

# Package ‘pipeFrame’

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**Type** Package

**Title** Pipeline framework for bioinformatics in R

**Version** 1.29.0

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**Description** pipeFrame is an R package for building a componentized bioinformatics pipeline. Each step in this pipeline is wrapped in the framework, so the connection among steps is created seamlessly and automatically. Users could focus more on fine-tuning arguments rather than spending a lot of time on transforming file format, passing task outputs to task inputs or installing the dependencies. Componentized step elements can be customized into other new pipelines flexibly as well. This pipeline can be split into several important functional steps, so it is much easier for users to understand the complex arguments from each step rather than parameter combination from the whole pipeline. At the same time, componentized pipeline can restart at the breakpoint and avoid rerunning the whole pipeline, which may save a lot of time for users on pipeline tuning or such issues as power off or process other interrupts.

**License** GPL-3

**Encoding** UTF-8

**LazyData** FALSE

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|               |   |
|---------------|---|
| getObjsInPipe | <i>Obtain all of objects in the specific pipeline</i> |
|---------------|---|

---

### Description

Obtain all of objects in the specific pipeline

### Usage

```
getObjsInPipe(pipeName = "pipe")
```

### Arguments

pipeName            Character scalar or vector. Pipeline name(s) of objects to be selected.

### Value

List scalar. A list containing all objects that belongs to the pipe name.

### Examples

```
getObjsInPipe("pipe")
```

---

graphMng

*Step graph management*


---

### Description

The step relations are managed and restricted to directed acyclic graph. The direction of data flow is from upstream to downstream. So when users create a new step object, restricting its relation with existing steps is necessary.

### Usage

```
addEdges(edges, argOrder)

getPrevSteps(stepType, argOrder)

getAttachedStep(stepType)

regAttachedStep(newStepType, stepType)

getNextSteps(stepType, argOrder)

printMap(stepType = NULL, display = TRUE, ...)
```

### Arguments

|             |  |
|-------------|--|
| edges       | Character vector. Contain the names of start and end points for all edges. It needs to follow the format like c("startpt1", "endpt1", "startpt2", "endpt2", "startpt3", "endpt3"). |
| argOrder    | Numeric scalar. The argument order of the input Step object.   |
| stepType    | Character scalar. Step class name of each step.  |
| newStepType | Logical scalar. give a new step step type name to the original step type with different default parameter value  |
| display     | Logical scalar. Wether show the picture on device or not.  |
| ...         | Additional arguments, currently used.  |

### Value

|                 |  |
|-----------------|--|
| addEdges        | No value will be returned.             |
| getPrevSteps    | Names of previous steps                |
| getAttachedStep | get the step that is generated from    |
| regAttachedStep | Add different step type for exist step |
| getNextSteps    | Names of next steps                    |
| printMap        | Print the flow map for the pipeline.   |

**Examples**

```
addEdges(edges = c("RandomRegionOnGenome",
                  "OverlappedRandomRegion"),argOrder = 1)
printMap()

getPrevSteps("OverlappedRandomRegion",1)
```

---

|             |  |
|-------------|--|
| ignoreCheck | <i>ignore checking input and output file (for developer)</i> |
|-------------|--|

---

**Description**

ignore checking input and output file (for developer)

**Usage**

```
ignoreCheck(ignore = TRUE)
```

**Arguments**

|        |   |
|--------|---|
| ignore | Logical scalar. Ignore checking input and output file MD5 value when skipping the step. |
|--------|---|

**Value**

|             |                           |
|-------------|---------------------------|
| ignoreCheck | No value will be returned |
|-------------|---------------------------|

**Examples**

```
ignoreCheck(FALSE)
```

---

|               |   |
|---------------|---|
| initPipeFrame | <i>initialize the pipeFrame package</i> |
|---------------|---|

---

**Description**

This function should be called first in R terminal for general users. And it should be used in .onLoad() function for package developers. In this function, several parameters need to be defined and configured, including genome, job name, reference directory, temporary directory, check and install function, threads number, reference list, etc.

