

```
install.packages("TreeAndLeaf") # Pacote Bioconductor
install.packages("RedeR") # Pacote Bioconductor
install.packages("RColorBrewer") # Pacote CRAN
install.packages("igraph") # Pacote CRAN
install.packages("SummarizedExperiment") # Pacote Bioconductor
install.packages("ComplexHeatmap") # Pacote Bioconductor
install.packages("circlize") # Pacote CRAN
install.packages("RColorBrewer") # Pacote CRAN
install.packages("survival") # Pacote CRAN
install.packages("survminer") # Pacote CRAN
install.packages("shiny") # Pacote CRAN

if (!require("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install(c("TreeAndLeaf", "RedeR", "SummarizedExperiment", "ComplexHeatmap"))

# Carregamento dos pacotes em R:
library(TreeAndLeaf) # Pacote Bioconductor
library(RedeR) # Pacote Bioconductor
library(RColorBrewer) # Pacote CRAN
library(igraph) # Pacote CRAN
library(SummarizedExperiment) # Pacote Bioconductor
library(ComplexHeatmap) # Pacote Bioconductor
library(circlize) # Pacote CRAN
library(RColorBrewer) # Pacote CRAN
library(survival) # Pacote CRAN
library(survminer) # Pacote CRAN
library(shiny) # Pacote CRAN

install.packages("ggplot2")
library(ggplot2)
```

Accessing package: survival

The following object is masked from 'package:survival':

```
dataset.df <- read.csv(file="./dataset-absolute-numbers-inc-both-sexes-in-2040-breast.csv")

year <- dataset.df$Year[(dataset.df$Year == 2020 | dataset.df$Year == 2040)]
breast_cancer.df <- data.frame("pop"= dataset.df$Population[(dataset.df$Year == 2020 | dataset.df$Year == 2040)],
                              "year"=dataset.df$Year[(dataset.df$Year == 2020 | dataset.df$Year == 2040)],
                              "n_cases"=dataset.df$Prediction[(dataset.df$Year == 2020 | dataset.df$Year == 2040)])

breast_cancer.df$year[breast_cancer.df$year == 2020] = "2020"
breast_cancer.df$year[breast_cancer.df$year == 2040] = "2040"

breast_cancer.df
save(dataset.df, file = "dataset.RData")
```

A data.frame: 12 × 3

	pop	year	n_cases
	<chr>	<chr>	<int>
	Africa	2020	186598
	Africa	2040	346587
Latin America and Caribbean	2020	210100	
Latin America and Caribbean	2040	314356	
Northern America	2020	281591	
Northern America	2040	343676	
Europe	2020	531086	
Europe	2040	568439	
Oceania	2020	25873	
Oceania	2040	35935	
Asia	2020	1026171	
Asia	2040	1416478	

```
# Criar objeto ggplot
grafico <- ggplot(data = breast_cancer.df, aes(x = breast_cancer.df$pop,
                                              y = breast_cancer.df$n_cases,
                                              fill = breast_cancer.df$year))

# Adicionar camada de barras
grafico <- grafico + geom_bar(stat = "identity", position = "dodge")

# Adicionar rótulos aos eixos e título
grafico <- grafico + xlab("População") + ylab("Número de casos") + ggtitle("Casos por população e ano")

# Personalizar a aparência do gráfico
grafico <- grafico + theme(panel.background = element_rect(fill = "white"),
                          panel.grid.major = element_line(colour = "gray"),
                          panel.grid.minor = element_blank(),
                          axis.line = element_line(colour = "black"),
                          legend.position = "top")

# Mostrar gráfico
grafico
```



```
Warning message:
"Use of `breast_cancer.df$pop` is discouraged.
i Use `pop` instead."
Warning message:
"Use of `breast_cancer.df$n_cases` is discouraged.
i Use `n_cases` instead."
Warning message:
"Use of `breast_cancer.df$year` is discouraged.
i Use `year` instead."
Casos por população e ano
```

