

# 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 (>= 3.0.0), tcltk, tcltk2, cgdsr

**Imports** GSEABase,GSEAlm,tkrplot, geNetClassifier,RUnit, Formula, rpart, Biobase, phenoTest

**biocViews** GUI, GeneExpression, Software

**NeedsCompilation** no

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---

about	<i>get brief information and help.</i>
-------	--

---

## Description

This function is run by the botton "Help" in strating window.

## Examples

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

canceR

*Main function of canceR package.*

---

**Description**

This function get Studies from cbio portal (<http://www.cbioportal.org/>) and list them in starting window. User can select easily multiple studies to get specific data.

**Author(s)**

Karim Mezhoud Nuclear Safety Department, Nuclear Science Center of Tunisia.

**References**

canceR: A Graphical User Interface for accessing and modeling the MSKCC Cancer Genomics Data.

**Examples**

```
## Not run:  
library(canceR)  
canceR()  
  
## End(Not run)
```

---

canceRHelp

*canceRHelp*

---

**Description**

Help

**Examples**

```
## Not run:  
library(canceR)  
canceRHelp()  
  
## End(Not run)
```

---

`canceR_Vignette`*Get Vignette*

---

**Description**

This function open the canceR Vignette pdf file from Help menu.

**Usage**

```
canceR_Vignette()
```

**Author(s)**

Karim Mezhoud Nuclear Safety Department, Nuclear Science Center. Tunisia

**References**

canceR: A Graphical User Interface for accessing and modeling the MSKCC Cancer Genomics Data.

**Examples**

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

---

`cbind.na`*cbind.na*

---

**Description**

This function allows user to bind non equal columns

**Examples**

```
col1 <- c("a", "b", "c", "d")  
col2 <- c("A", "B", "C")  
col3 <- canceR::cbind.na(col1, col2)
```

---

ClinicalData

*ClinicalData*

---

## Description

Exmaple of Clinical Data

## Usage

```
data("ClinicalData")
```

## Format

A data frame with 770 observations on the following 4 variables.

DFS\_MONTHS a numeric vector

DFS\_STATUS a factor with levels DiseaseFree Recurred/Progressed

OS\_MONTHS a numeric vector

OS\_STATUS a factor with levels DECEASED LIVING

## Value

Value

## Source

cbioportal

## Examples

```
## Not run  
##library(cancer)  
##getClinicalData()  
## End(Not run)
```

---

dialogGeneClassifier *dialogGeneClassifier*

---

### Description

Dialog box to get gene classifier options.

### Usage

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

### Arguments

```
Lchecked_Cases  Number of checked Cases
entryWidth      10
returnValOnCancel
                 "ID_CANCEL"
```

### Examples

```
## Not run
library(canceR)
library(Biobase)
library(geNetClassifier)
## Load workspace
load(paste(path.package("canceR"), "/data/brca_tcgaClassifier223.RData", sep=""))
##getGenesClassifier()
##dialogGeneClassifier
## End(Not run)
```

---

dialogMetOption *dialog box to specify Methylation rate threshold of silencing genes.*

---

### Description

dialog box to specify Methylation rate threshold of silencing genes.

### Arguments

```
ProfData
k: integer
```

### See Also

```
getMetDataMultipleGenes
```

**Examples**

```
## Not run
##Load Session
##load(paste(path.package("cancer"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case from Prostate Cancer
##myGlobalEnv$curselectCases <- 19
##Select Genetic Profile from Prostate Cancer
##myGlobalEnv$curselectGenProfs <- 17
## get Methylation data for 73 Genes list
##getMetDataMultipleGenes()
##dialogMetOption(myGlobalEnv$ProfData,1)
## End(Not run)
```

---

dialogMut

*dialog box to specify Animo Acid changes using regular expression*

---

**Description**

dialog box to specify Animo Acid changes using regular expression.

