Package ‘HiBED’

April 10, 2025

Type Package

Title HiBED

Version 1.5.0

Description Hierarchical deconvolution for extensive cell type resolution in the human brain using DNA methylation. The HiBED deconvolution estimates proportions up to 7 cell types (GABAergic neurons, glutamatergic neurons, astrocytes, microglial cells, oligodendrocytes, endothelial cells, and stromal cells) in bulk brain tissues.

License GPL-3

Encoding UTF-8

LazyData false

VignetteBuilder knitr

biocViews ExperimentData, Homo_sapiens_Data, Tissue, MicroarrayData, Genome, MethylationArrayData, PackageTypeData

RoxygenNote 7.2.3

URL `https://github.com/SalasLab/HiBED`

Imports dplyr, FlowSorted.Blood.EPIC, tibble, FlowSorted.DLPFC.450k, minfi, utils, AnnotationHub, SummarizedExperiment

Suggests knitr, rmarkdown, testthat, IlluminaHumanMethylation450kmanifest

BugReports `https://github.com/SalasLab/HiBED/issues.`

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Contents

`HiBED_deconvolution` *HiBED_deconvolution*

Description

The function estimates proportions up to 7 cell types in brain tissues.

Usage

```
HiBED_deconvolution(Beta, h = 2)
```

Arguments

`Beta`	Methylation beta in the format of matrix or data frame or Mset or SummarizedExperiment from brain samples.
`h`	Numeric variable. Specify the layer of deconvolution in the hierarchical model. Default is 2.

Value

A matrix with predicted cell proportions in brain tissues.

Examples

```
#Step 1: Load required libraries
library(FlowSorted.Blood.EPIC)
library(FlowSorted.DLPFC.450k)
#Step 2: Load example data and preprocess
Mset<-minfi::preprocessRaw(FlowSorted.DLPFC.450k)
Examples_Betas<-minfi::getBeta(Mset)
#Step 3: Run HiBED and show results
HiBED_result<-HiBED_deconvolution(Examples_Betas, h=2)
head(HiBED_result)
```

`HiBED_Libraries` ***HiBED library CpGs matrix stored in SummarizedExperiment for brain tissue DNA methylation deconvolution***

Description

This object contains 4 matrices of the the average DNA methylation values of the probes included in 4 layers of the HiBED deconvolution. These CpGs are used as the backbone for deconvolution and were selected because their methylation signature differs across the seven brain cell subtypes.

Usage

```
data("HiBED_Libraries")
```

Format

The list contains matrices are 81 x 3, 183 x 4, 237 x 5, 120 x 4

The format is: num [1:81, 1:3] 0.04592944 0.02268472 0.88886150 ...

Value

A list with 4 libraries in SummarizedExperiment formats

Examples

```
data("HiBED_Libraries")
head(HiBED_Libraries)
```

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