Time Series Analysis

ARMA Models

Nicoleta Serban, Ph.D.

Professor

Stewart School of Industrial and Systems Engineering

ARMA Modeling: Data Example

Georgia Tech

About This Lesson

Georgia Tech

Emergency Department Care

Have you ever experienced long waits in the Emergency Department?

- Good predictions of daily inflow in an emergency department can assist in staffing and diversion
- Time series modeing can be useful in achieving good predictions.

Georgia Tech

Case Study Overview

Objective:

- Identify temporal patterns in the Emergency Department (ED) volume of patients
- Develop a model to predict ED volume

Time Series Data:

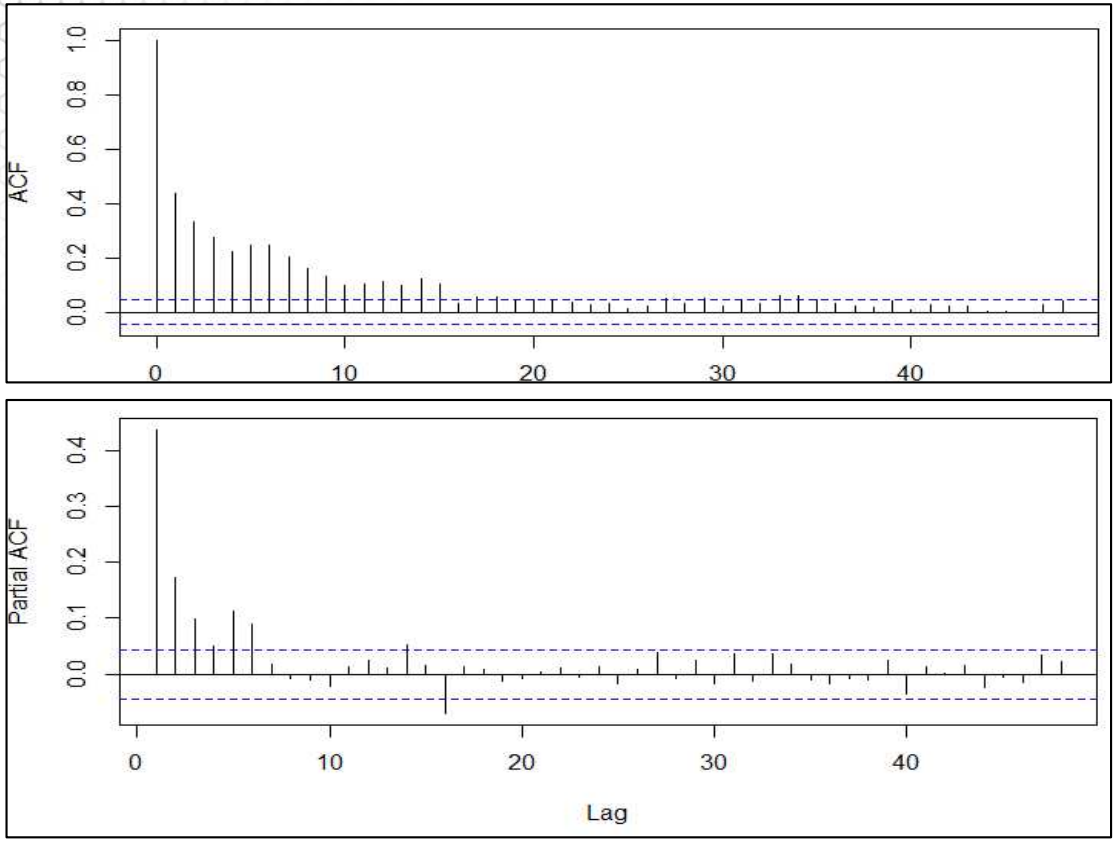
- Daily number of patients visiting an emergency department of a hospital in the Atlanta area with observations from 2010 until mid 2015
- Other predicting variables were made available by the hospital but we will only focus on the predictability of the time series with respect to temporal factors

Model Trend and Seasonality

```
## Model Trend + Monthly Seasonality
library(mgcv)
time.pts = c(1:length(Volume))
time.pts = c(time.pts - min(time.pts))/max(time.pts)
month = as.factor(format(dates,"%b"))
week = as.factor(weekdays(dates))
gam.fit.seastr = gam(Volume.tr~s(time.pts)+month+week)
vol.fit.gam.seastr = fitted(gam.fit.seastr)
resid.process = Volume.tr-vol.fit.gam.seastr

acf(resid.process,lag.max=12*4,main="ACF: Residual Plot")
pacf(resid.process,lag.max=12*4,main="PACF: Residual Plot")
```

