Package 'IOBR'

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Description Provides six modules for tumor microenvironment (TME) analysis based on multi-omics data. These modules cover data preprocessing, TME estimation, TME infiltrating patterns, cellular interactions, genome and TME interaction, and visualization for TME relevant features, as well as modelling based on key features. It integrates multiple microenvironmental analysis algorithms and signature estimation methods, simplifying the analysis and downstream visualization of the TME. In addition to providing a quick and easy way to construct gene signatures from single-cell RNA-seq data, it also provides a way to construct a reference matrix for TME deconvolution from single-cell RNA-seq data. The analysis pipeline and feature visualization are user-friendly and provide a comprehensive description of the complex TME, offering insights into tumour-immune interactions (Zeng D, et al. (2024) <doi:10.1016/j.crmeth.2024.100910>. Fang Y, et al. (2025) <doi:10.1002/mdr2.70001>).

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URL https://doi.org/10.3389/fimmu.2021.687975 (paper), https://iobr.github.io/book/ (docs), https://iobr.github.io/IOBR/

BugReports https://github.com/IOBR/IOBR/issues

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add_iobr_mirror *Add Custom Download Mirror*

Description

Adds a custom mirror URL to the default mirrors for the current session. The mirror URL should be a base URL. If it contains 'github.com', it will be treated as a GitHub proxy and the relative path to IOBR releases will be appended. Otherwise, it will be treated as a direct repository path.

Usage

```
add_iobr_mirror(url, position = c("first", "last", "before_github"))
```

Arguments

url	Character string. The mirror URL to add.
position	Character. Where to add the mirror: "first", "last", or "before_github". Default: "first".

Value

Invisibly returns the updated mirror list.

Examples

```
## Not run:
add_iobr_mirror("https://my-mirror.com/https://github.com")

## End(Not run)
```

add_riskscore *Add Risk Score to Dataset*

Description

Computes a risk score for each observation based on Cox proportional hazards regression or binary logistic regression. The function fits the specified model and returns the dataset with an added risk score column.

Usage

```
add_riskscore(
  input,
  family = c("cox", "binary"),
  target = NULL,
  time = NULL,
  status = NULL,
  vars,
  new_var_name = "riskscore"
)
```

Arguments

input	Data frame containing the variables for analysis.
family	Character string specifying the model family: ‘"cox"‘ for Cox proportional hazards regression or ‘"binary"‘ for logistic regression. Default is ‘"cox"‘.
target	Character string specifying the target variable name. Required when ‘family = "binary"‘.
time	Character string specifying the time-to-event variable name. Required when ‘family = "cox"‘.
status	Character string specifying the event status variable name. Required when ‘family = "cox"‘.
vars	Character vector of variable names to include in the model.
new_var_name	Character string specifying the name for the new risk score column. Default is ‘"riskscore"‘.

Value

Data frame identical to ‘input‘ with an additional column containing risk scores (linear predictors for Cox models or predicted probabilities for logistic models).

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
input_data <- data.frame(
  time = rexp(100),
  status = rbinom(100, 1, 0.5),
  age = rnorm(100, 60, 10),
  score1 = rnorm(100),
  score2 = rnorm(100)
)
result <- add_riskscore(
  input_data,
  time = "time", status = "status",
```

```
  vars = c("age", "score1", "score2")
)
head(result$riskscore)
```

---

anno_eset *Annotate Gene Expression Matrix and Remove Duplicated Genes*

Description

Annotates an expression matrix with gene symbols using provided annotation data, filters out missing or invalid symbols, handles duplicate gene entries, and removes uninformative rows. The function supports multiple aggregation methods for resolving duplicate gene symbols.

Usage

```
anno_eset(
  eset,
  annotation,
  symbol = "symbol",
  probe = "probe_id",
  method = "mean"
)
```

Arguments

eset	Expression matrix or ExpressionSet object containing gene expression data.
annotation	Data frame containing annotation information for probes. Built-in options include ‘anno_hug133plus2‘, ‘anno_rnaseq‘, and ‘anno_illumina‘.
symbol	Character string specifying the column name in ‘annotation‘ that represents gene symbols. Default is ‘"symbol"‘.
probe	Character string specifying the column name in ‘annotation‘ that represents probe identifiers. Default is ‘"probe_id"‘.
method	Character string specifying the aggregation method for duplicate gene symbols. Options are ‘"mean"‘, ‘"sum"‘, or ‘"sd"‘. Default is ‘"mean"‘.

Details

The function performs the following operations:

1. Filters probes with missing symbols or labeled as ‘"NA_NA"‘
2. Matches probes between expression set and annotation data
3. Merges annotation with expression data
4. Handles duplicate gene symbols using specified aggregation method
5. Removes rows with all zeros, all NAs, or missing values in the first column

Value

Annotated and cleaned gene expression matrix with gene symbols as row names.

Author(s)

Dongqiang Zeng

Examples

```
# Create a small example expression matrix
eset_mat <- matrix(runif(100), nrow = 10, ncol = 10)
rownames(eset_mat) <- paste0("Probe", 1:10)
colnames(eset_mat) <- paste0("Sample", 1:10)

# Create a matching annotation data frame
anno_df <- data.frame(
  probe_id = paste0("Probe", 1:10),
  symbol = c("Gene1", "Gene1", "Gene2", "Gene3", "Gene4",
             "Gene5", "Gene6", "Gene7", "Gene8", "Gene9")
)

# Annotate
result <- anno_eset(eset = eset_mat, annotation = anno_df)
head(result)
```

---

assimilate_data *Harmonize Two Data Frames by Column Structure*

Description

Adds missing columns (filled with 'NA') to a secondary data frame so that its column set and order match a reference data frame. This is useful when combining data frames from different sources that should have the same structure but may be missing some columns.

Usage

```
assimilate_data(data_a, data_b)
```

Arguments

data_a	Data frame. Reference data frame whose column structure should be matched.
data_b	Data frame. Data frame to be conformed to 'data_a'.

Value

Data frame 'data_b' with added missing columns (NA-filled) and reordered to match 'data_a'.

Examples

```
# Create reference data frame
pdata_a <- data.frame(
  A = 1:5, B = 2:6, C = 3:7, D = 4:8, E = 5:9
)

# Create data frame with subset of columns
pdata_b <- data.frame(A = 1:3, C = 4:6, E = 7:9)

# Harmonize pdata_b to match pdata_a structure
pdata_b_harmonized <- assimilate_data(data_a = pdata_a, data_b = pdata_b)
print(names(pdata_b_harmonized)) # Now has A, B, C, D, E
```

---

batch_cor *Batch Correlation Analysis*

Description

Performs correlation analysis between a target variable and multiple feature variables. Computes correlation coefficients, p-values, and adjusts for multiple testing using the Benjamini-Hochberg method.

Usage

```
batch_cor(data, target, feature, method = c("spearman", "pearson", "kendall"))
```

Arguments

data	Data frame containing the target and feature variables.
target	Character string specifying the name of the target variable.
feature	Character vector specifying the names of feature variables to correlate with the target.
method	Character string specifying the correlation method. Options are ‘"spearman"‘, ‘"pearson"‘, or ‘"kendall"‘. Default is ‘"spearman"‘.

Value

Tibble containing the following columns for each feature:

sig_names Feature name

p.value Raw p-value

statistic Correlation coefficient

p.adj Adjusted p-value (Benjamini-Hochberg)

log10pvalue Negative log10-transformed p-value

stars Significance stars: **** p<0.0001, *** p<0.001, ** p<0.01, * p<0.05, + p<0.5

Author(s)

Dongqiang Zeng

Examples

```
# Create a small example dataset
set.seed(123)
data_df <- as.data.frame(matrix(runif(100 * 10), 100, 10))
colnames(data_df) <- paste0("Signature", 1:10)

# Perform batch correlation
results <- batch_cor(
  data = data_df,
  target = "Signature1",
  feature = colnames(data_df)[2:10]
)
head(results)
```

---

batch_kruskal *Batch Kruskal-Wallis Test*

Description

Performs Kruskal-Wallis rank sum tests on multiple continuous features across different groups. Computes p-values, adjusts for multiple testing, and ranks features by significance.

Usage

```
batch_kruskal(data, group, feature = NULL, feature_manipulation = FALSE)
```

Arguments

`data`	Data frame containing the dataset for analysis.
`group`	Character string specifying the name of the grouping variable.
`feature`	Character vector specifying the names of feature variables to test. If 'NULL', the user is prompted to select features (interactive mode only). Default is 'NULL'.
`feature_manipulation`	Logical indicating whether to apply feature manipulation to filter valid features. Default is 'FALSE'.

Value

Tibble containing:

sig_names Feature name

p.value Raw p-value from Kruskal-Wallis test

statistic Test statistic (chi-squared)

p.adj Adjusted p-value (Benjamini-Hochberg)

log10pvalue Negative log10-transformed p-value

stars Significance stars: **** p<0.0001, *** p<0.001, ** p<0.01, * p<0.05, + p<0.5

group columns Mean-centered values for each group

Author(s)

Dongqiang Zeng

Examples

```
# Create small example data
set.seed(123)
test_data <- data.frame(
  Gender = rep(c("Male", "Female"), each = 50),
  Signature1 = rnorm(100),
  Signature2 = rnorm(100)
)
# Test features by gender
res <- batch_kruskal(
  data = test_data,
  group = "Gender",
  feature = c("Signature1", "Signature2")
)
head(res)
```

---

batch_pcc *Batch Calculation of Partial Correlation Coefficients*

Description

Computes partial correlation coefficients between multiple features and a target variable while controlling for an interference (confounding) variable. Adjusts p-values for multiple testing using the Benjamini-Hochberg method.

Usage

```
batch_pcc(
  input,
  interferenceid,
  target,
  features,
  method = c("pearson", "spearman", "kendall")
)
```

Arguments

input	Data frame containing feature variables, target variable, and interference variable.
interferenceid	Character string specifying the column name of the interference (confounding) variable to control for.
target	Character string specifying the column name of the target variable.
features	Character vector specifying the column names of feature variables to correlate with the target.
method	Character string specifying the correlation method. Options are ‘"pearson"‘, ‘"spearman"‘, or ‘"kendall"‘. Default is ‘"pearson"‘.

Value

Tibble containing the following columns for each feature:

sig_names Feature name

p.value Raw p-value

statistic Partial correlation coefficient

p.adj Adjusted p-value (Benjamini-Hochberg method)

log10pvalue Negative log10-transformed p-value

stars Significance stars: **** p.adj<0.0001, *** p.adj<0.001, ** p.adj<0.01, * p.adj<0.05, + p.adj<0.5

Author(s)

Rongfang Shen

Examples

```
# Create small example data
set.seed(123)
test_data <- data.frame(
  TumorPurity = runif(100),
  TargetVar = rnorm(100),
  Signature1 = rnorm(100),
  Signature2 = rnorm(100)
)
# Calculate partial correlations controlling for tumor purity
res <- batch_pcc(
  input = test_data,
  interferenceid = "TumorPurity",
  target = "TargetVar",
  method = "pearson",
  features = c("Signature1", "Signature2")
)
head(res)
```

batch_sig_surv_plot *Batch Signature Survival Plot*

Description

Generates Kaplan-Meier survival plots for multiple projects or cohorts based on signature scores. Automatically determines optimal cutpoints for signature stratification and creates publication-ready survival curves.

Usage

```
batch_sig_surv_plot(
  input_pdata,
  signature,
  id = "ID",
  column_of_project = "ProjectID",
  project = NULL,
  time = "time",
  status = "status",
  time_type = "day",
  break_month = "auto",
  palette = "jama",
  cols = NULL,
  mini_sig = "score",
  save_path = NULL,
  show_col = TRUE,
  fig_type = "pdf"
)
```

Arguments

input_pdata	Data frame containing survival data and signature scores.
signature	Character string specifying the column name of the target signature for survival analysis.
id	Character string specifying the column name containing unique identifiers. Default is ‘"ID"‘.
column_of_project	Character string specifying the column name containing project identifiers. Default is ‘"ProjectID"‘.
project	Character string or vector specifying project name(s) to analyze. If ‘NULL‘, all projects are analyzed. Default is ‘NULL‘.
time	Character string specifying the column name containing time-to-event data. Default is ‘"time"‘.
status	Character string specifying the column name containing event status. Default is ‘"status"‘.

time_type	Character string specifying the time unit. Options are ‘"day"‘ or ‘"month"‘. Default is ‘"day"‘.
break_month	Numeric value or ‘"auto"‘ specifying the interval for time axis breaks in months. Default is ‘"auto"‘.
palette	Character string specifying the color palette. Default is ‘"jama"‘.
cols	Character vector of custom colors. If ‘NULL‘, palette is used. Default is ‘NULL‘.
mini_sig	Character string for the signature label in the legend. Default is ‘"score"‘.
save_path	Character string or ‘NULL‘. Directory path for saving plots. If ‘NULL‘, plots are not saved. Default is ‘NULL‘.
show_col	Logical indicating whether to display color information. Default is ‘TRUE‘.
fig_type	Character string specifying the output file format (‘"pdf"‘, ‘"png"‘, etc.). Default is ‘"pdf"‘.

Value

Data frame containing combined survival analysis results from all projects.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_pdata <- data.frame(
  ID = paste0("S", 1:20),
  ProjectID = rep("P1", 20),
  OS_time = runif(20, 1, 60),
  OS_status = sample(c(0, 1), 20, replace = TRUE),
  Marker = rnorm(20)
)
result <- batch_sig_surv_plot(
  input_pdata = test_pdata, signature = "Marker",
  id = "ID", column_of_project = "ProjectID",
  time = "OS_time", status = "OS_status", time_type = "month"
)
if (!is.null(result)) head(result)
```

---

batch_surv *Batch Survival Analysis*

Description

Performs Cox proportional hazards regression analysis on multiple variables. Optionally determines optimal cutoffs to dichotomize continuous predictors before modeling. Returns hazard ratios, confidence intervals, and p-values for each variable.

Usage

```
batch_surv(
  pdata,
  variable,
  time = "time",
  status = "status",
  best_cutoff = FALSE
)
```

Arguments

pdata	Data frame containing survival time, event status, and predictor variables.
variable	Character vector specifying the names of predictor variables to analyze.
time	Character string specifying the column name containing follow-up time. Default is ‘"time"‘.
status	Character string specifying the column name containing event status (1 = event occurred, 0 = censored). Default is ‘"status"‘.
best_cutoff	Logical indicating whether to compute optimal cutoffs for continuous variables and analyze dichotomized versions. Default is ‘FALSE‘.

Value

Data frame containing hazard ratios (HR), 95 and p-values for each variable, sorted by p-value.

Author(s)

Dongqiang Zeng

Examples

```
# Create small example data
set.seed(123)
test_data <- data.frame(
  OS_time = runif(100, 0, 100),
  OS_status = sample(c(0, 1), 100, replace = TRUE),
  Signature1 = rnorm(100),
  Signature2 = rnorm(100)
)
batch_surv(
  pdata = test_data,
  variable = c("Signature1", "Signature2"),
  time = "OS_time",
  status = "OS_status"
)
```

batch_wilcoxon *Batch Wilcoxon Rank-Sum Test Between Two Groups*

Description

Performs Wilcoxon rank-sum tests (Mann-Whitney U tests) to compare the distribution of specified features between two groups. Computes p-values, adjusts for multiple testing, and ranks features by significance.

Usage

```
batch_wilcoxon(
  data,
  target = "group",
  feature = NULL,
  feature_manipulation = FALSE
)
```

Arguments

data	Data frame containing the dataset for analysis.
target	Character string specifying the column name of the grouping variable. Default is '"group"'.
feature	Character vector specifying feature names to analyze. If 'NULL', prompts for selection (interactive mode only). Default is 'NULL'.
feature_manipulation	Logical indicating whether to apply feature manipulation filtering. Default is 'FALSE'.

Value

Tibble with columns:

sig_names Feature name

p.value Raw p-value

statistic Difference in means between groups

p.adj Adjusted p-value (Benjamini-Hochberg)

log10pvalue Negative log10-transformed p-value

stars Significance stars: **** p<0.0001, *** p<0.001, ** p<0.01, * p<0.05, + p<0.5

group1, group2 Mean values for each group

Author(s)

Dongqiang Zeng

Examples

```
# Create small example data
set.seed(123)
test_data <- data.frame(
  Gender = rep(c("Male", "Female"), each = 50),
  Signature1 = rnorm(100),
  Signature2 = rnorm(100)
)
# Compare features by gender
res <- batch_wilcoxon(
  data = test_data,
  target = "Gender",
  feature = c("Signature1", "Signature2")
)
head(res)
```

`best_cutoff` *Extract Best Cutoff and Add Binary Variable to Data Frame*

Description

Determines the optimal cutoff point for a continuous variable in survival analysis using the maximally selected rank statistics method. Creates a binary variable based on the identified cutoff and adds it to the input data frame.

Usage

```
best_cutoff(
  pdata,
  variable,
  time = "time",
  status = "status",
  print_result = TRUE
)
```

Arguments

`pdata`	Data frame containing survival information and the continuous variable.
`variable`	Character string specifying the name of the continuous variable for which the optimal cutoff should be determined.
`time`	Character string specifying the column name containing time-to-event data. Default is ‘"time"‘.
`status`	Character string specifying the column name containing event status (censoring information). Default is ‘"status"‘.
`print_result`	Logical indicating whether to print detailed results including cutoff value and Cox model summaries. Default is ‘TRUE‘.

Value

Data frame identical to ‘pdata‘ with an additional binary column named ‘<variable>_binary‘ containing "High" and "Low" categories based on the optimal cutoff.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
pdata <- data.frame(
  time = rexp(100),
  status = rbinom(100, 1, 0.5),
  score = rnorm(100, mean = 50, sd = 10)
)
result <- best_cutoff(pdata, variable = "score", print_result = FALSE)
table(result$score_binary)
```

---

best_cutoff2 *Extract Best Cutoff and Add Binary Variable to Data Frame*

Description

Finds the best cutoff point for a continuous variable in survival analysis. Takes input data containing a continuous variable and survival information (time and status). Returns the modified input data with a new binary variable created based on the best cutoff point.

Usage

```
best_cutoff2(
  pdata,
  variable,
  time = "time",
  status = "status",
  print_result = TRUE
)
```

Arguments

pdata	Data frame containing survival information and features.
variable	Character string specifying the continuous variable name.
time	Character string specifying the time-to-event column name. Default is ‘"time"‘.
status	Character string specifying the event status column name. Default is ‘"status"‘.
print_result	Logical indicating whether to print results. Default is ‘TRUE‘.

Value

List containing:

pdata Data frame with binary variable added

best_cutoff Numeric cutoff value

cox_continuous_object Cox model summary for continuous variable

summary_binary_variable Summary of binary variable

cox_binary_object Cox model summary for binary variable

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
pdata <- data.frame(
  time = rexp(100),
  status = rbinom(100, 1, 0.5),
  score = rnorm(100, mean = 50, sd = 10)
)
result <- best_cutoff2(pdata, variable = "score", print_result = FALSE)
result$best_cutoff
```

BinomialAUC *Calculate AUC for Binomial Model*

Description

Computes Area Under the ROC Curve (AUC) for model predictions using the ROCR package. Handles binary classification models from glmnet.

Usage

```
BinomialAUC(model, newx, s, acture.y)
```

Arguments

model	Fitted glmnet model object.
newx	New data matrix for prediction.
s	Lambda value for prediction (e.g., "lambda.min" or numeric).
acture.y	Actual binary outcomes (numeric 0/1 or factor).

Value

Numeric AUC value between 0 and 1.

Examples

```
if (requireNamespace("glmnet", quietly = TRUE) &&
  requireNamespace("ROCR", quietly = TRUE)) {
  set.seed(123)
  train_data <- matrix(rnorm(100 * 5), ncol = 5)
  train_outcome <- rbinom(100, 1, 0.5)
  test_data <- matrix(rnorm(50 * 5), ncol = 5)
  test_outcome <- rbinom(50, 1, 0.5)
 fitted_model <- glmnet::cv.glmnet(train_data, train_outcome, family = "binomial", nfolds = 5)
 auc_value <- BinomialAUC(fitted_model, test_data, fitted_model$lambda.min, test_outcome)
  print(auc_value)
}
```

BinomialModel *Binomial Model Construction*

Description

Constructs and evaluates binomial logistic regression models using Lasso and Ridge regularization. Processes input data, scales features if specified, splits data into training/testing sets, and fits both Lasso and Ridge models. Optionally generates AUC plots for model evaluation.

Usage

```
BinomialModel(
  x,
  y,
  seed = 123456,
  scale = TRUE,
  train_ratio = 0.7,
  nfold = 10,
  plot = TRUE,
  palette = "jama",
  cols = NULL
)
```

Arguments

x	A data frame containing sample ID and features. First column must be sample ID.
y	A data frame where first column is sample ID and second column is outcome (numeric or factor).
seed	Integer for random seed. Default is '123456'.
scale	Logical indicating whether to scale features. Default is 'TRUE'.
train_ratio	Numeric between 0 and 1 for training proportion. Default is '0.7'.
nfold	Integer for cross-validation folds. Default is '10'.

plot	Logical indicating whether to generate AUC plots. Default is 'TRUE'.
palette	Character string for color palette. Default is '"jama"'.
cols	Optional color vector for ROC curves. Default is 'NULL'.

Value

List containing:

lasso_result Lasso model results

ridge_result Ridge model results

train.x Training data with IDs

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
x <- data.frame(
  ID = paste0("Sample", 1:50),
  Feature1 = rnorm(50),
  Feature2 = rnorm(50),
  Feature3 = rnorm(50)
)
y <- data.frame(
  ID = x$ID,
  Outcome = factor(rbinom(50, 1, 0.5))
)
result <- BinomialModel(x = x, y = y, plot = FALSE, nfold = 5)
str(result, max.level = 1)
```

CalculatePref *Calculate Performance Metrics*

Description

Computes True Positive Rate (TPR) and False Positive Rate (FPR) for ROC analysis using the ROCR package. Used internally for ROC curve generation.

Usage

```
CalculatePref(model, newx, s, acture.y)
```

Arguments

model	Fitted glmnet model.
newx	New data matrix for prediction.
s	Lambda value for prediction.
acture.y	Actual binary outcomes.

Value

ROCR performance object containing TPR and FPR values.

Examples

```
if (requireNamespace("glmnet", quietly = TRUE) &&
  requireNamespace("ROCR", quietly = TRUE)) {
 fitted_model <- glmnet::cv.glmnet(matrix(rnorm(100), ncol = 2), rbinom(50, 1, 0.5), nfolds = 3)
 perf <- CalculatePref(fitted_model, matrix(rnorm(20), ncol = 2), "lambda.min", rbinom(10, 1, 0.5))
}
```

CalculateTimeROC *Calculate Time-Dependent ROC Curve*

Description

Computes time-dependent ROC curve for survival models using the ‘timeROC‘ package. Evaluates predictive accuracy at a specified time quantile.

Usage

```
CalculateTimeROC(model, newx, s, acture.y, modelname, time_prob = 0.9)
```

Arguments

model	A fitted survival model object.
newx	A matrix or data frame of new data for prediction.
s	Lambda value for prediction.
acture.y	Data frame with ‘time‘ and ‘status‘ columns.
modelname	Character string for model identification.
time_prob	Numeric quantile for ROC calculation. Default is ‘0.9‘.

Value

An object of class ‘timeROC‘ containing ROC curve information.

Author(s)

Dongqiang Zeng

Examples

```
if (requireNamespace("glmnet", quietly = TRUE) &&
  requireNamespace("survival", quietly = TRUE) &&
  requireNamespace("timeROC", quietly = TRUE)) {
  library(survival)
  dat <- na.omit(lung[, c("time", "status", "age", "sex", "ph.ecog")])
  dat$status <- dat$status - 1
  x <- as.matrix(dat[, c("age", "sex", "ph.ecog")])
  y <- Surv(dat$time, dat$status)
  fit <- glmnet::glmnet(x, y, family = "cox")
  actual_outcome <- data.frame(time = dat$time, status = dat$status)
  roc_info <- CalculateTimeROC(
    model = fit, newx = x, s = 0.01, acture.y = actual_outcome,
    modelname = "glmnet Cox Model", time_prob = 0.5
  )
  print(roc_info$AUC)
}
```

---

calculate_break_month *Break Time Into Blocks*

Description

Divides time duration into specified blocks for analysis.

Usage

```
calculate_break_month(input, block = 6, time_type = c("month", "day"))
```

Arguments

input	Numeric vector of time durations.
block	Number of blocks. Default is 6.
time_type	Units: "month" or "day". Default is "month".

Value

Numeric vector of breakpoints, rounded to nearest multiple of 5.

Author(s)

Dongqiang Zeng

Examples

```
time_data <- c(24, 36, 12, 48)
blocks <- calculate_break_month(input = time_data)
```

`calculate_sig_score` *Calculate Signature Score*

Description

Main interface for calculating signature scores from gene expression data. Supports PCA, z-score, ssGSEA, and integration methods.

Usage

```
calculate_sig_score(
  pdata = NULL,
  eset,
  signature = NULL,
  method = c("pca", "ssgsea", "zscore", "integration"),
  mini_gene_count = 3,
  column_of_sample = "ID",
  print_gene_proportion = FALSE,
  print_filtered_signatures = FALSE,
  adjust_eset = FALSE,
  parallel.size = 1L,
  ...
)
```

Arguments

`pdata`	Phenotype data. If 'NULL', created from 'eset' column names.
`eset`	Expression matrix (CPM, TPM, RPKM, FPKM, etc.).
`signature`	List of gene signatures. Can also be a character string naming a built-in signature collection (e.g., '"signature_collection"', '"signature_tme"', '"go_bp"', '"kegg"', '"hallmark"').
`method`	Scoring method: '"pca"', '"ssgsea"', '"zscore"', or '"integration"'. Default is '"pca"'.
`mini_gene_count`	Minimum genes required per signature. Default is 3 (or 5 for ssGSEA).
`column_of_sample`	Column with sample IDs in 'pdata'. Default is '"ID"'.
`print_gene_proportion`	Logical: print gene coverage. Default is 'FALSE'.
`print_filtered_signatures`	Logical: print filtered signatures. Default is 'FALSE'.
`adjust_eset`	Logical: clean problematic features. Default is 'FALSE'.
`parallel.size`	Parallel workers for ssGSEA. Default is 1.
`...`	Additional arguments passed to specific methods.

Value

Tibble with phenotype data and signature scores.

Author(s)

Dongqiang Zeng

References

1. Hänzelmann S, Castelo R, Guinney J. GSVA: gene set variation analysis. BMC Bioinformatics. 2013;14:7.
2. Mariathasan S, et al. TGFβ attenuates tumour response to PD-L1 blockade. Nature. 2018;554:544-548.

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
signature <- list(
  Signature1 = paste0("Gene", 1:10),
  Signature2 = paste0("Gene", 11:20)
)

result <- calculate_sig_score(eset = eset, signature = signature, method = "pca")
```

---

calculate_sig_score_integration

Calculate Signature Score Using Integration Method

Description

Computes signature scores using PCA, z-score, and ssGSEA methods combined.

Usage

```
calculate_sig_score_integration(
  pdata = NULL,
  eset,
  signature,
  mini_gene_count = 2,
  column_of_sample = "ID",
  adjust_eset = FALSE,
  parallel.size = 1L
)
```

Arguments

pdata	Data frame with phenotype data. If 'NULL', created from 'eset' column names.
eset	Expression matrix (genes as rows, samples as columns).
signature	List of gene signatures.
mini_gene_count	Minimum genes required per signature. Default is 3.
column_of_sample	Column in 'pdata' with sample IDs. Default is '"ID"'.
adjust_eset	Logical: remove problematic features. Default is 'FALSE'.
parallel.size	Number of parallel workers. Default is 1.

Value

Tibble with signature scores from all three methods.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
signature <- list(
  Signature1 = paste0("Gene", 1:15),
  Signature2 = paste0("Gene", 16:30)
)

result <- calculate_sig_score_integration(eset = eset, signature = signature)
```

---

calculate_sig_score_pca

Calculate Signature Score Using PCA Method

Description

Computes signature scores using Principal Component Analysis. The first principal component is used as the signature score.

Usage

```
calculate_sig_score_pca(
  pdata = NULL,
  eset,
  signature,
  mini_gene_count = 3,
  column_of_sample = "ID",
  adjust_eset = FALSE
)
```

Arguments

pdata	Data frame with phenotype data. If 'NULL', created from 'eset' column names.
eset	Expression matrix (genes as rows, samples as columns).
signature	List of gene signatures.
mini_gene_count	Minimum genes required per signature. Default is 3.
column_of_sample	Column in 'pdata' with sample IDs. Default is '"ID"'.
adjust_eset	Logical: remove problematic features. Default is 'FALSE'.

Value

Tibble with signature scores.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
signature <- list(
  Signature1 = paste0("Gene", 1:10),
  Signature2 = paste0("Gene", 11:20)
)

result <- calculate_sig_score_pca(eset = eset, signature = signature)
```

`calculate_sig_score_ssgsea` *Calculate Signature Score Using ssGSEA Method*

Description

Computes signature scores using single-sample Gene Set Enrichment Analysis.