**Usage**

```

initPipeFrame(
  defaultJobName,
  availableGenome = c("hg19", "hg38", "mm9", "mm10", "danRer10", "galGal5", "galGal4",
    "rheMac3", "rheMac8", "panTro4", "rn5", "rn6", "sacCer2", "sacCer3", "susScr3",
    "testgenome"),
  defaultCheckAndInstallFunc = NULL,
  defaultThreads = 2,
  defaultTmpDir = getwd(),
  defaultRefDir = file.path(getwd(), "refdir"),
  defaultReference = list(test = list(file = "fileName", rc = "obj"))
)

```

**Arguments**

`defaultJobName` Character scalar. The default job name for the package. When users use pipeFrame package, defaultJobName is "pipeFrame-pipeline".

`availableGenome` Character scalar or vector. Configure the available valid genome such as "hg19", "mm10", etc.

`defaultCheckAndInstallFunc` Function scalar. The function needs to call [runWithFinishCheck](#)

`defaultThreads` Numeric scalar. The maximum thread limit for each step. Default:2

`defaultTmpDir` Character scalar. The directory of intermediate results for all steps. Default: Current working directory.

`defaultRefDir` Character scalar. The directory of reference data. Default: `file.path(getwd(), "refdir")`

`defaultReference` List scalar. List of reference files.

**Value**

No value will be returned.

**Examples**

```

initPipeFrame(availableGenome = c("hg19", "hg38", "mm9", "mm10"),
  defaultJobName = paste0("pkgname", "-pipeline")
)

```

---

loadConfig

*load configure from file*


---

**Description**

load configure from file

**Usage**

```
loadConfig(configFile)

saveConfig(configFile)

configRegName()
```

**Arguments**

configFile      Character scalar. The directory to configuration file.

**Value**

loadConfig      No value will be returned  
 saveConfig      save the configuration into a RDS file  
 configRegName   character vector, registered configuration name

**Examples**

```
configRegName()
saveConfig("test.rds")
loadConfig("test.rds")
```

---

|          |                                       |
|----------|---------------------------------------|
| loadStep | <i>load step object from rds file</i> |
|----------|---------------------------------------|

---

**Description**

load PipeFrame Step (or its inherit class) object from rds file

**Usage**

```
loadStep(rdsfile, regClass = TRUE)
```

**Arguments**

rdsfile            Character scalar. The rds file directory for Step (or its inherit class) Object  
 regClass          Logical scalar. Register the Class of object to inherit from Step Class. Default: TRUE. Note: make sure corresponding packages depending on pipeFrame is loaded

**Value**

Step (or its inherit class) object

**Examples**

```
objrds <- system.file(package = "pipeFrame", "extdata", "pipeFrame.obj.rds")
obj <- loadStep(objrds)
```

---

runWithFinishCheck      *Install dependent data or software with finishing check*

---

## Description

Install dependent data or software with finishing check

## Usage

```
runWithFinishCheck(func, refName, refFilePath = NULL, genome = NULL)

checkAndInstallBSgenome(refFilePath, genome = getGenome())

checkAndInstallOrgDb(refFilePath, genome = getGenome())

checkAndInstallTxDb(refFilePath, genome = getGenome())

checkAndInstallGenomeFa(refFilePath)
```

## Arguments

|             |   |
|-------------|---|
| func        | Function scalar. The function with refFilePath argument (reference file directory). The returned value will be set as the reference object. |
| refName     | Character scalar. Reference name for <a href="#">getRef</a> , <a href="#">getRefFiles</a> and <a href="#">getRefRc</a> .                    |
| refFilePath | Character scalar. The reference file relative directory under the "refdir/genome/"  |
| genome      | Character scalar. The genome like "hg19". Default: <code>getGenome()</code>   |

## Value

|                         |  |
|-------------------------|--|
| runWithFinishCheck      | No value will be returned  |
| checkAndInstallBSgenome | check if there is the BSgenome package installed for curent genome and install it if not. No value will be returned. |
| checkAndInstallOrgDb    | check if there is the OrgDb package installed for curent genome and install it if not. No value will be returned.    |
| checkAndInstallTxDb     | check if there is the TxDb package installed for curent genome and install it if not. Nothing will be returned.      |
| checkAndInstallGenomeFa | check if genome FASTA file exist and install if not. No value will be returned                                       |

