Package 'CopyNeutralIMA'

October 27, 2026

Title Copy Neutral Illumina Methylation Arrays

Version 1.30.0

Description Provides a set of genomic copy neutral samples hybridized using Illumina Methylation arrays (450k and EPIC).

Depends R (>= 3.5.0)

License Artistic-2.0

Encoding UTF-8

LazyData true

biocViews ExperimentData,Homo_sapiens_Data,MicroarrayData,TwoChannelData,MethylationArrayData,GEO

Imports ExperimentHub,Rdpack (>= 0.8)

Suggests BiocStyle,knitr,rmarkdown,minfi,conumee,minfiData

RdMacros Rdpack

VignetteBuilder knitr

RoxygenNote 6.0.1

NeedsCompilation no

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`CopyNeutralIMA-package` *Reference samples for analysis of IlluminaHumanMethylation arrays.*

Description

The CopyNeutralIMA package provides a set of 51 samples for IlluminaHumanMethylation450k arrays and a set of 13 samples for IlluminaHumanMethylationEPIC arrays.

Details

The package includes two RGChannelSetExtended objects, one with 51 samples hybridized with the IlluminaHumanMethylation450k array and another one with 13 samples hybridized with the IlluminaHumanMethylationEPIC array.

For the 450k arrays, samples from GEO series GSE49618 (Ley et al. 2013), GSE61441 (Wei et al. 2015) and GSE106089 (Tomlinson et al. 2017) are provided.

For the EPIC arrays, samples from GEO series GSE86831/ GSE86833 #' (Pidsley et al. 2016), GSE98990 (Zhou et al. 2017) and GSE100825 (Guastafierro et al. 2017) are also provided.

The provided samples consist of material from healthy patients with nominally no copy number aberrations.

Users may use this data package as controls for their copy number profiling analysis or for testing other tools.

Check the vignette on how to use these data as control samples for **conumee**.

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References

Guastafierro T, Bacalini MG, Marcoccia A, Gentilini D, Pisoni S, Di Blasio AM, Corsi A, Franceschi C, Raimondo D, Spanò A, Garagnani P, Bondanini F (2017). "Genome-wide DNA methylation analysis in blood cells from patients with Werner syndrome." *Clinical Epigenetics*, **9**, 92. doi:10.1186/s1314801703894.

Ley TJ, Miller C, Ding L, Network TCGAR (2013). "Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia." *The New England of Journal Medicine*, **368**(22), 2059–74. doi:10.1056/NEJMoa1301689.

Pidsley R, Zotenko E, Peters TJ, Lawrence MG, Risbridger GP, Molloy P, Van Djik S, Muhlhausler B, Stirzaker C, Clark SJ (2016). "Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling." *Genome Biology*, **17**(1), 208.

doi:10.1186/s1305901610661.

Tomlinson MS, Bommarito PA, Martin EM, Smeester L, Fichorova RN, Onderdonk AB, Kuban KCK, O'Shea TM, Fry RC (2017). "Microorganisms in the human placenta are associated with altered CpG methylation of immune and inflammation-related genes." *PLoS One*, **12**(12), e0188664. doi:10.1371/journal.pone.0188664.

Wei JH, Haddad A, Luo JH, others (2015). "A CpG-methylation-based assay to predict survival in clear cell renal cell carcinoma." *Nature Communications*, **30**(6), 8699. doi:10.1038/ncomms9699.

Zhou W, Laird PW, Shen H (2017). "Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes." *Nucleic Acids Research*, **45**(4), e22. doi:10.1093/nar/gkw967.

`getCopyNeutralRGSet` *Accessor to the data objects.*

Description

igetCopyNeutralRGSet simplifies the access to the data of the package in ExperimentHub. The allowed values matched of those in the array definition of the RGChannelSet objects from package 'minfi'. If 'ima' is set to 'IlluminaHumanMethylation450k' it will return the object with index 'EH1453' in ExperimentHub; if set to 'IlluminaHumanMethylationEPIC' it will return the object with index 'EH1454'.

Usage

```
getCopyNeutralRGSet(ima = c("IlluminaHumanMethylation450k",
  "IlluminaHumanMethylationEPIC"))
```

Arguments

`ima`	a character string specifying for which array type to retrieve data. Valid values are 'IlluminaHumanMethylation450k' and 'IlluminaHumanMethylationEPIC'.

Value

A `RGChannelSet-class` object

Examples

```
rgset_450k <- getCopyNeutralRGSet('IlluminaHumanMethylation450k')
rgset_450k
```

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