values.

Usage

```
calculate_GR_value(
  rel_viability,
  corrected_readout,
  day0_readout,
  untrt_readout,
  ndigit_rounding,
  duration,
  ref_div_time,
  cap = 1.25
)

calculate_time_dep_GR_value(
  corrected_readout,
  day0_readout,
  untrt_readout,
  ndigit_rounding
)

calculate_endpt_GR_value(
  rel_viability,
  duration,
  ref_div_time,
  cap = 1.25,
  ndigit_rounding
)
```

Arguments

`rel_viability`	numeric vector representing the Relative Viability.
`corrected_readout`	numeric vector containing the corrected readout.
`day0_readout`	numeric vector containing the day 0 readout.
`untrt_readout`	numeric vector containing the untreated readout.
`ndigit_rounding`	integer specifying the number of digits to use for calculation rounding.
`duration`	numeric value specifying the length of time the cells were treated (in hours).
`ref_div_time`	numeric value specifying the reference division time for the cell line in the experiment.
`cap`	numeric value representing the value to cap the highest allowed relative viability at.

Details

Note that this function expects that all numeric vectors are of the same length. `calculate_GR_value` will try to greedily calculate a GR value. If no day 0 readouts are available, the `duration` and `ref_div_time` will be used to try to back-calculate a day 0 value in order to produce a GR value.

In the case of calculating the reference GR value from multiple reference readout values, the vectorized calculation is performed and then the resulting vector should be averaged outside of this function.

Note that it is expected that the `ref_div_time` and `duration` are reported in the same units.

Value

numeric vector containing GR values, one value for each element of the input vectors.

See Also

normalize_SE2

Examples

```
duration <- 144
rv <- seq(0.1, 1, 0.1)
corrected <- seq(41000, 50000, 1000)
day0 <- seq(91000, 95500, 500)
untrt <- rep(c(115000, 118000), 5)

calculate_GR_value(
  rel_viability = rv,
  corrected_readout = corrected,
  day0_readout = day0,
  untrt_readout = untrt,
  ndigit_rounding = 4,
  duration = duration,
  ref_div_time = duration / 2
)

readouts <- rep(10000, 5)
calculate_time_dep_GR_value(readouts, readouts * 1.32, readouts * 2, 2)

readouts <- rep(10000, 5)
calculate_endpt_GR_value(readouts, 72, 1, ndigit_rounding = 2)
```

---

calculate_matrix_metric

Calculate a metric for combination data.

Description

Calculate a metric based off of single-agent values in combination screens.

Usage

```
calculate_HSA(sa1, series_id1, sa2, series_id2, metric)

calculate_Bliss(
  sa1,
  series_id1,
  sa2,
  series_id2,
  metric,
  measured_col = "smooth"
)

.calculate_matrix_metric(
  sa1,
  series_id1,
  sa2,
  series_id2,
  metric,
  FXN,
  measured_col = "x"
)
```

Arguments

sa1	data.table containing single agent data where entries in series_id2 are all 0. Columns of the data.table include identifiers and the metric of interest. Metric is stored in the 'x' column.
series_id1	String representing the column within sa1 that represents id1.
sa2	data.table containing single agent data where entries in series_id1 are all 0. Columns of the data.table include identifiers and the metric of interest.n Metric is stored in the 'x' column.
series_id2	String representing the column within sa2 that represents id2.
metric	String specifying the metric of interest. Usually either 'GRvalue' or 'Relative-Viability'.
measured_col	String specyfying the measured colname.
FXN	Function to apply to the single-agent fits to calculate a metric.

Details

calculate_HSA takes the minimum of the two single agents readouts. calculate_Bliss performs Bliss additivity calculation based on the single agent effects, defined as 1-x for the corresponding normalization. See https://www.sciencedirect.com/science/article/pii/S1359644619303460?via%3Dihub#tb0005 for more details.

Value

data.table containing a single row for every unique combination of the two series identifiers and the corresponding calculated metric for each row.

