MethylAid-summarized data on 2800 Illumina 450k array samples

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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:

```r
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.

## 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

