

# Package ‘canceR’

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**Type** Package

**Title** A Graphical User Interface for accessing and modeling the Cancer Genomics Data of MSKCC

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**Description** The package is user friendly interface based on the cgdsr and other modeling packages to explore, compare, and analyse all available Cancer Data (Clinical data, Gene Mutation, Gene Methylation, Gene Expression, Protein Phosphorylation, Copy Number Alteration) hosted by the Computational Biology Center at Memorial-Sloan-Kettering Cancer Center (MSKCC).

**License** GPL-2

**LazyLoad** yes

**Depends** R (>= 4.1), tcltk

**Imports** GSEABase, tkrplot, geNetClassifier, RUnit, Formula, rpart, survival, Biobase, phenoTest, circlize, plyr, graphics, stats, utils, grDevices, R.oo, R.methodsS3, httr

**Suggests** testthat (>= 3.1), knitr, rmarkdown, BiocStyle

**SystemRequirements** Tktable, BWidget

**VignetteBuilder** knitr

**BugReports** <https://github.com/kmezhoud/canceR/issues>

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about

*about canceR*

---

**Description**

about canceR

**Usage**

about()

**Value**

dialog box with text

**Examples**

```
## Not run:  
about()  
  
## End(Not run)
```

---

canceR

*main function*

---

**Description**

main function

**Usage**

canceR()

**Value**

open the starting windows with cancer studies

**Examples**

```
myGlobalEnv <- new.env(parent = emptyenv())  
## Not run:  
canceR()  
  
## End(Not run)
```

---

canceR_Issue	<i>canceR Report Issue</i>
--------------	----------------------------

---

**Description**

canceR Report Issue

**Usage**

```
canceR_Issue()
```

**Value**

link to github issues

**Examples**

```
## Not run:  
canceR_Issue()  
  
## End(Not run)
```

---

canceR_Vignette	<i>open pdf vignette</i>
-----------------	--------------------------

---

**Description**

open pdf vignette

**Usage**

```
canceR_Vignette()
```

**Value**

open pdf vignette

**Examples**

```
## Not run:  
canceR_Vignette()  
  
## End(Not run)
```

---

cbind.na	<i>bind non equal column</i>
----------	------------------------------

---

**Description**

bind non equal column

**Usage**

```
cbind.na(..., deparse.level = 1)
```

**Arguments**

... (generalized) vectors or matrices.

deparse.level integer controlling the construction of labels in the case of non-matrix-like arguments (for the default method): deparse.level = 0 constructs no labels; the default, deparse.level = 1 or 2 constructs labels from the argument names.

**Value**

a data frame with merged columns

**Examples**

```
## Not run:
col1 <- c("a", "b", "c", "d")
col2 <- c("A", "B", "C")
col3 <- cbind.na(col1, col2)

## End(Not run)
```

---

dialogGeneClassifier	<i>Dialogue Box for gene classifier setting: sample size and postprob threshold</i>
----------------------	---

---

**Description**

Dialogue Box for gene classifier setting: sample size and postprob threshold

**Usage**

```
dialogGeneClassifier(Lchecked_Cases, entryWidth = 10, returnValOnCancel = "ID_CANCEL")
```

### Arguments

Lchecked\_Cases integer with a number of checked cases  
entryWidth integer default 10  
returnValOnCancel  
"ID\_CANCEL"

### Value

a dataframe with genes classes

### Examples

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/gbm_tcgaPlotTwoGenProf.rds", sep=""))  
## Not run:  
getGenesClassifier()  
dialogGeneClassifier(1,10,returnValOnCancel = "ID_CANCEL")  
  
## End(Not run)
```

---

dialoggetGeneListMSigDB

*Multi-select choice of gene sets from loaded MSigDB*

---

### Description

Multi-select choice of gene sets from loaded MSigDB

### Usage

```
dialoggetGeneListMSigDB(MSigDB)
```

### Arguments

MSigDB object with MSigDB. A list of genesets

### Value

a dataframe with genes classes

**Examples**

```
z <- 7
## Not run:
##MSigDB <- readLines(paste(.libPaths(), "/cancer/extdata/MSigDB/c5.bp.v4.0.symbols.gmt", sep=""))
dialoggetGeneListMSigDB(MSigDB)

## End(Not run)
```

---

dialogMetOption	<i>Dialog Box to set methylation options</i>
-----------------	--

---

**Description**

Dialog Box to set methylation options

**Usage**

```
dialogMetOption(ProfData, k)
```

**Arguments**

ProfData	adataframe with methylation data
k	threshold of silencing gene 0:1

**Value**

a dialog box to set methylation option (threshold of silencing gene)

**Examples**

```
readRDS(paste(path.package("cancerR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
getMetDataMultipleGenes()
#dialogMetOption(ProfData, 0.7)

## End(Not run)
```



---

dialogMut	<i>Dialog box to set returned Mutation information</i>
-----------	--

---

**Description**

Dialog box to set returned Mutation information

**Usage**

