

# Package ‘normalize450K’

September 24, 2025

**Type** Package

**Title** Preprocessing of Illumina Infinium 450K data

**Version** 1.37.0

**Date** 2016-11-29

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## Description

Precise measurements are important for epigenome-wide studies investigating DNA methylation in whole blood samples, where effect sizes are expected to be small in magnitude. The 450K platform is often affected by batch effects and proper preprocessing is recommended. This package provides functions to read and normalize 450K '.idat' files. The normalization corrects for dye bias and biases related to signal intensity and methylation of probes using local regression. No adjustment for probe type bias is performed to avoid the trade-off of precision for accuracy of beta-values.

**Depends** R (>= 3.3), Biobase, illuminaio, quadprog

**Imports** utils

**License** BSD\_2\_clause + file LICENSE

**biocViews** Normalization, DNAMethylation, Microarray, TwoChannel,  
Preprocessing, MethylationArray

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/normalize450K>

**git\_branch** devel

**git\_last\_commit** 456fa4e

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-09-23

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estimateLC

*Estimation of Leukocyte composition for whole blood samples***Description**

Estimate leukocyte composition from whole blood DNA methylation

**Usage**

```
estimateLC(eSet)
```

**Arguments**

eSet                      A Biobase eSet object as returned from a call of `normalize450K`

**Details**

Cell proportions are estimated using the algorithm developed by Houseman et al. (2012) by two different models. The first model was trained on a dataset of purified leukocytes (Reinius et al., 2012) and provides predictions for six cell types (granulocytes, monocytes, CD8+ T cells, CD4+ T cells, natural killer cells and CD19+ B cells), the second model was trained on whole blood samples from the LOLIPOP study as described by Heiss et al. (2016) and provides predictions for 4 cell types (neutrophils, eosinophils, lymphocytes, monocytes – ignore the prediction for basophils). Use this function only for normalized data (with `normalize450K(..., tissue='Blood')`).

**Value**

Returns the eSet object with cell proportions estimates added to the `phenoData` slot.

**Author(s)**

Jonathan A. Heiss

**References**

- Houseman EA, et al. (2012) DNA methylation arrays as surrogate measures of cell mixture distribution. BMC Bioinformatics, doi:[10.1186/1471-2105-13-86](https://doi.org/10.1186/1471-2105-13-86)
- Reinius LE, et al. (2012) Differential DNA methylation in purified human blood cells: implications for cell lineage and studies on disease susceptibility. PloS ONE, doi:[10.1371/journal.pone.0041361](https://doi.org/10.1371/journal.pone.0041361)
- Heiss JA, et al. (2016). Training a model for estimating leukocyte composition using whole-blood DNA methylation and cell counts as reference. Epigenomics, doi:[10.2217/epi-2016-0091](https://doi.org/10.2217/epi-2016-0091)

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`read_and_normalize450K`*Normalization of 450K data by LOESS method*

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## Description

Read 450K '.idat' files and compute raw or normalized beta-values.

## Usage

```
read450K(idat_files)
normalize450K(intensities, tissue='')
dont_normalize450K(intensities)
```

## Arguments

|                          |                                                                                                                                                                                                           |
|--------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>idat_files</code>  | a character vector containing the paths to the .idat files stripped from the '_Grn.idat' suffix with one entry for each sample (.idat files for green and red intensities have to be in the same folder). |
| <code>intensities</code> | List object containing raw signal intensities. Result of calling <code>read450K</code> .                                                                                                                  |
| <code>tissue</code>      | If set to 'Blood', a set of prespecified reference values are used for normalization. This is recommended if you plan to use <code>estimateLC</code> .                                                    |

## Details

Function `read450K` reads .idat files and returns a list object containing raw signal intensities. `dont_normalize450K` returns an `ExpressionSet` containing beta-values without normalization. `normalize450K` performs dye bias correction using the extension controls probes followed by normalization by local regression (Heiss and Brenner, 2015) and returns an `ExpressionSet` containing beta-values, too.

## Value

For `read450K` a list containing the methylated, unmethylated and control signal intensities. For `dont_normalize450K` and `normalize450K` an `ExpressionSet` containing beta-values, rows corresponding to CpG sites (named) and columns to samples (in the same order as 'idat\_files').

## Note

A benchmark comparing the performance of this method with other normalization approaches is provided in the vignette.

## Author(s)

Jonathan A. Heiss

## References

Heiss JA, Brenner H (2015). Between-array normalization for 450K data. *Frontiers in Genetics*, doi:[10.3389/fgene.2015.00092](https://doi.org/10.3389/fgene.2015.00092)

**Examples**

```
## Not run:
library(minfiData) ## this package includes some .idat files
library(data.table)

path <- system.file("extdata",package="minfiData")
samples = fread(file.path(path, 'SampleSheet.csv'),integer64='character')

samples[,file:=file.path(path,Sentrix_ID,paste0(Sentrix_ID,'_',Sentrix_Position))]
## samples$file is a character vector containing the location of the
## .idat files, but without the suffixes "_Red.idat" or "_Grn.idat"

raw = read450K(samples$file)
none = dont_normalize450K(raw) ## no normalization
norm = normalize450K(raw)

## End(Not run)
```

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