**Usage**

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

**Arguments**

```
title
question      question= enter gene Symbol
entryInit     entryInit= P53
entryWidth    entryWidth = 10
returnValOnCancel
              returnValOnCancel= ID_CANCEL h
```

**See Also**

getMutData

**Examples**

```
## Not run:
## library(cancer)
##Load Session
##load(paste(path.package("cancer"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case
myGlobalEnv$curselectCases <- 2
##Select Genetic Profile
myGlobalEnv$curselectGenProfs <- 9
## get Mutation data for 73 Genes list
```



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

## End(Not run)
```

---

dialogOptionGSEAlm      *Dialog Box Option for GSEAlm*

---

## Description

Specifying Options for GSEA linear modeling: Variables/Phenotypes, Permutation and p-value

## Usage

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

## Arguments

k  
ClinicalData

## See Also

```
getGSEAlm_Variables()
```

## Examples

```
## Not run:
##Load Session
##load(paste(path.package("cancerR"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case from Breast Cancer
##myGlobalEnv$curselectCases <- 9
##Select Genetic Profile from Breast Cancer
myGlobalEnv$curselectGenProfs <- 4
## get GSEAlm data for 73 Genes list
##library(GSEAlm)
##getGSEAlm_Variables()
##dialogOptionGSEAlm(k, ClinicalData)

## End(Not run)
```

dialogOptionPhenoTest *Dialog Box to specify Variables for PhenoTest function.*

---

**Description**

Specifying PhenoTest Options.

**Arguments**

eSet                    Expression Set function to built eSet from gene expression and clinical data.

**See Also**

PhenoTest package

**Examples**

```
## Not run:
library(canceR)
library(Biobase)
library(phenoTest)
## Load workspace
load(paste(path.package("canceR"),"/data/prad_michPhenoTest1021.RData", sep=""))

getPhenoTest()
## Empty Survival rvariables
## Select DSF_STATUS for categorical variable
## Select PSA Level for Numeric variable
## BH
##dialogOptionPhenoTest()

## End(Not run)
```

---

dialogPlotOption\_SkinCor  
*dialogPlotOption\_SkinCor*

---

**Description**

Specifying Skin and Correlation Options.

**See Also**

cgdsr package

**Examples**

```
## Not run:
library(canceR)
##Load workspace
load(paste(path.package("canceR"),"/data/ucec_tcga_pubGSEA1021.RData", sep=""))
plot_2Genes_1GenProf()

##dialogPlotOption_SkinCor(2)

## End(Not run)
```

---

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

---

**Description**

Samoling Cases from cbiportal for GSEA.

**Usage**

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

**Arguments**

```
Lchecked_Cases  Number of checked Cases
entryWidth      entryWidth=10
returnValOnCancel
                 returnValOnCancel="ID_CANCEL"
```

**Examples**

```
## Not run:
##library(canceR)
## Load workspace
##load(paste(path.package("canceR"),"/data/ucec_tcga_pubGSEA1021.RData", sep=""))
##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

This function select GCT, CLS, GMT and output Files for GSEA-R.

### Examples

```
## Not run
library(canceR)
## Load workspace
load(paste(path.package("canceR"),"/data/ucec_tcga_pubGSEA1021.RData", sep=""))
##dialogSelectFiles_GSEA()
## End(Not run)
```

---

```
dialogSpecificMut
```

*dialog box to Specify Mutation using Regular Expression.*

---

### Description

Search specific mutation using regular expression.

### Arguments

```
MutData
c
```

### See Also

```
getSpecificMut
```

### Examples

```
## Not run

##Load Session
load(paste(path.package("canceR"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case
myGlobalEnv$curselectCases <- 2
##Select Genetic Profile
myGlobalEnv$curselectGenProfs <- 9
## get Specific Mutation data for 73 Genes list
##getSpecificMut()
##dialogSpecificMut()
## End(Not run)
```

---

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

---

**Description**

This function ask the user to specify the phenotype (variable).