## Examples

```
checkAndInstall <- function(){
  runWithFinishCheck(func = checkAndInstallBSgenome,refName = "bsgenome")
  runWithFinishCheck(func = checkAndInstallGenomeFa,refName = "fasta",
    refFilePath = paste0(getGenome(),".fa"))
}
initPipeFrame(availableGenome = c("hg19", "hg38","mm9","mm10","testgenome"),
```

```

        defaultJobName = paste0("pkgname", "-pipeline")
    )
    setGenome("hg19")

```

---

|           |                                       |
|-----------|---------------------------------------|
| setGenome | <i>Configure genome for all steps</i> |
|-----------|---------------------------------------|

---

### Description

Configure the reference genome assembly for all steps.

### Usage

```

getValidGenome()

setGenome(genome)

getGenome()

```

### Arguments

genome            Character scalar. Valid genome to be configured.

### Value

getValidGenome    Character scalar. All valid genome assemblies for this package.

setGenome         All packages and dependencies are configured and installed. No value will be returned.

getGenome         Character scalar. Display the configured genome.

### Examples

```

getValidGenome()
setGenome("hg19")
getGenome()

```

---

|            |  |
|------------|--|
| setJobName | <i>Configure the job name for following steps.</i> |
|------------|--|

---

### Description

Configure the job name for following steps.

**Usage**

```
setJobName(jobName)
```

```
getJobName()
```

```
getJobDir()
```

**Arguments**

|         |   |
|---------|---|
| jobName | Character scalar. Job name for following steps. |
|---------|---|

**Value**

|            |                           |
|------------|---------------------------|
| setJobName | No value will be returned |
|------------|---------------------------|

|            |                                     |
|------------|-------------------------------------|
| getJobName | Set a job name for following steps. |
|------------|-------------------------------------|

|           |                       |
|-----------|-----------------------|
| getJobDir | get the job directory |
|-----------|-----------------------|

**Examples**

```
setJobName("testJobName")
getJobName()
getJobDir()
```

---

```
setPipeName
```

*Configure the pipe name for following steps.*

---

**Description**

Configure the pipe name for following steps.

**Usage**

```
setPipeName(pipeName)
```

```
getPipeName(all = FALSE)
```

**Arguments**

|          |  |
|----------|--|
| pipeName | Character scalar. Pipeline name for following steps. |
|----------|--|

|     |   |
|-----|---|
| all | Logical scalar. If TRUE, return all exist pipeName. Default FALSE, return current default pipeName. |
|-----|---|

**Value**

|             |                           |
|-------------|---------------------------|
| setPipeName | No value will be returned |
|-------------|---------------------------|

|             |  |
|-------------|--|
| getPipeName | Set a pipeline name for following steps. |
|-------------|--|

**Examples**

```
setPipeName("pipe")
getPipeName()
```

---

|           |                                    |
|-----------|------------------------------------|
| setRefDir | <i>Set the reference directory</i> |
|-----------|------------------------------------|

---

**Description**

Set the reference directory

**Usage**

```
setRefDir(refdir, createDir = TRUE)
```

```
getRefDir()
```

```
getRef(refName)
```

```
getRefFiles(refName)
```

```
getRefRc(refName)
```

**Arguments**

|           |   |
|-----------|---|
| refdir    | Character scalar. The directory to store the reference data.                        |
| createDir | Logical scalar. Create the directory if the directory does not exist. Default: TRUE |
| refName   | Character scalar. The name of reference data.                                       |

**Value**

|             |  |
|-------------|--|
| setRefDir   | No value will be returned  |
| getRefDir   | Character scalar. Display the directory of reference data.   |
| getRef      | List scalar. A list object which contains "files" (reference file paths) and "rc" (reference R object) |
| getRefFiles | Character scalar or vector. Display the reference file directory.                                      |
| getRefRc    | Uncertain scalar or vector. Display any reference R object.  |

**Examples**

```
setRefDir("./refdir")  
getRefDir()  
getRef("test")  
  
getRefFiles("test")  
getRefRc("test")
```

---

|            |  |
|------------|--|
| setThreads | <i>Configure the maximum number of threads</i> |
|------------|--|

