

Package ‘Imetagene’

April 12, 2018

Type Package

Title A graphical interface for the metagene package

Version 1.8.0

Date 2015-09-18

Author@R c(person("Audrey", "Lemacon", email =
"audrey.lemacon.1@ulaval.ca"), person("Charles", "Joly
Beauparlant", email =
"charles.joly-beauparlant@crchul.ulaval.ca"), person("Arnaud",
"Droit", email = "arnaud.droit@crchuq.ulaval.ca"))

Author Audrey Lemacon <audrey.lemacon.1@ulaval.ca>, Charles Joly
Beauparlant <charles.joly-beauparlant@crchul.ulaval.ca>, Arnaud
Droit <arnaud.droit@crchuq.ulaval.ca>

Maintainer Audrey Lemacon <audrey.lemacon.1@ulaval.ca>

Description This package provide a graphical user interface to the
metagene package. This will allow people with minimal R
experience to easily complete metagene analysis.

License Artistic-2.0 | file LICENSE

biocViews ChIPSeq, Genetics, MultipleComparison, Coverage, Alignment,
Sequencing

BugReports <https://github.com/andronekomimi/Imetagene/issues>

VignetteBuilder knitr

Depends R (>= 3.2.0), metagene, shiny

Imports d3heatmap, shinyBS, shinyFiles, shinythemes, ggplot2

Suggests knitr, BiocStyle, rmarkdown

NeedsCompilation no

R topics documented:

shiny_metagene 2

Index 3

`shiny_metagene`*Launch interactive metagene session*

Description

Launch interactive metagene session

Usage

```
shiny_metagene()
```

Value

Interactive metagene session

Examples

```
if (interactive()) {  
  shiny_metagene()  
}
```

Index

shiny_metagene, [2](#)