Package ‘ggrisk’

August 10, 2020

Title Risk Score Plot for Cox Regression

Version 1.2

Description The risk plot may be one of the most commonly used figures in tumor genetic data analysis. We can conclude the following two points: Comparing the prediction results of the model with the real survival situation to see whether the survival rate of the high-risk group is lower than that of the low-level group, and whether the survival time of the high-risk group is shorter than that of the low-risk group. The other is to compare the heat map and scatter plot to see the correlation between the predictors and the outcome.

License GPL-2

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Depends R (>= 2.10)

Imports ggplot2, survival, egg, do, set, cutoff, fastStat, grid, rms, nomogramFormula

URL https://github.com/yikeshu0611/ggrisk

BugReports https://github.com/yikeshu0611/ggrisk/issues

NeedsCompilation no

Author Jing Zhang [aut, cre],
    Zhi Jin [aut]

Maintainer Jing Zhang <zj391120@163.com>

Repository CRAN

Date/Publication 2020-08-10 10:40:06 UTC

R topics documented:

  ggrisk ............................................................... 2
  LIRI ................................................................. 8
  two_scatter ......................................................... 8
Description

Risk Score Plot for Cox Regression

Usage

```
ggrisk(
  fit,
  heatmap.genes = NULL,
  new.data = NULL,
  code.0 = "Alive",
  code.1 = "Dead",
  code.highrisk = "High",
  code.lowrisk = "Low",
  cutoff.show = TRUE,
  cutoff.value = "median",
  cutoff.x = NULL,
  cutoff.y = NULL,
  cutoff.label = NULL,
  title.A.ylab = "Risk Score",
  title.B.ylab = "Survival Time",
  title.A.legend = "Risk Group",
  title.B.legend = "Status",
  title.C.legend = "Expression",
  size.ABC = 1.5,
  size.ylab.title = 14,
  size.Atext = 11,
  size.Btext = 11,
  size.Ctext = 11,
  size.yticks = 0.5,
  size.yline = 0.5,
  size.points = 2,
  size.dashline = 1,
  size.cutoff = 5,
  size.legendtitle = 13,
  size.legendtext = 12,
  color.A = c(low = "blue", high = "red"),
  color.B = c(code.0 = "blue", code.1 = "red"),
  color.C = c(low = "blue", median = "white", high = "red"),
  vjust.A.ylab = 1,
  vjust.B.ylab = 2,
  family = "sans",
  expand.x = 3,
)```
relative_heights = c(0.1, 0.1, 0.01, 0.15)
)

Arguments

- **fit**: cox regression results of coxph() from 'survival' package or cph() from 'rms' package
- **heatmap.genes**: (optional) numeric variables. Name for genes
- **new.data**: new data for validation
- **code.0**: string. Code for event 0. Default is 'Alive'
- **code.1**: string. Code for event 1. Default is 'Dead'
- **code.highrisk**: string. Code for highrisk in risk score. Default is 'High'
- **code.lowrisk**: string. Code for lowrisk in risk score. Default is 'Low'
- **cutoff.show**: logical, whether to show text for cutoff in figure A. Default is TRUE
- **cutoff.value**: string, which can be 'median', 'roc' or 'cutoff'. Even you can define it by yourself
- **cutoff.x**: numeric (optional), ordination x for cutoff text
- **cutoff.y**: numeric (optional), ordination y for cutoff text
- **cutoff.label**: (should be) string. Define cutoff label by yourself
- **title.A.ylab**: string, y-lab title for figure A. Default is 'Risk Score'
- **title.B.ylab**: string, y-lab title for figure B. Default is 'Survival Time'
- **title.A.legend**: string, legend title for figure A. Default is 'Risk Group'
- **title.B.legend**: string, legend title for figure B. Default is 'Status'
- **title.C.legend**: string, legend title for figure C. Default is 'Expression'
- **size.ABC**: numeric, size for ABC. Default is 1.5
- **size.ylab.title**: numeric, size for y-axis label title. Default is 14
- **size.Atext**: numeric, size for y-axis text in figure A. Default is 11
- **size.Btext**: numeric, size for y-axis text in figure B. Default is 11
- **size.Ctext**: numeric, size for y-axis text in figure C. Default is 11
- **size.yticks**: numeric, size for y-axis ticks. Default is 0.5
- **size.yline**: numeric, size for y-axis line. Default is 0.5
- **size.points**: numeric, size for scatter points. Default is 2
- **size.dashline**: numeric, size for dashline. Default is 1
- **size.cutoff**: numeric, size for cutoff text. Default is 5
- **size.legendtitle**: numeric, size for legend title. Default is 13
- **size.legendtext**: numeric, size for legend text. Default is 12
- **color.A**: color for figure A. Default is low = 'blue', high = 'red'
color.B  color for figure B. Default is code.0 = 'blue', code.1 = 'red'
color.C  color for figure C. Default is low = 'blue', median = 'white', high = 'red'
vjust.A.ylab numeric, vertical just for y-label in figure A. Default is 1
vjust.B.ylab numeric, vertical just for y-label in figure B. Default is 2
family family, default is sans
expand.x numeric, expand for x-axis
relative_heights numeric, relative heights for figure A, B, colored side bar and heatmap. Default is 0.1 0.1 0.01 and 0.15

**Value**

A risk score picture

**Examples**