```
dialogMut(title, question, entryInit, entryWidth = 40, returnValOnCancel = "ID_CANCEL")
```

**Arguments**

title	title of the table
question	question
entryInit	entryInit
entryWidth	40
returnValOnCancel	"ID_CANCEL"

**Value**

a check box with mutations variables

**Examples**

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
dialogMut("title", "question", "entryInit", entryWidth = 40, returnValOnCancel = "ID_CANCEL")

## End(Not run)
```

---

dialogOptionCircos	<i>Checkbox to select dimensions</i>
--------------------	--------------------------------------

---

**Description**

Checkbox to select dimensions

**Usage**

```
dialogOptionCircos()
```

**Value**

a checkbox with all dimensions

**Examples**

```
readRDS(paste(path.package("canceR"),"/extdata/rdata/Circos.rds", sep=""))
## Not run:
dialogOptionCircos()
#getCircos(dimension ="All")

## End(Not run)
```

---

dialogOptionGSEAlm      *Dialogbox to select variables from Clinical data*

---

**Description**

Dialogbox to select variables from Clinical data

**Usage**

```
dialogOptionGSEAlm(k,ClinicalData)
```

**Arguments**

k	integer 1
ClinicalData	dataframe with clinical variables

**Value**

permutaion value, p-value, coVariables

**Examples**

```
#data(ClinicalData)
## Not run:
getOptionGSEAlm()

## End(Not run)
```

---

dialogOptionPhenoTest *Checkbox to select variables from clinical data*

---

**Description**

Checkbox to select variables from clinical data

**Usage**

```
dialogOptionPhenoTest(eSet)
```

**Arguments**

eSet                    Expression Set

**Value**

vectors: variables to test Survival status, AGE, p-value

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/prad_michPhenoTest1021.rds", sep=""))
## Not run:
dialogOptionPhenoTest(myGlobalEnv$eSet)

## End(Not run)
```

---

dialogPlotOption\_SkinCor  
*Checkbox to select variables for plotting*

---

**Description**

Checkbox to select variables for plotting

**Usage**

```
dialogPlotOption_SkinCor(s)
```

**Arguments**

s                        integer number of Studies

**Value**

Dialog box with setting of correlation method

**Examples**

```
readRDS(paste(path.package("cancerR"), "/extdata/rdata/gbm_tcgaPlotTwoGenProf.rds", sep=""))
## Not run:
dialogPlotOption_SkinCor(1)

## End(Not run)
```

---

dialogSamplingGSEA	<i>Dialog Box for Sampling patients from expression profile data used for GSEA-R (Broad Institute)</i>
--------------------	--

---

**Description**

Dialog Box for Sampling patients from expression profile data used for GSEA-R (Broad Institute)

**Usage**

```
dialogSamplingGSEA( Lchecked_Cases, entryWidth = 10, returnValOnCancel = "ID_CANCEL")
```

**Arguments**

Lchecked_Cases	Number of checked Cases
entryWidth	10
returnValOnCancel	"ID_CANCEL"

**Value**

A vector with sampling size

**Examples**

```
readRDS(paste(path.package("cancerR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
Run.GSEA()
#dialogSamplingGSEA(1, entryWidth=10, returnValOnCancel = "ID_CANCEL")

## End(Not run)
```

---

`dialogSelectFiles_GSEA`

*Dialog Box to Select GCT, CLS, GMT and output Files for GSEA-R (Broad Institute)*

---

**Description**

Dialog Box to Select GCT, CLS, GMT and output Files for GSEA-R (Broad Institute)

**Usage**

```
dialogSelectFiles_GSEA()
```

**Value**

A vector with files paths

**Examples**

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
dialogSelectFiles_GSEA()

## End(Not run)
```

---

`dialogSpecificMut`

*dialog box to Specify Mutation using Regular Expression. Search specific mutation using regular expression.*

---

**Description**

dialog box to Specify Mutation using Regular Expression. Search specific mutation using regular expression.

**Usage**

```
getSpecificMut()
```

**Value**

a dataframe with specific mutation informations

### Examples

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
getSpecificMut()

## End(Not run)
```

---

dialogSummary_GSEA	<i>Dialog Box to specify phenotype (variable) used in last GSEA-R to get Summary Results. This function ask the user to specify the phenotype (variable).</i>
--------------------	---

---

### Description

Dialog Box to specify phenotype (variable) used in last GSEA-R to get Summary Results. This function ask the user to specify the phenotype (variable).

### Usage

```
dialogSummary_GSEA(Variable,returnValOnCancel ="ID_CANCEL")
```

### Arguments

Variable	phenotype
returnValOnCancel	"ID_CANCEL"

### Value

variables

### Examples

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
#Run.GSEA()
#getSummaryGSEA()

## End(Not run)
```

---

displayInTable	<i>Display matrix in tcltk table</i>
----------------	--------------------------------------

---

**Description**

Display matrix in tcltk table

**Usage**

```
displayInTable(tclarray, title="", height=-1, width=-1, nrow=-1, ncol=-1)
```

**Arguments**

tclarray	a dataframe
title	title of the table
height	-1
width	-1
nrow	-1
ncol	-1

**Value**

display a Table

**Examples**

```
#data(ClinicalData)
## Not run:
getInTable(Table= ClinicalData, title= "Clinical Data")

## End(Not run)
```

---

getCases	<i>Get cases for selected Studies. The Cases are the description of the samples from patients. The samples can be subdivided by the type of assays as, sequencing, CNA, Mutation, Methylation.</i>
----------	--

---

**Description**

Get cases for selected Studies. The Cases are the description of the samples from patients. The samples can be subdivided by the type of assays as, sequencing, CNA, Mutation, Methylation.

