# Package 'HiBED'

May 5, 2026

**Type** Package

**Title** HiBED

**Version** 1.11.0

**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.

**git_url** https://git.bioconductor.org/packages/HiBED

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`HiBED_deconvolution` *HiBED_deconvolution*

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## 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)
```

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

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## 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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