Package 'FlowSorted.CordBloodNorway.450k'

November 10, 2026

Version 1.38.0

Title Illumina HumanMethylation data on sorted cord blood cell populations

Description Raw data objects for the Illumina 450k DNA methylation microarrays, for cell type composition estimation.

License Artistic-2.0

URL https://bitbucket.com/kasperdanielhansen/Illumina_CordBlood

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

LazyData yes

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

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

Description

The FlowSorted.CordBloodNorway.450k package contains Illumina HumanMethylation450 ("450k")) DNA methylation microarray data provided by Kristina Gervin and coworkers (manuscript in preparation), consisting of 77 umbilical cord blood samples, formatted as an RGset object for easy integration and normalization using existing Bioconductor packages.

This package contains data equivalent to the FlowSorted.Blood.450k package consisting of data from peripheral blood samples generated from adult men. However, minfi estimates of cell type composition in umbilical cord blood samples using the FlowSorted.Blood.450k package does not correlate well with cell counts (see references). Hence, this package consists of appropriate data for deconvolution of cord blood samples used in for example EWAS.

Researchers may find this package useful as these samples represent different cellular populations (lymphocytes (CD4+ and CD8+), B cells (CD19+), monocytes (CD14+), NK cells (CD56+) and granulocytes of whole umbilical cord blood generated on the same 11 (6 girls and 5 boys) individuals using flow sorting, an experimental procedure that can separate heterogeneous biological samples like umbilical blood into pure cellular populations. This data can be directly integrated with the minfi Bioconductor package to estimate cellular composition in users' whole blood Illumina 450k samples using a modified version of the algorithm described in Houseman et al. 2012.

Usage

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

Format

An object of class `RGset`.

Details

The `FlowSorted.CordBloodNorway.450k` objects is based an samples assayed by Kristina Gervin and collegaues; manuscript in preparation.

References

P Yousefi et al. (2015). *Estimation of blood cellular heterogeneity in newborns and children for epigenome-wide association studies*. Environ. Mol. Mutagen. 56, 751-758.

EA Houseman et al. (2012) *DNA methylation arrays as surrogate measures of cell mixture distribution*. BMC Bioinformatics 13, 86.

See Also

See the **minfi** package for tools for estimating cell type composition in blood using these data. See the **FlowSorted.CordBlood.450k** for an alternative reference dataset for Cord Blood samples.

Examples

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

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