

HW6 Solution

1 (a):

```
set.seed(1000)
y <- arima.sim(n=100, list(ma=c(0.7)))
```

The elements of the covariance matrix is given by:

$$\Sigma_{ij} = \begin{cases} (1 + \theta_1^2 + \theta_2^2)\sigma_e^2, & \text{if } i = j, \\ (-\theta_1 + \theta_1\theta_2)\sigma_e^2, & \text{if } |i - j| = 1, \\ -\theta_2\sigma_e^2, & \text{if } |i - j| = 2, \\ 0, & \text{otherwise.} \end{cases}$$

(b): Since we assume the innovations to be iid normally distributed, the sample is from a multivariate normal distribution with zero mean covariance matrix Σ , we can write down the likelihood equation of the sample in terms of Σ and find the value of θ_1 and θ_2 that maximize the likelihood function. \

(c,d)

```
arima(y, order = c(0, 0, 2), method = "ML")

##
## Call:
## arima(x = y, order = c(0, 0, 2), method = "ML")
##
## Coefficients:
##          ma1          ma2  intercept
##          0.5246   -0.1835         0.0107
## s.e.    0.1072    0.1101    0.1336
##
## sigma^2 estimated as 0.9948:  log likelihood = -141.94,  aic = 289.87
```

The above code provide the result of the MLE of the parameters and their standard errors.

7.1 Using $\hat{\phi}_1 = \frac{r_1(1-r_2)}{1-r_1^2}$ and $\hat{\phi}_2 = \frac{r_2-r_1^2}{1-r_1^2}$, we have $\hat{\phi}_1 = \frac{0.8(1-0.5)}{1-0.8^2} = 1.11$ and $\hat{\phi}_2 = \frac{0.5-0.8^2}{1-0.8^2} = -0.389$. Then from $\theta_0 = \mu(1 - \phi_1 - \phi_2)$ we have $\hat{\theta}_0 = \hat{\mu}(1 - \hat{\phi}_1 - \hat{\phi}_2) = 2(1 - 1.11 - (-0.389)) = 0.558$. Finally, from $\hat{\sigma}_e^2 = (1 - \hat{\phi}_1 r_1 - \hat{\phi}_2 r_2) s^2 = [1 - (1.11)(0.8) - (-0.389)(0.5)]5 = 1.5325$.

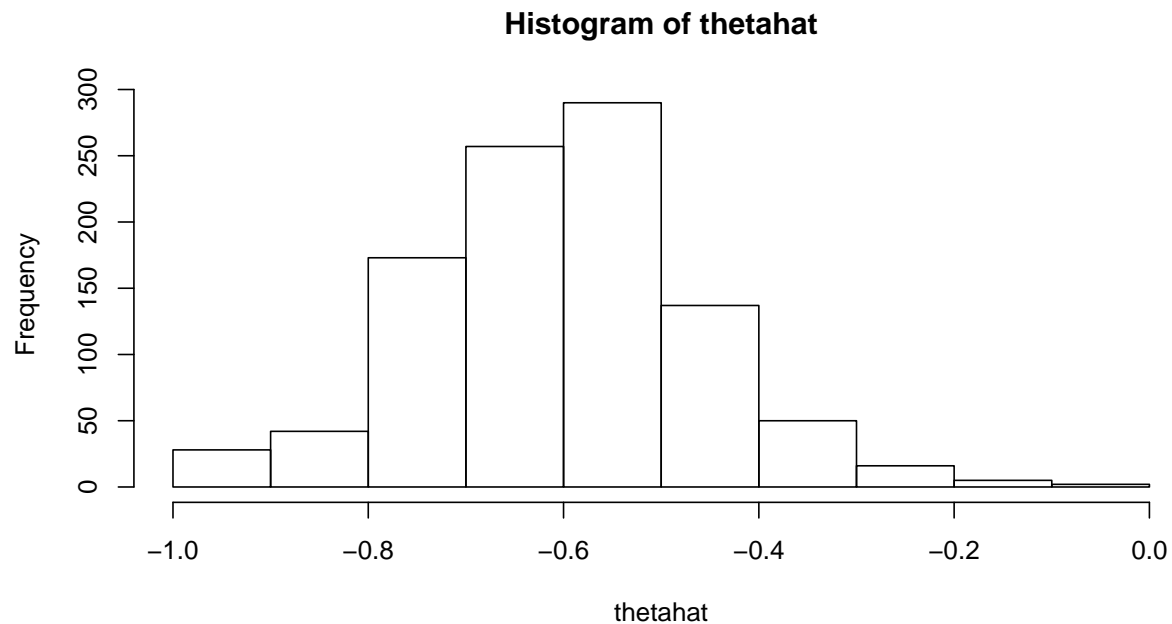
7.11 (a) The following code generate an MA(1) series with $\theta = -0.6$ and $n = 48$ and give the mle of θ (Note that the sign convention in the textbook is opposite that of the R software)

```
set.seed(1352);
series <- arima.sim(n=48, list(ma=0.6))
arima(series, order=c(0,0,1), method='ML')$coef[1]

##          ma1
## 0.5081146
```

