STAT429 HW4

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Question1

```
rec = scan("cmort.dat")
data=rec
y=mean(data)
data_new=data-y
rec.yw=ar.yw(data_new,order=2)
n=length(rec)
```

The mean value of x is $\mu = E(X_t) =$ y

```
rec.yw$ar
```

```
## [1] 0.4339481 0.4375768
```

```
phi1=rec.yw$ar[1]
phi2=rec.yw$ar[2]
```

These are the point estimates of ϕ_1 and ϕ_2.

```
rec.yw$var.pred
```

```
## [1] 32.84056
```

This is the point estimate of σ^2.

```
sd=sqrt(diag(rec.yw$asy.var.coef))
stat1=(phi1-0.4)/sd[1]
stat2=(phi2-0.4)/sd[2]
2*pnorm(abs(stat1),lower.tail = FALSE)
```

```
## [1] 0.3962005
```

```
2*pnorm(abs(stat2),lower.tail = FALSE)
```

```
## [1] 0.3476723
```

Both p-value is over 30%. This means that we cannot reject the null hypothesis. The data is compatible with the hypothesis.

Question 4

```
P=4
Q=4
crit1=matrix(0,P+1,Q+1)
crit2=matrix(0,P+1,Q+1)
for (j in 0:P)
{
for (k in 0:Q)
{
```

```r
dataML=arima(data,order=c(j,0,k),method="ML")
#AICC
crit1[j+1,k+1]=n*log(dataML$sigma)+2*(j+k+1)*n/(n-j-k-2)
#BIC
crit2[j+1,k+1]=n*log(dataML$sigma)+(j+k+1)*log(n)

}
}
```

```
## Warning in arima(data, order = c(j, 0, k), method = "ML"): possible
## convergence problem: optim gave code = 1

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```

```r
crit1
```

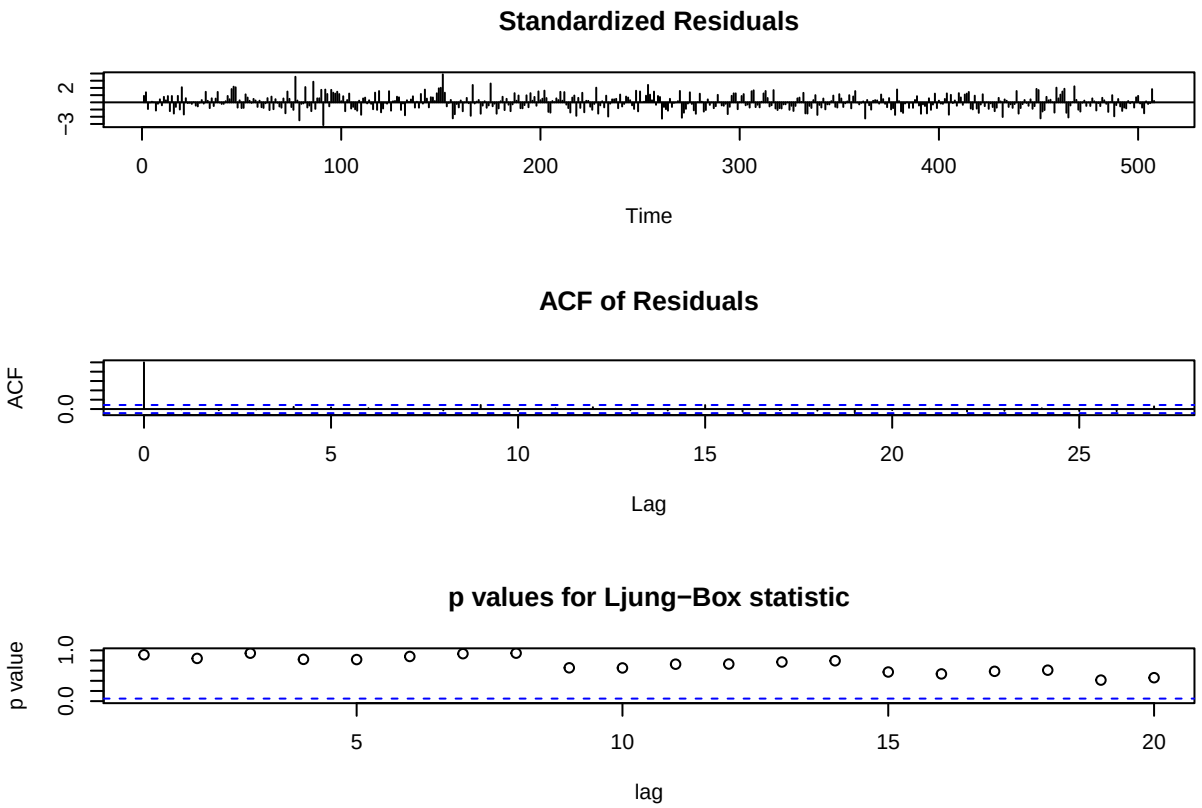
```
##          [,1]     [,2]     [,3]     [,4]     [,5]
## [1,] 2340.300 2135.475 1971.191 1920.154 1874.984
## [2,] 1881.363 1791.966 1777.992 1778.289 1776.332
## [3,] 1772.495 1774.153 1775.905 1777.951 1779.914
## [4,] 1774.198 1776.465 1770.877 1775.110 1780.032
## [5,] 1775.809 1777.855 1779.132 1781.943 1772.909
```

```r
crit2
```

```
##          [,1]     [,2]     [,3]     [,4]     [,5]
## [1,] 2344.523 2143.913 1983.835 1936.997 1896.017
## [2,] 1889.800 1804.610 1794.834 1799.322 1801.547
## [3,] 1785.139 1790.995 1796.937 1803.166 1809.303
## [4,] 1791.040 1797.497 1796.092 1804.499 1813.588
## [5,] 1796.842 1803.071 1808.522 1815.499 1810.622
```

The best model is ARIMA(3,0,1) because the BIC is the smallest when the model is ARIMA(3,0,1)

```
rec.ML<-arima(data,order=c(3,0,1),method="ML")
tsdiag(rec.ML,gof.lag=20)
```



If you see this, you can know that ACF of Residuals is between the blue line and p-values for Ljung-Box statistics are all above the blue line. This means that this model has almost 0 ACF of residuals. In addition we can be in favor of the fact that autocorrelations of data is zero.