Examples

```
n <- 10
sa1 <- data.table::data.table(conc = seq(n), conc2 = rep(0, n), smooth = seq(n))
sa2 <- data.table::data.table(conc = rep(0, n), conc2 = seq(n), smooth = seq(n))
calculate_HSA(sa1, "conc", sa2, "conc2", "smooth")
n <- 10
sa1 <- data.table::data.table(conc = seq(n), conc2 = rep(0, n), smooth = seq(n))
sa2 <- data.table::data.table(conc = rep(0, n), conc2 = seq(n), smooth = seq(n))
calculate_Bliss(sa1, "conc", sa2, "conc2", "smooth")
```

---

calculate_score *Calculate score for HSA and Bliss*

Description

Calculate score for HSA and Bliss

Usage

```
calculate_score(excess)
```

Arguments

excess	numeric vector with excess

Value

numeric vector with calculated score

Examples

```
metric <- data.table::data.table(
  Concentration = c(1, 2, 3, 1, 2, 3),
  Concentration_2 = c(1, 1, 1, 2, 2, 2),
  GRvalue = c(100, 200, 300, 400, 500, 600)
)
measured <- data.table::data.table(
  Concentration = c(3, 1, 2, 2, 1, 3),
  Concentration_2 = c(1, 1, 1, 2, 2, 2),
  testvalue = c(200, 0, 100, 400, 300, 500)
)
series_identifiers <- c("Concentration", "Concentration_2")
metric_col <- "GRvalue"
measured_col <- "testvalue"
x <- calculate_excess(
  metric,
  measured,
  series_identifiers,
  metric_col,
  measured_col
)
calculate_score(x$x)
```

cleanup_metadata *cleanup_metadata*

Description

Cleanup a data.table with metadata

Usage

```
cleanup_metadata(df_metadata)
```

Arguments

df_metadata	a data.table with metadata

Details

Adds annotations and check whether user provided correct input data.

Value

a data.table with cleaned metadata

Examples

```
df <- data.table::data.table(
  clid = "CELL_LINE",
  Gnumber = "DRUG_1",
  Concentration = c(0, 1),
  Duration = 72
)
cleanup_df <- cleanup_metadata(df)
```

convert_mae_to_raw_data *Transform mae into raw data*

Description

Transform mae into raw data

Usage

```
convert_mae_to_raw_data(mae)
```

Arguments

mae	MultiAssayExperiment object with SummarizedExperiments containing "RawTreated" and "Controls" assays

Value

data.table with raw data

Examples

```
mae <- gDRutils::get_synthetic_data("finalMAE_small")
convert_mae_to_raw_data(mae)
```

`convert_se_to_raw_data` *Transform se into raw_data*

Description

Transform se into raw_data

Usage

```
convert_se_to_raw_data(se)
```

Arguments

se	SummarizedExperiment object with "RawTreated" and "Controls" assays

Value

data.table with raw data

Examples

```
mae <- gDRutils::get_synthetic_data("finalMAE_small")
se <- mae[[1]]
convert_se_to_raw_data(se)
```

`data_model` *Detect model of data*

Description

Detect model of data

Usage

```
data_model(x)
```

Arguments

x	data.table with raw data or SummarizedExperiment object with gDR assays

Value

string with the information of the raw data follows single-agent or combination data model

Examples

```
data_model("single-agent")
```

---

data_model.character *Detect model of data from experiment name*

Description

Detect model of data from experiment name

Usage

```
## S3 method for class 'character'
data_model(x)
```

Arguments

x	character with experiment name

Value

string with the information of the raw data follows single-agent or combination data model

---

data_model.data.table *Detect model of data in data.table*

Description

Detect model of data in data.table

Usage

```
## S3 method for class 'data.table'
data_model(x)
```

Arguments

x	data.table of raw drug response data containing both treated and untreated values.

Value

string with the information of the raw data follows single-agent or combination data model

do_skip_step *check if the given step can be skipped if partial run is chosen*

Description

check if the given step can be skipped if partial run is chosen

Usage

```
do_skip_step(current_step, start_from, steps = get_pipeline_steps())
```

Arguments

current_step	string with the step to be evaluated
start_from	string indicating the pipeline step from which partial run should be launched
steps	charvect with all available steps

Value

logical

fit_SE.combinations *fit_SE for combination screens*

Description

Perform fittings for combination screens.

Usage

```
fit_SE.combinations(
  se,
  data_type = gDRutils::get_supported_experiments("combo"),
  series_identifiers = NULL,
  normalization_types = c("GR", "RV"),
  averaged_assay = "Averaged",
  metrics_assay = "Metrics",
  score_FUN = calculate_score
)
```

Arguments

se	SummarizedExperiment object with a BumpyMatrix assay containing averaged data.
data_type	single-agent vs combination
series_identifiers	character vector of the column names in the nested DFrame corresponding to nested identifiers.

normalization_types
: character vector of normalization types used for calculating combo matrix.

averaged_assay
: string of the name of the averaged assay to use as input. in the se.

metrics_assay
: string of the name of the metrics assay to output in the returned SummarizedExperiment. whose combination represents a unique series for which to fit curves.

score_FUN
: function used to calculate score for HSA and Bliss

Details

This function assumes that the combination is set up with both concentrations nested in the assay.