**Usage**

```
getCases()
```

**Value**

a dataframe with cases

**Examples**

```
## Not run:
# Create CGDS object
cgds<-CGDS("http://www.cbioportal.org/")
# Get list of cancer studies at server
Studies <- getCancerStudies(cgds)[,2]
# Get available case lists (collection of samples) for a given cancer study
mycancerstudy <- getCancerStudies(cgds)[2,1]
mycaselist <- getCaseLists(cgds,mycancerstudy)[1,1]

##getCases()

## End(Not run)
```

---

getCasesGenProfs      *get Cases and Genetic Profiles of selected Studies.*

---

**Description**

get Cases and Genetic Profiles of selected Studies.

**Usage**

```
getCasesGenProfs()
```

**Value**

This function is run by the "Get Cases and Genetic Profiles for selected Studies in starting window. This function needs to select at least one study and display Cases and genetic profiles in the main window.

**Examples**

```
##Load Session
readRDS(paste(path.package("canceR"),"/extdata/rdata/brca_tcga73genes.rds", sep=""))
## load Cases and Genetic Profiles
## Not run:
getCasesGenProfs()

## End(Not run)
```



---

getCircos	<i>get Circos Layout for selected studies and selected dimensions</i>
-----------	---

---

**Description**

get Circos Layout for selected studies and selected dimensions

**Usage**

```
getCircos(dimension)
```

**Arguments**

dimension      string (All,mRNA, CNA, Met,RPPA, miRNA, Mut)

**Value**

a plot with Circos style

**Examples**

```
readRDS(paste(path.package("canceR"),"/extdata/rdata/Circos.rds", sep=""))
## Not run:
getCircos(dimension ="All")

## End(Not run)
```

---

getClinicalDataMatrix	<i>get matrix with clinical from file</i>
-----------------------	---

---

**Description**

get matrix with clinical from file

**Usage**

```
getClinicalDataMatrix()
```

**Value**

dataframe of clinicaldata

**Examples**

```
readRDS(paste(path.package("canceR"),"/extdata/rdata/brca_tcga73genes.rds", sep=""))
## Not run:
getClinicalDataMatrix()

## End(Not run)
```

---

```
getClinicData_MultipleCases
```

*get Clinical Data for Multiple Cases. User needs to select at least one case to run this function. Get clinical data for more one or multiple cases.*

---

### Description

get Clinical Data for Multiple Cases. User needs to select at least one case to run this function. Get clinical data for more one or multiple cases.

### Usage

```
getClinicData_MultipleCases(getSummaryGSEAEExists)
```

### Arguments

```
getSummaryGSEAEExists
```

if equal to 0, the clinical data is displayed in table. if the argument is equal to 1, the clinical data is used to summarise GSEA analysis results.

### Value

dataframe with clinical data

### Examples

```
##Load Session
readRDS(paste(path.package("canceR"), "/extdata/rdata/brca_tcga73genes.rds", sep=""))
## Select Case
myGlobalEnv <- new.env(parent = emptyenv())
myGlobalEnv$curselectCases <- 2
## get Clinical data
## Not run:
getClinicData_MultipleCases(getSummaryGSEAEExists = 0)

## End(Not run)
```

---

```
getCor_ExpCNAMet
```

*Get gene correlation for multiple dimensions.*

---

### Description

Get gene correlation for multiple dimensions.

**Usage**

```
getCor_ExpCNAMet(ListMatrix, dimension)
```

**Arguments**

```
ListMatrix    is a List of numeric matrices  
dimension     Exp,CNA, Met , miRNA , RPPA
```

**Value**

correlation matrix

**Examples**

```
readRDS(paste(path.package("cancerR"),"/extdata/rdata/Circos.rds", sep=""))  
## Not run:  
getListProfData()  
getCor_ExpCNAMet(myGlobalEnv$ListProfData$Expression, dimension="mRNA")  
head(myGlobalEnv$Cor_Exp)  
  
## End(Not run)
```

---

geteSet

*Built Expression Set (eSet) from profile data.*

---

**Description**

Built Expression Set (eSet) from profile data.

