Package: cbpManager (via r-universe)

November 18, 2026

Type Package

Title Generate, manage, and edit data and metadata files suitable for the import in cBioPortal for Cancer Genomics

Version 1.20.0

Date 2021-03-16

Description This R package provides an R Shiny application that enables the user to generate, manage, and edit data and metadata files suitable for the import in cBioPortal for Cancer Genomics. Create cancer studies and edit its metadata. Upload mutation data of a patient that will be concatenated to the data_mutation_extended.txt file of the study. Create and edit clinical patient data, sample data, and timeline data. Create custom timeline tracks for patients.

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

VignetteBuilder knitr

URL https://arsenij-ust.github.io/cbpManager/index.html

BugReports https://github.com/arsenij-ust/cbpManager/issues

Depends shiny, shinydashboard

Imports utils, DT, htmltools, vroom, plyr, dplyr, magrittr, jsonlite, rapportools, basilisk, reticulate, shinyBS, shinycssloaders, rintrojs, rlang, markdown

Suggests knitr, BiocStyle, rmarkdown, testthat (>= 3.0.0)

StagedInstall no

Collate 'basilisk.R' 'dynamicTable.R' 'modulesResourceButtons.R' 'cbpManager-pkg.R' 'functions.R' 'global.R' 'cbpManager.R' 'shinyAppServer.R' 'shinyAppUI.R'

biocViews ImmunoOncology, DataImport, DataRepresentation, GUI, ThirdPartyClient, Preprocessing, Visualization

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Contents

addColumn_Server . . . 3
addColumn_UI . . . 3
addRow_Server . . . 4
addRow_UI . . . 5
addRowRc_Server . . . 5
addRowRc_UI . . . 6
cBioPortalToDataFrame . . . 7
cbpManager . . . 7
cbpManager-pkg . . . 8
check_input_dates . . . 8
convertDataFrame . . . 9
create_name . . . 10
deleteColumn_Server . . . 10
deleteColumn_UI . . . 11
deleteRow_Server . . . 11
deleteRow_UI . . . 12
deleteRowRc_Server . . . 12
deleteRowRc_UI . . . 13
editRow_Server . . . 14
editRow_UI . . . 15
editRowRc_Server . . . 15
editRowRc_UI . . . 16
fncols . . . 17
generateOncotreeUIwidgets . . . 17
generateUIwidgets . . . 18
getSampleIDs . . . 19
importPatientData . . . 19
IsDate . . . 20
saveResource_Server . . . 21
saveResource_UI . . . 22
saveTimeline_Server . . . 22
saveTimeline_UI . . . 23
setupConda_cbpManager . . . 23
shinyAppServer . . . 24
shinyAppUI . . . 24
updateOncotreeUIwidgets . . . 25

validateResourceDefinition 25
validateResourcePatient 26
validateResourceSample 26
validateResourceStudy 27
ValidationDependencies 27
writeLogfile 28

Index **29**

`addColumn_Server` *Server logic of module for adding a column*

Description

Server logic of module for adding a column

Usage

```
addColumn_Server(input, output, session, data)
```

Arguments

`input`	Shiny input
`output`	Shiny output
`session`	Shiny session
`data`	source data as data.frame

Value

reactive data.frame of modified source data

`addColumn_UI` *UI elements of module for adding a column*

Description

UI elements of module for adding a column

Usage

```
addColumn_UI(id, label = "Add column")
```

Arguments

`id`	module id
`label`	label of the button

Value

UI module

`addRow_Server` *Server logic of module for adding a row*

Description

Server logic of module for adding a row

Usage

```
addRow_Server(
  input,
  output,
  session,
  data,
  patient_ids = NULL,
  dates_first_diagnosis = NULL,
  mode = c("timeline", "timepoint")
)
```

Arguments

`input`	Shiny input
`output`	Shiny output
`session`	Shiny session
`data`	source data as data.frame
`patient_ids`	reactive vector of existing patient IDs
`dates_first_diagnosis`	data.frame with dates of the first diagnosis and patient IDs
`mode`	Mode of the timeline data. Controls which columns are displayed.