```r
library(rms)
library(ggrisk)
fit <- cph(Surv(time,status)~ANLN+CENPA+GPR182+BCO2,LIRI)
ggrisk(fit,
   cutoff.value='median',
   cutoff.x = 145,
   cutoff.y = -0.8)

#more detailed example
#plot
ggrisk(fit)

#heatmap.genes
ggrisk(fit,
   heatmap.genes=c('GPR182','CENPA','BCO2'))

#cutoff
ggrisk(fit,
   cutoff.value='median') #default
ggrisk(fit,
   cutoff.value='roc')
ggrisk(fit,
   cutoff.value='cutoff')
ggrisk(fit,
   cutoff.value=-1)
ggrisk(fit,
   cutoff.value='median',
   cutoff.x = 145,
   cutoff.y = -0.8)
ggrisk(fit,
   cutoff.value='median',
   cutoff.x = 145,
   cutoff.y = -0.8,
```
cutoff.label='This is cutoff')
#
#code for 0 and 1
#code for high and low risk group
#title
#size

ggrisk(fit,  
cutoff.value='median',  
cutoff.x = 145,  
cutoff.y = -0.8,  
code.0 = 'Still Alive',  
code.1 = 'Already Dead',  
code.highrisk = 'High Risk',  
code.lowrisk = 'Low Risk',  
title.A.ylab='Risk Score',  
title.B.ylab='Survival Time(year)',  
title.A.legend='Risk Group',  
title.B.legend='Status',  
title.C.legend='Expression',  
size.ABC=1.5,  
size.ylab.title=14,  
size.Atext=11,  
size.Btext=11,  
size.Ctext=11,  
size.yticks=0.5,  
size.yline=0.5,  
size.points=2,  
size.dashline=1,  
size.cutoff=5,  
size.legendtitle=13,  
size.legendtext=12,  

color.A=c(low='blue',high='red'),  
color.B=c(code.0='blue',code.1='red'),  
color.C=c(low='blue',median='white',high='red'))

#vjust
ggrisk(fit,  
cutoff.value='median',  
cutoff.x = 145,  
cutoff.y = -0.8,  
code.0 = 'Still Alive',  
code.1 = 'Already Dead',  
code.highrisk = 'High Risk',  
code.lowrisk = 'Low Risk',  
title.A.ylab='Risk Score',  
title.B.ylab='Survival Time(year)',  
title.A.legend='Risk Group',  
title.B.legend='Status',  
title.C.legend='Expression',  
size.ABC=1.5,  
size.ylab.title=14,  
size.Atext=11,  
size.Btext=11,  
size.Ctext=11,  
size.yticks=0.5,  
size.yline=0.5,  
size.points=2,  
size.dashline=1,  
size.cutoff=5,  
size.legendtitle=13,  
size.legendtext=12,  

color.A=c(low='blue',high='red'),  
color.B=c(code.0='blue',code.1='red'),  
color.C=c(low='blue',median='white',high='red'))
size.Btext=11,
size.Ctext=11,
size.yticks=0.5,
size.yline=0.5,
size.points=2,
size.dashline=1,
size.cutoff=5,
size.legendtitle=13,
size.legendtext=12,

color.A=c(low='blue', high='red'),

color.B=c(code.0='blue', code.1='red'),

color.C=c(low='blue', median='white', high='red'),

vjust.A.ylab=1,
vjust.B.ylab=2)

# family, expand, relative height

ggrisk(fit,
cutoff.value='median',
cutoff.x = 145,
cutoff.y = -0.8,
code.0 = 'Still Alive',
code.1 = 'Already Dead',
code.highrisk = 'High Risk',
code.lowsrisk = 'Low Risk',
title.A.ylab='Risk Score',
title.B.ylab='Survival Time(year)',
title.A.legend='Risk Group',
title.B.legend='Status',
title.C.legend='Expression',
size.ABC=1.5,
size.ylab.title=14,
size.Atext=11,
size.Btext=11,
size.Ctext=11,
size.yticks=0.5,
size.yline=0.5,
size.points=2,
size.dashline=1,
size.cutoff=5,
size.legendtitle=13,
size.legendtext=12,
color.A=c(low='blue', high='red'),
color.B=c(code.0='blue', code.1='red'),
color.C=c(low='blue', median='white', high='red'),
vjust.A.ylab=1,
vjust.B.ylab=2,
family='sans',
expand.x=3,
relative_heights=c(0.1, 0.1, 0.01, 0.15))
LIRI  

**ICGC Liver Data from Japan**

**Description**
This data is a liver cancer data from Japan Data released in ICGC database ([Link](#)). It contains time, event and four genes.

**Usage**
```
data(LIRI)
```

**Format**
An object of class `data.frame` with 232 rows and 6 columns.

**Examples**
```
data(LIRI)
```

two_scatter  

**Two Scatter Plot Plot for Cox Regression**

**Description**
Two Scatter Plot Plot for Cox Regression

**Usage**
```
two_scatter(
  fit,
  new.data = NULL,
  code.0 = "Alive",
  code.1 = "Dead",
  code.highrisk = "High",
  code.lowrisk = "Low",
  cutoff.show = TRUE,
  cutoff.value = "median",
  cutoff.x,
  cutoff.y,
  cutoff.label,
  title.A.ylab = "Risk Score",
  title.B.ylab = "Survival Time",
  title.xlab = "Rank",
  title.A.legend = "Risk Group",
  title.B.legend = "Status",
)
two_scatter

