

# Package ‘RIPAT’

October 18, 2022

**Title** Retroviral Integration Pattern Analysis Tool (RIPAT)

**Version** 1.6.0

**Description** RIPAT is developed as an R package for retroviral integration sites annotation and distribution analysis. RIPAT needs local alignment results from BLAST and BLAT. Specific input format is depicted in RIPAT manual. RIPAT provides RV integration pattern analysis result as forms of R objects, excel file with multiple sheets and plots.

**biocViews** Annotation

**Depends** R (>= 4.0)

**Imports** biomaRt (>= 2.38.0), GenomicRanges (>= 1.34.0), ggplot2 (>= 3.1.0), grDevices (>= 3.5.3), IRanges (>= 2.16.0), karyoploteR (>= 1.6.3), openxlsx (>= 4.1.4), plyr (>= 1.8.4), regioneR (>= 1.12.0), rtracklayer (>= 1.42.2), stats (>= 3.5.3), stringr (>= 1.3.1), utils (>= 3.5.3)

**Suggests** knitr (>= 1.28)

**VignetteBuilder** knitr

**License** Artistic-2.0

**URL** <https://github.com/bioinfo16/RIPAT/>

**Encoding** UTF-8

**RoxygenNote** 7.1.0

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annoByCpG	<i>Annotate integration sites by CpG sites.</i>
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### Description

Annotate vector integration sites by CpG site data.

### Usage

```
annoByCpG(hits, mapTool = 'blast', organism = 'GRCh37', interval = 5000,
          range = c(-20000, 20000), doRandom = TRUE,
          randomSize = if(doRandom){10000}else{NULL},
          includeUndecided = FALSE, outPath = getwd(),
          outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

### Arguments

hits	a GR object. This object made by makeInputObj function.
mapTool	a single character. Function serves two types of object such as outputs from BLAST and BLAT. Default is 'blast'. If you want to use BLAT result, use 'blat'.
organism	a single character. This function can run by two versions of organisms such as GRCh37, GRCh38 (Human). Default is 'GRCh37'.
interval	an integer vector. This number means interval number for distribution analysis. Default is 5000.

range	an integer array. The range of highlight region for analysis. Default range is c(-20000, 20000).
doRandom	TRUE or FALSE. If user types TRUE, random set is generated and user can do random distribution analysis. Default is TRUE. If this value is FALSE, random distribution analysis is not executed.
randomSize	an integer vector. A random set size. Default is 10000.
includeUndecided	TRUE or FALSE. If user want to use undecided hits in analysis, enter TRUE. Default is FALSE.
outPath	an string vector. Plots are saved in this path. Default value is R home directory.
outFileName	a character vector. Attached ID to the result file name.

### Value

Return a result list that is made up of insertion and distribution result tables and GenomicRange object of CpG data.

### Examples

```
data(blast_obj); data(cpg_exam_db)
saveRDS(cpg_exam_db, paste0(system.file("extdata", package = 'RIPAT'), '/GRCh37_cpg.rds'))

blast_cpg = annoByCpG(hits = blast_obj, doRandom = FALSE, outFileName = 'blast_res')
```

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annoByGene	<i>Annotate integration sites by genes and TSSs.</i>
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### Description

Annotate vector integration sites by gene data.

### Usage

```
annoByGene(hits, mapTool = 'blast', organism = 'GRCh37', interval = 5000,
           range = c(-20000, 20000), doRandom = TRUE,
           randomSize = if(doRandom){10000}else{NULL},
           includeUndecided = FALSE, outPath = getwd(),
           outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

### Arguments

hits	a GR object. This object made by makeInputObj function.
mapTool	a single character. Function serves two types of object such as outputs from BLAST and BLAT. Default is 'blast'. If you want to use BLAT result, use 'blat'.

organism	a single character. This function can run by two versions of organisms such as GRCh37, GRCh38 (Human). Default is 'GRCh37'.
interval	an integer vector. This number means interval number for distribution analysis. Default is 5000.
range	an integer array. The range of highlight region for analysis. Default range is c(-20000, 20000).
doRandom	TRUE or FALSE. If user types TRUE, random set is generated and user can do random distribution analysis. Default is TRUE. If this value is FALSE, random distribution analysis is not executed.
randomSize	an integer vector. A random set size. Default is 10000.
includeUndecided	TRUE or FALSE. If user want to use undecided hits in analysis, enter TRUE. Default is FALSE.
outPath	an string vector. Plots are saved in this path. Default value is R home directory.
outFileName	a character vector. Attached ID to the result file name.