Value

reactive data.frame of modified source data

addRow_UI *UI elements of module for adding a row*

Description

UI elements of module for adding a row

Usage

```
addRow_UI(id, label = "Add")
```

Arguments

id	module id
label	label of the button

Value

UI module

addRowRc_Server *Server logic of Resource tab module for adding a row*

Description

Server logic of Resource tab module for adding a row

Usage

```
addRowRc_Server(
  input,
  output,
  session,
  data,
  patient_ids = NULL,
  sample_ids = NULL,
  resource_ids = NULL,
  resource_type = c("definition", "sample", "patient", "study")
)
```

Arguments

input	Shiny input
output	Shiny output
session	Shiny session
data	Source data as data.frame
patient_ids	Reactive vector of existing patient IDs
sample_ids	Reactive data.frame of existing patient IDs and sample IDs
resource_ids	Reactive data.frame of data_resource_definition
resource_type	The type of the resource. Can be "definition", "sample", "patient", "study"

Value

reactive data.frame of modified source data

---

addRowRc_UI *UI elements of Resource tab module for adding a row*

Description

UI elements of Resource tab module for adding a row

Usage

```
addRowRc_UI(id, label = "Add")
```

Arguments

id	module id
label	label of the button

Value

UI module

cBioPortalToDataFrame *Convert the cBioPortal sample- and patient-data file format into a data.frame*

Description

This function takes a file object (from read.table), removes the # symbol, sets the 5th row as the column names of the data.frame and removes the rows containing the priority, data type and column name. use read.table as follows: `read.table(file, sep='\t', colClasses = 'character', comment.char = '')`

Usage

```
cBioPortalToDataFrame(data)
```

Arguments

data	The data.frame of a cBioPortal sample/patient data file

Value

data.frame

Examples

```
df <- data.frame(
        V1=c("#attr_1", "#attribute 1", "#STRING", "#1", "ATTRIBUTE_1", "value_1"),
        V2=c("attr_2", "attribute 2", "STRING", "1", "ATTRIBUTE_2", "value_2")
    )
cbpManager:::cBioPortalToDataFrame(df)
```

cbpManager *Launch cbpManager*

Description

Launch the cbpManager Shiny application.

Usage

```
cbpManager(studyDir = NULL, logDir = NULL, returnAppObj = FALSE, ...)
```

Arguments

studyDir	Path to study folder containing studies of cBioPortal.
logDir	Path where a logfile should be saved. If NULL, logs are not stored
returnAppObj	Logical value, whether to return the app object if set to TRUE. Default behavior: directly runs the app (FALSE)
...	Further parameters that are used by shiny::runApp, e.g. host or port.

Value

shiny application object

Examples

```
if (interactive()) {
  cbpManager()
}
```

---

cbpManager-pkg *cbpManager*

Description

'cbpManager' is an R package that provides an interactive Shiny-based graphical user interface for...

Author(s)

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---

check_input_dates *Check the input of dates*

Description

Check the input of dates

Usage

```
check_input_dates(diagnosisDate, startDate = NULL, endDate = NULL)
```

Arguments

diagnosisDate	date of first diagnosis
startDate	start date of timeline event
endDate	end date of timeline event

Value

Returns a number indicating the warning

Examples

```
cbpManager:::check_input_dates(
    diagnosisDate = "2020-01-01",
    startDate = "2020-02-01",
    endDate = "2020-03-01"
) #returns 0
cbpManager:::check_input_dates(
    diagnosisDate = "2020-01-01",
    startDate = "2019-02-01"
) #returns 2
cbpManager:::check_input_dates(
    diagnosisDate = "2020-01-01",
    endDate = "2019-02-01"
) #returns 2
cbpManager:::check_input_dates(
    diagnosisDate = "2020-01-01",
    startDate = "2020-03-01",
    endDate = "2020-02-01"
) #returns 1
```

---

convertDataFrame *Convert the data.frame to the appropriate file format for cBioPortal*

Description

Convert the data.frame to the appropriate file format for cBioPortal

Usage

```
convertDataFrame(df)
```

Arguments

df	data.frame

Value

Data.frame formated for the cBioPortal file format

Examples

```
cbpManager:::convertDataFrame(
    data.frame(
        ATTRIBUTE1=c("attr_1", "attribute 1", "STRING", "value_a1"),
        ATTRIBUTE2=c("attr_2", "attribute 2", "STRING", "value_b1")
    )
)
```

---

create_name *Sanitize names*

Description

This function takes a character string, replaces spaces by underscores and runs make.names.

Usage

```
create_name(x, toupper = TRUE)
```

Arguments

x	A character string.
toupper	If TRUE, the name wil be upper-case; if FALSE, the name will be lower-case.

Value

A sanitized string.