**Usage**

```
geteSet()
```

**Value**

ExpressionSet

**Examples**

```
f <- 9  
## Not run:  
readRDS(paste(path.package("cancerR"),"/extdata/rdata/prad_michPhenoTest1021.rds", sep=""))  
geteSet()  
  
## End(Not run)
```

---

getGCTCLSExample	<i>get GCT and CLS example files.</i>
------------------	---------------------------------------

---

**Description**

get GCT and CLS example files.

**Usage**

```
getGCTCLSExample()
```

**Value**

GCT and CLS files

**Examples**

```
## Load workspace
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
getGCTCLSExample()

## End(Not run)
```

---

getGCT_CLSfiles	<i>get Profile (GCT file) and Phenotype (CLS file) Data from Disease.</i>
-----------------	---

---

**Description**

get Profile (GCT file) and Phenotype (CLS file) Data from Disease.

**Usage**

```
getGCT_CLSfiles()
```

**Value**

GCT and CLS files paths

**Examples**

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
getGCT_CLSfiles()

## End(Not run)
```

---

getGeneExpMatrix	<i>get matrix with gene expression from file</i>
------------------	--

---

**Description**

get matrix with gene expression from file

**Usage**

```
getGeneExpMatrix()
```

**Value**

dataframe of gene expression

---

getGeneList	<i>User needs to specify which gene is interesting to get genomic cancer data. The gene must be with Symbol and one gene by line.</i>
-------------	---

---

**Description**

User needs to specify which gene is interesting to get genomic cancer data. The gene must be with Symbol and one gene by line.

**Usage**

```
getGeneList()
```

**Value**

Gene list path of file

**Examples**

```
myGlobalEnv <- new.env(parent = emptyenv())  
## Not run:  
getGeneList()  
  
## End(Not run)
```

---

```
getGeneListExample    get Gene List from examples. User can select one from available gene list
```

---

**Description**

get Gene List from examples. User can select one from available gene list

**Usage**

```
getGeneListExample()
```

**Value**

Gene list path of file

**Examples**

```
myGlobalEnv <- new.env(parent = emptyenv())  
## Not run:  
getGeneListExample()  
  
## End(Not run)
```

---

```
getGeneListFromMSigDB get gene list from MSigDB
```

---

**Description**

get gene list from MSigDB

**Usage**

```
getGeneListFromMSigDB()
```

**Value**

a vector with gene list

**Examples**

```
readRDS(paste(path.package("cancerR"), "/extdata/rdata/brca_tcgaGSEA1m1021.rds", sep=""))  
## Not run:  
getGeneListFromMSigDB()  
  
## End(Not run)
```

---

getGenesClassifier     *get Genes Classifier*

---

**Description**

get Genes Classifier

**Usage**

```
getGenesClassifier()
```

**Value**

a data frma with genes classes

**Examples**

```
x <- 0
## Not run:
readRDS(paste(path.package("canceR"), "/extdata/rdata/brca_tcga73genes.rds", sep=""))
getGenesClassifier()

## End(Not run)
```

---

getGenesTree\_MultipleCases  
*Get successively trees of genes list for multiple cases*

---

**Description**

Get successively trees of genes list for multiple cases

**Usage**

```
getGenesTree_MultipleCases(entryWidth = 10)
```

**Arguments**

entryWidth     10

**Value**

plot tree

**Examples**

```
q <- readRDS(paste(path.package("cancerR"), "/extdata/rdata/brca_tcga73genes.rds", sep=""))
## Not run:
readRDS(paste(.libPaths(), "/cancerR/data/brca_tcga73genes.rds", sep=""))
getGenesTree_MultipleCases(entryWidth = 10)

## End(Not run)
```

---

getGenesTree\_SingleCase  
*classify genes in tree for two phenotypes in the same case(disease).*

---

**Description**

classify genes in tree for two phenotypes in the same case(disease).

**Usage**

```
getGenesTree_SingleCase()
```

**Value**

tree plot

**Examples**

```
readRDS(paste(path.package("cancerR"), "/extdata/rdata/prad_michPhenoTest1021.rds", sep=""))
## Not run:
getGenesTree_SingleCase()

## End(Not run)
```

---

getGenProfs                      *Get Genetic Profile from selected Studies*

---

**Description**

Get Genetic Profile from selected Studies

**Usage**

```
getGenProfs()
```

**Value**

dataframe with genetic profil



**Examples**

```
## Not run:
cgds<-CGDS("http://www.cbioportal.org/")
# Get list of cancer studies at server
Studies <- getCancerStudies(cgds)[,2]
# Get available case lists (collection of samples) for a given cancer study
mycancerstudy <- getCancerStudies(cgds)[2,1]
mycaselist <- getCaseLists(cgds,mycancerstudy)[1,1]
# Get available genetic profiles
mygeneticprofile <- getGeneticProfiles(cgds,mycancerstudy)[4,1]

getGenProfs()

## End(Not run)
```

---

getGSEAlm\_Diseases      *get GSEA linear modeling by studies (diseases)*

---

**Description**

get GSEA linear modeling by studies (diseases)

**Usage**