Value

A SummarizedExperiment object with an additional assay containing the combination metrics.

Examples

```
fmae_cms <- gDRutils::get_synthetic_data("finalMAE_combo_matrix_small")

se1 <- fmae_cms[[gDRutils::get_supported_experiments("combo")]]
SummarizedExperiment::assays(se1) <-
  SummarizedExperiment::assays(se1)["Averaged"]
fit_SE.combinations(se1[1, 1])
```

---

generateCodilution *generateCodilution*

Description

generateCodilution

Usage

```
generateCodilution(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateCodilutionSmall *generateCodilutionSmall*

Description

generateCodilutionSmall

Usage

```
generateCodilutionSmall(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateComboMatrix *generateComboMatrix*

Description

generateComboMatrix

Usage

```
generateComboMatrix(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateComboMatrixSmall *generateComboMatrixSmall*

Description

generateComboMatrixSmall

Usage

```
generateComboMatrixSmall(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateComboNoNoiseData
generateComboNoNoiseData

Description

generateComboNoNoiseData

Usage

```
generateComboNoNoiseData(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateComboNoNoiseData2
generateComboNoNoiseData2

Description

generateComboNoNoiseData2

Usage

```
generateComboNoNoiseData2(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateComboNoNoiseData3
generateComboNoNoiseData3

Description

generateComboNoNoiseData3

Usage

```
generateComboNoNoiseData3(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateLigandData *generateLigandData*

Description

generateLigandData

Usage

```
generateLigandData(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateMediumData *generateMediumData*

Description

generateMediumData

Usage

```
generateMediumData(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

generateNoiseRawData *generateNoiseRawData*

Description

generateNoiseRawData

Usage

```
generateNoiseRawData(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

`generateNoNoiseRawData` *generateNoNoiseRawData*

Description

generateNoNoiseRawData

Usage

```
generateNoNoiseRawData(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

`generateTripleComboMatrix` *generateTripleComboMatrix*

Description

generateTripleComboMatrix

Usage

```
generateTripleComboMatrix(cell_lines, drugs, save = TRUE)
```

Value

data.table with raw input data or MAE with processed data

`get_assays_per_pipeline_step` *get info about created/present assays in SE at the given pipeline step*

Description

get info about created/present assays in SE at the given pipeline step

Usage

```
get_assays_per_pipeline_step(
  step,
  data_model,
  status = c("created", "present")
)
```

Arguments

step	string with pipeline step
data_model	single-agent vs combination
status	string return vector of assays created or present at the given step?

Value

assay

---

get_cellline_annotation_from_dt

Retrieve the cell line annotation from the annotated dt input

---

Description

Retrieve the cell line annotation from the annotated dt input

Usage

```
get_cellline_annotation_from_dt(dt)
```

Arguments

dt	annotated data.table

Value

data.table with cell line annotation

Examples

```
dt <- data.table::data.table(Gnumber = "A",
clid = "CL123",
CellLineName = "cl name",
Tissue = "Bone",
parental_identifier = "some cl",
subtype = "cortical",
ReferenceDivisionTime = 5)
get_cellline_annotation_from_dt(dt)
```

get_cell_line_annotation *get_cell_line_annotation*

Description

Get cell line annotation data table

Usage

```
get_cell_line_annotation(
  data,
  fname = "cell_lines.csv",
  fill = "unknown",
  annotation_package = if ("gDRinternal" %in% .packages(all.available = TRUE)) {

    "gDRinternal"
 } else {
     "gDRtestData"
 }
)
```

Arguments

data	data.table with cell line identifiers to be matched
fname	string with file name containing the annotation
fill	string indicating how unknown cell lines should be filled in the DB
annotation_package	string indicating name of the package containing cell line annotation

Value

data.table with cell line annotations

Examples

```
data <- data.table::data.table(clid = c("CL1", "CL2", "CL3"))
cell_line_annotation <- get_cell_line_annotation(data)
```

get_default_nested_identifiers *Get default nested identifiers*

Description

Get default nested identifiers

Usage

```
get_default_nested_identifiers(x, data_model = NULL)

## S3 method for class 'data.table'
get_default_nested_identifiers(x, data_model = NULL)

## S3 method for class 'SummarizedExperiment'
get_default_nested_identifiers(x, data_model = NULL)
```

Arguments

x	data.table with raw data or SummarizedExperiment object with gDR assays
data_model	single-agent vs combination

Value

vector of nested identifiers

Examples