**Usage**

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

**Arguments**

```
Variable  
returnValOnCancel
```

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
##getSummaryGSEA()  
  
## End(Not run)
```

---

displayInTable	<i>Display In Table</i>
----------------	-------------------------

---

**Description**

Display matrix in tcltk table

**Usage**

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

**Arguments**

```
tclarray      tclarray=Matrix
title         title="Title"
height       height=ncol(Matrix)
width        width= nrow(Matrix)
nrow
ncol
```

**Examples**

```
## Not run
##library(cancer)
##displayInTable()
## End(Not run)
```

---

GeneExpMatrix	<i>Profile data</i>
---------------	---------------------

---

**Description**

Example of gene expression matrix

**Usage**

```
data("GeneExpMatrix")
```

**Format**

A data frame with 958 observations on the following 18 variables.

BEGAIN a numeric vector  
CD83 a numeric vector  
CD93 a numeric vector  
CEP164 a numeric vector  
FOXN2 a numeric vector  
IGFBP2 a numeric vector  
IL18 a numeric vector  
KDEL1R1 a numeric vector  
NCSTN a numeric vector  
NOTCH2 a numeric vector  
NPY a numeric vector  
NT5E a numeric vector

PARP4 a numeric vector  
SIGLEC1 a numeric vector  
SLC16A2 a numeric vector  
SLC35B1 a numeric vector  
SLC9A2 a numeric vector  
VPS16 a numeric vector

### Source

cbioportal

### Examples

```
## Not run  
##cancerRHelp()  
## End(Not run)
```

---

getCases

*Get cases for selected Studies*

---

### Description

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.

### See Also

cgdsr package

### Examples

```
## Not run:  
# Create CGDS object  
cgds<-CGDS("http://www.cbioportal.org/public-portal/")  
# 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

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

```
## Not Run
##Load Session
load(paste(path.package("cancerR"),"/data/brca_tcga73genes.RData", sep=""))
## load Cases and Genetic Profiles
##getCasesGenProfs()
## End(Not run)
```

---

getClinicalDataMatrix    *getClinicalDataMatrix*

---

### Description

Load clinical data from file.

### Usage

```
getClinicalDataMatrix()
```

### Value

Value

### Examples

```
## Not run
##getClinicalDataMatrix()
## End(Not run)
```



---

```
getClinicData_MultipleCases
```

*get Clinical Data for Multiple Cases*

---

**Description**

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.

**Examples**

```
## Not run:  
##Load Session  
load(paste(path.package("cancerR"),"/data/brca_tcga73genes.RData", sep=""))  
## Select Case  
myGlobalEnv$curselectCases <- 2  
## get Clinical data  
##getClinicData_MultipleCases(getSummaryGSEAEExists = 0)  
  
## End(Not run)
```

---

```
geteSet
```

*Build expression Set (Biobase)*

---

**Description**

Built Expression Set (eSet) from profile data.

**Usage**

```
geteSet()
```

**Examples**

```
## Not run:  
library(canceR)  
##load(paste(path.package("canceR"),"/data/brca_tcgaGSEA1m1021.RData", sep=""))  
##geteSet()  
  
## End(Not run)
```

---

getGCTCLSExample	<i>getGCTCLSExample</i>
------------------	-------------------------

---

**Description**

get GCT and CLS example files.

**Usage**

```
getGCTCLSExample()
```

**Value**

Value

**Examples**

```
## Not run:  
library(canceR)  
##getGCTCLSExample()  
  
## End(Not run)
```

---

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

---

**Description**

This function load gene expression data frame and clinical data and built GCT, CLS files and save them in /Results/GCT\_CLS folder.

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
  
##getGCT_CLSfiles()  
  
## End(Not run)
```

---

getGeneExpMatrix	<i>load matrix from file</i>
------------------	------------------------------

---

**Description**

load matrix from file

**Usage**

```
getGeneExpMatrix()
```

**Value**

Value

**Examples**

```
## Not run  
library(canceR)  
#getGeneExpMatrix()  
## End(Not run)
```

---

getGeneList	<i>get Gene List from file.</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.

**Examples**

```
## Not run  
library(canceR)  
##getGeneList()  
## End(Not run)
```

---

getGeneListExample     *get Gene List from examples*

---

### Description

User can select one from available gene list

### Examples

```
## Not run
##library(cancer)
##getGeneListExample()
## End(Not run)
```

---

getGenesClassifier     *Ranking Genes by Diseases.*

---

### Description

refers to geNetClassifier package.

### See Also

geNetClassifier package

### Examples

