Package

`FlowSorted.CordBloodCombined.450k`

March 12, 2024

Type  Package
Title  Illumina 450k/EPIC data on FACS and MACS umbilical blood cells
Version  1.18.0
Date  2019-10-24
Description  Raw data objects to be used for umbilical cord blood cell proportion estimation in minfi and similar packages. The FlowSorted.CordBloodCombined.450k object is based in samples assayed by Bakulski et al, Gervin et al., de Goede et al., and Lin et al.
License  GPL-3
Depends  R (>= 3.6), minfi (>= 1.21.2), ExperimentHub(>= 1.9.1)
Imports  SummarizedExperiment,
IlluminaHumanMethylation450kanno.ilmn12.hg19(>= 0.2.1),
IlluminaHumanMethylationEPICanno.ilm10b4.hg19, utils,
AnnotationHub
biocViews  ExperimentData, Homo_sapiens_Data, Tissue, MicroarrayData,
Genome, TissueMicroarrayData, MethylationArrayData,
ExperimentHub
NeedsCompilation  no
LazyData  yes
LazyDataCompression  gzip
Suggests  FlowSorted.Blood.EPIC, knitr, rmarkdown, testthat,
IlluminaHumanMethylation450kmanifest(>= 0.2.0),
IlluminaHumanMethylationEPICanno.ilm10b2.hg19
VignetteBuilder  knitr
RoxygenNote  7.1.2
Description

The FlowSorted.CordBloodCombined.450k package contains data derived from Illumina HumanMethylation450K and Illumina HumanMethylationEPIC DNA methylation microarrays (Gervin K, Salas L.A et al. under review), consisting of 263 blood cell references and 26 umbilical cord blood samples, formatted as an RGChannelSet object for integration and normalization using most of the existing Bioconductor packages.

This package contains cleaned data from four different umbilical cord blood references similar to the FlowSorted.CordBlood.450K package consisting of data from umbilical cord blood samples generated from healthy newborns. However, when using the cleaned dataset (eliminating potential cell cross contamination) and using the IDOL procedure compared to minfi estimates the cell type composition obtained through FlowSorted.CordBlood.450k package were less precise and biased compared to actual cell counts. Hence, this package consists of appropriate data for deconvolution of umbilical cord blood samples used in for example EWAS relying in both 450K and EPIC technology.
Researchers may find this package useful as these samples represent different cellular populations (T lymphocytes (CD4+ and CD8+), B cells (CD19+), monocytes (CD14+), NK cells (CD56+), granulocytes, and nucleated red blood cells of cell sorted umbilical cord blood. The estimates were contrasted versus FACS proportions in 22 umbilical samples, and validated using 197 umbilical cord blood samples.

These data can be integrated with the minfi Bioconductor package to estimate cellular composition in users’ umbilical cord blood Illumina 450K and EPIC samples using a modified version of the algorithm constrained projection/quadratic programming described in Houseman et al. 2012. However, for more accurate estimations we suggest that the user prefers IDOL over minfi automatic estimations, using the function estimateCellCounts2 from the package FlowSorted.Blood.EPIC which allows using customized sets of probes from IDOL (see IDOLOptimizedCpGsCordBlood for an example).

Usage

FlowSorted.CordBloodCombined.450k

# See ?estimateCellCounts2 for cell deconvolution guidelines

Format

A class: RGChannelSet, dimensions: 575130 289

Value

RGChannelSet 289 samples

See Also

References


9. **minfi** package for tools for estimating cell type composition in blood using these data

**Examples**

```r
FlowSorted.CordBloodCombined.450k
#libraryDataGet('FlowSorted.CordBloodCombined.450k')
#table(FlowSorted.CordBloodCombined.450k$CellType)
```

**Description**

The FlowSorted.CordBloodCombined.450k.compTable contains the average DNA methylation values used for IDOL deconvolution (Gervin K, Salas LA et al. under review), these data are derived from 263 umbilical blood cell references available in ExperimentHub (FlowSorted.CordBloodCombined.450k).

Researchers who want to project directly their estimates can use this matrix of different cellular populations (T lymphocytes (CD4+ and CD8+), B cells (CD19+), monocytes (CD14+), NK cells (CD56+), Granulocytes, and nucleated red blood cells of cell sorted umbilical cord blood. The estimates were contrasted versus FACS proportions in 22 umbilical samples, and validated using 197 umbilical cord blood samples.

**Usage**

```r
#data("FlowSorted.CordBloodCombined.450k.compTable")
#head(FlowSorted.CordBloodCombined.450k.compTable)
#See ?estimateCellCounts2 for deconvolution
```

**Format**

A class: matrix, dimensions: 517 7 The format is: num [1:517, 1:7] 0.0568 0.214 0.908 0.839 ...

**Value**

numeric matrix 517 rows 7 columns
See Also

References


9. minfi package for tools for estimating cell type composition in blood using these data

Examples

```r
# Explore the reference library
#data("FlowSorted.CordBloodCombined.450k.compTable")
#head(FlowSorted.CordBloodCombined.450k.compTable)
```

Description

This object is a vector of length 517 consisting of the names of the IDOL optimized CpGs. These CpGs are used as the backbone for deconvolution and were selected because their methylation signature differs across the six normal leukocyte subtypes and the nucleated red blood cells.
Usage

```r
#data ("IDOLOptimizedCpGsCordBlood")
#head(IDOLOptimizedCpGsCordBlood)
#See ?estimateCellCounts2 for deconvolution examples
```

Format

An object of class "character" of length 517. The format is: `chr [1:517] "cg12603453" "cg24765783" "cg06975018" "cg19708055" ...

References


Examples

```r
#data ("IDOLOptimizedCpGsCordBlood")
#head(IDOLOptimizedCpGsCordBlood)
#See ?estimateCellCounts2 for deconvolution examples
```
Examples

FlowSorted.CordBloodCombined.450k <-
libraryDataGet('FlowSorted.CordBloodCombined.450k')
FlowSorted.CordBloodCombined.450k
Index

* datasets
  FlowSorted.CordBloodCombined.450k,  2
  FlowSorted.CordBloodCombined.450k.compTable,  4
  IDOLOptimizedCpGsCordBlood,  5

FlowSorted.CordBloodCombined.450k,  2
FlowSorted.CordBloodCombined.450k.compTable,  4

IDOLOptimizedCpGsCordBlood,  5

libraryDataGet,  6