```
get_default_nested_identifiers(data.table::data.table())
```

`get_drug_annotation` *get_drug_annotation*

Description

Get drug annotation data table

Usage

```
get_drug_annotation(
  data,
  fname = "drugs.csv",
  fill = "unknown",
  annotation_package = if ("gDRinternal" %in% .packages(all.available = TRUE)) {

    "gDRinternal"
 } else {
    "gDRtestData"
 }
)
```

Arguments

data	data.table with drug identifiers to be matched
fname	string with file name containing the annotation
fill	string indicating how unknown drugs should be filled in the DB
annotation_package	string indicating name of the package containing drug annotation

Value

data.table with drug annotations

Examples

```
data <- data.table::data.table(Gnumber = c("drug1", "drug2", "drug3"))
drug_annotation <- get_drug_annotation(data)
```

---

get_drug_annotation_from_dt

Retrieve the drug annotation from the annotated dt input

Description

Retrieve the drug annotation from the annotated dt input

Usage

```
get_drug_annotation_from_dt(dt)
```

Arguments

dt	annotated data.table

Value

data.table with drug annotation

Examples

```
dt <- data.table::data.table(Gnumber = "A",
DrugName = "drugA",
drug_moa = "drug_moa_A")
get_drug_annotation_from_dt(dt)
```

---

get_mae_from_intermediate_data

get mae dataset from intermediate data

Description

get mae dataset from intermediate data

Usage

```
get_mae_from_intermediate_data(data_dir)
```

Arguments

data_dir	directory with intermediate data

Value

MAE object

`get_pipeline_steps` *get pipeline steps*

Description

get pipeline steps

Usage

```
get_pipeline_steps()
```

Value

vector with steps

`get_relevant_ids` *Function to get relevant identifiers from the environment*

Description

Function to get relevant identifiers from the environment

Usage

```
get_relevant_ids(identifiers, dt)
```

Arguments

`identifiers`	A character vector of identifier names to fetch from the environment
`dt`	A data.table containing the columns to be checked against the identifiers

Value

A character vector of relevant identifiers that are present in the data.table

grr_matches *Value Matching*

Description

Returns a lookup table or list of the positions of ALL matches of its first argument in its second and vice versa. Similar to match, though that function only returns the first match.

Usage

```
grr_matches(
  x,
  y,
  all.x = TRUE,
  all.y = TRUE,
  list = FALSE,
  indexes = TRUE,
  nomatch = NA
)
```

Arguments

x	vector. The values to be matched. Long vectors are not currently supported.
y	vector. The values to be matched. Long vectors are not currently supported.
all.x	logical; if TRUE, then each value in x will be included even if it has no matching values in y
all.y	logical; if TRUE, then each value in y will be included even if it has no matching values in x
list	logical. If TRUE, the result will be returned as a list of vectors, each vector being the matching values in y. If FALSE, result is returned as a data.table with repeated values for each match.
indexes	logical. Whether to return the indices of the matches or the actual values.
nomatch	the value to be returned in the case when no match is found. If not provided and indexes=TRUE, items with no match will be represented as NA. If set to NULL, items with no match will be set to an index value of length+1. If indexes=FALSE, they will default to NA.

Details

This behavior can be imitated by using joins to create lookup tables, but matches is simpler and faster: usually faster than the best joins in other packages and thousands of times faster than the built in merge.

all.x/all.y correspond to the four types of database joins in the following way:

left all.x=TRUE, all.y=FALSE

right all.x=FALSE, all.y=TRUE

inner all.x=FALSE, all.y=FALSE

full all.x=TRUE, all.y=TRUE

Note that NA values will match other NA values.

Source of the function: https://github.com/cran/grr/blob/master/R/grr.R

Value

data.table

Examples

```
mat_elem <- data.table::data.table(
  DrugName = rep(c("untreated", "drugA", "drugB", "untreated"), 2),
  DrugName_2 = rep(c("untreated", "vehicle", "drugA", "drugB"), 2),
  clid = rep(c("C1", "C2"), each = 4)
)
untreated_tag <- gDRutils::get_env_identifiers("untreated_tag")
ref_idx <- which(
  mat_elem$DrugName %in% untreated_tag |
   mat_elem$DrugName_2 %in% untreated_tag
)
ref <- mat_elem[ref_idx, ]
treated <- mat_elem[-ref_idx, ]
valid <- c("DrugName", "DrugName_2")
trt <- lapply(valid, function(x) {
  colnames <- c("clid", x)
  treated[, colnames, with = FALSE]
})
trt <- do.call(paste,
  do.call(rbind, lapply(trt, function(x) setNames(x, names(trt[[1]]))))
)
ref <- lapply(valid, function(x) {
  colnames <- c("clid", x)
  ref[, colnames, with = FALSE]
})
ref <- do.call(paste,
  do.call(rbind, lapply(ref, function(x) setNames(x, names(ref[[1]]))))
)
grr_matches(trt, ref, list = FALSE, all.y = FALSE)
```

---

identify_data_type *Identify type of data*

Description

Identify type of data

Usage