Examples

```
cbpManager:::create_name("Study name 1") #returns "STUDY_NAME_1"
cbpManager:::create_name("FANCY;name", toupper = FALSE) #returns "fancy.name"
```

---

deleteColumn_Server *Server logic of module for deleting a column*

Description

Server logic of module for deleting a column

Usage

```
deleteColumn_Server(input, output, session, data, exclude)
```

Arguments

input	Shiny input
output	Shiny output
session	Shiny session
data	source data as data.frame
exclude	column names that shoud be excluded from deletion

Value

reactive data.frame of modified source data

---

deleteColumn_UI *UI elements of module for deleting a column*

Description

UI elements of module for deleting a column

Usage

```
deleteColumn_UI(id, label = "Delete column(s)")
```

Arguments

id	module id
label	label of the button

Value

UI module

---

deleteRow_Server *Server logic of module for removing a row*

Description

Server logic of module for removing a row

Usage

```
deleteRow_Server(input, output, session, data, selected_row)
```

Arguments

input	Shiny input
output	Shiny output
session	Shiny session
data	source data as data.frame
selected_row	Index of the selected row from the table

Value

reactive data.frame of modified source data

---

deleteRow_UI *UI elements of module for removing a row*

Description

UI elements of module for removing a row

Usage

```
deleteRow_UI(id, label = "Delete")
```

Arguments

id	module id
label	label of the button

Value

UI module

---

deleteRowRc_Server *Server logic of Resource tab module for deleting a row*

Description

Server logic of Resource tab module for deleting a row

Usage

```
deleteRowRc_Server(
  input,
  output,
  session,
  data,
  selected_row,
  mode = "default",
  sample_data = NULL,
  patient_data = NULL,
  study_data = NULL
)
```

Arguments

input	Shiny input
output	Shiny output
session	Shiny session
data	Source data as data.frame
selected_row	Index of the selected row from the table
mode	If 'recursive' the resources bind to the resource definition will be deleted.
sample_data	Data of the resource from type 'sample'
patient_data	Data of the resource from type 'patient'
study_data	Data of the resource from type 'study'

Value

reactive data.frame of modified source data

---

deleteRowRc_UI *UI elements of module for removing a row*

Description

UI elements of module for removing a row

Usage

```
deleteRowRc_UI(id, label = "Delete")
```

Arguments

id	Module id
label	Label of the button

Value

UI module

`editRow_Server` *Server logic of module for editing a row*

Description

Server logic of module for editing a row

Usage

```
editRow_Server(
  input,
  output,
  session,
  data,
  patient_ids = NULL,
  dates_first_diagnosis = NULL,
  selected_row = NULL,
  mode = c("timeline", "timepoint")
)
```

Arguments

`input`	Shiny input
`output`	Shiny output
`session`	Shiny session
`data`	source data as data.frame
`patient_ids`	reactive vector of existing patient IDs
`dates_first_diagnosis`	data.frame with dates of the first diagnosis and patient IDs
`selected_row`	the index of the selected row
`mode`	Mode of the timeline data. Controls which columns are displayed.

Value

reactive data.frame of modified source data

editRow_UI *UI elements of module for editing a row*

Description

UI elements of module for editing a row

Usage

```
editRow_UI(id, label = "Edit")
```

Arguments

id	module id
label	label of the button

Value

UI module

editRowRc_Server *Server logic of Resource tab module for editing a row*

Description

Server logic of Resource tab module for editing a row

Usage

```
editRowRc_Server(
  input,
  output,
  session,
  data,
  patient_ids = NULL,
  sample_ids = NULL,
  resource_ids = NULL,
  selected_row = NULL,
  resource_type = c("definition", "sample", "patient", "study")
)
```

Arguments

input	Shiny input
output	Shiny output
session	Shiny session
data	Source data as data.frame
patient_ids	Reactive vector of existing patient IDs
sample_ids	Reactive data.frame of existing patient IDs and sample IDs
resource_ids	Reactive data.frame of data_resource_definition
selected_row	Index of the selected row
resource_type	The type of the resource. Can be "definition", "sample", "patient", "study"

Value

reactive data.frame of modified source data

---

editRowRc_UI *UI elements of module for editing a row*

Description

UI elements of module for editing a row

Usage

```
editRowRc_UI(id, label = "Edit")
```

Arguments

id	Module id
label	Label of the button

Value

UI module

fncols — *Add empty column to a data.frame, if column does not exist in the data.frame*

Description

Add empty column to a data.frame, if column does not exist in the data.frame

Usage

```
fncols(data, cname)
```

Arguments

data	data.frame
cname	column name

Value

data.frame

Examples

```
cbpManager:::fncols(data.frame(a=c(1,2,3), b=c(4,5,6)), "new")
```

generateOncotreeUIwidgets — *Create shiny UI-widget for specific columns of oncotree entries*

