

STAT2003: Assignment 2

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Question 1

Kandanamond (2013) Factorial Design:

Two simulations were conducted under the ARIMA model: ARMA (stationary) and the IMA (non-stationary). In the literature by Kandanamond (2013), once the dataset for both ARMA and IMA are obtained, the SVM and ANN methods along with the other AR and MA settings are applied to obtain the MAPEs (Mean Absolute Percentage Error). Kandanamond (2013) concluded that the ANN worked better in forecasting the stationary model and the SVM worked better in forecasting the non-stationary model. The factorial components of the experiments are as follows:

Response	MAPE
Factor	Machine Learning Algorithms, AR (ϕ), and MA (θ)
Levels	2 levels for each factor. Machine Learning: ANN and SVM. AR: -0.9 and 0.9. MA: -0.9 and 0.9
Replicates	5
Structure: Stationary	2^3 Factorial Experiment with 5 replications. Total number of observations are 40
Structure: Non-stationary	2^2 Factorial Experiment with 5 replications. Total number of observations are 20

Recreated Experimental Results:

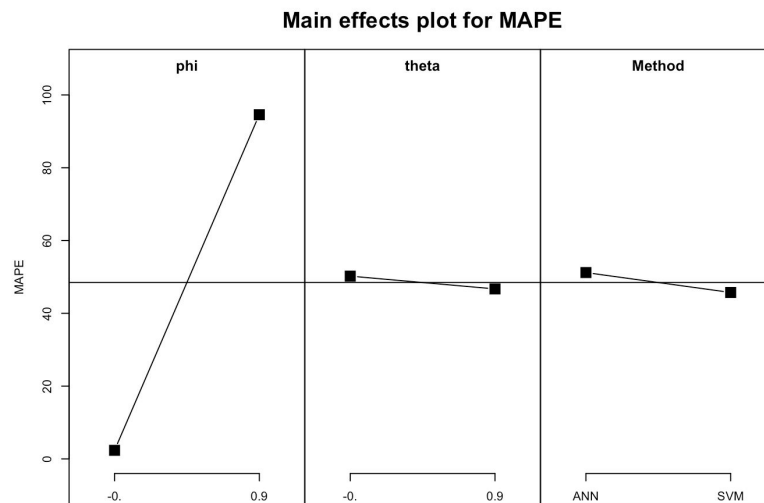
Stationary:

The MAPEs recorded in the literature were duplicated for the purposes of the current study (with inversed MAPE values) and ANOVA was applied.

After running the ANOVA, there is evidence to suggest that there exists a significant interaction effect between ϕ , θ and the method (ANN or SVM). Below are the ANOVA table output

and the Main Effects Plot for stationary. The ANOVA table is identical to that shown in the literature for the stationary process.

```
##               Df Sum Sq Mean Sq  F value    Pr(>F)
## phi             1  85026    85026 3664.386 < 2e-16 ***
## theta           1   124      124   5.325 0.02764 *
## Method          1   300      300  12.928 0.00107 **
## phi:theta       1   256      256  11.039 0.00224 **
## phi:Method      1   231      231   9.960 0.00347 **
## theta:Method    1   256      256  11.029 0.00225 **
## phi:theta:Method 1   250      250  10.792 0.00247 **
## Residuals      32    743        23
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



Assumptions:

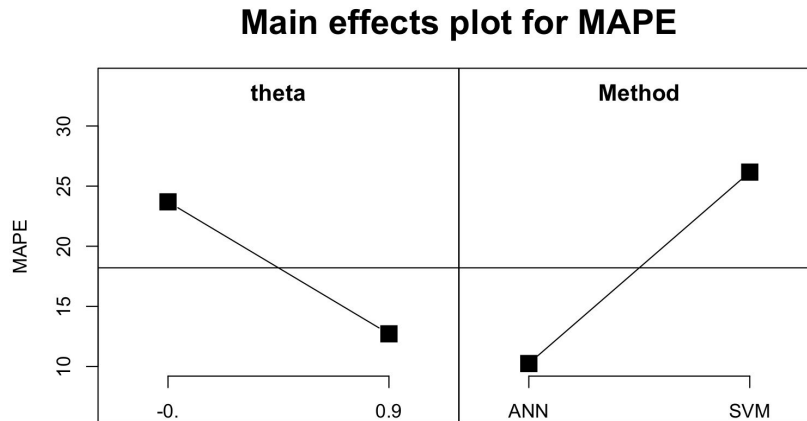
The literature failed to look at the assumptions of ANOVA. Shapiro-Wilk test of normality of residuals shows that $p = 0.1781$ which is larger than 0.05. Thus, the assumption of normality of residuals has been met. Levene's Test of homogeneity of variance indicates that at 5% level of significance there is insufficient evidence ($F(7,32) = 1.6237$, $P = 0.1645$) to conclude that assumption of homogeneity of variance has been met. Thus all assumptions have been satisfied for the stationary case.

Non-Stationary:

However, for the non-stationary data, the ANOVA table does not match that shown in the literature. There exists a significant interaction effect between theta and the method (ANN or SVM) when looking at the MAPEs.

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
theta	1	602.4	602.4	20.64	0.000333	***
Method	1	1267.0	1267.0	43.41	6.24e-06	***
theta:Method	1	662.5	662.5	22.70	0.000211	***
Residuals	16	467.0	29.2			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1



Assumptions:

Shapiro-Wilk test of normality of residuals shows that $p = 0.008475$ which is less than 0.05. Thus, the assumption of normality of residuals has not been met. Levene's Test of homogeneity of variance indicates that at 5% level of significance there is sufficient evidence ($F(3,16) = 5.52$, $P = 0.008498$) to conclude that the assumption of homogeneity of variance has been met.

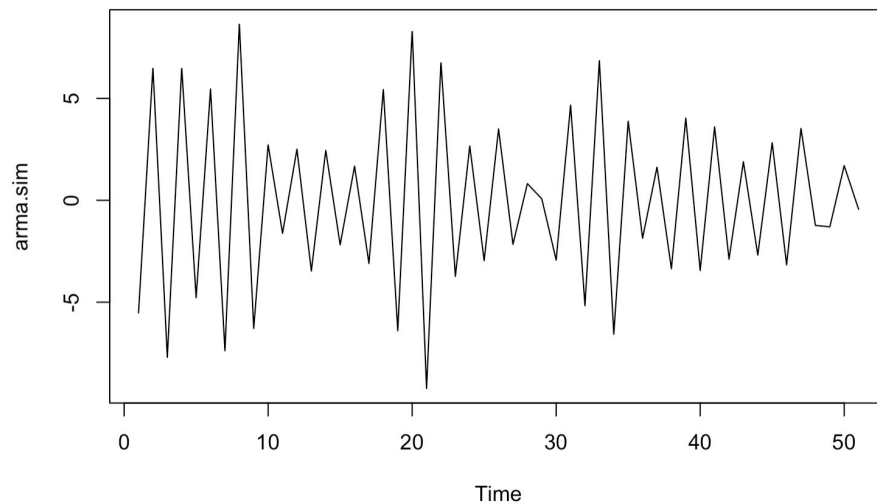
The non-stationary data failed the Shapiro Wilk's Test but passed the Levene Test when MAPE was inversed. However, this was not the case when the inverse was removed. Without inversed MAPEs, the dataset passed Shapiro Wilk's Test but failed to pass the Levene's Test (as shown in the Appendix). Other transformations such as square root, log, square, were also trialed but did not satisfy all assumptions. Thus it will be necessary to trial non-parametric model on the non-stationary data.

Question 2

Simulating using ARMA & IMA Models

Stationary Process:

ARMA model was used to simulate time series data based on random phi and theta values ranging from -0.9 to 0.9 as shown in the plot below.



51 values were simulated at one time, then the first 50 values were used to train the SVM model to predict the 51st value. MAPE was then calculated using the equation: $|(\text{actual} - \text{pred})/\text{actual}|$. This model training was repeated 50 times using 50 sets of ARMA simulated values. The mean of the 50 MAPEs was then derived. This whole process was then repeated to produce 100 MAPE values in the end.

Non-Stationary Process:

The process is identical to that discussed for Stationary but now only theta (from -0.9 to 0.9) is used to simulate the values using IMA.

Dace Kriging Model

Stationary Process:

```
-----
Dace Kriging model.
```

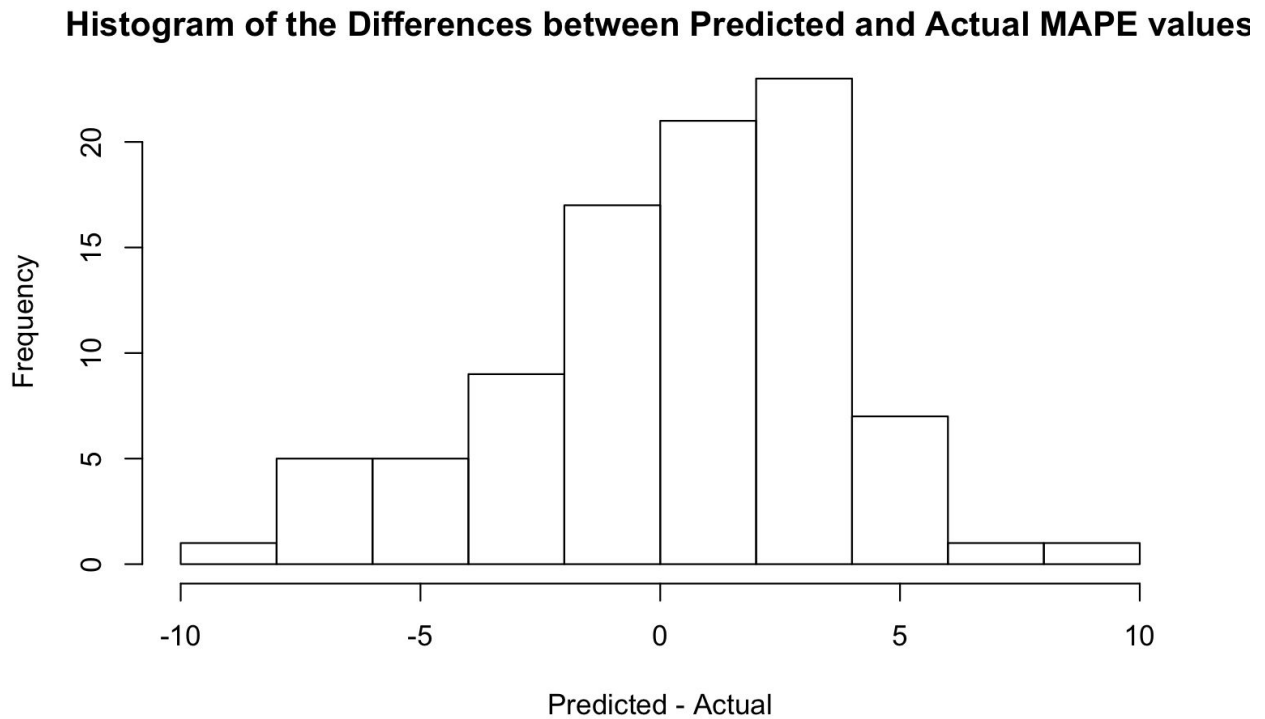
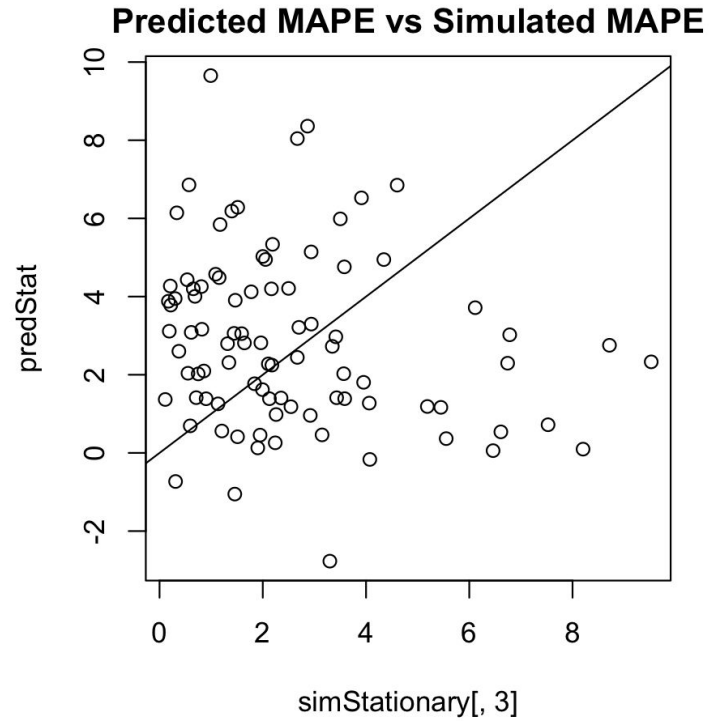
```
-----
Estimated activity parameters (theta) sorted
from most to least important variable
x1 x2
2.818383 2.818383
```