```
getGSEAlm_Diseases()
```

**Value**

a dataframe with annotation (GO, BP)

**Examples**

```
readRDS(paste(path.package("cancerR"),"/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
getGSEAlm_Diseases

## End(Not run)
```

---

getGSEAlm\_Variables     *get GSEA linear modeling by variables (phenotype)*

---

**Description**

get GSEA linear modeling by variables (phenotype)

**Usage**

```
getGSEAlm_Variables()
```

**Value**

a dataframe with annotation (GO, BP)

**Examples**

```
x <- 3
## Not run:
readRDS(paste(path.package("cancerR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
getGSEAlm_Variables()

## End(Not run)
```

---

getInTable     *get dataframe in TK/TCL table*

---

**Description**

get dataframe in TK/TCL table

**Usage**

```
getInTable(table, title)
```

**Arguments**

table	Dataframe
title	string a title of the table

**Value**

display a Table

**Examples**

```
#data(ClinicalData)
## Not run:
getInTable(Table= ClinicalData, title= "Clinical Data")

## End(Not run)
```

---

getListProfData	<i>get a list of Profile Data of every available dimensions. This function load matrices of every dimension (Exp, CNA, Met, RPPA,miRNA,Mut) and save them in a list for every disease.</i>
-----------------	--

---

**Description**

get a list of Profile Data of every available dimensions. This function load matrices of every dimension (Exp, CNA, Met, RPPA,miRNA,Mut) and save them in a list for every disease.

**Usage**

```
getListProfData()
```

**Value**

a list of data frame with Profiles Data

**Examples**

```
readRDS(paste(path.package("canceR"),"/extdata/rdata/brca_tcga73genes.rds", sep=""))
## Not run:
getListProfData()
head(myGlobalEnv$ProfData$Expression)

## End(Not run)
```

---

getMegaProfData	<i>Get profile data for more than 500 genes list.</i>
-----------------	---

---

**Description**

Get profile data for more than 500 genes list.

**Usage**

```
getMegaProfData(MegaGeneList,k)
```

**Arguments**

MegaGeneList    Genelist >500  
k                integer number of studies

**Value**

dataframewith profile data

**Examples**

```
myGlobalEnv <- new.env(parent = emptyenv())  
readRDS(paste(path.package("cancerR"), "/extdata/rdata/brca_tcgaGSEA1m1021.rds", sep=""))  
## Not run:  
getMegaProfData(myGlobalEnv$MegaGeneList, 1)  
  
## End(Not run)
```

---

getMetDataMultipleGenes

*get Methylation data for multiple genes*

---

**Description**

get Methylation data for multiple genes

**Usage**

```
getMetDataMultipleGenes()
```

**Value**

a dataframe with mean and median of methylation rate (threshold of silencing gene)

**Examples**

```
readRDS(paste(path.package("cancerR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
## Not run:  
getMetDataMultipleGenes()  
  
## End(Not run)
```

---

getMSigDB                      *Reduce MSigDB size for only gene list*

---

**Description**

Reduce MSigDB size for only gene list

**Usage**

```
getMSigDB(eSet, k)
```

**Arguments**

eSet	Expression Set
k	integer Number of studies

**Value**

MSigDB for user gene List

**Examples**

```
d <- 7
## Not run:
setWorkspace()
getMSigDB(eSet = myGlobalEnv$eSetClassifier,k = 1)

## End(Not run)
```

---

getMSigDBExample              *get example of .gmt file from MSigDB (Broad Institute)*

---

**Description**

get example of .gmt file from MSigDB (Broad Institute)

**Usage**

```
getMSigDBExample()
```

**Value**

path of GMT file

**Examples**

```
readRDS(paste(path.package("cancerR"),"/extdata/rdata/brca_tcga73genes.rds", sep=""))
## Not run:
getMSigDBExample()

## End(Not run)
```

---

getMSigDBfile

*Dialog Box to Select MSigDB Files from drive*

---

**Description**

Dialog Box to Select MSigDB Files from drive

**Usage**

```
getMSigDBfile()
```

**Value**

A path of MSigDB file

**Examples**

```
f <- 5+2
## Not run:
readRDS(paste(path.package("cancerR"),"/extdata/rdata/prad_michPhenoTest1021.rds", sep=""))
geteSet()
getMSigDBfile()

## End(Not run)
```

---

getMutData

*get Mutation data for multiple genes*

---

**Description**

get Mutation data for multiple genes

**Usage**

```
getMutData()
```

**Value**

a dataframe with mutation informations

**Examples**

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
getMutData()

## End(Not run)
```

---

getPhenoTest	<i>Associate phenotype to Studies (cancers)</i>
--------------	---

---

**Description**

Associate phenotype to Studies (cancers)

**Usage**

```
getPhenoTest()
```

**Value**

a dataframe with disease/ variables association

**Examples**

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/prad_michPhenoTest1021.rds", sep=""))
## Not run:
getPhenoTest(myGlobalEnv$set)