Model Trend and Seasonality

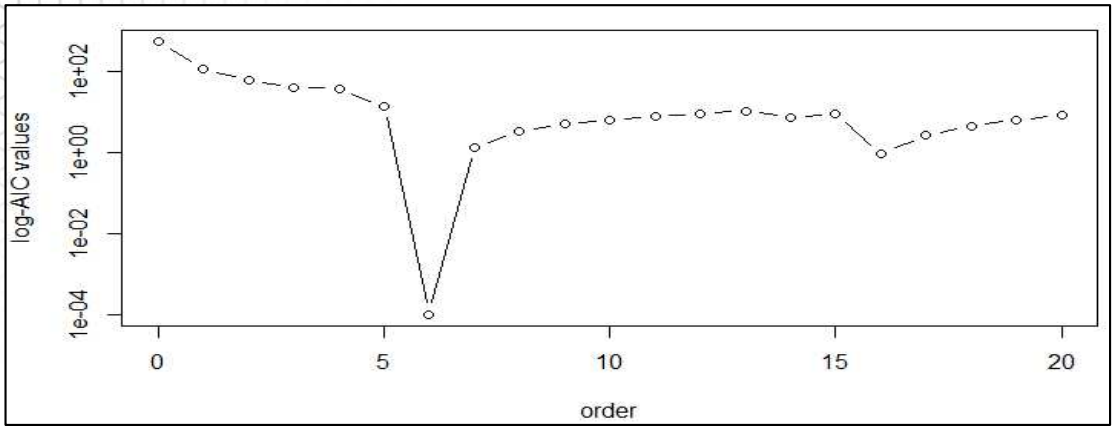


Fitting an AR process

```
## Fit an AR(p) process for for p<= order.max
mod = ar(resid.process,order.max=20)
## What is the selected order?
print(mod$order)
## Find the list of arguments provided by AR fit
summary(mod)
## Plot AIC values on the log scale to easily identify minimum
plot(c(0:20), mod$aic+.0001, type="b",log="y",xlab="order",ylab="log-AIC
values")
```

Georgia Tech

Fitting an AR process

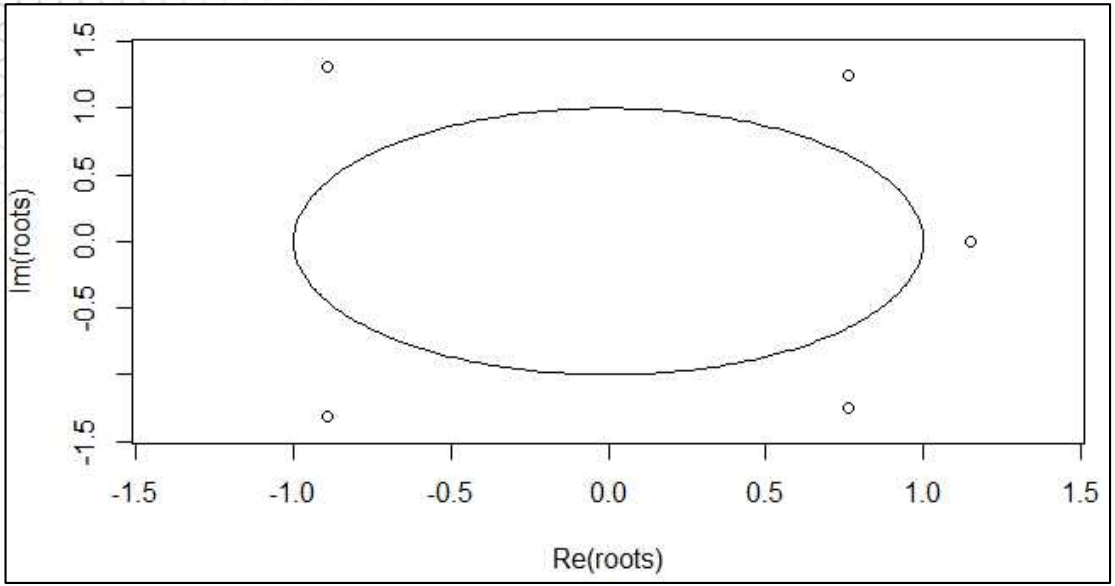


Georgia Tech

Fitted AR process: Properties

```
## Are the roots of fitted AR within the unit circle?
## Extract roots from the model output:
roots = polyroot(c(1,(-mod$ar)))
## Adjust the x and y -axis limits to include the full circle
plot(roots,xlim=c(-1.5,1.5),ylim=c(-1.5,1.5))
## Draw a unit root circle
lines(complex(arg = seq(0,2*pi,len=300)))
```