```
exponent(s) p:
1.9 1.9
```

```
Estimated regularization constant (or nugget) lambda:
0.999
```

```
Number of Likelihood evaluations during MLE:
```

```
-----
```



As can be seen, the majority of the differences between predicted MAPE values and actual values centre around 0, when using the Krigging model to produce new MAPE values for the

stationary process. Thus the current model is not bad at predicting MAPE values - although note that there are also quite a few bad predictions.

Non-Stationary Process:

Dace Kriging model.

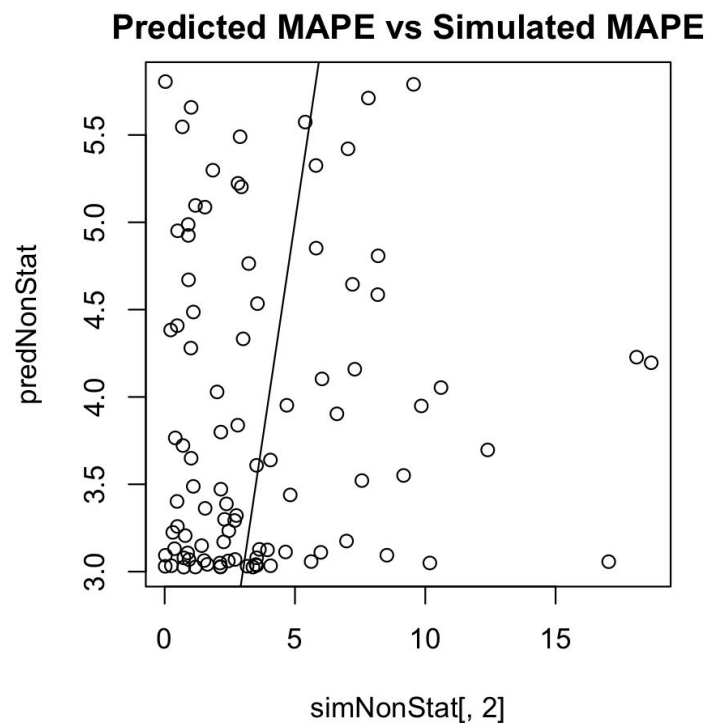
Estimated activity parameters (theta) sorted
from most to least important variable

x1
0.03406543

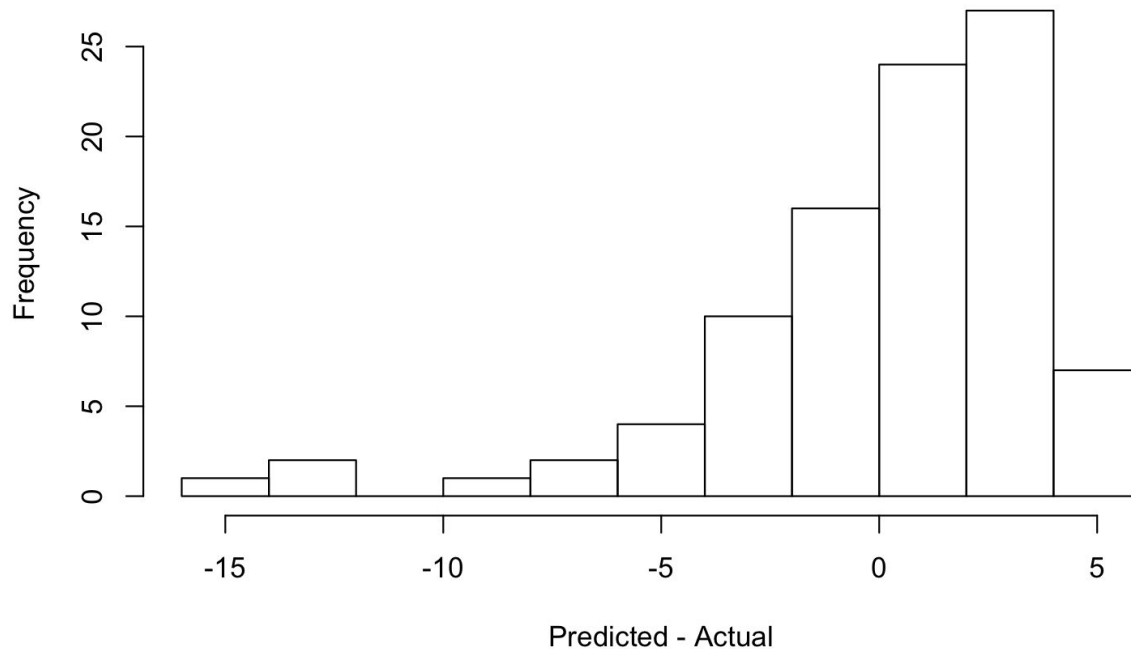
exponent(s) p:
2

Estimated regularization constant (or nugget) lambda:
0.7406117

Number of Likelihood evaluations during MLE:



Histogram of the Differences between Predicted and Actual MAPE values



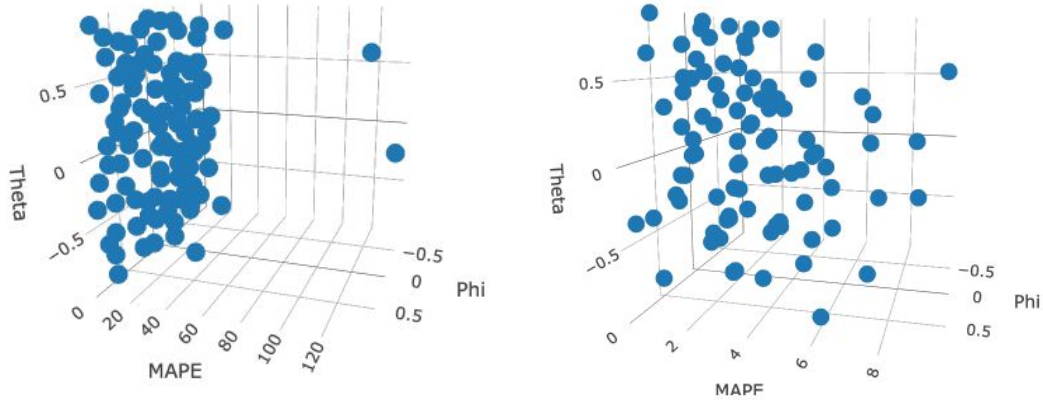
As can be seen, the majority of the differences between predicted MAPE values and actual values centre around 0, when using the Krigging model to produce new MAPE values for non-stationary process. However there is some skew to the left which may indicate that a transformation is necessary and it also exposes the fact that many of the predicted values are smaller than the actual value of the MAPEs.

Optimality Criterion

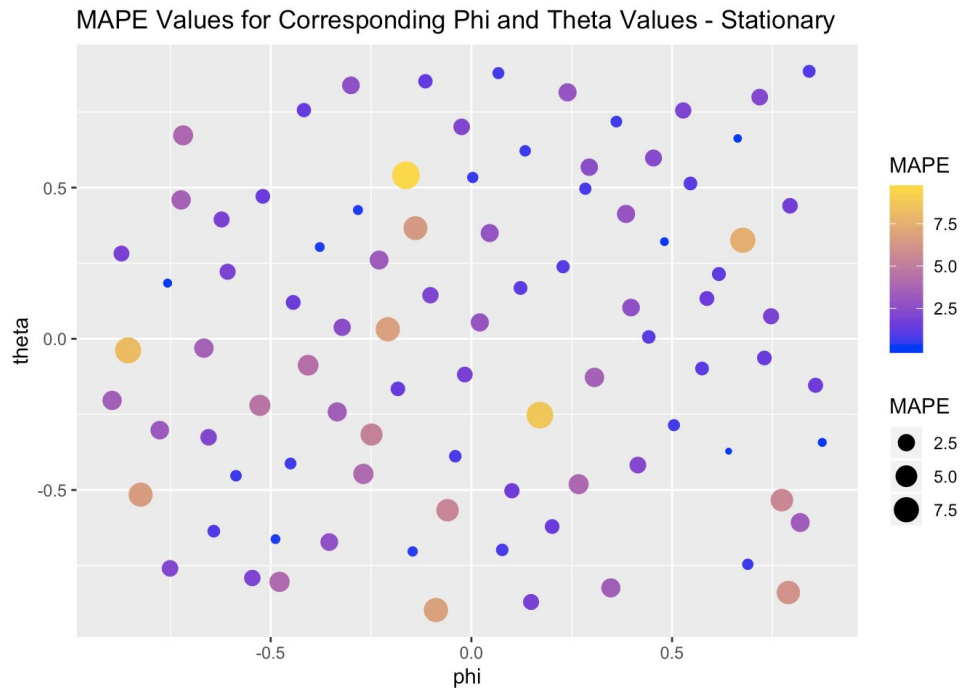
Overall Methodology:

Firstly we generated the design for the Phi (AR) and Theta (MA) parameters using the maximin LHS criterion. We generated 100 pairs of phi and theta and simulated 100 sequences of time series data. Each sequence used to train the SVM to predict the last value in the sequence. This process was repeated 50 times (for each sequence out of the 100) to obtain the average of the SVM's prediction MAPEs. We resulted in having 100 data points for both stationary and non-stationary processes. The non-stationary only required the theta parameter, so slight adjustments had been made.

Stationary Process:

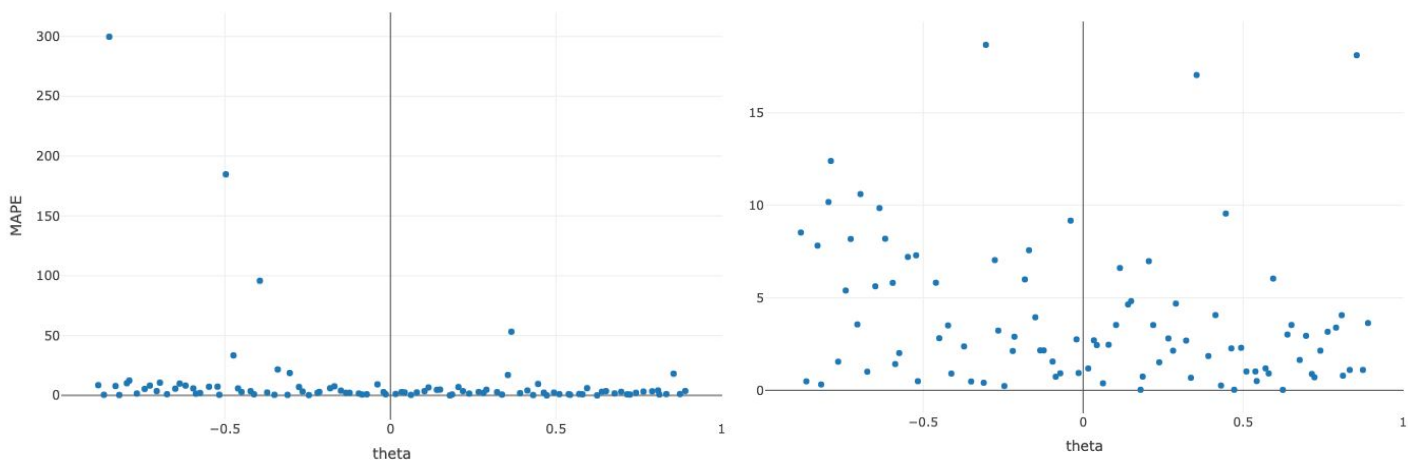


We originally had 100 MAPE values, however, certain extreme outliers affected the analysis. So they were deleted to produce a clear and in-depth display of the results.

