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("#E7E7E7", "#208200"), legend = "bottom", legend.title = "Sex", legendlabs = 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)
ggcoxzph(fit)
```

```
Global Schoenfeld Test p: 0.2656
Schoenfeld Individual Test p: 0.1174
Schoenfeld Individual Test p: 0.7192
```

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".

```
library("survival")
ggcoxdiagnostics(fit, data = lung)
ggcoxdiagnostics(fit, type = "deviance")
ggcoxdiagnostics(fit, type = "schoenfeld")
ggcoxdiagnostics(fit, type = "dfbeta")
ggcoxdiagnostics(fit, type = "dfbetas")
ggcoxdiagnostics(fit, type = "scaledsch")
```

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

```
## GLOBAL      NA 2.651 0.266
##           coef exp(coef) se(coef)     z       p
## sex Male    1.00  2.707e+00  0.470     2.14 1.3e-01
## Female     1.00  2.707e+00  0.470     2.14 1.3e-01
## ph.ecog    0.10  1.103e+00  0.050     2.06 1.3e-01
## age>70     1.00  2.707e+00  0.470     2.14 1.3e-01
## age<70     1.00  2.707e+00  0.470     2.14 1.3e-01
##```

```
library("survminer")
lungSage <- ifelse(lungSage == 1, "Male", "Female")
```

```
library("survminer")
library("survival")
lungSage3 <- cut(lungSage, c(35, 55, 65, 85))
ggcoxdiagnostics(fit, data = lung, variable = "age3")
```

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.

```
lungSage3 <- cut(lungSage, c(35, 55, 65, 85))
ggcoxdiagnostics(fit, data = lung, variable = "age3")
```