Package ‘BeadSorted.Saliva.EPIC’

April 7, 2026

Title Illumina EPIC data on BeadSorted child saliva cells

Version 1.19.0

Description Raw data objects used to estimate saliva cell proportion estimates in ewastools. The FlowSorted.Saliva.EPIC object is constructed from samples assayed by Lauren Middleton et. al. (2021).

Depends R (>= 4.1), minfi(>= 1.36.0), ExperimentHub

biocViews ExperimentData, Homo_sapiens_Data, MicroarrayData, Genome, MethylationArrayData, ExperimentHub

License GPL-3

Encoding UTF-8

LazyData true

VignetteBuilder knitr

RoxygenNote 7.1.1

Suggests knitr, rmarkdown

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Author Jonah Fisher [aut, cre],
Kelly Bakulski [aut],
Lauren Middleton [aut]

Maintainer Jonah Fisher <`jazzfish@umich.edu`>

Contents

`BeadSorted.Saliva.EPIC`

DNA Methylation RGChannelSet

Description

Illumina Human Methylation data from EPIC on cell-sorted child saliva cell populations. The BeadSorted.Saliva.EPIC package contains Illumina HumanMethylationEPIC ("EPIC")) DNA methylation microarray data from Middleton and colleagues, consisting of 38 magnetic bead sorted saliva cell references from 22 samples, formatted as an RGChannelSet object for easy integretion with other bioconductor packages.

This package contains data similar to other data packages for cell-type deconvolution, such as FlowSorted.Blood.450k and FlowSorted.Blood.EPIC. However, this package provides novel data from saliva biosamples.

Researchers may find this package useful as these samples represent cell populations (immune and epithelial cells) from cell-sorted saliva.

Implementation of cell-type estimation using these data can be performed using the **ewastools** package's function estimateLC.

Format

An RGChannelSet, dimensions: 1051815 60

Source

`https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE147318` The BeadSorted.Saliva.EPIC object is based on samples assayed by Lauren Middleton et a. (2021).

See Also

References

1. Lauren Y. M. Middleton, John Dou, Jonah Fisher, Jonathan A. Heiss, Vy K. Nguyen, Allan C. Just, Jessica Faul, Erin B. Ware, Colter Mitchell, Justin A. Colacino & Kelly M. Bakulski (2021) *Saliva cell type DNA methylation reference panel for epidemiological studies in children* , Epigenetics, DOI: 10.1080/15592294.2021.1890874
2. EA Houseman et al. (2012) *DNA methylation arrays as surrogate measures of cell mixture distribution*. BMC Bioinformatics 13, 86. doi:10.1186/1471-2105-13-86.
3. **ewastools** package with implementation for estimating cell type proportions in saliva using these data

`https://github.com/hhhh5/ewastools`

Examples

```
library(ExperimentHub)
query(ExperimentHub(), "BeadSorted.Saliva.EPIC")

BeadSorted.Saliva.EPIC <- ExperimentHub()[["EH4539"]]
BeadSorted.Saliva.EPIC
```

`BeadSorted.Saliva.EPIC.compTable`

Cell Proportion Association Table

Description

Association of each probe in the Illumina EPIC array with saliva cell type composition.

Format

A data frame with 795694 rows and 7 columns

probeName	CpG identifier
t-statistic	test statistic for the t-test between immune and epithelial compositions
p-value	p-value for the t-test between immune and epithelial compositions
averageMethylationImmune	average methylation beta value across immune cell samples
averageMethylationEpithelial	average methylation beta value across epithelial cell samples
low	minimum methylation beta across all samples
high	maximum methylation beta across all samples

Examples

```
library(ExperimentHub)
query(ExperimentHub(), "BeadSorted.Saliva.EPIC.compTable")

BeadSorted.Saliva.EPIC.compTable <- ExperimentHub()[["EH4540"]]
BeadSorted.Saliva.EPIC.compTable
```

`BeadSorted.Saliva.EPIC.estimates`

Estimated cell proportion for samples

Description

Cell-type proportion estimates for each of 60 samples from 22 children. Proportions were estimated using the estimateLC function from the **ewastools** package.

Usage

```
BeadSorted.Saliva.EPIC.estimates
```

Format

A data frame with 60 rows and 4 columns

sampid Sample identifier

immuneCells Estimated proportion of immune cells in sample

epithelialCells Estimate proportion of epithelial cells in sample

See Also

References

1. EA Houseman et al. (2012) *DNA methylation arrays as surrogate measures of cell mixture distribution*. BMC Bioinformatics 13, 86. doi:10.1186/1471-2105-13-86.
2. **ewastools** package with implementation for estimating cell-type proportion in saliva using these data

`https://github.com/hhhh5/ewastools`

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