Fitted AR process: Properties

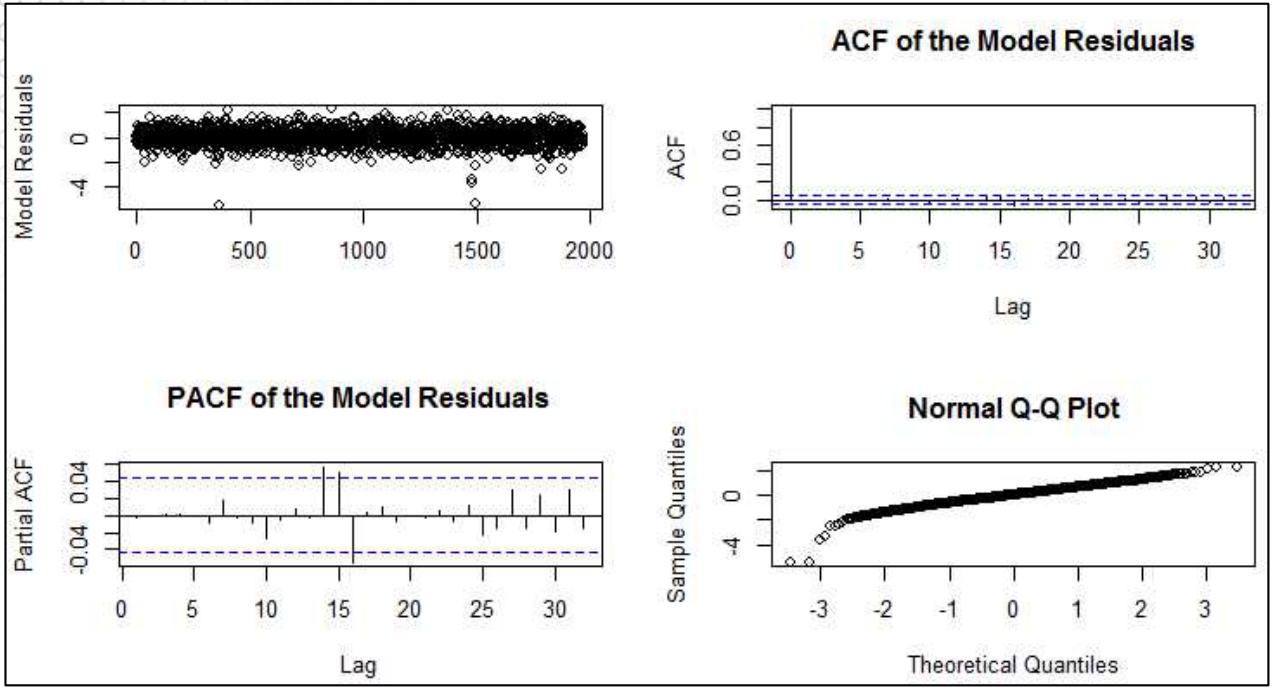


Georgia Tech

Fitted AR process: Residual Analysis

```
## Obtain the standardized residuals
resids = mod$resid[(mod$order+1): length(mod$resid)]
## Plot the residuals
par(mfrow=c(2,2))
plot(resids,xlab="",ylab="Model Residuals")
acf(resids,main='ACF of the Model Residuals')
pacf(resids,main='PACF of the Model Residuals')
qqnorm(resids)
```

