# Time Series Analysis: Fourth laboratory

19 de febrero de 2020

#### Laboratory contents.

- Performance of the four methods for estimation of AR(p).
- Performance of MLE versus sample size

```
arfun<-function(N,n,phi,s,c){
#simulates N AR(p) processes with n observations, parameter phi standard deviation of a=s
phiest=matrix(nrow=N,ncol=4)
colnames(phiest) <-c("OLS", "BURGS", "YW", "MLE")
for (i in 1:N) {
x=arima.sim(list(ar=phi),sd=s,n)
f.ar.ols<-ar.ols(x,aic=F,inter=F,order=1)
phiest[i,1]=f.ar.ols$ar
f.ar.burg<-ar.burg(x,aic=F,inter=F,order=1)
phiest[i,2]=f.ar.burg$ar
f.ar.vw<-ar.burg(x,aic=F,inter=F,order=1)
phiest[i,3]=f.ar.yw$ar
f.ar.mle < -arima(x, order = c(1,0,0))
phiest[i,4]=f.ar.mle$coef[1]
#boxplots for the phi estimates
boxplot(phiest, main="Phi estimation versus method", col=c("green", "red", "blue", "yellow"))
```

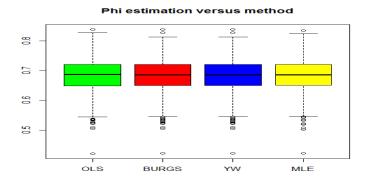


Figura: 1000 replications of an AR(1) with phi=0.7 and 200 observations

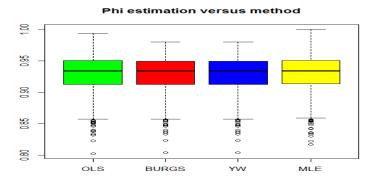


Figura: 1000 replications of an AR(1) with phi=0.95 and 200 observations

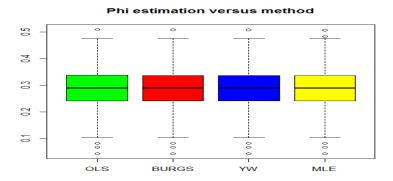


Figura: 1000 replications of an AR(1) with phi=0.3 and 200 observations

```
arfun<-function(N,n1,n2,n3,n4,phi,s,c){
#simulates N AR(p) processes with n observations, parameter phi standard deviation of a=s
phiest=matrix(nrow=N,ncol=4)
colnames(phiest)<-c("n=20", "n=60", "n=100", "n=200")
for (i in 1:N) {
x1=arima.sim(list(ar=phi).sd=s.n1)
x2=arima.sim(list(ar=phi).sd=s.n2)
x3=arima.sim(list(ar=phi).sd=s.n3)
x4=arima.sim(list(ar=phi),sd=s,n4)
f.ar.mle < -arima(x1, order=c(1, 0, 0))
phiest[i,1]=f.ar.mle$coef[1]
f.ar.mle < -arima(x2, order=c(1,0,0))
phiest[i,2]=f.ar.mle$coef[1]
f.ar.mle < -arima(x3, order=c(1,0,0))
phiest[i,3]=f.ar.mle$coef[1]
f.ar.mle < -arima(x4.order=c(1.0.0))
phiest[i,4]=f.ar.mle$coef[1]
}
boxplot(phiest, main="Phi estimation versus n", col=c("green", "red", "blue", "yellow"))
```

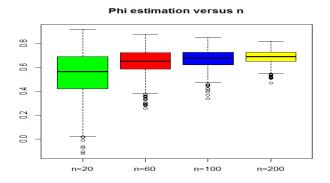


Figura: 1000 replications of an AR(1) with phi=0.7 and MLE

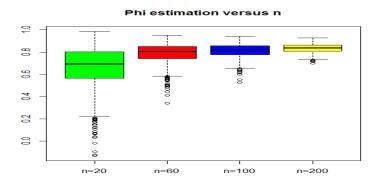


Figura: 1000 replications of an AR(1) with phi=0.85 and MLE

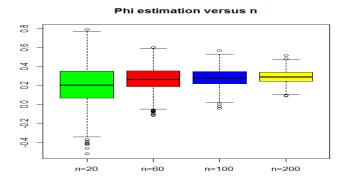


Figura: 1000 replications of an AR(1) with phi=0.3 and MLE

```
arfun<-function(N,n1,n2,n3,n4,phi,s,c){
#simulates N AR(p) processes with n observations, parameter phi standard deviation of a=s
phiest=matrix(nrow=N,ncol=4)
colnames(phiest)<-c("n=20", "n=60", "n=100", "n=200")
for (i in 1:N) {
x1=arima.sim(list(ar=phi).sd=s.n1)
x2=arima.sim(list(ar=phi),sd=s,n2)
x3=arima.sim(list(ar=phi),sd=s,n3)
x4=arima.sim(list(ar=phi),sd=s,n4)
f.ar.mle < -arima(x1, order=c(1, 0, 0))
phiest[i,1]=f.ar.mle$sigma
f.ar.mle < -arima(x2.order=c(1.0.0))
phiest[i,2]=f.ar.mle$sigma
f.ar.mle < -arima(x3.order=c(1.0.0))
phiest[i,3]=f.ar.mle$sigma
f.ar.mle < -arima(x4, order=c(1,0,0))
phiest[i,4]=f.ar.mle$sigma
boxplot(phiest.main="Sigma estimation versus n".col=c("green", "red", "blue", "vellow"))
```

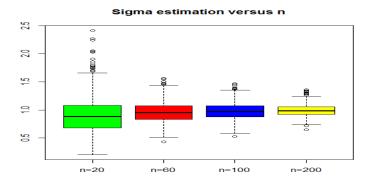


Figura: 1000 replications of an AR(1) with phi=0.4 and MLE

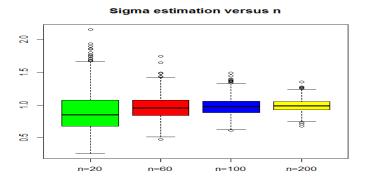


Figura: 1000 replications of an AR(1) with phi=0.85 and MLE