

University of Edinburgh, School of Mathematics
Biostatistics (MATH11230), 2021/2022

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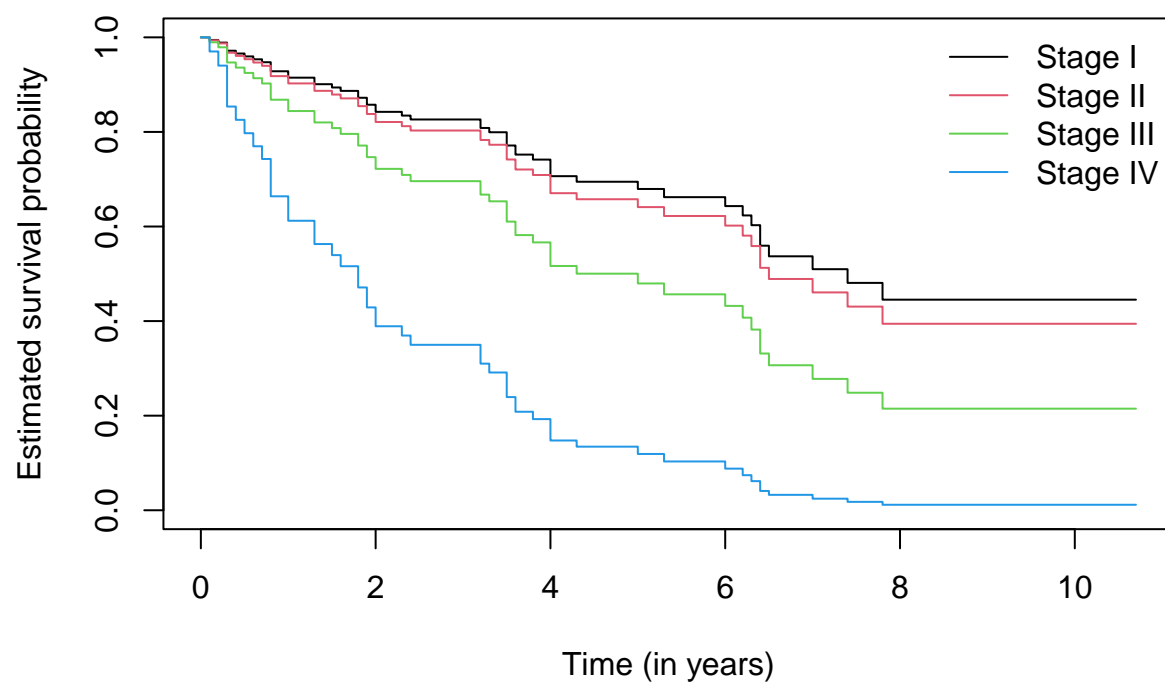
Here we reproduce the results presented in the slides.

```
require(survival)
require(KMsurv)
data(larynx)
res_1 <- coxph(Surv(time, delta) ~ as.factor(stage) + age, data = larynx)

#adjusted survival curve for the mean age
newdf <- data.frame("stage" = levels(as.factor(larynx$stage)),
                    "age" = rep(mean(larynx$age), 4))
fit <- survfit(res_1, newdata = newdf)

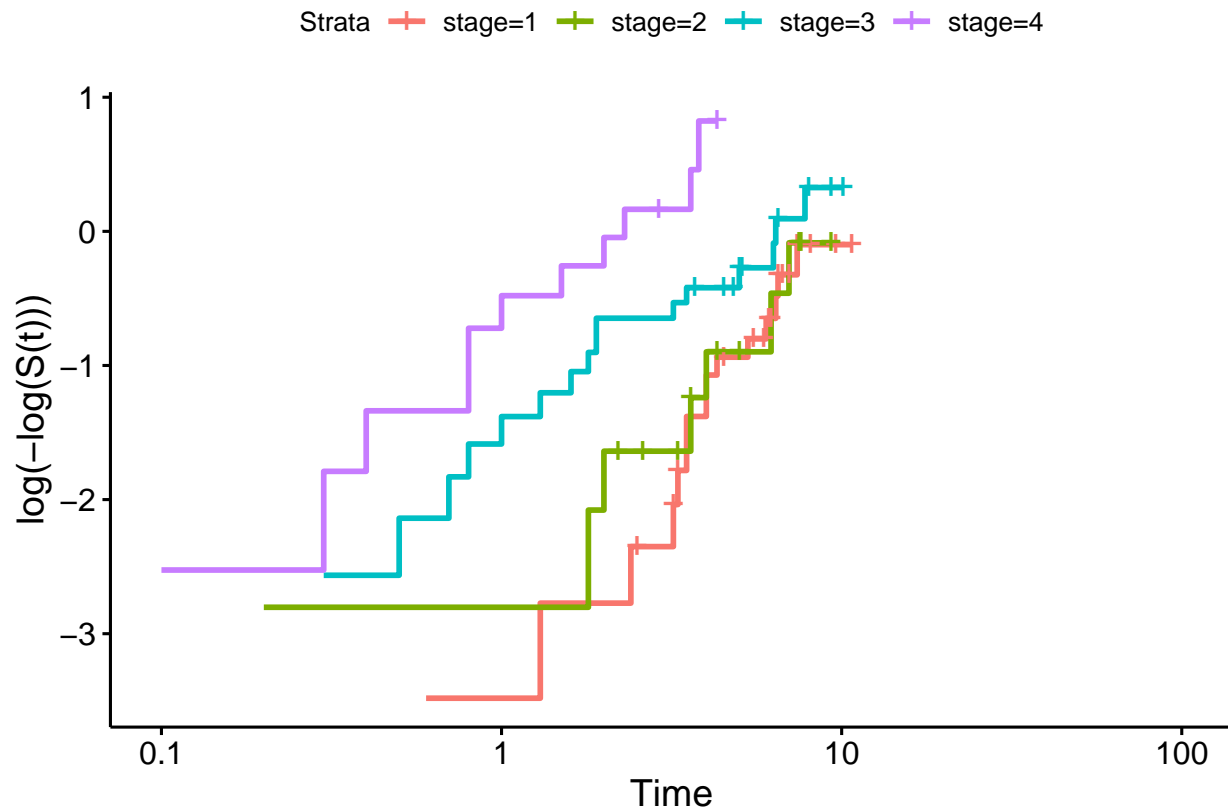
plot(fit, conf.int = FALSE, col = c(1:4),
     ylab = "Estimated survival probability",
     xlab = "Time (in years)",
     main = "Age = 64.6 years (mean age)")
legend("topright", legend = c("Stage I", "Stage II", "Stage III", "Stage IV"),
     col = c(1:4), lty = c(1,1,1,1), bty = "n")
```

