

Creating Survival Plots

Informative and Elegant with *survminer*

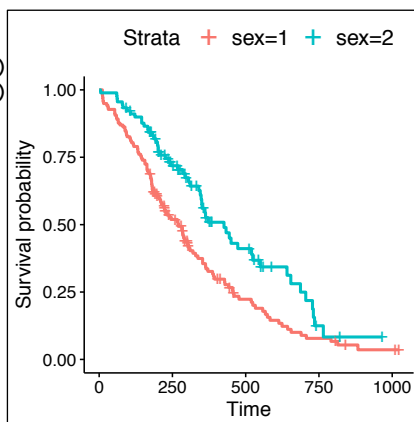
Survival Curves

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

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

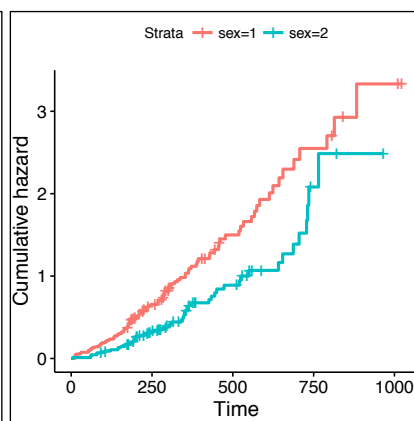
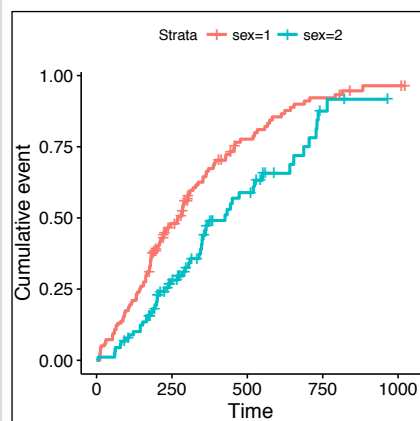
class(fit)
## [1] "survfit"

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



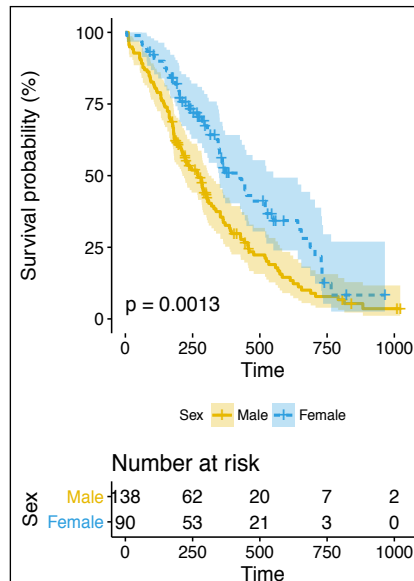
Use the `fun` argument to set the transformation of the survival curve. E.g. `"event"` for cumulative events, `"cumhaz"` for the cumulative hazard function or `"pct"` for survival probability in percentage.

```
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.

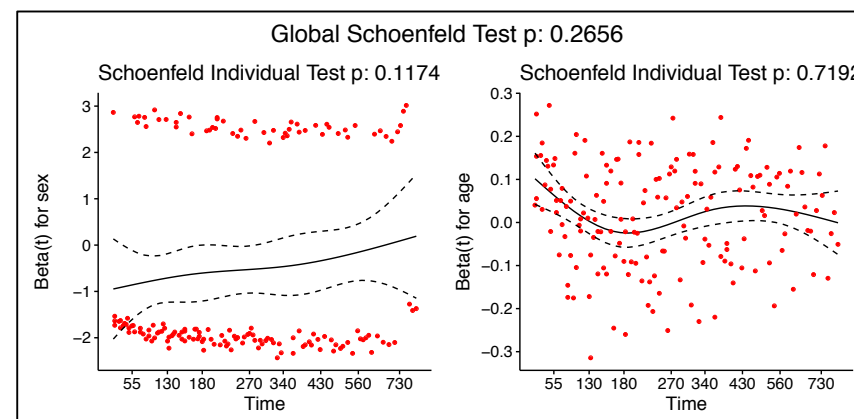
```
ggsurvplot(fit, data = lung,
conf.int = TRUE,
pval = TRUE,
fun = "pct",
risk.table = TRUE,
size = 1,
linetype = "strata",
palette = c("#E7B800", "#2E9FDF"),
legend = "bottom",
legend.title = "Sex",
legend.labs = c("Male", "Female"))
```



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)
fctest <- cox.zph(fit)
fctest
##          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(fctest)
```



