

Package ‘canceR’

April 22, 2016

Type Package

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

Version 1.2.0

Date 2015-07-12

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

Maintainer Karim Mezhoud <kmezhoud@gmail.com>

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,survival, Biobase, phenoTest, Formula, rpart, Biobase, circlize, plyr

biocViews GUI, GeneExpression, Software

NeedsCompilation no

R topics documented:

about	3
canceR	4
canceRHelp	4
canceR_Vignette	5
cbind.na	5
ClinicalData	6

dialogGeneClassifier	7
dialoggetGeneListMSigDB	7
dialogMetOption	8
dialogMut	9
dialogOptionCircos	10
dialogOptionGSEAlm	10
dialogOptionPhenoTest	11
dialogPlotOption_SkinCor	12
dialogSamplingGSEA	12
dialogSelectFiles_GSEA	13
dialogSpecificMut	13
dialogSummary_GSEA	14
displayInTable	15
GeneExpMatrix	15
getCases	16
getCasesGenProfs	17
getCircos	17
getClinicalDataMatrix	18
getClinicData_MultipleCases	18
getCor_ExpCNAMet	19
geteSet	20
getGCTCLSExample	20
getGCT_CLSfiles	21
getGeneExpMatrix	21
getGeneList	22
getGeneListExample	22
getGeneListFromMSigDB	22
getGenesClassifier	23
getGenesTree_MultipleCases	23
getGenesTree_SingleCase	24
getGenProfs	24
getGSEAlm_Diseases	25
getGSEAlm_Variables	26
getInTable	26
getListProfData	27
getMegaProfData	28
getMetDataMultipleGenes	29
getMSigDB	29
getMSigDBExample	30
getMSigDBfile	31
getMutData	31
getPhenoTest	32
getProfilesDataMultipleGenes	32
getProfilesDataSingleGene	33
getSpecificMut	33
getSummaryGSEA	34
getSurvival	35
getTextWin	35

GSEA	36
GSEA.Analyze.Sets	37
GSEA.ConsPlot	38
GSEA.EnrichmentScore	38
GSEA.EnrichmentScore2	39
GSEA.Gct2Frame	40
GSEA.Gct2Frame2	40
GSEA.GeneRanking	41
GSEA.HeatMapPlot	41
GSEA.HeatMapPlot2	42
GSEA.NormalizeCols	42
GSEA.NormalizeRows	43
GSEA.ReadClsFile	43
GSEA.Res2Frame	44
GSEA.Threshold	44
GSEA.VarFilter	45
GSEA.write.gct	46
Match_GeneList_MSigDB	46
modalDialog	47
myGlobalEnv	48
OLD.GSEA.EnrichmentScore	48
plotModel	49
plot_1Gene_2GenProfs	49
plot_2Genes_1GenProf	50
rbind.na	50
Run.GSEA	51
setWorkspace	51
testCheckedCaseGenProf	52

Index 53

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)
```

```
dialoggetGeneListMSigDB
```

Multi-select choice of gene sets from loaded MSigDB

Description

This function

Usage

```
dialoggetGeneListMSigDB(MSigDB)
```

Arguments

```
MSigDB          dialoggetGeneListMSigDB(MSigDB)
```

Value

myGlobalEnv\$regex
A list of Gene Sets

Author(s)

Karim Mezhoud

See Also

getGeneListMSigDB()

Examples

```
## Not run:  
library(canceR)  
getGeneListMSigDB()  
head(myGlobalEnv$GeneListMSigDB)  
head(myGlobalEnv$GeneList)  
  
## 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	<i>dialog box to specify Animo Acid changes using regular expression</i>
-----------	--

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)
```

dialogOptionCircos *Select with dimensions to plot*

Description

This dialg Box allow user to select which dimensions to plot and gene Symbol using Threshold of correlation rate of every dimension.

Usage

```
dialogOptionCircos()
```

Author(s)

Karim Mezhoud

See Also

```
getCircos(dimension="All")
```

Examples

```
## Not run:  
library(canceR)  
dialogOptionCircos()  
getCircos()  
myGlobalEnv$returnCBoxCircos  
myGlobalEnv$returnCBoxThrCircos  
myGlobalEnv$returnThreshCircos  
  