(b,c)

```
set.seed(1352); thetahat <- rep(0,1000)
for (k in 1:1000) {series=arima.sim(n=48,list(ma=0.6));
thetahat[k] <- -arima(series,order=c(0,0,1),method='ML')$coef[1]}
hist(thetahat)
```



The distribution is roughly normal but skewed a little toward zero.

(d,e)

```
mean(thetahat)
```

```
## [1] -0.6042001
```

```
sd(thetahat)^2
```

```
## [1] 0.02080749
```

The mean of the sampling distribution is -0.6042001, so the estimate is nearly unbiased. The sample variance from the 1000 replications is 0.02080749. Compare this to the large-sample result of $\text{Var}(\hat{\theta}) \approx \frac{1-\theta^2}{n} = \frac{1-(-0.6)^2}{48} = 0.013$, things are somewhat better in standard variance terms.

7.31

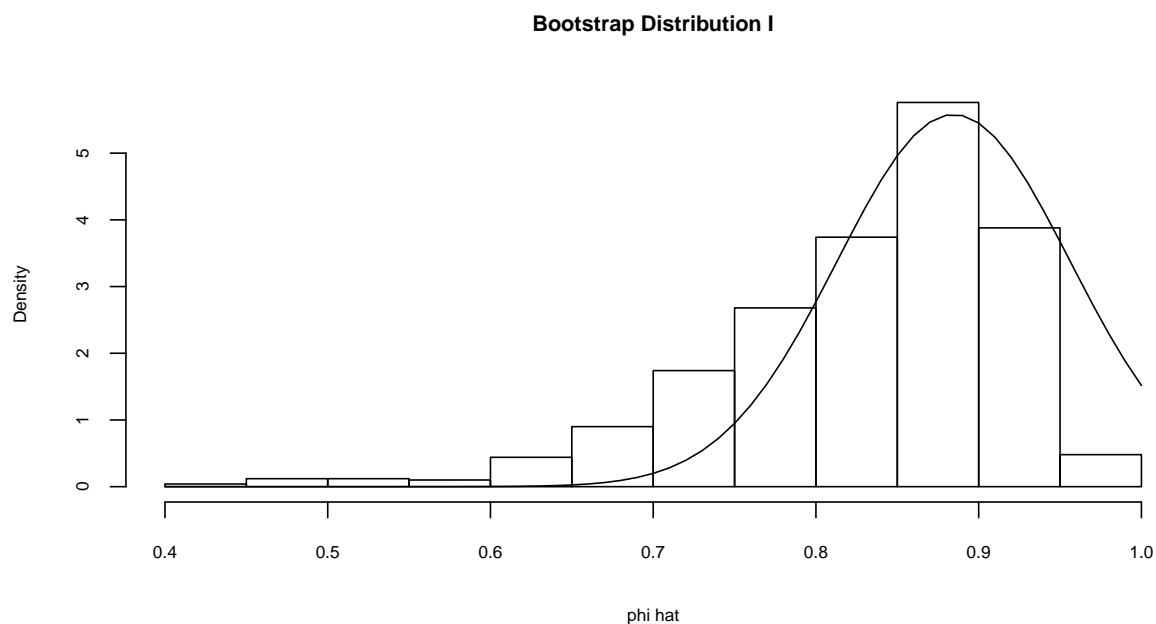
```
set.seed(54321); series <- arima.sim(n=48,list(ar=0.7))
result <- arima(series,order=c(1,0,0))
```

The standard deviation 0.0715 is based on the large-sample theory.