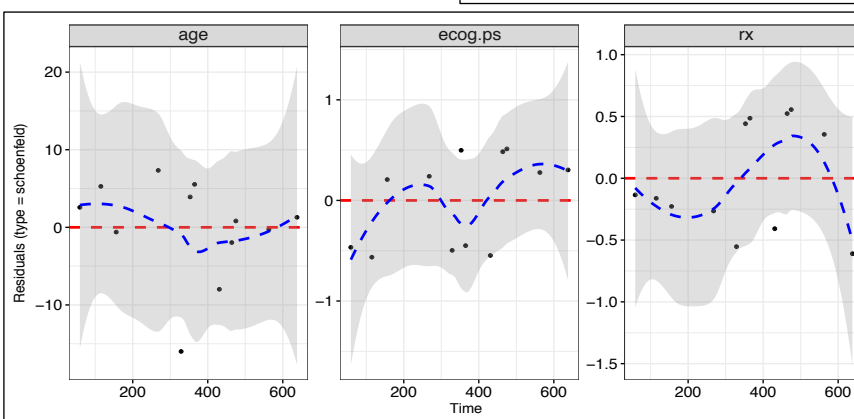
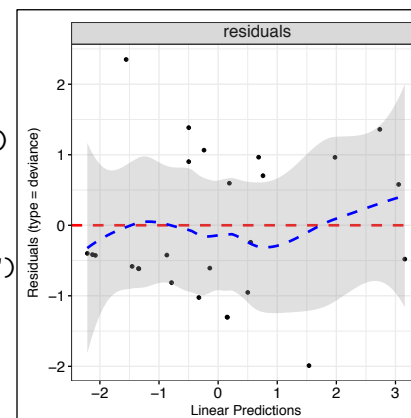
The function `ggcoxdiagnostics()` plots different types of residuals as a function of time, linear predictor or observation id. The type of residual is selected with `type` argument. Possible values are `"martingale"`, `"deviance"`, `"score"`, `"schoenfeld"`, `"dfbeta"`, `"dfbetas"`, and `"scaledsch"`.

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

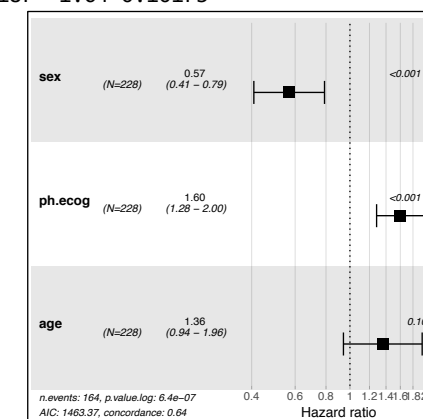
The function `ggforest()` from the `survminer` package creates a forest plot for a Cox regression model fit. Hazard ratio estimates along with confidence intervals and p-values are plotted for each variable.

```
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
##
```

```
## Likelihood ratio test=31.6 on
## n= 227, number of events= 164
```

```
ggforest(fit)
```



The function `ggadjustedcurves()` 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.

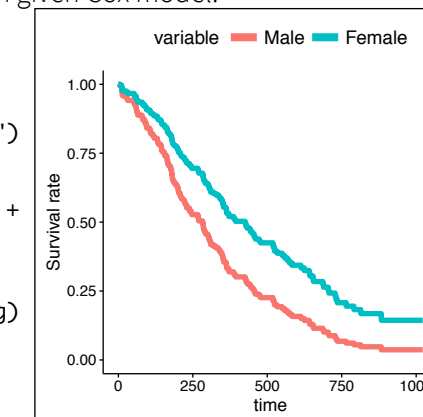
Note that these curves differ from Kaplan Meier estimates since they present expected survival based on given Cox model.

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

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

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

```
ggcoxadjustedcurves(fit, data=lung)
```



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="lage3")
```

