

Lecture 24 R code

Survival Modeling

Part 1: Set up

```
# Read in srt data and set up
srt <- read.csv("~/Desktop/srt.csv")
#View(srt)
head(srt)
```

```
srt$sex = factor(srt$sex)
srt$sorb = factor(srt$sorb)
```

Set up survival analysis

```
library(survival)
library(survminer)
survobj = Surv(srt$fup,srt$status)
print(survobj)
```

```
hist(srt$fup)
```

Part 2: Kaplan-Meier estimate

```
model1 = survfit(survobj~sorb, data=srt)
summary(model1)
```

#Plot Kaplan-Meier estimate

```
ggsurvplot(model1)
```

Part 3: Done in lab: Log-Rank Test

```
survdifff(survobj~sorb,data=srt) # Test equality of treatment and placebo survival curves
```

```
survdifff(survobj~sorb+strata(sex),data=srt) # Test equality, stratified by sex
```

```
survdifff(survobj~sorb+sex,data=srt) # Test equality of all four curves
```

PART 4: Cox Proportional Hazards Models

```
model4 = coxph(survobj~sorb+tgh+dur+sex, data=srt)
plot(survfit(model4))
summary(model4)
```

```
#exp(coef(model4))
#ggsurvplot(survfit(model4, newdata = with(srt, data.frame(sex = factor(c(1, 1)),
sorb = factor(c(0,1)), #tgh = rep(mean(tgh, na.rm = TRUE), 2), dur = rep(mean(dur,
na.rm = TRUE), 2))), data=srt)
```

Part 5: Assessing PH assumption using *scaled Schoenfeld residuals then log-log plots*.

```
## Using Schoenfeld residuals
test.ph <- cox.zph(model4)
test.ph
```

```
# Plot 1 parameter at a time
plot(test.ph)
```

```
# Plot all on 1 page
ggcoxzph(test.ph)
```

```
## Using Log-Log plots
# First using sorb
model5 = survfit(survobj~sorb, data=srt)
ggsurvplot(model5, fun = "cloglog")
```

```
# Next using sex
model5 = survfit(survobj~sex,data=srt)
ggsurvplot(model5, fun = "cloglog")
```

```
##### Part 6: Assessing influence
## First using dfbetas
model4 = coxph(survobj~sorb+tgh+dur+sex, data=srt)
ggcoxdiagnostics(model4, type = "dfbeta",
  linear.predictions = FALSE, ggtheme = theme_bw())
```

```
## Next using deviance residuals
ggcoxdiagnostics(model4, type = "deviance",
  linear.predictions = FALSE, ggtheme = theme_bw())
```

```
##### Part 7: Assessing linearity of (continuous only) covariate effects
# First for tgh
ggcoxfunctional(survobj~tgh, data=srt)
```

```
# Next for dur  
ggcoxfunctional(survobj~dur, data=srt)
```

```
# Now fit GAM with nonlinear functions of dur and tgh  
model7 <- mgcv::gam(fup ~ s(dur) + sex + s(tgh) + sorb, data=srt, family=cox.ph,  
weights=status)  
plot(model7, pages=1, all.terms=TRUE)
```

```
##### Part 8: Assessing Effect modification
```

```
# Consider sex*dur  
model8 = coxph(survobj~sex+dur+sex*dur, data=srt)  
# Consider sorb*tgh  
model8 = survfit(survobj~sorb + agh + sorb*tgh, data=srt)  
ggsurvplot(model8)
```