### Value

Return a result list that is made up of insertion and distribution result tables and GenomicRange object of Gene and TSS data.

### Examples

```
data(blast_obj); data(gene_exam_db); data(tss_exam_db)
saveRDS(gene_exam_db, paste0(system.file("extdata", package = 'RIPAT'), '/GRCh37_gene.rds'))
saveRDS(tss_exam_db, paste0(system.file("extdata", package = 'RIPAT'), '/GRCh37_TSS.rds'))

blast_gene = annoByGene(hits = blast_obj, doRandom = FALSE, outFileName = 'blast_res')
```

---

annoByRepeat	<i>Annotate integration sites by repeats and microsatellites.</i>
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---

### Description

Annotate vector integration sites by repeat and microsatellite data.

### Usage

```
annoByRepeat(hits, mapTool = 'blast', organism = 'GRCh37', interval = 5000,
             range = c(-20000, 20000), doRandom = TRUE,
             randomSize = if(doRandom){10000}else{NULL},
             includeUndecided = FALSE, outPath = getwd(),
             outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

**Arguments**

hits	a GR object. This object made by makeInputObj function.
mapTool	a single character. Function serves two types of object such as outputs from BLAST and BLAT. Default is 'blast'. If you want to use BLAT result, use 'blat'.
organism	a single character. This function can run by two versions of organisms such as GRCh37, GRCh38 (Human). Default is 'GRCh37'.
interval	an integer vector. This number means interval number for distribution analysis. Default is 5000.
range	an integer array. The range of highlight region for analysis. Default range is c(-20000, 20000).
doRandom	TRUE or FALSE. If user types TRUE, random set is generated and user can do random distribution analysis. Default is TRUE. If this value is FALSE, random distribution analysis is not executed.
randomSize	an integer vector. A random set size. Default is 10000.
includeUndecided	TRUE or FALSE. If user want to use undecided hits in analysis, enter TRUE. Default is FALSE.
outPath	an string vector. Plots are saved in this path. Default value is R home directory.
outFileName	a character vector. Attached ID to the result file name.

**Value**

Return a result list that is made up of insertion and distribution result tables and GenomicRange object of Rpeat and microsatellite data.

**Examples**

```
data(blast_obj); data(repeat_exam_db); data(micro_exam_db)
saveRDS(repeat_exam_db, paste0(system.file("extdata", package = 'RIPAT'), '/GRCh37_repeat.rds'))
saveRDS(micro_exam_db, paste0(system.file("extdata", package = 'RIPAT'), '/GRCh37_microsat.rds'))

blast_repeat = annoByRepeat(hits = blast_obj, doRandom = FALSE, outFileName = 'blast_res')
```

---

annoByVar

*Annotate integration sites by clinical variants.*


---

**Description**

Annotate vector integration sites by clinical variant data.

**Usage**

```
annoByVar(hits, mapTool = 'blast', organism = 'GRCh37', interval = 5000,
          range = c(-20000, 20000), doRandom = TRUE,
          randomSize = if(doRandom){10000}else{NULL},
          includeUndecided = FALSE, outPath = getwd(),
          outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