```
## Not run
##library(cancer)
##library(Biobase)
##library(geNetClassifier)
## Load workspace
#load(paste(path.package("cancer"),"/data/brca_tcgaClassifier223.RData", sep=""))
##getGenesClassifier()
## End(Not run)
```

---

getGenesTree\_MultipleCases  
*getGenesTree\_MultipleCases*

---

**Description**

Get successively trees of genes list for multiple cases

**Value**

Value

**Examples**

```
## Not run
##library(cancerR)
##load(paste(path.package("cancerR"),"/data/brca_tcgaClassifier223.RData", sep=""))
##getGenesTree_MultipleCases()
## End(Not run)
```

---

getGenesTree\_SingleCase  
*getGenesTree\_SingleCase*

---

**Description**

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

**Usage**

```
getGenesTree_SingleCase()
```

**Value**

Value

**Examples**

```
## Not run
##library(cancerR)
##load(paste(path.package("cancerR"),"/data/brca_tcgaClassifier223.RData", sep=""))
##getGenesTree_SingleCase()
##end(Not run)
```

---

getGenProfs

*Get Genetic Profile from selected Studies*


---

### Description

The Genetic Profiles are subdivided by the type of assays as, CNA, Mutation, Methylation, Gene expression.

### Examples

```
## Not run:
##library(cancer)
##library(cgdsr)
## Create CGDS object
##cgds<-CGDS("http://www.cbioportal.org/public-portal/")
# 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 Gene Set Enrichment Analysis linear modeling for two Diseases.*


---

### Description

Get Gene Set Enrichment Analysis linear modeling for two phenotypes (Diseases). Users needs to browse MSigDB file from ~R/x86\_64-unknown-linux-gnu-library/3.2/cancer/extdata/MSigDB/c2.cp.reactome.v4.0.symbol

### Usage

```
getGSEAlm_Diseases()
```

### Examples

```
## Not run:
##library(cancer)
##library(GSEAlm)
##Load Session
##load(paste(path.package("cancer"),"/data/brca_tcgaGSEAlm1021.RData", sep=""))
##getGSEAlm_Diseases()

## End(Not run)
```

---

getGSEAlm_Variables	<i>Get Gene Set Enrichment Analysis linear modeling for two phenotypes (variables) in the same disease.</i>
---------------------	---

---

**Description**

Get Gene Set Enrichment Analysis linear modeling for two phenotypes (variables) in the same disease. Users needs to browse MSigDB file from ~R/x86\_64-unknown-linux-gnu-library/3.2/canceR/extdata/MSigDB/c2.cp.re And check DFS\_STATUS. The results change depending the profile data and cbio portal updates.

**Usage**

```
getGSEAlm_Variables()
```

**Examples**

```
## Not run:  
##Load Session  
##load(paste(path.package("canceR"),"/data/brca_tcga73genes.RData", sep=""))  
## Select Case from Breast Cancer  
##myGlobalEnv$curselectCases <- 9  
##Select Genetic Profile from Breast Cancer  
##myGlobalEnv$curselectGenProfs <- 4  
## get GSEAlm data for 73 Genes list  
##library(GSEAlm)  
##getGSEAlm_Variables()  
  
## End(Not run)
```

---

getInTable	<i>getInTable</i>
------------	-------------------

---

**Description**

get in matrix in table

**Usage**

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

**Arguments**

table  
title

**Value**

Value

**Examples**

```
## Not run
##library(cancer)
##getInTable(matrix(2,3,4))
## end(Not run)
```

---

getMegaProfData	<i>getMegaProfData</i>
-----------------	------------------------

---

**Description**

Get profile data for more than 500 genes list.

**Usage**

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

**Arguments**

MegaGeneList

k

**Value**

Value

**Examples**

```
## Not run:
##library(cancer)
##load(paste(path.package("cancer"),"/data/brca_tcgaGSEA1m1021.RData", sep=""))
##getMegaProfData(myGloboEnv$MegaGeneList,1)

## End(Not run)
```



---

```
getMetDataMultipleGenes
```

*get Methylation Data for Multiple Genes.*

---

**Description**

Get methylation data for gene list. User needs to specify correlation rate threshold between Methylation and Silencing of genes(default rate: 0.8).

