

# Package ‘Imetagene’

September 23, 2017

**Type** Package

**Title** A graphical interface for the metagene package

**Version** 1.6.0

**Date** 2015-09-18

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

**Author** Audrey Lemacon <audrey.lemacon.1@ulaval.ca>, Charles Joly  
Beuparlant <charles.joly-beuparlant@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](#)