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

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Here we 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)
## 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
                                1.01921 0.01426 1.335
## age
                      0.01903
                                                           0.1820
##
## Likelihood ratio test=18.31 on 4 df, p=0.001072
## n= 90, number of events= 50
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.
res_2 <- coxph(Surv(time, delta) ~ age, data = larynx)</pre>
res_2
## Call:
## coxph(formula = Surv(time, delta) ~ age, data = larynx)
##
##
          coef exp(coef) se(coef)
                                        z
## 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 P(>|Chi|)
## 1 -187.71
## 2 -195.55 15.681 3 0.001318 **
```

```
## ---
## Signif. codes: 0 '***' 0.001 '**' 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$loglik[2])</pre>
pchisq(test_stat, df = 4 - 1, lower.tail = FALSE)
## [1] 0.001318283
If we want to compare non nested models, we can use the AIC or the BIC.
AIC(res_1)
## [1] 383.4147
-2*res_1$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
```