```
identify_data_type(dt, codilution_conc = 2, matrix_conc = 1)
```

Arguments

dt	data.table of raw drug response data containing both treated and untreated values
codilution_conc	integer of maximum number of concentration ratio of co-treatment to classify as codilution data type; defaults to 2
matrix_conc	integer of minimum number of concentration pairs of co-treatment to classify as co-treatment or matrix data type; defaults to 1

Value

data.table of raw drug response data with additional column `type` with the info of data type for a given row of data.table

Author(s)

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Examples

```
conc <- rep(seq(0, 0.3, 0.1), 2)
ctrl_dt <- S4Vectors::DataFrame(
  ReadoutValue = c(2, 2, 1, 1, 2, 1),
  Concentration = rep(0, 6),
  masked = FALSE,
  DrugName = rep(c("DRUG_10", "vehicle", "DRUG_8"), 2),
  CellLineName = "CELL1"
)

trt_dt <- S4Vectors::DataFrame(
  ReadoutValue = rep(seq(1, 4, 1), 2),
  Concentration = conc,
  masked = rep(FALSE, 8),
  DrugName = c("DRUG_10", "DRUG_8"),
  CellLineName = "CELL1"
)
input_dt <- data.table::as.data.table(rbind(ctrl_dt, trt_dt))
input_dt$Duration <- 72
input_dt$CorrectedReadout2 <- input_dt$ReadoutValue
identify_data_type(input_dt)
```

---

identify_keys *identify_keys*

Description

Group columns from a data.table that correspond to different

Usage

```
identify_keys(
  df_,
  nested_keys = NULL,
  override_untrt_controls = NULL,
  identifiers = gDRutils::get_env_identifiers()
)
```

Arguments

`df_`	a data.table to identify keys for.
`nested_keys`	character vector of keys to exclude from the returned list. The keys discarded should be identical to the keys in the third dimension of the SummarizedExperiment. Defaults to the `"Barcode"` and the `masked` identifier.

override_untrt_controls
: named list containing defining factors in the treatments. Defaults to NULL.

identifiers
: named list containing all identifiers to use during processing. By default, this value will be obtained by the environment.

Details

This is most likely to be used for provenance tracking and will be placed on the SummarizedExperiment metadata for downstream analyses to reference.

Value

named list of key types and their corresponding key values.

See Also

map_df, create_SE

Examples

```
n <- 64
md_df <- data.table::data.table(
  Gnumber = rep(c("vehicle", "untreated", paste0("G", seq(2))), each = 16),
  DrugName = rep(c("vehicle", "untreated", paste0("GN", seq(2))), each = 16),
  clid = paste0("C", rep_len(seq(4), n)),
  CellLineName = paste0("N", rep_len(seq(4), n)),
  replicates = rep_len(paste0("R", rep(seq(4), each = 4)), 64),
  drug_moa = "inhibitor",
  ReferenceDivisionTime = rep_len(c(120, 60), n),
  Tissue = "Lung",
  parental_identifier = "CL12345",
  Duration = 160
)
md_df <- unique(md_df)
ref <- md_df$Gnumber %in% c("vehicle", "untreated")
trt_df <- md_df[!ref, ]
identify_keys(trt_df)
```

---

is_preceding_step *check if the given step is preceding the step chosen in the partial run*

Description

check if the given step is preceding the step chosen in the partial run

Usage

```
is_preceding_step(current_step, start_from, steps = get_pipeline_steps())
```

Arguments

current_step	string with the step to be evaluated
start_from	string indicating the pipeline step from which partial run should be launched
steps	charvect with all available steps

Value

logical

---

map_df *Map treated conditions to their respective references.*

Description

Map treated conditions to their respective Day0, untreated, or single-agent references using condition metadata.

Usage