## 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("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()
##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      Dialog Box for Sampling patients from expression profile data used for
                        GSEA-R (Broad Institute)
```

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("cancerR"),"/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 *Dialog Box to specify phenotype (variable) used in last GSEA-R to get Summary Results.*

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(cancerR)
## Load workspace
load(paste(path.package("cancerR"),"/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

KDELR1 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)
```

```
getCircos      Get Circos plot of multiple dimensions.
```

Description

This function plot correlation rate between diseases of multiple dimensions (mRNA, CNA, Met,RPPA, miRNA, Mut)

Usage

```
getCircos(dimension)
```

Arguments

```
dimension      All
```

Author(s)

Karim Mezhoud

Examples

```
## Not run:  
library(canceR)  
##Load Session  
load(paste(path.package("canceR"),"/data/Circos.RData", sep=""))  
##getListProfData()  
getCircos(dimension ="All")  
  
## 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)
```

```
getCor_ExpCNAMet      Get gene correlation for multiple dimensions.
```

Description

Get Correlation of the same gene between two diseases from matrices of mRNA, CNA and Methylation Data

Usage

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

Arguments

ListMatrix is a List of numeric matrices

dimension Exp: get correlation for mRNA Profiles Data
CNA: get correlation for CNA Profiles Data
Met: get correlation for Methylation Profiles Data
miRNA: get correlation for miRNA Profiles Data
RPPA: get correlation for RPPA Profiles Data

Author(s)

Karim Mezhoud

See Also

```
getCircos(dimension= "All")
```

Examples

```
## Not run:
library(canceR)
load(paste(path.package("canceR"), "/data/Circos.RData", sep=""))
getListProfData()
getCor_ExpCNAMet(myGlobalEnv$ListProfData$CNA, dimension="CNA")
head(myGlobalEnv$Cor_CNA)
head(myGlobalEnv$Cor_Exp)

## End(Not run)
```

geteSet	<i>Build expression Set (Biobase)</i>
---------	---------------------------------------

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          get Gene List from file.
```

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)
```

```
getGeneListFromMSigDB Get Gene List from MSigDB.gmt file.
```

Description

This function builds data frame with two columns (Gene Sets and Genes). This function deletes duplicate genes through gene sets. The input file is MSigDB.gmt file.

Usage

```
getGeneListFromMSigDB()
```

Value

```
myGlobalEnv$GeneListMSigDB
      Data frame of genes sets and its genes
```

Author(s)

Karim Mezhoud

Examples

```
## Not run:  
library(canceR)  
getGeneListFromMSigDB()  
head(myGlobalEnv$GeneListMSigDB)  
  
## 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(cancer)
##load(paste(path.package("cancer"),"/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(cancer)
##load(paste(path.package("cancer"),"/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(cancerR)
##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/cancerR/extdata/MSigDB/c2.cp.reactome.v4.0.symbol

Usage

```
getGSEAlm_Diseases()
```

Examples

```
## Not run:
##library(cancerR)
##library(GSEAlm)
##Load Session
##load(paste(path.package("cancerR"),"/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)
```

getListProfData	<i>get a list of Profile Data of every available dimensions;</i>
-----------------	--

Description

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

```
myGlobalEnv$ProfData$Expression
    Matrices of mRNA expression
myGlobalEnv$ProfData$CNA
    Matrices of Copy Number Alteration
myGlobalEnv$Met
    Matrices of Methylation Data
myGlobalEnv$ProfData$RPPA
    Matrices of Reverse Phase Protein Activities
myGlobalEnv$ProfData$miRNA
    Matrices of miRNA expression
myGlobalEnv$Mut
    Matrices of Mutation Data
```

Author(s)

Karim Mezhoud

Examples

```
## Not run:  
library(canceR)  
getListProfData()  
head(myGlobalEnv$ProfData$Expression)  
  
## 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(myGlobalEnv$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)
```

getSurvival	<i>Survival plot</i>
-------------	----------------------

Description

This function plot Kaplan-Meier curves and Cox proportional Hazard model.

Usage

```
getSurvival(Coxph)
```

Arguments

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

Examples

```
## Not run:  
load("~/CGDS-R/canceR/data/gbm_tcgaPlotTwoGenProf.RData")  
  
getSurvival(Coxph = 1)  
getSurvival(Coxph = 0)  
  
