Package ‘FlowSorted.Blood.450k’

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Version 1.41.0

Title Illumina HumanMethylation data on sorted blood cell populations

Description Raw data objects for the Illumina 450k DNA methylation microarrays, and an object depicting which CpGs on the array are associated with cell type.

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License Artistic-2.0

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`FlowSorted.Blood.450k` *Illumina Human Methylation data from 450k on sorted blood cell populations*

Description

This `RGset` contains Illumina 450k DNA methylation measurements on 60 samples from Reinius et al. 2012, which can be used by the minfi package to estimate cellular composition from whole blood samples. This data may also be useful to individuals as example Illumina 450k data for trying preprocessing methods across a variety of Bioconductor packages.

Usage

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

Format

An object of class `RGChannelSet`.

Details

The `FlowSortedBlood.450k` objects is based an samples assayed as part of Reinius et al (2012). Please cite this paper, if the data is used. If you're using this data together with the minfi package, please see the package vignette for details on how to cite that package.

A script for obtaining this dataset is available in the `scripts` directory of this package.

References

Reinius, L. E. et al. *Differential DNA Methylation in Purified Human Blood Cells: Implications for Cell Lineage and Studies on Disease Susceptibility*. PLoS ONE (2012), 7:e41361. doi:10.1371/journal.pone.0041361

Houseman E.A. et al *DNA methylation arrays as surrogate measures of cell mixture distribution.* BMC Bioinformatics (2012), 13:p86. doi:10.1186/147121051386

Jaffe A.E. and Irizarry R.A. *Accounting for cellular heterogeneity is critical in epigenome-wide association studies* Genome Biology (2013), 15:R31. doi:10.1186/gb2014152r31

See Also

`FlowSorted.Blood.450k.JaffeModelPars` and `FlowSorted.Blood.450k.compTable` for additional datasets derived from this one. See the minfi package for tools for estimating cell type composition in blood using these data..

Examples

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

FlowSorted.Blood.450k.compTable

Cell Composition Association Table

Description

Association of each probe on the Illumina 450k with blood cell composition Note that probes on the sex chromosomes and those that contain annotated single nucleotide polymorphisms (SNPs) have been filtered (see Methods section of Jaffe and Irizarry 2013, below)

Usage

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

Format

Name: CpG identifier from the Illumina 450k Fstat: f-statistic for composition from the ANOVA containing 6 samples/biological replicates per cell type across 6 cell types p.value: corresponding p-value for f-statistic CD8T_mean: mean DNA methylation (DNAm) across the 6 CD8+ T-cell replicates, on the beta/proportion methylation scale CD4T_mean: mean DNA methylation (DNAm) across the 6 CD4+ T-cell replicates, on the beta/proportion methylation scale NK_mean: mean DNA methylation (DNAm) across the 6 Natural Killer cell replicates, on the beta/proportion methylation scale Bcell_mean: mean DNA methylation (DNAm) across the 6 B-cell replicates, on the beta/proportion methylation scale Mono_mean: mean DNA methylation (DNAm) across the 6 monocyte replicates, on the beta/proportion methylation scale Gran_mean: mean DNA methylation (DNAm) across the 6 granulocyte replicates, on the beta/proportion methylation scale DNAm_min: minimum beta values across the 36 samples DNAm_max: maximum beta values DNAm_range: range of beta values

Details

We recommend using the CpG identifiers to match each probe from a user's differential methylation analysis in their whole blood data to obtain the corresponding composition p-value - if there are many small p-values for significant differentially methylated sites for the exposure/outcome/trait of interest, this may be a sign of confounding via composition differences, in which case we recommend estimating cellular components using the minfi Bioconductor package, and formally exploring this potential correlation between the trait, composition, and DNA methylation.

References

Reinius, L. E. et al. *Differential DNA Methylation in Purified Human Blood Cells: Implications for Cell Lineage and Studies on Disease Susceptibility*. PLoS ONE 7, e41361 (2012). http://dx.doi.org/10.1371/journal.pone.0041361

Houseman E.A. et al *DNA methylation arrays as surrogate measures of cell mixture distribution.* BMC Bioinformatics 13, p86 (2012). http://dx.doi.org/10.1186/1471-2105-13-86

Jaffe A.E. and Irizarry R.A. *Accounting for cellular heterogeneity is critical in epigenome-wide association studies* Under Review (2013).

See Also

FlowSorted.Blood.450k for the original data, FlowSorted.Blood.450k.JaffeModelPars for an additional dataset derived from this one. See the minfi package for tools for estimating cell type composition in blood using these data.

Examples

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

FlowSorted.Blood.450k.JaffeModelPars

Model Parameters for Blood Cell Type Estimation

Description

This object can be used by minfi to estimate the relative proportion of each cell type, given user's whole blood Illumina 450k data.

Usage

```
data(FlowSorted.Blood.450k.JaffeModelPars)
```

Format

A matrix where rows are selected CpGs that are differentially methylated by cell type, and columns are particular cell types.

Details

For details on how this coefficient object was created, see Methods section of Jaffe and Irizarry, 2013, below. For statistical details on how the cell estimation procedure is performed, refer to Houseman et al 2012.

References

Reinius, L. E. et al. *Differential DNA Methylation in Purified Human Blood Cells: Implications for Cell Lineage and Studies on Disease Susceptibility*. PLoS ONE 7, e41361 (2012). http://dx.doi.org/10.1371/journal.pone.0041361

Houseman E.A. et al *DNA methylation arrays as surrogate measures of cell mixture distribution.* BMC Bioinformatics 13, p86 (2012). http://dx.doi.org/10.1186/1471-2105-13-86

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See Also

FlowSorted.Blood.450k for the original data, FlowSorted.Blood.450k.compTable for an additional dataset derived from this one. See the minfi package for tools for estimating cell type composition in blood using these data.

Examples

```
data(FlowSorted.Blood.450k.JaffeModelPars)
```

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