

MethylAid-summarized data on 2800 Illumina 450k array samples

Maarten van Iterson, Elmar Tobi, Roderick Slieker, Wouter den Hollander, Rene Luijk,

Eline Slagboom and Bas Heijmans
Department of Molecular Epidemiology,
Leiden University Medical Center, Leiden, The Netherlands

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1 Introduction

MethylAidData contains *MethylAid*-summarized data on 2800 Illumina 450k array samples. These DNA methylation samples are a subset from a large-scale multiple omics study conducted by several Dutch Biobanks; the BIOS consortium (<http://www.bbmri.nl/en-gb/activities/rainbow-projects/bios>). The raw Illumina 450k array data, idat-files, will be made available through the EGA archive (<https://www.ebi.ac.uk/ega/home>).

The summarization performed by *MethylAid* entails the following for each sample:

1. calculation of the median Methylated and Unmethylation intensities
2. extraction of all quality control probe intensities
3. construction of quality control metrics e.g. sample-dependent, sample-independent and detection p-values
4. storing everything efficiently to allow fast rendering of the various quality control plots provided by *MethylAid*,

see van Iterson *et al.*[1] for detailed description of *MethylAid*.

2 Preparation of the data

The raw Illumina 450k array data, idat-files, will be made available this summer from EGA archive (accession number:EGAS00###). Access to the data must be approved by the Data Access Committee (###). Once the raw idat-files have been downloaded and a targets file is constructed, *MethylAid* can be used to summarize the data and perform quality control using the interactive *shiny*[2] application.

Data sets of this size are preferably summarized in parallel and batches to overcome long run times or memory issues. *MethylAid* provides several options to do this using the *BiocParallel*-package[3]. For example, if multiple cores are available these could be used like this:

```
library(MethylAid)
targets ##constructed from EGA
BPPARAM <- MulticoreParam(workers = 8, verbose=TRUE)
summarize(targets, batchSize = 100, BPPARAM = BPPARAM, file="exampleDataLarge")
```

Another option would be thus use a cluster, see the vignette of *MethylAid* how to set this up.

3 Using MethylAidData

The summarized data contained in *MethylAidData* can be used in two ways, 1) to explore a large data set using *MethylAid* and 2) use this data as a background data set on top of own data. Since version 1.1.4, *MethylAid* has the functionality to show as background data set in the filter control plots. As such it can be used as a reference data set and can give guidance to when removing outlying samples. Furthermore, the data gives confirmation of the default thresholds used to determine outlying samples.

Additionally, since *MethylAid*(1.1.4) functionality is added to construct your own background data and several summarizedData-objects can be merged to give one larger summarizedData-object to use as your own reference or to determine filter thresholds, for example for hydroxymethylation data for which there are currently no thresholds available.

References

- [1] M. van Iterson, E. W. Tobi, R. C. Sliker, W. den Hollander, R. Luijk, P. E. Slagboom, and B. T. Heijmans. MethylAid: visual and interactive quality control of large Illumina 450k datasets. *Bioinformatics*, 30(23):3435–3437, 2014.
- [2] RStudio and Inc. *shiny: Web Application Framework for R*, 2014. R package version 0.9.1. URL: <http://CRAN.R-project.org/package=shiny>.
- [3] Martin Morgan, Michel Lang, and Ryan Thompson. *BiocParallel: Bioconductor facilities for parallel evaluation*. R package version 1.0.3.