Lab 10

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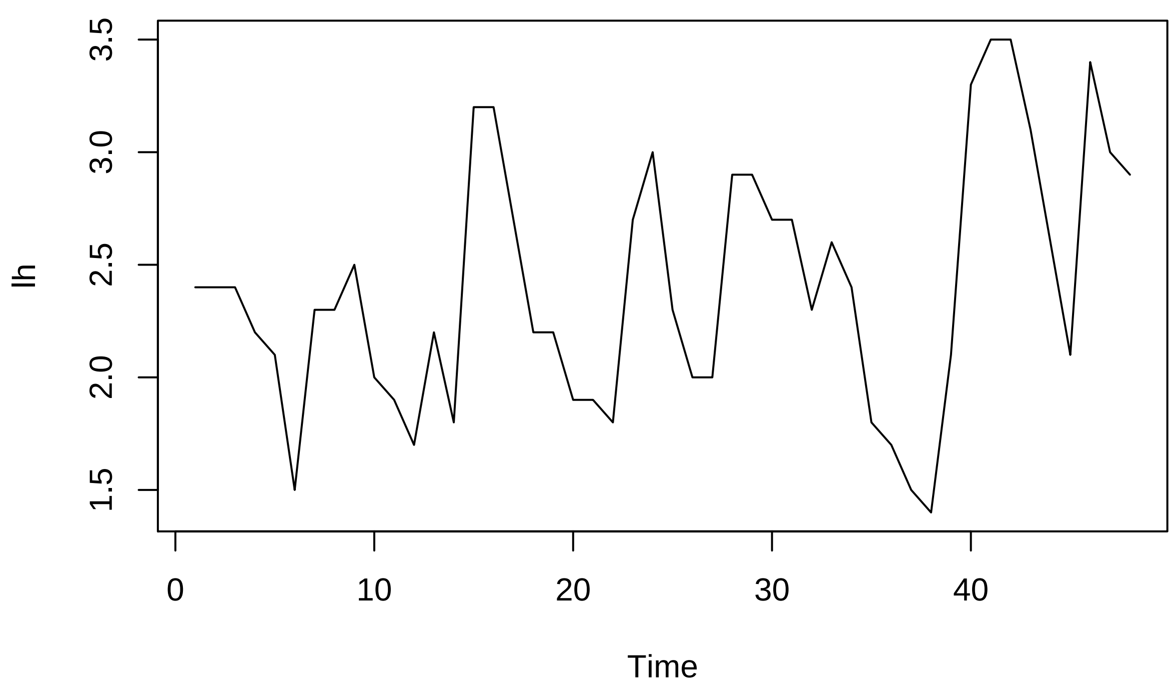
```
library(TSA)
library(astsa)
library(datasets)
library(forecast)
library(tseries)
```

Apply the Box-Jenkins method (transform to stationarity if necessary and identify the time series model(e.g., ARMA(p,q))) for the luteinizing hormone data. Write down the algebraic expression of the fitted model. How is your "final" model compared with an AR(3)?