## End(Not run)
```

---

getProfilesDataMultipleGenes	<i>get Profiles Data of multiple genes</i>
------------------------------	--

---

**Description**

get Profiles Data of multiple genes

**Usage**

```
getProfilesDataMultipleGenes(getSummaryGSEAEExists)
```

**Arguments**

```
getSummaryGSEAEExists
```

if equal to 0, the clinical data is displayed in table. if the argument is equal to 1, the clinical data is used to summarise GSEA analysis results.

**Value**

a file with a dataframe of profile data

**Examples**

```
readRDS(paste(path.package("canceR"),"/extdata/rdata/prad_michPhenoTest1021.rds", sep=""))
## Not run:
getProfilesDataMultipleGenes(getSummaryGSEAEExists = 0)

## End(Not run)
```

---

getProfilesDataSingleGene

*get Profiles Data for a Single Gene.*

---

**Description**

get Profiles Data for a Single Gene.

**Usage**

```
getProfilesDataSingleGene()
```

**Value**

dataframe with profiles data for a single gene

**Examples**

```
readRDS(paste(path.package("canceR"),"/extdata/rdata/brca_tcga73genes.rds", sep=""))
## Select Case from Breast Cancer
myGlobalEnv <- new.env(parent = emptyenv())
myGlobalEnv$curselectCases <- 9
##Select Genetic Profile from Breast Cancer
myGlobalEnv$curselectGenProfs <- 4
## get Specific Mutation data for 73 Genes list
## Not run:
getProfilesDataSingleGene()

## End(Not run)
```



---

getSpecificMut	<i>get specific Mutation data for multiple genes</i>
----------------	--

---

**Description**

get specific Mutation data for multiple genes

**Usage**

```
getSpecificMut()
```

**Value**

a dataframe with specific mutation informations

**Examples**

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
getSpecificMut()

## End(Not run)
```

---

getSummaryGSEA	<i>get Summary results from GSEA-R (Broad Institute)</i>
----------------	--

---

**Description**

get Summary results from GSEA-R (Broad Institute)

**Usage**

```
getSummaryGSEA()
```

**Value**

Dataframe with summary results

**Examples**

```
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
Run.GSEA()
getSummaryGSEA()

## End(Not run)
```

getSurvival                      *Survival plot*

---

**Description**

Survival plot

**Usage**

```
getSurvival(Coxph)
```

**Arguments**

Coxph                      if Coxph = 0 : plot Kaplan-Meier curves else Coxph= 1 : plot Cox Proportional Hazard Model

**Value**

Survival plot

**Examples**

```
surv <- 11
## Not run:
readRDS(paste(path.package("canceR"), "/extdata/rdata/gbm_tcgaPlotTwoGenProf.rds", sep=""))
getSurvival(Coxph = 1)

## End(Not run)
```

---

getTextWin                      *get text in tcltk windows*

---

**Description**

get text in tcltk windows

**Usage**

```
getTextWin(text)
```

**Arguments**

text                      string

**Value**

tcltk windows with text

**Examples**

```
text <- "mytext"
## Not run:
getTextWin(text)

## End(Not run)
```

---

GSEA

*GSEA-R (Broad Institute)*

---

**Description**

See [http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/R-GSEA\\_Readme](http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/R-GSEA_Readme)

**Value**

GSEA

**Author(s)**

Subramanian, Tamayo, et al. (2005, PNAS 102, 15545-15550) and Mootha, Lindgren, et al. (2003, Nat Genet 34, 267-273)

**Examples**

```
## Not run:
library(canceR)
## Load workspace
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
##Run.GSEA()

## End(Not run)
```

---

GSEA.Analyze.Sets

*GSEA.Analyze.Sets*

---

**Description**

[http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/R-GSEA\\_Readme](http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/R-GSEA_Readme)

**Usage**

```
GSEA.Analyze.Sets(directory, topgs="", non.interactive.run= FALSE, height=12, width=17)
```

**Arguments**

```
directory      directory= fname.Output
topgs          topgs = 20
non.interactive.run
               non.interactive.run= FALSE
height        height=16
width         width=16
```

**Value**

GSEA.Analyze.Sets

**Author(s)**

Subramanian, Tamayo, et al. (2005, PNAS 102, 15545-15550) and Mootha, Lindgren, et al. (2003, Nat Genet 34, 267-273)

**References**

[http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/Main\\_Page](http://www.broadinstitute.org/cancer/software/gsea/wiki/index.php/Main_Page).