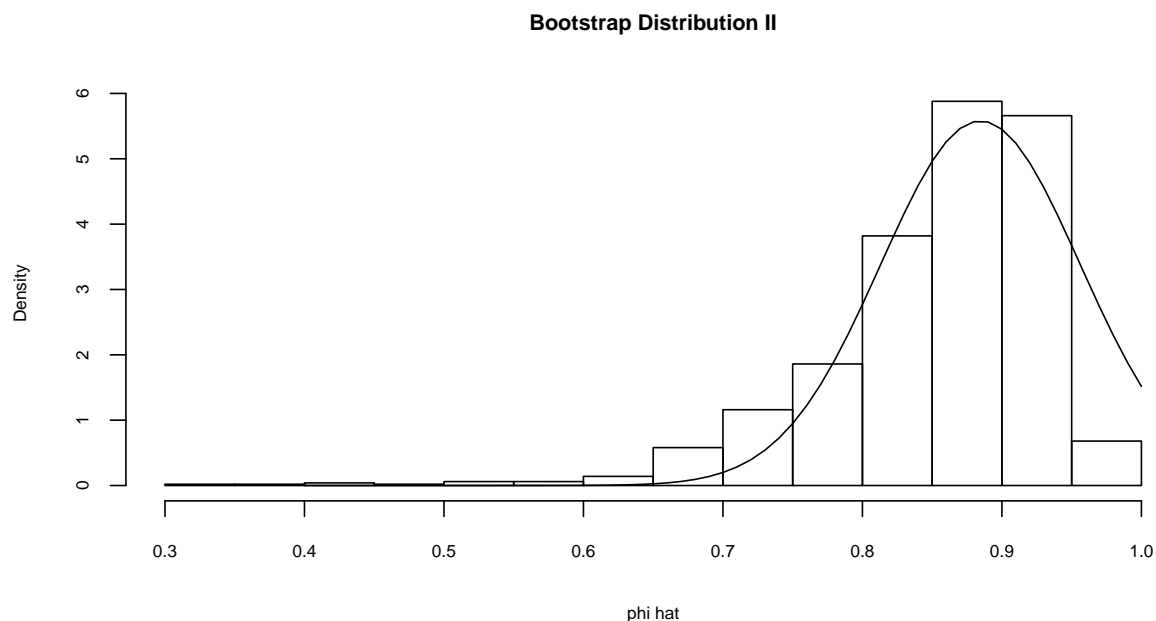
```
x=seq(from=0.4,to=1,by=0.01); y=dnorm(x,mean=0.8846,sd=0.0715)
# Setup asymptotic distribution.
```

```
set.seed(12345)
# Bootstrap Method I
```

```
coefmI <- arima.boot(result,cond.boot=T,is.normal=T,B=1000,init=series)
win.graph(width=4,height=3,points=8)
hist(coefmI[,1],xlab='phi hat',main='Bootstrap Distribution I',freq=F)
lines(x,y,type='l')
```



```
# Method II
coefmII <- arima.boot(result,cond.boot=T,is.normal=F,B=1000,init=series)
hist(coefmII[,1],xlab='phi hat',main='Bootstrap Distribution II',freq=F)
lines(x,y,type='l')
```



The method I bootstrap distribution is skewed somewhat strongly toward lower values and, ofcourse, the asymptotic normal distribution is symmetric. The asymptotic distribution has significant probability above $\phi = 1$.

The Method II bootstrap distribution is also skewed strongly toward lower values and, of course, the asymptotic normal distribution is symmetric. The asymptotic distribution has significant probablty above $\phi = 1$.

