## Start with nickel worker data.

```r
# library(survival)
# nickel <- read.table("nickel.dat", +  col.names=c("id", "icd", "exposure", "dob", "agefe", "agefml"))
# nickel$1deaths <- (nickel$icd1 %in% c(162:163)) + 1
```

## compute years from start of employment

```r
# nickel$tstart <- nickel$agefe - nickel$agefml
# nickel$tfeend <- nickel$agefml - nickel$agefe
# km.exp <- survfit(Surv(tstart, tfeend, lcdeath)~I(exposure>0), data=nickel)
```

## Log-log survivor function

```r
# plot(log(km.exp$surv[km.exp$event>0]), type="n")
# for(i in 1:2) with(km.exp[i], lines(log(time), log(-log(surv)), col=i))
# km.apefe <- survfit(Surv(tstart, tfeend, lcdeath)~ +
# cut(agefe, c(0,20,30,100))) +
# + data=nickel)
```

## get scaled Shoenfeld residuals and plot them.

```r
# scsch.res <- residuals(cox.exp.agefe, type="sca")
# plot(as.numeric(row.names(scsch.res)), scsch.res[,1])
```

## testing the proportional hazards assumption

```r
# cox.zph(cox.exp.agefe)
```

## Now consider endometrial cancer data

## This example shows how one can do conditional analysis of 1:M matched data

```r
# load("endo.RData")
```

## conditional analysis using only first control

```r
# summary(glm(cc ~ estro−1, data=endo, family=binomial))
```

## Deviance Residuals:

```
Min 1Q Median 3Q Max
−20.63 −5.15  0.59  0.92  1.38
```

## Null deviance: 87.337 on 63 degrees of freedom

## Residual deviance: 62.887 on 62 degrees of freedom

## AIC: 64.887

## Likelihood ratio test=35.4 on 1 df, p=2.76e−09

## Number of Fisher Scoring iterations: 4

## Now use coxph to do conditional analysis of complete data

## Note that OR estimate is not too much different, and standard error
## of coefficient is smaller, since we're using more data

```r
# coxph(formula = Surv(set, cc) ~ estro + strata(set), data=endo.all)
```

## coef exp(coef) se(coef) z p

```
estro  2.07  7.95  0.421 4.93 8.3e−07
```

## Likelihood ratio test=35.4 on 1 df, p=2.76e−09

```
```