**Examples**

```
## Not run:
## Load workspace
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
##Run.GSEA()

## End(Not run)
```

---

GSEA.ConsPlot

*GSEA.ConsPlot*

---

**Description**

GSEA.ConsPlot

**Usage**

```
GSEA.ConsPlot(V, col.names, main = " ", sub = " ", xlab = " ", ylab = " ")
```

**Arguments**

V	V="Itable"
col.names	col.names = colnames
main	main= " "
sub	sub = " "
xlab	xlab= " "
ylab	ylab = " "

**Value**

GSEA.ConsPlot

**Examples**

```
## Not run:
library(canceR)
## Load workspace
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
##Run.GSEA()

## End(Not run)
```

---

GSEA.EnrichmentScore *GSEA.EnrichmentScore*

---

**Description**

GSEA.EnrichmentScore

**Usage**

```
GSEA.EnrichmentScore(gene.list, gene.set, weighted.score.type = 1, correl.vector = NULL)
```

**Arguments**

gene.list  
gene.set  
weighted.score.type  
  
correl.vector

**Value**

GSEA.EnrichmentScore

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.EnrichmentScore2 *GSEA.EnrichmentScore2*

---

**Description**

GSEA.EnrichmentScore2

**Usage**

```
GSEA.EnrichmentScore2(gene.list, gene.set, weighted.score.type = 1, correl.vector = NULL)
```

**Arguments**

gene.list  
gene.set  
weighted.score.type  
  
correl.vector

**Value**

GSEA.EnrichmentScore2

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.Gct2Frame	<i>GSEA.Gct2Frame</i>
----------------	-----------------------

---

**Description**

GSEA.Gct2Frame

**Usage**

GSEA.Gct2Frame(filename = "NULL")

**Arguments**

filename

**Value**

GSEA.GCT2Frame

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.Gct2Frame2	<i>GSEA.Gct2Frame2</i>
-----------------	------------------------

---

**Description**

GSEA.Gct2Frame2

**Usage**

GSEA.Gct2Frame2(filename = "NULL")

**Arguments**

filename

**Value**

GSEA.GCT2Frame2

**Examples**

```
## Not run:
library(canceR)
## Load workspace
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
##Run.GSEA()

## End(Not run)
```

---

GSEA.GeneRanking

*GSEA.GeneRanking*

---

**Description**

GSEA.GeneRanking

**Arguments**

A  
class.labels  
gene.labels  
nperm  
permutation.type  
  
sigma.correction  
  
fraction  
replace  
reverse.sign

**Value**

GSEA.GeneRanking

**Examples**

```
## Not run:
library(canceR)
## Load workspace
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
##Run.GSEA()

## End(Not run)
```



---

GSEA.HeatMapPlot	<i>GSEA.HeatMapPlot</i>
------------------	-------------------------

---

**Description**

GSEA.HeatMapPlot

**Value**

GSEA.HeatMapPlot

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.HeatMapPlot2	<i>GSEA.HeatMapPlot2</i>
-------------------	--------------------------

---

**Description**

GSEA.HeatMapPlot2

**Value**

GSEA.HeatMapPlot2

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

GSEA.NormalizeCols     *GSEA.NormalizeCols*

---

**Description**

GSEA.NormalizeCols

**Usage**

GSEA.NormalizeCols(V)

**Arguments**

V

**Value**

GSEA.NormalizeCols

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
## Load workspace
##Run.GSEA()

## End(Not run)
```

---

GSEA.NormalizeRows     *GSEA.NormalizeRows*

---

**Description**

GSEA.NormalizeRows

**Usage**

GSEA.NormalizeRows(V)

**Arguments**

V

**Value**

GSEA.NormalizeRows

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.ReadClsFile	<i>GSEA.ReadClsFile</i>
------------------	-------------------------

---

**Description**

GSEA.ReadClsFile

**Usage**

```
GSEA.ReadClsFile(file = "NULL")
```

**Arguments**

file

**Value**

GSEA.ReadClsFile

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
## Not run:  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.Res2Frame	<i>GSEA.Res2Frame</i>
----------------	-----------------------

---

**Description**

GSEA.Res2Frame

**Usage**

```
GSEA.Res2Frame(filename = "NULL")
```

**Arguments**

filename

**Value**

GSEA.NormalizeCols

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
## Not run:  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.Threshold

*GSEA.Threshold*

---

**Description**

GSEA.Threshold

**Usage**

GSEA.Threshold(V, thres, ceil)

**Arguments**

V

thres

ceil

**Value**

GSEA.Threshold

**Examples**

```
## Load workspace  
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
## Not run:  
  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.VarFilter	<i>GSEA.VarFilter</i>
----------------	-----------------------

---

**Description**

GSEA.VarFilter

**Usage**

```
GSEA.VarFilter(V, fold, delta, gene.names = "NULL")
```

**Arguments**

```
V  
fold  
delta  
gene.names
```

**Value**

GSEA.VarFilter

**Examples**

```
## Load workspace  
readRDS(paste(path.package("cancer"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
## Not run:  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.write.gct	<i>GSEA.write.gct</i>
----------------	-----------------------

---

**Description**

GSEA.write.gct

**Usage**

```
GSEA.write.gct(gct, filename)
```

**Arguments**

```
gct  
filename
```

**Value**

GSEA.Write.gct

**Examples**

```
## Load workspace
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:

##Run.GSEA()

## End(Not run)
```

---

Match\_GeneList\_MSigDB *Search MSigDb that overlap gene list*

---

**Description**

Search MSigDb that overlap gene list

**Usage**

Match\_GeneList\_MSigDB

**Value**

GeneList

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/prad_michPhenoTest1021.rds", sep=""))
## Not run:
Match_GeneList_MSigDB()

## End(Not run)
```

---

modalDialog *Dialog box to specify Gene Symbol.*

---

**Description**

Dialog box to specify Gene Symbol.