**See Also**

dialogMetOption

**Examples**

```
## Not run:
##Load Session
load(paste(path.package("cancerR"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case from Prostate Cancer
myGlobalEnv$curselectCases <- 19
##Select Genetic Profile from Prostate Cancer
myGlobalEnv$curselectGenProfs <- 17
## get Methylation data for 73 Genes list
getMetDataMultipleGenes()

## End(Not run)
```

---

```
getMSigDB
```

*getMSigDB*

---

**Description**

Reduce MSigDB size for only gene list.

**Usage**

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

**Arguments**

eSet  
k

**Value**

Value

## Examples

```
## Not run:  
library(canceR)  
##load(paste(path.package("canceR"), "/data/brca_tcgaGSEA1m1021.RData", sep=""))  
getMSigDB()  
  
## End(Not run)
```

---

getMSigDBExample	<i>getMSigDBExample</i>
------------------	-------------------------

---

## Description

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

## Usage

```
getMSigDBExample()
```

## Details

<http://www.broadinstitute.org/gsea/index.jsp>

## Value

Value

## Examples

```
## Not run:  
library(canceR)  
getMSigDBExample()  
  
## End(Not run)
```

---

getMSigDBfile	<i>getMSigDBfile</i>
---------------	----------------------

---

**Description**

get MSigDB file in .gmt format.

**Usage**

```
getMSigDBfile()
```

**Value**

Value

**Examples**

```
## Not run:  
library(canceR)  
getMSigDBfile()  
  
## End(Not run)
```

---

getMutData	<i>get Mutation Data for gene list.</i>
------------	---

---

**Description**

User needs to select gene list, all samples with sequencing data from cases and Mutations from Genetic profiles

**Examples**

```
## Not run:  
##Load Session  
load(paste(path.package("canceR"),"/data/brca_tcga73genes.RData", sep=""))  
## Select Case  
myGlobalEnv$curselectCases <- 2  
##Select Genetic Profile  
myGlobalEnv$curselectGenProfs <- 9  
## get Mutation data for 73 Genes list  
getMutData()  
  
## End(Not run)
```

---

getPhenoTest	<i>Associate Phenotypes (variables) from Clinical data to gene expression profile.</i>
--------------	--

---

### Description

see phenoTest package

### Examples

```
## Not run:
#library(cancer)
#library(Biobase)
#library(phenoTest)
## Load workspace
#load(paste(path.package("cancer"),"/data/prad_michPhenoTest1021.RData", sep=""))

#getPhenoTest()
## Empty Survival rvariables
## Select DSF_STATUS for categorical variable
## Select PSA Level for Numeric variable
## BH

## End(Not run)
```

---

getProfilesDataMultipleGenes	<i>get Profiles Data of Multiple Genes.</i>
------------------------------	---

---

### Description

This function get Profile data for Gene list and save table in workspace/Results/ProfileData

### 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.

**Examples**

```
## Not run:
##Load Session
##load(paste(path.package("cancerR"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case from Breast Cancer
##myGlobalEnv$curselectCases <- 9
##Select Genetic Profile from Breast Cancer
##myGlobalEnv$curselectGenProfs <- 4
##getProfilesDataMultipleGenes(getSummaryGSEAEExists=0)

## End(Not run)
```

---

```
getProfilesDataSingleGene
```

*get Profiles Data for a Single Gene.*

---

**Description**

Get profile data for single gene. Users must write a right Symbol gene in dialog box.

**See Also**

modalDialog

**Examples**

```
## Not run
##Load Session
##load(paste(path.package("cancerR"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case from Breast Cancer
myGlobalEnv$curselectCases <- 9
##Select Genetic Profile from Breast Cancer
myGlobalEnv$curselectGenProfs <- 4
## get Specific Mutation data for 73 Genes list
##getProfilesDataSingleGene()
## End(Not run)
```

---

```
getSpecificMut
```

*get Specific Mutation using Amino Acid changes.*

---

**Description**

This function search only mutation with specific Amino Acid changes using Regular Expression. User needs to specify Amino Acid change in dialog box.