---

**Description**

Configure the maximum number of threads for all steps

**Usage**

```
setThreads(threads = detectCores())
```

```
getThreads()
```

**Arguments**

|         |   |
|---------|---|
| threads | Numeric scalar. The maximum number of threads that can be allocated to each step. |
|---------|---|

**Value**

|            |                           |
|------------|---------------------------|
| setThreads | No value will be returned |
|------------|---------------------------|

|            |   |
|------------|---|
| getThreads | Numeric scalar. Display the maximum number of threads that can be allocated to each step. |
|------------|---|

**Examples**

```
setThreads()
getThreads()
```

---

|           |  |
|-----------|--|
| setTmpDir | <i>Configure the directory for intermediate results of all steps</i> |
|-----------|--|

---

**Description**

Configure the directory for intermediate results of all steps

**Usage**

```
setTmpDir(tmpDir = getwd())
```

```
getTmpDir()
```

**Arguments**

|        |   |
|--------|---|
| tmpDir | Character scalar. The directory to store intermediate results of all steps. Default: Current directory. |
|--------|---|

**Value**

|           |                           |
|-----------|---------------------------|
| setTmpDir | No value will be returned |
|-----------|---------------------------|

|           |  |
|-----------|--|
| getTmpDir | Character scalar. Display the directory for intermediate results of all steps. |
|-----------|--|

**Examples**

```
setTmpDir()
getTmpDir()
```

---

Step-class

*Methods for Step objects*


---

**Description**

Users can call Step object operation methods below to obtain information in objects.

**Usage**

```
## S4 method for signature 'Step'
init(.Object, prevSteps = list(), ...)

## S4 method for signature 'Step'
stepName(.Object, ...)

## S4 method for signature 'Step'
stepType(.Object, attachedTypes = TRUE, ...)

## S4 method for signature 'Step'
pipeName(.Object, ...)

## S4 method for signature 'Step'
input(.Object)

## S4 replacement method for signature 'Step'
input(.Object) <- value

## S4 method for signature 'Step'
output(.Object)

## S4 replacement method for signature 'Step'
output(.Object) <- value

## S4 method for signature 'Step'
param(.Object)

## S4 replacement method for signature 'Step'
param(.Object) <- value

## S4 method for signature 'Step'
property(.Object, ..., pipeName = NULL)

## S4 replacement method for signature 'Step'
property(.Object, pipeName = NULL) <- value

## S4 method for signature 'Step'
report(.Object)
```

```
## S4 replacement method for signature 'Step'
report(.Object) <- value

## S4 method for signature 'Step'
argv(.Object)

## S4 method for signature 'Step'
x$name

## S4 replacement method for signature 'Step'
x$name <- value

## S4 method for signature 'Step'
getParam(.Object, item, type = c("input", "output", "other"), ...)

## S4 method for signature 'Step'
getParamItems(.Object, type = c("input", "output", "other"), ...)

## S4 method for signature 'Step'
isReady(.Object, ...)

## S4 method for signature 'Step'
clearStepCache(.Object, ...)

## S4 method for signature 'Step'
getAutoPath(.Object, originPath, regexSuffixName, suffix, ...)

## S4 method for signature 'Step'
checkRequireParam(.Object, ...)

## S4 method for signature 'Step'
checkAllPath(.Object, ...)

## S4 method for signature 'Step'
getParamMD5Path(.Object, ...)

## S4 method for signature 'Step'
getStepWorkDir(.Object, filename = NULL, ...)

## S4 method for signature 'Step'
stepID(.Object, ...)

## S4 method for signature 'Step'
writeLog(
  .Object,
  msg,
  ...,
  isWarning = FALSE,
  appendLog = TRUE,
  showMsg = TRUE
)
```

```
processing(.Object, ...)
```

```
genReport(.Object, ...)
```

