

# 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

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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(  
  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))
```

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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(  
  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)
```

# Index

\* **datasets**

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