**See Also**

dilogSpecificMut

**Examples**

```
## Not run:
##Load Session
##load(paste(path.package("cancer"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case
##myGlobalEnv$curselectCases <- 2
##Select Genetic Profile
##myGlobalEnv$curselectGenProfs <- 9
## get Specific Mutation data for 73 Genes list
##getSpecificMut()

## End(Not run)
```

---

getSummaryGSEA

*get Summary results from GSEA-R (Broad Institute)*

---

**Description**

This function select only significant modulated gene set and display them in table. user needs to specify save files from Run.GSEA function in /Results/GSEA/Disease/.

**Author(s)**

Karim Mezhoud

**References**

Karim Mezhoud cancerR: A Graphical User Interface for accessing and modeling the MSKCC Cancer Genomics Data.

**Examples**

```
## Not run
##library(cancer)
## Load workspace
##load(paste(path.package("cancer"),"/data/ucec_tcga_pubGSEA1021.RData", sep=""))
##Run.GSEA()
##getSummaryGSEA()
## End(Not run)
```

---

getTextWin

*getTextWin*

---

### **Description**

output capture and getting text in editing windows.

### **Usage**

getTextWin(text)

### **Arguments**

text

### **Details**

detail

### **Value**

Value

### **Author(s)**

Karim Mezhoud

### **References**

Karim Mezhoud (in press) *canceR*: A Graphical User Interface for accessing and modeling the MSKCC Cancer Genomics Data.

### **Examples**

```
## Not run
##library(canceR)
##getTextWin()
## end(Notrun)
```

---

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)

### 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
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", 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= F, height=12, width=17)
```

### Arguments

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

### 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:
library(canceR)
## Load workspace
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", 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 = " "

**Examples**

```
## Not run:
library(canceR)
## Load workspace
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", 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
```

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", 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
```

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.Gct2Frame

*GSEA.Gct2Frame*

---

**Description**

GSEA.Gct2Frame

**Usage**

```
GSEA.Gct2Frame(filename = "NULL")
```

**Arguments**

filename

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.Gct2Frame2

*GSEA.Gct2Frame2*

---

**Description**

GSEA.Gct2Frame2

**Usage**

```
GSEA.Gct2Frame2(filename = "NULL")
```

**Arguments**

filename

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", 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

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

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

---

**Description**

GSEA.HeatMapPlot

**Examples**

```
## Not run:
library(canceR)
## Load workspace
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))
##Run.GSEA()

## End(Not run)
```

---

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

---

**Description**

GSEA.HeatMapPlot2

**Examples**

```
## Not run:
library(canceR)
## Load workspace
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))
##Run.GSEA()

## End(Not run)
```

---

GSEA.NormalizeCols	<i>GSEA.NormalizeCols</i>
--------------------	---------------------------

---

**Description**

GSEA.NormalizeCols

**Usage**

GSEA.NormalizeCols(V)

**Arguments**

V

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.NormalizeRows      *GSEA.NormalizeRows*

---

**Description**

GSEA.NormalizeRows

**Usage**

GSEA.NormalizeRows(V)

**Arguments**

V

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

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

---

**Description**

GSEA.ReadClsFile

**Usage**

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

**Arguments**

file

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

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

---

**Description**

GSEA.Res2Frame

**Usage**

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

**Arguments**

filename

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

GSEA.Threshold      *GSEA.Threshold*

---

**Description**

GSEA.Threshold

**Usage**

```
GSEA.Threshold(V, thres, ceil)
```

**Arguments**

V  
thres  
ceil

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.VarFilter      *GSEA.VarFilter*

---

**Description**

GSEA.VarFilter

**Usage**

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

**Arguments**

V  
fold  
delta  
gene.names



**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

GSEA.write.gct

*GSEA.write.gct*

---

**Description**

GSEA.write.gct

**Usage**

GSEA.write.gct(gct, filename)

**Arguments**

gct  
filename

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

Match\_GeneList\_MSigDB *Match\_GeneList\_MSigDB*

---

**Description**

Search MSigDb that overlap gene list

**Usage**

Match\_GeneList\_MSigDB()

**Value**

Value

**Examples**

```
##not run
##library(cancer)
##Match_GeneList_MSigDB()
## End(Not run)
```

---

modalDialog

*Dialog box to specify Gene Symbol.*

---

**Description**

This function get Profile Data for one gene Symbol.

