Creating Survival Plots
Informative and Elegant with *survminer*
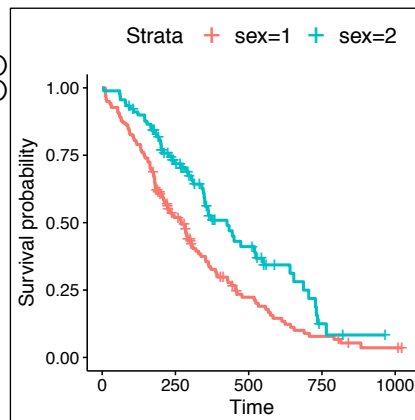
Survival Curves

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

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

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

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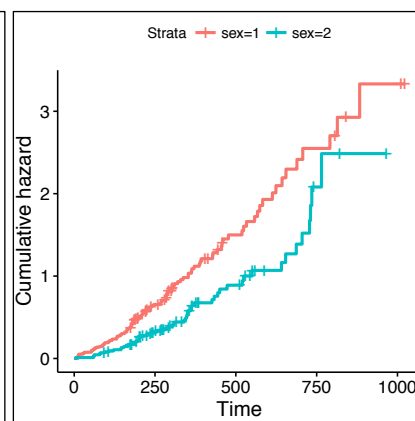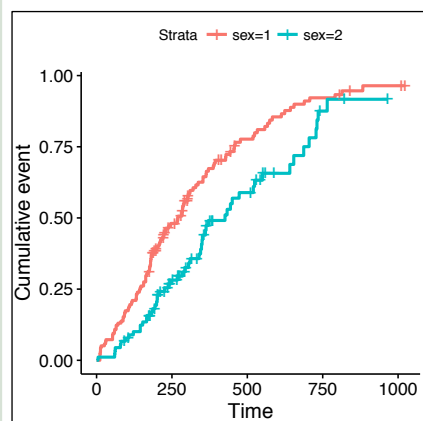

Use the **fun** argument to set the transformation of the survival curve. E.g. **"event"** for cumulative events, **"cumhaz"** for the cumulative hazard function or **"pct"** for survival probability in percentage.

```r
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.

```r
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"))
```
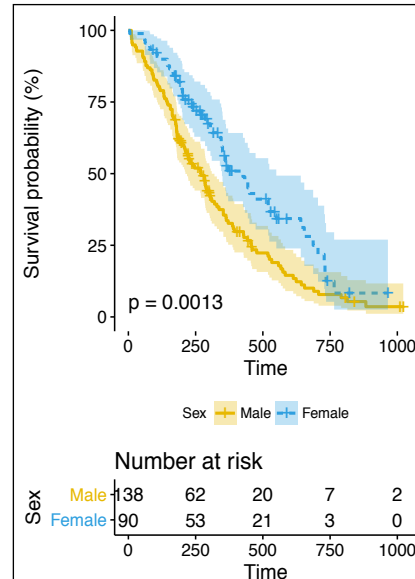

Diagnostics of Cox Model

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.

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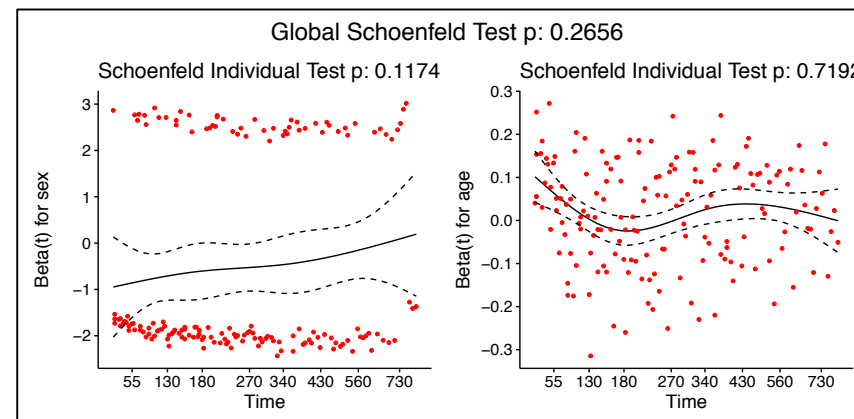

The function **ggcoxdiagnostics()** plots different types of residuals as a function of time, linear predictor or observation id. The type of residual is selected with **type** argument. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta"', "dfbetas", and "scaledsch".

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.

