

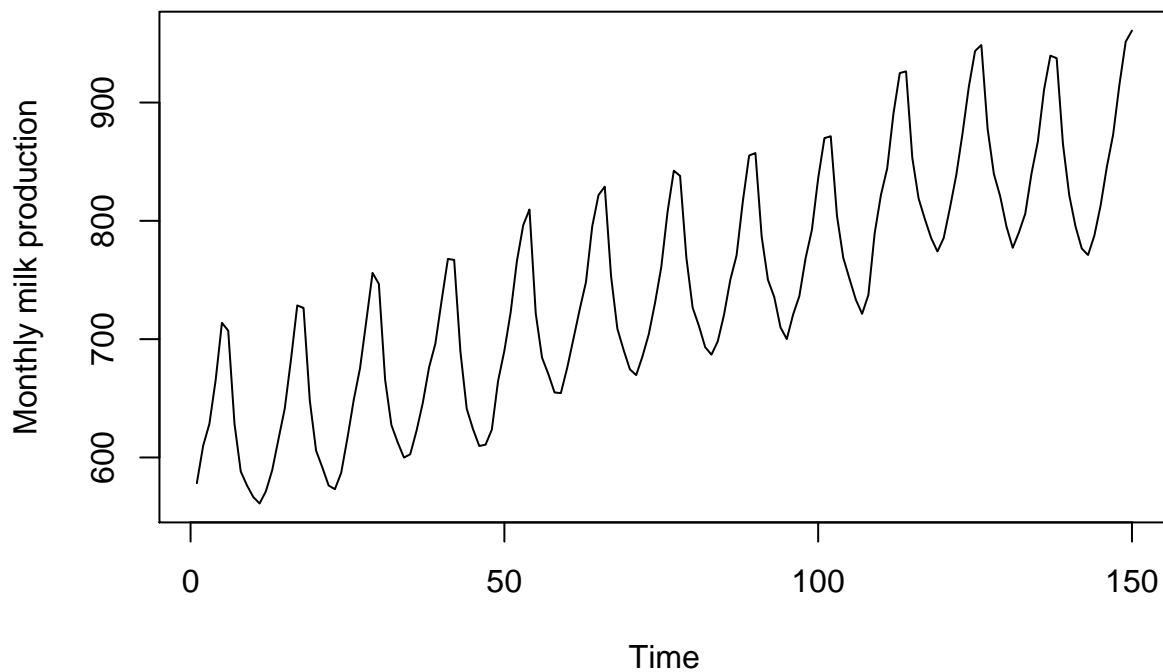
# PSTAT174\_Lab07

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1. We will again analyze adjusted monthly milk production measured in pounds per from Jan. 1962 to Dec. 1975. And we can import the dataset from `tsdl` package as `milk` in R, and denote the milk time series as  $X_t$ . For comparison, we split the dataset into training set `train` and testing set `test`. The training set is used for model building, and the testing set is used for prediction verification and comparison.

```
library(tsd1)
milk <- subset(tsd1, 12, "Agriculture")[[3]]
train <- milk[1:150]
test <- milk[151:156]
ts.plot(train, ylab = "Monthly milk production")
```