8.9

```
data(robot)
mod1 <- arima(robot,order=c(1,0,0)); res1=rstandard(mod1)
mod1

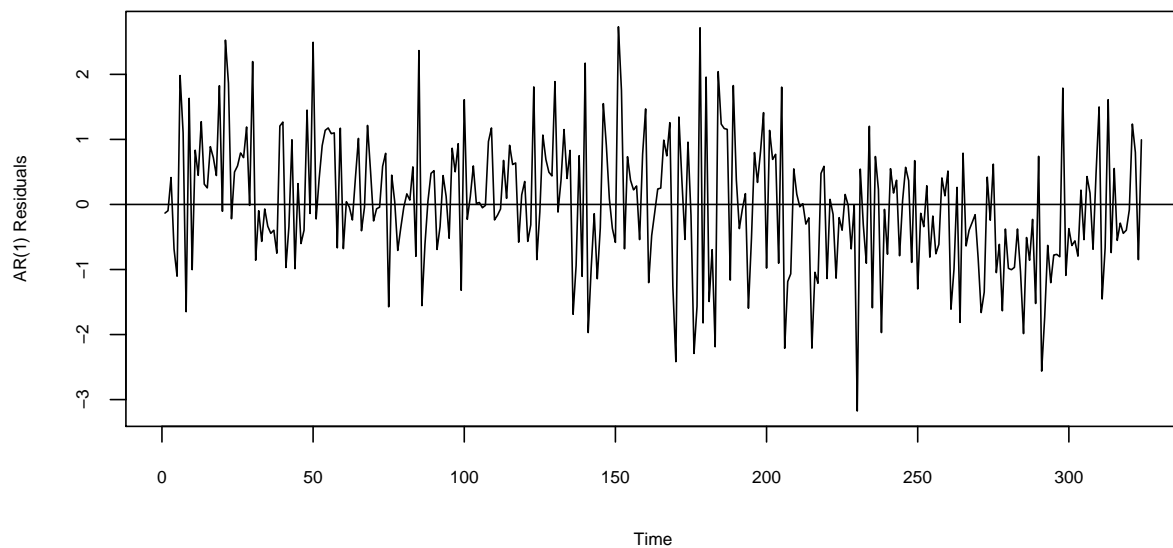
##
## Call:
## arima(x = robot, order = c(1, 0, 0))
##
## Coefficients:
##          ar1  intercept
##      0.3074    0.0015
## s.e.  0.0528    0.0002
##
## sigma^2 estimated as 6.482e-06:  log likelihood = 1475.54,  aic = -2947.08
mod2 <- arima(robot,order=c(0,1,1)); res2=rstandard(mod2);
mod2

##
## Call:
## arima(x = robot, order = c(0, 1, 1))
##
## Coefficients:
```

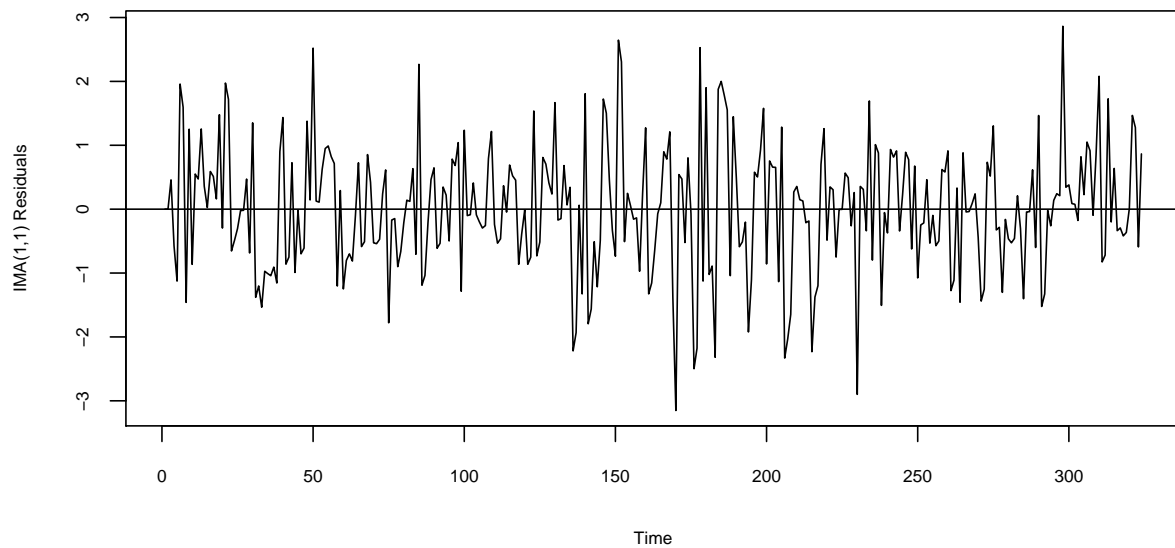
```
##          ma1
##        -0.8713
## s.e.    0.0389
##
## sigma^2 estimated as 6.069e-06:  log likelihood = 1480.95,  aic = -2959.9
```

Both models have statistically significant parameter estimates. The log likelihood and AIC values are just a little better in the IMA(1,1) model.

```
win.graph(width=6.5,height=3,pointsize=8)
plot(res1,ylab='AR(1) Residuals'); abline(h=0)
```