```r
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")
```
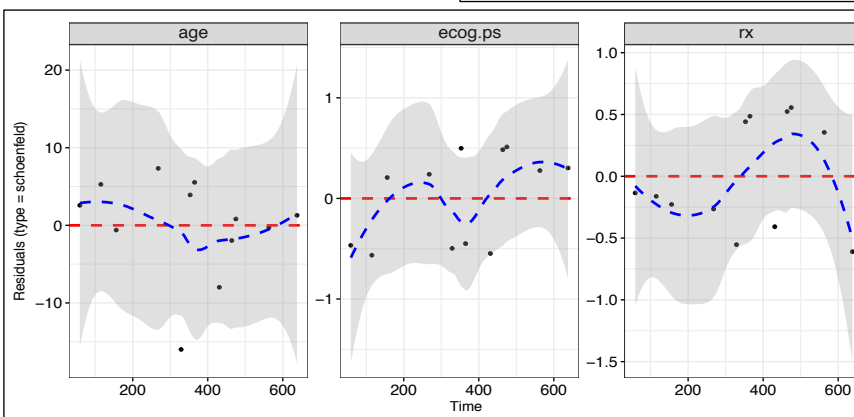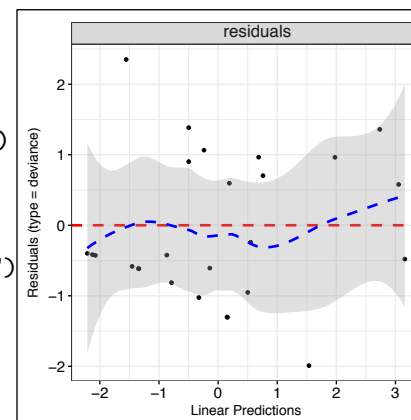

Summary of Cox Model

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 plotter for each variable.

```r
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)
```
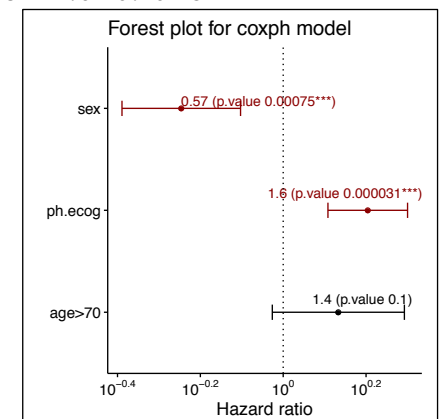

The function **ggcoxadjustedcurves()** from the **survminer** package plots Adjusted Survival Curves for Cox Proportional Hazards Model. Adjusted Survival Curves show how a selected factor influences survival estimated from a Cox model.
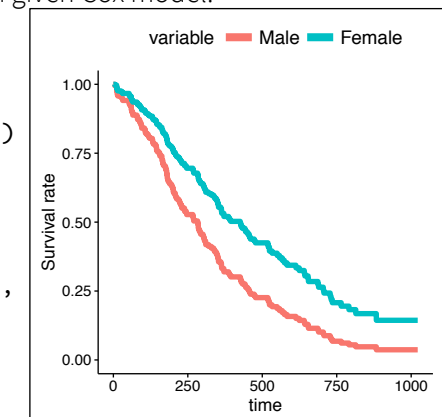
Note that these curves differ from Kaplan Meier estimates since they present expected ssurvival based on given Cox model.

```r
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.

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

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