**Usage**

```
modalDialog(title, question, entryInit, entryWidth = 40, returnValOnCancel = "ID_CANCEL")
```

**Arguments**

title	string
question	string
entryInit	entryInit
entryWidth	40
returnValOnCancel	"ID_CANCEL"

**Value**

dialog box

**Examples**

```
readRDS(paste(path.package("canceR"),"/extdata/rdata/brca_tcga73genes.rds", sep=""))
## Select Case from Breast Cancer
myGlobalEnv <- new.env(parent = emptyenv())
myGlobalEnv$curselectCases <- 9
##Select Genetic Profile from Breast Cancer
myGlobalEnv$curselectGenProfs <- 4
## get Specific Mutation data for 73 Genes list
## Not run:
getProfilesDataSingleGene()

## End(Not run)
```

---

myGlobalEnv

*myGlobalEnv*

---

**Description**

Global environment to store canceR variables.

**Format**

The format is: <environment: 0xb3eb240>

**Examples**

```
myGlobalEnv <- new.env(parent = emptyenv())
```

---

OLD.GSEA.EnrichmentScore  
*OLD.GSEA.EnrichmentScore*

---

**Description**

OLD.GSEA.EnrichmentScore

**Arguments**

gene.list  
 gene.set

**Value**

OLD.GSEA.EnchmentScore

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
##Run.GSEA()

## End(Not run)
```

---

plotModel                    *model plotting with tcltk*

---

**Description**

model plotting with tcltk

**Usage**

```
plotModel(plotCommand, title= "TITLE", hscale=1, vscale=1 )
```

**Arguments**

plotCommand	plotcommand
title	title of plot
hscale	horizintal scale
vscale	vertical scale

**Value**

plot



**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/gbm_tcgaPlotTwoGenProf.rds", sep=""))
## Not run:
plot_1Gene_2GenProfs()

## End(Not run)
```

---

plot\_1Gene\_2GenProfs *Plotting two genetic profiles for one Gene*

---

**Description**

Plotting two genetic profiles for one Gene

**Usage**

```
plot_1Gene_2GenProfs()
```

**Value**

plot

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/gbm_tcgaPlotTwoGenProf.rds", sep=""))
## Not run:
plot_1Gene_2GenProfs()

## End(Not run)
```

---

plot\_2Genes\_1GenProf *plot correlation of two genes expressions.*

---

**Description**

plot correlation of two genes expressions.

**Usage**

```
plot_2Genes_1GenProf()
```

**Value**

plot

## Examples

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))
## Not run:
plot_2Genes_1GenProf()

## End(Not run)
```

---

rbind.na	<i>bind non equal row</i>
----------	---------------------------

---

## Description

bind non equal row

## Usage

```
rbind.na(..., deparse.level = 1)
```

## Arguments

... (generalized) vectors or matrices.

deparse.level integer controlling the construction of labels in the case of non-matrix-like arguments (for the default method): deparse.level = 0 constructs no labels; the default, deparse.level = 1 or 2 constructs labels from the argument names.

## Value

a data frame with merged rows

## Examples

```
## Not run:
row1 <- c("a", "b", "c", "d")
row2 <- c("A", "B", "C")
row3 <- rbind.na(row1, row2)

## End(Not run)
```

---

Run.GSEA	<i>The main function to run GSEA-R from Broad Institute</i>
----------	---

---

**Description**

The main function to run GSEA-R from Broad Institute

**Usage**

```
Run.GSEA()
```

**Value**

A vector with sampling size

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/ucec_tcga_pubGSEA1021.rds", sep=""))  
## Not run:  
Run.GSEA()  
  
## End(Not run)
```

---

setWorkspace	<i>Setting work Directory and output folders.At starting window, user needs to set work directory for output data. The function is foud in File menu.</i>
--------------	---

---

**Description**

Setting work Directory and output folders.At starting window, user needs to set work directory for output data. The function is foud in File menu.

**Usage**

```
setWorkspace()
```

**Value**

paths of output files

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/brca_tcga73genes.rds", sep=""))  
## Not run:  
setWorkspace()  
  
## End(Not run)
```

---

testCheckedCaseGenProf

*Testing checked appropriate Cases for appropriate Genetic profiles.*

---

**Description**

Testing checked appropriate Cases for appropriate Genetic profiles.

**Usage**

```
testCheckedCaseGenProf()
```

**Value**

dialog box with warning message

**Examples**

```
readRDS(paste(path.package("canceR"), "/extdata/rdata/brca_tcga73genes.rds", sep=""))  
## Not run:  
testCheckedCaseGenProf()  
  
## End(Not run)
```

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