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
                     0.01903
                               1.01921 0.01426 1.335
                                                        0.1820
## age
##
## 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 ***
                               1.01921 0.01426 1.335
## age
                     0.01903
                                                        0.1820
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
##
                     exp(coef) exp(-coef) lower .95 upper .95
                                   0.8693
## as.factor(stage)2
                         1.150
                                             0.4647
                                                        2.848
## as.factor(stage)3
                         1.901
                                   0.5260
                                             0.9459
                                                        3.820
## as.factor(stage)4
                         5.507
                                                       12.590
                                   0.1816
                                             2.4086
                         1.019
                                   0.9811
                                             0.9911
                                                        1.048
## age
## Concordance= 0.682 (se = 0.039)
                                            p=0.001
## Likelihood ratio test= 18.31 on 4 df,
## 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</pre>
```

```
##
## 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 '**' 0.05 '.' 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
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$stage)),</pre>
                    "age" = rep(mean(larynx$age), 4))
fit <- survfit(res_1, newdata = newdf)</pre>
```

```
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)