## End(Not run)
```

getTextWin	<i>getTextWin</i>
------------	-------------------

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

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

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.

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

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

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	<i>GSEA.GeneRanking</i>
------------------	-------------------------

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 *GSEA.HeatMapPlot2*

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 *GSEA.NormalizeCols*

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 *GSEA.ReadClsFile*

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

GSEA.Res2Frame

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	<i>Dialog box to specify Gene Symbol.</i>
-------------	---

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	<i>plot Model</i>
-----------	-------------------

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	<i>Plotting two genetic profiles for one Gene</i>
----------------------	---

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)
```

Index

*Topic **datasets**

- ClinicalData, [6](#)
- GeneExpMatrix, [15](#)
- myGlobalEnv, [48](#)

- (cancerR), [4](#)

- about, [3](#)

- cancerR, [4](#)
- cancerR (cancerR), [4](#)
- cancerR_Vignette, [5](#)
- cancerRHelp, [4](#)
- cbind.na, [5](#)
- ClinicalData, [6](#)

- dialogGeneClassifier, [7](#)
- dialoggetGeneListMSigDB, [7](#)
- dialogMetOption, [8](#)
- dialogMut, [9](#)
- dialogOptionCircos, [10](#)
- dialogOptionGSEALm, [10](#)
- dialogOptionPhenoTest, [11](#)
- dialogPlotOption_SkinCor, [12](#)
- dialogSamplingGSEA, [12](#)
- dialogSelectFiles_GSEA, [13](#)
- dialogSpecificMut, [13](#)
- dialogSummary_GSEA, [14](#)
- displayInTable, [15](#)

- GeneExpMatrix, [15](#)
- getCases, [16](#)
- getCasesGenProfs, [17](#)
- getCircos, [17](#)
- getClinicalDataMatrix, [18](#)
- getClinicData_MultipleCases, [18](#)
- getCor_ExpCNAMet, [19](#)
- geteSet, [20](#)
- getGCT_CLSfiles, [21](#)
- getGCTCLSExample, [20](#)
- getGeneExpMatrix, [21](#)

- getGeneList, [22](#)
- getGeneListExample, [22](#)
- getGeneListFromMSigDB, [22](#)
- getGenesClassifier, [23](#)
- getGenesTree_MultipleCases, [23](#)
- getGenesTree_SingleCase, [24](#)
- getGenProfs, [24](#)
- getGSEALm_Diseases, [25](#)
- getGSEALm_Variables, [26](#)
- getInTable, [26](#)
- getListProfData, [27](#)
- getMegaProfData, [28](#)
- getMetDataMultipleGenes, [29](#)
- getMSigDB, [29](#)
- getMSigDBExample, [30](#)
- getMSigDBfile, [31](#)
- getMutData, [31](#)
- getPhenoTest, [32](#)
- getProfilesDataMultipleGenes, [32](#)
- getProfilesDataSingleGene, [33](#)
- getSpecificMut, [33](#)
- getSummaryGSEA, [34](#)
- getSurvival, [35](#)
- getTextWin, [35](#)
- GSEA, [36](#)
- GSEA.Analyze.Sets, [37](#)
- GSEA.ConsPlot, [38](#)
- GSEA.EnrichmentScore, [38](#)
- GSEA.EnrichmentScore2, [39](#)
- GSEA.Gct2Frame, [40](#)
- GSEA.Gct2Frame2, [40](#)
- GSEA.GeneRanking, [41](#)
- GSEA.HeatMapPlot, [41](#)
- GSEA.HeatMapPlot2, [42](#)
- GSEA.NormalizeCols, [42](#)
- GSEA.NormalizeRows, [43](#)
- GSEA.ReadClsFile, [43](#)
- GSEA.Res2Frame, [44](#)
- GSEA.Threshold, [44](#)

GSEA.VarFilter, [45](#)
GSEA.write.gct, [46](#)

Match_GeneList_MSigDB, [46](#)
modalDialog, [47](#)
myGlobalEnv, [48](#)

OLD.GSEA.EnrichmentScore, [48](#)

plot_1Gene_2GenProfs, [49](#)
plot_2Genes_1GenProf, [50](#)
plotModel, [49](#)

rbind.na, [50](#)
Run.GSEA, [51](#)

setWorkspace, [51](#)

testCheckedCaseGenProf, [52](#)