Usage

```
calculate_sig_score_ssgsea(
  pdata = NULL,
  eset,
  signature,
  mini_gene_count = 5,
  column_of_sample = "ID",
  adjust_eset = FALSE,
  parallel.size = 1L
)
```

Arguments

`pdata`	Data frame with phenotype data. If ‘NULL‘, created from ‘eset‘ column names.
`eset`	Expression matrix (genes as rows, samples as columns).
`signature`	List of gene signatures.
`mini_gene_count`	Minimum genes required per signature. Default is 3.
`column_of_sample`	Column in ‘pdata‘ with sample IDs. Default is ‘"ID"‘.
`adjust_eset`	Logical: remove problematic features. Default is ‘FALSE‘.
`parallel.size`	Number of parallel workers. Default is 1.

Value

Tibble with signature scores.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
```

```
signature <- list(
  Signature1 = paste0("Gene", 1:15),
  Signature2 = paste0("Gene", 16:30)
)

result <- calculate_sig_score_ssgsea(eset = eset, signature = signature)
```

`calculate_sig_score_zscore` *Calculate Signature Score Using Z-Score Method*

Description

Computes signature scores using z-score transformation.

Usage

```
calculate_sig_score_zscore(
  pdata = NULL,
  eset,
  signature,
  mini_gene_count = 3,
  column_of_sample = "ID",
  adjust_eset = FALSE
)
```

Arguments

`pdata`	Data frame with phenotype data. If ‘NULL‘, created from ‘eset‘ column names.
`eset`	Expression matrix (genes as rows, samples as columns).
`signature`	List of gene signatures.
`mini_gene_count`	Minimum genes required per signature. Default is 3.
`column_of_sample`	Column in ‘pdata‘ with sample IDs. Default is ‘"ID"‘.
`adjust_eset`	Logical: remove problematic features. Default is ‘FALSE‘.

Value

Tibble with signature scores.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
signature <- list(
  Signature1 = paste0("Gene", 1:10),
  Signature2 = paste0("Gene", 11:20)
)

result <- calculate_sig_score_zscore(eset = eset, signature = signature)
```

---

cell_bar_plot *Visualize Cell Fractions as Stacked Bar Chart*

Description

Creates stacked bar charts to visualize tumor microenvironment (TME) cell fractions. Supports batch visualization of deconvolution results from methods such as CIBERSORT, EPIC, and quanTIseq.

Usage

```
cell_bar_plot(
  input,
  id = "ID",
  title = "Cell Fraction",
  features = NULL,
  pattern = NULL,
  legend.position = "bottom",
  coord_flip = TRUE,
  palette = 3,
  show_col = FALSE,
  cols = NULL
)
```

Arguments

input	Data frame containing deconvolution results.
id	Character string specifying the column name containing sample identifiers. Default is "ID".
title	Character string specifying the plot title. Default is "Cell Fraction".
features	Character vector specifying column names representing cell types to plot. If NULL, columns are selected based on ‘pattern‘. Default is NULL.
pattern	Character string or regular expression to match column names for automatic feature selection. Used when ‘features‘ is NULL. Default is NULL.

legend.position	Character string specifying legend position ("bottom", "top", "left", "right"). Default is "bottom".
coord_flip	Logical indicating whether to flip plot coordinates using ‘coord_flip()‘. Default is TRUE.
palette	Integer specifying the color palette to use. Default is 3.
show_col	Logical indicating whether to display color information. Default is FALSE.
cols	Character vector of custom colors. If NULL, palette is used. Default is NULL.

Value

A ggplot2 object representing the stacked bar chart.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
input_data <- data.frame(
  ID = paste0("Sample", 1:10),
  Cell_A = runif(10, 0, 0.4),
  Cell_B = runif(10, 0, 0.3),
  Cell_C = runif(10, 0, 0.3)
)
cell_bar_plot(input = input_data, id = "ID", features = c("Cell_A", "Cell_B", "Cell_C"))
```

---

check_cancer_types *Process Batch Table and Validate Cancer Types*

Description

Processes input data containing cancer types and validates each category against a predefined list of supported cancer types (‘timer_available_cancers‘).

Usage

```
check_cancer_types(args)
```

Arguments

args	A list containing input parameters: **batch** Character. Path to a CSV file (optional). **expression** Character vector of expression identifiers (used if ‘batch‘ is NULL). **category** Character vector of cancer types (used if ‘batch‘ is NULL).

Value

A character matrix with two columns:

Column 1 Expression identifiers

Column 2 Cancer categories

Examples

```
args <- list(
  expression = c("exp1", "exp2"),
  category = c("luad", "brca"),
  batch = NULL
)
result <- check_cancer_types(args)
```

---

check_eset *Check Integrity and Outliers of Expression Set*

Description

Performs quality checks on an expression matrix to identify missing values, infinite values, and features with zero variance. Issues warnings when potential problems are detected that may affect downstream analyses.

Usage

```
check_eset(eset, print_result = FALSE, estimate_sd = FALSE)
```

Arguments

eset	Expression matrix or data frame with genes/features in rows and samples in columns.
print_result	Logical indicating whether to print detailed check results to the console. Default is 'FALSE'.
estimate_sd	Logical indicating whether to check for features with zero standard deviation. Default is 'FALSE'.

Value

Invisibly returns 'NULL'. Function is called for its side effects (printing messages and issuing warnings).

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
check_eset(eset, print_result = TRUE)
```

CIBERSORT *CIBERSORT Deconvolution Algorithm*

Description

An analytical tool to estimate cell type abundances in mixed cell populations using gene expression data.

Usage

```
CIBERSORT(
  sig_matrix = NULL,
  mixture_file,
  perm,
  QN = TRUE,
  absolute = FALSE,
  abs_method = "sig.score",
  parallel = FALSE,
  num_cores = 2,
  seed = NULL
)
```

Arguments

sig_matrix	Cell type GEP barcode matrix: row 1 = sample labels; column 1 = gene symbols; no missing values; default = LM22.txt download from CIBERSORT (https://cibersortx.stanford.edu/runci
mixture_file	GEP matrix: row 1 = sample labels; column 1 = gene symbols; no missing values
perm	Set permutations for statistical analysis (>=100 permutations recommended).
QN	Quantile normalization of input mixture (default = TRUE)
absolute	Run CIBERSORT in absolute mode (default = FALSE) - note that cell subsets will be scaled by their absolute levels and will not be represented as fractions (to derive the default output, normalize absolute levels such that they sum to 1 for each mixture sample) - the sum of all cell subsets in each mixture sample will be added to the output ('Absolute score'). If LM22 is used, this score will capture total immune content.

abs_method	If absolute is set to TRUE, choose method: 'no.sumto1' or 'sig.score' - sig.score = for each mixture sample, define S as the median expression level of all genes in the signature matrix divided by the median expression level of all genes in the mixture. Multiple cell subset fractions by S. - no.sumto1 = remove sum to 1 constraint
parallel	Logical. Enable parallel execution? (default = FALSE)
num_cores	Integer. Number of cores to use when parallel = TRUE (default = 2)
seed	Integer. Random seed for reproducible permutation testing. If NULL (default), uses current random state. Set to a specific value (e.g., 123) for reproducible results across runs. Applies to both parallel and serial permutation.

Value

A matrix object containing the estimated cibersort-cell fractions, p-values, correlation coefficients, and RMSE values.

Author(s)

Aaron M. Newman, Stanford University (amnewman@stanford.edu)

Examples

```
# Simulate data
set.seed(123)
sim_sig <- matrix(rnorm(100 * 5), 100, 5)
rownames(sim_sig) <- paste0("Gene", 1:100)
colnames(sim_sig) <- paste0("Cell", 1:5)

sim_mixture <- as.data.frame(matrix(
  rnorm(100 * 3), 100, 3
))
rownames(sim_mixture) <- paste0("Gene", 1:100)
colnames(sim_mixture) <- paste0("Sample", 1:3)

# Run deconvolution
result <- CIBERSORT(
  sig_matrix = sim_sig,
  mixture_file = sim_mixture,
  perm = 10, QN = FALSE, absolute = FALSE,
  parallel = FALSE
)
if (!is.null(result)) head(result)
```

---

clear_iobr_cache *Clear IOBR Data Cache*

Description

Removes all cached data files downloaded from GitHub.

Usage

```
clear_iobr_cache(cache_dir = NULL)
```

Arguments

cache_dir	Character string. Custom cache directory. If NULL, uses the option 'IOBR.cache_dir' or the default system cache location.

Value

Invisible NULL. Called for side effects of clearing the cache.

Examples

```
clear_iobr_cache()
```

---

combine_pd_eset *Combine Phenotype Data and Expression Set*

Description

Merges phenotype data with an expression matrix by matching sample IDs. Optionally filters features, applies feature manipulation, and scales expression data before combining.

Usage

```
combine_pd_eset(
  eset,
  pdata,
  id_pdata = "ID",
  feas = NULL,
  feature_manipulation = TRUE,
  scale = TRUE,
  choose_who_when_duplicate = c("eset", "pdata")
)
```

Arguments

eset	Expression matrix with genes/features in rows and samples in columns.
pdata	Data frame containing phenotype/clinical data.
id_pdata	Character string specifying the column name in 'pdata' containing sample identifiers. Default is '"ID"'.
feas	Character vector specifying features to include from 'eset'. If 'NULL', all features are used. Default is 'NULL'.
feature_manipulation	Logical indicating whether to apply feature manipulation to filter valid features. Default is 'TRUE'.

scale — Logical indicating whether to scale (standardize) expression data. Default is 'TRUE'.

choose_who_when_duplicate — Character string specifying which data to prefer when duplicate columns exist. Options are '"eset"' or '"pdata"'. Default is '"eset"'.

Value

Data frame combining phenotype data and (transposed) expression data, with samples in rows and features/phenotypes in columns.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
pdata <- data.frame(
  ID = colnames(eset),
  group = rep(c("A", "B"), each = 5),
  age = rnorm(10, 50, 10)
)
result <- combine_pd_eset(eset = eset, pdata = pdata, scale = FALSE)
dim(result)
```

Construct_con *Construct Contrast Matrix*

Description

Creates a contrast matrix for differential analysis, where each phenotype level is contrasted against all other levels combined.

Usage

```
Construct_con(pheno)
```

Arguments

pheno — Factor with different levels representing groups to contrast.

Value

Square matrix with dimensions equal to the number of levels in 'pheno'. Each row represents a contrast where the corresponding level is compared against the average of others.

Examples

```
pheno <- factor(c("A", "B", "C", "D"))
contrast_matrix <- Construct_con(pheno)
print(contrast_matrix)
```

`ConvertRownameToLoci` *Convert Rowname To Loci*

Description

Processes a gene expression data matrix by modifying its row names. Extracts the gene identifier from row names formatted as 'GENE|ID', simplifying them to 'GENE'.

Usage

```
ConvertRownameToLoci(cancerGeneExpression)
```

Arguments

`cancerGeneExpression`
: Matrix or data frame. Gene expression data with row names in the format 'GENE|ID'.

Value

Matrix with modified gene expression data with updated row names. Rows without a valid identifier are removed.

Examples

```
example_data <- matrix(runif(20), ncol = 5)
rownames(example_data) <- c("LOC101", "LOC102", "LOC103", "LOC104")
processed_data <- ConvertRownameToLoci(example_data)
print(processed_data)
```

`CoreAlg` *Core Algorithm for CIBERSORT Deconvolution*

Description

Performs nu-regression using support vector machines (SVM) to estimate cell type proportions. This is the core computational engine of CIBERSORT, using nu-SVR with linear kernel to decompose mixed gene expression signals.

Usage

```
CoreAlg(X, y, absolute, abs_method)
```

Arguments

X	Matrix or data frame containing signature matrix (predictor variables). Rows are genes, columns are cell types.
y	Numeric vector containing the mixture sample expression (response variable).
absolute	Logical indicating whether to use absolute space for weights. Default is FALSE (relative proportions).
abs_method	String specifying the method for absolute space weights: ‘"sig.score"‘ or ‘"no.sumto1"‘.

Value

List containing:

w Estimated cell type weights/proportions

mix_rmse Root mean squared error of the deconvolution

mix_r Correlation coefficient between observed and predicted mixture

Examples

```
# Simulate data
set.seed(123)
X <- matrix(rnorm(100), nrow = 10)
rownames(X) <- paste0("Gene", 1:10)
colnames(X) <- paste0("Cell", 1:10)
y <- rnorm(10)
names(y) <- paste0("Gene", 1:10)

# Run core algorithm
result <- CoreAlg(X, y, absolute = FALSE, abs_method = "sig.score")
if (!is.null(result)) str(result)
```

---

count2tpm *Convert Read Counts to Transcripts Per Million (TPM)*

Description

Transforms gene expression count data into Transcripts Per Million (TPM) values, normalizing for gene length and library size. Supports multiple gene ID types and can retrieve gene length information from BioMart or use local datasets.

Usage

```
count2tpm(
  countMat,
  idType = "Ensembl",
  org = c("hsa", "mmus"),
  source = c("local", "biomart"),
  effLength = NULL,
```

```
  id = "id",
  gene_symbol = "symbol",
  length = "eff_length",
  check_data = FALSE
)
```

Arguments

countMat	Numeric matrix of raw read counts with genes in rows and samples in columns.
idType	Character string specifying the gene identifier type. Options are ‘"Ensembl"‘, ‘"Entrez"‘, or ‘"Symbol"‘. Default is ‘"Ensembl"‘.
org	Character string specifying the organism. Options include ‘"hsa"‘ (human) or ‘"mmus"‘ (mouse). Default is ‘"hsa"‘.
source	Character string specifying the source for gene length information. Options are ‘"biomart"‘ (retrieve from Ensembl BioMart) or ‘"local"‘ (use local dataset). Default is ‘"local"‘.
effLength	Data frame containing effective gene length information. If ‘NULL‘, lengths are retrieved based on ‘source‘. Default is ‘NULL‘.
id	Character string specifying the column name in ‘effLength‘ containing gene identifiers. Default is ‘"id"‘.
gene_symbol	Character string specifying the column name in ‘effLength‘ containing gene symbols. Default is ‘"symbol"‘.
length	Character string specifying the column name in ‘effLength‘ containing gene lengths. Default is ‘"eff_length"‘.
check_data	Logical indicating whether to check for missing values in the count matrix. Default is ‘FALSE‘.

Value

Data frame of TPM-normalized expression values with genes in rows and samples in columns. Gene identifiers are converted to gene symbols in the output, regardless of the input ‘idType‘.

Author(s)

Wubing Zhang, Dongqiang Zeng, Yiran Fang

Examples

```
# Simulated count data
set.seed(123)
count_matrix <- matrix(
  rpois(100, lambda = 10),
  ncol = 5,
  dimnames = list(
    paste0("ENSG00000", 101:120),
    paste0("Sample", 1:5)
  )
)
```

```
# Simulated effective length data
eff_len <- data.frame(
  id = paste0("ENSG00000", 101:120),
  symbol = paste0("Gene", 1:20),
  eff_length = runif(20, 500, 5000)
)
# Transform to TPM using local gene annotation
eset <- count2tpm(
  countMat = count_matrix, effLength = eff_len,
  id = "id", length = "eff_length", gene_symbol = "symbol"
)
head(eset)
```

`creat_folder` *Create Nested Output Folders*

Description

Creates one to three nested folders (if not existing) under the current working directory and returns their names and absolute paths.

Usage

```
creat_folder(f1, f2 = NULL, f3 = NULL, return = NULL)
```

Arguments

`f1`	Character. First-level folder name.
`f2`	Character or 'NULL'. Second-level folder name. Default is 'NULL'.
`f3`	Character or 'NULL'. Third-level folder name. Default is 'NULL'.
`return`	Deprecated (not used). Kept for backward compatibility.

Value

List with elements:

folder_name Relative path to the created folder

abspath Absolute path ending with '/'

Examples

```
creat_folder(file.path(tempdir(), "1-result"))
creat_folder(file.path(tempdir(), "1-result"), "figures", "correlation")
```

`deconvolute_quantiseq.default` *Use quanTIseq to Deconvolute a Gene Expression Matrix*

Description

Deconvolutes gene expression data to estimate immune cell fractions using the quanTIseq method. Source code from https://github.com/FFinotello/quanTIseq.

Usage

```
deconvolute_quantiseq.default(
  mix.mat,
  arrays = FALSE,
  signame = "TIL10",
  tumor = FALSE,
  mRNAscale = TRUE,
  method = c("lsei", "hampel", "huber", "bisquare"),
  rmgenes = "unassigned"
)
```

Arguments

`mix.mat`	Data frame or matrix. Gene expression matrix with gene symbols on the first column and sample IDs on the first row. Expression data must be on non-log scale (TPM for RNA-seq or expression values for microarrays).
`arrays`	Logical. Whether expression data are from microarrays. Default is FALSE. If TRUE, the rmgenes parameter is set to "none".
`signame`	Character. Name of the signature matrix. Currently only "TIL10" is available. Default is "TIL10".
`tumor`	Logical. Whether expression data are from tumor samples. If TRUE, signature genes with high expression in tumor samples are removed. Default is FALSE.
`mRNAscale`	Logical. Whether cell fractions must be scaled to account for cell-type-specific mRNA content. Default is TRUE.
`method`	Character. Deconvolution method: "hampel", "huber", "bisquare" for robust regression, or "lsei" for constrained least squares. Default is "lsei".
`rmgenes`	Character. Genes to remove: "unassigned" (default), "default", "none", or "path".

Value

Data frame with cell fractions for each sample.

Author(s)

Finotello F, et al. (adapted for IOBR)

References

F. Finotello, C. Mayer, C. Plattner, G. Laschober, D. Rieder, H. Hackl, A. Krogsdam, W. Posch, D. Wilflingseder, S. Sopper, M. Jsselsteijn, D. Johnsons, Y. Xu, Y. Wang, M. E. Sanders, M. V. Estrada, P. Ericsson-Gonzalez, J. Balko, N. F. de Miranda, Z. Trajanoski. "quanTIseq: quantifying immune contexture of human tumors". bioRxiv 223180. https://doi.org/10.1101/223180.

Examples

```
## Not run:
quantiseq_data <- load_data("quantiseq_data")
if (!is.null(quantiseq_data)) {
  common_genes <- rownames(quantiseq_data$TIL10_signature)
  tpm_matrix <- as.data.frame(matrix(
    abs(rnorm(length(common_genes) * 2, mean = 5, sd = 2)),
    nrow = length(common_genes), ncol = 2
  ))
  rownames(tpm_matrix) <- common_genes
  colnames(tpm_matrix) <- paste0("Sample", 1:2)
  results <- deconvolute_quantiseq.default(mix.mat = tpm_matrix)
  if (!is.null(results)) head(results)
}

## End(Not run)
```

---

deconvolute_timer.default

Deconvolute Tumor Microenvironment Using TIMER

Description

Performs deconvolution of the tumor microenvironment using the TIMER algorithm. Processes multiple cancer datasets, removes batch effects, and estimates immune cell type abundances.

Usage

```
deconvolute_timer.default(args)
```

Arguments

`args`	List or environment containing parameters:
	outdir Character. Output directory path.
	batch Character. File containing paths to expression data and cancer types.

Value

Matrix of abundance scores for different immune cell types across multiple cancer samples.

Examples

```
## Not run:
set.seed(123)
immune <- load_data("immuneCuratedData")
cancer_genes <- load_data("cancer_type_genes")
if (!is.null(immune) && !is.null(cancer_genes)) {
  gene_names <- unique(c(head(rownames(immune$genes), 30), cancer_genes[["stad"]]))
  sample_names <- paste0("Sample", 1:2)
  n_genes <- length(gene_names)
  expr <- matrix(runif(n_genes * 2, 1, 100), n_genes, 2,
                 dimnames = list(gene_names, sample_names))
  tf <- tempfile(fileext = ".tsv")
  write.table(as.data.frame(expr), tf, sep = "\t", quote = FALSE)
  batch_tf <- tempfile(fileext = ".csv")
  write.table(data.frame(path = tf, type = "stad"), batch_tf,
              sep = ",", col.names = FALSE, row.names = FALSE, quote = FALSE)
  args <- list(outdir = tempdir(), batch = batch_tf)
  result <- deconvolute_timer.default(args)
  if (!is.null(result)) head(result)
}

## End(Not run)
```

---

deconvo_cibersort *Deconvolve Using CIBERSORT*

Description

CIBERSORT is freely available to academic users. License and binary can be obtained from https://cibersortx.stanford.edu.

Usage

```
deconvo_cibersort(
  eset,
  project = NULL,
  arrays = FALSE,
  perm = 1000,
  absolute = FALSE,
  abs_method = "sig.score",
  parallel = FALSE,
  num_cores = 2,
  seed = NULL
)
```

Arguments

eset	Expression matrix with gene symbols as row names.

project	Optional project name. Default is ‘NULL‘.
arrays	Logical: optimized for microarray data. Default is ‘FALSE‘.
perm	Permutations for statistical analysis. Default is 1000.
absolute	Logical: run in absolute mode. Default is ‘FALSE‘.
abs_method	Method for absolute mode: ‘"sig.score"‘ or ‘"no.sumto1"‘. Default is ‘"sig.score"‘.
parallel	Enable parallel execution. Default is ‘FALSE‘.
num_cores	Number of cores for parallel mode. Default is 2.
seed	Random seed for reproducibility. Default is ‘NULL‘.

Value

Data frame with CIBERSORT cell fractions. Columns suffixed with ‘_CIBERSORT‘.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
lm22 <- load_data("lm22")
if (!is.null(lm22)) {
  set.seed(123)
  sim_eset <- matrix(rnorm(nrow(lm22) * 2), nrow(lm22), 2)
  rownames(sim_eset) <- rownames(lm22)
  colnames(sim_eset) <- paste0("Sample", 1:2)
  result <- deconvo_cibersort(eset = sim_eset, project = "TCGA-STAD", perm = 10)
  if (!is.null(result)) head(result)
}

## End(Not run)
```

---

deconvo_epic *Deconvolve Immune Microenvironment Using EPIC*

Description

Estimates immune cell fractions using EPIC algorithm.

Usage

```
deconvo_epic(eset, project = NULL, tumor = TRUE)
```

Arguments

eset	Gene expression matrix with genes as row names.
project	Optional project name. Default is ‘NULL‘.
tumor	Logical indicating tumor (‘TRUE‘) or normal (‘FALSE‘) samples.

Value

Data frame with EPIC cell fraction estimates. Columns suffixed with '_EPIC'.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
TRef <- load_data("TRef")
if (!is.null(TRef)) {
  set.seed(123)
  sim_eset <- matrix(rnorm(nrow(TRef$refProfiles) * 2), nrow(TRef$refProfiles), 2)
  rownames(sim_eset) <- rownames(TRef$refProfiles)
  colnames(sim_eset) <- paste0("Sample", 1:2)
  result <- deconvo_epic(eset = sim_eset, project = "Example", tumor = TRUE)
  if (!is.null(result)) head(result)
}

## End(Not run)
```

---

deconvo_estimate *Calculate ESTIMATE Scores*

Description

Calculates stromal, immune, and ESTIMATE scores from gene expression.

Usage

```
deconvo_estimate(eset, project = NULL, platform = "affymetrix")
```

Arguments

eset	Gene expression matrix with gene symbols.
project	Optional project name. Default is 'NULL'.
platform	Platform type: '"affymetrix"' or '"illumina"'. Default is '"affymetrix"'.

Value

Data frame with ESTIMATE scores. Columns suffixed with '_estimate'.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
common_genes <- load_data("common_genes")
if (!is.null(common_genes)) {
  set.seed(123)
  sim_eset <- matrix(rnorm(nrow(common_genes) * 2), nrow(common_genes), 2)
  rownames(sim_eset) <- common_genes$GeneSymbol
  colnames(sim_eset) <- paste0("Sample", 1:2)
  result <- deconvo_estimate(sim_eset, project = "TCGA-STAD")
  if (!is.null(result)) head(result)
}

## End(Not run)
```

`deconvo_ips` *Calculate Immunophenoscore (IPS)*

Description

Calculates immune phenotype scores from gene expression data.

Usage

```
deconvo_ips(eset, project = NULL, plot = FALSE)
```

Arguments

`eset`	Gene expression matrix.
`project`	Optional project name. Default is 'NULL'.
`plot`	Logical: generate visualization. Default is 'FALSE'.

Value

Data frame with IPS scores. Columns suffixed with '_IPS'.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
ips_genes <- load_data("ips_gene_set")
if (!is.null(ips_genes)) {
  set.seed(123)
  sim_eset <- matrix(rnorm(nrow(ips_genes) * 2), nrow(ips_genes), 2)
  rownames(sim_eset) <- ips_genes$GENE
  colnames(sim_eset) <- paste0("Sample", 1:2)
```

```
  result <- deconvo_ips(eset = sim_eset, project = "Example")
  if (!is.null(result)) head(result)
}

## End(Not run)
```

---

deconvo_mcpcounter *Deconvolve Immune Microenvironment Using MCP-Counter*

Description

Estimates immune cell abundances using MCP-counter.

Usage

```
deconvo_mcpcounter(eset, project = NULL)
```

Arguments

eset	Gene expression matrix with HGNC symbols as row names.
project	Optional project name. Default is 'NULL'.

Value

Data frame with MCP-counter scores. Columns suffixed with '_MCPcounter'.

Author(s)

Dongqiang Zeng

Examples

```
mcp_genes <- load_data("mcp_genes")
if (!is.null(mcp_genes)) {
  set.seed(123)
  sim_eset <- matrix(rnorm(nrow(mcp_genes) * 3), nrow(mcp_genes), 3)
  rownames(sim_eset) <- mcp_genes$`HUGO symbols`
  colnames(sim_eset) <- paste0("Sample", 1:3)

  # Run deconvolution
  result <- deconvo_mcpcounter(eset = sim_eset, project = "TCGA-STAD")
  if (!is.null(result)) head(result)
}
```

deconvo_quantiseq *Deconvolve Using quanTIseq*

Description

quanTIseq deconvolution for RNA-seq immune cell fractions.

Usage

```
deconvo_quantiseq(eset, project = NULL, tumor, arrays, scale_mrna)
```

Arguments

eset	Gene expression matrix.
project	Optional project name. Default is 'NULL'.
tumor	Logical: tumor samples. Must be specified.
arrays	Logical: microarray data. Must be specified.
scale_mrna	Logical: correct for mRNA content. Must be specified.

Value

Data frame with quanTIseq cell fractions. Columns suffixed with '_quantiseq'.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
quantiseq_data <- load_data("quantiseq_data")
if (!is.null(quantiseq_data)) {
  set.seed(123)
  n_sig <- nrow(quantiseq_data$TIL10_signature)
  sim_eset <- matrix(rnorm(n_sig * 2), n_sig, 2)
  rownames(sim_eset) <- rownames(quantiseq_data$TIL10_signature)
  colnames(sim_eset) <- paste0("Sample", 1:2)
  result <- deconvo_quantiseq(eset = sim_eset, project = "Example", tumor = TRUE,
                              arrays = FALSE, scale_mrna = FALSE)
  if (!is.null(result)) head(result)
}

## End(Not run)
```

deconvo_ref *Deconvolve Using Custom Reference*

Description

Cell fraction estimation using SVR or lsei methods with custom reference.

Usage

```
deconvo_ref(
  eset,
  project = NULL,
  arrays = TRUE,
  method = c("svr", "lsei"),
  perm = 100,
  reference,
  scale_reference = TRUE,
  absolute.mode = FALSE,
  abs.method = "sig.score"
)
```

Arguments

eset	Gene expression matrix.
project	Optional project name. Default is 'NULL'.
arrays	Logical: use quantile normalization. Default is 'TRUE'.
method	Method: '"svr"' or '"lsei"'. Default is '"svr"'.
perm	Permutations for SVR. Default is 100.
reference	Custom reference matrix (e.g., lm22, lm6).
scale_reference	Logical: scale reference. Default is 'TRUE'.
absolute.mode	Logical: absolute mode for SVR. Default is 'FALSE'.
abs.method	Method for absolute mode. Default is '"sig.score"'.

Value

Data frame with cell fractions. Columns suffixed with '_CIBERSORT'.

Author(s)

Dongqiang Zeng, Rongfang Shen

Examples

```
# Simulate data
set.seed(123)
sim_ref <- matrix(rnorm(100 * 5), 100, 5)
rownames(sim_ref) <- paste0("Gene", 1:100)
colnames(sim_ref) <- paste0("CellType", 1:5)

sim_eset <- matrix(rnorm(100 * 3), 100, 3)
rownames(sim_eset) <- paste0("Gene", 1:100)
colnames(sim_eset) <- paste0("Sample", 1:3)

# Run deconvolution
result <- deconvo_ref(eset = sim_eset, reference = sim_ref, method = "lsei")
if (!is.null(result)) head(result)
```

`deconvo_timer` *Deconvolve Using TIMER*

Description

TIMER deconvolution for cancer-specific immune estimation.

