

Package ‘Imetagene’

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Type Package

Title A graphical interface for the metagene package

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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.

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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

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

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R topics documented:

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shiny_metagene	<i>Launch interactive metagene session</i>
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Description

Launch interactive metagene session

Usage

```
shiny_metagene()
```

Value

Interactive metagene session

Examples

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

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