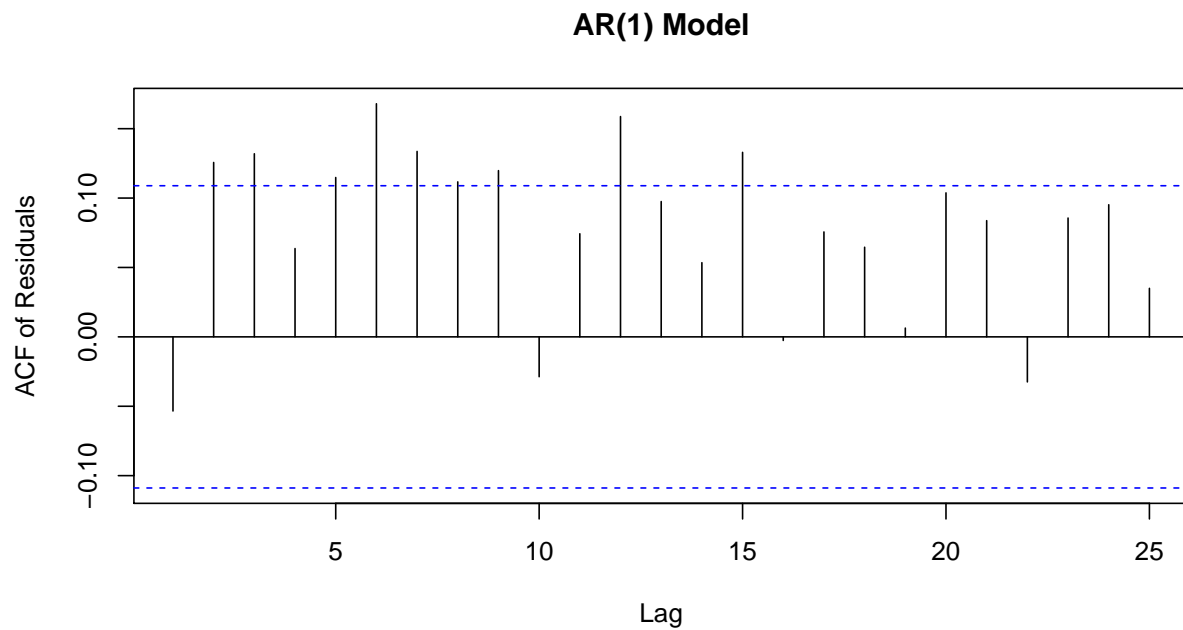


```
plot(res2,ylab='IMA(1,1) Residuals'); abline(h=0)
```



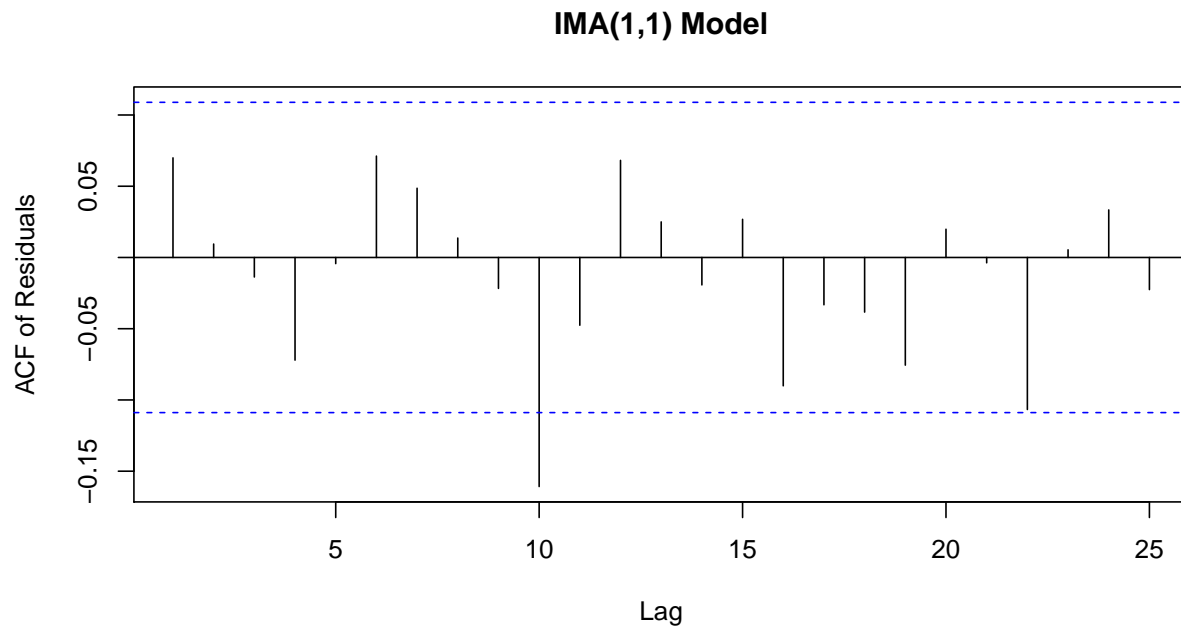
There may be a little drift in these residuals over time. There are more positive residuals in the first half of the series and more negative in the last half. The drift observed in the residuals of the AR(1) model does not seem to appear with the IMA(1,1) model residuals. We proceed to look at correlation in the residuals.

```
acf(residuals(mod1), main='AR(1) Model', ylab='ACF of Residuals'); LB.test(mod1)
```



