

# 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.

**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

**git\_url** <https://git.bioconductor.org/packages/Imetagene>

**git\_branch** RELEASE\_3\_9

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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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