Description

Create shiny UI-widget for specific columns of oncotree entries

Usage

```
generateOncotreeUIwidgets(
  colname,
  mode = c("add", "edit"),
  tab = c("Patient", "Sample")
)
```

Arguments

colname	column name
mode	determines the inputId prefix of the UI-widget
tab	"Patient", "Sample" - The used tab; sets the html id prefix of the input

Value

A oncotree specific shiny UI-widget

Examples

```
oncotree <- jsonlite::fromJSON(system.file("extdata", "oncotree.json", package = "cbpManager"))
cancer_type <- unique(oncotree$mainType[which(!is.na(oncotree$mainType))])
cbpManager:::generateOncotreeUIwidgets("CANCER_TYPE", "add")
```

---

generateUIwidgets *Generate UI input widget*

Description

Generate UI input widget

Usage

```
generateUIwidgets(
  colname,
  mode = c("add", "edit"),
  tab = c("Patient", "Sample", "Mutation"),
  data = NULL,
  selected_row = NULL,
  patientIDs = NULL,
  sampleIDs = NULL
)
```

Arguments

colname	A character string - the name of the column, that will be the label of the input
mode	"add" or "edit" - whether to use existing values or not
tab	"Patient", "Sample" - The used tab; sets the html id prefix of the input
data	A data.frame.
selected_row	A number indicating the row number of the selected row in the data.frame.
patientIDs	Vector of patient IDs used for drop down menu of the PATIENT_ID column

Value

A sanitized string.

Examples

```
cbpManager:::generateUIwidgets(colname = "attribute", mode = "add", tab = "Patient")
```

`getSampleIDs` *Get Sample IDs associated with Patient IDs from the data_clinical_sample.txt file*

Description

Get Sample IDs associated with Patient IDs from the data_clinical_sample.txt file

Usage

```
getSampleIDs(file_path, patIDs)
```

Arguments

`file_path`	A character string.
`patIDs`	A character string.

Value

vector with Sample IDs

Examples

```
cbpManager:::getSampleIDs(
    system.file("study/testpatient/data_clinical_sample.txt", package = "cbpManager"),
    patIDs = "Testpatient")
```

`importPatientData` *Import patient data into current study data.frames*

Description

Import patient data into current study data.frames

Usage

```
importPatientData(
  mode = c("patient", "sample", "mutations", "timelines"),
  file_name,
  file_path,
  patIDs,
  data,
  associatedSampleIDs = NULL
)
```

Arguments

mode	Defines the type of imported data
file_name	Filename of source data
file_path	Filepath with filename of source data
patIDs	PATIENT_IDs of patients that should be imported
data	Source data, to be subsetted according to patIDs
associatedSampleIDs	The sample IDs associated to the patIDs

Value

data.frame

IsDate *Check if input is in the appropriate date format*

Description

Check if input is in the appropriate date format

Usage

```
IsDate(mydate, date.format = "%Y-%m-%d")
```

Arguments

mydate	date
date.format	string describig the date format

Value

boolean

Examples

```
cbpManager:::IsDate("2020-02-20")
cbpManager:::IsDate("20.01.2020", date.format = "%d.%m.%Y")
```

saveResource_Server *Server logic of module for saving the resource data*

Description

Server logic of module for saving the resource data

Usage

```
saveResource_Server(
  input,
  output,
  session,
  data,
  study_id,
  data_filename,
  meta_filename,
  resource_type = c("SAMPLE", "DEFINITION", "PATIENT", "STUDY")
)
```

Arguments

input	Shiny input
output	Shiny output
session	Shiny session
data	Source data as data.frame
study_id	The current study ID
data_filename	File name of the data file
meta_filename	file name of the meta file
resource_type	The type of the resource. Can be "definition", "sample", "patient", "study"

Value

boolean value; TRUE if function was used.

saveResource_UI *UI elements of module for saving the resource data*

Description

UI elements of module for saving the resource data

Usage

```
saveResource_UI(id, label = "Save")
```

Arguments

id	module id
label	label of the button

Value

UI module

saveTimeline_Server *Server logic of module for saving the source data*

Description

Server logic of module for saving the source data

Usage

```
saveTimeline_Server(input, output, session, data, study_id)
```

Arguments

input	Shiny input
output	Shiny output
session	Shiny session
data	source data as data.frame
study_id	the current study ID

Value

boolean value; TRUE if function was used.

