Package 'FlowSorted.CordBlood.450k'

Type Package

Title Illumina 450k data on sorted cord blood cells

Version 1.24.0

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Description Raw data objects to be used for cord blood cell proportion estimation in minfi.

License Artistic-2.0

Depends R (>= 3.2.0), minfi (>= 1.21.2)

LazyData yes

biocViews ExperimentData, Homo_sapiens_Data, Tissue, MicroarrayData, TissueMicroarrayData, MethylationArrayData

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R topics documented:

FlowSorted.CordBlood.450k

Illumina 450k data on sorted cord blood cell populations

Description

This `RGChannelSet` contains Illumina 450k measurements on 17 cord blood samples, each of which contribute between 4 and 7 sorted cell populations. These 7 cell populations are: B cells, CD4 T cells, CD8 T cells, granulocytes, monocytes, natural killer cells, and nucleated red blood cells.

Usage

```
data(FlowSorted.CordBlood.450k)
```

Details

Please see manuscript for additional details on cord blood samples and prediction pipeline.

Value

An `RGChannelSet`.

References

Bakulski KM, Feinberg JI, Yang J, Brown S, Andrews SV, McKenney S, Witter F, Walston J, Feinberg AP, Fallin MD. *DNA methylation of cord blood cell types: Applications for mixed cell birth studies.* Epigenetics (2016), 11:354-362. doi:10.1080/15592294.2016.1161875.

Examples

```
data(FlowSorted.CordBlood.450k)
```

FlowSorted.CordBlood.450k.compTable

Cell composition association table

Description

Association of probes on the 450k with cord blood cell composition. Please see manuscript for probe filtering criteria.

Usage

```
data(FlowSorted.CordBlood.450k.compTable)
```

Format

A data frame with 429794 observations on the following 12 variables.

`Fstat` f-statistic for composition from ANOVA. See estimateCellCounts in minfi.

`p.value` p-value corresponding to f-statistic.

`Bcell` mean methylation level across 15 B cell replicates.

`CD4T` mean methylation level across 15 CD4 T-cell replicates.

`CD8T` mean methylation level across 14 CD8 T-cell replicates.

`Gran` mean methylation level across 12 granulocyte replicates.

`Mono` mean methylation level across 15 monocyte replicates.

`NK` mean methylation level across 14 natural killer cell replicates.

`nRBC` mean methylation level across 4 nucleated red blood cell replicates.

`low` low value of methylation across all samples.

`high` high value of methylation across all samples.

`range` range of methylation values across all samples.

Details

Our recommedations for this object parallel those given in the (adult) blood companion package, FlowSorted.Blood.450k. Briefly, this object can be used to evaluate the potetial for cofounding by cell-type heterogeneity at 450k probes following an associaton study.

Value

A data frame with 429794 observations and 12 variables.

References

Bakulski KM, Feinberg JI, Yang J, Brown S, Andrews SV, McKenney S, Witter F, Walston J, Feinberg AP, Fallin MD. *DNA methylation of cord blood cell types: Applications for mixed cell birth studies.* Manuscript in review.

Examples

```
data(FlowSorted.CordBlood.450k.compTable)
```

FlowSorted.CordBlood.450k.ModelPars
Model parameters for cord blood cell type estimation

Description

This object is generated during the course of cord blood cell proportion estimation in the minfi
estimateCellCounts function.

Usage

```
data(FlowSorted.CordBlood.450k.ModelPars)
```

Details

A matrix of 700 rows and 7 columns, the latter corresponding to 7 cell types. 100 probes were
selected as being differentially methylated by each cell type from the reference RGset contained
herein (FlowSorted.CordBlood.450k). In the implementation of the estimateCellCounts func-
tion, probes are selected based on a combined RGset of user and reference data. Please see
manuscript for details on the probe selection process.

Value

A matrix with 700 rows and 7 columns.

References

Bakulski KM, Feinberg JI, Yang J, Brown S, Andrews SV, McKenney S, Witter F, Walston J, Fein-
berg AP, Fallin MD. *DNA methylation of cord blood cell types: Applications for mixed cell birth
studies.* Manuscript in review.

Examples

```
data(FlowSorted.CordBlood.450k.ModelPars)
```

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