Package: shinyepico (via r-universe)

May 30, 2026

Title ShinyÉPICo

Version 1.20.0

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.

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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

Config/pak/sysreqs cmake make libmagick++-dev gsfonts libbz2-dev libicu-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

Repository https://bioc-release.r-universe.dev

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RemoteUrl https://github.com/bioc/shinyepico

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Contents

`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()
  }
}
```

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