**Usage**

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

**Arguments**

title  
question  
entryInit  
entryWidth  
returnValOnCancel

**See Also**

getProfilesDataSingleGene

**Examples**

```
## Not run:
##Load Session
##load(paste(path.package("cancer"),"/data/brca_tcga73genes.RData", sep=""))
## Select Case from Breast Cancer
##myGlobalEnv$curselectCases <- 9
##Select Genetic Profile from Breast Cancer
##myGlobalEnv$curselectGenProfs <- 4
## get Specific Mutation data for 73 Genes list
##getProfilesDataSingleGene()

## End(Not run)
```

---

`myGlobalEnv``myGlobalEnv`

---

**Description**

Global environment to store `canceR` variables.

**Format**

The format is: `<environment: 0xb3eb240>`

**Examples**

```
library(canceR)
myGlobalEnv
```

---

`OLD.GSEA.EnrichmentScore``OLD.GSEA.EnrichmentScore`

---

**Description**

`OLD.GSEA.EnrichmentScore`

**Arguments**`gene.list``gene.set`**Examples**

```
## Not run:
library(canceR)
## Load workspace
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))
##Run.GSEA()

## End(Not run)
```

plotModel

*plot Model*

---

**Description**

model plotting with tcltk

**Usage**

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

**Arguments**

plotCommand

title

hscale

vscale

**Examples**

```
## Not run:  
##library(cancerR)  
## Load workspace  
##load(paste(path.package("cancerR"),"/data/gbm_tcgaPlotTwoGenProf.RData", sep=""))  
##plot_1Gene_2GenProfs()  
##use default options  
  
## End(Not run)
```

---

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

---

**Description**

Tcltk plotting of 1 gene depending two genetic profiles (expression vs mutation or expression vs methylation)

**Usage**

```
plot_1Gene_2GenProfs()
```

**Examples**

```
## Not run:  
##library(canceR)  
## Load workspace  
##load(paste(path.package("canceR"),"/data/gbm_tcgaPlotTwoGenProf.RData", sep=""))  
##plot_1Gene_2GenProfs()  
##use default options  
  
## End(Not run)
```

---

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

---

**Description**

Plotting the correlation between two genes.

**Examples**

```
## Not run:  
##library(canceR)  
## Load workspace  
##load(paste(path.package("canceR"),"/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##plot_2Genes_1GenProf()  
  
## End(Not run)
```

---

rbind.na                    *rbind.na*

---

**Description**

No equal rows binding

**Usage**

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

**Arguments**

```
...  
deparse.level
```

**Value**

Value

**Examples**

```
rbind.na()
```

---

Run.GSEA

*The main function to run GSEA-R from Broad Institute*

---

**Description**

this function runs the GSEA-R version of Broad Institute at (<http://www.broadinstitute.org/gsea/index.jsp>)

**Usage**

```
Run.GSEA()
```

**Examples**

```
## Not run:  
library(canceR)  
## Load workspace  
load(paste(path.package("canceR"), "/data/ucec_tcga_pubGSEA1021.RData", sep=""))  
##Run.GSEA()  
  
## End(Not run)
```

---

setWorkspace

*Setting work Directory and output folders.*

---

**Description**

At starting window, user needs to set work directory for output data. The function is found in File menu.

**Examples**

```
## Not run:  
library(canceR)  
setWorkspace()  
  
## End(Not run)
```

---

`testCheckedCaseGenProf`*Testing checked appropriate Cases for appropriate Genetic profiles.*

---

**Description**

Testing checked appropriate Cases for appropriate Genetic profiles.

**Usage**

```
testCheckedCaseGenProf()
```

**Examples**

```
## Not run:  
##Load Session  
load(paste(path.package("cancerR"),"/data/brca_tcga73genes.RData", sep=""))  
## Select Case from Breast Cancer  
##myGlobalEnv$curselectCases <- 9  
##Select Genetic Profile from Breast Cancer  
##myGlobalEnv$curselectGenProfs <- 4  
##testCheckedCaseGenProf()  
  
## End(Not run)
```

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