

# Package ‘ggrisk’

February 9, 2020

**Title** Risk Score Plot for Cox Regression

**Version** 1.0

**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** 6.1.1

**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

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**Repository** CRAN

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ggrisk *Risk Score Plot for Cox Regression*

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### Description

Risk Score Plot for Cox Regression

### Usage

```
ggrisk(data, time, event, heatmap.genes, 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.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

data	dataframe data
time	numeric variable. Name for following time
event	must be numeric variable. Name for event, which must be coded as 0 and 1
heatmap.genes	(optional) numeric variables. Name for genes
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'

<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'
<code>color.B</code>	color for figure B. Default is code.0 = 'blue', code.1 = 'red'
<code>color.C</code>	color for figure C. Default is low = 'blue', median = 'white', high = 'red'
<code>vjust.A.ylab</code>	numeric, vertical just for y-label in figure A. Default is 1
<code>vjust.B.ylab</code>	numeric, vertical just for y-label in figure B. Default is 2
<code>family</code>	family, default is sans
<code>expand.x</code>	numeric, expand for x-axis
<code>relative_heights</code>	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**

```
ggrisk(data=LIRI,time='time',event='status',
        cutoff.value='median',
        cutoff.x = 145,
        cutoff.y = -0.8)
```

```
#more detailed example
library(ggrisk)
```

```
#plot
ggrisk(data=LIRI,time='time',event='status')

#heatmap.genes
ggrisk(data=LIRI,time='time',event='status',
       heatmap.genes=c('GPR182','CENPA','BCO2'))

#cutoff
ggrisk(data=LIRI,time='time',event='status',
       cutoff.value='median') #default
ggrisk(data=LIRI,time='time',event='status',
       cutoff.value='roc')
ggrisk(data=LIRI,time='time',event='status',
       cutoff.value='cutoff')
ggrisk(data=LIRI,time='time',event='status',
       cutoff.value=-1)
ggrisk(data=LIRI,time='time',event='status',
       cutoff.value='median',
       cutoff.x = 145,
       cutoff.y = -0.8)
ggrisk(data=LIRI,time='time',event='status',
       cutoff.value='median',
       cutoff.x = 145,
       cutoff.y = -0.8,
       cutoff.label='This is cutoff')

#code for 0 and 1
ggrisk(data=LIRI,time='time',event='status',
       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(data=LIRI,time='time',event='status',
       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(data=LIRI,time='time',event='status',
       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(data=LIRI,time='time',event='status',
    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(data=LIRI,time='time',event='status',
    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(data=LIRI,time='time',event='status',
       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(data=LIRI,time='time',event='status',
       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))
```

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LIRI

*ICGC Liver Data from Japan*

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### 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(data, time, event, 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**

data	dataframe data
time	numeric variable. Name for following time
event	must be numeric variable. Name for event, which must be coded as 0 and 1
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

```

two_scatter(data=LIRI,time='time',event='status',
            cutoff.value = 'median',
            cutoff.x = 142,
            cutoff.y = -0.5)

#more detailed example
library(ggrisk)
#plot
two_scatter(data=LIRI,time='time',event='status')
#regulate cutoff
##hidden cutoff
two_scatter(data=LIRI,time='time',event='status',
            cutoff.show = FALSE)
two_scatter(data=LIRI,time='time',event='status',

```

```

        cutoff.value = 'median')
two_scatter(data=LIRI,time='time',event='status',
            cutoff.value = 'roc')
two_scatter(data=LIRI,time='time',event='status',
            cutoff.value = 'cutoff')
two_scatter(data=LIRI,time='time',event='status',
            cutoff.value = -1)
two_scatter(data=LIRI,time='time',event='status',
            cutoff.value = 'median',
            cutoff.x = 142,
            cutoff.y = -0.5)
#code for 0 and 1
two_scatter(data=LIRI,time='time',event='status',
            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(data=LIRI,time='time',event='status',
            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(data=LIRI,time='time',event='status',
            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(data=LIRI,time='time',event='status',
            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(data=LIRI,time='time',event='status',
            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(data=LIRI,time='time',event='status',
            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(data=LIRI,time='time',event='status',
  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 Arail, serif for Times New Roman
  expand.x=10)

```

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