Fitted AR process: Residual Analysis

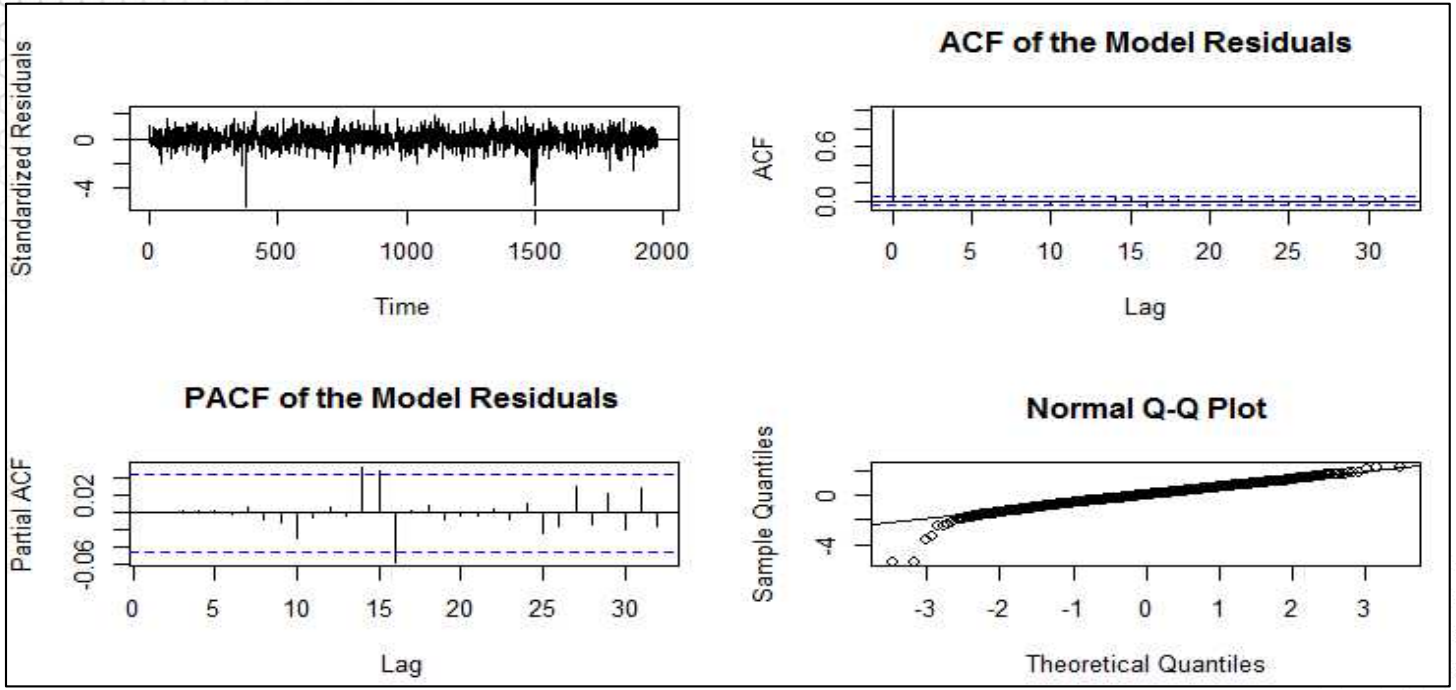


Georgia Tech

Fit an ARMA Model

```
## Fit ARMA(6,1)
modarma = arima(resid.process, order = c(6,0,1),method = "ML")
## Residual Analysis
par (mfrow=c(2,2))
plot(resid(modarma), ylab='Standardized Residuals')
abline(h=0)
acf(as.vector(resid(modarma)),main= 'ACF of the Model Residuals')
pacf(as.vector(resid(modarma)),main='PACF of the Model Residuals')
qqnorm(resid(modarma))
qqline(resid(modarma))
```

