Package 'DAssemble'

December 18, 2025

Type Package

Title Ensemble models for differential analysis

Version 0.99.0

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.

License MIT + file LICENSE

Encoding UTF-8

biocViews Software, StatisticalMethod, DifferentialExpression, RNASeq, SingleCell, Microbiome

Depends R (>= 4.3.0)

Imports methods,
stats,
utils,
graphics,
grDevices,
dplyr,
DESeq2,
edgeR,
limma,
dearseq,
metagenomeSeq,
MAST,
Tweedieverse,
Maaslin2,
maaslin3,
LOCOM,
LinDA,
ANCOMBC,
ALDEx2,
Robseq,
SummarizedExperiment,
TreeSummarizedExperiment,
S4Vectors

Suggests scran,

> SingleCellExperiment,
> knitr,
> rmarkdown,
> BiocStyle,
> Seurat,
> KernSmooth,
> foreign,
> nnet,
> rpart,
> spatial,
> boot,
> class

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

VignetteBuilder knitr

URL https://github.com/Ziyu-Liu-WCM/DAssemble

Contents

DAssemble   *Differential analysis using 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,
  core_method = NULL,
  enhancers = NULL,
  expVar = "group",
  p_adj = "BY",
  enhancer_norm = "TSS",
  return_components = TRUE,
  return_subensembles = FALSE
)
```

Index