

# Creating Survival Plots

## Informative and Elegant with *survminer*

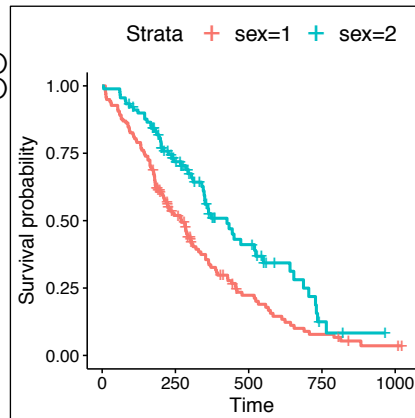
### Survival Curves

The **ggsurvplot()** function creates **ggplot2** plots from **survfit** objects.

```
library("survival")
fit <- survfit(Surv(time,status) ~ sex, data = lung)

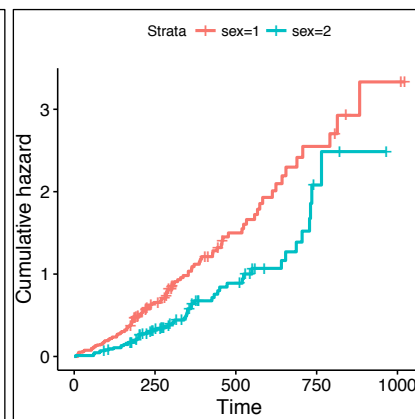
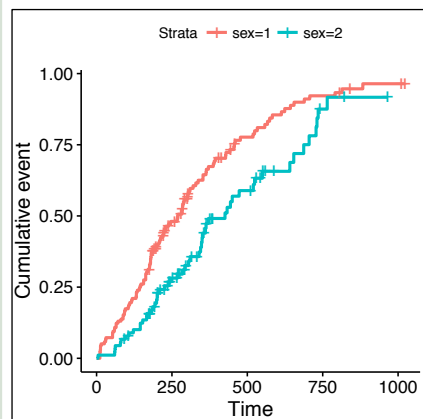
class(fit)
## [1] "survfit"

library("survminer")
ggsurvplot(fit, data = lung)
```



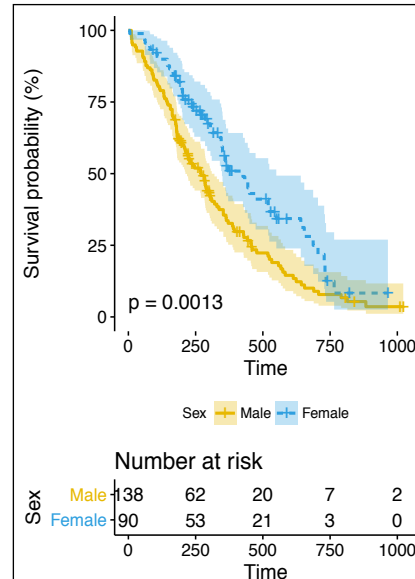
Use the **fun** argument to set the transformation of the survival curve. E.g. **"event"** for cumulative events, **"cumhaz"** for the cumulative hazard function or **"pct"** for survival probability in percentage.

```
ggsurvplot(fit, data = lung, fun="event")
ggsurvplot(fit, data = lung, fun="cumhaz")
```



With lots of graphical parameters you have full control over look and feel of the survival plots; position and content of the legend; additional annotations like p-value, title, subtitle.

```
ggsurvplot(fit, data = lung,
  conf.int = TRUE,
  pval = TRUE,
  fun = "pct",
  size = 1,
  linetype = "strata",
  palette = c("#E7B800", "#2E9FDF"),
  legend = "bottom",
  legend.title = "Sex",
  legend.labs = c("Male", "Female"),
  risk.table = TRUE)
```

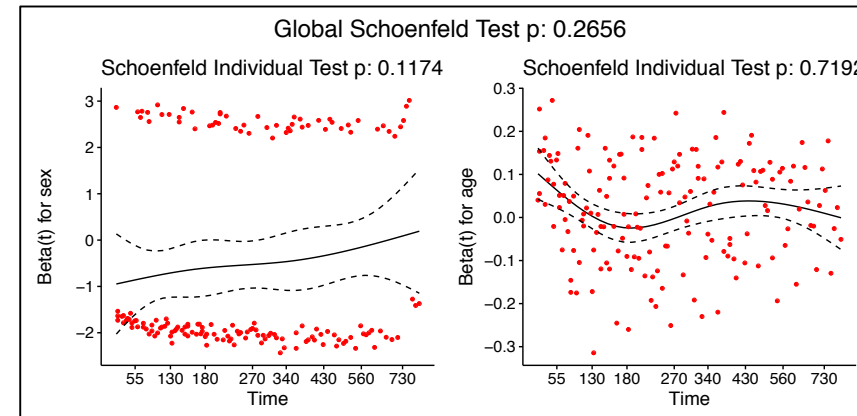


### Diagnostics of Cox Model

The function **cox.zph()** from **survival** package may be used to test the proportional hazards assumption for a Cox regression model fit. The graphical verification of this assumption may be performed with the function **ggcoxzph()** from the **survminer** package. For each covariate it produces plots with scaled Schoenfeld residuals against the time.

```
library("survival")
fit <- coxph(Surv(time, status) ~ sex + age, data = lung)
fetest <- cox.zph(fit)
fetest
```

```
##               rho chisq    p
## sex          0.1236 2.452 0.117
## age         -0.0275 0.129 0.719
## GLOBAL             NA 2.651 0.266
library("survminer")
ggcoxzph(fetest)
```