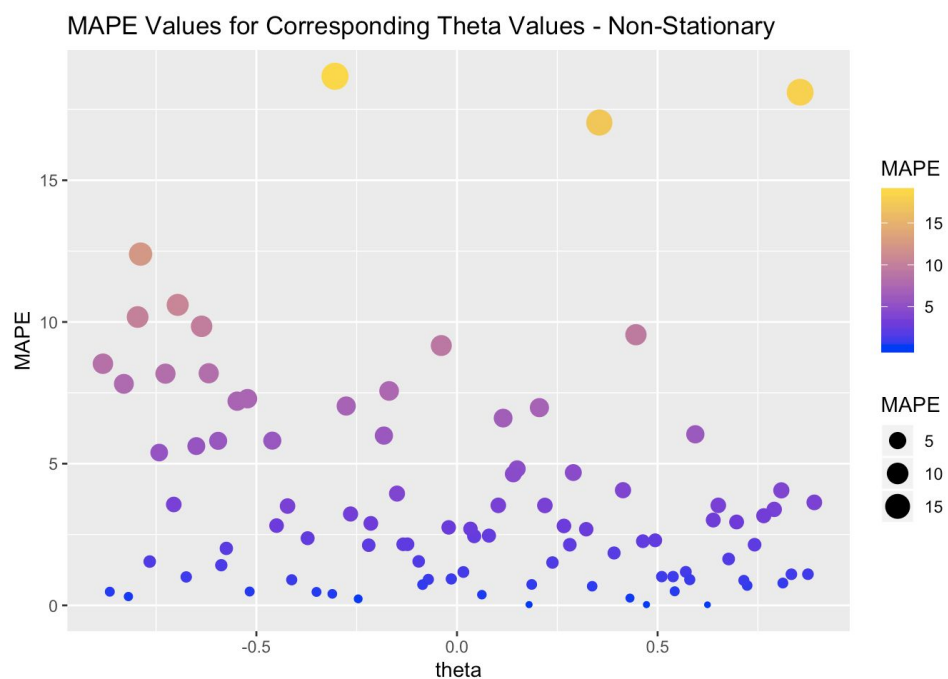


As can be seen the distribution is quite random, so it seems that SVM performance was not dependent on the different phi and theta settings. Upon closer inspection however it may be argued that smaller values of phi and theta result in higher MAPEs.

Non-Stationary Process:



Extreme outliers were also removed, as seen on the left plot.



As the non-stationary process only had the theta as the parameter, the plot above shows the effect of theta towards MAPE directly. There is a bit of clustering around medium MAPE values and the lower theta values. There seem to be smaller MAPE values as the value of theta increases, except for a few outliers. Note that the predicted MAPE values alongside theta values are also shown in the appendix.

Appendix:

Non-Stationary without Inverse Transformation that the paper applies:

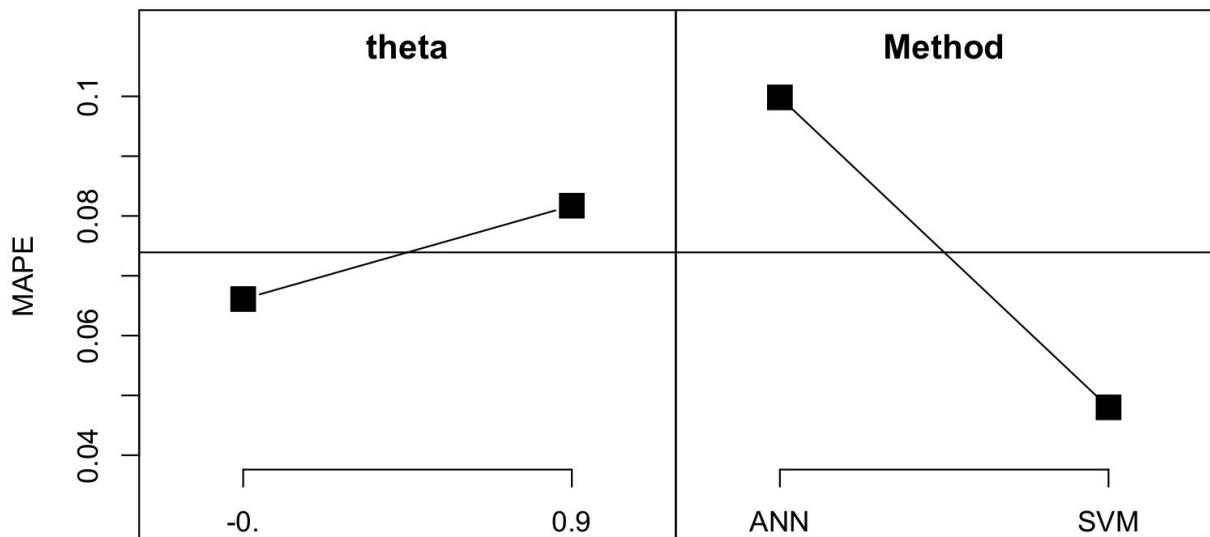
ANOVA:

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
theta	1	0.001218	0.001218	6.954	0.0179 *
Method	1	0.013424	0.013424	76.661	1.69e-07 ***
theta:Method	1	0.002649	0.002649	15.130	0.0013 **
Residuals	16	0.002802	0.000175		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Main Effects:

Main effects plot for MAPE

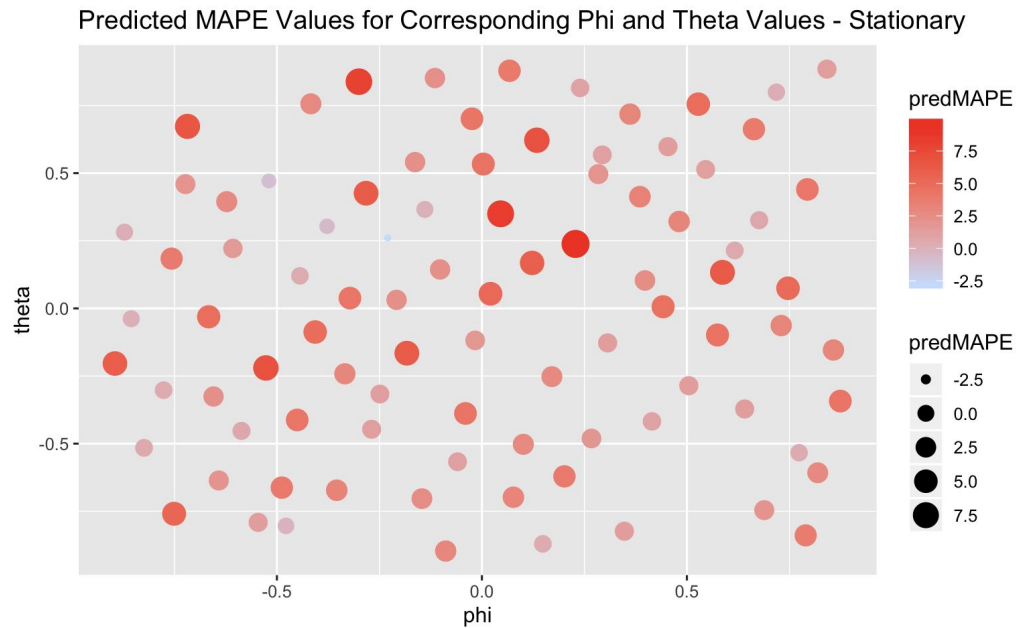


Assumptions when MAPE is not inversed:

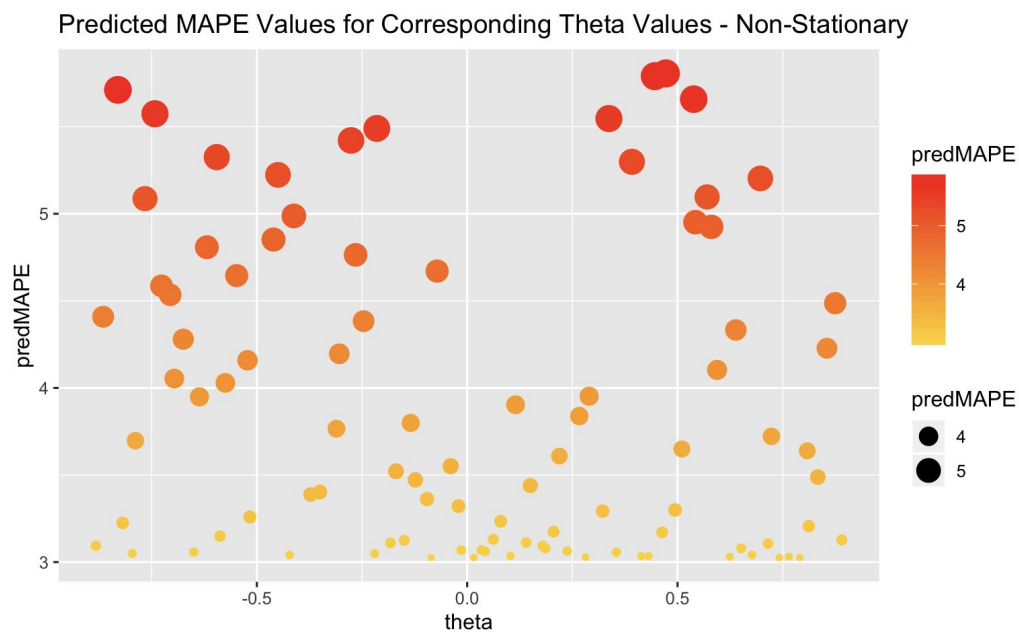
Shapiro-Wilk test of normality of residuals shows that $p = 0.1838$ which is larger than 0.05. Thus, the assumption of normality of residuals has been met.

Levene's Test of homogeneity of variance indicates that at 5% level of significance there is insufficient evidence ($F(3,16) = 1.30$, $P = 0.2814$) to conclude that assumption of homogeneity of variance has been met.

Predicted MAPE for Stationary:



Predicted MAPE for Non-Stationary:



R Code for Assignment 2

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13/10/2019

```
library(FrF2)
library(lhs)
library(ggplot2)
library(SPOT)
library(lattice)
```

Stationary Case

```
stationary = read.csv("stationary.csv", header = TRUE, row.names = 1)
stationary$phi <- as.factor(stationary$phi)
stationary$theta <- as.factor(stationary$theta)
stationary$MAPE <- 1/(stationary$MAPE)
head(stationary)
```

