Package 'pipeFrame'

November 12, 2026

Type Package

Title Pipeline framework for bioinformatics in R

Version 1.28.0

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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

Depends R (>= 4.0.0),

Imports BSgenome, digest, visNetwork, magrittr, methods, Biostrings,
Seqinfo, parallel, stats, utils, rmarkdown

Suggests BiocManager, knitr, rtracklayer, testthat,
BSgenome.Hsapiens.UCSC.hg19

RoxygenNote 7.0.2

VignetteBuilder knitr

biocViews Software, Infrastructure, WorkflowStep

URL https://github.com/wzthu/pipeFrame

BugReports https://github.com/wzthu/pipeFrame/issues

git_url https://git.bioconductor.org/packages/pipeFrame

git_branch RELEASE_3_23

git_last_commit 7f13528

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`getObjsInPipe` *Obtain all of objects in the specific pipeline*

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 *ignore checking input and output file (for developer)*

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` *initialize the pipeFrame package*

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`	charactor vector, registered configuration name

Examples

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

loadStep *load step object from rds file*

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 getRef, getRefFiles and getRefRc.
refFilePath	Character scalar. The reference file relative directory under the "refdir/genome/"
genome	Character scalar. The genome like "hg19". Default: getGenome()

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 *Configure genome for all steps*

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 *Configure the job name for following steps.*

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 *Set the reference directory*

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	Logica 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 *Configure the maximum number of threads*

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 *Configure the directory for intermediate results of all steps*

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,
  ...,
  isWarnning = 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 scaler. The name of file under step working directiory
msg	Character scalar. The message to write into log file.
isWarnning	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

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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 ingnore 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
        # runOerlappedRandomRegion 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
        # runOerlappedRandomRegion
        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)$randomBed <- randomBed
        }
        # begin to set output parameters
        # the output is recemended to set under the step work directory
        if(!is.null(outputBed)){
            output(.Object)$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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