```
map_df(
  trt_md,
  ref_md,
  override_untrt_controls = NULL,
  ref_cols,
  ref_type = c("Day0", "untrt_Endpoint")
)
```

Arguments

trt_md	data.table of treated metadata.
ref_md	data.table of untreated metadata.
override_untrt_controls	named list indicating what treatment metadata fields should be used as a control. Defaults to NULL.
ref_cols	character vector of the names of reference columns to include. Likely obtained from identify_keys().
ref_type	string of the reference type to map to. Should be one of c("Day0", "untrt_Endpoint", "ref_Endpoint").

Details

If override_untrt_controls is specified, TODO: FILL ME!

Value

named list mapping treated metadata to untreated metadata.

See Also

identify_keys

Examples

```
n <- 64
md_df <- data.table::data.table(
  Gnumber = rep(c("vehicle", "untreated", paste0("G", seq(2))), each = 16),
  DrugName = rep(c("vehicle", "untreated", paste0("GN", seq(2))), each = 16),
  clid = paste0("C", rep_len(seq(4), n)),
  CellLineName = paste0("N", rep_len(seq(4), n)),
  replicates = rep_len(paste0("R", rep(seq(4), each = 4)), 64),
  drug_moa = "inhibitor",
  ReferenceDivisionTime = rep_len(c(120, 60), n),
  Tissue = "Lung",
  parental_identifier = "CL12345",
  Duration = 160
)
md_df <- unique(md_df)
ref <- md_df$Gnumber %in% c("vehicle", "untreated")
ref_df <- md_df[ref, ]
trt_df <- md_df[!ref, ]
Keys <- identify_keys(trt_df)
ref_type <- "untrt_Endpoint"
map_df(
  trt_df,
  ref_df,
  ref_cols = Keys[[ref_type]],
  ref_type = ref_type
)
```

`map_ids_to_fits` *Get predicted values for a given fit and input.*

Description

Map fittings to identifiers and compute the predicted values for corresponding fits.

Usage

```
map_ids_to_fits(pred, match_col, fittings, fitting_id_col)
```

Arguments

`pred`	numeric vector for which you want predictions.
`match_col`	vector to match on `fittings` to get the correct fit.
`fittings`	data.table of fit metrics.
`fitting_id_col`	string of the column name in `fittings` that should be used to match with `match_col` .

Value

Numeric vector of predicted values given `pred` inputs and `fittings` values.

Examples

```
pred <- c(1, 5, 5)
match_col <- c(1, 1, 2)
fitting_id_col <- "match_on_me"

fit1 <- data.table::data.table(h = 2.09, x_inf = 0.68, x_0 = 1, ec50 = 0.003)
fit2 <- data.table::data.table(h = 0.906, x_inf = 0.46, x_0 = 1, ec50 = 0.001)
fittings <- do.call(rbind, list(fit1, fit2))
fittings[[fitting_id_col]] <- c(1, 2)

map_ids_to_fits(pred, match_col, fittings, fitting_id_col)
```

---

map_untreated *Identify untreated rows based on Drug treatment alone*

Description

Identify untreated rows based on Drug treatment alone

Usage

```
map_untreated(mat_elem)
```

Arguments

mat_elem	input data frame

Details

Using the given rownames, map the untreated conditions

Value

list

---

merge_data *merge_data*

Description

Merge all the input data into a single data.table

Usage

```
merge_data(manifest, treatments, data)
```

Arguments

manifest	a data.table with a manifest info
treatments	a data.table with a treaatments info
data	a data.table with a raw data info

Value

a data.table with merged data and metadata.

Examples

```
td <- gDRimport::get_test_data()
l_tbl <- gDRimport::load_data(
  manifest_file = gDRimport::manifest_path(td),
  df_template_files = gDRimport::template_path(td),
  results_file = gDRimport::result_path(td)
)
merge_data(
  l_tbl$manifest,
  l_tbl$treatments,
  l_tbl$data
)
```

---

order_result_df *Order_result_df*

Description

Order a data.table with results

Usage

```
order_result_df(df_)
```

Arguments

df_	a data.table with results

Value

a ordered data.table with results

---

prepare_input *Prepare input data common for all experiments*

Description

Current steps

- refining nested confounders
- refining nested identifiers
- splitting df_ into (per experiment) df_list

Usage

```
prepare_input(x, ...)
```

Arguments

x	data.table with raw data or MAE object with dose-response data
...	additional parameters

Value

list of input data

Examples

```
td <- gDRimport::get_test_data()
l_tbl <- gDRimport::load_data(
  manifest_file = gDRimport::manifest_path(td),
  df_template_files = gDRimport::template_path(td),
  results_file = gDRimport::result_path(td)
)
df_ <- merge_data(
  l_tbl$manifest,
  l_tbl$treatments,
  l_tbl$data
)
nested_confounders = intersect(
  names(df_),
  gDRutils::get_env_identifiers("barcode")
)
prepare_input(df_, nested_confounders, NULL)
```

---

prepare_input.data.table

Prepare input data common for all experiments

Description

Current steps

- refining nested confounders
- refining nested identifiers
- splitting df_ into (per experiment) df_list

Usage