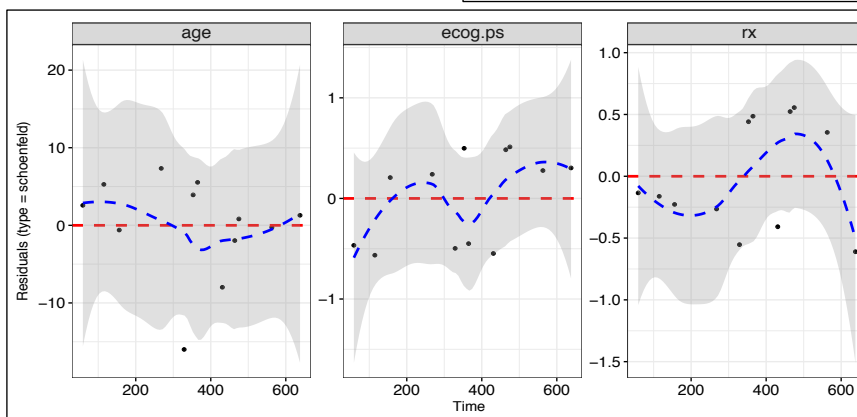
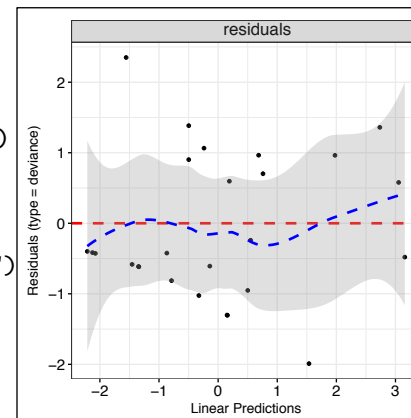


The function **ggcoxdiagnostics()** plots different types of residuals as a function of time, linear predictor or observation id. The type of residual is selected with **type** argument. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", and "scaledsch". The **ox.scale** argument defines what shall be plotted on the OX axis. Possible values are "linear.predictions", "observation.id", "time". Logical arguments **hline** and **sline** may be used to add horizontal line or smooth line to the plot.

```
library("survival")
library("survminer")
fit <- coxph(Surv(time, status) ~ sex + age, data = lung)
```

```
ggcoxdiagnostics(fit,
  type = "deviance",
  ox.scale = "linear.predictions")
```

```
ggcoxdiagnostics(fit,
  type = "schoenfeld",
  ox.scale = "time")
```



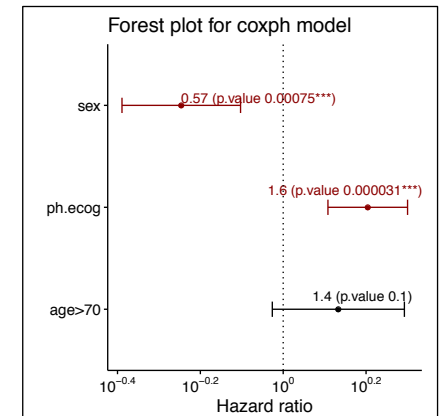
### Summary of Cox Model

The function **ggforest()** from the **survival** package creates a forest plot for a Cox regression model fit. Hazard ratio estimates along with confidence intervals and p-values are plotted for each variable.

```
library("survival")
library("survminer")
lung$age <- ifelse(lung$age > 70, ">70", "<= 70")
fit <- coxph( Surv(time, status) ~ sex + ph.ecog + age, data = lung)
fit
```

```
## Call:
## coxph(formula = Surv(time, status) ~ sex+ph.ecog+age, data=lung)
##
##               coef exp(coef) se(coef)      z      p
## sex          -0.567    0.567    0.168 -3.37 0.00075
## ph.ecog       0.470    1.600    0.113  4.16 3.1e-05
## age>70        0.307    1.359    0.187  1.64 0.10175
```

```
ggforest(fit)
```



The function **ggcoxadjustedcurves()** from the **survminer** package plots Adjusted Survival Curves for Cox Proportional Hazards Model. Adjusted Survival Curves show how a selected factor influences survival estimated from a Cox model.

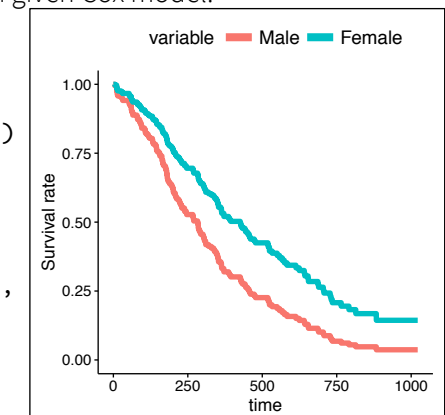
Note that these curves differ from Kaplan Meier estimates since they present expected survival based on given Cox model.

```
library("survival")
library("survminer")
```

```
lung$sex <- ifelse(lung$sex == 1,
  "Male", "Female")
```

```
fit <- coxph(Surv(time, status) ~ sex + ph.ecog + age,
  data = lung)
```

```
ggcoxadjustedcurves(fit, data=lung,
  variable=lung$sex)
```



Note that it is not necessary to include the grouping factor in the Cox model. Survival curves are estimated from Cox model for each group defined by the factor independently.

```
lung$age3 <- cut(lung$age,
  c(35,55,65,85))
```

```
ggcoxadjustedcurves(fit, data=lung,
  variable=lung$age3)
```