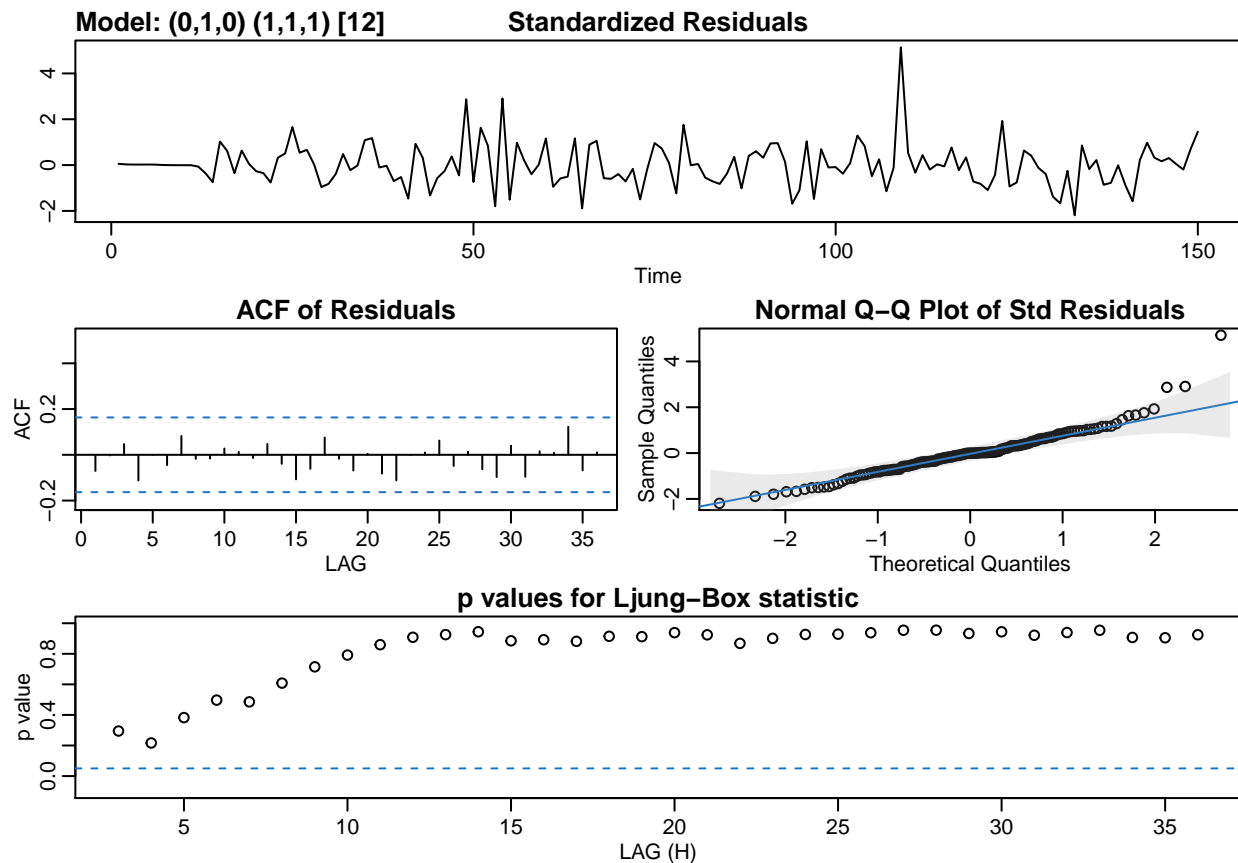
From the above graph, we can conclude that  $X_t$  is non-stationary because of the upward trend and seasonality. (You can think about whether we need to transform the series or not.) To make it more stationary, we need to remove trend and seasonality with the following code:

```
dmilk <- diff(train, 12)
ddmilk <- diff(dmilk, 1)
```

Let  $Y_t$  denote the series `ddmilk`. Then,  $Y_t = (1 - B)(1 - B^{12})X_t$ . As Lab Assignment 5, we can use `SARIMA(0, 1, 0) × (1, 1, 1)12`. Now, we will conduct model diagnostic analysis.

```
library(astsa)
fit.i <- sarima(xdata=train, p=0, d=1, q=0, P=1, D=1, Q=1, S=12)
```

```
## initial value 1.989465
## iter 2 value 1.850408
## iter 3 value 1.824156
## iter 4 value 1.800049
## iter 5 value 1.791131
## iter 6 value 1.789958
## iter 7 value 1.789636
## iter 8 value 1.789235
## iter 9 value 1.789186
## iter 10 value 1.789182
## iter 10 value 1.789182
## iter 10 value 1.789182
## final value 1.789182
## converged
## initial value 1.803940
## iter 2 value 1.803675
## iter 3 value 1.803165
## iter 4 value 1.803164
## iter 5 value 1.803163
## iter 6 value 1.803163
## iter 6 value 1.803163
## final value 1.803163
## converged
```



(a) Perform diagnostics on the chosen model fit. Do the residuals appear to be white noise? Are they normally distributed? You should conduct hypothesis testing and plot some graphs to answer this questions. (You can think about why we want to check normality of the residuals.)

