

Package ‘ggrisk’

October 13, 2022

Title Risk Score Plot for Cox Regression

Version 1.3

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, grid, rms,
nomogramFormula, reshape2

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

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

NeedsCompilation no

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`ggrisk`*Risk Score Plot for Cox Regression*

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

<code>fit</code>	cox regression results of <code>coxph()</code> from 'survival' package or <code>cph()</code> from 'rms' package
<code>heatmap.genes</code>	(optional) numeric variables. Name for genes
<code>new.data</code>	new data for validation
<code>code.0</code>	string. Code for event 0. Default is 'Alive'
<code>code.1</code>	string. Code for event 1. Default is 'Dead'
<code>code.highrisk</code>	string. Code for highrisk in risk score. Default is 'High'
<code>code.lowrisk</code>	string. Code for lowrisk in risk score. Default is 'Low'
<code>cutoff.show</code>	logical, whether to show text for cutoff in figure A. Default is TRUE
<code>cutoff.value</code>	string, which can be 'median', 'roc' or 'cutoff'. Even you can define it by yourself
<code>cutoff.x</code>	numeric (optional), ordination x for cutoff text
<code>cutoff.y</code>	numeric (optional), ordination y for cutoff text
<code>cutoff.label</code>	(should be) string. Define cutoff label by yourself
<code>title.A.ylab</code>	string, y-lab title for figure A. Default is 'Risk Score'
<code>title.B.ylab</code>	string, y-lab title for figure B. Default is 'Survival Time'
<code>title.A.legend</code>	string, legend title for figure A. Default is 'Risk Group'
<code>title.B.legend</code>	string, legend title for figure B. Default is 'Status'
<code>title.C.legend</code>	string, legend title for figure C. Default is 'Expression'
<code>size.ABC</code>	numeric, size for ABC. Default is 1.5
<code>size.ylab.title</code>	numeric, size for y-axis label title. Default is 14
<code>size.Atext</code>	numeric, size for y-axis text in figure A. Default is 11
<code>size.Btext</code>	numeric, size for y-axis text in figure B. Default is 11
<code>size.Ctext</code>	numeric, size for y-axis text in figure C. Default is 11
<code>size.yticks</code>	numeric, size for y-axis ticks. Default is 0.5
<code>size.yline</code>	numeric, size for y-axis line. Default is 0.5
<code>size.points</code>	numeric, size for scatter points. Default is 2
<code>size.dashline</code>	numeric, size for dashline. Default is 1
<code>size.cutoff</code>	numeric, size for cutoff text. Default is 5
<code>size.legendtitle</code>	numeric, size for legend title. Default is 13
<code>size.legendtext</code>	numeric, size for legend text. Default is 12
<code>color.A</code>	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

```
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
ggrisk(fit,
      cutoff.value='median',
      cutoff.x = 145,
      cutoff.y = -0.8,
      code.0 = 'Still Alive',
      code.1 = 'Already Dead')

#code for high and low risk group
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
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
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
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'),
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.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.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",
```



```

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

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

```
                vjust.B.ylab = 3)
#size
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
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'))
#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)
```

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* **datasets**

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