Package 'FlowSorted.CordBloodCombined.450k'

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Type Package

Title Illumina 450k/EPIC data on FACS and MACS umbilical blood cells

Version 1.28.0

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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

URL https://github.com/immunomethylomics/FlowSorted.CordBloodCombined.450k

BugReports https://github.com/immunomethylomics/FlowSorted.CordBloodCombined.450k/issues.

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`FlowSorted.CordBloodCombined.450k`
FlowSorted.CordBloodCombined.450k

Description

The FlowSorted.CordBloodCombined.450k package contains data derived from Illumina HumanMethylation450K and Illumina HumanMethylationEPIC DNA methylation microarrays (Gervin K, Salas LA 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 suggests 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

1. K Gervin, LA Salas et al. (2019) *Systematic evaluation and validation of references and library selection methods for deconvolution of cord blood DNA methylation data*. Clin Epigenetics 11,125. doi: 10.1186/s13148-019-0717-y
2. KM Bakulski, et al. (2016) *DNA methylation of cord blood cell types: Applications for mixed cell birth studies*. Epigenetics 11:5. doi:10.1080/15592294.2016.1161875.
3. K Gervin, et al. (2016) *Cell type specific DNA methylation in cord blood: A 450K-reference data set and cell count-based validation of estimated cell type composition*. Epigenetics 11:690-8. doi:10.1080/15592294.2016.1214782.
4. OM de Goede, et al. (2015) *Nucleated red blood cells impact DNA methylation and expression analyses of cord blood hematopoietic cells*. Clin Epigenetics. 7:95. doi:10.1186/s13148-015-0129-6.
5. X Lin, et al. (2018) *Cell type-specific DNA methylation in neonatal cord tissue and cord blood: A 850K-reference panel and comparison of cell-types*. Epigenetics. 13:941-58. doi:10.1080/15592294.2018.1522929.
6. LA Salas et al. (2018). *An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray*. Genome Biology 19, 64. doi: 10.1186/s13059-018-1448-7.

7. DC Koestler et al. (2016). *Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL)*. BMC bioinformatics. 17, 120. doi: 10.1186/s12859-016-0943-7.

8. 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.

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

Examples

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

FlowSorted.CordBloodCombined.450k.compTable

FlowSorted.CordBloodCombined.450k.compTable

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

```
#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

1. K Gervin, LA Salas et al. (2019) *Systematic evaluation and validation of references and library selection methods for deconvolution of cord blood DNA methylation data*. Clin Epigenetics 11,125. doi: 10.1186/s13148-019-0717-y
2. KM Bakulski, et al. (2016) *DNA methylation of cord blood cell types: Applications for mixed cell birth studies*. Epigenetics 11:5. doi:10.1080/15592294.2016.1161875.
3. K Gervin, et al. (2016) *Cell type specific DNA methylation in cord blood: A 450K-reference data set and cell count-based validation of estimated cell type composition*. Epigenetics 11:690-8. doi:10.1080/15592294.2016.1214782.
4. OM de Goede, et al. (2015) *Nucleated red blood cells impact DNA methylation and expression analyses of cord blood hematopoietic cells*. Clin Epigenetics. 7:95. doi:10.1186/s13148-015-0129-6.
5. X Lin, et al. (2018) *Cell type-specific DNA methylation in neonatal cord tissue and cord blood: A 850K-reference panel and comparison of cell-types*. Epigenetics. 13:941-58. doi:10.1080/15592294.2018.1522929.
6. LA Salas et al. (2018). *An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray*. Genome Biology 19, 64. doi: 10.1186/s13059-018-1448-7.
7. DC Koestler et al. (2016). *Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL)*. BMC bioinformatics. 17, 120. doi: 10.1186/s12859-016-0943-7.
8. 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.
9. **minfi** package for tools for estimating cell type composition in blood using these data

Examples

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

`IDOLOptimizedCpGsCordBlood` *IDOL Optimized CpGs for umbilical cord blood DNA methylation deconvolution*

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

```
#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

K Gervin, LA Salas et al. (2019) *Systematic evaluation and validation of references and library selection methods for deconvolution of cord blood DNA methylation data*. Clin Epigenetics 11,125. doi: 10.1186/s13148-019-0717-y

LA Salas et al. (2018). *An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray*. Genome Biology 19, 64. doi: 10.1186/s13059-018-1448-7.

DC Koestler et al. (2016). *Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL)*. BMC bioinformatics. 17, 120. doi: 10.1186/s12859-016-0943-7.

Examples

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

---

libraryDataGet *libraryDataGet*

Description

Function to load the library data from ExperimentHub

Usage

```
libraryDataGet(title)
```

Arguments

title	title of the data, e.g., 'FlowSorted.CordBloodCombined.450k'

Value

The function will look for the dataset in ExperimentHub and load the object

This function will return an object matching the title of the ExperimentHub

Examples

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

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