Fit an ARMA Model



Georgia Tech

ARMA Model: Order Selection

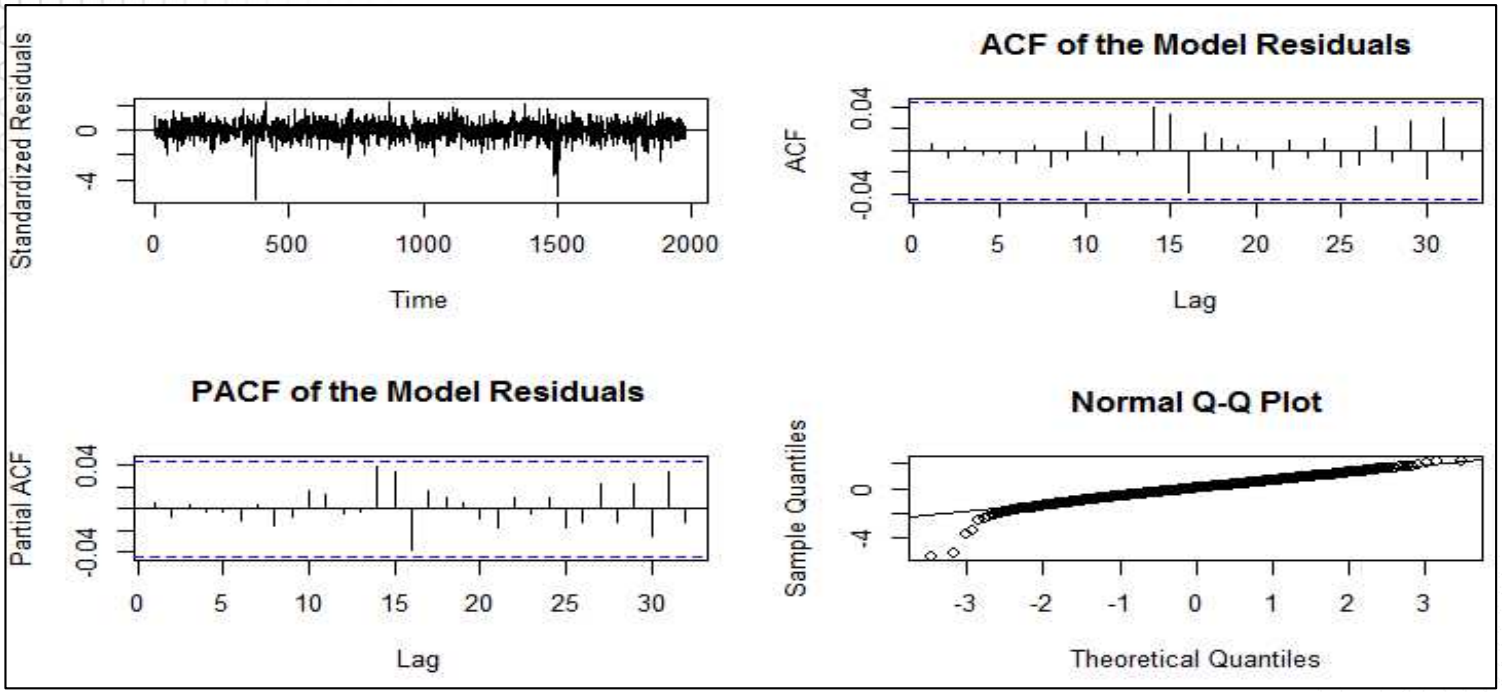
```
## Order selection – AIC
n = length(resid.process)
norder = 6
p = c(1:norder)-1; q = c(1:norder)-1
aic = matrix(0,norder,norder)
for(i in 1:norder){
   for(j in 1:norder){
    modij = arima(resid.process,order = c(p[i],0,q[j]), method='ML')
    aic[i,j] = modij$aic-2*(p[i]+q[j]+1)+2*(p[i]+q[j]+1)*n/(n-p[i]-q[j]-2)
   }
 }
```

Georgia Tech

ARMA Model: Order Selection (cont'd)

```
## Which order to select?
aicv = as.vector(aic)
plot(aicv,ylab="AIC values")
indexp = rep(c(1:norder),norder)
indexq = rep(c(1:norder),each=norder)
indexaic = which(aicv == min(aicv))
porder = indexp[indexaic]-1
qorder = indexq[indexaic]-1
## Final Model
final_model = arima(resid.process,order = c(porder,0,qorder), method='ML')
```

ARMA Model: Residual Analysis



Georgia Tech

Testing for Uncorrelated Residuals

Test for Uncorrelated Residuals for the final model

Box.test(final_model$resid, lag = (porder+qorder+1), type = "Box-Pierce", fitdf = (porder+qorder))

Box.test(final_model$resid, lag = (porder+qorder+1), type = "Ljung-Box", fitdf = (porder+qorder))

Test for Uncorrelated Residuals for the smaller model

Box.test(modarma$resid, lag = (porder+qorder+1), type = "Box-Pierce", fitdf = (porder+qorder))

Box.test(modarma$resid, lag = (porder+qorder+1), type = "Ljung-Box", fitdf = (porder+qorder))

Georgia Tech

Testing for Uncorrelated Residuals (cont'd)

```
> Box.test(final_model$resid, lag = (porder+qorder+1), type = "Box-Pierce", fitdf = (porder+qord
r))

        Box-Pierce test

data:  final_model$resid
X-squared = 1.9958, df = 1, p-value = 0.1577

> Box.test(final_model$resid, lag = (porder+qorder+1), type = "Ljung-Box", fitdf = (porder+qorde
))

        Box-Ljung test

data:  final_model$resid
X-squared = 2.0062, df = 1, p-value = 0.1567

> Box.test(modarma$resid, lag = (porder+qorder+1), type = "Box-Pierce", fitdf = (porder+qorder))

        Box-Pierce test

data:  modarma$resid
X-squared = 2.2056, df = 1, p-value = 0.1375

> Box.test(modarma$resid, lag = (porder+qorder+1), type = "Ljung-Box", fitdf = (porder+qorder))

        Box-Ljung test

data:  modarma$resid
X-squared = 2.2186, df = 1, p-value = 0.1364
```

Georgia Tech

Summary

Georgia Tech