

# Package ‘cbpManager’

May 29, 2024

**Type** Package

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

**Version** 1.12.0

**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.

**License** AGPL-3 + file LICENSE

**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

**Config/testthat/edition 3****git\_url** <https://git.bioconductor.org/packages/cbpManager>**git\_branch** RELEASE\_3\_19**git\_last\_commit** 0eee05c**git\_last\_commit\_date** 2024-04-30**Repository** Bioconductor 3.19**Date/Publication** 2024-05-29**Author** Arsenij Ustjanzew [aut, cre, cph](<<https://orcid.org/0000-0002-1014-4521>>),Federico Marini [aut] (<<https://orcid.org/0000-0003-3252-7758>>)**Maintainer** Arsenij Ustjanzew <[arsenij.ustjanzew@gmail.com](mailto:arsenij.ustjanzew@gmail.com)>**Contents**

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---

<code>addColumn_Server</code>	<i>Server logic of module for adding a column</i>
-------------------------------	---

---

## Description

Server logic of module for adding a column

## Usage

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

## Arguments

<code>input</code>	Shiny input
<code>output</code>	Shiny output
<code>session</code>	Shiny session
<code>data</code>	source data as <code>data.frame</code>

## Value

reactive `data.frame` of modified source data

---

addColumn_UI	<i>UI elements of module for adding a column</i>
--------------	--

---

**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

---

addRowRc_Server	<i>Server logic of Resource tab module for adding a row</i>
-----------------	---

---

**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

---

addRow_Server	<i>Server logic of module for adding a row</i>
---------------	--

---

**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	<i>UI elements of module for adding a row</i>
-----------	---

---

**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

---

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**

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

Arsenij Ustjanzew <arsenij.ustjanzew@gmail.com>

---

check_input_dates	<i>Check the input of dates</i>
-------------------	---------------------------------

---

### 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	<i>Convert the data.frame to the appropriate file format for cBioPortal</i>
------------------	---

---

**Description**

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

**Usage**

```
convertDataFrame(df)
```

**Arguments**

df	data.frame
----	------------

**Value**

Data.frame formatted 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	<i>Sanitize names</i>
-------------	-----------------------

---

**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 will 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 should 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

---

deleteRowRc_Server	<i>Server logic of Resource tab module for deleting a row</i>
--------------------	---

---

**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	<i>UI elements of module for removing a row</i>
----------------	---

---

**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

---

deleteRow_Server	<i>Server logic of module for removing a row</i>
------------------	--

---

**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	<i>UI elements of module for removing a row</i>
--------------	---

---

**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

---

editRowRc_Server	<i>Server logic of Resource tab module for editing a row</i>
------------------	--

---

**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	<i>UI elements of module for editing a row</i>
--------------	--

---

**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

---

editRow_Server	<i>Server logic of module for editing a row</i>
----------------	---

---

### 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	<i>UI elements of module for editing a row</i>
------------	--

---

**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

---

fncols	<i>Add empty column to a data.frame, if column does not exist in the data.frame</i>
--------	---

---

**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	<i>Get Sample IDs associated with Patient IDs from the data_clinical_sample.txt file</i>
--------------	--

---

**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	<i>Import patient data into current study data.frames</i>
-------------------	---

---

**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	<i>Check if input is in the appropriate date format</i>
--------	---

---

**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	<i>Server logic of module for saving the resource data</i>
---------------------	--

---

**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")
```

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