Usage

```
deconvo_timer(eset, project = NULL, indications = NULL)
```

Arguments

`eset`	Gene expression matrix.
`project`	Optional project name. Default is 'NULL'.
`indications`	Cancer type for each sample (e.g., '"brca"', '"stad"'). Must match number of columns in 'eset'.

Value

Data frame with TIMER cell fractions. Columns suffixed with '_TIMER'.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
immune <- load_data("immuneCuratedData")
cancer_genes <- load_data("cancer_type_genes")
if (!is.null(immune) && !is.null(cancer_genes)) {
  set.seed(123)
```

```
  genes <- unique(c(head(rownames(immune$genes), 100), cancer_genes[["stad"]]))
  sim_eset <- matrix(rnorm(length(genes) * 2), length(genes), 2)
  rownames(sim_eset) <- genes
  colnames(sim_eset) <- paste0("Sample", 1:2)
  result <- deconvo_timer(eset = sim_eset, project = "TCGA-STAD",
                          indications = rep("stad", 2))
  if (!is.null(result)) head(result)
}

## End(Not run)
```

---

deconvo_tme *Main TME Deconvolution Function*

Description

Unified interface for multiple TME deconvolution methods.

Usage

```
deconvo_tme(
  eset,
  project = NULL,
  method = tme_deconvolution_methods,
  arrays = FALSE,
  tumor = TRUE,
  perm = 1000,
  reference,
  scale_reference = TRUE,
  plot = FALSE,
  scale_mrna = TRUE,
  group_list = NULL,
  platform = "affymetrix",
  absolute.mode = FALSE,
  abs.method = "sig.score",
  ...
)
```

Arguments

eset	Gene expression matrix with HGNC symbols as row names.
project	Optional project name. Default is 'NULL'.
method	Deconvolution method. See [tme_deconvolution_methods].
arrays	Logical: microarray-optimized mode. Default is 'FALSE'.
tumor	Logical: tumor-optimized mode (EPIC). Default is 'TRUE'.
perm	Permutations (CIBERSORT/SVR). Default is 1000.

reference	Custom reference matrix (SVR/lsei).
scale_reference	Logical: scale reference (SVR/lsei).
plot	Logical: generate plots (IPS). Default is 'FALSE'.
scale_mrna	Logical: mRNA correction (quanTIseq/EPIC).
group_list	Cancer types for TIMER (vector).
platform	Platform for ESTIMATE. Default is '"affymetrix"'.
absolute.mode	Logical: absolute mode (CIBERSORT/SVR). Default is 'FALSE'.
abs.method	Absolute mode method. Default is '"sig.score"'.
...	Additional arguments passed to method.

Value

Tibble with cell fractions and 'ID' column.

Author(s)

Dongqiang Zeng, Rongfang Shen

References

1. Newman et al. (2015). Robust enumeration of cell subsets from tissue expression profiles. Nature Methods.
2. Vegesna et al. (2013). Inferring tumour purity and stromal/immune cell admixture. Nature Communications.
3. Finotello et al. (2019). Molecular and pharmacological modulators of the tumor immune contexture. Genome Medicine.
4. Li et al. (2016). Comprehensive analyses of tumor immunity. Genome Biology.
5. Charoentong et al. (2017). Pan-cancer Immunogenomic Analyses. Cell Reports.
6. Becht et al. (2016). Estimating population abundance of tissue-infiltrating immune cells. Genome Biology.
7. Aran et al. (2017). xCell: digitally portraying tissue cellular heterogeneity. Genome Biology.
8. Racle et al. (2017). Simultaneous enumeration of cancer and immune cell types. ELife.

Examples

```
mcp_genes <- load_data("mcp_genes")
if (!is.null(mcp_genes)) {
  set.seed(123)
  sim_eset <- matrix(rnorm(nrow(mcp_genes) * 3), nrow(mcp_genes), 3)
  rownames(sim_eset) <- mcp_genes$`HUGO symbols`
  colnames(sim_eset) <- paste0("Sample", 1:3)

  # Run deconvolution
  result <- deconvo_tme(eset = sim_eset, method = "mcpcounter")
  if (!is.null(result)) head(result)
}
```

deconvo_xcell *Deconvolve Immune Microenvironment Using xCell*

Description

Estimates immune cell fractions using the xCell algorithm. xCell provides cell type enrichment scores for 64 immune and stromal cell types from gene expression data.

Usage

```
deconvo_xcell(eset, project = NULL, arrays = FALSE)
```

Arguments

eset	Gene expression matrix with HGNC gene symbols as row names and samples as columns.
project	Optional project name to add as 'ProjectID' column. Default is 'NULL'.
arrays	Logical indicating microarray data ('TRUE') or RNA-seq ('FALSE'). Default is 'FALSE'.

Value

Data frame with xCell enrichment scores. Cell type columns are suffixed with '_xCell'.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
xcell <- load_data("xCell.data")
if (!is.null(xcell)) {
  set.seed(123)
  sim_eset <- matrix(rnorm(length(xcell$genes) * 2), length(xcell$genes), 2)
  rownames(sim_eset) <- xcell$genes
  colnames(sim_eset) <- paste0("Sample", 1:2)
  result <- deconvo_xcell(eset = sim_eset, project = "TCGA-STAD")
  if (!is.null(result)) head(result)
}

## End(Not run)
```

`design_mytheme` *Design Custom Theme for ggplot2 Plots*

Description

Creates a customized ggplot2 theme based on user-specified parameters for plot elements such as title size, axis sizes, legend settings, and theme style. Supports various base themes and allows fine-tuning of visual aspects.

Usage

```
design_mytheme(
  theme = c("light", "bw", "classic", "classic2"),
  plot_title_size = 2,
  axis_title_size = 2,
  axis_text_size = 12,
  axis_angle = 60,
  hjust = 1,
  legend.position = "bottom",
  legend.direction = "horizontal",
  legend.size = 0.25,
  legend.key.height = 0.5,
  legend.key.width = 0.5,
  legend.size.text = 10,
  legend.box = "horizontal"
)
```

Arguments

`theme`	Base theme: "light", "bw", "classic", "classic2". Default is "light".
`plot_title_size`	Relative size of plot title. Default is 2.
`axis_title_size`	Relative size of axis titles. Default is 2.
`axis_text_size`	Size of axis tick labels. Default is 12.
`axis_angle`	Angle of x-axis tick labels. Default is 60.
`hjust`	Horizontal justification for x-axis text. Default is 1.
`legend.position`	Legend position: "none", "left", "right", "bottom", "top". Default is "bottom".
`legend.direction`	Direction of legend items: "horizontal" or "vertical". Default is "horizontal".
`legend.size`	Size of legend key. Default is 0.25.
`legend.key.height`	Height of legend key in cm. Default is 0.5.

`legend.key.width`
: Width of legend key in cm. Default is 0.5.

`legend.size.text`
: Size of legend text labels. Default is 10.

`legend.box`
: Orientation of legend box: "horizontal" or "vertical". Default is "horizontal".

Value

A ggplot2 theme object.

Author(s)

Dongqiang Zeng

Examples

```
library(ggplot2)
p <- ggplot(mtcars, aes(wt, mpg)) +
  geom_point()
mytheme <- design_mytheme(theme = "bw", plot_title_size = 1.5, axis_text_size = 14)
p + mytheme + ggtitle("Example Plot")
```

---

doPerm *Permutation Test for CIBERSORT*

Description

Performs permutation-based sampling to generate an empirical null distribution of correlation coefficients for p-value calculation in CIBERSORT analysis. Randomly samples from the mixture data to create null distributions.

Usage

```
doPerm(perm, X, Y, absolute, abs_method, seed = NULL)
```

Arguments

`perm`
: Integer. Number of permutations to perform ($\geq$100 recommended for reliable p-value estimation).

`X`
: Matrix or data frame containing signature matrix (predictor variables).

`Y`
: Numeric vector containing the mixture sample expression.

`absolute`
: Logical indicating whether to use absolute space for weights.

`abs_method`
: String specifying the method for absolute space weights: ‘"sig.score"‘ or ‘"no.sumto1"‘.

`seed`
: Integer. Random seed for reproducibility. If NULL (default), uses current random state.

Value

List containing:

dist Numeric vector of correlation coefficients from permutations

Examples

```
# Simulate data
set.seed(123)
X <- matrix(rnorm(100), nrow = 10)
rownames(X) <- paste0("Gene", 1:10)
colnames(X) <- paste0("Cell", 1:10)
Y <- rnorm(10)
names(Y) <- paste0("Gene", 1:10)

# Run permutation test
result <- doPerm(10, X, Y, absolute = FALSE, abs_method = "sig.score")
if (!is.null(result)) str(result)
```

---

download_iobr_data *Download IOBR Data from GitHub with Mirror Support*

Description

Downloads large datasets from GitHub releases to avoid CRAN size limits. Supports multiple download mirrors for users in different regions. Data is cached locally after first download. Cache directory can be customized via ‘options(IOBR.cache_dir = "your/path")‘.

Usage

```
download_iobr_data(
  name,
  force = FALSE,
  verbose = TRUE,
  mirrors = get_default_mirrors(),
  cache_dir = NULL
)
```

Arguments

name	Character string. Name of the dataset to download.
force	Logical. Whether to force re-download even if cached. Default: FALSE.
verbose	Logical. Whether to print progress messages. Default: TRUE.
mirrors	Character vector. URLs of mirrors to try. Default uses get_default_mirrors().
cache_dir	Character string. Custom cache directory. If NULL, uses the option ‘IOBR.cache_dir‘ or the default system cache location.

Value

The requested dataset.

Examples

```
## Not run:
tcga_sig <- download_iobr_data("tcga_stad_sig")

## End(Not run)
```

`DrawQQPlot` *Draw QQ Plot Comparing Cancer and Immune Expression*

Description

Creates a quantile-quantile (QQ) plot to compare gene expression distributions between cancer and immune samples. Points along the diagonal indicate similar distributions.

Usage

```
DrawQQPlot(cancer.exp, immune.exp, name = "")
```

Arguments

`cancer.exp`	Vector. Gene expression data for cancer samples.
`immune.exp`	Vector. Gene expression data for immune samples.
`name`	Character. Optional subtitle with additional information.

Value

Generates a QQ plot.

Examples

```
cancer_exp <- rnorm(100, mean = 5, sd = 1.5)
immune_exp <- rnorm(100, mean = 5, sd = 1.5)
DrawQQPlot(
  cancer.exp = cancer_exp,
  immune.exp = immune_exp,
  name = "Comparison of Gene Expression"
)
```

Enet *Elastic Net Model Fitting*

Description

Fits elastic net model with cross-validation to find optimal alpha and lambda. Searches across a grid of alpha values (0 to 1) and lambda values to minimize cross-validation error.

Usage

```
Enet(train.x, train.y, lambdamax, nfold = 10)
```

Arguments

train.x	Training predictors matrix.
train.y	Training binary outcomes (0/1 or factor).
lambdamax	Maximum lambda value for the grid search.
nfold	Number of CV folds. Default is '10'.

Value

List containing:

chose_alpha Optimal alpha value (0-1)

chose_lambda Optimal lambda value

Examples

```
if (requireNamespace("glmnet", quietly = TRUE)) {
  set.seed(123)
  train_data <- matrix(rnorm(50 * 5), ncol = 5)
  train_outcome <- rbinom(50, 1, 0.5)
  result <- Enet(train.x = train_data, train.y = train_outcome, lambdamax = 1, nfold = 5)
}
```

enrichment_barplot *Enrichment Bar Plot with Two Directions*

Description

Creates a bar plot visualizing enrichment results for up-regulated and down-regulated terms, using -log10(p-values) to indicate significance.

Usage

```
enrichment_barplot(
  up_terms,
  down_terms,
  terms = "Description",
  pvalue = "pvalue",
  group = "group",
  palette = "jama",
  cols = NULL,
  title = "Gene Ontology Enrichment",
  width_wrap = 30,
  font_terms = 15
)
```

Arguments

up_terms	Data frame for up-regulated terms.
down_terms	Data frame for down-regulated terms.
terms	Column name for term descriptions. Default is "Description".
pvalue	Column name for p-values. Default is "pvalue".
group	Column name for group indicator. Default is "group".
palette	Color palette. Default is "jama".
cols	Character vector. Custom colors for bars. If NULL, uses palette. Default is NULL.
title	Plot title. Default is "Gene Ontology Enrichment".
width_wrap	Maximum width for wrapping pathway names. Default is 30.
font_terms	Font size for axis labels. Default is 15.

Value

A ggplot object of the enrichment bar plot.

Author(s)

Dongqiang Zeng

Examples

```
up_terms <- data.frame(
  Description = c("Pathway1", "Pathway2"),
  pvalue = c(0.001, 0.01)
)
down_terms <- data.frame(
  Description = c("Pathway4", "Pathway5"),
  pvalue = c(0.005, 0.02)
)
p <- enrichment_barplot(
```

```
  up_terms = up_terms,
  down_terms = down_terms,
  title = "Custom Enrichment Plot"
)
p
```

EPIC *Estimate the proportion of immune and cancer cells.*

Description

EPIC takes as input bulk gene expression data (RNA-seq) and returns the proportion of mRNA and cells composing the various samples.

Usage

```
EPIC(
  bulk,
  reference = NULL,
  mRNA_cell = NULL,
  mRNA_cell_sub = NULL,
  sigGenes = NULL,
  scaleExprs = TRUE,
  withOtherCells = TRUE,
  constrainedSum = TRUE,
  rangeBasedOptim = FALSE
)
```

Arguments

bulk	A matrix (nGenes x nSamples) of the genes expression from each bulk sample (the counts should be given in TPM, RPKM or FPKM when using the prebuilt reference profiles). This matrix needs to have rownames telling the gene names (corresponds to the gene symbol in the prebuilt reference profiles (e.g. CD8A, MS4A1) - no conversion of IDs is performed at the moment). It is advised to keep all genes in the bulk instead of a subset of signature genes (except if scaleExprs = FALSE in which case it doesn't make any difference).
reference	(optional): A string or a list defining the reference cells. It can take multiple formats: - 'NULL': to use the default reference profiles and genes signature TRef - A character: either "BRef" or "TRef" to use the reference cells and genes signature of the corresponding datasets (see BRef and TRef) - A list containing: - '$refProfiles': a matrix (nGenes x nCellTypes) of the reference cells genes expression (don't include a column of the 'other cells' (representing usually the cancer cells for which such a profile is usually not conserved between samples); the rownames needs to be defined as well as the colnames giving the names of each gene and reference cell types respectively. It is advised to keep all genes in this refProfiles matrix instead of a subset of signature genes - '$sigGenes':

a character vector of the gene names to use as signature - sigGenes can also be given as a direct input to EPIC function - '$refProfiles.var' (optional): a matrix (`nGenes` x `nCellTypes`) of the variability of each gene expression for each cell type, which is used to define weights on each gene for the optimization (if this is absent, we assume an identical variability for all genes in all cells) - it needs to have the same dimnames than refProfiles

`mRNA_cell` (optional): A named numeric vector: tells (in arbitrary units) the amount of mRNA for each of the reference cells and of the other uncharacterized (cancer) cell. Two names are of special meaning: *"otherCells"* - used for the mRNA/cell value of the "other cells" from the sample (i.e. the cell type that don't have any reference gene expression profile) ; and *default* - used for the mRNA/cell of the cells from the reference profiles for which no specific value is given in mRNA_cell (i.e. if mRNA_cell=c(Bcells=2, NKcells=2.1, otherCells=3.5, default=1), then if the refProfiles described Bcells, NKcells and Tcells, we would use a value of 3.5 for the "otherCells" that didn't have any reference profile and a default value of 1 for the Tcells when computing the cell fractions). To note: if data is in tpm, this mRNA per cell would ideally correspond to some number of transcripts per cell.

`mRNA_cell_sub` (optional): This can be given instead of `mRNA_cell` (or in addition to it). It is also a named numeric vector, used to replace only the mRNA/cell values from some cell types (or to add values for new cell types). The values given in mRNA_cell_sub will overwrite the default values as well as those that might have been given by mRNA_cell.

`sigGenes` (optional): a character vector of the gene names to use as signature for the deconvolution. In principle this is given with the reference as the "reference$sigGenes" but if we give a value for this input variable, it is these signature genes that will be used instead of the ones given with the reference profile.

`scaleExprs` (optional, default is TRUE): boolean telling if the bulk samples and reference gene expression profiles should be rescaled based on the list of genes in common between the them (such a rescaling is recommanded).

`withOtherCells` (optional, default is TRUE): if EPIC should allow for an additional cell type for which no gene expression reference profile is available or if the bulk is assumed to be composed only of the cells with reference profiles.

`constrainedSum` (optional, default is TRUE): tells if the sum of all cell types should be constrained to be < 1. When `withOtherCells=FALSE`, there is additionally a constrain the the sum of all cell types with reference profiles must be > 0.99.

`rangeBasedOptim`

(optional): when this is FALSE (the default), the least square optimization is performed as described in *Racle et al., 2017, eLife*, which is recommanded. When this variable is TRUE, EPIC uses the variability of each gene from the reference profiles in another way: instead of defining weights (based on the variability) for the fit of each gene, we define a range of values accessible for each gene (based on the gene expression value in the reference profile +/- the variability values). The error that the optimization tries to minimize is by how much the predicted gene expression is outside of this allowed range of values.

Details

This function uses a constrained least square minimization to estimate the proportion of each cell type with a reference profile and another uncharacterized cell type in bulk gene expression samples.

The names of the genes in the bulk samples, the reference samples and in the gene signature list need to be the same format (gene symbols are used in the predefined reference profiles). The full list of gene names don't need to be exactly the same between the reference and bulk samples: *EPIC* will use the intersection of the genes. In case of duplicate gene names, *EPIC* will use the median value per duplicate - if you want to consider these cases differently, you can remove the duplicates before calling *EPIC*.

Value

A list of 3 matrices: - 'mRNAProportions': (`nSamples` x (`nCellTypes+1`)) the proportion of mRNA coming from all cell types with a ref profile + the uncharacterized other cell - 'cellFractions': (`nSamples` x (`nCellTypes+1`)) this gives the proportion of cells from each cell type after accounting for the mRNA / cell value - 'fit.gof': (`nSamples` x 12) a matrix telling the quality for the fit of the signature genes in each sample. It tells if the minimization converged, and other info about this fit comparing the measured gene expression in the sigGenes vs predicted gene expression in the sigGenes

Examples

```
melanoma_counts <- matrix(abs(rnorm(80)), nrow = 20, ncol = 4)
rownames(melanoma_counts) <- paste0("Gene", 1:20)
colnames(melanoma_counts) <- paste0("Sample", 1:4)
mock_ref <- list(
  refProfiles = matrix(abs(rnorm(80)), nrow = 20, ncol = 4),
  sigGenes = paste0("Gene", 1:10)
)
rownames(mock_ref$refProfiles) <- paste0("Gene", 1:20)
colnames(mock_ref$refProfiles) <- c("Bcells", "CD4T", "CD8T", "NK")
res1 <- EPIC(melanoma_counts, reference = mock_ref)
if (!is.null(res1)) head(res1$cellFractions)
```

---

eset_distribution *Visualize Expression Set Distribution*

Description

Generates boxplots and density plots to analyze the distribution of expression values in an expression set. Useful for quality control and assessing data normalization.

Usage

```
eset_distribution(eset, quantile = 3, log = TRUE, project = NULL)
```

Arguments

eset	Expression matrix or data frame with genes in rows and samples in columns.
quantile	Integer specifying the divisor for sampling columns. Default is 3 (samples 1/3 of columns).
log	Logical indicating whether to perform log2 transformation. Default is 'TRUE'.
project	Optional output directory path for saving files. If 'NULL', no files are saved. Default is 'NULL'.

Value

Invisibly returns 'NULL'. If 'project' is provided, saves PNG files to disk.

Examples

```
# Simulate data
set.seed(123)
sim_eset <- matrix(rnorm(1000 * 10, mean = 5, sd = 2), 1000, 10)
rownames(sim_eset) <- paste0("Gene", 1:1000)
colnames(sim_eset) <- paste0("Sample", 1:10)

# Run distribution plot
result <- eset_distribution(sim_eset)
```

---

estimateScore *estimateScore*

Description

This function reads a gene expression dataset in GCT format, calculates enrichment scores for specific gene sets, and writes the computed scores to an output file. It supports multiple platform types and performs platform-specific calculations if necessary.

Usage

```
estimateScore(
  input.ds,
  output.ds,
  platform = c("affymetrix", "agilent", "illumina")
)
```

Arguments

input.ds	A character string specifying the path to the input dataset file in GCT format. The file should have gene expression data with appropriate headers.
output.ds	A character string specifying the path to the output dataset file, where the calculated scores will be written.

platform A character vector indicating the platform type. Must be one of "affymetrix", "agilent", or "illumina". Platform-specific calculations are performed based on this parameter.

Value

This function does not return a value but writes the computed scores to the specified output file in GCT format.

Examples

```
## Not run:
set.seed(123)
si_geneset_data <- load_data("SI_geneset")
if (!is.null(si_geneset_data)) {
  gene_names <- unique(c(si_geneset_data[1, -1], si_geneset_data[2, -1]))
  gene_names <- gene_names[!is.na(gene_names) & gene_names != ""]
  gene_names <- head(gene_names, 200)
  n_genes <- length(gene_names)
  eset_sim <- as.data.frame(matrix(rnorm(n_genes * 2, mean = 5, sd = 1), n_genes, 2))
  rownames(eset_sim) <- gene_names
  colnames(eset_sim) <- c("Sample1", "Sample2")
  eset_sim <- tibble::rownames_to_column(eset_sim, var = "symbol")
  input_file <- tempfile(pattern = "estimate_", fileext = ".gct")
  output_file <- tempfile(pattern = "estimate_score_", fileext = ".gct")
 writeLines(c("#1.2", paste(nrow(eset_sim), ncol(eset_sim) - 1, sep = "\t")), input_file)
  utils::write.table(eset_sim, input_file, sep = "\t", row.names = FALSE,
                     col.names = TRUE, append = TRUE, quote = FALSE)
  score_res <- estimateScore(input.ds = input_file, output.ds = output_file,
                             platform = "affymetrix")
  if (!isFALSE(score_res) && file.exists(output_file)) {
    head(read.table(output_file, skip = 2, header = TRUE, sep = "\t"))
  }
}

## End(Not run)
```

---

exact_pvalue *Calculate Exact P-Value for Correlation*

Description

Computes the exact p-value for the correlation between two numeric variables using a specified correlation method.

Usage

```
exact_pvalue(x, y, method)
```

Arguments

x	Numeric vector representing the first variable.
y	Numeric vector representing the second variable.
method	Character string specifying the correlation method: ‘"spearman"‘, ‘"pearson"‘, or ‘"kendall"‘.

Value

Numeric value representing the exact p-value.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
x <- rnorm(100)
y <- rnorm(100)
p_val <- exact_pvalue(x = x, y = y, method = "spearman")
print(p_val)
```

---

extract_sc_data *Extract Data Frame from Seurat Object*

Description

Extracts and combines a data frame with cells as rows and features as columns from Seurat assay data. Supports multiple assays and optional metadata integration.

Usage

```
extract_sc_data(
  sce,
  vars = NULL,
  assay,
  slot = "scale.data",
  combine_meta_data = TRUE
)
```

Arguments

sce	Seurat object.
vars	Character vector of feature names to extract. If 'NULL', all features are extracted.
assay	Character vector specifying assay(s) to pull data from.
slot	Character string specifying the assay data slot. Default is '"scale.data"'.
combine_meta_data	Logical indicating whether to combine metadata with the extracted data frame. Default is 'TRUE'.

Value

Data frame with cells as rows and features as columns.

Author(s)

Dongqiang Zeng

Examples

```
if (requireNamespace("Seurat", quietly = TRUE)) {
  pbmc <- SeuratObject::pbmc_small
  vars <- c("PPBP", "IGLL5", "VDAC3", "CD1C", "AKR1C3")
  eset <- extract_sc_data(sce = pbmc, vars = vars, assay = "RNA")
}
```

---

feature_manipulation *Feature Quality Control and Filtering*

Description

Filters features (variables) in a matrix or data frame by removing those with missing values, non-numeric types, infinite values, or zero variance. This is useful for preparing data for downstream statistical analyses.

Usage

```
feature_manipulation(
  data,
  feature = NULL,
  is_matrix = FALSE,
  print_result = FALSE
)
```

Arguments

data	A matrix or data frame containing features to filter.
feature	Character vector of feature names to check. If 'is_matrix = TRUE', features are extracted from row names of the matrix.
is_matrix	Logical indicating whether 'data' is a gene expression matrix (features as rows, samples as columns). If 'TRUE', the matrix is transposed for processing. Default is 'FALSE'.
print_result	Logical indicating whether to print filtering statistics. Default is 'FALSE'.

Value

Character vector of feature names that pass all quality checks.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_data <- data.frame(
  A = c(1, 2, 3),
  B = c(1, 1, 1), # zero variance
  C = c(1, NA, 3), # missing value
  D = c("a", "b", "c") # non-numeric
)
feas <- feature_manipulation(data = test_data, feature = colnames(test_data), print_result = TRUE)
print(feas)
```

---

feature_select *Feature Selection via Correlation or Differential Expression*

Description

Selects informative features using either correlation with a quantitative response or differential expression (limma) for binary/continuous responses.

Usage

```
feature_select(
  x,
  y,
  method = c("cor", "dif"),
  family = c("spearman", "pearson"),
  cutoff = NULL,
  padjcut = NULL
)
```

Arguments

x	Numeric matrix. Features (rows) by samples (columns).
y	Numeric or factor. Response vector (quantitative or binary).
method	Character. "cor" (correlation) or "dif" (differential expression). Default c("cor","dif").
family	Character. Correlation method if method = "cor": "spearman" or "pearson".
cutoff	Numeric. Absolute correlation (for cor) or |log2FC| (for dif) threshold.
padjcut	Numeric. Adjusted p-value cutoff.

Value

Character vector of selected feature names.

Examples

```
# Simulate data
set.seed(123)
sim_eset <- matrix(rnorm(100 * 50), 100, 50)
rownames(sim_eset) <- c("PDCD1", paste0("Gene", 2:100))
colnames(sim_eset) <- paste0("Sample", 1:50)
pd1 <- as.numeric(sim_eset["PDCD1", ])
group <- ifelse(pd1 > mean(pd1), "high", "low")

# Correlation method
pd1_cor <- feature_select(
  x = sim_eset, y = pd1, method = "cor",
  family = "pearson", padjcut = 0.05, cutoff = 0.5
)

# Differential expression method
pd1_dif <- feature_select(
  x = sim_eset, y = pd1, method = "dif",
  padjcut = 0.05, cutoff = 2
)
pd1_dif_2 <- feature_select(
  x = sim_eset, y = group,
  method = "dif", padjcut = 0.05, cutoff = 2
)
```

---

filterCommonGenes *filterCommonGenes*

Description

This function filters and merges a dataset with a set of common genes.

Usage

```
filterCommonGenes(input.f, output.f, id = c("GeneSymbol", "EntrezID"))
```

Arguments

input.f	A character string specifying the path to the input file or a connection object. The file should be a tab-separated table with row names.
output.f	A character string specifying the path to the output file.
id	A character string indicating the type of gene identifier to use. Can be either "GeneSymbol" or "EntrezID".

Value

No return value. The function writes the merged dataset to the specified output file.

Examples

```
## Not run:
input_data <- data.frame(
  GeneSymbol = c("BRCA1", "TP53", "EGFR", "NOTCH1"),
  Value = c(10, 15, 8, 12),
  stringsAsFactors = FALSE
)
input_file <- tempfile(fileext = ".txt")
output_file <- tempfile(fileext = ".txt")
write.table(input_data, file = input_file, sep = "\t", row.names = TRUE, quote = FALSE)
filterCommonGenes(input_file, output_file, id = "GeneSymbol")

## End(Not run)
```

---

find_markers_in_bulk *Identify Marker Features in Bulk Expression Data*

Description

Identifies informative marker features across groups from bulk gene expression or signature score matrices using Seurat workflows. Performs feature selection, scaling, PCA, clustering, and marker discovery.

Usage

```
find_markers_in_bulk(
  pdata,
  eset,
  group,
  id_pdata = "ID",
  nfeatures = 2000,
  top_n = 20,
  thresh.use = 0.25,
  only.pos = TRUE,
  min.pct = 0.25,
  npcs = 30
)
```

Arguments

pdata	Data frame. Sample metadata.
eset	Matrix. Gene expression or signature score matrix.
group	Character. Column name in pdata specifying grouping variable.
id_pdata	Character. Column name for sample IDs. Default is "ID".
nfeatures	Integer. Number of top variable features to select. Default is 2000.
top_n	Integer. Number of top markers to retain per cluster. Default is 20.
thresh.use	Numeric. Threshold for marker selection. Default is 0.25.
only.pos	Logical. Whether to retain only positive markers. Default is TRUE.
min.pct	Numeric. Minimum expression percentage threshold. Default is 0.25.
npcs	Integer. Number of principal components to use. Default is 30.