```
## S3 method for class 'data.table'
prepare_input(
  x,
  nested_confounders = gDRutils::get_env_identifiers("barcode"),
  nested_identifiers_l = .get_default_nested_identifiers(),
  ...
)
```

Arguments

x	data.table with raw data
nested_confounders	Character vector of the nested_confounders for a given assay. nested_keys is character vector of column names to include in the data.tables in the assays of the resulting SummarizedExperiment object. Defaults to the nested_identifiers and nested_confounders if passed through
nested_identifiers_l	list with the nested_identifiers(character vectors) for single-agent and (optionally) for combination data
...	additional parameters

Value

list of input data

---

prepare_input.MultiAssayExperiment

Prepare input data common for all experiments

Description

Current steps

- refining nested confounders
- refining nested identifiers
- splitting df_ into (per experiment) df_list

Usage

```
## S3 method for class 'MultiAssayExperiment'
prepare_input(
  x,
  nested_confounders = gDRutils::get_SE_identifiers(x[[1]], "barcode"),
  nested_identifiers_l = .get_default_nested_identifiers(x[[1]]),
  raw_data_field = "experiment_raw_data",
  split_data = TRUE,
  ...
)
```

Arguments

x	MAE object with dose-response data
nested_confounders	Character vector of the nested_confounders for a given assay. nested_keys is character vector of column names to include in the data.tables in the assays of the resulting SummarizedExperiment object. Defaults to the nested_identifiers and nested_confounders if passed through

`nested_identifiers_l`
: list with the nested_identifiers(character vectors) for `single-agent` and (optionally) for `combination` data

`raw_data_field`
: metadata field with raw data

`split_data`
: Boolean indicating need of splitting the data into experiment types

`...`
: additional parameters

Value

list of input data

`process_perturbations` *Cleanup additional perturbations in the data.table*

Description

This function processes drug and concentration columns in a data.table. It checks if there is only one unique drug (excluding a specified untreated tag) and if there are exactly two doses (one of which is 0). If these conditions are met, it creates a new column named after the drug and fills it with the doses, then removes the original drug and concentration columns.

Usage

```
process_perturbations(
  dt,
  drugs_cotrt_ids,
  conc_cotrt_ids,
  untreated_tag = "vehicle"
)
```

Arguments

`dt`
: A data.table containing the data.

`drugs_cotrt_ids`
: A vector of column names related to drugs.

`conc_cotrt_ids`
: A vector of column names related to concentrations.

`untreated_tag`
: A string representing the untreated tag (default is "vehicle").

Value

A modified data.table with new columns for the drugs and removed original drug and concentration columns.

Examples

```
dt <- data.table::data.table(
  drug1 = c("vehicle", "drugA", "drugA"),
  conc1 = c(0, 10, 0),
  drug2 = c("vehicle", "drugB", "drugB"),
  conc2 = c(0, 20, 0)
)
drugs_cotrt_ids <- c("drug1", "drug2")
conc_cotrt_ids <- c("conc1", "conc2")
dt <- process_perturbations(dt, drugs_cotrt_ids, conc_cotrt_ids)
print(dt)
```

---

read_intermediate_data

read intermediate data for the given experiment and step to qs file

---

Description

read intermediate data for the given experiment and step to qs file

Usage

```
read_intermediate_data(path, step, experiment)
```

Arguments

path	string with the input directory of the qs file
step	string with the step name
experiment	string with the experiment name

Value

se

---

replace_conc_with_standardized_conc

Standardize concentrations.

Description

Utilize a map to standardize concentrations.

Usage

```
replace_conc_with_standardized_conc(
  original_concs,
  conc_map,
  original_conc_col,
  standardized_conc_col
)
```

Arguments

original_concs	numeric vector of concentrations to replace using conc_map.
conc_map	data.table of two columns named original_conc_col and standardized_conc_col.
original_conc_col	string of the name of the column in conc_map containing the original concentrations to replace.
standardized_conc_col	string of the name of the column in conc_map containing the standardized concentrations to use for replacement.

Value

numeric vector of standardized concentrations.

See Also

map_conc_to_standardized_conc

Examples