### Arguments

|                 |  |
|-----------------|--|
| .Object         | Step object scalar. Step object is returned by functions in each step.   |
| prevSteps       | List list of Step objects  |
| ...             | Additional arguments, currently unused.  |
| attachedTypes   | Logical scalar. Show the new type name or show the original type name Default: TRUE  |
| value           | any type scalar. The value to be set for corresponding item in a list.   |
| pipeName        | Character scalar. The pipeline name that this step belongs to. Default: NULL. It will be replace by the only pipeline name.                      |
| x               | Step object scalar. Step object is returned by functions in each step.   |
| name            | Character scalar. Name can be one of inputList, outputList, paramList, allList, propList or the item names of inputList, outputList or paramList |
| item            | Character scalar. The items in parameter list (input, output and other) or report list.  |
| type            | Character scalar. Valid types of parameters including "input", "output" and "other"  |
| originPath      | Character scalar. The file name for output file is based on this original path name.   |
| regexSuffixName | Character scalar. The suffix for replacement.  |
| suffix          | Character scalar. The new suffix for the file.   |
| filename        | Character scalar. The name of file under step working directory  |
| msg             | Character scalar. The message to write into log file.  |
| isWarning       | Logical scalar. Set this message as warning message. Default: FALSE  |
| appendLog       | Logical scalar. Append to the log file. Default: TRUE  |
| showMsg         | Logical scalar. Show the message on screen. Default: TRUE  |

### Details

Step is a S4 class for generating Step S4 objects. All Step objects generated by child classes inherit from Step. To generate new Step objects, a function wrapper with fixed arguments needs to be implemented. Users use this function to generate new Step functions rather than Step S4 class to generate objects.

### Value

the function and result of functions:

|          |  |
|----------|--|
| init     | (For package developer only) A Step child class object with initialized input, output and other parameters |
| stepName | get Step object Character name   |
| stepType | get Step object Character type name (class name)   |

|                   |   |
|-------------------|---|
| pipeName          | get Step object pipe name   |
| input             | get input list  |
| input<-           | set input list  |
| output            | get output list   |
| output<-          | set output list   |
| param             | get other parameters list   |
| param<-           | set other parameters list   |
| property          | get property list   |
| property<-        | set property list   |
| report            | get report list   |
| report<-          | set report list   |
| argv              | get arguments list  |
| \$                | get inputList, outputList, paramList, allList, propList or any item value in inputList, outputList or paramList |
| \$<-              | set inputList, outputList, paramList, allList, propList or any item value in inputList, outputList or paramList |
| getParam          | Get parameter value set by process function. See getParamItems to obtain valid items for query.                 |
| getParamItems     | Get parameter name list   |
| isReady           | Is the process ready for downstream process   |
| clearStepCache    | Clear cache of Step object  |
| getAutoPath       | (For package developer) Developer can use this method to generate new file name based on exist input file name  |
| checkRequireParam | (For package developer) Check required inputs or parameters are filled.   |
| checkRequireParam | (For package developer) Check required inputs are filled.   |
| getParamMD5Path   | The Step object storage directory   |
| getStepWorkDir    | Get the step work directory of this object  |
| stepID            | Get the step ID   |
| writeLog          | (For package developer) write log.  |
| processing        | (For package developer) Run pipeline step   |
| genReport         | (For package developer) Generate report list  |

**Author(s)**

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**See Also**[setGenome setThreads](#)

**Examples**

```

library(BSgenome)
library(rtracklayer)
library(magrittr)

# generate new Step : RandomRegionOnGenome
setClass(Class = "RandomRegionOnGenome",
         contains = "Step"
)

setMethod(
  f = "init",
  signature = "RandomRegionOnGenome",
  definition = function(.Object,prevSteps = list(),...){
    # All arguments in function randomRegionOnGenome
    # will be passed from "..."
    # so get the arguments from "..." first.
    allparam <- list(...)
    sampleNumb <- allparam[["sampleNumb"]]
    regionLen <- allparam[["regionLen"]]
    genome <- allparam[["genome"]]
    outputBed <- allparam[["outputBed"]]
    # no previous steps for this step so ignore the "prevSteps"
    # begin to set input parameters
    # no input for this step
    # begin to set output parameters
    if(is.null(outputBed)){
      output(.Object)$outputBed <-
        getStepWorkDir(.Object,"random.bed")
    }else{
      output(.Object)$outputBed <- outputBed
    }
    # begin to set other parameters
    param(.Object)$regionLen <- regionLen
    param(.Object)$sampleNumb <- sampleNumb
    if(is.null(genome)){
      param(.Object)$bsgenome <- getBSgenome(getGenome())
    }else{
      param(.Object)$bsgenome <- getBSgenome(genome)
    }
    # don't forget to return .Object
    .Object
  }
)

setMethod(
  f = "processing",
  signature = "RandomRegionOnGenome",
  definition = function(.Object,...){
    # All arguments are set in .Object
    # so we can get them from .Object
    allparam <- list(...)
    sampleNumb <- getParam(.Object,"sampleNumb")
    regionLen <- getParam(.Object,"regionLen")
    bsgenome <- getParam(.Object,"bsgenome")
  }
)