```
##      phi theta Method      MAPE
## 1 -0.9  -0.9    ANN  3.3048019
## 2 -0.9  -0.9    ANN  3.5511364
## 3 -0.9  -0.9    ANN  1.2526462
## 4 -0.9  -0.9    ANN  0.6029109
## 5 -0.9  -0.9    ANN  0.7708852
## 6  0.9  -0.9    ANN 100.8064516
```

```
st_anova = aov(MAPE ~ phi * theta * Method, data = stationary)
summary(st_anova)
```

```
##              Df Sum Sq Mean Sq  F value    Pr(>F)
## phi              1   85026    85026 3664.386 < 2e-16 ***
## theta            1    124      124   5.325 0.02764 *
## Method           1     300      300  12.928 0.00107 **
## phi:theta         1     256      256  11.039 0.00224 **
## phi:Method        1     231      231   9.960 0.00347 **
## theta:Method       1     256      256  11.029 0.00225 **
## phi:theta:Method   1     250      250  10.792 0.00247 **
## Residuals        32      743       23
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

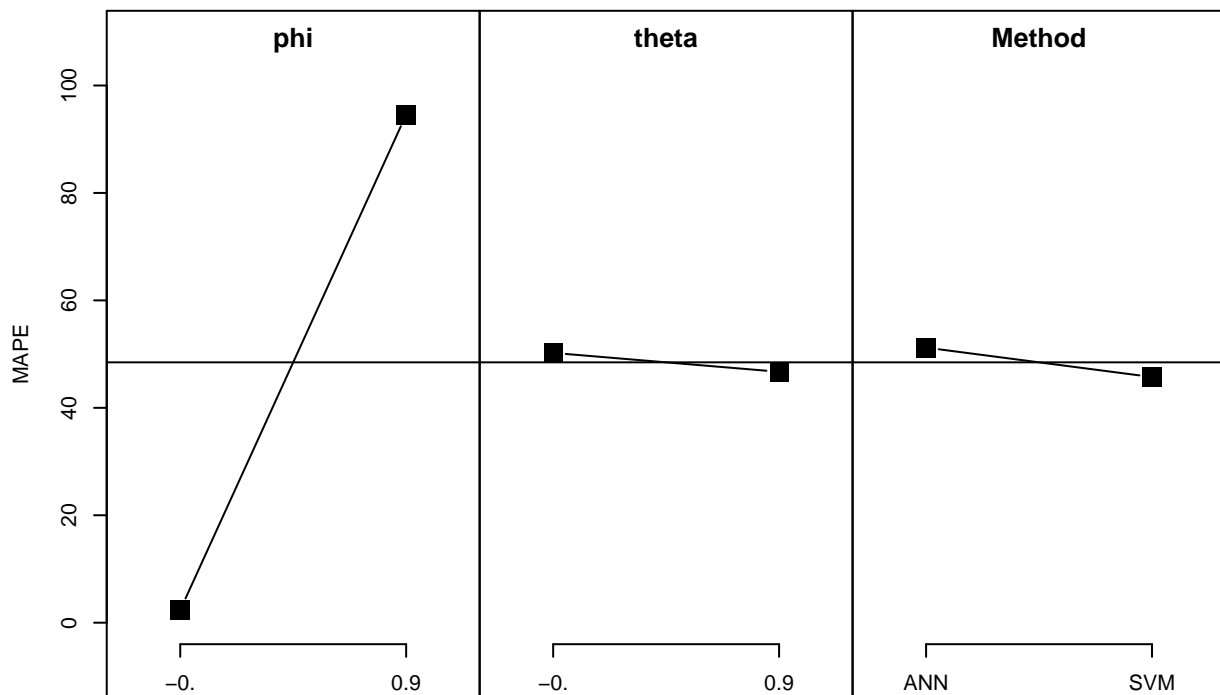
```
step(st_anova)
```

```
## Start:  AIC=132.85
## MAPE ~ phi * theta * Method
##
##              Df Sum of Sq    RSS    AIC
## <none>                742.51 132.85
## - phi:theta:Method   1    250.41  992.92 142.47
##
## Call:
## aov.default(formula = MAPE ~ phi * theta * Method, data = stationary)
```

```
##
## Terms:
##           phi      theta  Method phi:theta phi:Method
## Sum of Squares 85025.95  123.56   299.98   256.14   231.11
## Deg. of Freedom      1      1      1      1      1
##           theta:Method phi:theta:Method Residuals
## Sum of Squares      255.90      250.41   742.51
## Deg. of Freedom      1      1      32
##
## Residual standard error: 4.816983
## Estimated effects may be unbalanced
```

```
#from library FrF2
MEPlot(st_anova)
```

Main effects plot for MAPE



```
shapiro.test(st_anova$residuals)
```

```
##
## Shapiro-Wilk normality test
##
## data: st_anova$residuals
## W = 0.96078, p-value = 0.1781
```

```
library(car)
leveneTest(st_anova)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value Pr(>F)
## group 7  1.6237 0.1645
##      32
```

Non-Stationary Case

```
nonstationary = read.csv("non-stationary.csv", header = TRUE, row.names = 1)
nonstationary
```

```
##      theta Method      MAPE
## 1   -0.9     ANN 0.094206
## 2   -0.9     ANN 0.090310
## 3   -0.9     ANN 0.081850
## 4   -0.9     ANN 0.133830
## 5   -0.9     ANN 0.117440
## 6    0.9     ANN 0.091490
## 7    0.9     ANN 0.088000
## 8    0.9     ANN 0.116300
## 9    0.9     ANN 0.089100
## 10   0.9     ANN 0.095680
## 11  -0.9     SVM 0.020776
## 12  -0.9     SVM 0.024260
## 13  -0.9     SVM 0.039130
## 14  -0.9     SVM 0.022100
## 15  -0.9     SVM 0.037200
## 16   0.9     SVM 0.066770
## 17   0.9     SVM 0.062580
## 18   0.9     SVM 0.076060
## 19   0.9     SVM 0.066620
## 20   0.9     SVM 0.064560
```

```
nonstationary$theta <- as.factor(nonstationary$theta)
nonstationary$MAPE <- (1/nonstationary$MAPE)
head(nonstationary)
```

```
##      theta Method      MAPE
## 1   -0.9     ANN 10.615035
## 2   -0.9     ANN 11.072971
## 3   -0.9     ANN 12.217471
## 4   -0.9     ANN  7.472166
## 5   -0.9     ANN  8.514986
## 6    0.9     ANN 10.930156
```

```
non_st_anova = aov(MAPE ~ theta * Method, data = nonstationary)
summary(non_st_anova)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)
## theta          1  602.4   602.4   20.64 0.000333 ***
## Method          1 1267.0  1267.0   43.41 6.24e-06 ***
## theta:Method    1  662.5   662.5   22.70 0.000211 ***
## Residuals      16  467.0    29.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
step(non_st_anova)
```

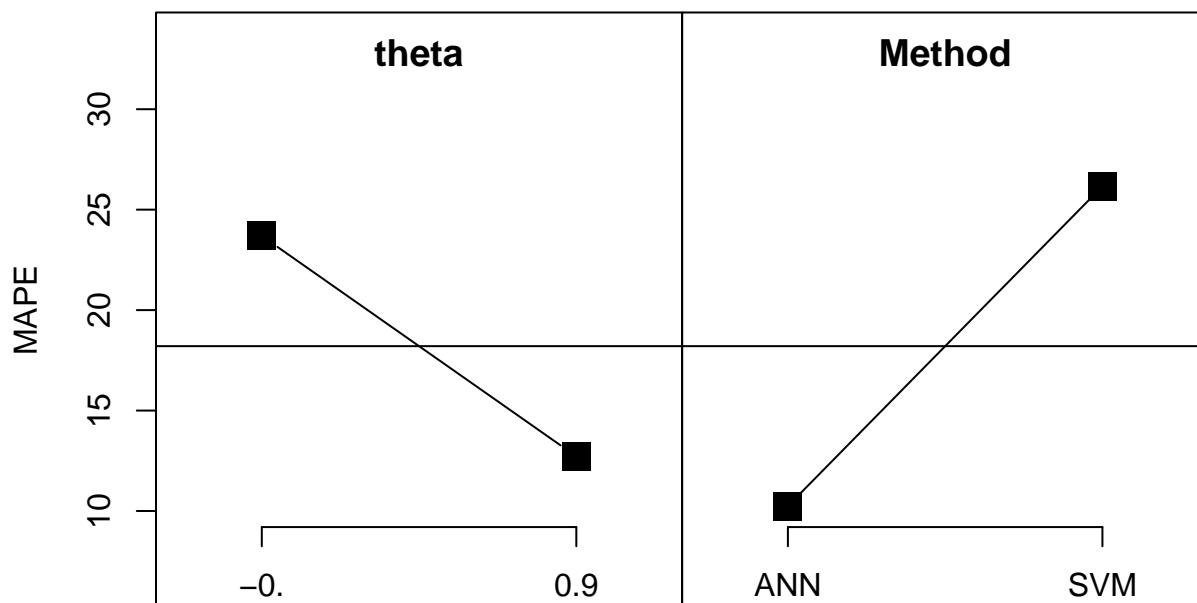
```
## Start:  AIC=71.01
## MAPE ~ theta * Method
##
##              Df Sum of Sq    RSS    AIC
```

```
## <none>                                467.01 71.012
## - theta:Method 1      662.51 1129.52 86.676

## Call:
## aov.default(formula = MAPE ~ theta * Method, data = nonstationary)
##
## Terms:
##              theta      Method theta:Method Residuals
## Sum of Squares  602.3708 1266.9630      662.5116  467.0129
## Deg. of Freedom      1          1          1       16
##
## Residual standard error: 5.40262
## Estimated effects may be unbalanced
```

```
MEPlot(non_st_anova)
```

Main effects plot for MAPE



```
shapiro.test(non_st_anova$residuals)
```

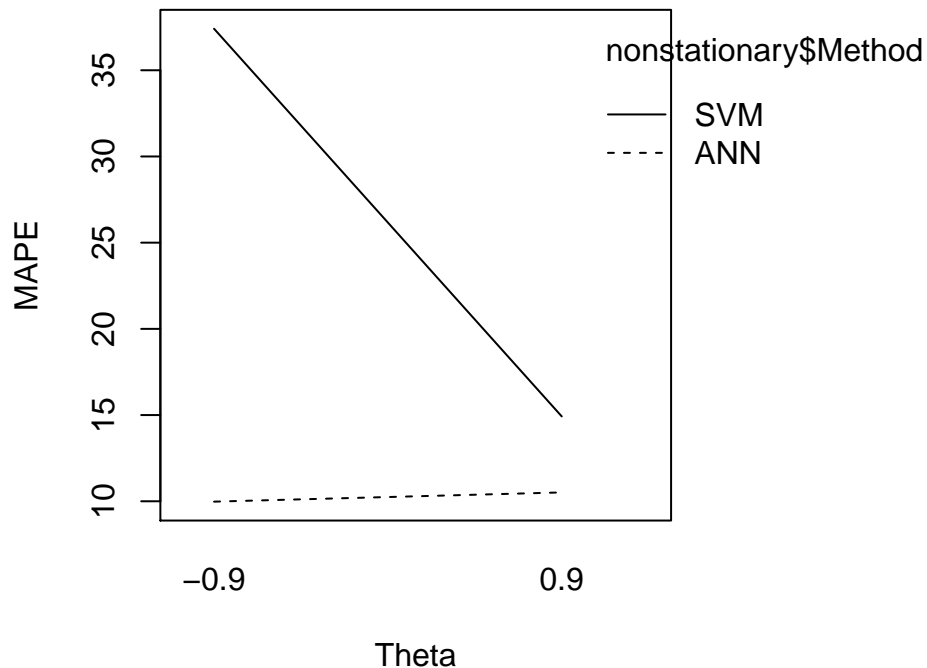
```
##
## Shapiro-Wilk normality test
##
## data:  non_st_anova$residuals
## W = 0.86185, p-value = 0.008475
```

```
leveneTest(non_st_anova)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##      Df F value    Pr(>F)
## group 3  5.5222 0.008498 **
##      16
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
par(pty='s')
interaction.plot(nonstationary$theta, nonstationary$Method, nonstationary$MAPE, xlab='Theta', ylab='MAPE')
```

Non-Stationary – Interaction



Check for Normality and Homogeneity of Variance

High theta and low theta error is other way around for the STAT2003 assignment Q1 because inverting the model will make larger errors small and small errors large. This means that it is now the larger errors that show smaller error!