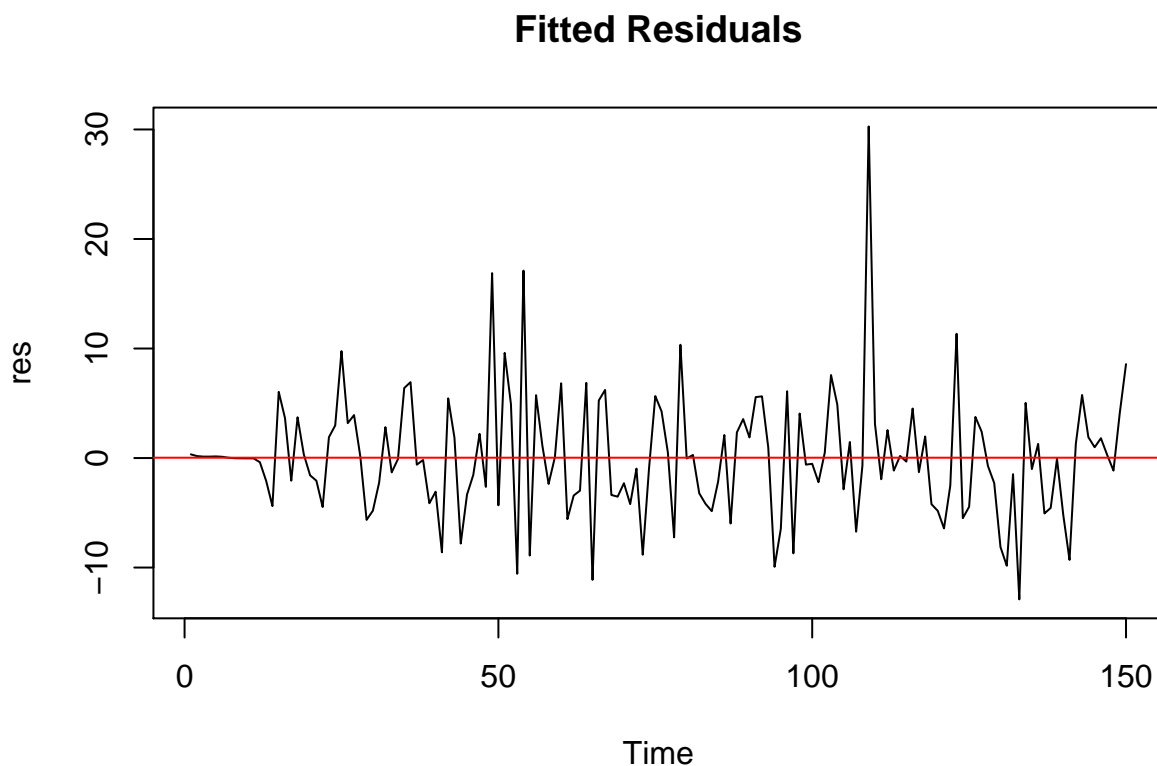
```
# Diagnostics on model
res <- residuals(fit.i$fit)
mean(res)
```

```
## [1] 0.03021635
```

```
var(res)
```