Value

List with components: ‘sce‘ (Seurat object), ‘markers‘ (all markers), ‘top_markers‘ (top markers per group).

Examples

```
if (requireNamespace("Seurat", quietly = TRUE) && requireNamespace("Matrix", quietly = TRUE)) {
  # Simulate data
  set.seed(123)
  sim_eset <- matrix(abs(rnorm(100 * 30)), 100, 30)
  rownames(sim_eset) <- paste0("Gene", 1:100)
  colnames(sim_eset) <- paste0("Sample", 1:30)

  sim_pdata <- data.frame(
    ID = paste0("Sample", 1:30),
    TMEcluster = rep(c("A", "B", "C"), each = 10)
  )

  res <- find_markers_in_bulk(
    pdata = sim_pdata, eset = sim_eset,
    group = "TMEcluster", npcs = 5
  )
  if (!is.null(res)) head(res$top_markers)
}
```

---

find_mutations *Analyze Mutations Related to Signature Scores*

Description

This function identifies mutations associated with a specific signature score, performs statistical tests for significance, and generates oncoprints and box plots to visualize relationships.

Usage

```
find_mutations(
  mutation_matrix,
  signature_matrix,
  id_signature_matrix = "ID",
  signature,
  min_mut_freq = 0.05,
  plot = TRUE,
  method = "multi",
  point_alpha = 0.1,
  save_path = NULL,
  palette = "jco",
  cols = NULL,
  show_plot = TRUE,
  show_col = FALSE,
  width = 8,
  height = 4,
  oncoprint_group_by = "mean",
  oncoprint_col = "#224444",
  gene_counts = 10,
  jitter = FALSE,
  genes = NULL,
  point_size = 4.5
)
```

Arguments

mutation_matrix	A matrix of mutation data with samples in rows and genes in columns.
signature_matrix	A data frame with sample identifiers and signature scores.
id_signature_matrix	Column name in ‘signature_matrix‘ for sample identifiers.
signature	Name of the target signature for analysis.
min_mut_freq	Minimum mutation frequency required for gene inclusion. Default is 0.05.
plot	Logical indicating whether to generate and save plots. Default is TRUE.
method	Statistical test method: "multi" for both Cuzick and Wilcoxon, or "Wilcoxon" only. Default is "multi".
point_alpha	Transparency of points in box plot. Default is 0.1.
save_path	Directory to save plots and results. If NULL, no files are saved.
palette	Color palette for box plots(used when cols is NULL). Default is "jco".
cols	Character vector. Custom colors for box plots. If NULL, uses palette. Default is NULL.
show_plot	Logical indicating whether to display plots. Default is TRUE.
show_col	Logical indicating whether to show color codes. Default is FALSE.

width	Width of oncoprint plot. Default is 8.
height	Height of oncoprint plot. Default is 4.
oncoprint_group_by	Grouping method for oncoprint: "mean" or "quantile". Default is "mean".
oncoprint_col	Color for mutations in oncoprint. Default is "#224444".
gene_counts	Number of genes to display in oncoprint. Default is 10.
jitter	Logical indicating whether to add jitter to box plot points. Default is FALSE.
genes	Optional vector of gene names; if NULL, selects based on frequency.
point_size	Size of points in box plot. Default is 4.5.

Value

A list containing statistical test results, oncoprint plots, and box plots.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
# This example requires a MAF file from TCGA or maftools
# See maftools or TCGAbiolinks documentation for obtaining MAF files
mut_list <- make_mut_matrix(
  maf = "path_to_maf_file", isTCGA = TRUE,
  category = "multi"
)
mut <- mut_list$snp
results <- find_mutations(
  mutation_matrix = mut, signature_matrix = signature_data,
  id_signature_matrix = "ID", signature = "CD_8_T_effector",
  min_mut_freq = 0.01, plot = TRUE, method = "multi"
)

## End(Not run)
```

---

find_outlier_samples *Identify Outlier Samples in Gene Expression Data*

Description

Analyzes gene expression data to identify potential outlier samples using connectivity analysis via the WGCNA package. Calculates normalized adjacency and connectivity z-scores for each sample, generates connectivity plots, and optionally performs hierarchical clustering.

Usage

```
find_outlier_samples(
  eset,
  yinter = -3,
  project = NULL,
  plot_hculst = FALSE,
  show_plot = TRUE,
  index = NULL,
  save = FALSE
)
```

Arguments

eset	Numeric matrix. Gene expression data with genes as rows and samples as columns.
yinter	Numeric. Z-score threshold for identifying outliers. Default is -3.
project	Character or 'NULL'. Output directory path for saving plots. Required if 'save = TRUE'. Default is 'NULL'.
plot_hculst	Logical. Whether to plot hierarchical clustering. Default is 'FALSE'.
show_plot	Logical. Whether to display the connectivity plot. Default is 'TRUE'.
index	Integer or 'NULL'. Index for output file naming. Default is 'NULL'.
save	Logical. Whether to save plots to files. Default is 'FALSE'.

Value

Character vector of sample names identified as potential outliers.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_eset <- matrix(rnorm(100 * 10), 100, 10)
rownames(sim_eset) <- paste0("Gene", 1:100)
colnames(sim_eset) <- paste0("Sample", 1:10)

# Add one extreme outlier
sim_eset[, 10] <- sim_eset[, 10] + 50

# Identify outliers
if (requireNamespace("WGCNA", quietly = TRUE)) {
  outs <- find_outlier_samples(eset = sim_eset, show_plot = FALSE)
  print(outs)
}
```

`find_variable_genes` *Identify Variable Genes in Expression Data*

Description

Identifies variable genes from a gene expression dataset using specified selection criteria. Supports multiple methods, including expression thresholding and variability estimation via median absolute deviation (MAD).

Usage

```
find_variable_genes(
  eset,
  data_type = c("count", "normalized"),
  methods = c("low", "mad"),
  prop = 0.7,
  quantile = 0.75,
  min.mad = 0.1,
  feas = NULL
)
```

Arguments

`eset`	Numeric matrix. Gene expression data (genes as rows, samples as columns).
`data_type`	Character. Type of data: ‘"count"‘ or ‘"normalized"‘. Default is ‘"count"‘.
`methods`	Character vector. Methods for gene selection: ‘"low"‘, ‘"mad"‘. Default is ‘c("low", "mad")‘.
`prop`	Numeric. Proportion of samples in which a gene must be expressed. Default is 0.7.
`quantile`	Numeric. Quantile threshold for minimum MAD (0.25, 0.5, 0.75). Default is 0.75.
`min.mad`	Numeric. Minimum allowable MAD value. Default is 0.1.
`feas`	Character vector or ‘NULL‘. Additional features to include. Default is ‘NULL‘.

Value

Matrix subset of ‘eset‘ containing variable genes.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_eset <- matrix(rnorm(100 * 20), 100, 20)
rownames(sim_eset) <- paste0("Gene", 1:100)
colnames(sim_eset) <- paste0("Sample", 1:20)

# Identify variable genes
eset_var <- find_variable_genes(
  eset = sim_eset,
  data_type = "normalized",
  methods = "mad",
  quantile = 0.25
)
head(eset_var)
```

`format_msigdb` *Format Input Signatures from MSigDB*

Description

Reads a GMT file from MSigDB and converts it into a named list of gene sets suitable for IOBR functions.

Usage

```
format_msigdb(gmt, ont = "term", gene = "gene")
```

Arguments

gmt	Character string. Path to a GMT file.
ont	Character string. Name of the signature/set column in the parsed GMT table. Default is ‘"term"‘.
gene	Character string. Name of the gene column in the parsed GMT table. Default is ‘"gene"‘.

Value

Named list of character vectors, where each element contains the genes belonging to one signature.

Examples

```
if (rlang::is_installed("clusterProfiler")) {
  tf <- tempfile(fileext = ".gmt")
  writeLines(
    c(
      "HALLMARK_TNFA_SIGNALING_VIA_NFKB\tNA\tTNF\tNFKB1\tNFKB2",
      "HALLMARK_P53_PATHWAY\tNA\tTP53\tMDM2\tCDKN1A"
```

```
    ),
    con = tf
  )

  sig_list <- format_msigdb(tf, ont = "term", gene = "gene")
  names(sig_list)
  sig_list[[1]]
}
```

---

format_signatures *Transform Signature Data into List Format*

Description

Converts signature data from a data frame (with signatures as columns and genes as rows) into a list format suitable for IOBR functions. Handles NA values appropriately.

Usage

```
format_signatures(sig_data, save_signature = FALSE, output_path = NULL)
```

Arguments

sig_data	Data frame with signature names as columns and genes in rows. Use 'NA' for missing values.
save_signature	Logical. Whether to save the signature list as RData. Default is 'FALSE'.
output_path	Character. Full path (without extension) for output file. Required if 'save_signature = TRUE'. Default is 'NULL'.

Value

List of signatures.

Author(s)

Dongqiang Zeng

Examples

```
sig_data <- data.frame(
  Signature1 = c("Gene1", "Gene2", "Gene3", NA),
  Signature2 = c("Gene4", "Gene5", NA, NA)
)
format_signatures(sig_data)
```

generateRef *Generate Reference Signature Matrix*

Description

Generates a reference signature matrix for cell types based on differential expression analysis. Supports both limma for normalized data and DESeq2 for raw count data.

Usage

```
generateRef(dds, pheno, FDR = 0.05, dat, method = "limma")
```

Arguments

dds	Matrix. Raw count data from RNA-seq. Required if ‘method = "DESeq2"‘.
pheno	Character vector. Cell type class of the samples.
FDR	Numeric. Genes with BH adjusted p-value < FDR are considered significant. Default is 0.05.
dat	Matrix or data frame. Normalized transcript quantification data (e.g., FPKM, TPM).
method	Character. Method for differential expression: ‘"limma"‘ or ‘"DESeq2"‘. Default is ‘"limma"‘.

Value

List containing: - ‘reference_matrix‘: Data frame of median expression for significant genes across cell types. - ‘G‘: Optimal number of probes minimizing condition number. - ‘condition_number‘: Minimum condition number. - ‘whole_matrix‘: Full median expression matrix.

Examples

```
expressionData <- matrix(runif(1000 * 4, min = 0, max = 10), ncol = 4)
rownames(expressionData) <- paste("Gene", 1:1000, sep = "_")
colnames(expressionData) <- paste("Sample", 1:4, sep = "_")

phenotype <- c("celltype1", "celltype2", "celltype1", "celltype2")

rawCountData <- matrix(sample(1:100, 1000 * 4, replace = TRUE), ncol = 4)
rownames(rawCountData) <- paste("Gene", 1:1000, sep = "_")
colnames(rawCountData) <- paste("Sample", 1:4, sep = "_")


result <- generateRef(
  dds = rawCountData, pheno = phenotype,
  FDR = 0.05, dat = expressionData, method = "DESeq2"
)
```

generateRef_DEseq2 *Generate Reference Signature Matrix Using DESeq2*

Description

Uses DESeq2 to perform differential expression analysis across cell types, identifies significantly expressed genes, and creates a reference signature matrix from median expression levels.

Usage

```
generateRef_DEseq2(dds, pheno, FDR = 0.05, dat)
```

Arguments

dds	Matrix. Raw count data from RNA-seq.
pheno	Character vector. Cell type classes for samples.
FDR	Numeric. Threshold for adjusted p-values. Default is 0.05.
dat	Matrix. Normalized expression data (e.g., FPKM, TPM) for calculating median expression.

Value

List containing: - ‘reference_matrix‘: Data frame of median expression for significant genes across cell types. - ‘G‘: Optimal number of probes minimizing condition number. - ‘condition_number‘: Minimum condition number. - ‘whole_matrix‘: Full median expression matrix.

Examples

```
set.seed(123)
dds <- matrix(sample(0:1000, 2000, replace = TRUE), nrow = 100, ncol = 20)
colnames(dds) <- paste("Sample", 1:20, sep = "_")
rownames(dds) <- paste("Gene", 1:100, sep = "_")
pheno <- rep(c("Type1", "Type2"), each = 10)
dat <- matrix(runif(2000), nrow = 100, ncol = 20)
rownames(dat) <- rownames(dds)
colnames(dat) <- colnames(dds)

result <- generateRef_DEseq2(dds = dds, pheno = pheno, FDR = 0.05, dat = dat)
print(result$reference_matrix)
```

generateRef_limma *Generate Reference Signature Matrix Using Limma*

Description

Performs differential expression analysis using the limma package to identify significantly expressed genes across different cell types. Computes median expression levels of these significant genes to create a reference signature matrix.

Usage

```
generateRef_limma(dat, pheno, FDR = 0.05)
```

Arguments

dat	Matrix or data frame. Gene probes in rows and samples in columns.
pheno	Character vector. Cell type class of the samples.
FDR	Numeric. Genes with BH adjusted p-value < FDR are considered significant. Default is 0.05.

Value

List containing: - ‘reference_matrix‘: Data frame of median expression values for significantly expressed genes. - ‘G‘: Number of probes used that resulted in the lowest condition number. - ‘condition_number‘: Minimum condition number obtained. - ‘whole_matrix‘: Matrix of median values across all samples.

Examples

```
dat <- matrix(rnorm(2000), nrow = 100)
rownames(dat) <- paste("Gene", 1:100, sep = "_")
colnames(dat) <- paste("Sample", 1:20, sep = "_")
pheno <- sample(c("Type1", "Type2", "Type3"), 20, replace = TRUE)
results <- generateRef_limma(dat, pheno)
print(results)
```

generateRef_rnaseq *Generate Reference Gene Matrix from RNA-seq DEGs*

Description

Uses DESeq2 to identify differentially expressed genes and create a reference matrix from median expression levels across cell types.

Usage

```
generateRef_rnaseq(dds, pheno, mode = "oneVSothers", FDR = 0.05, dat)
```

Arguments

dds	Matrix. Raw count data from RNA-seq.
pheno	Character vector. Cell type classes.
mode	Character. DEG identification mode: ‘"oneVSothers"‘ or ‘"pairs"‘. Default is ‘"oneVSothers"‘.
FDR	Numeric. Threshold for adjusted p-values. Default is 0.05.
dat	Matrix. Normalized expression data (e.g., FPKM, TPM).

Value

List containing: - ‘reference_matrix‘: Data frame of median expression for significant genes across cell types. - ‘G‘: Optimal number of probes minimizing condition number. - ‘condition_number‘: Minimum condition number. - ‘whole_matrix‘: Full median expression matrix.

Author(s)

Rongfang Shen

Examples

```
dds <- matrix(rpois(200 * 10, lambda = 10), ncol = 10)
rownames(dds) <- paste("Gene", 1:200, sep = "_")
colnames(dds) <- paste("Sample", 1:10, sep = "_")
pheno <- sample(c("Type1", "Type2", "Type3"), 10, replace = TRUE)
dat <- matrix(rnorm(200 * 10), ncol = 10)
rownames(dat) <- rownames(dds)
colnames(dat) <- colnames(dds)

results <- generateRef_rnaseq(dds = dds, pheno = pheno, FDR = 0.05, dat = dat)
```

---

generateRef_seurat *Generate Reference Matrix from Seurat Object*

Description

Generates reference gene expression data from a Seurat object by identifying marker genes for each cell type and aggregating expression data.

Usage

```
generateRef_seurat(
  sce,
  celltype = NULL,
  proportion = NULL,
  assay_deg = "RNA",
  slot_deg = "data",
  adjust_assay = FALSE,
  assay_out = "RNA",
  slot_out = "data",
  verbose = FALSE,
  only.pos = TRUE,
  n_ref_genes = 50,
  logfc.threshold = 0.15,
  test.use = "wilcox"
)
```

Arguments

sce	Seurat object containing single-cell RNA-seq data.
celltype	Character. Cell type column name in metadata. Default is 'NULL' (uses default identity).
proportion	Numeric. Proportion of cells to randomly select for analysis. Default is 'NULL' (use all cells).
assay_deg	Character. Assay for finding markers. Default is '"RNA"'.
slot_deg	Character. Slot for finding markers. Default is '"data"'.
adjust_assay	Logical. Whether to adjust assay for SCT. Default is 'FALSE'.
assay_out	Character. Assay for output. Default is '"RNA"'.
slot_out	Character. Slot for output. Default is '"data"'.
verbose	Logical. Print verbose messages. Default is 'FALSE'.
only.pos	Logical. Return only positive markers. Default is 'TRUE'.
n_ref_genes	Integer. Number of reference genes per cell type. Default is 50.
logfc.threshold	Numeric. Log fold change threshold. Default is 0.15.
test.use	Character. Statistical test for marker identification. Default is '"wilcox"'.

Value

Matrix containing aggregated expression data for reference genes.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
if (requireNamespace("Seurat", quietly = TRUE)) {
  # Requires a Seurat object with sufficient cells and markers
  sm <- generateRef_seurat(sce = seurat_obj, celltype = "cell_type", slot_out = "data")
}

## End(Not run)
```

GetFractions.Abbas *Constrained Regression Method (Abbas et al., 2009)*

Description

Implements a constrained regression approach described by Abbas et al. (2009). Estimates proportions of immune cell types within mixed cancer tissue samples based on gene expression data. Iteratively adjusts regression coefficients to ensure non-negative values.

Usage

```
GetFractions.Abbas(XX, YY, w = NA)
```

Arguments

XX	Matrix. Immune expression data with genes as rows and cell types as columns.
YY	Vector. Cancer expression data with gene expression levels.
w	Vector or NA. Weights for regression. Default is NA (no weights).

Value

Vector with non-negative coefficients representing proportions of each cell type.

Examples

```
XX <- matrix(runif(100), nrow = 10, ncol = 10)
colnames(XX) <- paste("CellType", 1:10, sep = "")
YY <- runif(10)
results <- GetFractions.Abbas(XX, YY)
print(results)
```

getHRandCIfromCoxph *Extract Hazard Ratio and Confidence Intervals from Cox Model*

Description

Extracts hazard ratio (HR) and 95 Cox proportional hazards model.

Usage

```
getHRandCIfromCoxph(coxphData)
```

Arguments

coxphData	Fitted Cox model object from 'survival::coxph()'.

Value

Data frame with p-values, HR, and confidence intervals.

Author(s)

Dorothee Nickles

Dongqiang Zeng

Examples

```
library(survival)
set.seed(123)
df <- data.frame(
  TTE = rexp(200, rate = 0.1),
  Cens = rbinom(200, size = 1, prob = 0.7),
  group = sample(c("Treatment", "Control"), 200, replace = TRUE)
)
coxphData <- survival::coxph(survival::Surv(TTE, Cens) ~ group, data = df)
results <- getHRandCIfromCoxph(coxphData)
print(results)
```

GetOutlierGenes *Get Outlier Genes*

Description

Identifies outlier genes from multiple cancer datasets. Treats the top 5 expressed genes in each sample as outliers and returns unique outlier genes.

Usage

```
GetOutlierGenes(cancers)
```

Arguments

cancers	Data frame. One column containing paths to gene expression files.

Value

Vector of unique gene names identified as outliers.

Examples

```
tf1 <- tempfile(fileext = ".tsv")
tf2 <- tempfile(fileext = ".tsv")

expr1 <- data.frame(
  gene = c("GeneA", "GeneB", "GeneC", "GeneD", "GeneE", "GeneF"),
  Sample1 = c(10, 50, 30, 80, 60, 20),
  Sample2 = c(15, 40, 25, 90, 55, 10)
)

expr2 <- data.frame(
  gene = c("GeneA", "GeneB", "GeneC", "GeneD", "GeneE", "GeneF"),
  Sample3 = c(100, 20, 10, 60, 30, 80),
  Sample4 = c(95, 25, 15, 70, 35, 85)
)

write.table(expr1, tf1, sep = "\t", row.names = FALSE, quote = FALSE)
write.table(expr2, tf2, sep = "\t", row.names = FALSE, quote = FALSE)

cancers <- data.frame(ExpressionFiles = c(tf1, tf2))
outlier_genes <- GetOutlierGenes(cancers)
```

---

get_cols *Set and View Color Palettes*

Description

Retrieves color palettes from the IOBR package with options for randomization and visualization. Users can specify predefined palettes or provide custom colors.

Usage

```
get_cols(cols = "normal", palette = 1, show_col = TRUE, seed = 123)
```

Arguments

cols	Character vector of colors, or one of: - ‘"normal"‘: Use standard palette - ‘"random"‘: Randomly shuffle the palette Default is ‘"normal"‘.
palette	Numeric or character specifying the palette. Options are 1, 2, 3, 4, or palette name. Default is 1.
show_col	Logical indicating whether to display the color palette. Default is ‘TRUE‘.
seed	Integer seed for random number generator when ‘cols = "random"‘. Default is 123.

Value

Character vector of colors.

Examples

```
# Get default palette
mycols <- get_cols()

# Get random palette
mycols <- get_cols(cols = "random", seed = 456)

# Use custom colors
mycols <- get_cols(cols = c("red", "blue", "green"))
```

---

get_cor *Calculate and Visualize Correlation Between Two Variables*

Description

Calculates and visualizes the correlation between two variables with options for scaling, handling missing values, and incorporating grouping data.

Usage

```
get_cor(
  eset,
  pdata = NULL,
  var1,
  var2,
  is.matrix = FALSE,
  id_eset = "ID",
  id_pdata = "ID",
  scale = TRUE,
  subtype = NULL,
  na.subtype.rm = FALSE,
  color_subtype = NULL,
  palette = "jama",
```

```
  index = NULL,
  method = c("spearman", "pearson", "kendall"),
  show_cor_result = TRUE,
  col_line = NULL,
  id = NULL,
  show_label = FALSE,
  point_size = 4,
  title = NULL,
  alpha = 0.5,
  title_size = 1.5,
  text_size = 10,
  axis_angle = 0,
  hjust = 0,
  show_plot = TRUE,
  save_plot = FALSE,
  path = NULL,
  fig.format = "png",
  fig.width = 7,
  fig.height = 7.3,
  add.hdr.line = FALSE
)
```

Arguments

eset	Dataset containing the variables (data frame or matrix).
pdata	Optional phenotype data frame. Default is 'NULL'.
var1	Name of the first variable.
var2	Name of the second variable.
is.matrix	Logical indicating if 'eset' is a matrix with features as rows. Default is 'FALSE'.
id_eset	ID column in 'eset'. Default is '"ID"'.
id_pdata	ID column in 'pdata'. Default is '"ID"'.
scale	Logical indicating whether to scale data. Default is 'TRUE'.
subtype	Optional grouping variable for coloring points. Default is 'NULL'.
na.subtype.rm	Logical indicating whether to remove NA in subtype. Default is 'FALSE'.
color_subtype	Colors for subtypes. Default is 'NULL'.
palette	Color palette name. Default is '"jama"'.
index	Plot index for filename. Default is 'NULL' (uses 1).
method	Correlation method: '"spearman"', '"pearson"', or '"kendall"'. Default is '"spearman"'.
show_cor_result	Logical indicating whether to print correlation result. Default is 'TRUE'.
col_line	Color of regression line. Default is 'NULL' (auto-determine).
id	Column for point labels. Default is 'NULL'.
show_label	Logical indicating whether to show labels. Default is 'FALSE'.

point_size	Size of points. Default is 4.
title	Plot title. Default is 'NULL'.
alpha	Transparency of points. Default is 0.5.
title_size	Title font size. Default is 1.5.
text_size	Text font size. Default is 10.
axis_angle	Axis label angle. Default is 0.
hjust	Horizontal justification. Default is 0.
show_plot	Logical indicating whether to display plot. Default is 'TRUE'.
save_plot	Logical indicating whether to save plot. Default is 'FALSE'.
path	Save path. Default is 'NULL'.
fig.format	Figure format: '"png"' or '"pdf"'. Default is '"png"'.
fig.width	Figure width in inches. Default is 7.
fig.height	Figure height in inches. Default is 7.3.
add.hdr.line	Logical for adding HDR (high density region) lines. Default is 'FALSE'.

Value

A ggplot object of the correlation plot.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_eset <- matrix(rnorm(100 * 20), 100, 20)
rownames(sim_eset) <- c("GZMB", "CD274", paste0("Gene", 3:100))
colnames(sim_eset) <- paste0("Sample", 1:20)

# Calculate and plot correlation
p <- get_cor(eset = sim_eset, is.matrix = TRUE, var1 = "GZMB", var2 = "CD274", show_plot = FALSE)
if (!is.null(p)) print(p)
```

---

get_cor_matrix *Calculate and Visualize Correlation Matrix Between Two Variable Sets*

Description

Calculates and visualizes the correlation matrix between two sets of variables. Supports Pearson, Spearman, and Kendall correlation methods. The function generates a customizable heatmap with significance stars.

Usage

```
get_cor_matrix(
  data,
  feas1,
  feas2,
  method = c("pearson", "spearman", "kendall"),
  path = NULL,
  index = 1,
  fig.type = "pdf",
  width = NULL,
  height = NULL,
  project = NULL,
  is.matrix = FALSE,
  scale = TRUE,
  font.size = 15,
  fill_by_cor = FALSE,
  round.num = 1,
  font.size.star = 8,
  cols = NULL
)
```

Arguments

data	Input data frame or matrix. Variables should be in columns.
feas1	Character vector of variable names for the first set.
feas2	Character vector of variable names for the second set.
method	Correlation method: ‘"pearson"‘, ‘"spearman"‘, or ‘"kendall"‘. Default is ‘"pearson"‘.
path	Directory to save the plot. If ‘NULL‘, plot is not saved. Default is ‘NULL‘.
index	Numeric prefix for output filename. Default is 1.
fig.type	File format: ‘"pdf"‘, ‘"png"‘, etc. Default is ‘"pdf"‘.
width	Plot width in inches. Auto-calculated if ‘NULL‘.
height	Plot height in inches. Auto-calculated if ‘NULL‘.
project	Project name for plot title. Default is ‘NULL‘.
is.matrix	Logical: if ‘TRUE‘, data is transposed. Default is ‘FALSE‘.
scale	Logical: scale variables before correlation. Default is ‘TRUE‘.
font.size	Font size for axis labels. Default is 15.
fill_by_cor	Logical: show correlation values instead of stars. Default is ‘FALSE‘.
round.num	Decimal places for correlation values. Default is 1.
font.size.star	Font size for significance stars. Default is 8.
cols	Custom colors for gradient (low, mid, high). If ‘NULL‘, uses blue-white-red. Default is ‘NULL‘.

Value

ggplot object displaying the correlation matrix heatmap.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
data <- as.data.frame(matrix(rnorm(1000), nrow = 100, ncol = 10))
colnames(data) <- paste0("Gene_", 1:10)

feas1 <- c("Gene_1", "Gene_2", "Gene_3")
feas2 <- c("Gene_4", "Gene_5", "Gene_6")

cor_plot <- get_cor_matrix(
  data = data,
  feas1 = feas1,
  feas2 = feas2,
  method = "spearman",
  project = "Example Correlation"
)
```

---

get_iobr_cache_dir *Get IOBR Cache Directory*

Description

Returns the current cache directory for IOBR downloaded data. To comply with CRAN policies, the default cache directory is a session-specific temporary directory. Users can opt-in to a persistent cache by setting ‘options(IOBR.cache_dir = "your/path")‘ or using ‘set_iobr_cache_dir()‘.

The cache directory is determined in the following priority order: 1. Function argument ‘cache_dir‘ (if provided) 2. Option ‘IOBR.cache_dir‘ (if set via ‘options()‘) 3. Default: A session-specific temporary directory (‘file.path(tempdir(), "IOBR_cache")‘)

Usage

```
get_iobr_cache_dir(cache_dir = NULL)
```

Arguments

cache_dir	Optional character string to override the current setting.

Value

Character string with the cache directory path.

Examples

```
# Get current cache directory (defaults to tempdir)
get_iobr_cache_dir()

# Set custom cache directory via options (use tempdir() for examples)
options(IOBR.cache_dir = tempdir())
get_iobr_cache_dir()
```

`get_sig_sc` *Extract Top Marker Genes from Single-Cell Differential Results*

Description

Selects the top N marker genes per cluster from a ranked differential expression result table.

Usage

```
get_sig_sc(
  deg,
  cluster = "cluster",
  gene = "gene",
  avg_log2FC = "avg_log2FC",
  n = 100
)
```

Arguments

`deg`	Data frame or matrix. Ranked marker statistics.
`cluster`	Character. Column name containing cluster identifiers. Default is ‘"cluster"‘.
`gene`	Character. Column name containing gene identifiers. Default is ‘"gene"‘.
`avg_log2FC`	Character. Column name for average log2 fold change. Default is ‘"avg_log2FC"‘.
`n`	Integer. Number of top markers per cluster. Default is 100.

Value

List of character vectors; each element contains the top N genes for a cluster.

Examples

```
# Simulate marker data
set.seed(123)
sim_deg <- data.frame(
  cluster = rep(c("A", "B"), each = 50),
  gene = paste0("Gene", 1:100),
  avg_log2FC = rnorm(100, 2, 1)
)
```

```
# Extract top 5 markers per cluster
markers <- get_sig_sc(sim_deg, n = 5)
print(markers)
```

`high_var_fea` *Identify High-Variance Features from Statistical Results*

Description

Selects top variable (up- and down-regulated) features based on adjusted p-value and log fold-change thresholds.