saveTimeline_UI *UI elements of module for saving the data*

Description

UI elements of module for saving the data

Usage

```
saveTimeline_UI(id, label = "Save")
```

Arguments

id	module id
label	label of the button

Value

UI module

setupConda_cbpManager *Install conda environment with basilisk before launching the app*

Description

Install conda environment with basilisk before launching the app

Usage

```
setupConda_cbpManager()
```

Value

Nothing to return

Examples

```
## Not run:
setupConda_cbpManager()

## End(Not run)
```

shinyAppServer *Shiny app server function*

Description

Shiny app server function

Usage

```
shinyAppServer(input, output, session)
```

Arguments

input	provided by shiny
output	provided by shiny
session	provided by shiny

Value

nothing to return

shinyAppUI *Shiny app server object create the shiny application user interface*

Description

Shiny app server object create the shiny application user interface

Usage

```
shinyAppUI
```

Format

An object of class shiny.tag of length 3.

updateOncotreeUIwidgets *Updates UI-widgets for specific columns of oncotree entries*

Description

Updates UI-widgets for specific columns of oncotree entries

Usage

```
updateOncotreeUIwidgets(
  session,
  row_last_clicked,
  mode = c("add", "edit"),
  tab = c("Patient", "Sample")
)
```

Arguments

session	Shiny session
row_last_clicked	the index of the row last clicked in the oncotree_table
mode	determines the inputId prefix of the UI-widget
tab	"Patient", "Sample" - The used tab; sets the html id pr

Value

nothing to return

validateResourceDefinition *Validate resource_definition input*

Description

Validate resource_definition input

Usage

```
validateResourceDefinition(values, resourceDf, mode = "add")
```

Arguments

values	List of input values
resourceDf	data.frame of data_resource_definition
mode	The mode of the function ('add' or 'edit')

Value

boolean

`validateResourcePatient` *Validate resource_patient input*

Description

Validate resource_patient input

Usage

```
validateResourcePatient(values)
```

Arguments

`values`	List of input values

Value

boolean

`validateResourceSample` *Validate resource_sample input*

Description

Validate resource_sample input

Usage

```
validateResourceSample(values)
```

Arguments

`values`	List of input values

Value

boolean

validateResourceStudy *Validate resource_study input*

Description

Validate resource_study input

Usage

```
validateResourceStudy(values)
```

Arguments

values	List of input values

Value

boolean

ValidationDependencies *Validation Dependencies*

Description

Vector defining a set of Python dependencies and versions required to operate with the validation scripts for cBioPortal

Usage

```
.validation_dependencies
```

Format

A character vector containing the pinned versions of all Python packages on which the import validation depends.

`writeLogfile` *Write a line to a logfile containing the date, time, username (from Shinyproxy), and the name of the modified file.*

Description

Write a line to a logfile containing the date, time, username (from Shinyproxy), and the name of the modified file.

Usage

```
writeLogfile(outdir, modified_file, log_filename = "cbpManager_logfile.txt")
```

Arguments

`outdir`	directory, where the logfile should be saved
`modified_file`	Name of the modified file
`log_filename`	Name of the logfile

Value

Nothing to return

Examples

```
cbpManager:::writeLogfile(tempdir(), "data_clinical_patient.txt")
```

Index

∗ **datasets**
    shinyAppUI, 24
    ValidationDependencies, 27
.validation_dependencies
        *(*ValidationDependencies*)*, 27

addColumn_Server, 3
addColumn_UI, 3
addRow_Server, 4
addRow_UI, 5
addRowRc_Server, 5
addRowRc_UI, 6

cBioPortalToDataFrame, 7
cbpManager, 7
cbpManager-pkg, 8
check_input_dates, 8
convertDataFrame, 9
create_name, 10

deleteColumn_Server, 10
deleteColumn_UI, 11
deleteRow_Server, 11
deleteRow_UI, 12
deleteRowRc_Server, 12
deleteRowRc_UI, 13

editRow_Server, 14
editRow_UI, 15
editRowRc_Server, 15
editRowRc_UI, 16

fncols, 17

generateOncotreeUIwidgets, 17
generateUIwidgets, 18
getSampleIDs, 19

importPatientData, 19
IsDate, 20

saveResource_Server, 21
saveResource_UI, 22
saveTimeline_Server, 22
saveTimeline_UI, 23
setupConda_cbpManager, 23
shinyAppServer, 24
shinyAppUI, 24

updateOncotreeUIwidgets, 25

validateResourceDefinition, 25
validateResourcePatient, 26
validateResourceSample, 26
validateResourceStudy, 27
ValidationDependencies, 27

writeLogfile, 28