Age = 64.6 years (mean age)

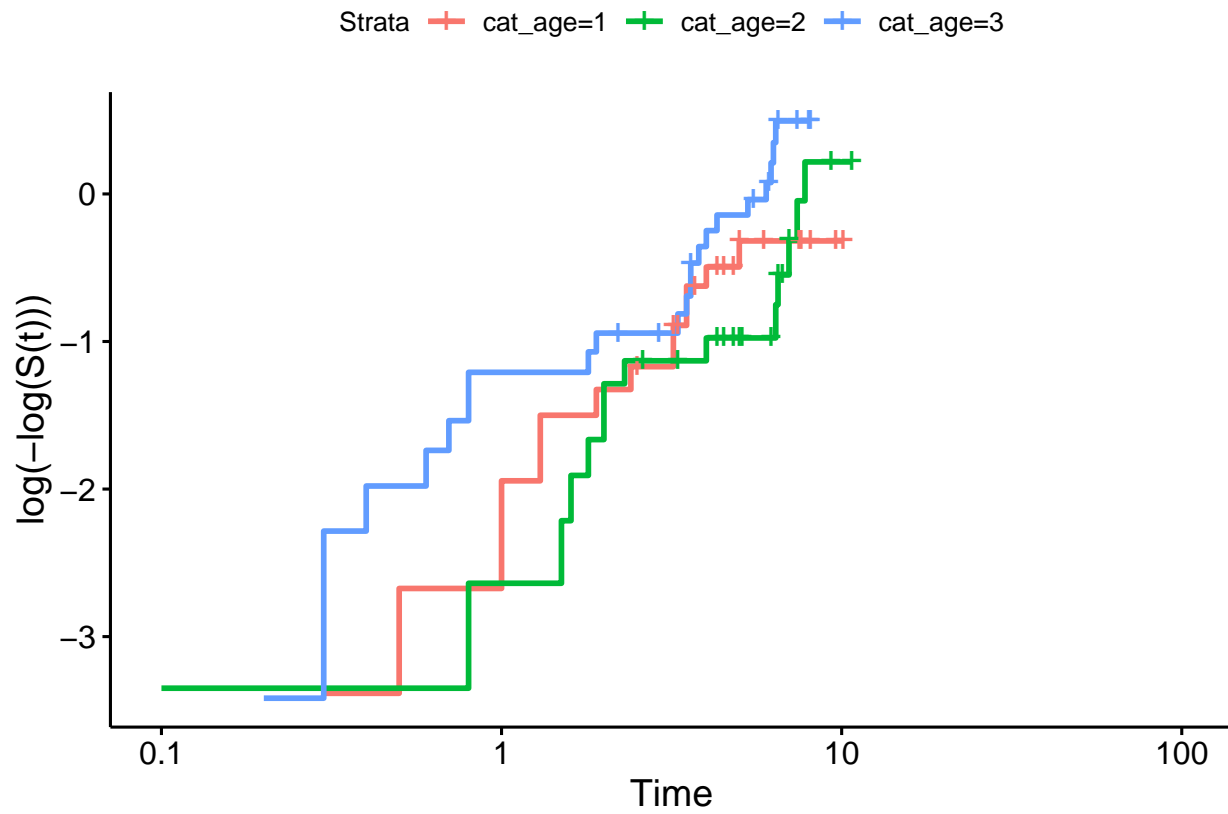


Below the code for the log cumulative hazard plot.

```
km_fit_stage <- survfit(Surv(time, delta) ~ stage, data = larynx)
require(survminer)
ggsurvplot(km_fit_stage, fun = "cloglog")
```

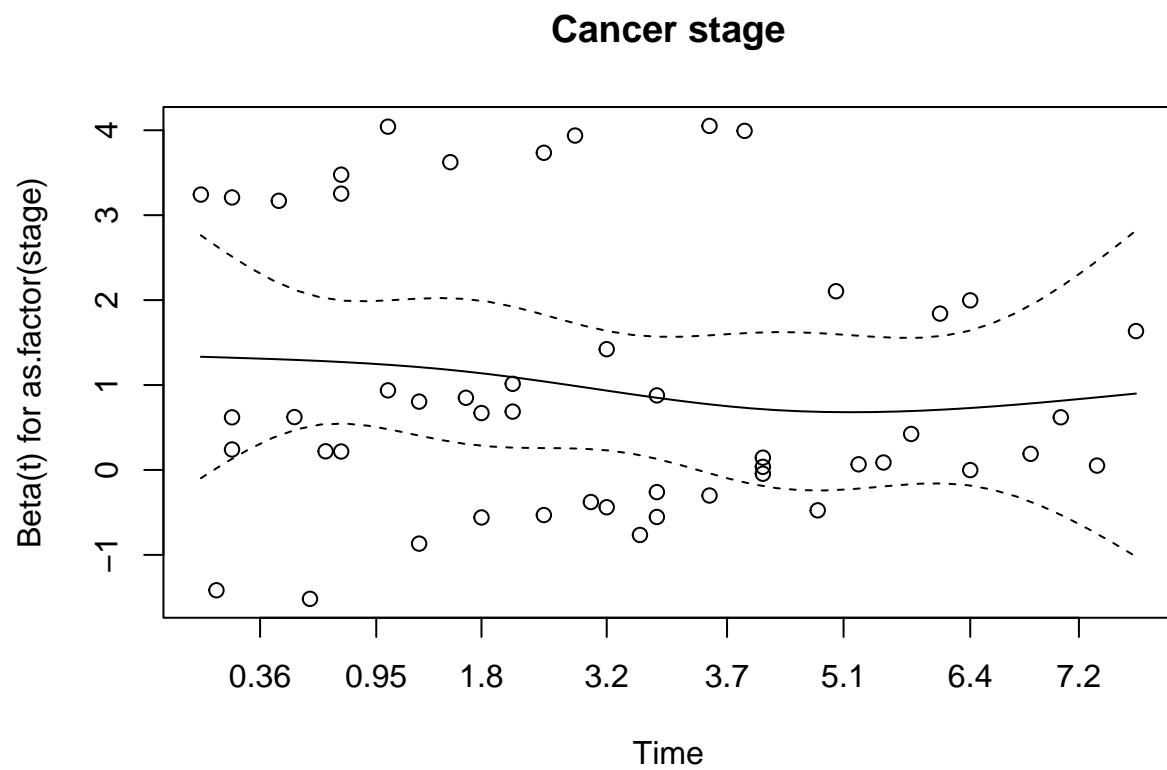


```
larynx$cat_age <- numeric(length(larynx$age))
for(i in 1:length(larynx$age)){
  if(larynx$age[i] < quantile(larynx$age, 0.33)) {larynx$cat_age[i] <- 1}
  else{
    if(larynx$age[i] >= quantile(larynx$age, 0.33) & larynx$age[i] < quantile(larynx$age, 0.66)) {larynx$cat_age[i] <- 2}
    else {larynx$cat_age[i] <- 3}
  }
}
km_fit_age <- survfit(Surv(time, delta) ~ larynx$cat_age, data = larynx)
ggsurvplot(km_fit_age, fun = "cloglog")
```