Make sure to use multidimensional krigging in the second question of the assignment.

Applying inverse on non-stationary actually makes it fail the Levene test of homogeneity although it makes up for the other assumption of normality. But Levene homogeneity of variance is arguably the more important assumption to hold.

Thus the article does both stationary and non-stationary cases wrong!

Question 2

```
library(mvtnorm)
library(e1071)
```

Stationary Process

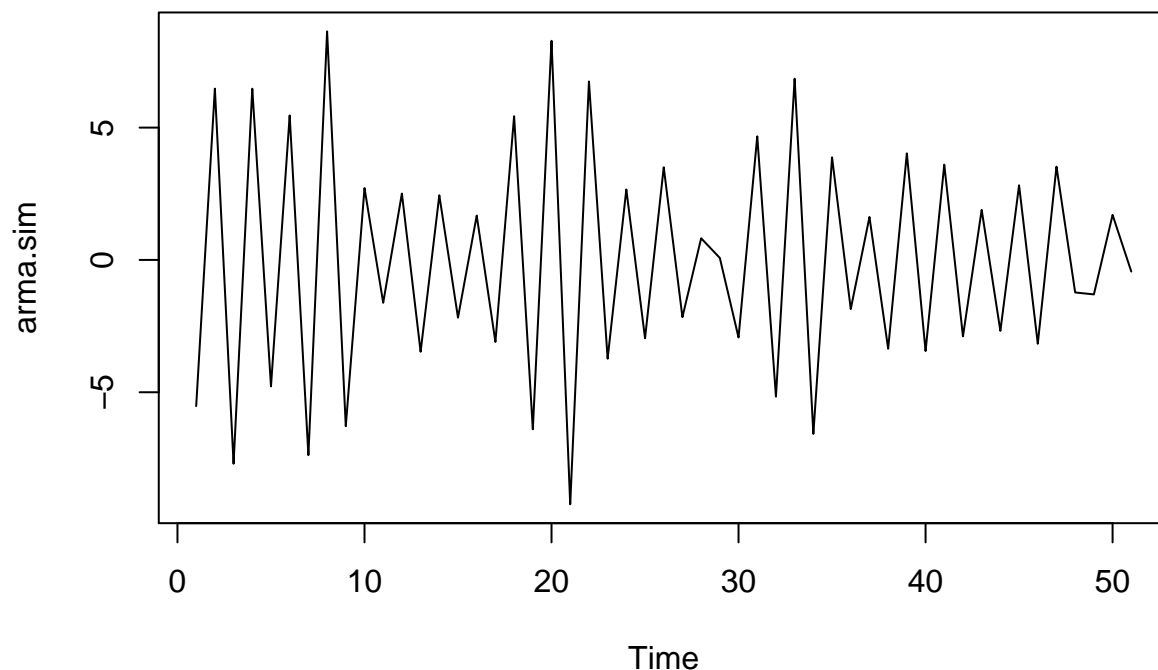
```
#Stationary process - Simulation Test
set.seed(61)
arma.sim <- arima.sim(model=list(ar=-0.9,ma=-0.9),n=51)
arma.sim
```

```
## Time Series:
```



```
## Start = 1
## End = 51
## Frequency = 1
## [1] -5.52412295  6.47309097 -7.70124679  6.46978196 -4.77689181
## [6]  5.45929444 -7.37829255  8.63630155 -6.28486440  2.71437507
## [11] -1.61894120  2.50796915 -3.47061185  2.44251798 -2.18049648
## [16]  1.67534722 -3.09863685  5.43139381 -6.40205106  8.27961566
## [21] -9.23274825  6.74451014 -3.73189614  2.66370874 -2.95950364
## [26]  3.50133309 -2.16212065  0.81852349  0.07435405 -2.93009761
## [31]  4.67010294 -5.16661964  6.84739078 -6.57443077  3.87830163
## [36] -1.85745259  1.62376942 -3.35658313  4.02793098 -3.44350568
## [41]  3.60182569 -2.88885637  1.89381802 -2.68262368  2.82001595
## [46] -3.16803091  3.52396275 -1.22926979 -1.30301083  1.70207093
## [51] -0.43889334
```

```
ts.plot(arma.sim)
```



Function for simulating data

```
# Simulate ARIMA based on the phi and theta parameter as function input
# Output the result as a 51x1 matrix with each row having 51 sequences of ts data
```

```
simData <- function(phi,theta){
  all_training=NULL
  for (i in 1:50){
    armaSet = arima.sim(model=list(ar=phi, ma=theta),n=51)
    all_training = rbind(all_training, armaSet[1:51])
  }
  return(all_training)
}
```

```
#LLdata means low setting for both phi and theta
#LLdata has 50 rows and 51 columns
```

```
#set.seed(61)
#phi;theta <- runif(2,-0.9,0.9)
#data = simData(phi,theta)
```

TRIAL - start SVM prediction using first row

```
# training data is column 1 to 50
# test data is column 51st
# we only use the first row to test out.. not sure how to run all 50 rows..
#trainSVMDat = data.frame(timestamp=c(seq(1,50,1)),value=data[1,1:50])
#testSVMDat = data.frame(timestamp=1,value=data[1,51])

# svm(y~x,data=training)
# the epsilon, gamma and cost values were taken from the paper
# the syntax we used is "to predict value using timestamp"
# predict(trainingmodel, newdata=testset)
#modelSVM = svm(value~timestamp,data=trainSVMDat,epsilon=0.1,gamma=0.1,cost=10)
#predSVM = predict(LHmodelSVM,newdata=testSVMDat); predSVM

# MAPE is the prediction - actual data divided by the prediction
#MAPE = (LHpredSVM - testSVMDat[,2])/LHpredSVM; abs(MAPE)
```

Function for automating the generation of MAPE values in SVM (Nina did after Basement Cafe :))

```
#Automating the MEAN ABSOLUTE VALUE of MAPE - 1 replication
calc_mape = function(data_name){
  mape_matrix = NULL
  for (i in 1:50){
    #create the training and testing dataset from the chosen dataset (as per input)
    #each train and test is only one row of the 50 rows dataset
    trainDat = data.frame(timestamp=c(seq(1,50,1)),value=data_name[i,1:50]);trainDat
    testDat = data.frame(timestamp=1,value=data_name[i,51])

    #create a SVM model with the paramteres taken from the paper
    modelSVM = svm(value~timestamp,data=trainDat,epsilon=0.1,gamma=0.1,cost=10)
    predSVM = predict(modelSVM,newdata=testDat)

    #calculate the MAPE and "append" the value into the matrix
    MAPE = (predSVM - testDat[,2])/predSVM
    mape_matrix = rbind(mape_matrix, MAPE)
  }
  #label <- paste("MAPE", data_name, sep = "_")
  #assign(label, mape_matrix)

  #return the absolute value of the mean of the 50 rows of MAPE
  return (abs(mean(mape_matrix)))
}
```

Replicating the functions above 5 times for each setting

```
#Calculate the MAPE again but for all 20 random parameters
#This is like a wrapper function
```

```

replicatedMAPE = function(){
  #set the parameters as NULL
  phi=NULL
  theta=NULL
  #variables to contain results
  replicates = NULL
  param = NULL
  #set up the LHS design for input into simData
  design = maximinLHS(100,2,method='build')
  LHSdesign = qunif(design,-0.9,0.9)
  for (i in 1:100){
    phi <- LHSdesign[i,1]
    theta <- LHSdesign[i,2]
    #simulate stationary data using simData
    dataset = simData(phi,theta)
    #calculate MAPE
    newRep = calc_mape(dataset)
    #append results into existing variable
    replicates = rbind(replicates, newRep)
    param = rbind(param, c(phi, theta))
  }
  dataset = cbind(param,replicates)
  return(dataset)
}

```

Create the final dataset for MAPEs from Stationary

```

set.seed(88)
simStationary = replicatedMAPE()

colnames(simStationary) <- c("phi","theta","MAPE")
simStationary <- as.data.frame(simStationary)

```

Plotting MAPE

```

library(plotly)
p <- plot_ly(simStationary, x = ~phi, y = ~MAPE, z = ~theta, colors = c('#BF382A', '#0C4B8E')) %>%
  add_markers() %>%
  layout(scene = list(xaxis = list(title = 'Phi'),
                      yaxis = list(title = 'MAPE'),
                      zaxis = list(title = 'Theta')))
p

```

```

#DONT RUN THIS CHUNK AGAIN
simStationary <- simStationary[simStationary$MAPE<10,]

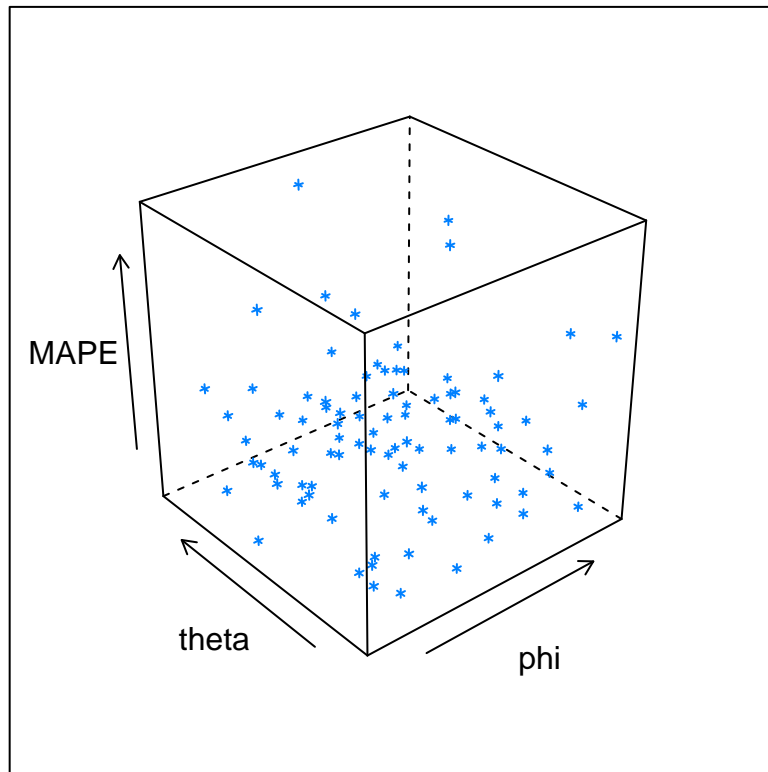
```

```

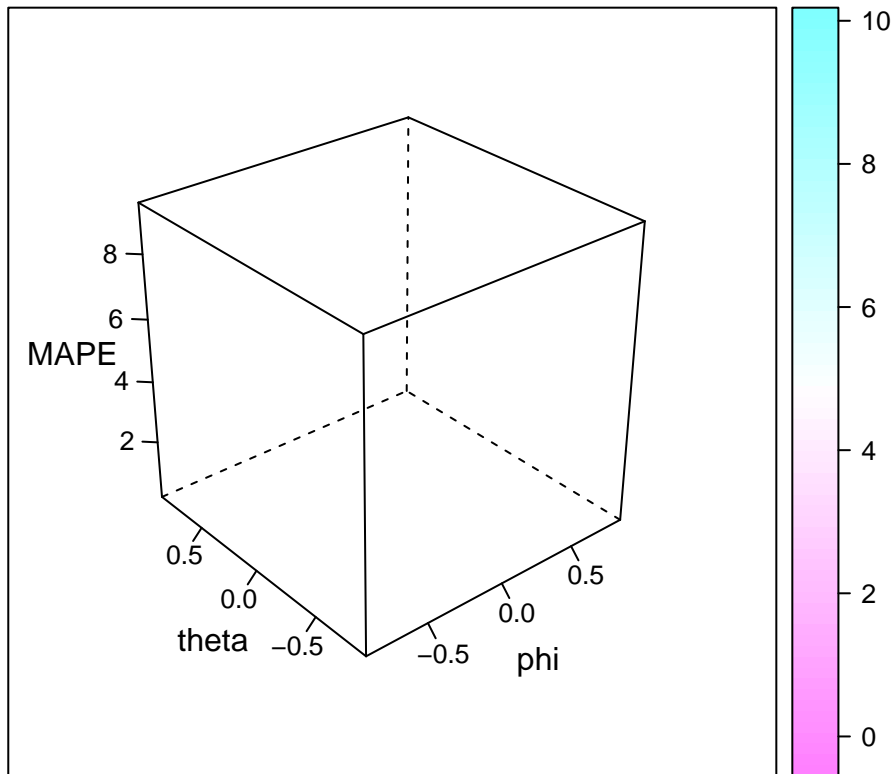
p <- plot_ly(as.data.frame(simStationary), x = ~phi, y = ~MAPE, z = ~theta, colors = c('#BF382A', '#0C4B8E')) %>%
  add_markers() %>%
  layout(scene = list(xaxis = list(title = 'Phi'),
                      yaxis = list(title = 'MAPE'),
                      zaxis = list(title = 'Theta')))
p