size.AB = 1.5,
size.ylab.title = 14,
size.xlab.title = 14,
size.Atext = 11,
size.Btext = 11,
size.xtext = 11,
size.xyticks = 0.5,
size.xyline = 0.5,
size.points = 2,
size.dashline = 1,
size.cutoff = 5,
size.legendtitle = 13,
size.legendtext = 12,
color.A = c(low = "blue", high = "red"),
color.B = c(code.0 = "blue", code.1 = "red"),
vjust.A.ylab = 1,
vjust.B.ylab = 2,
family = "sans",
expand.x = 3
)

Arguments

fit             cox regression results of coxph() from 'survival' package or cph() from 'rms' package
new.data        new data for validation
code.0          string. Code for event 0. Default is 'Alive'
code.1          string. Code for event 1. Default is 'Dead'
code.highrisk   string. Code for highrisk in risk score. Default is 'High'
code.lowrisk    string. Code for lowrisk in risk score. Default is 'Low'
cutoff.show     logical, whether to show text for cutoff in figure A. Default is TRUE
cutoff.value    string, which can be 'median', 'roc' or 'cutoff'. Even you can define it by yourself
cutoff.x        numeric (optional), ordination x for cutoff text
cutoff.y        numeric (optional), ordination y for cutoff text
cutoff.label    (should be) string. Define cutoff label by yourself
title.A.ylab    string, y-lab title for figure A. Default is 'Riskscore'
title.B.ylab    string, y-lab title for figure B. Default is 'Survival Time'
title.xlab      string, x-lab title for figure B. Default is 'Rank'
title.A.legend  string, legend title for figure A. Default is 'Risk Group'
title.B.legend  string, legend title for figure B. Default is 'Status'
size.AB         numeric, size for ABC. Default is 1.5
size.ylab.title numeric, size for y-axis label title. Default is 14
size.xlab.title
  numeric, size for x-axis lab title. Default is 11

size.Atext
  numeric, size for y-axis text in figure A. Default is 11

size.Btext
  numeric, size for y-axis text in figure B. Default is 11

size.xtext
  numeric, size for x-axis text. Default is 11

size.xyticks
  numeric, size for y-axis ticks. Default is 0.5

size.xyline
  numeric, size for y-axis line. Default is 0.5

size.points
  numeric, size for scatter points. Default is 2

size.dashline
  numeric, size for dashline. Default is 1

size.cutoff
  numeric, size for cutoff text. Default is 5

size.legendtitle
  numeric, size for legend title. Default is 13

size.legendtext
  numeric, size for legend text. Default is 12

color.A
  color for figure A. Default is low = 'blue', high = 'red'

color.B
  color for figure B. Default is code.0 = 'blue', code.1 = 'red'

vjust.A.ylab
  numeric, vertical just for y-label in figure A. Default is 1

vjust.B.ylab
  numeric, vertical just for y-label in figure B. Default is 2

family
  family, default is sans

expand.x
  numeric, expand for x-axis

Value

A riskscore picture

Examples

library(rms)
fit <- cph(Surv(time,status)~ANLN+CENPA+GPR182+BCO2,LIRI)
two_scatter(fit, 
  cutoff.value = 'median', 
  cutoff.x = 142, 
  cutoff.y = 0.5)

#more detailed example
library(ggrisk)
#plot

#regulate cutoff
##hidden cutoff
two_scatter(fit, 
  cutoff.show = FALSE)
two_scatter(fit, 
  cutoff.value = 'median')
two_scatter(fit, 
  cutoff.value = 'roc')
two_scatter(fit,
cutoff.value = 'cutoff')
two_scatter(fit,
cutoff.value = -1)
two_scatter(fit,
cutoff.value = 'median',
cutoff.x = 142,
cutoff.y = -0.5)