```

```

outputBed <- getParam(.Object,"outputBed")
# begin the calculation
chrlens <- seqlengths(bsgenome)
selchr <- grep("_|M",names(chrlens),invert=TRUE)
chrlens <- chrlens[selchr]
startchrlens <- chrlens - regionLen
spchrs <- sample(x = names(startchrlens),
size = sampleNumb, replace = TRUE,
prob = startchrlens / sum(startchrlens))
gr <- GRanges()
for(chr in names(startchrlens)){
  startpt <- sample(x = 1:startchrlens[chr],
size = sum(spchrs == chr),replace = FALSE)
  gr <- c(gr,GRanges(seqnames = chr,
ranges = IRanges(start = startpt, width = 1000)))
}
result <- sort(gr,ignore.strand=TRUE)
rtracklayer::export.bed(object = result, con = outputBed)
# don't forget to return .Object
.Object
}
)

setMethod(
  f = "genReport",
  signature = "RandomRegionOnGenome",
  definition = function(.Object, ...){
    .Object
  }
)

# This function is exported in NAMESPACE for user to use
randomRegionOnGenome <- function(sampleNumb, regionLen = 1000,
genome = NULL, outputBed = NULL, ...){
  allpara <- c(list(Class = "RandomRegionOnGenome", prevSteps = list()),
as.list(environment()),list(...))
  step <- do.call(new,allpara)
  invisible(step)
}

# generate another new Step : OverlappedRandomRegion
setClass(Class = "OverlappedRandomRegion",
contains = "Step"
)

setMethod(
  f = "init",
  signature = "OverlappedRandomRegion",
  definition = function(.Object,prevSteps = list(),...){

```

```

# All arguments in function overlappedRandomRegion and
# runOverlappedRandomRegion will be passed from "..."
# so get the arguments from "..." first.
allparam <- list(...)
inputBed <- allparam[["inputBed"]]
randomBed <- allparam[["randomBed"]]
outputBed <- allparam[["outputBed"]]
# inputBed can obtain from previous step object when running
# runOverlappedRandomRegion
if(length(prevSteps)>0){
  prevStep <- prevSteps[[1]]
  input(.Object)$randomBed <- getParam(prevStep,"outputBed")
}
# begin to set input parameters
if(!is.null(inputBed)){
  input(.Object)$inputBed <- inputBed
}
if(!is.null(randomBed)){
  input(.Object)$randomBed <- randomBed
}
# begin to set output parameters
# the output is recommended to set under the step work directory
if(!is.null(outputBed)){
  output(.Object)$outputBed <- outputBed
}else{
  output(.Object)$outputBed <-
    getAutoPath(.Object, getParam(.Object, "inputBed"),
                "bed", suffix = "bed")
  # the path can also be generate in this way
  # ib <- getParam(.Object,"inputBed")
  # output(.Object)$outputBed <-
  #   file.path(getStepWorkDir(.Object),
  #             paste0(substring(ib,1,nchar(ib)-3), "bed"))
}
# begin to set other parameters
# no other parameters
# don't forget to return .Object

.Object
}
)
setMethod(
  f = "processing",
  signature = "OverlappedRandomRegion",
  definition = function(.Object,...){
    # All arguments are set in .Object
    # so we can get them from .Object
    allparam <- list(...)
    inputBed <- getParam(.Object,"inputBed")
    randomBed <- getParam(.Object,"randomBed")
    outputBed <- getParam(.Object,"outputBed")

    # begin the calculation
    gr1 <- import.bed(con = inputBed)
    gr2 <- import.bed(con = randomBed)
    gr <- second(findOverlapPairs(gr1,gr2))
  }
)