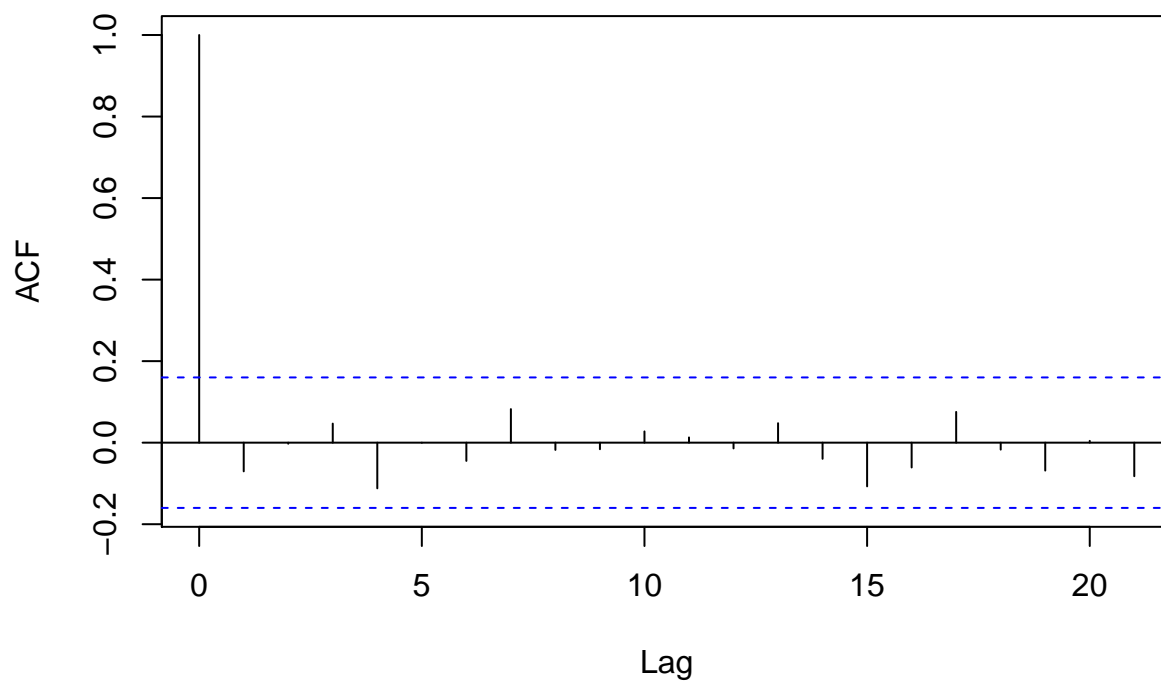
```
## [1] 31.89208
```

```
# Plots on model
ts.plot(res, main = "Fitted Residuals")
abline(h = mean(res), col = "red")
```

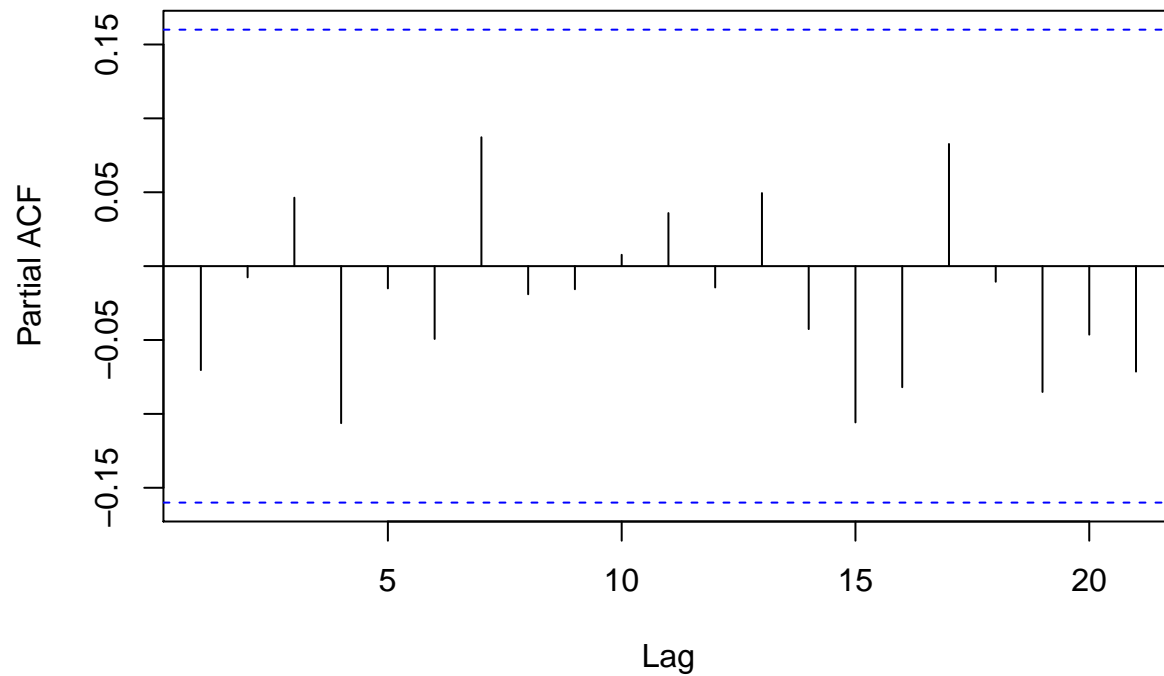


```
acf(res, main = "Autocorrelation"); pacf(res, main = "Partial Autocorrelation")
```