**Arguments**

hits	a GR object. This object made by makeInputObj function.
mapTool	a single character. Function serves two types of object such as outputs from BLAST and BLAT. Default is 'blast'. If you want to use BLAT result, use 'blat'.
organism	a single character. This function can run by two versions of organisms such as GRCh37, GRCh38 (Human). Default is 'GRCh37'.
interval	an integer vector. This number means interval number for distribution analysis. Default is 5000.
range	an integer array. The range of highlight region for analysis. Default range is c(-20000, 20000).
doRandom	TRUE or FALSE. If user types TRUE, random set is generated and user can do random distribution analysis. Default is TRUE. If this value is FALSE, random distribution analysis is not executed.
randomSize	an integer vector. A random set size. Default is 10000.
includeUndecided	TRUE or FALSE. If user want to use undecided hits in analysis, enter TRUE. Default is FALSE.
outPath	an string vector. Plots are saved in this path. Default value is R home directory.
outFileName	a character vector. Attached ID to the result file name.

**Value**

Return a result list that is made up of insertion and distribution result tables and GenomicRange object of clinical variant data.

**Examples**

```
data(blast_obj); data(var_exam_db)
saveRDS(var_exam_db, paste0(system.file("extdata", package = 'RIPAT'), '/GRCh37_clinvar.rds'))

blast_clivar = annoByVar(hits = blast_obj, doRandom = FALSE, outFileName = 'blast_res')
```

---

blast\_gene

*Integration site annotation by gene data*

---

**Description**

Data used in example code of drawingKaryo and makeDocument

**Usage**

data(blast\_gene)

**Format**

List object

**Examples**

data(blast\_gene)

---

blast\_obj

*Retroviral vector integration site object*

---

**Description**

Data used in example code of integration site annotation functions

**Usage**

data(blast\_obj)

**Format**

GRange object

**Examples**

data(blast\_obj)

---

 cpg\_exam\_db

*Data file for annoByCpG vignette*


---

**Description**

Data used in example code of annoByCpG

**Usage**

```
data(cpg_exam_db)
```

**Format**

Data table object

**Examples**

```
data(cpg_exam_db)
```

---

drawingKaryo

*Draw the karyogram plot.*


---

**Description**

Draw a karyogram plot and show integration site.

**Usage**

```
drawingKaryo(hits, feature, organism = 'GRCh37',
             includeUndecided = FALSE, outPath = getwd(),
             outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

**Arguments**

hits	a GR object. This object made from makeInputObj function.
feature	a GR object. This object made from annotation function.
organism	a character vector. This function serves 2 versions of organisms such as GRCh37, GRCh38 (Human). Default is 'GRCh37'.
includeUndecided	TRUE or FALSE. If user want to use undecided hits in analysis, enter TRUE. Default is FALSE.
outPath	a string vector. Type path to save a plot.
outFileName	a character vector. This value used when saving the idegoram image file.



**Value**

Return the ideogram plot and object.

**Examples**

```
data(blast_obj)
data(blast_gene)
drawingKaryo(hits = blast_obj, feature = blast_gene$Gene_data, outFileNames = 'blast_res')
```

---

gene_exam_db	<i>Data file for annoByGene vignette</i>
--------------	--

---

**Description**

Data used in example code of annoByGene

**Usage**

```
data(gene_exam_db)
```

**Format**

Data table object

**Examples**

```
data(gene_exam_db)
```

---

makeData	<i>Make data files for RIPAT.</i>
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---

**Description**

Download datafiles for running RIPAT.

**Usage**

```
makeData(organism = 'GRCh37', dataType = 'gene')
```

**Arguments**

organism	a single character. Two versions of organism such as GRCh37, GRCh38 (Human). Default is 'GRCh37'.
dataType	a single character. Data type what user needs (gene, cpg, repeat and variant). Default is 'gene'.

**Value**

Database files are saved in the extdata directory of RIPAT.

**Examples**

```
makeData(organism = 'GRCh37')
```

---

makeDocument	<i>Make the result object and document.</i>
--------------	---

---

**Description**

Rearrange the result from annotation functions.

**Usage**

```
makeDocument(res, dataType, excelOut = TRUE,
             includeUndecided = FALSE, outPath = getwd(),
             outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

**Arguments**

res	a GR object. This object is output of annoByGene, annoByCpG, annoByRepeat, annoByVar function.
dataType	a character vector. User enter the annotation type of input such as gene, cpg, repeat and variant.
excelOut	TRUE or FALSE. If user want to make excel file, enter TRUE. Default is TRUE.
includeUndecided	TRUE or FALSE. If user want to use undecided hits in analysis, enter TRUE. Default is FALSE.
outPath	an string vector. Plots are saved in this path. Default value is R home directory.
outFileName	a character vector. Attached ID to the result file name.