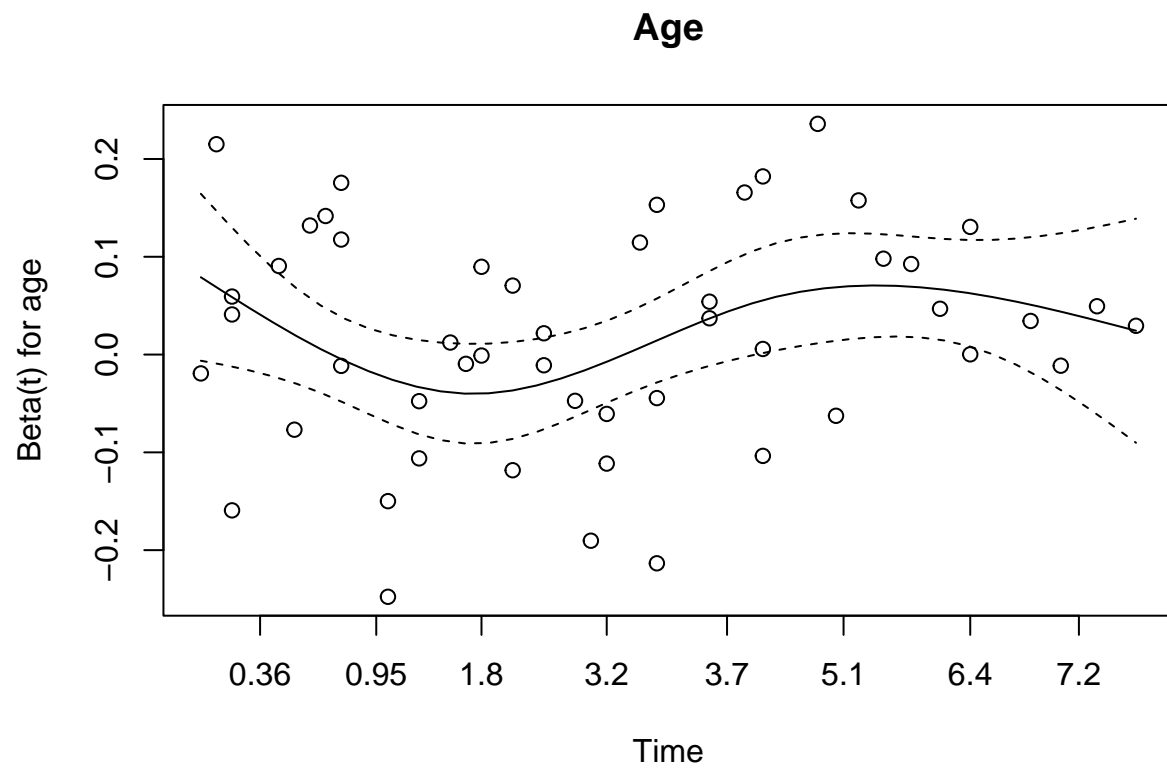


And finally the results for Schoenfeld residuals.

```
zph <- cox.zph(res_1)
plot(zph, var = 1, main = "Cancer stage")
```



```
plot(zph, var = 2, main = "Age")
```



```
zph
```

| ## | chisq | df | p |
|---------------------|-------|----|------|
| ## as.factor(stage) | 3.72 | 3 | 0.29 |
| ## age | 1.13 | 1 | 0.29 |
| ## GLOBAL | 5.14 | 4 | 0.27 |