## Autocorrelation



## Partial Autocorrelation



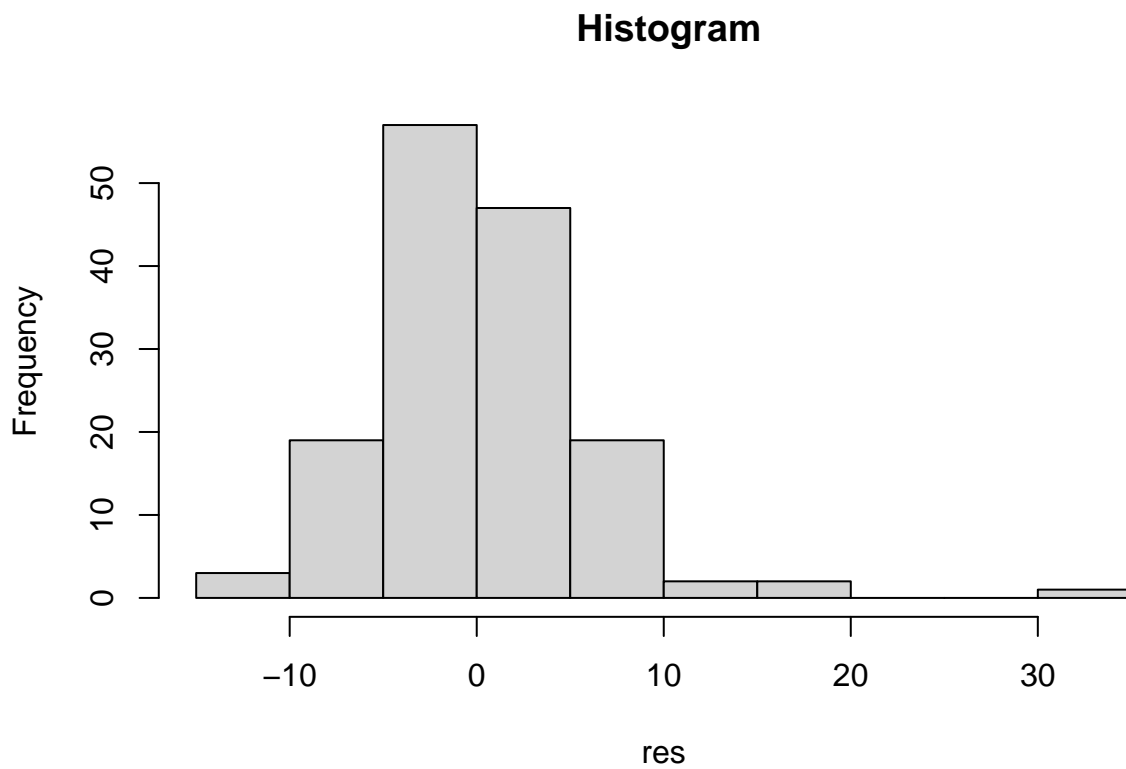
```
# Independence test  
Box.test(res, lag = 12, type = c("Box-Pierce"), fitdf = 2)
```

```
##  
## Box-Pierce test
```

```
##
## data:  res
## X-squared = 4.5287, df = 10, p-value = 0.9204
Box.test(res, lag = 12, type = c("Ljung-Box"), fitdf = 2)

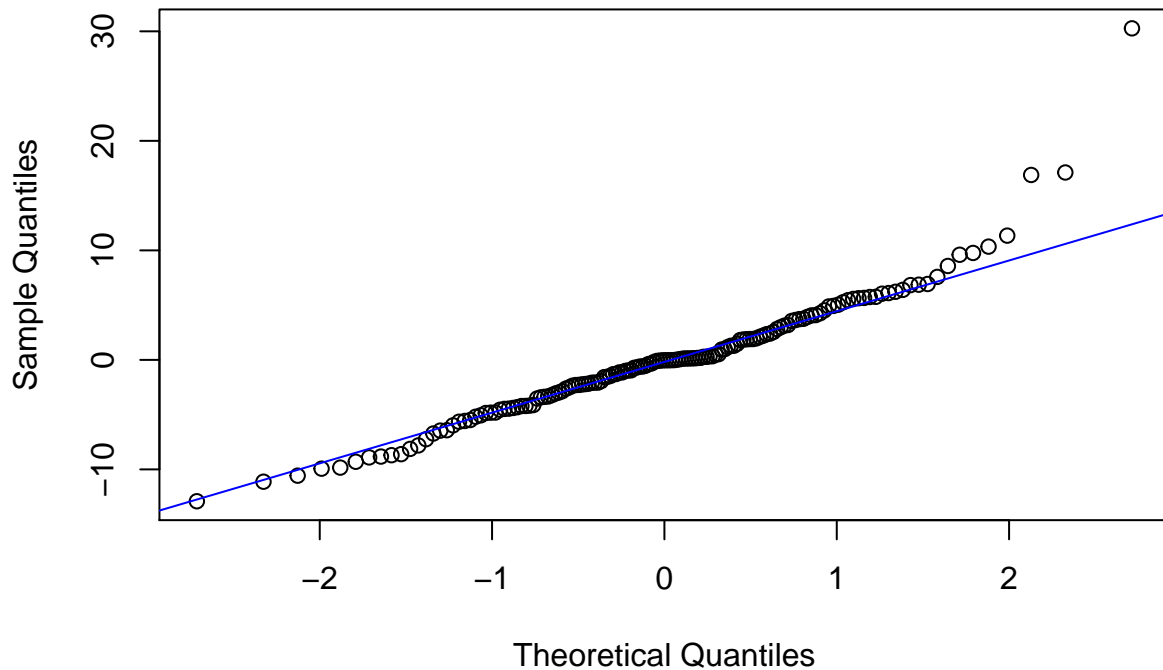
##
## Box-Ljung test
##
## data:  res
## X-squared = 4.7345, df = 10, p-value = 0.9082
Box.test(res^2, lag = 12, type = c("Ljung-Box"), fitdf = 0)

##
## Box-Ljung test
##
## data:  res^2
## X-squared = 1.9858, df = 12, p-value = 0.9994
# Checking the normality assumption
hist(res, main = " Histogram")
```



```
qqnorm(res)
qqline(res, col = "blue")
```

## Normal Q-Q Plot



```
# Test normality of residual
shapiro.test(res)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  res
## W = 0.93109, p-value = 1.183e-06
```

(b) Forecast the next 6 observations using `sarima.for()`, and plot your predictions. And you should also add true milk production points in test.

```
pred.milk <- sarima.for(train, n.ahead = 6, plot.all = F,
                        p=0, d=1, q=0, P=1, D=1, Q=1, S=12)

lines(151:156, pred.milk$pred, col = "red")
lines(151:156, test, col = "blue")
points(151:156, test, col = "blue")
legend("bottomright", pch = 1, col = c("red", "blue"),
      legend = c("Forecasted values", "True Values"))
```