**Value**

Make output table and excel files about vector integration sites and proportion test result.

**Examples**

```
data(blast_gene)
makeDocument(res = blast_gene, dataType = 'gene', outFileName = 'blast_gene_res')
```

---

makeInputObj	<i>Make the retroviral vector integration site object.</i>
--------------	--

---

## Description

Make an input object for annotation functions.

## Usage

```
makeInputObj(inFile, mapTool = 'blast',  
             vectorPos = 'front', outPath = getwd(),  
             outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

## Arguments

inFile	a string vector. The path of a local alignment result file. File do not include any header and comment.
mapTool	a character vector. Function serves two types of file such as outputs from BLAST and BLAT. Default is 'blast'. If you want to use BLAT result, use 'blat'.
vectorPos	a character vector. Sets the position of vector on sequences. Default value is 'front'. If the vector is located at the behind of sequence, you can change it to 'behind'.
outPath	a string vector. Directory path of tab-delimited hit files generated by this function.
outFileName	a character vector. Attached character to the result file name.

## Value

Return two types of outputs. Text file and R object. Available hit data from input is written in text file and generated as a list of GenomicRange(GR) format object.

## Examples

```
blast_obj = makeInputObj(inFile = paste0(.libPaths()[1], '/RIPAT/scripts/A5_15856M_BLASTn.txt'))
```

---

makeInputObj2                    *Make the retroviral vector integration site object.*

---

### Description

Make an input object for annotation functions.

### Usage

```
makeInputObj2(inDir, id, mapTool = 'blast',  
              vectorPos = 'front', outPath = getwd(),  
              outFileName = paste0('RIPAT', round(unclass(Sys.time()))))
```

### Arguments

inDir	a string vector. Location of a directory that has a local alignment result files. All alignment result files do not include any header and comment.
id	a character vector. the specific words that can appoint alignment file names exclusively.
mapTool	a character vector. Function serves two types of file such as outputs from BLAST and BLAT. Default is 'blast'. If you want to use BLAT result, use 'blat'.
vectorPos	a character vector. Sets the position of vector on sequences. Default value is 'front'. If the vector is located at the behind of sequence, you can change it to 'behind'.
outPath	a string vector. Directory path of tab-delimited hit files generated by this function.
outFileName	a character vector. Attached character to the result file name.

### Value

Return two types of outputs. Text file and R object. Available hit data from input is written in text file and generated as a list of GenomicRange(GR) format object.

### Examples

```
blast_obj = makeInputObj2(inDir = system.file("scripts", package = "RIPAT"), id = 'BLASTn')
```

---

micro\_exam\_db

*Data file for annoByRepeat vignette*

---

**Description**

Data used in example code of annoByRepeat

**Usage**

```
data(micro_exam_db)
```

**Format**

Data table object

**Examples**

```
data(micro_exam_db)
```

---

repeat\_exam\_db

*Data file for annoByRepeat vignette*

---

**Description**

Data used in example code of annoByRepeat

**Usage**

```
data(repeat_exam_db)
```

**Format**

Data table object

**Examples**

```
data(repeat_exam_db)
```

---

`tss_exam_db`*Data file for annoByGene vignette*

---

**Description**

Data used in example code of annoByGene

**Usage**

```
data(tss_exam_db)
```

**Format**

Data table object

**Examples**

```
data(tss_exam_db)
```

---

`var_exam_db`*Data file for annoByVar vignette*

---

**Description**

Data used in example code of annoByVar

**Usage**

```
data(var_exam_db)
```

**Format**

Data table object

**Examples**

```
data(var_exam_db)
```

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