# code for 0 and 1
two_scatter(fit,
cutoff.value = 'median',
cutoff.x = 142,
cutoff.y = -0.5,
code.0 = 'Still Alive',
code.1 = 'Dead')

# code for high and low risk group
two_scatter(fit,
cutoff.value = 'median',
cutoff.x = 142,
cutoff.y = -0.5,
code.0 = 'Still Alive',
code.1 = 'Dead',
code.highrisk = 'High Group',
code.lowrisk = 'Low Group')

# title for legend, x and y lab
two_scatter(fit,
cutoff.value = 'median',
cutoff.x = 142,
cutoff.y = -0.5,
code.0 = 'Still Alive',
code.1 = 'Dead',
code.highrisk = 'High Group',
code.lowrisk = 'Low Group',
title.A.legend = 'Riskscore',
title.B.legend = 'Event Status',
title.A.ylab = 'Riskscore',
title.B.ylab = 'Survival Time(year)',
title.xlab = 'This is rank')

# vertical just for y-axis lab
two_scatter(fit,
cutoff.value = 'median',
cutoff.x = 142,
cutoff.y = -0.5,
code.0 = 'Still Alive',
code.1 = 'Dead',
code.highrisk = 'High Group',
code.lowrisk = 'Low Group',
title.A.legend = 'Riskscore',
title.B.legend = 'Event Status',
title.A.ylab = 'Riskscore',
title.B.ylab = 'Survival Time(year)',
title.xlab = 'This is rank',
vjust.A.ylab = 1,
two_scatter(fit, 
  cutoff.value = 'median',
  cutoff.x = 142,
  cutoff.y = -0.5,
  code.0 = 'Still Alive',
  code.1 = 'Dead',
  code.highrisk = 'High Group',
  code.lowrisk = 'Low Group',
  title.A.legend = 'Riskscore',
  title.B.legend = 'Event Status',
  title.A.ylab = 'Riskscore',
  title.B.ylab = 'Survival Time(year)',
  title.xlab = 'This is rank',
  vjust.A.ylab = 1,
  vjust.B.ylab = 3,
  size.AB = 2,
  size.ylab.title = 14,
  size.xlab.title = 14,
  size.Atext = 12,
  size.Btext = 12,
  size.xtext = 12,
  size.xyticks = 0.5,
  size.xyline = 0.5,
  size.dashline = 1.5,
  size.points = 1,
  size.cutoff = 5,
  size.legendtitle = 14,
  size.legendtext = 13)

two_scatter(fit, 
  cutoff.value = 'median',
  cutoff.x = 142,
  cutoff.y = -0.5,
  code.0 = 'Still Alive',
  code.1 = 'Dead',
  code.highrisk = 'High Group',
  code.lowrisk = 'Low Group',
  title.A.legend = 'Riskscore',
  title.B.legend = 'Event Status',
  title.A.ylab = 'Riskscore',
  title.B.ylab = 'Survival Time(year)',
  title.xlab = 'This is rank',
  vjust.A.ylab = 1,
  vjust.B.ylab = 3,
  size.AB = 2,
  size.ylab.title = 14,
  size.xlab.title = 14,
  size.Atext = 12,
  size.Btext = 12,
  size.xtext = 12,
  size.xyticks = 0.5,
two_scatter

size.xyline = 0.5,
size.dashline = 1.5,
size.points = 1,
size.cutoff = 5,
size.legendtitle = 14,
size.legendtext = 13,
color.A = c(low='green', high='red'),
color.B = c(code.0='green', code.1='red'))

# famli and expand
two_scatter(fit,
cutoff.value = 'median',
cutoff.x = 142,
cutoff.y = -0.5,
code.0 = 'Still Alive',
code.1 = 'Dead',
code.highrisk = 'High Group',
code.lowrisk = 'Low Group',
title.A.legend = 'Riskscore',
title.B.legend = 'Event Status',
title.A.ylab = 'Riskscore',
title.B.ylab = 'Survival Time(year)',
title.xlab = 'This is rank',
vjust.A.ylab = 1,
vjust.B.ylab = 3,
size.AB = 2,
size.ylab.title = 14,
size.xlab.title = 14,
size.Atext = 12,
size.Btext = 12,
size.xtext = 12,
size.xyticks = 0.5,
size.xyline = 0.5,
size.dashline = 1.5,
size.points = 1,
size.cutoff = 5,
size.legendtitle = 14,
size.legendtext = 13,
color.A = c(low='green', high='red'),
color.B = c(code.0='green', code.1='red'),
family = 'sans', # sans for Arial, serif for Times New Roman
expand.x=10)
Index

* datasets
  LIRI, 8

ggrisk, 2
LIRI, 8
two_scatter, 8