```

```

        export.bed(gr, con = outputBed)
        # don't forget to return .Object
        .Object
    }
)

setMethod(
  f = "genReport",
  signature = "OverlappedRandomRegion",
  definition = function(.Object, ...){
    .Object
  }
)

# This function is exported in NAMESPACE for user to use
overlappedRandomRegion <- function(inputBed, randomBed,
                                   outputBed = NULL, ...){
  allpara <- c(list(Class = "OverlappedRandomRegion",
                    prevSteps = list()), as.list(environment()), list(...))
  step <- do.call(new, allpara)
  invisible(step)
}

setGeneric("runOverlappedRandomRegion",
           function(prevStep,
                    inputBed,
                    randomBed = NULL,
                    outputBed = NULL,
                    ...) standardGeneric("runOverlappedRandomRegion"))

setMethod(
  f = "runOverlappedRandomRegion",
  signature = "Step",
  definition = function(prevStep,
                        inputBed,
                        randomBed = NULL,
                        outputBed = NULL,
                        ...){
    allpara <- c(list(Class = "OverlappedRandomRegion",
                      prevSteps = list(prevStep)), as.list(environment()), list(...))
    step <- do.call(new, allpara)
    invisible(step)
  }
)

# add to graph
addEdges(edges = c("RandomRegionOnGenome", "OverlappedRandomRegion"),
         argOrder = 1)
# begin to test pipeline
setGenome("hg19")
# generate test BED file

```

```
test_bed <- file.path(tempdir(),"test.bed")
library(rtracklayer)
export.bed(GRanges("chr7:1-127473000"),test_bed)

rd <- randomRegionOnGenome(10000)
overlap <- runOverlappedRandomRegion(rd, inputBed = test_bed)

randombed <- getParam(rd,"outputBed")

randombed

overlap1 <-
  overlappedRandomRegion(inputBed = test_bed, randomBed = randombed)

clearStepCache(overlap1)
overlap1 <-
  overlappedRandomRegion(inputBed = test_bed, randomBed = randombed)
clearStepCache(rd)
clearStepCache(overlap1)
rd <- randomRegionOnGenome(10000) %>%
runOverlappedRandomRegion(inputBed = test_bed)

stepName(rd)
stepID(rd)

isReady(rd)
```

---

Utils

*Functions for directory operations*

---

## **Description**

Functions for directory operations

## **Usage**

```
getBasenamePrefix(filepath, words, ...)
```

```
getPathPrefix(filepath, words, ...)
```

```
checkFileExist(filePath, ...)
```

```
checkPathExist(filePath, ...)
```

```
checkFileCreatable(filePath, ...)
```

```
addFileSuffix(filePath, suffix, ...)
```

## **Arguments**

filepath            character scalar or vector.

|          |  |
|----------|--|
| words    | character scalar. Remove substring of the path characters starting to match the word |
| ...      | Additional arguments, currently unused   |
| filePath | Character scalar.  |
| suffix   | Character scalar. File suffix.   |

**Value**

|                    |   |
|--------------------|---|
| getBasenamePrefix  | Get the filepath basename with removed suffix                       |
| getPathPrefix      | Get the filepath with removed suffix                                |
| checkFileExist     | (For package developer) Check file is exist.                        |
| checkPathExist     | (For package developer) Check directory is exist.                   |
| checkFileCreatable | (For package developer) Check file creatable.                       |
| addFileSuffix      | (For package developer) Check if file suffix existed and add suffix |

**Examples**

```

getBasenamePrefix("aaa/bbb.ccc.ddd", "cCc")

getBasenamePrefix("aaa/bbb.ccc.ddd", "ddd")

getPathPrefix("aaa/bbb.ccc.ddd", "dDd")

getPathPrefix("aaa/bbb.ccc.ddd", "ccc")

file.create("test.bed")

checkFileExist("test.bed")

tryCatch({checkFileExist("test.bed1")}, error = function(e) e)

dir.create("testdir")

checkPathExist(file.path(getwd(), "testdir"))

tryCatch({checkPathExist(file.path(dirname(getwd()),
"notexistfolder", "testdir")}, error = function(e) e)

checkFileCreatable("aaa.bed")

tryCatch({checkFileCreatable("testdir1/aaa.bed")}, error = function(e) e)

```

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