##

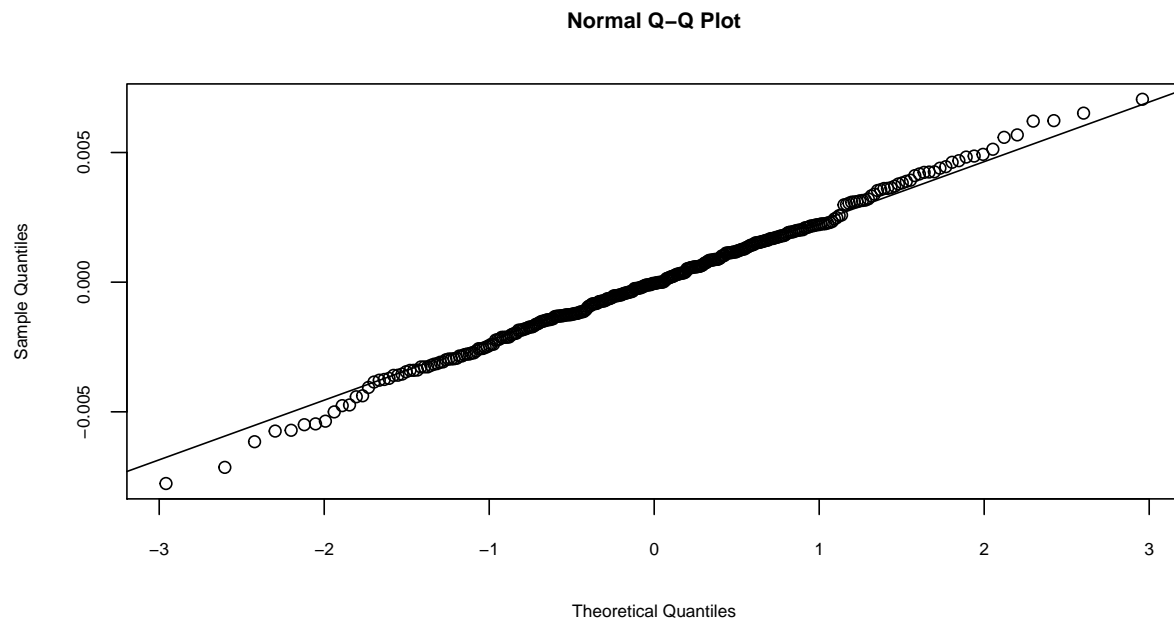
```
## Box-Ljung test
##
## data: residuals from mod1
## X-squared = 52.512, df = 11, p-value = 2.201e-07
acf(residuals(mod2), main='IMA(1,1) Model',ylab='ACF of Residuals'); LB.test(mod2)
```



```
##
## Box-Ljung test
##
## data: residuals from mod2
## X-squared = 17.081, df = 11, p-value = 0.1055
```

The residuals from the AR(1) model clearly have too much autocorrelation. The residuals from the IMA(1,1) model are much less correlated with only one significant autocorrelation at lag 10. The Ljung-Box test indicates that, jointly, the residual autocorrelations are not too large. Next we check out normality of the error terms by first displaying a Q-Q plot of the residuals.

```
win.graph(width=3,height=3,pointsize=8)
qqnorm(residuals(mod2)); qqline(residuals(mod2))
```