Usage

```
high_var_fea(
  result,
  target,
  name_padj = "padj",
  padj_cutoff = 1,
  name_logfc,
  logfc_cutoff = 0,
  n = 10,
  data_type = NULL
)
```

Arguments

`result`	Data frame or tibble. Statistical results containing feature, adjusted p-value, and logFC columns.
`target`	Character. Column name of feature identifiers.
`name_padj`	Character. Adjusted p-value column name. Default is ‘"padj"‘.
`padj_cutoff`	Numeric. Adjusted p-value threshold. Default is 1.
`name_logfc`	Character. log2 fold-change column name.
`logfc_cutoff`	Numeric. Absolute log2 fold-change threshold. Default is 0.
`n`	Integer. Number of top up and top down features to select. Default is 10.
`data_type`	Character or ‘NULL‘. If ‘"survival"‘, adjusts logFC interpretation. Default is ‘NULL‘.

Value

Character vector of selected feature names (combined up and down sets).

Author(s)

Dongqiang Zeng

Examples

```
result_data <- data.frame(
  gene = c("Gene1", "Gene2", "Gene3", "Gene4", "Gene5"),
  padj = c(0.01, 0.02, 0.05, 0.001, 0.03),
  logfc = c(-2, 1.5, -3, 2.5, 0.5)
)
high_var_fea(
  result = result_data,
  target = "gene",
  name_padj = "padj",
  name_logfc = "logfc",
  n = 2,
  padj_cutoff = 0.05,
  logfc_cutoff = 1.5
)
```

---

imvigor210_pdata *IMvigor210 Bladder Cancer Immunotherapy Cohort Data*

Description

Clinical and biomarker data from the IMvigor210 clinical trial cohort. Includes treatment response, survival outcomes, and immune biomarker measurements for bladder cancer patients treated with atezolizumab.

Usage

```
data(imvigor210_pdata)
```

Format

A data frame with patients as rows and variables as columns:

ID Patient sample identifier

BOR Best overall response (CR, PR, SD, PD, NA)

BOR_binary Binary response classification (R=responder, NR=non-responder)

OS_days Overall survival time in days

OS_status Overall survival status (0=alive, 1=dead)

Mutation_Load Tumor mutation burden

Neo_antigen_Load Neoantigen load

CD_8_T_effector CD8+ T effector signature score

Immune_Checkpoint Immune checkpoint signature score

Pan_F_TBRs Pan-fibroblast TGF-β response signature

Mismatch_Repair Mismatch repair status or signature

TumorPurity Estimated tumor purity

Source

IMvigor210 clinical trial (NCT02108652)

References

Mariathasan S et al. TGFβ attenuates tumour response to PD-L1 blockade by contributing to exclusion of T cells. Nature 554, 544-548 (2018). doi:10.1038/nature25501

Examples

```
data(imvigor210_pdata)
head(imvigor210_pdata)
```

---

iobr_cor_plot *Integrative Correlation Analysis Between Phenotype and Features*

Description

Performs comprehensive correlation analysis between phenotype data and feature data, supporting both continuous and categorical phenotypes. Filters features based on statistical significance and generates publication-ready visualizations including box plots, heatmaps, and correlation plots.

Usage

```
iobr_cor_plot(
  pdata_group,
  id1 = "ID",
  feature_data,
  id2 = "ID",
  target = NULL,
  group = "group3",
  is_target_continuous = TRUE,
  padj_cutoff = 1,
  index = 1,
  category = "signature",
  signature_group = NULL,
  ProjectID = "TCGA",
  palette_box = "nrc",
  cols_box = NULL,
  palette_corplot = "pheatmap",
  palette_heatmap = 2,
  feature_limit = 26,
  character_limit = 60,
  show_heatmap_col_name = FALSE,
  show_col = FALSE,
  show_plot = FALSE,
  path = NULL,
```

```
  discrete_x = 20,
  discrete_width = 20,
  show_palettes = FALSE,
  fig.type = "pdf"
)
```

Arguments

pdata_group	Data frame containing phenotype data with an identifier column.
id1	Character string specifying the column name in ‘pdata_group‘ serving as the sample identifier. Default is ‘"ID"‘.
feature_data	Data frame containing feature data with corresponding identifiers.
id2	Character string specifying the column name in ‘feature_data‘ serving as the sample identifier. Default is ‘"ID"‘.
target	Character string specifying the target variable column name for continuous analysis. Default is ‘NULL‘.
group	Character string specifying the grouping variable name for categorical analysis. Default is ‘"group3"‘.
is_target_continuous	Logical indicating whether the target variable is continuous, which affects grouping strategy. Default is ‘TRUE‘.
padj_cutoff	Numeric value specifying the adjusted p-value cutoff for filtering features. Default is ‘1‘.
index	Numeric index used for ordering output file names. Default is ‘1‘.
category	Character string specifying the data category: ‘"signature"‘ or ‘"gene"‘.
signature_group	List specifying the grouping variable for signatures. Options include ‘"sig_group"‘ for signature grouping or ‘"signature_collection"‘/‘"signature_tme"‘ for gene grouping.
ProjectID	Character string specifying the project identifier for file naming.
palette_box	Character string or integer specifying the color palette for box plots. Default is ‘"nrc"‘.
cols_box	Character vector of specific colors for box plots. Default is ‘NULL‘.
palette_corplot	Character string or integer specifying the color palette for correlation plots. Default is ‘"pheatmap"‘.
palette_heatmap	Integer specifying the color palette index for heatmaps. Default is ‘2‘.
feature_limit	Integer specifying the maximum number of features to display. Default is ‘26‘.
character_limit	Integer specifying the maximum number of characters for variable labels. Default is ‘60‘.
show_heatmap_col_name	Logical indicating whether to display column names on heatmaps. Default is ‘FALSE‘.

show_col	Logical indicating whether to display color codes for palettes. Default is 'FALSE'.
show_plot	Logical indicating whether to display plots. Default is 'FALSE'.
path	Character string specifying the directory path for saving output files. Default is 'NULL'.
discrete_x	Numeric threshold for character length beyond which labels are discretized. Default is '20'.
discrete_width	Numeric value specifying the width for label wrapping in plots. Default is '20'.
show_palettes	Logical indicating whether to display color palettes. Default is 'FALSE'.
fig.type	Character string specifying the format for saving figures ('"pdf"', '"png"', etc.). Default is '"pdf"'.

Value

Depending on configuration, returns ggplot2 objects (box plots, heatmaps, correlation plots) and/or a data frame containing statistical analysis results.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)

pdata_group <- data.frame(
  ID = 1:100,
  phenotype_score = rnorm(100)
)

feature_data <- data.frame(
  ID = 1:100,
  Feature1 = rnorm(100),
  Feature2 = rnorm(100),
  Feature3 = rnorm(100)
)

sig_group_example <- list(
  signature = c("Feature1", "Feature2", "Feature3")
)

results <- iobr_cor_plot(
  pdata_group = pdata_group,
  feature_data = feature_data,
  id1 = "ID",
  id2 = "ID",
  target = "phenotype_score",
  is_target_continuous = TRUE,
  category = "signature",
  signature_group = sig_group_example,
  show_plot = FALSE,
```

```
  path = tempdir()
)

print(results)
```

`iobr_deconvo_pipeline` *Tumor Microenvironment (TME) Deconvolution Pipeline*

Description

Executes an integrated TME analysis on a gene expression matrix: performs immune/stromal cell deconvolution using multiple algorithms, computes signature scores, and aggregates results. Designed for exploratory immunogenomic profiling.

Usage

```
iobr_deconvo_pipeline(
  eset,
  project,
  array,
  tumor_type,
  path = NULL,
  permutation = 1000
)
```

Arguments

`eset`	Numeric matrix. Gene expression (TPM/log scale) with genes in rows.
`project`	Character. Project name (used in output naming).
`array`	Logical. Whether data originated from an array platform. Affects deconvolution choices.
`tumor_type`	Character. Tumor type code (e.g., "stad") used by certain methods.
`path`	Character. Output directory. Default is NULL (uses tempdir()).
`permutation`	Integer. Number of permutations for CIBERSORT (and similar). Default is 1000.

Value

Data frame integrating cell fractions and signature scores (also writes intermediate outputs to disk).

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
lm22 <- load_data("lm22")
cancer_genes <- load_data("cancer_type_genes")
if (!is.null(lm22) && !is.null(cancer_genes)) {
  set.seed(123)
  genes <- rownames(lm22)
  xcell <- load_data("xCell.data")
  if (!is.null(xcell)) genes <- unique(c(genes, xcell$genes))
  genes <- unique(c(genes, cancer_genes[["stad"]]))
  eset <- matrix(runif(length(genes) * 2), nrow = length(genes), ncol = 2)
  rownames(eset) <- genes
  colnames(eset) <- paste0("Sample", 1:2)
  res <- iobr_deconvo_pipeline(
    eset = eset, project = "TEST",
    array = FALSE, tumor_type = "stad",
    path = tempdir(), permutation = 2
  )
  if (!is.null(res)) head(res)
}

## End(Not run)
```

---

iobr_deg *Differential Expression Analysis*

Description

Performs differential expression analysis on gene expression data using either DESeq2 or limma. Includes pre-processing steps like filtering low count data, and calculates fold changes and adjusted p-values. Optionally generates volcano plots and heatmaps.

Usage

```
iobr_deg(
  eset,
  annotation = NULL,
  id_anno = NULL,
  pdata,
  group_id = "group",
  pdata_id = "ID",
  array = FALSE,
  method = c("DESeq2", "limma"),
  contrast = c("High", "Low"),
  path = NULL,
  padj_cutoff = 0.01,
  logfc_cutoff = 0.5,
```

```
  volcano_plot = FALSE,
  col_volcano = 1,
  heatmap = TRUE,
  col_heatmap = 1,
  parallel = FALSE
)
```

Arguments

eset	A matrix of gene expression data where rows represent genes and columns represent samples.
annotation	Optional data frame for mapping gene IDs to gene names. Default is 'NULL'.
id_anno	Character string specifying the identifier column in annotation. Default is 'NULL'.
pdata	A data frame containing sample information and grouping labels.
group_id	Character string specifying the column name in 'pdata' containing grouping labels. Default is '"group"'.
pdata_id	Character string specifying the column name in 'pdata' for sample IDs. Default is '"ID"'.
array	Logical indicating whether to perform quantile normalization. Default is 'FALSE'.
method	Character string specifying the method: '"DESeq2"' or '"limma"'. Default is '"DESeq2"'.
contrast	Character vector of length 2 specifying contrast groups. Default is 'c("High", "Low")'.
path	Character string for output directory. Default is 'NULL'.
padj_cutoff	Numeric cutoff for adjusted p-values. Default is '0.01'.
logfc_cutoff	Numeric log2 fold change cutoff. Default is '0.5'.
volcano_plot	Logical indicating whether to generate a volcano plot. Default is 'FALSE'.
col_volcano	Integer specifying color index for volcano plot. Default is '1'.
heatmap	Logical indicating whether to generate a heatmap. Default is 'TRUE'.
col_heatmap	Integer specifying color index for heatmap. Default is '1'.
parallel	Logical indicating whether to run in parallel. Default is 'FALSE'.

Value

Data frame containing differentially expressed genes with statistics including log2 fold changes and adjusted p-values.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_eset <- matrix(abs(rnorm(100 * 20)), 100, 20)
rownames(sim_eset) <- paste0("Gene", 1:100)
colnames(sim_eset) <- paste0("Sample", 1:20)

sim_pdata <- data.frame(
  ID = paste0("Sample", 1:20),
  group = rep(c("High", "Low"), each = 10)
)

# Run DEG analysis
deg <- iobr_deg(
  eset = sim_eset, pdata = sim_pdata,
  group_id = "group", pdata_id = "ID",
  method = "limma", contrast = c("High", "Low"),
  heatmap = FALSE
)
if (!is.null(deg)) head(deg)
```

---

iobr_pca *Principal Component Analysis (PCA) Visualization*

Description

This function performs Principal Component Analysis (PCA) on gene expression data, reduces dimensionality while preserving variance, and generates a scatter plot visualization.

Usage

```
iobr_pca(
  data,
  is.matrix = TRUE,
  scale = TRUE,
  is.log = FALSE,
  pdata,
  id_pdata = "ID",
  group = NULL,
  geom.ind = "point",
  cols = "normal",
  palette = "jama",
  repel = FALSE,
  ncp = 5,
  axes = c(1, 2),
  addEllipses = TRUE
)
```

Arguments

data	Input data for PCA: matrix or data frame.
is.matrix	Logical indicating if input is a matrix. Default is TRUE.
scale	Logical indicating whether to scale the data. Default is TRUE.
is.log	Logical indicating whether to log-transform the data. Default is FALSE.
pdata	Data frame with sample IDs and grouping information.
id_pdata	Column name in ‘pdata‘ for sample IDs. Default is "ID".
group	Column name in ‘pdata‘ for grouping variable. Default is NULL.
geom.ind	Type of geometric representation for points. Default is "point".
cols	Color scheme for groups. Default is "normal".
palette	Color palette for groups. Default is "jama".
repel	Logical indicating whether to repel overlapping points. Default is FALSE.
ncp	Number of principal components to retain. Default is 5.
axes	Principal components to plot (e.g., c(1, 2)). Default is c(1, 2).
addEllipses	Logical indicating whether to add concentration ellipses. Default is TRUE.

Value

A ggplot object of the PCA plot.

Author(s)

Dongqiang Zeng

Examples

```
if (requireNamespace("FactoMineR", quietly = TRUE) &&
  requireNamespace("factoextra", quietly = TRUE)) {
  set.seed(123)
  eset <- matrix(rnorm(1000), nrow = 100, ncol = 10)
  rownames(eset) <- paste0("Gene", 1:100)
  colnames(eset) <- paste0("Sample", 1:10)
  pdata <- data.frame(
    ID = colnames(eset),
    group = rep(c("A", "B"), each = 5)
  )
  iobr_pca(eset, pdata = pdata, id_pdata = "ID", group = "group", addEllipses = FALSE)
}
```

ipsmap *Map Score to Immunophenoscore*

Description

Maps input score to Immunophenoscore (IPS) on a 0-10 scale. Scores ≤ 0 map to 0, scores ≥ 3 map to 10, and intermediate scores are linearly scaled.

Usage

```
ipsmap(x)
```

Arguments

x	Numeric value representing the aggregate z-score.

Value

Integer value between 0 and 10 representing the Immunophenoscore.

Examples

```
ips <- ipsmap(2.5)
ips <- ipsmap(-1)
ips <- ipsmap(5)
```

IPS_calculation *Calculate Immunophenoscore (IPS)*

Description

Calculates Immunophenoscore (IPS) from gene expression data. IPS is a composite score measuring immunophenotype based on four major categories: MHC molecules, immunomodulators, effector cells, and suppressor cells.

Usage

```
IPS_calculation(eset, project = NULL, plot = FALSE)
```

Arguments

eset	Gene expression matrix with official human gene symbols (HGNC) as rownames. Expression values should be log2(TPM+1) or will be transformed if max value > 100.
project	Character string for project identifier. Default is NULL.
plot	Logical. Whether to generate immunophenogram plots. Default is FALSE.

Value

Data frame containing:

MHC MHC molecules score

EC Effector cells score

SC Suppressor cells score

CP Checkpoints/Immunomodulators score

AZ Aggregate score (sum of MHC, CP, EC, SC)

IPS Immunophenoscore (0-10 scale)

Examples

```
## Not run:
example_genes <- c(
  "HLA-A", "HLA-B", "HLA-C", "CD274", "PDCD1", "CTLA4",
  "CD8A", "CD8B", "GZMB", "PRF1", "FOXP3", "IL10"
)
sim_eset <- as.data.frame(matrix(
  rnorm(length(example_genes) * 5, mean = 5, sd = 2),
  nrow = length(example_genes), ncol = 5
))
rownames(sim_eset) <- example_genes
colnames(sim_eset) <- paste0("Sample", 1:5)
ips_result <- IPS_calculation(eset = sim_eset, project = "Example", plot = FALSE)
if (!is.null(ips_result)) head(ips_result)

## End(Not run)
```

---

lasso_select *Feature Selection for Predictive or Prognostic Models Using LASSO Regression*

Description

Applies LASSO (Least Absolute Shrinkage and Selection Operator) regression to construct predictive or prognostic models. Supports both binary and survival response variables, utilizing cross-validation for optimal model selection.

Usage

```
lasso_select(
  x,
  y,
  type = c("binary", "survival"),
  nfold = 10,
  lambda = c("lambda.min", "lambda.1se")
)
```

Arguments

x	A numeric matrix. Features (e.g., gene symbols or CGI) as row names and samples as column names.
y	A response variable vector. Can be binary (0/1) or survival data (e.g., survival time and event status).
type	Character. Model type: "binary" for binary response or "survival" for survival analysis. Default is "binary".
nfold	Integer. Number of folds for cross-validation. Default is 10.
lambda	Character. Regularization parameter selection: "lambda.min" (minimum mean cross-validated error) or "lambda.1se" (one standard error from minimum). Default is "lambda.min".

Value

Character vector of selected feature names with non-zero coefficients in the optimal LASSO model.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
gene_expression <- matrix(rnorm(100 * 20), nrow = 100, ncol = 20)
rownames(gene_expression) <- paste0("Gene", 1:100)
colnames(gene_expression) <- paste0("Sample", 1:20)

# Binary response example
binary_outcome <- sample(c(0, 1), 20, replace = TRUE)
lasso_select(
  x = gene_expression,
  y = binary_outcome,
  type = "binary",
  nfold = 5
)
```

---

limma.dif *Differential Expression Analysis Using Limma*

Description

Performs differential expression analysis using the limma package on a given gene expression dataset. Constructs a design matrix from phenotype data, fits a linear model, applies contrasts, and computes statistics for differential expression.

Usage

```
limma.dif(exprdata, pdata, contrastfml)
```

Arguments

exprdata	A matrix with rownames as features like gene symbols or cgi, and colnames as samples.
pdata	A two-column dataframe where the first column matches the colnames of exprdata and the second column contains the grouping variable.
contrastfml	A character vector for contrasts to be tested (see ?makeContrasts for more details).

Value

Returns a dataframe from limma::topTable, which includes genes as rows and columns like genelist, logFC, AveExpr, etc.

Examples

```
# Toy example with 100 genes and 6 samples
set.seed(123)
exprdata <- matrix(
  rnorm(100 * 6),
  nrow = 100,
  ncol = 6,
  dimnames = list(
    paste0("gene", 1:100),
    paste0("sample", 1:6)
  )
)

# Phenotype data: 3 vs 3
pdata <- data.frame(
  sample = colnames(exprdata),
  group = rep(c("group1", "group2"), each = 3),
  stringsAsFactors = FALSE
)

# Differential expression: group1 vs group2
res <- limma.dif(
  exprdata = exprdata,
  pdata = pdata,
  contrastfml = "group1 - group2"
)
head(res)
```

---

list_github_datasets *List Available GitHub Datasets*

Description

List Available GitHub Datasets

Usage

```
list_github_datasets()
```

Value

Character vector of available dataset names.

Examples

```
list_github_datasets()
```

---

list_iobr_mirrors *List Current Download Mirrors*

Description

Returns the current list of download mirrors.

Usage

```
list_iobr_mirrors()
```

Value

Character vector of mirror URLs.

Examples

```
list_iobr_mirrors()
```

---

load_data *Load IOBR Datasets*

Description

Loads internal datasets from the IOBR package. Supports both sysdata (internal) and exported data files included in the package.

Usage

```
load_data(name)
```

Arguments

name	Character string. Name of the dataset to load. Must be a single value. Available datasets include: - Expression data: ‘"eset_stad"‘, ‘"imvigor210_eset"‘, ‘"melanoma_data"‘ - Signatures: ‘"signature_tme"‘, ‘"signature_metabolism"‘, ‘"signature_collection"‘ - Gene sets: ‘"hallmark"‘, ‘"kegg"‘, ‘"go_bp"‘, ‘"go_cc"‘, ‘"go_mf"‘ - Cell markers: ‘"cellmarkers"‘, ‘"mcp_genes"‘ - Phenotype data: ‘"pdata_stad"‘, ‘"pdata_sig_tme"‘, ‘"pdata_acrg"‘ - Reference data: ‘"xCell.data"‘, ‘"quantiseq_data"‘, ‘"TRef"‘, ‘"BRef"‘ - Color palettes: ‘"palette1"‘, ‘"palette2"‘, ‘"palette3"‘, ‘"palette4"‘

Value

Dataset object, typically a ‘list‘, ‘data.frame‘, or ‘matrix‘. The exact type depends on the requested dataset.

Examples

```
# Load signature collection (stored in sysdata, no download)
sig_tme <- load_data("signature_tme")

# Load color palette (stored in sysdata, no download)
colors <- load_data("palette1")

# Error handling with suggestions for similar names
try(load_data("sign_tme")) # Will suggest "signature_tme"

## Not run:
# Load expression data (triggers download from GitHub)
eset <- load_data("eset_stad")

## End(Not run)
```

---

log2eset *Log2 Transformation of Gene Expression Matrix*

Description

Determines whether a gene expression matrix requires log2 transformation based on the distribution of values, and applies it if necessary. This is useful for automatically detecting raw counts or linear-scale data that should be log-transformed for downstream analysis.

Usage

```
log2eset(eset)
```

Arguments

eset	Numeric matrix. Gene expression data with genes as rows and samples in columns.

Value

Numeric matrix. Log2-transformed gene expression data (if transformation was needed), or the original data otherwise.

Examples

```
set.seed(123)
eset <- matrix(rnorm(1000, mean = 10, sd = 2), nrow = 100, ncol = 10)
rownames(eset) <- paste0("Gene", 1:100)
colnames(eset) <- paste0("Sample", 1:10)
eset_transformed <- log2eset(eset)
```

LR_cal *Calculate Ligand-Receptor Interaction Scores*

Description

Quantifies ligand-receptor interactions in the tumor microenvironment from bulk gene expression data using the easier package. This function processes raw counts or TPM data and computes interaction scores for each sample.

Usage

```
LR_cal(
  eset,
  data_type = c("count", "tpm"),
  id_type = "ensembl",
  cancer_type = "pancan"
)
```

Arguments

eset	Gene expression matrix with genes as rows and samples as columns.
data_type	Type of input data. Options are ‘"count"‘ or ‘"tpm"‘. If ‘"count"‘, data will be converted to TPM before analysis.
id_type	Type of gene identifier. Default is ‘"ensembl"‘.
cancer_type	Character string specifying the cancer type for easier. Default is ‘"pancan"‘ for pan-cancer analysis.

Value

Data frame containing ligand-receptor interaction scores with sample IDs as row names.

References

Lapuente-Santana, van Genderen, M., Hilbers, P., Finotello, F., & Eduati, F. (2021). Interpretable systems biomarkers predict response to immune-checkpoint inhibitors. Patterns (New York, N.Y.), 2(8), 100293. https://doi.org/10.1016/j.patter.2021.100293

Examples

```
# LR_cal requires HGNC gene symbols as rownames
# Create a simple example with gene symbols
example_genes <- c(
  "TGFB1", "EGFR", "VEGFA", "PDGFB", "FGF2", "CXCL12",
  "CXCR4", "IL6", "IL6R", "TNF", "TNFRSF1A", "IFNG"
)
sim_eset <- as.data.frame(matrix(
  rnorm(length(example_genes) * 10, mean = 5, sd = 2),
  nrow = length(example_genes), ncol = 10
))
rownames(sim_eset) <- example_genes
colnames(sim_eset) <- paste0("Sample", 1:10)
## Not run:
if (requireNamespace("easier", quietly = TRUE)) {
  tryCatch({
    lr <- LR_cal(eset = sim_eset, data_type = "tpm")
    head(lr)
  }, error = function(e) {
    message("Example skipped: could not download ExperimentHub data")
  })
}

## End(Not run)
```

---

make_mut_matrix *Construct Mutation Matrices from MAF Data*

Description

Builds mutation presence/absence matrices from MAF input (file path or MAF object). Supports multiple categories: all mutations, SNPs, indels, and frameshift mutations. When category = "multi", returns a list of matrices for each category. Compatible with TCGA-formatted data.

Usage

```
make_mut_matrix(
  maf = NULL,
  mut_data = NULL,
  isTCGA = TRUE,
  category = c("multi", "all", "snp", "indel", "frameshift"),
  Tumor_Sample_Barcode = "Tumor_Sample_Barcode",
  Hugo_Symbol = "Hugo_Symbol",
  Variant_Classification = "Variant_Classification",
  Variant_Type = "Variant_Type"
)
```

Arguments

maf	Character or MAF object. Path to MAF file or an already loaded MAF object.
mut_data	Data frame or NULL. Preloaded MAF-like data (used if 'maf' is NULL).
isTCGA	Logical. Whether the MAF follows TCGA conventions. Default is TRUE.
category	Character. Mutation category: "all", "snp", "indel", "frameshift", or "multi". Default is "multi".
Tumor_Sample_Barcode	Character. Column name for tumor sample IDs. Default is "Tumor_Sample_Barcode".
Hugo_Symbol	Character. Column name for gene symbols. Default is "Hugo_Symbol".
Variant_Classification	Character. Column name for variant classification (e.g., Frame_Shift_Del). Default is "Variant_Classification".
Variant_Type	Character. Column name for variant type (e.g., SNP, INS, DEL). Default is "Variant_Type".

Value

List of mutation matrices (if category = "multi") or a single matrix for the specified category.

Note

Some users may encounter errors from upstream data import (e.g. "Can't combine ..$Tumor_Seq_Allele2" when using TCGAbiolinks or TCGAmutations). This is due to inconsistent column types in the source MAF tables, not an issue of this function. Please ensure your MAF or merged data frame uses consistent column types (e.g. convert allele columns to character before input).

Author(s)

Dongqian Zeng

Shixiang Huang

Examples

```
## Not run:
# See maftools or TCGAbiolinks documentation for obtaining MAF input
# Example: Download MAF file from TCGA portal
mut_list <- make_mut_matrix(maf = "path_to_maf_file.maf", isTCGA = TRUE, category = "multi")

## End(Not run)
```

mapbw *Map Score to Black and White Color*

Description

Maps a numeric input value to a color from a black-white gradient palette. Values are mapped to a 1001-color palette where -2 maps to black and +2 maps to white.

Usage

```
mapbw(x, my_palette2 = NULL)
```

Arguments

x	Numeric value to be mapped to a color (typically between -2 and 2).
my_palette2	Color palette vector (should have 1001 colors). Default uses black-white gradient.

Value

A color from the black-white palette as a hex code.

Examples

```
my_palette2 <- grDevices::colorRampPalette(c("black", "white"))(1001)
color <- mapbw(1.5, my_palette2)
color <- mapbw(-1, my_palette2)
```

mapcolors *Map Score to Color*

Description

Maps a numeric input value to a color from a blue-white-red gradient palette. Values are mapped to a 1001-color palette where -3 maps to blue, 0 maps to white, and +3 maps to red.

Usage

```
mapcolors(x, my_palette = NULL)
```

Arguments

x	Numeric value to be mapped to a color (typically between -3 and 3).
my_palette	Color palette vector (should have 1001 colors). Default uses blue-white-red gradient.

Value

A color from the palette as a hex code.

Examples

```
my_palette <- grDevices::colorRampPalette(c("blue", "white", "red"))(1001)
color <- mapcolors(2, my_palette)
color <- mapcolors(-2, my_palette)
```

`MCPcounter.estimate` *MCP-counter Cell Population Abundance Estimation*

Description

Estimates the abundance of different immune and stromal cell populations using the MCP-counter method. Works with various gene identifiers including Affymetrix probesets, HUGO gene symbols, Entrez IDs, and Ensembl IDs.

Usage

```
MCPcounter.estimate(
  expression,
 featuresType = c("affy133P2_probesets", "HUGO_symbols", "ENTREZ_ID", "ENSEMBL_ID"),
 probesets = read.table(system.file("extdata/probesets.txt", package = "IOBR"), sep =
    "\t", stringsAsFactors = FALSE, colClasses = "character"),
 genes = read.table(system.file("extdata/genes.txt", package = "IOBR"), sep = "\t",
  stringsAsFactors = FALSE, header = TRUE, colClasses = "character", check.names =
    FALSE)
)
```

Arguments

`expression`	Matrix or data.frame with features in rows and samples in columns.
`featuresType`	Type of identifiers for expression features. Options: "affy133P2_probesets", "HUGO_symbols", "ENTREZ_ID", "ENSEMBL_ID". Default is "affy133P2_probesets".
`probesets`	Probesets data table. Default loads from GitHub.
`genes`	Genes data table. Default loads from GitHub.

Value

Matrix with cell populations in rows and samples in columns.