```
conc_map <- data.table::data.table(
  orig = c(0.99, 0.6, 0.456, 0.4),
  std = c(1, 0.6, 0.46, 0.4)
)
original_concs <- c(0.456, 0.456, 0.4, 0.99)
exp <- c(0.46, 0.46, 0.4, 1)
obs <- replace_conc_with_standardized_conc(
  original_concs,
  conc_map,
  original_conc_col = "orig",
  standardized_conc_col = "std"
)
```

---

save_intermediate_data *save intermediate data for the given experiment and step to qs file*

Description

save intermediate data for the given experiment and step to qs file

Usage

```
save_intermediate_data(path, step, experiment, se)
```

Arguments

path	string with the save directory for the qs file
step	string with the step name
experiment	string with the experiment name
se	output se

Value

NULL

---

split_raw_data *Split raw data into list based on the data types*

Description

Split raw data into list based on the data types

Usage

```
split_raw_data(dt, type_col = "type")
```

Arguments

dt	data.table of raw drug response data containing both treated and untreated values with column specified in type_col argument.
type_col	string with column names in dt with info about data type. Defaults to "type".

Value

list with split data based on its data type

Author(s)

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Examples

```
cell_lines <- gDRtestData::create_synthetic_cell_lines()
drugs <- gDRtestData::create_synthetic_drugs()
dt_layout <- drugs[4:6, as.list(cell_lines[7:8, ]), names(drugs)]
dt_layout <- gDRtestData::add_data_replicates(dt_layout)
dt_layout <- gDRtestData::add_concentration(
  dt_layout,
  concentrations = 10 ^ (seq(-3, .5, .5))
)

dt_2 <-
 drugs[c(21, 26), as.list(cell_lines[which(cell_lines$clid %in% dt_layout$clid)]), names(drugs)]
dt_2 <- gDRtestData::add_data_replicates(dt_2)
dt_2 <- gDRtestData::add_concentration(
  dt_2,
  concentrations = 10 ^ (seq(-3, .5, .5))
)
colnames(dt_2)[colnames(dt_2) %in% c(colnames(drugs), "Concentration")] <-
  paste0(
    colnames(dt_2)[colnames(dt_2) %in% c(colnames(drugs), "Concentration")],
    "_2"
  )
dt_layout_2 <- dt_layout[dt_2, on = intersect(names(dt_layout), names(dt_2)),
                         allow.cartesian = TRUE]
```

```
dt_merged_data <- gDRtestData::generate_response_data(dt_layout_2, 0)
dt <- identify_data_type(dt_merged_data)
split_raw_data(dt)

conc <- rep(seq(0, 0.3, 0.1), 2)
ctrl_dt <- S4Vectors::DataFrame(
  ReadoutValue = c(2, 2, 1, 1, 2, 1),
  Concentration = rep(0, 6),
  masked = FALSE,
  DrugName = rep(c("DRUG_10", "vehicle", "DRUG_8"), 2),
  CellLineName = "CELL1"
)

trt_dt <- S4Vectors::DataFrame(
  ReadoutValue = rep(seq(1, 4, 1), 2),
  Concentration = conc,
  masked = rep(FALSE, 8),
  DrugName = c("DRUG_10", "DRUG_8"),
  CellLineName = "CELL1"
)
input_dt <- data.table::as.data.table(rbind(ctrl_dt, trt_dt))
input_dt$Duration <- 72
input_dt$CorrectedReadout2 <- input_dt$ReadoutValue
split_dt <- identify_data_type(input_dt)
split_raw_data(split_dt)
```

`test_synthetic_data` *Testing synthetic data form gDRtestData package*

Description

Testing synthetic data form gDRtestData package

Usage

```
test_synthetic_data(
  original,
  data,
  dataName,
  override_untrt_controls = NULL,
  assays = c("Normalized", "Averaged", "Metrics"),
  tolerance = 0.001
)
```

Arguments

`original`	original MAE assay
`data`	datase MAE or data.table
`dataName`	dataset name
`override_untrt_controls`	named list containing defining factors in the treatments
`assays`	assays to test
`tolerance`	tolerance factor

Value

NULL

Examples

```
set.seed(2)
cell_lines <- gDRtestData::create_synthetic_cell_lines()
drugs <- gDRtestData::create_synthetic_drugs()
data <- "finalMAE_small"
original <- gDRutils::get_synthetic_data(data)
test_synthetic_data(original, original, "test")
```

---

validate_data_models_availability

Validate availability of data models

Description

Validate availability of data models

Usage

```
validate_data_models_availability(d_types, s_d_models)
```

Arguments

d_types	character vector with experiment names in MultiAssayExperiment object
s_d_models	character vector with names of supported experiment

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