```

```
#from library(lattice)
cloud(MAPE~phi*theta, data=simStationary,
      aspect = c(1, 1),
      panel = "panel.cloud",
      scales = list(distance = rep(1, 3), arrows = TRUE),
      zoom = 0.8)
```



```
wireframe(MAPE ~ phi*theta, data = simStationary[simStationary$MAPE>0,], scales = list(arrows = FALSE),
```



Multi-dimensional Kriging

```
#Create design and response matrix of the SimulatedStationary for KrigingDace Model
# design is the phi and theta setting from LHS
# response is the MAPE
kriging_design = simStationary[1:2]
kriging_design = as.matrix(kriging_design)
kriging_response = simStationary[3]
kriging_response = as.matrix(kriging_response)

# Make the KRIGING MODEL
# MAPE ~ phi * theta, data = simStationary
fit = buildKrigingDACE(kriging_design, kriging_response)
fit

## -----
## Dace Kriging model.
## -----
## Estimated activity parameters (theta) sorted
## from most to least important variable
## x1 x2
## 2.818383 2.818383
##
## exponent(s) p:
## 1.9 1.9
##
## Estimated regularization constant (or nugget) lambda:
## 0.999
##
```

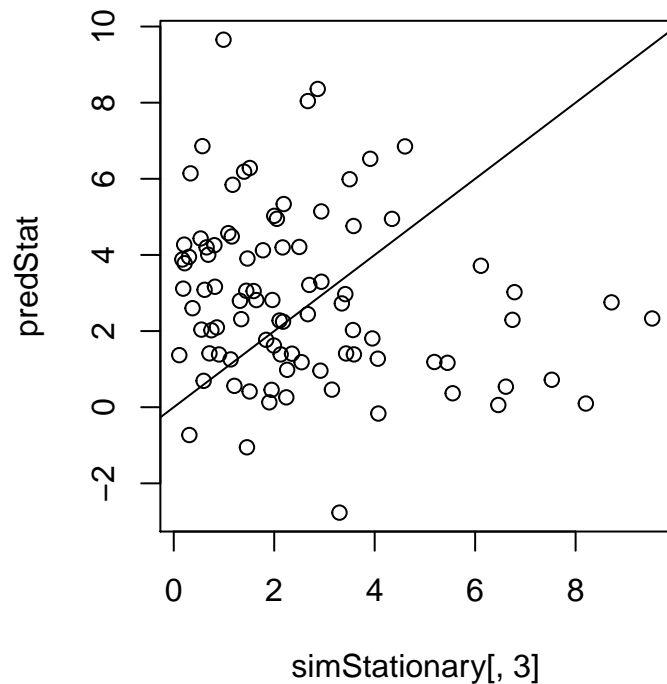
```
## Number of Likelihood evaluations during MLE:
##
## -----
```

Test the Kriging Model

```
#Create a new design
set.seed(57)
design <- maximinLHS(nrow(simStationary),2,method='build')
LHSdesign2 <- qunif(design, -0.9,0.9)
#Predict
predStat <- predict(fit,LHSdesign2)$y

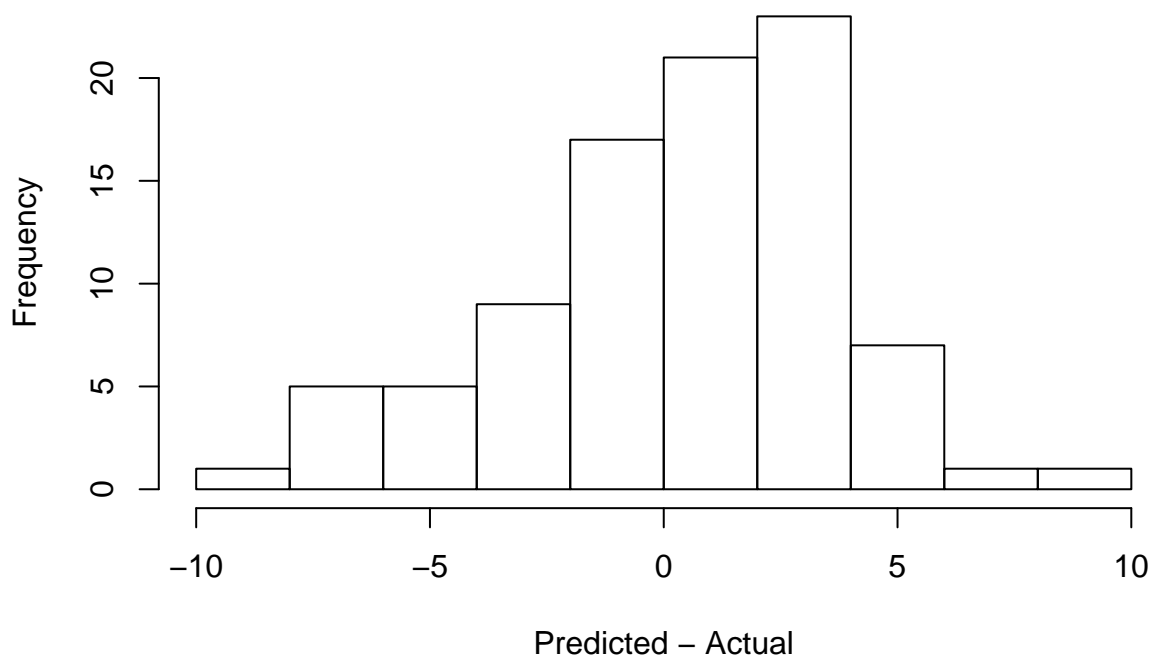
# TESTING PREDICTION ACCURACY
par(pty='s')
plot(predStat~simStationary[,3], main='Predicted MAPE vs Simulated MAPE')
abline(0,1)
```

Predicted MAPE vs Simulated MAPE



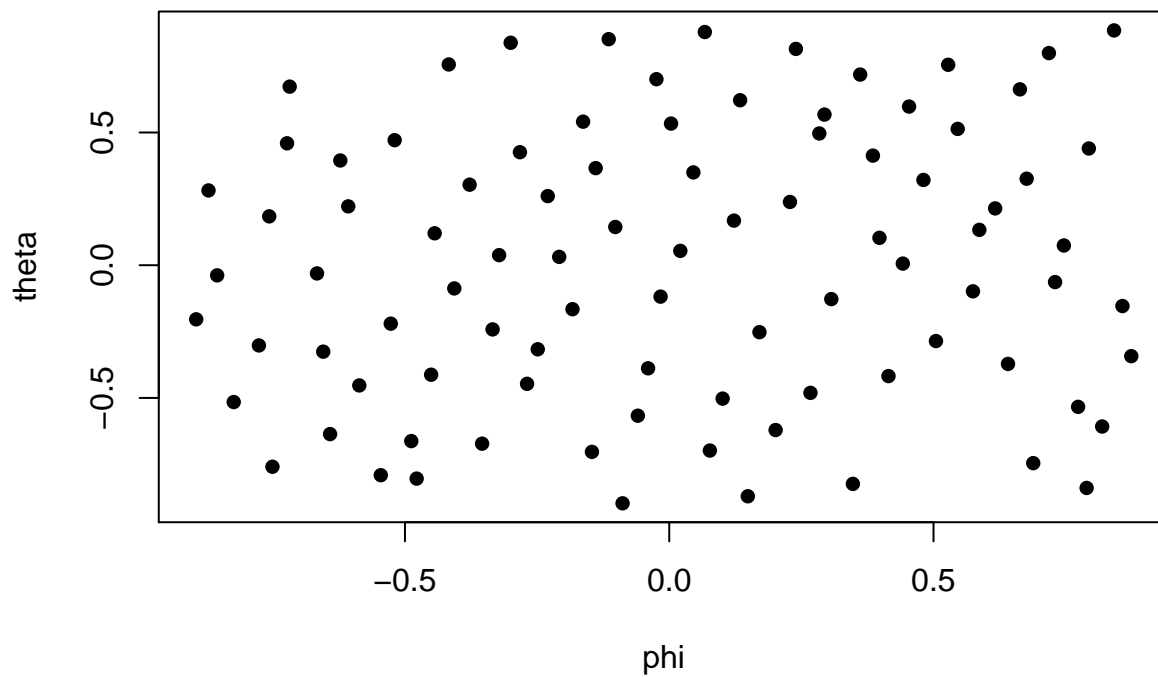
```
hist(predStat-simStationary[,3], main = "Histogram of the Differences between Predicted and Actual MAPE")
```