Author(s)

Etienne Becht

Examples

```
expr <- matrix(runif(1000), nrow = 100, ncol = 10)
rownames(expr) <- paste0("Gene", 1:100)
estimates <- MCPcounter.estimate(expr, featuresType = "HUGO_symbols")
```

`merge_duplicate` *Merge Data Frames with Duplicated Column Names*

Description

Merges two data frames, resolving duplicated column names according to user preference. Allows selection of which data frame's duplicated columns to retain, ensuring data integrity during merging.

Usage

```
merge_duplicate(
  x,
  y,
  by.x,
  by.y,
  all.x = FALSE,
  all.y = FALSE,
  all = NULL,
  choose = c("x", "y")
)
```

Arguments

`x`	Data frame. First data frame to merge.
`y`	Data frame. Second data frame to merge.
`by.x`	Character. Column name(s) in 'x' used for merging.
`by.y`	Character. Column name(s) in 'y' used for merging.
`all.x`	Logical. Include all rows from 'x' in output. Default is 'FALSE'.
`all.y`	Logical. Include all rows from 'y' in output. Default is 'FALSE'.
`all`	Logical or 'NULL'. If not 'NULL', include all rows from both 'x' and 'y', overriding 'all.x' and 'all.y'.
`choose`	Character. Which data frame's duplicated non-joining columns to retain: '"x"' or '"y"'. Default is '"x"'.

Value

Data frame resulting from merging 'x' and 'y' according to specified parameters.

Examples

```
df1 <- data.frame(ID = 1:3, Name = c("A", "B", "C"), Value = 1:3)
df2 <- data.frame(ID = 1:3, Name = c("X", "Y", "Z"), Score = 4:6)

# Merge keeping duplicated columns from x
merged_df <- merge_duplicate(df1, df2,
  by.x = "ID", by.y = "ID",
  all.x = TRUE, choose = "x"
)
print(merged_df)

# Merge keeping duplicated columns from y
merged_df2 <- merge_duplicate(df1, df2,
  by.x = "ID", by.y = "ID",
  all = TRUE, choose = "y"
)
```

---

merge_eset *Merge Expression Sets by Row Names*

Description

Merges two or three expression sets (matrices or data frames) by row names (gene symbols), removing duplicates. The function ensures common genes across all input expression sets are retained.

Usage

```
merge_eset(eset1, eset2, eset3 = NULL)
```

Arguments

eset1	First expression set (matrix or data frame with row names).
eset2	Second expression set (matrix or data frame with row names).
eset3	Optional third expression set. Default is 'NULL'.

Value

Merged expression set (data frame) with duplicates removed. Row names correspond to gene symbols.

Author(s)

Dongqiang Zeng

Examples

```
# Create mock expression sets with common genes
set.seed(123)
common_genes <- c("TP53", "BRCA1", "EGFR", "MYC")
eset1 <- matrix(rnorm(12),
  nrow = 4,
  dimnames = list(common_genes, paste0("S", 1:3))
)
eset2 <- matrix(rnorm(16),
  nrow = 4,
  dimnames = list(common_genes, paste0("S", 4:7))
)
# Merge two expression sets
merged_eset <- merge_eset(eset1, eset2)
print(dim(merged_eset))
```

---

mouse2human_eset *Convert Mouse Gene Symbols to Human Gene Symbols*

Description

Converts mouse gene symbols to human gene symbols in an expression dataset. Supports using either an online resource (Ensembl) or a local dataset for conversion.

Usage

```
mouse2human_eset(
  eset,
  source = c("local", "ensembl"),
  is_matrix = TRUE,
  column_of_symbol = NULL,
  verbose = FALSE
)
```

Arguments

eset	Matrix or data frame. Expression matrix with genes in rows.
source	Character. Data source for conversion: "ensembl" (online) or "local". Default is "ensembl". If Ensembl fails, use "local" which uses the internal ‘mus_human_gene_symbol‘ dataset.
is_matrix	Logical. Whether ‘eset‘ is a matrix with gene symbols as row names. Default is ‘TRUE‘. If ‘FALSE‘, ‘column_of_symbol‘ must be specified.
column_of_symbol	Character or ‘NULL‘. Column name containing gene symbols if ‘eset‘ is not a matrix. Default is ‘NULL‘.
verbose	Logical. If ‘TRUE‘, prints available Ensembl datasets. Default is ‘FALSE‘.

Value

Expression set with human gene symbols.

Author(s)

Dongqiang Zeng

Examples

```
## Not run:
set.seed(123)
data <- matrix(runif(50 * 3), nrow = 50, ncol = 3)
rownames(data) <- c("Tpt1", "Hmgb1", "Gapdh", paste0("Gene", 4:50))
colnames(data) <- paste0("Sample", 1:3)
human_data <- mouse2human_eset(data, source = "local", is_matrix = TRUE)
if (!is.null(human_data)) head(human_data)

## End(Not run)
```

---

null_models *NULL Model Coefficients for MCPcounter*

Description

NULL Model Coefficients for MCPcounter

Usage

```
data(null_models)
```

Format

A ‘data.frame‘ with cell types in rows and coefficients in columns.

Examples

```
data(null_models)
head(null_models)
```

outputGCT *outputGCT*

Description

This function converts a gene expression dataset to a GCT format file.

Usage

```
outputGCT(input.f, output.f)
```

Arguments

input.f	A data frame or a character string specifying the path to the input file. If a character string, the file should be a tab-separated table with row names.
output.f	A character string specifying the path to the output file.

Value

No return value. The function writes the dataset to the specified output file in GCT format.

Examples

```
# Create a sample input data frame
sample_data <- data.frame(
  Gene = c("BRCA1", "TP53", "EGFR"),
  Sample1 = c(10, 15, 8),
  Sample2 = c(12, 18, 7),
  stringsAsFactors = FALSE
)
rownames(sample_data) <- sample_data$Gene
sample_data <- sample_data[, -1]

# Convert the input data frame to GCT format and save to temporary file
output_file <- tempfile(fileext = ".gct")
outputGCT(sample_data, output_file)
```

output_sig *Save Signature Data to File*

Description

Saves signature data to a specified file format, supporting CSV or RData. Handles single signatures or lists of signatures, converting them to a data frame for storage.

Usage

```
output_sig(signatures, format = c("csv", "rdata"), file.name)
```

Arguments

signatures	Signature data: a list or single string of signatures.
format	Character. Output format: "csv" or "rdata". Default is "csv".
file.name	Character. Name of the output file without extension.

Value

Data frame containing the processed signature data, also saved to the specified file.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate signatures
set.seed(123)
sim_sigs <- list(
  Signature1 = paste0("Gene", 1:50),
  Signature2 = paste0("Gene", 51:100),
  Signature3 = paste0("Gene", 101:150)
)
tmpfile <- tempfile(fileext = ".csv")
output_sig(
  signatures = sim_sigs, format = "csv",
  file.name = tools::file_path_sans_ext(tmpfile)
)
```

---

palettes *Select Color Palettes for Visualization*

Description

Provides curated qualitative, sequential, and diverging palettes for multiple plot types. Supports intensity adjustment and preview.

Usage

```
palettes(
  category = "box",
  palette = "nrc",
  alpha = 1,
  counts = 50,
  show_col = TRUE,
```

```
  show_message = FALSE
)
```

Arguments

category	Character. Plot/palette category: one of 'box', 'continue2', 'continue', 'random', 'heatmap', 'heatmap3', 'tidyheatmap'.
palette	Character or numeric. Palette name or index (varies by category).
alpha	Numeric. Alpha (transparency) scaling factor. Default is 1.
counts	Integer. Number of colors (for continuous palettes). Default is 50.
show_col	Logical. If TRUE, prints the palette. Default is TRUE.
show_message	Logical. If TRUE, prints available options. Default is FALSE.

Value

Character vector of hex color codes.

Author(s)

Dongqiang Zeng

Examples

```
colors <- palettes(category = "box", palette = "nrc", show_col = FALSE)
heatmap_colors <- palettes(
  category = "heatmap", palette = 1, counts = 10, show_col = FALSE
)
```

---

parallel_doperm *Parallel Permutation Test for CIBERSORT*

Description

Parallel version of doPerm. Performs permutation-based sampling and runs the CoreAlg function iteratively using multiple CPU cores to accelerate computation. This function generates an empirical null distribution of correlation coefficients for p-value calculation in CIBERSORT analysis.

Usage

```
parallel_doperm(
  perm1,
  X1,
  Y1,
  absolute1,
  abs_method1,
  num_cores1 = 2,
  seed = NULL
)
```

Arguments

perm1	Integer. Number of permutations to perform ($\geq$100 recommended).
X1	Matrix or data frame. Signature matrix (cell type GEP barcode).
Y1	Matrix. Mixture file containing gene expression profiles.
absolute1	Logical. Whether to run in absolute mode (default: FALSE).
abs_method1	String. Method for absolute mode: 'sig.score' or 'no.sumto1'.
num_cores1	Integer. Number of CPU cores for parallel computation (default: 2).
seed	Integer. Random seed for reproducibility. If NULL (default), uses current random state. Set to a specific value (e.g., 123) for reproducible results across runs.

Details

This function utilizes the `foreach` and `doParallel` packages to distribute permutation iterations across multiple cores. It automatically handles cluster setup/teardown via `on.exit()` to prevent resource leaks.

Note: Windows users may experience slower performance due to socket-based parallelization (PSOCK) versus forking on Unix systems.

Value

List containing:

dist Numeric vector of correlation coefficients from permutations, representing the empirical null distribution.

See Also

`doPerm` for the sequential version, `CoreAlg`, `CIBERSORT`

Examples

```
# Simulate data
set.seed(123)
X <- matrix(rnorm(1000), nrow = 100)
Y <- matrix(rnorm(500), nrow = 100)
rownames(X) <- rownames(Y) <- paste0("Gene", 1:100)
colnames(X) <- paste0("Cell", 1:10)
colnames(Y) <- paste0("Sample", 1:5)

# Run parallel permutation test
result <- parallel_doperm(
  perm1 = 10, X1 = X, Y1 = Y,
  absolute1 = FALSE, abs_method1 = "sig.score", num_cores1 = 1
)
if (!is.null(result)) str(result$dist)
```

ParseInputExpression *Parse Input Gene Expression Data*

Description

Reads gene expression data from a tab-delimited text file, using the first column as row names. Converts data into a numeric matrix for analysis.

Usage

```
ParseInputExpression(path)
```

Arguments

path	Character. Path to a tab-delimited gene expression file. First column should contain gene identifiers.

Value

Numeric matrix of gene expression values with genes as rows and samples as columns.

Examples

```
tf <- tempfile(fileext = ".tsv")
expr <- data.frame(
  gene = c("GeneA", "GeneB", "GeneC"),
  Sample1 = c(10, 20, 30),
  Sample2 = c(15, 25, 35)
)
write.table(expr, tf, sep = "\t", row.names = FALSE, quote = FALSE)
gene_expression_data <- ParseInputExpression(tf)
print(gene_expression_data)
```

patterns_to_na *Default Pattern List for Name Cleaning*

Description

A character vector of common substrings to remove from feature names. Used in [remove_names()] and other helper functions.

Usage

```
patterns_to_na
```

Format

A character vector of length 12.

Value

Character vector of patterns to remove.

Examples

```
# View default patterns
patterns_to_na
```

---

pdata_stad *Toy STAD Phenotype Data*

Description

A data frame containing clinical and pathological annotations for the TCGA stomach adenocarcinoma (STAD) cohort. Each row corresponds to one tumour sample and can be matched to the columns of `eset_stad` via the `ID` column. This dataset is typically used together with `eset_stad` in examples of survival analysis, subgroup comparison and immune deconvolution in the IOBR package.

Usage

```
data(pdata_stad)
```

Format

A data frame with one row per TCGA-STAD sample and 8 variables:

ID Character. TCGA sample barcode, matching the column names of `eset_stad`.

stage Factor. Pathological stage (e.g. `"Stage_I"`, `"Stage_II"`, `"Stage_III"`, `"Stage_IV"`).

status Factor. Vital status at last follow-up (`"Alive"` or `"Dead"`).

Lauren Factor. Lauren classification of gastric cancer (`"Intestinal"`, `"Diffuse"`, `"Mixed"` or `NA`).

subtype Factor. Molecular subtype (e.g. `"CIN"`, `"EBV"`, `"GS"`, `"MSI"`).

EBV Factor. EBV status of the tumour (`"Positive"` or `"Negative"`).

time Numeric. Overall survival or follow-up time, typically measured in months.

OS_status Integer/binary. Overall survival status indicator. (`1` = death, `0` = censored)

Examples

```
data(pdata_stad)
head(pdata_stad)
```

`percent_bar_plot` *Create a Percent Bar Plot*

Description

Generates a bar plot visualizing the percentage distribution of a variable grouped by another variable.

Usage

```
percent_bar_plot(
  input,
  x,
  y,
  subset.x = NULL,
  color = NULL,
  palette = NULL,
  title = NULL,
  axis_angle = 0,
  coord_flip = FALSE,
  add_Freq = TRUE,
  Freq = "Proportion",
  size_freq = 8,
  legend.size = 0.5,
  legend.size.text = 10,
  add_sum = TRUE,
  print_result = TRUE,
  round.num = 2
)
```

Arguments

`input`	Input data frame.
`x`	Name of the x-axis variable.
`y`	Name of the y-axis (grouping) variable.
`subset.x`	Optional subset of x-axis values.
`color`	Optional color palette.
`palette`	Optional palette type.
`title`	Optional plot title.
`axis_angle`	Angle for axis labels (0-90). Default is 0.
`coord_flip`	Logical to flip coordinates. Default is FALSE.
`add_Freq`	Logical to add frequency count. Default is TRUE.
`Freq`	Name of frequency column.
`size_freq`	Size of frequency labels. Default is 8.

legend.size	Size of legend. Default is 0.5.
legend.size.text	Size of legend text. Default is 10.
add_sum	Logical to add sum to x-axis labels. Default is TRUE.
print_result	Logical to print result data frame. Default is TRUE.
round.num	Decimal places for proportion. Default is 2.

Value

A ggplot object.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_data <- data.frame(
  Subtype = sample(c("EBV", "GS", "MSI", "CIN"), 100, replace = TRUE),
  Lauren = sample(c("Diffuse", "Intestinal", "Mixed"), 100, replace = TRUE)
)

# Create percent bar plot
p <- percent_bar_plot(
  input = sim_data, x = "Subtype", y = "Lauren",
  axis_angle = 60
)
if (!is.null(p)) print(p)
```

---

pie_chart *Create Pie or Donut Charts*

Description

Generates a pie chart or donut chart from input data.

Usage

```
pie_chart(
  input,
  var,
  var2 = NULL,
  type = 2,
  show_freq = FALSE,
  color = NULL,
  palette = "jama",
```

```
  title = NULL,
  text_size = 10,
  title_size = 20,
  add_sum = FALSE
)
```

Arguments

input	Input dataframe.
var	Variable for the chart.
var2	Secondary variable for donut chart (type = 3).
type	Chart type: 1 (pie), 2 (donut), 3 (PieDonut via webr).
show_freq	Logical to show frequencies. Default is FALSE.
color	Optional color palette.
palette	Color palette name. Default is "jama".
title	Plot title. Default is NULL.
text_size	Text size. Default is 10.
title_size	Title size. Default is 20.
add_sum	Logical to add sum to labels. Default is FALSE.

Value

A ggplot object.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_data <- data.frame(
  Subtype = sample(c("EBV", "GS", "MSI", "CIN"), 100, replace = TRUE)
)

# Create pie chart
p1 <- pie_chart(input = sim_data, var = "Subtype", palette = "jama")
if (!is.null(p1)) print(p1)

# Create donut chart
p2 <- pie_chart(input = sim_data, var = "Subtype", type = 2)
if (!is.null(p2)) print(p2)
```

PlotAUC *Plot AUC ROC Curves*

Description

Generates ROC curves for model evaluation comparing training and testing performance at both lambda.min and lambda.1se. Creates a ggplot visualization with AUC values in the legend.

Usage

```
PlotAUC(
  train.x,
  train.y,
  test.x,
  test.y,
  model,
  modelname,
  cols = NULL,
  palette = "jama"
)
```

Arguments

train.x	Training predictors matrix.
train.y	Training outcomes (binary factor).
test.x	Testing predictors matrix.
test.y	Testing outcomes (binary factor).
model	Fitted cv.glmnet model.
modelname	Character string for plot title.
cols	Optional color vector for ROC curves.
palette	Color palette name from IOBR palettes. Default is ‘"jama"‘.

Value

ggplot object of ROC curves.

Examples

```
if (requireNamespace("glmnet", quietly = TRUE)) {
  set.seed(123)
  train_data <- matrix(rnorm(100 * 5), ncol = 5)
  train_outcome <- rbinom(100, 1, 0.5)
  test_data <- matrix(rnorm(50 * 5), ncol = 5)
  test_outcome <- rbinom(50, 1, 0.5)
 fitted_model <- glmnet::cv.glmnet(train_data, train_outcome, family = "binomial", nfolds = 5)
 p <- PlotAUC(train_data, train_outcome, test_data, test_outcome, fitted_model, "MyModel")
```

```
  print(p)
}
```

---

plotPurity *plotPurity*

Description

This function generates scatterplots of tumor purity based on ESTIMATE scores for given samples.

Usage

```
plotPurity(
  scores,
  samples = "all_samples",
  platform = c("affymetrix", "agilent", "illumina"),
  output.dir = NULL
)
```

Arguments

scores	A character string specifying the path to the input file containing ESTIMATE scores. The file should be a tab-separated table with appropriate headers.
samples	A character vector specifying the sample names to plot. The default is "all_samples", which plots all samples in the input file.
platform	A character string specifying the platform used for data collection. Can be "affymetrix", "agilent", or "illumina". Currently, only "affymetrix" is implemented.
output.dir	A character string specifying the directory to save the output plots. If 'NULL', plots are not saved. Default is 'NULL'.

Value

No return value. The function generates and saves scatterplots in the specified output directory.

Examples

```
# Create a sample ESTIMATE score matrix
scores_data <- data.frame(
  Sample1 = c(100, 200, 500, 0.80),
  Sample2 = c(120, 220, 450, 0.70),
  Sample3 = c(140, 240, 600, 0.90),
  row.names = c(
    "StromalScore", "ImmuneScore", "ESTIMATEScore",
    "TumorPurity"
  ),
  check.names = FALSE
)
```

```
# Write to a temporary GCT file
scores_file <- tempfile(fileext = ".gct")
outputGCT(scores_data, scores_file)
```

`PlotTimeROC` *Plot Time-Dependent ROC Curves*

Description

Generates time-dependent ROC curves for evaluating prognostic accuracy of survival models. Plots training and testing ROC curves at the 90th percentile survival time.

Usage

```
PlotTimeROC(
  train.x,
  train.y,
  test.x,
  test.y,
  model,
  modelname,
  cols = NULL,
  palette = "jama"
)
```

Arguments

`train.x`	Matrix or data frame of training predictors.
`train.y`	Training survival outcomes (time and status).
`test.x`	Matrix or data frame of testing predictors.
`test.y`	Testing survival outcomes (time and status).
`model`	Fitted survival model object.
`modelname`	Character string for model identification.
`cols`	Optional vector of colors for plotting.
`palette`	Character string specifying color palette. Default is ‘"jama"‘.

Value

A ‘ggplot‘ object representing the ROC curve plot.

Author(s)

Dongqiang Zeng

Examples

```
if (requireNamespace("glmnet", quietly = TRUE) &&
  requireNamespace("survival", quietly = TRUE) &&
  requireNamespace("timeROC", quietly = TRUE)) {
  library(survival)
  set.seed(123)
  train_x <- matrix(rnorm(100 * 5), ncol = 5)
  train_y <- data.frame(time = rexp(100), status = rbinom(100, 1, 0.5))
  test_x <- matrix(rnorm(50 * 5), ncol = 5)
  test_y <- data.frame(time = rexp(50), status = rbinom(50, 1, 0.5))
  fit <- glmnet::cv.glmnet(train_x, Surv(train_y$time, train_y$status), family = "cox")
  p <- PlotTimeROC(train_x, train_y, test_x, test_y, fit, "Cox Model")
  print(p)
}
```

ProcessingData *Process Data for Model Construction*

Description

Preprocesses data for binomial or survival analysis. Aligns and filters data based on sample IDs, optionally scales data, and ensures appropriate data types. Handles missing values by removing columns with NA values.

Usage

```
ProcessingData(x, y, scale, type = c("binomial", "survival"))
```

Arguments

x	Data frame of predictors with first column as IDs.
y	Data frame of outcomes with first column as IDs. For survival, expects two additional columns for time and status.
scale	Logical indicating whether to scale predictors.
type	Character string: ‘"binomial"‘ or ‘"survival"‘.

Value

List containing:

x_scale Processed predictor matrix

y Processed outcome variable

x_ID Sample IDs

Examples

```
x <- data.frame(ID = 1:10, predictor1 = rnorm(10), predictor2 = rnorm(10))
y <- data.frame(ID = 1:10, outcome = sample(c(0, 1), 10, replace = TRUE))
result <- ProcessingData(x, y, scale = TRUE, type = "binomial")
```

PrognosticAUC *Calculate Time-Dependent AUC for Survival Models*

Description

Evaluates prognostic ability of a survival model by calculating time-dependent AUC at the 30th and 90th percentiles of survival time. These thresholds assess short-term and long-term predictive accuracy.

Usage

```
PrognosticAUC(model, newx, s, acture.y)
```

Arguments

model	A fitted survival model object capable of generating risk scores.
newx	A matrix or data frame of new data for prediction.
s	Lambda value for prediction. Can be numeric or ‘"lambda.min"‘/‘"lambda.1se"‘.
acture.y	Data frame with ‘time‘ and ‘status‘ columns.

Value

A data frame with AUC values at 30th (‘probs.3‘) and 90th (‘probs.9‘) percentiles.

Author(s)

Dongqiang Zeng

Examples

```
if (requireNamespace("glmnet", quietly = TRUE) &&
  requireNamespace("survival", quietly = TRUE) &&
  requireNamespace("timeROC", quietly = TRUE)) {
  library(survival)
  set.seed(123)
  x <- matrix(rnorm(100 * 5), ncol = 5)
  y <- Surv(rexp(100), rbinom(100, 1, 0.5))
  fit <- glmnet::cv.glmnet(x, y, family = "cox")
  acture_y <- data.frame(time = y[, 1], status = y[, 2])
  auc_results <- PrognosticAUC(fit, newx = x, s = "lambda.min", acture.y = acture_y)
}
```

`PrognosticModel` *Build Prognostic Models Using LASSO and Ridge Regression*

Description

Prepares data, splits it into training and testing sets, and fits LASSO and Ridge regression models for survival analysis. Evaluates model performance using cross-validation and optionally generates time-dependent ROC curves for visual assessment of predictive accuracy.

Usage

```
PrognosticModel(
  x,
  y,
  scale = FALSE,
  seed = 123456,
  train_ratio = 0.7,
  nfold = 10,
  plot = TRUE,
  palette = "jama",
  cols = NULL
)
```

Arguments

`x`	A matrix or data frame of predictor variables (features).
`y`	A data frame of survival outcomes with two columns: survival time and event status.
`scale`	Logical indicating whether to scale predictor variables. Default is 'FALSE'.
`seed`	Integer seed for random number generation to ensure reproducibility. Default is '123456'.
`train_ratio`	Numeric proportion of data for training (e.g., 0.7). Default is '0.7'.
`nfold`	Integer number of folds for cross-validation. Default is '10'.
`plot`	Logical indicating whether to plot ROC curves. Default is 'TRUE'.
`palette`	String specifying color palette. Default is '"jama"'.
`cols`	Optional vector of colors for ROC curves. If 'NULL', uses default palette.

Value

A list containing:

lasso_result Results from LASSO model including coefficients and AUC

ridge_result Results from Ridge model including coefficients and AUC

train.x Training data with sample IDs

Author(s)

Dongqiang Zeng

Examples

```
if (requireNamespace("glmnet", quietly = TRUE) &&
  requireNamespace("survival", quietly = TRUE)) {
  library(survival)
  set.seed(123)
  # Create small example data (first column must be ID)
  x_sim <- as.data.frame(matrix(rnorm(100 * 5), 100, 5))
  colnames(x_sim) <- paste0("Sig", 1:5)
  x_sim$ID <- paste0("S", 1:100)
  x_sim <- x_sim[, c(6, 1:5)] # Move ID to first column

  y_sim <- data.frame(
    ID = paste0("S", 1:100),
    OS_days = rexp(100, 0.01),
    OS_status = rbinom(100, 1, 0.5)
  )
  prognostic_result <- PrognosticModel(
    x = x_sim, y = y_sim,
    scale = TRUE, seed = 123456,
    train_ratio = 0.7, nfold = 3, plot = FALSE
  )
  if (!is.null(prognostic_result)) head(prognostic_result)
}
```

`PrognosticResult` *Compute Prognostic Results for Survival Models*

Description

Computes and compiles prognostic results from a survival model fitted with ‘glmnet‘. Extracts model coefficients at optimal lambda values (‘lambda.min‘ and ‘lambda.1se‘) and calculates time-dependent AUC metrics for both training and testing datasets.

Usage

```
PrognosticResult(model, train.x, train.y, test.x, test.y)
```

Arguments

`model`	A fitted survival model object (e.g., from ‘glmnet::cv.glmnet‘).
`train.x`	Matrix or data frame of training predictors.
`train.y`	Training dataset survival outcomes (time and status).
`test.x`	Matrix or data frame of testing predictors.
`test.y`	Testing dataset survival outcomes (time and status).

Value

A list containing:

model The fitted model object

coefs Data frame of coefficients at ‘lambda.min‘ and ‘lambda.1se‘

AUC Data frame with AUC values for train/test at both lambda values

Author(s)

Dongqiang Zeng

Examples

```
if (requireNamespace("glmnet", quietly = TRUE) &&
  requireNamespace("survival", quietly = TRUE) &&
  requireNamespace("timeROC", quietly = TRUE)) {
  library(survival)
  set.seed(123)
  train_x <- matrix(rnorm(100 * 10), ncol = 10)
  train_y <- data.frame(time = rexp(100), status = rbinom(100, 1, 0.5))
  test_x <- matrix(rnorm(50 * 10), ncol = 10)
  test_y <- data.frame(time = rexp(50), status = rbinom(50, 1, 0.5))
  fit <- glmnet::cv.glmnet(train_x, Surv(train_y$time, train_y$status), family = "cox")
  results <- PrognosticResult(
    model = fit, train.x = train_x, train.y = train_y,
    test.x = test_x, test.y = test_y
  )
}
```

---

random_strata_cells *Stratified Random Sampling of Cells*

Description

Performs stratified random sampling of cells from single-cell data, ensuring proportional representation of each cell type while respecting minimum and maximum count constraints.

Usage

```
random_strata_cells(
  input,
  group,
  proportion = 0.1,
  minimum_count_include = 300,
  minimum_count = 200,
  maximum_count = 1000,
  sub_cluster = NULL,
  cell_type = NULL
)
```

Arguments

input	A data frame or Seurat object containing cell annotations.
group	Character string specifying the column name for cell type grouping.
proportion	Numeric value between 0 and 1 specifying the sampling proportion. Default is 0.1.
minimum_count_include	Integer specifying the minimum count threshold for a cell type to be included in sampling. Default is 300.
minimum_count	Integer specifying the minimum number of cells to sample per cell type. Default is 200.
maximum_count	Integer specifying the maximum number of cells to sample per cell type. Default is 1000.
sub_cluster	Optional character string specifying a sub-cluster column for filtering. Default is NULL.
cell_type	Optional character string specifying the cell type value to filter when 'sub_cluster' is provided. Default is NULL.

Value

A data frame containing the sampled cells with preserved cell type proportions.

Examples

```
# Create simulated cell annotation data
set.seed(123)
sim_cells <- data.frame(
  cell_id = paste0("Cell", 1:500),
  cell_type = sample(c("T_cell", "B_cell", "NK_cell", "Macrophage"), 500, replace = TRUE)
)
# Sample cells with stratified random sampling
sampled <- random_strata_cells(
  input = sim_cells,
  group = "cell_type",
  proportion = 0.2,
  minimum_count_include = 50,
  minimum_count = 20,
  maximum_count = 100
)
if (!is.null(sampled)) head(sampled)
```

---

rbind_iobr *Row Bind Multiple Data Sets*

Description

Combines two or three data frames or matrices vertically using 'rbind'. Ensures compatibility of input data before binding by aligning columns.

Usage

```
rbind_iobr(data1, data2, data3 = NULL)
```

Arguments

data1	Data frame or matrix. First dataset to combine.
data2	Data frame or matrix. Second dataset to combine.
data3	Data frame or matrix or 'NULL'. Optional third dataset. Default is 'NULL'.

Value

Combined data frame resulting from row binding the input datasets.

Author(s)

Dongqiang Zeng

Examples

```
data1 <- data.frame(A = 1:5, B = letters[1:5])
data2 <- data.frame(A = 6:10, B = letters[6:10])
combined_data <- rbind_iobr(data1, data2)