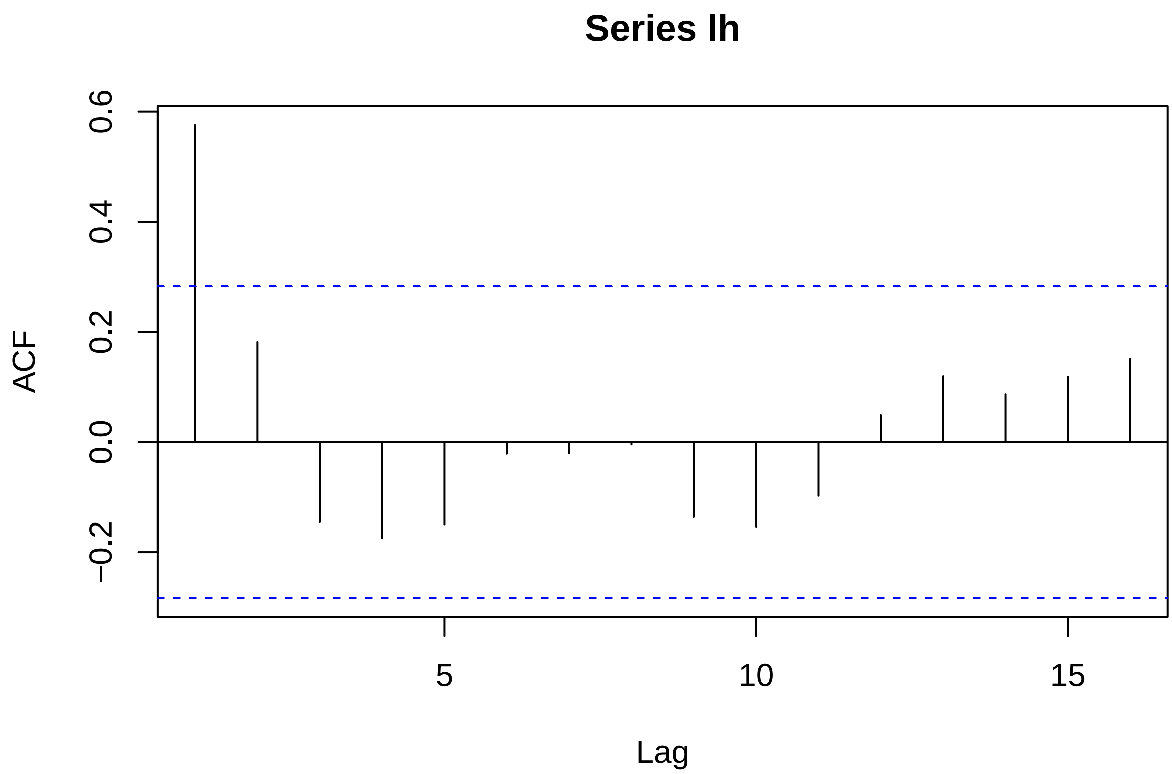
plot

```
data(lh)
plot(lh)
```

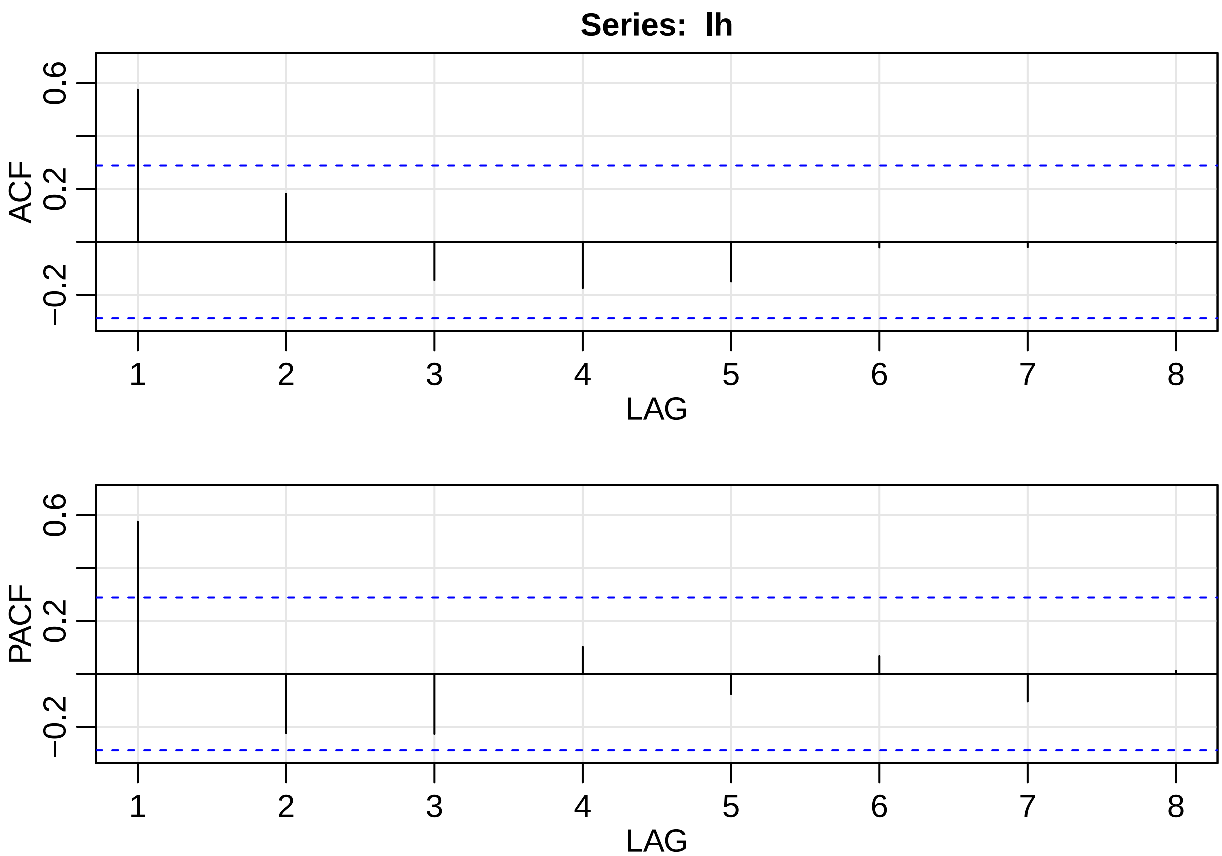


estimate p,q

```r
acf(lh)
```




```r
acf2(lh)[1:2]
```




```
## [1] 0.58 0.18
```

```r
eacf(lh)
```

```
## AR/MA
##   0 1 2 3 4 5 6 7 8 9 10 11 12 13
## 0 x o o o o o o o o o o  o  o  o
## 1 x o o o o o o o o o o  o  o  o
## 2 x x o o o o o o o o o  o  o  o
## 3 x o o o o o o o o o o  o  o  o
## 4 x o o o o o o o o o o  o  o  o
## 5 x o o o o o o o o o o  o  o  o
## 6 x o o o o o o o o o o  o  o  o
## 7 o o o o o o o o o o o  o  o  o
```

candiate models ARMA(1,1) or AR(1)

check residuals

```r
out1 <- arma(x = lh, order = c(1, 0))
summary(out1)
```

```
##
## Call:
## arma(x = lh, order = c(1, 0))
##
```

```
## Model:
## ARMA(1,0)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.73041 -0.35110 -0.08901  0.22820  1.16959
##
## Coefficient(s):
##            Estimate  Std. Error  t value Pr(>|t|)
## ar1          0.5861      0.1186    4.943  7.7e-07 ***
## intercept    0.9997      0.2906    3.440 0.000582 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Fit:
## sigma^2 estimated as 0.206,  Conditional Sum-of-Squares = 9.48,  AIC = 64.39
```

```r
out2 <- arma(x = lh, order = c(1, 1))
summary(out2)
```

```
##
## Call:
## arma(x = lh, order = c(1, 1))
##
## Model:
## ARMA(1,1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.7324 -0.3175 -0.1138  0.2214  1.2070
##
## Coefficient(s):
##            Estimate  Std. Error  t value Pr(>|t|)
## ar1          0.4631      0.1781    2.601  0.00929 **
## ma1          0.2003      0.1696    1.181  0.23745
## intercept    1.2943      0.4332    2.988  0.00281 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Fit:
## sigma^2 estimated as 0.2006,  Conditional Sum-of-Squares = 9.23,  AIC = 65.12
```

P value of ma(1) is large, which suggests that ar(1) is the better model.

$$X_t = 0.9997 + 0.5861 * X_{t-1} + w_t$$

compare to AR(3)

```r
out3 <- arma(x = lh, order = c(3, 0))
summary(out3)
```

```
##
## Call:
```