Histogram of the Differences between Predicted and Actual MAPE val

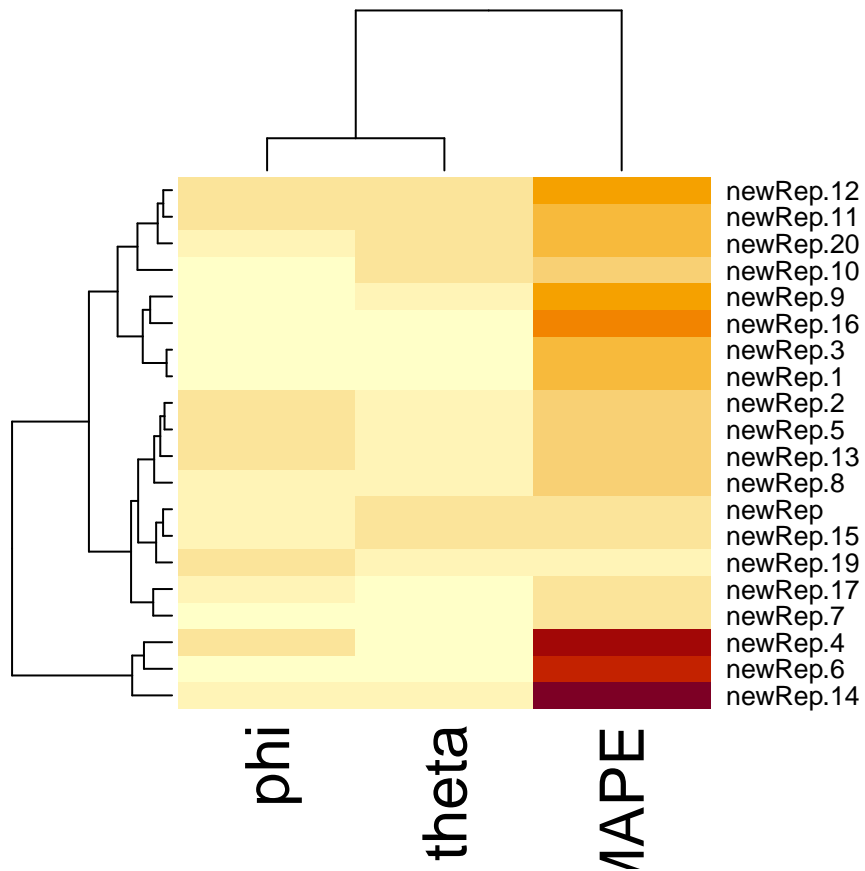


```
#(p <- ggplot(simStationary[simStationary$MAPE<10,], aes(phi, theta)) + geom_raster(aes(fill = MAPE), i  
plot(theta~phi, data=simStationary, main='Results of LHS', pch=16)
```

Results of LHS

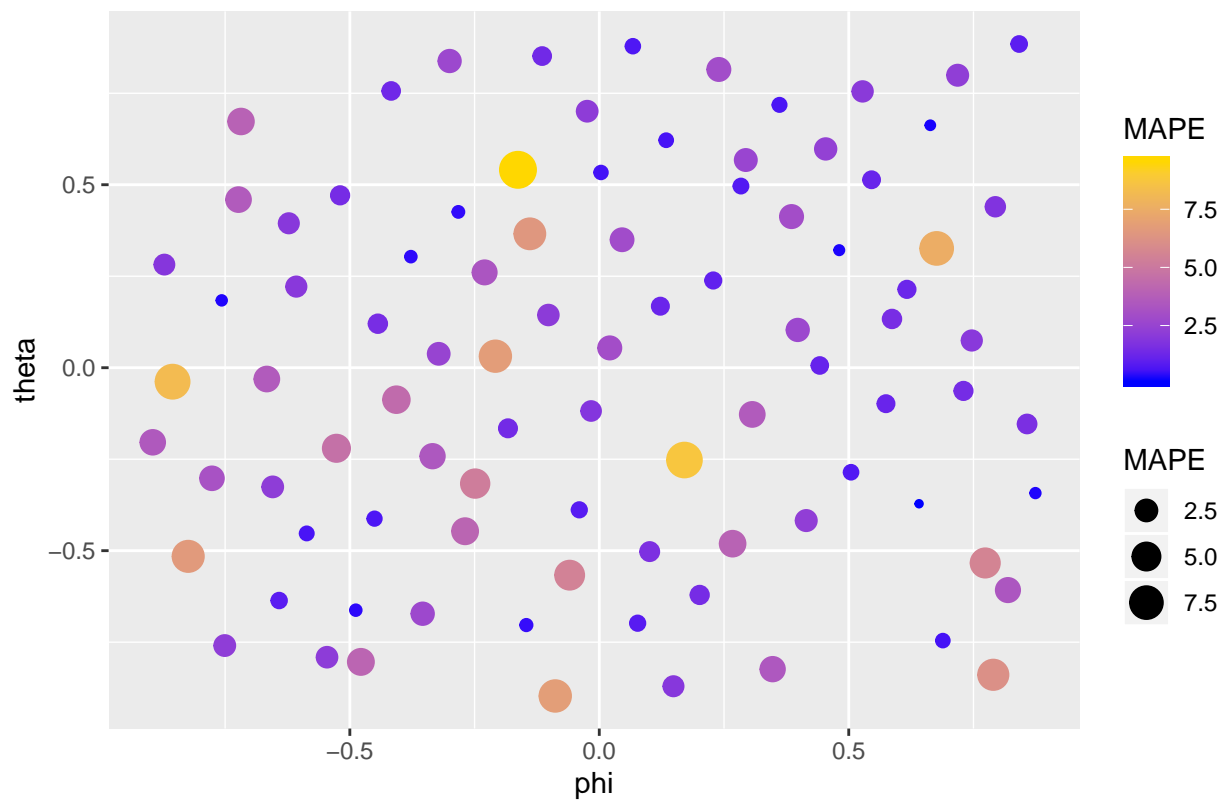


```
stationaryMatrix <- as.matrix(simStationary[1:20,])
heatmap(stationaryMatrix, scale='none')
```



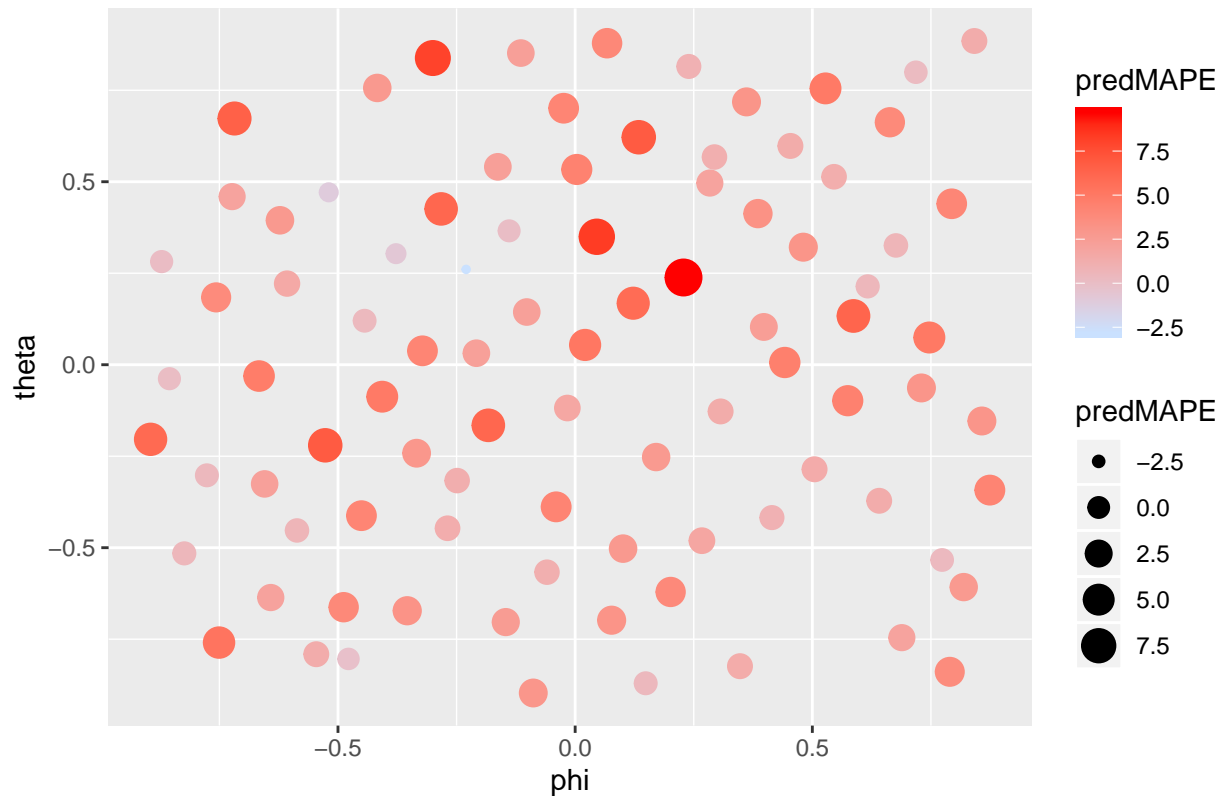
```
ggplot(simStationary, aes(x=phi, y=theta, color=MAPE, size=MAPE)) + geom_point() + scale_color_gradient
```


MAPE Values for Corresponding Phi and Theta Values – Stationary



```
predData <- data.frame(simStationary[,1:2], predMAPE = predStat)
ggplot(predData, aes(x=phi, y=theta, color=predMAPE, size=predMAPE)) + geom_point() + scale_color_gradient2()
```

Predicted MAPE Values for Corresponding Phi and Theta Values – Station



IMA MODEL

Functions (Simulate and Calc MAPE)

```
# Simulate IMA based model with theta parameter as function input
# Output the result as a 50x51 matrix with each row having 51 sequences of ts data

simData_nonst <- function(theta){
  all_training=NULL
  for (i in 1:50){
    arimaSet = arima.sim(model=list(ma=theta),n=51)
    all_training = rbind(all_training, arimaSet[1:51])
  }
  return(all_training)
}

#Automating the MEAN ABSOLUTE VALUE of MAPE - 1 replication
calc_mape_nonst = function(data_name){
  mape_matrix = NULL
  for (i in 1:50){
    #create the training and testing dataset from the chosen dataset (as per input)
    #each train and test is only one row of the 50 rows dataset
    trainDat = data.frame(timestamp=c(seq(1,50,1)),value=data_name[i,1:50]);trainDat
    testDat = data.frame(timestamp=1,value=data_name[i,51])

    #create a SVM model with the paramteres taken from the paper
    modelSVM = svm(value~timestamp,data=trainDat,epsilon=0.1,gamma=0.1,cost=10)
  }
}
```

```

predSVM = predict(modelSVM,newdata=testDat)

#calculate the MAPE and "append" the value into the matrix
MAPE = (predSVM - testDat[,2])/predSVM
mape_matrix = rbind(mape_matrix, MAPE)
}
#label <- paste("MAPE", data_name, sep = "_")
#assign(label, mape_matrix)

#return the absolute value of the mean of the 50 rows of MAPE
return (abs(mean(mape_matrix)))
}

```

Replicating the functions above 5 times for each setting

```

#Calculate the MAPE again but for all 20 random parameters
#This is like a wrapper function

replicatedMAPE_nonst = function(){
  theta=NULL
  replicates = NULL
  param = NULL
  design = maximinLHS(100,1,method='build')
  LHSdesign = qunif(design, -0.9, 0.9)
  for (i in 1:100){
    theta <- LHSdesign[i,1]
    dataset = simData_nonst(theta)
    newRep = calc_mape_nonst(dataset)
    replicates = rbind(replicates, newRep)
    param = rbind(param, theta)
  }
  dataset = cbind(param,replicates)
  return(dataset)
}

```

Create the final dataset for MAPEs from Non Stationary

```

set.seed(29)
simNonStat = replicatedMAPE_nonst()

colnames(simNonStat) <- c("theta", "MAPE")
simNonStat <- as.data.frame(simNonStat)

```

Plotting MAPE

```

p <- plot_ly(simNonStat, x = ~theta, y = ~MAPE, colors = c('#BF382A', '#0C4B8E')) %>%
  add_markers() %>%
  layout(scene = list(xaxis = list(title = 'Theta'),
    yaxis = list(title = 'MAPE')))
p

simNonStat <- simNonStat[simNonStat$MAPE<20,]

```

```

p <- plot_ly(simNonStat, x = ~theta, y = ~MAPE, colors = c('#BF382A', '#0C4B8E')) %>%
  add_markers() %>%
  layout(scene = list(xaxis = list(title = 'Theta'),
                        yaxis = list(title = 'MAPE')))
p