# With three datasets
data3 <- data.frame(A = 11:15, B = letters[11:15])
combined_data <- rbind_iobr(data1, data2, data3)
```

RegressionResult *Regression Result Computation*

Description

Computes regression results with coefficients at lambda.min and lambda.1se, and evaluates AUC for binomial outcomes. Returns a comprehensive summary of model performance on both training and testing datasets.

Usage

```
RegressionResult(train.x, train.y, test.x, test.y, model)
```

Arguments

train.x	Training predictors matrix.
train.y	Training outcomes (binary factor).
test.x	Testing predictors matrix.
test.y	Testing outcomes (binary factor).
model	Fitted cv.glmnet model object.

Value

List containing:

model The fitted cv.glmnet model

coefs Data frame with feature names and coefficients at lambda.min and lambda.1se

AUC Matrix of AUC values for train/test sets at both lambda values

Examples

```
if (requireNamespace("glmnet", quietly = TRUE)) {
  set.seed(123)
  train_data <- matrix(rnorm(100 * 10), ncol = 10)
  train_outcome <- rbinom(100, 1, 0.5)
  test_data <- matrix(rnorm(50 * 10), ncol = 10)
  test_outcome <- rbinom(50, 1, 0.5)
 fitted_model <- glmnet::cv.glmnet(train_data, train_outcome, family = "binomial", nfolds = 5)
  results <- RegressionResult(
    train.x = train_data, train.y = train_outcome,
    test.x = test_data, test.y = test_outcome, model = fitted_model
  )
}
```

RemoveBatchEffect *Remove Batch Effect of Expression Set*

Description

Removes batch effects between two gene expression datasets, typically representing different sample types such as cancer cells and immune cells. Uses ComBat from the sva package for batch correction.

Usage

```
RemoveBatchEffect(cancer.exp, immune.exp, immune.cellType)
```

Arguments

cancer.exp	Matrix or data frame. Cancer cell expression data with genes as rows and samples as columns.
immune.exp	Matrix or data frame. Immune cell expression data with genes as rows and samples as columns.
immune.cellType	Vector. Cell type for each column in ‘immune.exp‘.

Value

A list containing:

1. Batch effect corrected cancer expression data
2. Batch effect corrected immune expression data
3. Aggregated immune expression data (median per cell type)

Author(s)

Bo Li

Examples

```
set.seed(123)
gene_names <- paste0("Gene", 1:100)
sample_names_cancer <- paste0("CancerSample", 1:10)
cancer.exp <- matrix(runif(1000, 1, 1000),
  nrow = 100, ncol = 10,
  dimnames = list(gene_names, sample_names_cancer)
)

sample_names_immune <- paste0("ImmuneSample", 1:5)
immune.exp <- matrix(runif(500, 1, 1000),
  nrow = 100, ncol = 5,
  dimnames = list(gene_names, sample_names_immune)
)

immune.cellType <- c("T-cell", "B-cell", "T-cell", "NK-cell", "B-cell")
names(immune.cellType) <- sample_names_immune

result <- RemoveBatchEffect(cancer.exp, immune.exp, immune.cellType)
if (!is.null(result)) str(result)
```

---

remove_batcheffect *Removing Batch Effect from Expression Sets*

Description

Removes batch effects from expression datasets using sva::ComBat (for microarray/TPM data) or sva::ComBat_seq (for RNA-seq count data). Generates PCA plots to visualize data before and after correction.

Usage

```
remove_batcheffect(
  eset1,
  eset2,
  eset3 = NULL,
```

```
  id_type = "ensembl",
  data_type = c("array", "count", "tpm"),
  cols = "normal",
  palette = "jama",
  log2 = TRUE,
  check_eset = TRUE,
  adjust_eset = TRUE,
  repel = FALSE,
  path = NULL
)
```

Arguments

eset1	First expression set (matrix or data frame with genes as rows).
eset2	Second expression set.
eset3	Optional third expression set. Use 'NULL' if not available.
id_type	Type of gene ID in expression sets (e.g., '"ensembl"', '"symbol"'). Required for count data normalization.
data_type	Type of data: '"array"', '"count"', or '"tpm"'. Default is '"array"'.
cols	Color scale for PCA plot. Default is '"normal"'.
palette	Color palette for PCA plot. Default is '"jama"'.
log2	Whether to perform log2 transformation. Default is 'TRUE'. Ignored for count data.
check_eset	Whether to check expression sets for errors. Default is 'TRUE'.
adjust_eset	Whether to adjust expression sets by removing problematic features. Default is 'TRUE'.
repel	Whether to add repelling labels to PCA plot. Default is 'FALSE'.
path	Directory where results should be saved. Default is 'NULL' (display only).

Value

Expression matrix after batch correction.

Author(s)

Dongqiang Zeng

References

Zhang Y, et al. ComBat-seq: batch effect adjustment for RNA-seq count data. NAR Genomics and Bioinformatics. 2020;2(3):lqaa078. doi:10.1093/nargab/lqaa078

Leek JT, et al. The sva package for removing batch effects and other unwanted variation in high-throughput experiments. Bioinformatics. 2012;28(6):882-883.

Examples

```
# Simulate data
set.seed(123)
sim_eset1 <- matrix(rnorm(100 * 5, mean = 10, sd = 2), 100, 5)
sim_eset2 <- matrix(rnorm(100 * 5, mean = 12, sd = 2), 100, 5)
rownames(sim_eset1) <- rownames(sim_eset2) <- paste0("Gene", 1:100)
colnames(sim_eset1) <- paste0("S1_", 1:5)
colnames(sim_eset2) <- paste0("S2_", 1:5)

# Run batch correction
if (requireNamespace("sva", quietly = TRUE) && requireNamespace("BiocParallel", quietly = TRUE)) {
  eset_corrected <- remove_batcheffect(sim_eset1, sim_eset2, data_type = "tpm")
  if (!is.null(eset_corrected)) head(eset_corrected)
}
```

`remove_duplicate_genes` *Remove Duplicate Gene Symbols in Gene Expression Data*

Description

This function addresses duplicate gene symbols in a gene expression dataset by selecting the highest-expressing instance among duplicates. Users can choose between mean, standard deviation, or sum as the ranking criterion for selection. This is useful for preparing data where duplicates can lead to issues in downstream analyses.

Usage

```
remove_duplicate_genes(eset, column_of_symbol, method = c("mean", "sd", "sum"))
```

Arguments

`eset`	A data frame or matrix representing gene expression data, with gene symbols as one of the columns.
`column_of_symbol`	The name of the column containing gene symbols in ‘eset‘.
`method`	The ranking method to use for selecting among duplicate gene symbols: ‘"mean"‘ for mean expression, ‘"sd"‘ for standard deviation, or ‘"sum"‘ for sum of expression values. Default is ‘"mean"‘.

Value

A modified version of ‘eset‘ where duplicate gene symbols have been reduced to a single entry (the highest-ranking one). The gene symbols are set as row names in the returned data frame.

Note

Important: This function performs selection, not aggregation. For duplicate genes, it retains only the highest-ranking instance (based on the specified method) and discards others.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_eset <- data.frame(
  symbol = c("GeneA", "GeneA", "GeneB", "GeneC"),
  S1 = c(10, 5, 20, 15),
  S2 = c(12, 7, 22, 17)
)
# Remove duplicates using mean expression
test_eset_unique <- remove_duplicate_genes(
  eset = test_eset,
  column_of_symbol = "symbol",
  method = "mean"
)
print(test_eset_unique)
```

---

remove_names *Remove Patterns from Column Names or Variables*

Description

Modifies column names or specified variables in a data frame by replacing specified patterns with empty strings or spaces.

Usage

```
remove_names(
  input_df,
  variable = "colnames",
  patterns_to_na = patterns_to_na,
  patterns_space = NULL
)
```

Arguments

input_df	Data frame. Input data to modify.
variable	Character. Column to modify: "colnames" for column names, or a specific column name. Default is "colnames".
patterns_to_na	Character vector. Patterns to replace with empty string. Default uses [patterns_to_na].
patterns_space	Character vector or 'NULL'. Patterns to replace with spaces. Default is 'NULL'.

Value

Modified data frame with patterns replaced.

Author(s)

Dongqiang Zeng

Examples

```
df <- data.frame(
  "CellA_cibersort" = 1:5,
  "CellB_xCell" = 6:10,
  "CellC_TIMER" = 11:15
)
result <- remove_names(df, variable = "colnames", patterns_to_na = patterns_to_na)
colnames(result)
```

---

reset_iobr_cache_dir *Reset IOBR Cache Directory to Default*

Description

Resets the cache directory to the default session-specific temporary directory.

Usage

```
reset_iobr_cache_dir()
```

Value

Invisibly returns the default cache directory path.

Examples

```
reset_iobr_cache_dir()
```

---

reset_iobr_mirrors *Reset Download Mirrors to Default*

Description

Resets the download mirror list to the default values.

Usage

```
reset_iobr_mirrors()
```

Value

Invisibly returns the default mirror list.

Examples

```
reset_iobr_mirrors()
```

`roc_time` *Time-dependent ROC Curve for Survival Analysis*

Description

Generates a time-dependent Receiver Operating Characteristic (ROC) plot to evaluate the predictive performance of one or more variables in survival analysis. Calculates the Area Under the Curve (AUC) for each specified time point and variable, and creates a multi-line ROC plot with annotated AUC values.

Usage

```
roc_time(
  input,
  vars,
  time = "time",
  status = "status",
  time_point = 12,
  time_type = "month",
  palette = "jama",
  cols = "normal",
  seed = 1234,
  show_col = FALSE,
  path = NULL,
  main = "PFS",
  index = 1,
  fig.type = "pdf",
  width = 5,
  height = 5.2
)
```

Arguments

`input`	Data frame containing variables for analysis.
`vars`	Character vector. Variable(s) to be evaluated.
`time`	Character string. Name of the time variable. Default is ‘"time"‘.
`status`	Character string. Name of the status variable. Default is ‘"status"‘.
`time_point`	Integer or vector. Time point(s) for ROC analysis. Default is ‘12‘.
`time_type`	Character string. Time unit (‘"day"‘ or ‘"month"‘). Default is ‘"month"‘.
`palette`	Character string. Color palette for the plot. Default is ‘"jama"‘.
`cols`	Character vector or string. Color specification: ‘"normal"‘, ‘"random"‘, or custom color vector.

seed	Integer. Random seed for reproducibility. Default is ‘1234‘.
show_col	Logical indicating whether to display the color palette. Default is ‘FALSE‘.
path	Character string or ‘NULL‘. Path to save the plot. Default is ‘NULL‘.
main	Character string. Main title of the plot. Default is ‘"PFS"‘.
index	Integer. Index for plot filename. Default is ‘1‘.
fig.type	Character string. Output file type (e.g., ‘"pdf"‘, ‘"png"‘). Default is ‘"pdf"‘.
width	Numeric. Width of the plot. Default is ‘5‘.
height	Numeric. Height of the plot. Default is ‘5.2‘.

Value

A ggplot object representing the time-dependent ROC plot.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data for offline testing
set.seed(123)
sim_input <- data.frame(
  ID = paste0("Sample", 1:100),
  time = runif(100, 1, 60),
  status = sample(0:1, 100, replace = TRUE),
  Marker1 = rnorm(100),
  Marker2 = rnorm(100),
  Marker3 = rnorm(100)
)
## Not run:
roc_time(
  input = sim_input, vars = c("Marker1", "Marker2", "Marker3"),
  time = "time", status = "status", time_point = 12, path = NULL, main = "OS"
)

## End(Not run)
```

---

scale_matrix *Scale and Manipulate a Matrix*

Description

Scales a gene expression matrix, optionally applies logarithmic transformation, and performs feature manipulation to remove problematic variables (e.g., genes with zero variance or missing values).

Usage

```
scale_matrix(matrix, log2matrix = TRUE, manipulate = TRUE)
```

Arguments

matrix	Numeric matrix with genes as rows and samples as columns.
log2matrix	Logical indicating whether to apply log2 transformation using [log2eset()]. Default is 'TRUE'.
manipulate	Logical indicating whether to perform feature manipulation to remove problematic features. Default is 'TRUE'.

Value

A scaled matrix (genes as rows, samples as columns).

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_matrix <- matrix(
  rlnorm(100),
  ncol = 5,
  dimnames = list(paste0("Gene", 1:20), paste0("Sample", 1:5))
)
eset2 <- scale_matrix(test_matrix, log2matrix = FALSE, manipulate = TRUE)
head(eset2)
```

---

select_method *Select a Signature Scoring Method Subset*

Description

Filters an integrated signature score matrix to retain results from a specified method (PCA, ssGSEA, or zscore) and strips method suffixes from column names.

Usage

```
select_method(data, method = c("ssGSEA", "PCA", "zscore"))
```

Arguments

data	Data frame or matrix. Integrated signature score matrix.
method	Character. One of "PCA", "ssGSEA", or "zscore" (case-insensitive). Default is "ssGSEA".

Value

Matrix or data frame containing only the selected method's scores.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data with multiple method columns
set.seed(123)
sim_res <- data.frame(
  ID = paste0("Sample", 1:10),
  Sig1_PCA = rnorm(10),
  Sig1_ssGSEA = rnorm(10),
  Sig1_zscore = rnorm(10),
  Sig2_PCA = rnorm(10),
  Sig2_ssGSEA = rnorm(10),
  Sig2_zscore = rnorm(10)
)
# Select PCA method columns only
pca_res <- select_method(sim_res, method = "PCA")
print(colnames(pca_res))
```

---

set_iobr_cache_dir *Set IOBR Cache Directory*

Description

Sets a custom cache directory for IOBR downloaded data. This is useful when you want to store cached data in a specific location, such as a shared network drive or a custom directory.

To use the standard system cache location (persistent across sessions), you can use: 'set_iobr_cache_dir(tools::R_user_dir("IO which = "cache"))'.

Usage

```
set_iobr_cache_dir(path, create = TRUE)
```

Arguments

path	Character string. The path to the cache directory.
create	Logical. Whether to create the directory if it doesn't exist. Default: TRUE.

Value

Invisibly returns the cache directory path.

Examples

```
# Set a custom cache directory (use tempdir() for examples)
set_iobr_cache_dir(tempdir())

# Use standard system cache (persistent)
# set_iobr_cache_dir(tools::R_user_dir("IOBR", which = "cache"))

# Check the current cache directory
get_iobr_cache_dir()

# Download data will now use the custom cache
data <- download_iobr_data("lm22")
```

---

signature_collection *Gene signature collection for pathway and immune analysis*

Description

A named list of gene signatures used in the IOBR package for immune deconvolution, pathway scoring, functional annotation, and tumour microenvironment (TME) characterization. Each element corresponds to a predefined biological signature and contains a character vector of HGNC gene symbols.

Usage

```
data(signature_collection)
```

Format

A named list of length 323. Each element is a character vector of gene symbols. Representative entries include:

CD_8_T_effector Markers of $CD8^+$ effector T cells.

DDR DNA damage response and repair genes.

Immune_Checkpoint Immune checkpoint molecules.

CellCycle_Reg Core regulators of cell-cycle progression.

Mismatch_Repair Mismatch-repair pathway genes.

TMEsocreA_CIR TME-related signature used in TMEscore analysis.

... Additional signatures are included in the list but are not individually listed here; all follow the same structure.

Examples

```
data(signature_collection)
head(signature_collection)
```

signature_score_calculation_methods *Signature Score Calculation Methods*

Description

A named vector of supported methods for calculating signature scores.

Usage

```
signature_score_calculation_methods
```

Format

Named character vector:

PCA Principal Component Analysis method ("pca")

ssGSEA Single-sample Gene Set Enrichment Analysis ("ssgsea")

z-score Z-score transformation method ("zscore")

Integration Integration of multiple methods ("integration")

Examples

```
signature_score_calculation_methods
signature_score_calculation_methods["PCA"]
```

sigScore *Calculate Signature Score Using PCA, Mean, or Z-score Methods*

Description

Computes signature scores from gene expression data using Principal Component Analysis (PCA), mean-based, or z-score approaches.

Usage

```
sigScore(eset, methods = c("PCA", "mean", "zscore"))
```

Arguments

eset	Normalized expression matrix with genes (signature) as rows and samples as columns.
methods	Scoring method: ‘"PCA"‘ (default) for principal component 1, ‘"mean"‘ for mean expression, or ‘"zscore"‘ for z-score normalized mean.

Value

Numeric vector of length ‘ncol(eset)‘; a score summarizing the rows of ‘eset‘.

Author(s)

Dorothee Nickles, Dongqiang Zeng

Examples

```
# Create small example expression matrix
set.seed(123)
test_eset <- matrix(rnorm(1000), nrow = 10, ncol = 100)
rownames(test_eset) <- paste0("Gene", 1:10)
colnames(test_eset) <- paste0("Sample", 1:100)

# Calculate scores
score_pca <- sigScore(eset = test_eset, methods = "PCA")
score_mean <- sigScore(eset = test_eset, methods = "mean")
score_zscore <- sigScore(eset = test_eset, methods = "zscore")
```

---

sig_box *Signature Box Plot with Statistical Comparisons*

Description

Creates box plots to visualize signature distributions across groups with optional statistical pairwise comparisons. Supports both data frames and Seurat objects for single-cell data visualization.

Usage

```
sig_box(
  data,
  signature,
  variable,
  palette = "nrc",
  cols = NULL,
  jitter = FALSE,
  point_size = 5,
  angle_x_text = 0,
  hjust = 0.5,
  show_pairwise_p = TRUE,
  show_overall_p = FALSE,
  return_stat_res = FALSE,
  size_of_pvalue = 6,
  size_of_font = 10,
  assay = NULL,
  slot = "scale.data",
  scale = FALSE
)
```

Arguments

data	Data frame or Seurat object containing the signature and grouping variable.
signature	Character string specifying the column name (or feature name in Seurat) for the signature values to plot on the y-axis.
variable	Character string specifying the grouping variable column name for the x-axis.
palette	Character string specifying the color palette name. Default is ‘"nrc"‘.
cols	Character vector of custom fill colors. If ‘NULL‘, palette is used. Default is ‘NULL‘.
jitter	Logical indicating whether to add jittered points to the box plot. Default is ‘FALSE‘.
point_size	Numeric value specifying the size of jittered points. Default is 5.
angle_x_text	Numeric value specifying the rotation angle for x-axis labels (in degrees). Default is 0.
hjust	Numeric value specifying the horizontal justification of x-axis labels. Default is 0.5.
show_pairwise_p	Logical indicating whether to display pairwise comparison p-values between groups. Default is ‘TRUE‘.
show_overall_p	Logical indicating whether to display the overall group difference p-value. Default is ‘FALSE‘.
return_stat_res	Logical indicating whether to return statistical test results instead of the plot. Default is ‘FALSE‘.
size_of_pvalue	Numeric value specifying the font size for p-values. Default is 6.
size_of_font	Numeric value specifying the base font size. Default is 10.
assay	Character string specifying the assay name (for Seurat objects). Default is ‘NULL‘.
slot	Character string specifying the slot name (for Seurat objects). Default is ‘"scale.data"‘.
scale	Logical indicating whether to scale signature values (z-score transformation). Default is ‘FALSE‘.

Value

If ‘return_stat_res = FALSE‘, returns a ggplot2 object. If ‘return_stat_res = TRUE‘, returns a data frame containing statistical test results.

Author(s)

Dongqiang Zeng

Examples

```
# Create small example data
set.seed(123)
test_data <- data.frame(
  subtype = rep(c("A", "B"), each = 50),
  TMEscore_plus = rnorm(100)
)
sig_box(
  data = test_data,
  signature = "TMEscore_plus",
  variable = "subtype",
  jitter = TRUE,
  palette = "jco"
)
```

`sig_box_batch` *Batch Signature Box Plots for Group Comparisons*

Description

Generates multiple box plots for specified features (signatures) across groups in the input data. Supports customization of plot appearance, output path, statistical annotation, and compatibility with Seurat objects. Plots are saved to the specified directory or a default folder.

Usage

```
sig_box_batch(
  input,
  vars,
  groups,
  pattern_vars = FALSE,
  path = NULL,
  index = 0,
  angle_x_text = 0,
  hjust = 0.5,
  palette = "jama",
  cols = NULL,
  jitter = FALSE,
  point_size = 5,
  size_of_font = 8,
  size_of_pvalue = 4.5,
  show_pvalue = TRUE,
  return_stat_res = FALSE,
  assay = NULL,
  slot = "scale.data",
  scale = FALSE,
  height = 5,
```

```
  width = 3.5,
  fig_type = "pdf",
  max_count_feas = 30
)
```

Arguments

input	Data frame or Seurat object containing the data for analysis.
vars	Character vector. Features or variables to analyze. When 'pattern_vars = TRUE', these are treated as regular expression patterns.
groups	Character vector. Grouping variable(s) for comparison.
pattern_vars	Logical indicating whether to treat 'vars' as regular expression patterns for matching column names. Default is 'FALSE'.
path	Character string or 'NULL'. Directory to save plots. If 'NULL', plots are not saved. Default is 'NULL'.
index	Integer. Starting index for plot filenames. Default is '0'.
angle_x_text	Numeric. Angle of x-axis labels in degrees. Default is '0'.
hjust	Numeric. Horizontal justification of x-axis labels. Default is '0.5'.
palette	Character. Color palette for plots. Default is '"jama"'.
cols	Character vector or 'NULL'. Custom colors for plot elements.
jitter	Logical indicating whether to add jittered points. Default is 'FALSE'.
point_size	Numeric. Size of points. Default is '5'.
size_of_font	Numeric. Base font size. Default is '8'.
size_of_pvalue	Numeric. Size of p-value text. Default is '4.5'.
show_pvalue	Logical indicating whether to display p-values. Default is 'TRUE'.
return_stat_res	Logical indicating whether to return statistical results instead of saving plots. Default is 'FALSE'.
assay	Character string or 'NULL'. Assay type for Seurat objects.
slot	Character. Data slot for Seurat objects. Default is '"scale.data"'.
scale	Logical indicating whether to scale data before analysis. Default is 'FALSE'.
height	Numeric. Height of plots in inches. Default is '5'.
width	Numeric. Width of plots in inches. Default is '3.5'.
fig_type	Character. File format for plots (e.g., '"pdf"', '"png"'). Default is '"pdf"'.
max_count_feas	Integer. Maximum number of features to analyze when 'pattern_vars = TRUE'. If matched variables exceed this limit, only the first 'max_count_feas' features are used. Default is '30'.

Value

If 'return_stat_res = TRUE', returns a data frame of statistical results; otherwise, invisibly returns the path to saved plots.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_pdata <- data.frame(
  ID = paste0("Sample", 1:50),
  subtype = sample(c("TypeA", "TypeB", "TypeC"), 50, replace = TRUE),
  TMEscore_plus = rnorm(50),
  GZMB = rnorm(50)
)
sig_box_batch(
  input = sim_pdata,
  vars = c("TMEscore_plus", "GZMB"),
  groups = "subtype",
  jitter = TRUE,
  palette = "jco",
  path = tempdir()
)
```

---

sig_forest *Forest Plot for Survival Analysis Results*

Description

Generates a forest plot to visualize hazard ratios, confidence intervals, and p-values for gene signatures or features from survival analysis.

Usage

```
sig_forest(
  data,
  signature,
  pvalue = "P",
  HR = "HR",
  CI_low_0.95 = "CI_low_0.95",
  CI_up_0.95 = "CI_up_0.95",
  n = 10,
  max_character = 25,
  discrete_width = 35,
  color_option = 1,
  cols = NULL,
  text.size = 13
)
```

Arguments

data	Data frame with survival analysis results including p-values, hazard ratios, and confidence intervals.
signature	Character string. Column name for signatures or feature names.
pvalue	Character string. Column name for p-values. Default is '"P"'.
HR	Character string. Column name for hazard ratios. Default is '"HR"'.
CI_low_0.95	Character string. Column name for lower CI bound. Default is '"CI_low_0.95"'.
CI_up_0.95	Character string. Column name for upper CI bound. Default is '"CI_up_0.95"'.
n	Integer. Maximum number of signatures to display. Default is '10'.
max_character	Integer. Maximum characters for labels before wrapping. Default is '25'.
discrete_width	Integer. Width for discretizing long labels. Default is '35'.
color_option	Integer. Color option for p-value gradient (1, 2, or 3). Default is '1'.
cols	Character vector. Custom colors for p-value gradient (low to high). Default is 'NULL'.
text.size	Numeric. Text size for y-axis labels. Default is '13'.

Value

A ggplot2 object of the forest plot.

Author(s)

Dongqiang Zeng

Examples

```
# Example with sample survival results
sample_results <- data.frame(
  ID = c("Sig1", "Sig2", "Sig3"),
  HR = c(1.5, 0.8, 2.0),
  P = c(0.01, 0.05, 0.001),
  CI_low_0.95 = c(1.1, 0.6, 1.5),
  CI_up_0.95 = c(2.0, 1.0, 2.8)
)
sig_forest(data = sample_results, signature = "ID")
```

---

sig_group *Grouped gene signatures for IOBR analysis*

Description

A named list that organizes gene signatures into functional or biological categories. Each element of the list is a character vector containing the names of gene signatures defined in `signature_collection`. A total of 43 signature groups are included, covering tumour intrinsic pathways, immune-related processes, stromal activity, TME characteristics and immuno-oncology biomarkers. These groups are used in IOBR to conveniently select sets of signatures for scoring and visualization.

Usage

```
data(sig_group)
```

Format

A named list of length 43. Each element is a character vector of signature names. Representative groups include:

tumor_signature Signatures related to intrinsic tumour biology such as cell cycle, DNA damage repair and histone regulation.

EMT Epithelial–mesenchymal transition (EMT)–associated signatures.

io_biomarkers Immuno-oncology biomarker–related signatures.

immu_microenvironment Immune microenvironment–related signatures.

immu_suppression Immune suppression–related signatures.

immu_exclusion Signatures associated with immune exclusion and stromal barriers.

TCR_BCR T-cell and B-cell receptor pathway signatures.

tme_signatures1 Tumour microenvironment signature panel (set 1).

tme_signatures2 Tumour microenvironment signature panel (set 2).

... Additional groups are included (43 total), but not listed individually here; all groups follow the same structure.

Examples

```
data(sig_group)
head(sig_group)
```

---

sig_gsea *Perform Gene Set Enrichment Analysis (GSEA)*

Description

Conducts Gene Set Enrichment Analysis to identify significantly enriched gene sets from differential gene expression data. Supports MSigDB gene sets or custom gene signatures, and generates comprehensive visualizations and statistical results.

Usage

```
sig_gsea(
  deg,
  genesets = NULL,
  path = NULL,
  gene_symbol = "symbol",
  logfc = "log2FoldChange",
  org = c("hsa", "mus"),
  msigdb = TRUE,
```

```
  category = "H",
  subcategory = NULL,
  palette_bar = "jama",
  palette_gsea = 2,
  cols_gsea = NULL,
  cols_bar = NULL,
  show_bar = 10,
  show_col = FALSE,
  show_plot = FALSE,
  show_gsea = 8,
  show_path_n = 20,
  plot_single_sig = FALSE,
  project = "custom_sig",
  minGSSize = 10,
  maxGSSize = 500,
  verbose = TRUE,
  seed = FALSE,
  fig.type = "pdf",
  print_bar = TRUE
)
```

Arguments

deg	Data frame containing differential expression results with gene symbols and log fold changes.
genesets	List of custom gene sets for enrichment analysis. If 'NULL', MSigDB gene sets are used based on 'org' and 'category'. Default is 'NULL'.
path	Character string specifying the directory path for saving results. Default is 'NULL'.
gene_symbol	Character string specifying the column name in 'deg' containing gene symbols. Default is '"symbol"'.
logfc	Character string specifying the column name in 'deg' containing log fold change values. Default is '"log2FoldChange"'.
org	Character string specifying the organism. Options are '"hsa"' (Homo sapiens) or '"mus"' (Mus musculus). Default is '"hsa"'.
msigdb	Logical indicating whether to use MSigDB gene sets. Default is 'TRUE'.
category	Character string specifying the MSigDB category (e.g., '"H"' for Hallmark, '"C2"' for curated gene sets). Default is '"H"'.
subcategory	Character string specifying the MSigDB subcategory to filter gene sets. Default is 'NULL'.
palette_bar	Character string or integer specifying the color palette for bar plots. Default is '"jama"'.
palette_gsea	Integer specifying the color palette for GSEA plots. Default is '2'.
cols_gsea	Character vector specifying custom colors for GSEA enrichment plots. If 'NULL', colors are automatically generated. Default is 'NULL'.

cols_bar	Character vector specifying custom colors for the enrichment bar plot. If 'NULL', colors are automatically generated. Default is 'NULL'.
show_bar	Integer specifying the number of top enriched gene sets to display in the bar plot. Default is '10'.
show_col	Logical indicating whether to display color names in the bar plot. Default is 'FALSE'.
show_plot	Logical indicating whether to display GSEA enrichment plots. Default is 'FALSE'.
show_gsea	Integer specifying the number of top significant gene sets for which to generate GSEA plots. Default is '8'.
show_path_n	Integer specifying the number of pathways to display in GSEA plots. Default is '20'.
plot_single_sig	Logical indicating whether to generate separate plots for each significant gene set. Default is 'TRUE'.
project	Character string specifying the project name for output files. Default is '"custom_sig"'.
minGSSize	Integer specifying the minimum gene set size for analysis. Default is '10'.
maxGSSize	Integer specifying the maximum gene set size for analysis. Default is '500'.
verbose	Logical indicating whether to display progress messages. Default is 'TRUE'.
seed	Logical indicating whether to set a random seed for reproducibility. Default is 'FALSE'.
fig.type	Character string specifying the file format for saving plots (e.g., '"pdf"', '"png"'). Default is '"pdf"'.
print_bar	Logical indicating whether to save and print the bar plot. Default is 'TRUE'.

