

Package: DAssemble (via r-universe)

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Type Package

Title Ensemble Models for Differential Analysis

Version 0.99.3

Description The DAssemble package implements an ensemble framework for differential-abundance and differential-expression analysis across bulk RNA-seq, single-cell RNA-seq, and microbiome studies. It wraps a collection of popular DA/DE methods as core methods and combines them via Cauchy Combination Tests (CCT), optionally augmented by simple enhancers such as Wilcoxon, Kolmogorov–Smirnov, and presence–absence logistic regression.

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URL <https://github.com/himelmallick/DAssemble>

BugReports <https://github.com/himelmallick/DAssemble/issues>

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Description

DAssemble provides an ensemble framework for differential-abundance and differential-expression analysis across bulk RNA-seq, single-cell RNA-seq, and microbiome studies. The package combines a user-selected core method with optional enhancer tests and aggregates evidence using the Cauchy Combination Test.

Details

The main user-facing function is [DAssemble\(\)](#). It accepts either a MultiAssayExperiment object or a feature table paired with sample metadata. Core methods can be combined with enhancer tests including Wilcoxon rank-sum, Kolmogorov-Smirnov, and presence-absence logistic regression.

See Also

[DAssemble\(\)](#)

Description

The DAssemble function implements an ensemble strategy for differential analysis. Users can select a single *core* model and optionally augment it with up to three *enhancer* models. Enhancers are simple, often nonparametric tests that provide complementary evidence. P-values from the core and enhancer models are combined using the Cauchy Combination Test (CCT).

Usage

```
DAssemble(
  features,
  metadata = NULL,
  core_method = NULL,
  enhancers = NULL,
  expVar = "group",
  coVars = NULL,
  assay_name = NULL,
  p_adj = "BY",
  enhancer_norm = "TSS",
  return_components = TRUE,
  return_subensembles = FALSE
)
```

Arguments

features	A MultiAssayExperiment object, or a data.frame with samples in rows and features in columns.
metadata	A data.frame with sample metadata. Leave as NULL when features is a MultiAssayExperiment; sample metadata is then taken from colData(features).
core_method	Character scalar naming the core method to run, or NULL / "none" for enhancer-only analysis.
enhancers	Character vector containing any of "WLX", "LR", and "KS".
expVar	Character scalar naming the binary exposure variable in metadata or colData(features).
coVars	Optional character vector naming covariates to include in covariate-aware core methods and logistic-regression enhancers.
assay_name	Name of the assay/experiment to use when features is a MultiAssayExperiment. Required when the object contains multiple experiments.
p_adj	Multiple-testing correction method passed to stats::p.adjust .
enhancer_norm	Normalization method for enhancer tests. One of "TSS", "CLR", "TMM", or "SCRAN".
return_components	Logical; if TRUE, return per-method component result tables.

`return_subensembles`

Logical; if TRUE, return CCT sub-ensemble results for all available method sub-sets.

Value

A list containing combined results in `res`, the analyzed feature table in `features`, elapsed time in `Time.min`, and optionally components and ensembles.

Examples

```
features <- data.frame(
  taxon1 = c(12, 9, 11, 8, 25, 21, 23, 26),
  taxon2 = c(30, 28, 31, 29, 10, 12, 11, 9),
  taxon3 = c(5, 6, 4, 7, 5, 4, 6, 5),
  taxon4 = c(8, 7, 9, 6, 12, 13, 11, 14),
  row.names = paste0("sample", seq_len(8))
)
metadata <- data.frame(
  group = factor(rep(c("control", "case"), each = 4)),
  row.names = rownames(features)
)
result <- DAssemble(
  features = features,
  metadata = metadata,
  core_method = NULL,
  enhancers = "WLX",
  expVar = "group"
)
head(result$res)
```

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