

Package ‘ChAMP’

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Type Package

Title Chip Analysis Methylation Pipeline for Illumina
HumanMethylation450 and EPIC

Version 2.40.0

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Description The package includes quality control metrics, a selection of normalization methods and novel methods to identify differentially methylated regions and to highlight copy number alterations.

License GPL-3

VignetteBuilder knitr

Depends R (>= 3.3), minfi, ChAMPdata (>= 2.6.0),DMRcate,
Illumina450ProbeVariants.db,IlluminaHumanMethylationEPICmanifest,
DT, RPMM

Imports

prettydoc,Hmisc,globaltest,sva,illuminaio,rmarkdown,IlluminaHumanMethylation450kmanifest,IlluminaHumanMethylation450kmanifest,
limma, DNACopy, preprocessCore,impute, marray, wateRmelon,
plyr,goseq,missMethyl,ggplot2,
GenomicRanges,qvalue,isva,doParallel,bumphunter,quadprog,shiny,shinythemes,plotly
(>= 4.5.6),RColorBrewer,dendextend, matrixStats,combinat

biocViews Microarray, MethylationArray, Normalization, TwoChannel,
CopyNumber, DNAMethylation

Suggests knitr,rmarkdown

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NeedsCompilation no

LazyData true

git_url <https://git.bioconductor.org/packages/ChAMP>

git_branch RELEASE_3_22

git_last_commit fa068cf

