Package 'shinyepico'

November 13, 2026

Title ShinyÉPICo

Version 1.21.0

Description ShinyÉPICo is a graphical pipeline to analyze Illumina DNA methylation arrays (450k or EPIC). It allows to calculate differentially methylated positions and differentially methylated regions in a user-friendly interface. Moreover, it includes several options to export the results and obtain files to perform downstream analysis.

License AGPL-3 + file LICENSE

Depends R (>= 4.3.0)

Imports DT (>= 0.15.0), data.table (>= 1.13.0), doParallel (>= 1.0.0), dplyr (>= 1.0.9), foreach (>= 1.5.0), GenomicRanges (>= 1.38.0), ggplot2 (>= 3.3.0), gplots (>= 3.0.0), heatmaply (>= 1.1.0), limma (>= 3.42.0), minfi (>= 1.32.0), plotly (>= 4.9.2), reshape2 (>= 1.4.0), rlang (>= 1.0.2), rmarkdown (>= 2.3.0), rtracklayer (>= 1.46.0), shiny (>= 1.5.0), shinyWidgets (>= 0.5.0), shinycssloaders (>= 0.3.0), shinyjs (>= 1.1.0), shinythemes (>= 1.1.0), statmod (>= 1.4.0), tidyr (>= 1.2.0), zip (>= 2.1.0)

Suggests knitr (>= 1.30.0), mCSEA (>= 1.10.0), IlluminaHumanMethylation450kanno.ilmn12.hg19, IlluminaHumanMethylation450kmanifest, IlluminaHumanMethylationEPICanno.ilm10b4.hg19, IlluminaHumanMethylationEPICmanifest, testthat, minfiData, BiocStyle

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

URL https://github.com/omorante/shiny_epico

BugReports https://github.com/omorante/shiny_epico/issues

VignetteBuilder knitr

biocViews DifferentialMethylation,DNAMethylation,Microarray,Preprocessing,QualityControl

git_url https://git.bioconductor.org/packages/shinyepico

git_branch devel

git_last_commit f44c2c2

git_last_commit_date 2026-04-28

Repository Bioconductor 3.24

Date/Publication 2026-11-12

Author Octavio Morante-Palacios [cre, aut]

Maintainer Octavio Morante-Palacios <octaviompa@gmail.com>

Contents

shinyepico-package 2
run_shinyepico 2

Index **4**

`shinyepico-package` *shinyÉPICo: a graphical and interactive pipeline to analyze Illumina DNA Methylation Arrays*

Description

ShinyÉPICo is a web interface based on Shiny that makes it easy to do differentially methylated positions (DMP) and differentially methylated regions (DMR) analysis from Illumina EPIC or 450k DNA methylation arrays. This program allows following a standard pipeline of normalization (with minfi package), model creation and statistical analysis (with limma package), and DMR calculation (with mCSEA package) with different options in each step and plots to be able to choose properly. Moreover, you can select different options in the final heatmap and download an RMarkdown report with all the steps chosen.

Details

The package contains a vignette that describe throughly its features and options.

`run_shinyepico` *Run Shiny ÉPICo!*

Description

ShinyÉPICo! Interactive minfi and limma pipeline for Illumina methylation arrays

Usage

```
run_shinyepico(
  n_cores = parallel::detectCores()/2,
  max_upload_size = 2000,
  host = "127.0.0.1",
  port = NULL
)
```

Arguments

n_cores	Number of cores to be used in parallelized operations in the application. By default, half of your CPU cores. Parallelization affects only to mean and differences calculation and it does not suppose a significant memory overhead.
max_upload_size	The limit in MB of the .zip file size to be uploaded. By default, 2000MB.
host	IP used to deploy the server. By default, your local IP (127.0.0.1)
port	Port used to deploy the server.

Value

None

Examples

```
{
  if (interactive()) {
    run_shinyepico()
  }
}
```

Index

∗ **package**
shinyepico-package, 2

run_shinyepico, 2

shinyepico *(*shinyepico-package*)*, 2
shinyepico-package, 2