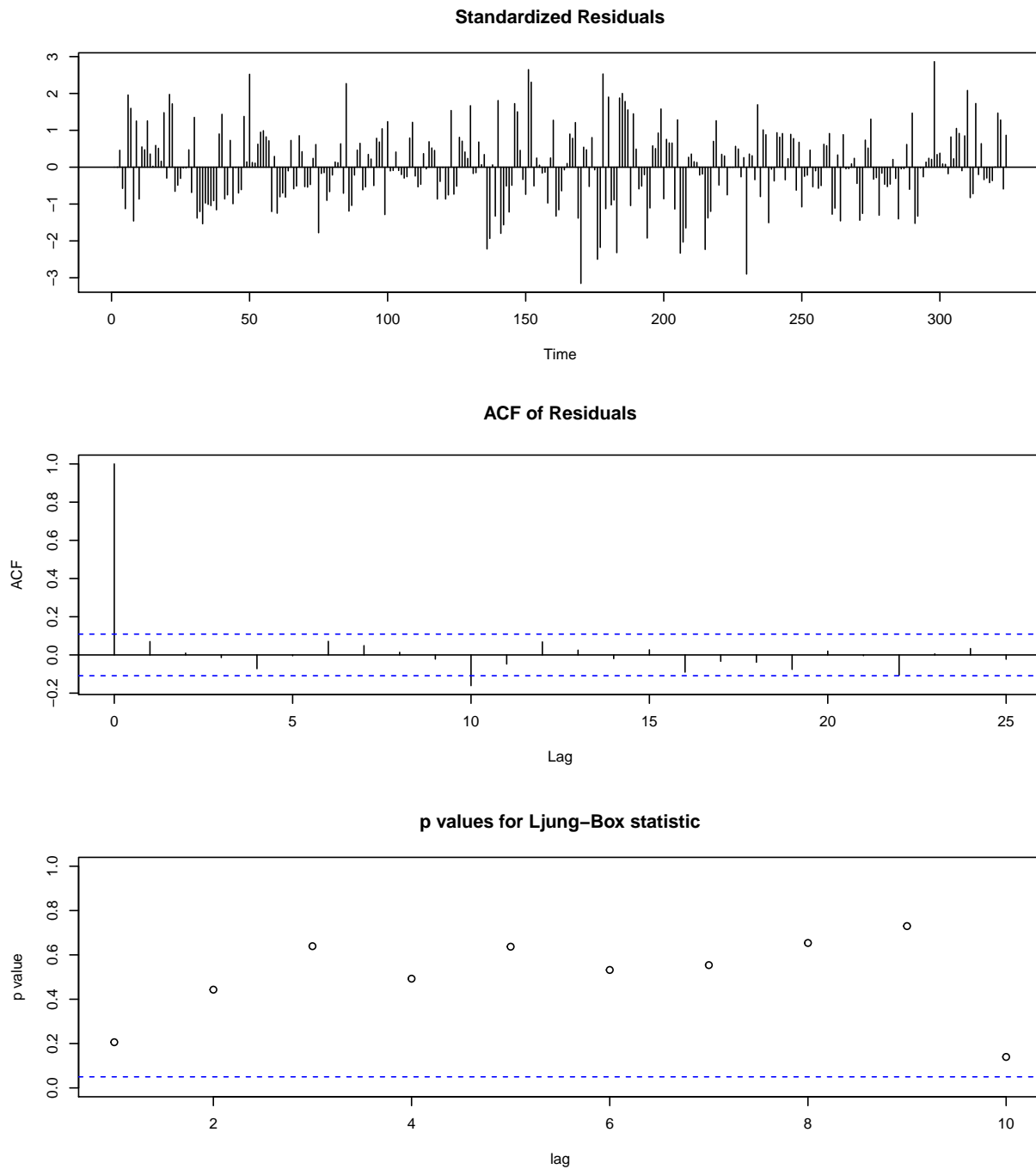


```
shapiro.test(residuals(mod2))
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  residuals(mod2)  
## W = 0.99689, p-value = 0.791
```

The Q-Q plot looks good. Normality looks like a viable assumption for the error terms in the IMA(1,1) model for the robot time series. Finally, let's look at the results from the `tsdiag` command.

```
tsdiag(mod2)
```

Summarizing: The robot time series seems to be well-represented by the IMA(1,1) model.