```

Multidimensional Kriging

```

#Create design and response matrix of the SimulatedStationary for KrigingDace Model
# design is the phi and theta setting from LHS
# response is the MAPE
kriging_design = simNonStat[1]
kriging_design = as.matrix(kriging_design)
kriging_response = simNonStat[2]
kriging_response = as.matrix(kriging_response)

# Make the KRIGING MODEL
# MAPE ~ phi * theta, data = simStationary
fit2 = buildKrigingDACE(kriging_design, kriging_response)
fit2

## -----
## Dace Kriging model.
## -----
## Estimated activity parameters (theta) sorted
## from most to least important variable
## x1
## 0.03406543
##
## exponent(s) p:
## 2
##
## Estimated regularization constant (or nugget) lambda:
## 0.7406117
##
## Number of Likelihood evaluations during MLE:
##
## -----

```

Test the Kriging Model

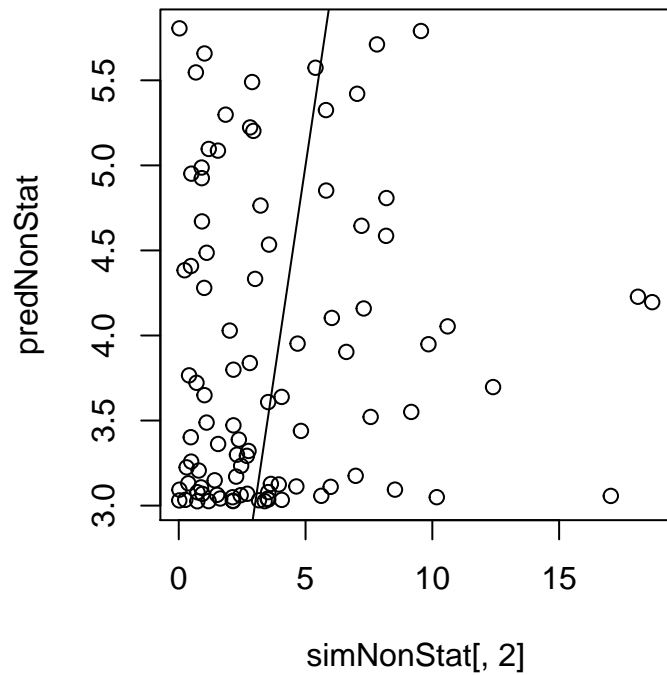
```

#Create a new design
set.seed(57)
design <- maximinLHS(nrow(simNonStat),1,method='build')
LHSdesign2 <- qunif(design, -0.9, 0.9)
#Predict
predNonStat <- predict(fit2,LHSdesign2)$y

# TESTING PREDICTION ACCURACY
par(pty='s')
plot(predNonStat~simNonStat[,2], main='Predicted MAPE vs Simulated MAPE')
abline(0,1)

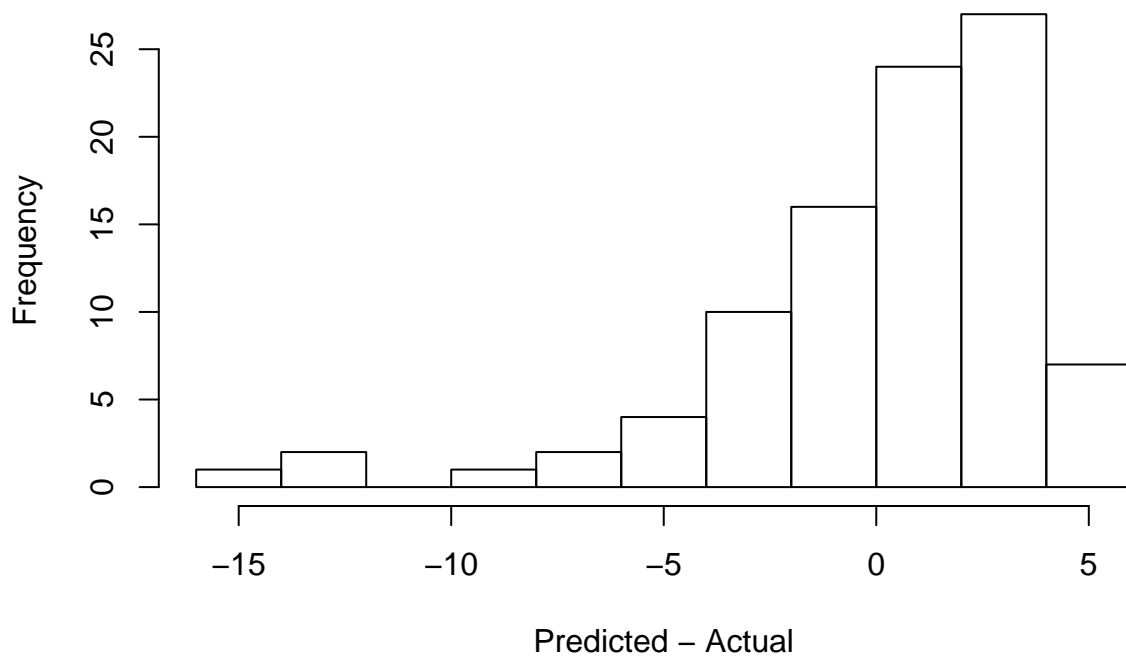
```

Predicted MAPE vs Simulated MAPE

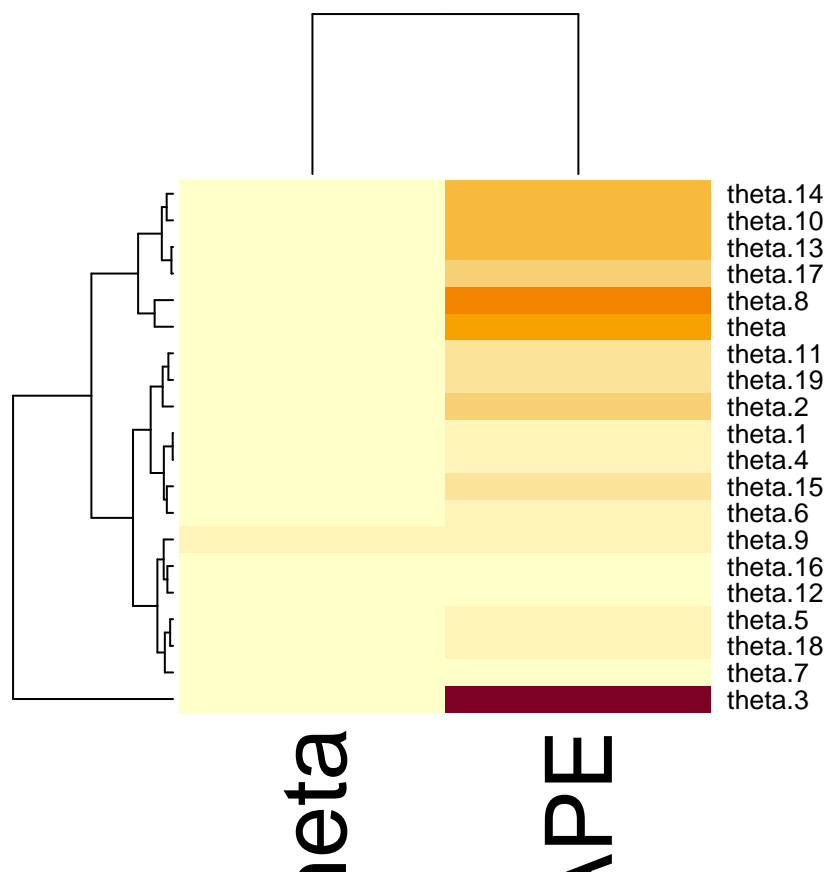


```
hist(predNonStat-simNonStat[,2], main = "Histogram of the Differences between Predicted and Actual MAPE")
```

Histogram of the Differences between Predicted and Actual MAPE values

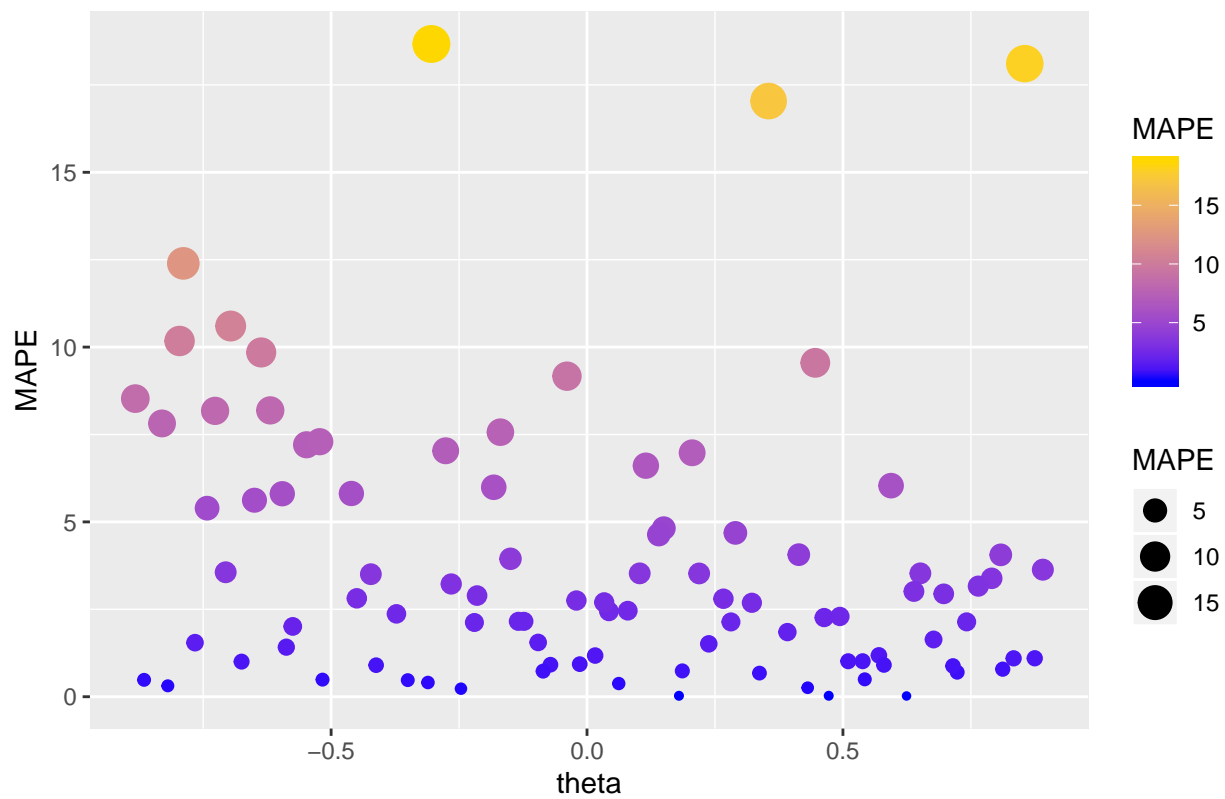


```
nonStatMatrix <- as.matrix(simNonStat[1:20,])
heatmap(nonStatMatrix, scale='none')
```



```
ggplot(simNonStat, aes(x=theta, y=MAPE, color=MAPE, size=MAPE)) + geom_point() + scale_color_gradient(1
```

MAPE Values for Corresponding Theta Values – Non-Stationary



```
predData <- data.frame(theta=simNonStat[,1], predMAPE = predNonStat)
ggplot(predData, aes(x=theta, y=predMAPE, color=predMAPE, size=predMAPE)) + geom_point() + scale_color_
```

Predicted MAPE Values for Corresponding Theta Values – Non-Stationary