Value

List containing:

up Data frame of up-regulated enriched gene sets

down Data frame of down-regulated enriched gene sets

all Complete GSEA results

plot_top GSEA enrichment plot for top gene sets

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
genes <- c(
  "TP53", "BRCA1", "EGFR", "MYC", "KRAS", "PTEN", "APC", "RB1",
  "CDKN2A", "VHL", "ATM", "ATR", "CHEK2", "PALB2", "RAD51", "MDM2",
  "CDK4", "CDK6", "CCND1", "CCNE1", "CDK2", "E2F1", "E2F2", "E2F3",
```

```
  "ARF1", "ARF3", "ARF4", "ARF5", "ARF6", "GSK3B", "AKT1", "AKT2",
  "PIK3CA", "PIK3CB", "PIK3CD", "PIK3CG", "PIK3R1", "PIK3R2", "PIK3R3"
)
deg <- data.frame(
  symbol = genes,
  log2FoldChange = rnorm(length(genes), mean = 0, sd = 2),
  padj = runif(length(genes), 0, 0.1)
)
signature <- list(
  DNA_Repair = c(
    "TP53", "BRCA1", "ATM",
    "ATR", "CHEK2", "PALB2", "RAD51"
  ),
  Cell_Cycle = c(
    "TP53", "MYC",
    "RB1", "CDKN2A", "CDK4",
    "CDK6", "CCND1", "CCNE1",
    "CDK2", "E2F1", "E2F2", "E2F3"
  ),
  PI3K_AKT = c(
    "AKT1", "AKT2",
    "PIK3CA", "PIK3CB", "PIK3CD",
    "PIK3CG", "PIK3R1", "PIK3R2", "PIK3R3"
  )
)

if (rlang::is_installed("clusterProfiler") && rlang::is_installed("org.Hs.eg.db")) {
  res <- sig_gsea(
    deg = deg,
    genesets = signature,
    path = tempdir(),
    show_plot = FALSE,
    print_bar = FALSE
  )
  print(names(res))
}
```

`sig_heatmap` *Signature Heatmap with Optional Annotations*

Description

Generates a heatmap of selected features grouped by a categorical variable, with optional conditional (annotation) bars. Supports palette customization, scaling, size controls, and output saving.

Usage

```
sig_heatmap(
  input,
```

```
  id = "ID",
  features,
  group,
  condition = NULL,
  id_condition = "vars",
  col_condition = "condition",
  cols_condition = NULL,
  scale = FALSE,
  palette = 2,
  cols_heatmap = NULL,
  palette_group = "jama",
  show_col = FALSE,
  show_palettes = FALSE,
  cols_group = NULL,
  show_plot = TRUE,
  width = 8,
  height = NULL,
  size_col = 10,
  size_row = 8,
  angle_col = 90,
  column_title = NULL,
  row_title = NULL,
  show_heatmap_col_name = FALSE,
  path = NULL,
  index = NULL
)
```

Arguments

input	Data frame containing ID, grouping variable, and feature columns.
id	Character string. Column name for sample identifier. Default is ‘"ID"‘.
features	Character vector. Feature (column) names to include in the heatmap.
group	Character string. Grouping variable column name.
condition	Data frame or ‘NULL‘. Optional annotation table with variable-condition mapping. Default is ‘NULL‘.
id_condition	Character string. Column name in ‘condition‘ for feature IDs. Default is ‘"vars"‘.
col_condition	Character string. Column name in ‘condition‘ for condition labels. Default is ‘"condition"‘.
cols_condition	Character vector. Colors for conditions.
scale	Logical indicating whether to scale values by row. Default is ‘FALSE‘.
palette	Integer or character. Palette index/name for heatmap colors. Default is ‘2‘.
cols_heatmap	Character vector. Custom colors for heatmap gradient.
palette_group	Character string. Palette name for group colors. Default is ‘"jama"‘.
show_col	Logical indicating whether to display the color vector. Default is ‘FALSE‘.
show_palettes	Logical indicating whether to print palette options. Default is ‘FALSE‘.

cols_group	Character vector. Custom colors for groups.
show_plot	Logical indicating whether to print the heatmap. Default is 'TRUE'.
width	Numeric. Plot width in inches. Default is '8'.
height	Numeric or 'NULL'. Plot height in inches. Auto-calculated if 'NULL'.
size_col	Numeric. Font size for column labels. Default is '10'.
size_row	Numeric. Font size for row labels. Default is '8'.
angle_col	Numeric. Rotation angle for column labels in degrees. Default is '90'.
column_title	Character string or 'NULL'. Title for column annotation.
row_title	Character string or 'NULL'. Title for row annotation.
show_heatmap_col_name	Logical indicating whether to show column names. Default is 'FALSE'.
path	Character string or 'NULL'. Output directory for saving the heatmap.
index	Integer or 'NULL'. Index appended to filename. Default is 'NULL'.

Value

A tidyHeatmap object. Saves PDF only when 'path' is provided.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_input <- data.frame(
  ID = paste0("Sample", 1:20),
  subtype = sample(c("TypeA", "TypeB"), 20, replace = TRUE),
  Sig1 = rnorm(20),
  Sig2 = rnorm(20)
)
sig_heatmap(input = test_input, features = c("Sig1", "Sig2"), group = "subtype", scale = TRUE)
```

---

sig_pheatmap *Generate Heatmap for Signature Data*

Description

Creates a heatmap from signature data with grouping variables, offering flexible options for colors, clustering, and output formats using ComplexHeatmap.

Usage

```
sig_pheatmap(
  input,
  feas,
  group,
  group2 = NULL,
  group3 = NULL,
  ID = "ID",
  path = NULL,
  cols1 = "random",
  cols2 = "random",
  cols3 = "random",
  seed = 54321,
  show_col = FALSE,
  palette1 = 1,
  palette2 = 2,
  palette3 = 3,
  cluster_cols = TRUE,
  palette_for_heatmape = 6,
  scale.matrix = TRUE,
  cellwidth = 1,
  cellheight = 9,
  show_colnames = FALSE,
  fig.type = "pdf",
  width = 6,
  height = NULL,
  file_name_prefix = 1
)
```

Arguments

input	Data frame with variables in columns.
feas	Character vector. Feature names (columns) to include in heatmap.
group	Character string. Column name for primary grouping variable.
group2	Character string or 'NULL'. Optional secondary grouping variable.
group3	Character string or 'NULL'. Optional tertiary grouping variable.
ID	Character string. Column name for sample identifiers. Default is '"ID"'.
path	Character string or 'NULL'. Directory to save output files. If 'NULL', the heatmap is not saved. Default is 'NULL'.
cols1	Character vector or '"random"' or '"normal"'. Colors for primary group. Default is '"random"'.
cols2	Character vector or '"random"' or '"normal"'. Colors for secondary group. Default is '"random"'.
cols3	Character vector or '"random"' or '"normal"'. Colors for tertiary group. Default is '"random"'.

seed	Integer. Random seed for color generation. Default is '54321'.
show_col	Logical indicating whether to display colors. Default is 'FALSE'.
palette1	Integer. Palette for primary group. Default is '1'.
palette2	Integer. Palette for secondary group. Default is '2'.
palette3	Integer. Palette for tertiary group. Default is '3'.
cluster_cols	Logical indicating whether to cluster columns. Default is 'TRUE'.
palette_for_heatmape	Integer. Palette number for heatmap. Default is '6'.
scale.matrix	Logical indicating whether to scale the matrix. Default is 'TRUE'.
cellwidth	Numeric. Width of each cell in points. Default is '1'.
cellheight	Numeric. Height of each cell in points. Default is '9'.
show_colnames	Logical indicating whether to show column names. Default is 'FALSE'.
fig.type	Character string. File format for saving. Default is '"pdf"'.
width	Numeric. Width of saved figure in inches. Default is '6'.
height	Numeric or 'NULL'. Height of saved figure in inches. Calculated if 'NULL'.
file_name_prefix	Character or numeric. Prefix for saved file name. Default is '1'.

Value

A list containing:

p_anno Annotation data frame

p_cols List of cluster colors

plot ComplexHeatmap object

eset Transformed expression matrix

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_input <- data.frame(
  ID = paste0("Sample", 1:20),
  subtype = sample(c("TypeA", "TypeB"), 20, replace = TRUE),
  Sig1 = rnorm(20),
  Sig2 = rnorm(20)
)
sig_pheatmap(
  input = test_input,
  feas = c("Sig1", "Sig2"),
  group = "subtype"
)
```

sig_roc *Plot ROC Curves and Compare Them*

Description

Generates Receiver Operating Characteristic (ROC) curves for multiple predictors and optionally performs statistical comparisons between them.

Usage

```
sig_roc(
  data,
  response,
  variables,
  fig.path = NULL,
  main = NULL,
  file.name = NULL,
  palette = "jama",
  cols = NULL,
  alpha = 1,
  compare = FALSE,
  smooth = TRUE,
  compare_method = "bootstrap",
  boot.n = 100
)
```

Arguments

data	Data frame containing the predictor variables and binary outcome.
response	Character. Name of the binary outcome variable in ‘data‘.
variables	Character vector. Names of predictor variables for ROC curves.
fig.path	Character or ‘NULL‘. Directory path to save output PDF. Default is ‘NULL‘.
main	Character or ‘NULL‘. Main title for the ROC plot. Default is ‘NULL‘.
file.name	Character or ‘NULL‘. Output PDF filename without extension. Default is ‘"0-ROC of multiple variables"‘.
palette	Character. Color palette for ROC curves. Default is ‘"jama"‘.
cols	Character vector or ‘NULL‘. Custom colors for ROC curves. Default is ‘NULL‘.
alpha	Numeric. Transparency level (1 = opaque, 0 = transparent). Default is ‘1‘.
compare	Logical. Whether to perform statistical comparison of AUCs. Default is ‘FALSE‘.
smooth	Logical. Whether to smooth ROC curves. Default is ‘TRUE‘.
compare_method	Character. Method for comparing ROC curves. Default is ‘"bootstrap"‘.
boot.n	Integer. Number of bootstrap replications. Default is ‘100‘.

Value

A list containing:

auc.out Data frame with AUC values and confidence intervals

legend.name Vector of legend entries for the plot

p.out If 'compare = TRUE', data frame with p-values from comparisons

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_data <- data.frame(
  OS_status = sample(c(0, 1), 20, replace = TRUE),
  Marker1 = rnorm(20),
  Marker2 = rnorm(20)
)
result <- sig_roc(data = test_data, response = "OS_status",
                  variables = c("Marker1", "Marker2"),
                  smooth = FALSE)
if (!is.null(result)) print(result$auc.out)
```

---

sig_surv_plot *Generate Kaplan-Meier Survival Plot for Signature*

Description

Creates Kaplan-Meier survival plots for a given signature or gene, with automatic cutoff determination. Generates three types of plots: optimal cutoff (best cutoff), tertile-based (3 groups), and median split (2 groups).

Usage

```
sig_surv_plot(
  input_pdata,
  signature,
  project = "KM",
  ID = "ID",
  time = "time",
  status = "status",
  time_type = "month",
  break_month = "auto",
  cols = NULL,
  palette = "jama",
  show_col = TRUE,
```

```
  mini_sig = "score",
  fig.type = "png",
  save_path = NULL,
  index = 1
)
```

Arguments

input_pdata	Data frame with survival data and signature scores.
signature	Character string. Column name of the target signature.
project	Character string. Project name for output. Default is '"KM"'.
ID	Character string. Column name for sample IDs. Default is '"ID"'.
time	Character string. Column name for survival time. Default is '"time"'.
status	Character string. Column name for survival status. Default is '"status"'.
time_type	Character string. Time unit ('"month"' or '"day"'). Default is '"month"'.
break_month	Numeric or '"auto"'. Time axis breaks. Default is '"auto"'.
cols	Character vector. Optional custom colors.
palette	Character string. Color palette if 'cols' not provided. Default is '"jama"'.
show_col	Logical indicating whether to show colors. Default is 'TRUE'.
mini_sig	Character string. Label for low score group. Default is '"score"'.
fig.type	Character string. File format. Default is '"png"'.
save_path	Character string or 'NULL'. Directory for saving plots. If 'NULL', plots are not saved. Default is 'NULL'.
index	Integer. Index for multiple plots. Default is '1'.

Value

A list containing:

data Processed input data with group assignments

plots Combined survival plots

Author(s)

Dongqiang Zeng

Examples

```
# Create small example data
set.seed(123)
test_data <- data.frame(
  time = runif(100, 0, 100),
  OS_status = sample(c(0, 1), 100, replace = TRUE),
  TMEscore_plus = rnorm(100),
  ID = paste0("S", 1:100)
)
```

```
sig_surv_plot(
  input_pdata = test_data,
  signature = "TMEscore_plus",
  time = "time",
  status = "OS_status"
)
```

SplitTrainTest *Split Data into Training and Testing Sets*

Description

Divides dataset into training and testing sets using random sampling. Maintains data integrity for both binomial and survival analysis types.

Usage

```
SplitTrainTest(x, y, train_ratio, type = c("binomial", "survival"), seed)
```

Arguments

x	Predictor matrix or data frame.
y	Outcome vector (binomial) or matrix with time/status (survival).
train_ratio	Proportion for training (0-1). Default is ‘0.7‘.
type	Analysis type: ‘"binomial"‘ or ‘"survival"‘.
seed	Random seed for reproducibility.

Value

List containing:

train.x Training predictors matrix

train.y Training outcomes

test.x Testing predictors matrix

test.y Testing outcomes

train_sample Indices of training samples

Examples

```
data_matrix <- matrix(rnorm(200), ncol = 2)
outcome_vector <- rbinom(100, 1, 0.5)
split_data <- SplitTrainTest(
  data_matrix, outcome_vector,
  train_ratio = 0.7,
  type = "binomial", seed = 123
)
```

stad_group *Example Clinical Data for TCGA-STAD Gastric Cancer Analysis*

Description

A small example dataset demonstrating the clinical data structure required for TCGA Stomach Adenocarcinoma (STAD) analysis using IOBR package functions. Contains simulated clinical variables, molecular subtypes, and survival data.

Usage

```
data(stad_group)
```

Format

A data frame with patient samples as rows and clinical variables as columns:

ID Unique patient identifier (TCGA barcode format)

stage AJCC pathological stage (Stage_II, Stage_III, Stage_IV)

status Patient vital status (Alive, Dead, NA)

Lauren Lauren histological classification (Intestinal, Diffuse, Mixed)

subtype Molecular subtype classification (EBV, GS)

EBV Epstein-Barr virus status (Positive, Negative)

time Overall survival time in months

OS_status Overall survival status (0=alive, 1=dead)

Examples

```
data(stad_group)
head(stad_group)
```

subgroup_data *Example Dataset for Subgroup Survival Analysis*

Description

An example dataset demonstrating the data structure required for subgroup survival analysis using the subgroup_survival function. Contains simulated clinical and biomarker data with survival outcomes.

Usage

```
data(subgroup_data)
```

Format

A data frame with clinical variables and biomarker scores:

Patient_ID Unique patient identifier

ProjectID Study or dataset identifier (e.g., "Dataset1")

AJCC_stage AJCC pathological stage (2, 3, 4)

status Event status (0=censored, 1=event)

time Follow-up time in months

score Continuous biomarker score (numeric values)

score_binary Binary biomarker classification ("High", "Low")

Examples

```
data(subgroup_data)
head(subgroup_data)
```

---

subgroup_survival *Subgroup Survival Analysis Using Cox Proportional Hazards Models*

Description

Extracts hazard ratios (HR) and 95 proportional hazards models across specified subgroups.

Usage

```
subgroup_survival(
  pdata,
  time_name = "time",
  status_name = "status",
  variables,
  object
)
```

Arguments

pdata	Data frame containing variables, follow-up time, and outcome.
time_name	Character. Column name of follow-up time. Default is ‘"time"‘.
status_name	Character. Column name of event status (1/0). Default is ‘"status"‘.
variables	Character vector. Subgrouping variables (each processed independently).
object	Character. Variable of interest used in Cox model. If it has levels "High" and "Low", recode "High" to 0 and "Low" to 1 before calling.

Value

Data frame summarizing subgroup Cox results (HR, CI, p-value).

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
test_pdata <- data.frame(
  time = runif(100, 1, 100),
  status = sample(c(0, 1), 100, replace = TRUE),
  subgroup = sample(c("A", "B"), 100, replace = TRUE),
  score = rnorm(100)
)
res <- subgroup_survival(
  pdata = test_pdata,
  time_name = "time",
  status_name = "status",
  variables = "subgroup",
  object = "score"
)
print(res)
```

---

surv_group *Generate Kaplan-Meier Survival Plots for Categorical Groups*

Description

Creates Kaplan-Meier survival plots for data grouped by a categorical variable. Handles both binary and multi-level categorical groups with customizable plot aesthetics.

Usage

```
surv_group(
  input_pdata,
  target_group,
  ID = "ID",
  levels = c("High", "Low"),
  reference_group = NULL,
  project = NULL,
  time = "time",
  status = "status",
  time_type = "month",
  break_month = "auto",
  cols = NULL,
  palette = "jama",
  mini_sig = "score",
  save_path = NULL,
  fig.type = "pdf",
  index = 1,
```

```
  width = 6,
  height = 6.5,
  font.size.table = 3
)
```

Arguments

input_pdata	Data frame containing survival data and grouping variables.
target_group	Name of column containing the grouping variable.
ID	Name of column with unique identifiers. Default is "ID".
levels	Names for levels of target_group (for binary groups). Default is c("High", "Low").
reference_group	Reference level for binary comparison. Default is NULL.
project	Optional title for plot. Default is NULL.
time	Name of column with follow-up times. Default is "time".
status	Name of column with event indicators. Default is "status".
time_type	Units: "month" or "day". Default is "month".
break_month	X-axis break interval. If "auto", calculated automatically. Default is "auto".
cols	Color vector for plot lines. Default is NULL.
palette	Color palette name. Default is "jama".
mini_sig	Prefix label for variables. Default is "score".
save_path	Directory for saving plot. Default is NULL.
fig.type	File format: "pdf" or "png". Default is "pdf".
index	Identifier for file naming. Default is 1.
width	Plot width. Default is 6.
height	Plot height. Default is 6.5.
font.size.table	Font size for risk table. Default is 3.

Value

Kaplan-Meier plot object.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate data
set.seed(123)
sim_pdata <- data.frame(
  ID = paste0("Sample", 1:100),
  Lauren = sample(c("Intestinal", "Diffuse"), 100, replace = TRUE),
  time = runif(100, 1, 60),
  OS_status = sample(0:1, 100, replace = TRUE)
)
# Run survival analysis (survival and survminer are imported packages)
result <- surv_group(
  input_pdata = sim_pdata,
  target_group = "Lauren",
  time = "time",
  status = "OS_status",
  save_path = NULL
)
if (!is.null(result)) print(result)
```

---

tcga_rna_preps *Preprocess TCGA RNA-seq Data*

Description

Preprocesses TCGA RNA-seq data by modifying sample types, transforming data, and annotating genes based on specified parameters.

Usage

```
tcga_rna_preps(
  eset,
  id_type = c("ensembl", "symbol"),
  input_type = c("log2count", "count"),
  output = c("tumor", "tumor_normal"),
  output_type = c("tpm", "log2tpm", "count"),
  annotation = TRUE
)
```

Arguments

eset	Matrix or data frame. RNA-seq gene expression matrix from TCGA.
id_type	Character. Gene identifier type: "ensembl" or "symbol". Default is "ensembl".
input_type	Character. Input data type: "log2count" or "count". Default is "log2count".
output	Character. Sample type: "tumor" or "tumor_normal". Default is "tumor".
output_type	Character. Output data type: "tpm", "log2tpm", or "count". Default is "tpm".
annotation	Logical. Whether to perform gene annotation. Default is TRUE.

Value

Preprocessed gene expression matrix.

Author(s)

Dongqiang Zeng

Examples

```
# Simulate TCGA-style data with Ensembl IDs
set.seed(123)
sim_eset <- matrix(
  abs(rnorm(500)),
  nrow = 100,
  ncol = 5,
  dimnames = list(
    paste0("ENSG00000", 101:200),
    paste0("TCGA-AB-123", 4:8, "-01A")
  )
)
# Process tumor samples only (output as count for offline testing)
eset <- tcga_rna_preps(
  eset = sim_eset, id_type = "ensembl", input_type = "count",
  output = "tumor", output_type = "count", annotation = FALSE
)
print(dim(eset))
```

---

tcga_stad_pdata *TCGA-STAD Clinical and Molecular Annotation Data*

Description

Clinical, molecular, and signature score data for TCGA stomach adenocarcinoma (STAD) samples. Includes patient demographics, tumor characteristics, molecular subtypes, and pre-computed signature scores.

Usage

```
data(tcga_stad_pdata)
```

Format

A data frame with samples as rows and variables as columns:

- ID – TCGA sample barcode
- stage – tumor stage (Stage_I, Stage_II, etc.)
- status – vital status (Alive/Dead)
- Lauren – histological classification

- subtype – molecular subtype (EBV, MSI, GS, CN, ...)
- EBV – EBV infection status
- TMEscore_plus – continuous tumor-micro-environment score
- TMEscore_plus_binary – High/Low TME classification
- time – follow-up time (months)
- OS_status – 0 = alive, 1 = dead
- ARID1A, PIK3CA – driver-gene mutation status
- MALAT1 – lncRNA expression
- remaining columns – gene-expression values and additional clinical/molecular annotations

Source

The Cancer Genome Atlas Stomach Adenocarcinoma (TCGA-STAD)

References

Cancer Genome Atlas Research Network. Comprehensive molecular characterization of gastric adenocarcinoma. Nature 513, 202-209 (2014). doi:10.1038/nature13480

Examples

```
data(tcga_stad_pdata)
head(tcga_stad_pdata)
```

---

test_for_infiltration *Test for Cell Population Infiltration*

Description

Returns p-values for the null hypothesis that samples are not infiltrated by the corresponding cell population.

Usage

```
test_for_infiltration(MCPcounterMatrix, platform = c("133P2", "133A", "HG1"))
```

Arguments

MCPcounterMatrix	Matrix, usually output from MCPcounter.estimate.
platform	Expression platform: "133P2", "133A", or "HG1". Default is "133P2".

Value

Matrix with samples in rows and cell populations in columns. Elements are p-values.

Author(s)

Etienne Becht

Examples

```
# This function requires null_models data which is loaded internally
# Create example data
scores <- matrix(runif(30), nrow = 3, ncol = 10)
rownames(scores) <- c("T cells", "B cells", "NK cells")
pvals <- test_for_infiltration(scores, platform = "133P2")
```

---

timer_available_cancers *TIMER Available Cancer Types*

Description

Character vector of cancer types supported by TIMER deconvolution. TIMER signatures are cancer-specific.

Usage

```
timer_available_cancers
```

Value

Character vector of available cancer type abbreviations.

Examples

```
# List all available cancer types for TIMER
timer_available_cancers

# Check if a cancer type is supported
"brca" %in% timer_available_cancers
```

---

timer_info *Source code for the TIMER deconvolution method.*

Description

Formats and displays informational messages for timing or logging purposes. Useful for tracking progress or stages of execution within scripts.

Usage

```
timer_info(string)
```

Arguments

string	Character. Message to be displayed.

Details

This code is adapted from https://github.com/hanfeisun/TIMER, which again is an adapted version of the original TIMER source code from http://cistrome.org/TIMER/download.html.

The method is described in Li et al. Genome Biology 2016;17(1):174., PMID 27549193. Display Timer Information Messages

Value

None; used for its side effect of printing a message.

Author(s)

Bo Li

Examples

```
timer_info("Data processing started.")
```

---

tme_cluster *Identification of TME Cluster*

Description

Performs TME (Tumor Microenvironment) clustering analysis using various clustering methods. Supports feature selection, scaling, and automatic determination of optimal cluster number.

Usage

```
tme_cluster(
  input,
  features = NULL,
  pattern = NULL,
  id = NULL,
  scale = TRUE,
  method = "kmeans",
  min_nc = 2,
  max.nc = 6
)
```

Arguments

input	Data frame containing the input dataset.
features	Vector of features to use for clustering. Default is NULL (uses all columns or pattern-selected columns).
pattern	Regular expression pattern for selecting features. Default is NULL.
id	Column name for identifiers. Default is NULL (uses row names).
scale	Logical indicating whether to scale features. Default is TRUE.
method	Clustering method. Default is "kmeans".
min_nc	Minimum number of clusters to evaluate. Default is 2.
max.nc	Maximum number of clusters to evaluate. Default is 6.

Value

Data frame with cluster assignments appended.

Author(s)

Dongqiang Zeng

Examples

```
set.seed(123)
input_data <- data.frame(
  ID = paste0("Sample", 1:20),
  xCell_Tcells = rnorm(20),
  xCell_Bcells = rnorm(20),
  xCell_Macrophages = rnorm(20),
  Other_feature = rnorm(20)
)
result <- tme_cluster(
  input = input_data,
  pattern = "xCell",
  id = "ID",
  method = "kmeans"
)
table(result$cluster)
```

---

tme_deconvolution_methods

TME Deconvolution Methods

Description

A named vector of supported tumor microenvironment (TME) deconvolution methods in the IOBR package.

Usage

```
tme_deconvolution_methods
```

Format

A named character vector where names are display names and values are internal method names.

Details

The methods currently supported are:

- ‘mcpcounter‘: MCP-counter for immune and stromal cell populations
- ‘epic‘: EPIC for immune, stromal, and cancer cell fractions
- ‘xcell‘: xCell for 64 immune and stromal cell types
- ‘cibersort‘: CIBERSORT for 22 immune cell types
- ‘cibersort_abs‘: CIBERSORT in absolute mode
- ‘ips‘: Immunophenoscore calculation
- ‘estimate‘: ESTIMATE for stromal/immune/estimate scores
- ‘svr‘: Support Vector Regression (custom reference)
- ‘lsei‘: Least Squares with Equality/Inequality constraints
- ‘timer‘: TIMER for cancer-specific immune estimation
- ‘quantiseq‘: quanTIseq for RNA-seq immune deconvolution

Value

Named character vector of available deconvolution methods.

Examples

```
# List all available TME deconvolution methods
tme_deconvolution_methods

# Get internal method name for a specific method
tme_deconvolution_methods["MCPcounter"]
```

Top_probe *Top Probe Selector*

Description

Extracts the top ‘i‘ probes based on their ordering in the provided data frame. If the number of rows is less than or equal to ‘i‘, returns all probes.

Usage

```
Top_probe(dat, i)
```

Arguments

dat	Data frame containing a column named "probe".
i	Integer. Number of top probes to return.

Value

Character vector containing the names of the top ‘i‘ probes.

Examples

```
dat <- data.frame(
  probe = c("Probe1", "Probe2", "Probe3", "Probe4", "Probe5"),
  value = c(5, 3, 2, 4, 1)
)
top_probes <- Top_probe(dat, 3)
print(top_probes)
```

---

transform_data *Transform NA, Inf, or Zero Values in Data*

Description

Replaces NA, Inf, or zero values in specified columns of a data frame with a user-defined value or the column mean.

Usage

```
transform_data(data, feature, data_type = c("NA", "Inf", "zero"), into = 0)
```

Arguments

data	Data frame. Input data to be transformed.
feature	Character vector. Column names in ‘data‘ to apply transformation.
data_type	Character. Type of value to replace: ‘"NA"‘, ‘"Inf"‘, or ‘"zero"‘.
into	Value to replace specified type with. Default is 0. If ‘"mean"‘, replaces with column mean (excluding NA/Inf values as appropriate).

Value

Data frame with specified transformations applied to selected features.

Author(s)

Dongqiang Zeng

Examples

```
data_matrix <- data.frame(
  A = c(1, 2, NA, 4, Inf),
  B = c(Inf, 2, 3, 4, 5),
  C = c(0, 0, 0, 1, 2)
)

# Replace NAs with 0
transform_data(data_matrix, feature = c("A", "B"), data_type = "NA")

# Replace Inf values with the mean of the column
transform_data(data_matrix,
  feature = c("A", "B"),
  data_type = "Inf", into = "mean"
)

# Replace zeros with -1 in column C
transform_data(data_matrix, feature = "C", data_type = "zero", into = -1)
```

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