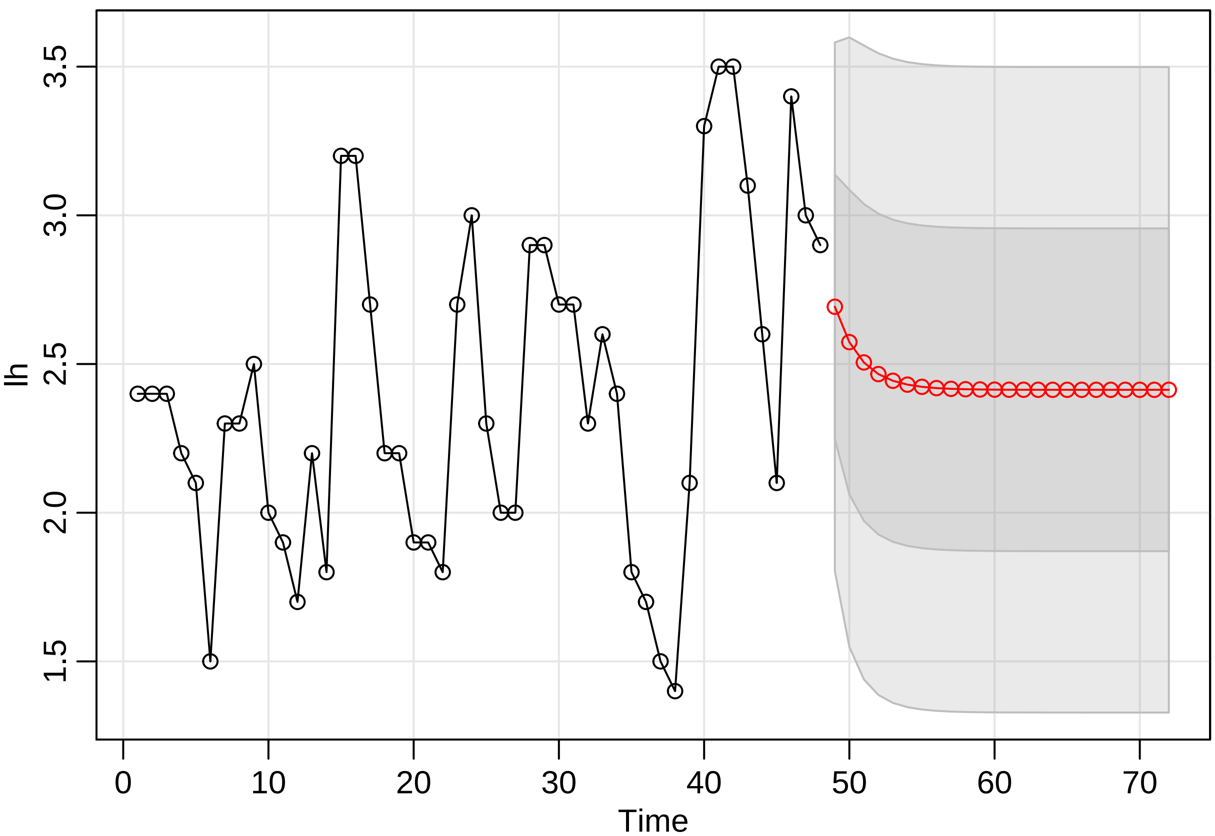
```
## arma(x = lh, order = c(3, 0))
##
## Model:
## ARMA(3,0)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.71055 -0.25307 -0.06248  0.25100  1.38012
##
## Coefficient(s):
##            Estimate  Std. Error  t value Pr(>|t|)
## ar1         0.65788     0.14141    4.652 3.28e-06 ***
## ar2        -0.06585     0.17022   -0.387    0.699
## ar3        -0.23475     0.14730   -1.594    0.111
## intercept   1.53729     0.36702    4.189 2.81e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Fit:
## sigma^2 estimated as 0.1948,  Conditional Sum-of-Squares = 8.57,  AIC = 65.7
```

Again we see that 2nd and 3rd AR terms are not significant, so AR(1) is prefered over AR(3).

forecast

Use your final model to forecast the next 24 luteinizing hormone measurements.

```r
n.ahead = 24
sarima.for(lh, n.ahead, 1, 0, 0)
```




```
## $pred
## Time Series:
## Start = 49
## End = 72
## Frequency = 1
##  [1] 2.692626 2.573609 2.505301 2.466097 2.443597 2.430683 2.423271
##  [8] 2.419018 2.416576 2.415175 2.414371 2.413910 2.413645 2.413493
## [15] 2.413405 2.413355 2.413327 2.413310 2.413301 2.413295 2.413292
## [22] 2.413290 2.413289 2.413289
##
## $se
## Time Series:
## Start = 49
## End = 72
## Frequency = 1
##  [1] 0.4443979 0.5123881 0.5328878 0.5394698 0.5416204 0.5423269 0.5425594
##  [8] 0.5426360 0.5426612 0.5426695 0.5426722 0.5426731 0.5426734 0.5426735
## [15] 0.5426736 0.5426736 0.5426736 0.5426736 0.5426736 0.5426736 0.5426736
## [22] 0.5426736 0.5426736 0.5426736
```