

Biostatistics (MATH11230)

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Here I reproduce the results for the larynx data.

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

## Call:
## coxph(formula = Surv(time, delta) ~ as.factor(stage) + age, data = larynx)
##
##               coef exp(coef) se(coef)      z      p
## as.factor(stage)2 0.14004   1.15032  0.46249 0.303  0.7620
## as.factor(stage)3 0.64238   1.90100  0.35611 1.804  0.0712
## as.factor(stage)4 1.70598   5.50678  0.42191 4.043 5.27e-05
## age               0.01903   1.01921  0.01426 1.335  0.1820
##
## Likelihood ratio test=18.31 on 4 df, p=0.001072
## n= 90, number of events= 50

summary(res_1)

## Call:
## coxph(formula = Surv(time, delta) ~ as.factor(stage) + age, data = larynx)
##
##      n= 90, number of events= 50
##
##               coef exp(coef) se(coef)      z Pr(>|z|)
## as.factor(stage)2 0.14004   1.15032  0.46249 0.303  0.7620
## as.factor(stage)3 0.64238   1.90100  0.35611 1.804  0.0712 .
## as.factor(stage)4 1.70598   5.50678  0.42191 4.043 5.27e-05 ***
## age               0.01903   1.01921  0.01426 1.335  0.1820
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##               exp(coef) exp(-coef) lower .95 upper .95
## as.factor(stage)2      1.150      0.8693    0.4647    2.848
## as.factor(stage)3      1.901      0.5260    0.9459    3.820
## as.factor(stage)4      5.507      0.1816    2.4086   12.590
## age                    1.019      0.9811    0.9911    1.048
##
## Concordance= 0.682 (se = 0.039 )
## Likelihood ratio test= 18.31 on 4 df, p=0.001
## Wald test               = 21.15 on 4 df, p=3e-04
## Score (logrank) test = 24.78 on 4 df, p=6e-05
```

In order to apply the likelihood ratio test, let us fit a proportional hazards model that does not include the stage of the cancer as risk factor. Our null hypothesis is then: $H_0 : \beta_1 = \beta_2 = \beta_3 = 0$ against the alternative that, at least, one of the coefficients is not zero.

```
res_2 <- coxph(Surv(time, delta) ~ age, data = larynx)
res_2

## Call:
## coxph(formula = Surv(time, delta) ~ age, data = larynx)
##
##          coef exp(coef) se(coef)      z      p
## age 0.02328    1.02356  0.01449 1.607 0.108
##
## Likelihood ratio test=2.63  on 1 df, p=0.1048
## n= 90, number of events= 50

anova(res_1, res_2)

## Analysis of Deviance Table
## Cox model: response is Surv(time, delta)
## Model 1: ~ as.factor(stage) + age
## Model 2: ~ age
##      loglik  Chisq Df Pr(>|Chi|)
## 1 -187.71
## 2 -195.55 15.681  3  0.001318 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can also obtain this value manually as follows.

```
#the first is the log likelihood of a model that contains none of the risk factors,
#so we need the second one
res_1$loglik
```

```
## [1] -196.8635 -187.7074

test_stat <- 2*(res_1$loglik[2] - res_2$loglik[2])
pchisq(test_stat, df = 4 - 1, lower.tail = FALSE)

## [1] 0.001318283
```

If we want to compare non nested models, we can use the AIC or the BIC.

```
AIC(res_1)

## [1] 383.4147

-2*res_1$loglik[2] + 2*4

## [1] 383.4147

BIC(res_1)

## [1] 391.0628

-2*res_1$loglik[2] + log(sum(larynx$delta))*4

## [1] 391.0628
```

Here we reproduce the results to obtain the adjusted survival curves (under a Cox model) presented in the last slide.

```

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)

