STA 137 Final Project

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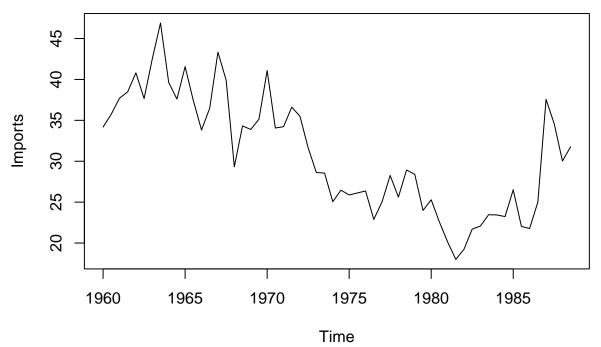
Col Removal

```
Keep Year, Imports, and Imports columns
finalPro_data <- finalPro_data[, c("Year", "Imports")]</pre>
```

Plot Time Series

```
# Plot Imports
imports_ts <- ts(finalPro_data$Imports, start = 1960, frequency = 2)
ts.plot(imports_ts, main="Imports Time Series", ylab="Imports")</pre>
```

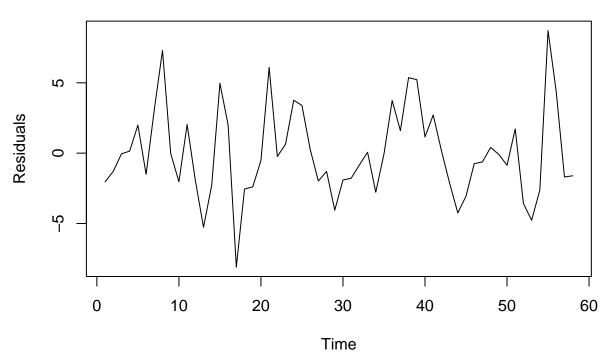
Imports Time Series



```
# Apply Polynomial Detrending
time_index <- 1:length(imports_ts)
poly_trend_model <- lm(imports_ts ~ poly(time_index, 3)) # 3rd-degree polynomial trend
detrended_imports <- residuals(poly_trend_model)</pre>
```

```
# Plot Detrended Imports
ts.plot(detrended_imports, main = "Detrended Imports (Polynomial)", ylab = "Residuals")
```

Detrended Imports (Polynomial)



Summary:

- Imports time series has U shape curve, this shows this is non-stationary
- It has peaks around every 10 year: 1980, 1990, 2010

Transform

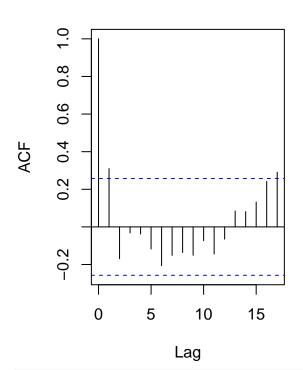
We tried log and Box-Cox, but neither stabilized the variance.

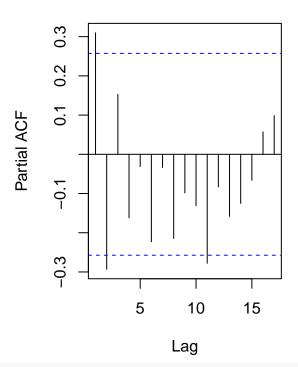
```
# Fit a basic linear model for demonstration
model_imports_bc <- lm(detrended_imports ~ time(detrended_imports))
resid_imports_bc <- residuals(model_imports_bc)

# Plot ACF and PACF of residuals
par(mfrow = c(1, 2)) # Side-by-side plots
acf(resid_imports_bc, main = "ACF of Residuals")
pacf(resid_imports_bc, main = "PACF of Residuals")</pre>
```

ACF of Residuals

PACF of Residuals





```
par(mfrow = c(1, 1)) # Reset layout

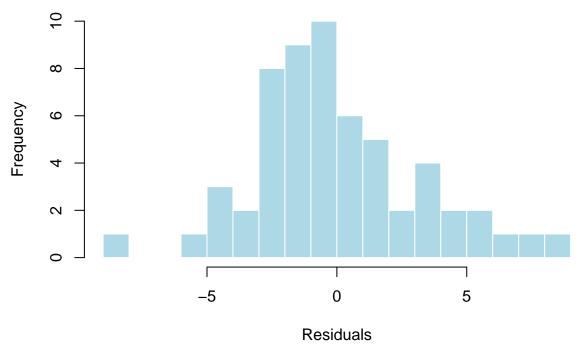
# Portmanteau (Box-Pierce) test for white noise
portmanteau_result <- Box.test(resid_imports_bc, lag = 10, type = "Box-Pierce")
print(portmanteau_result)
##</pre>
```

```
##
## Box-Pierce test
##
## data: resid_imports_bc
## X-squared = 14.672, df = 10, p-value = 0.1445
```

Assess Normality

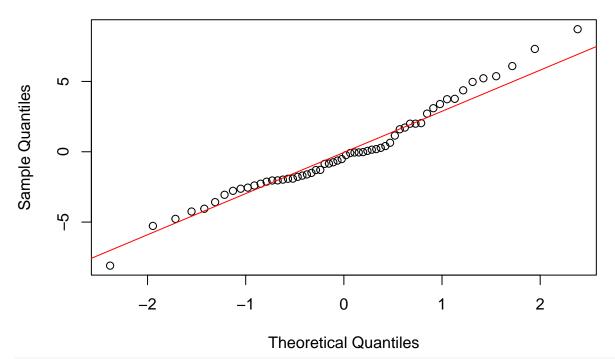
```
# Assess Normality of Residuals
# Histogram
hist(resid_imports_bc, breaks = 15, main = "Histogram of Residuals", xlab = "Residuals", col = "lightbl"
```

Histogram of Residuals



```
# Q-Q Plot
qqnorm(resid_imports_bc, main = "Q-Q Plot of Residuals")
qqline(resid_imports_bc, col = "red")
```

Q-Q Plot of Residuals



```
# Shapiro-Wilk Test
shapiro_test <- shapiro.test(resid_imports_bc)</pre>
```