

UNIVERSITY OF BAHÇEŞEHİR
Department of Computer Engineering
CMP5133 Artificial Neural Networks – Assignment 2

1. Abstract

The subject of the assignment is to implement RBF network using two dimensional data, one for input, one for output. To implement RBF network, it is required to use hybrid learning; K-means clustering algorithm will be implemented for unsupervised part, Single Layer Perceptron for the supervised part.

2. Implementation

I implemented the RBF network using R Studio. You can find the source code (Section 5) at the end of the document. To run the code successfully, you need to set input data directory as working directory. Source file and data should be in same folder.

Before implementing network, I didn't apply any preprocessing step.

For K-means, first I initiated centroids randomly. Then, I iterated process until no input data is assigned to different cluster (convergence). In case it doesn't converge, I limited iteration count to 10. In my tests, it always converged in less than 10 iterations. Each K-means iteration 3 steps:

- Assign input values to clusters by finding the closest one to input
- Re-calculate centroid values
- If any input changed cluster, go step 1.

During K-means clustering, I also calculated the most distant inputs in clusters to calculate spread after it converges.

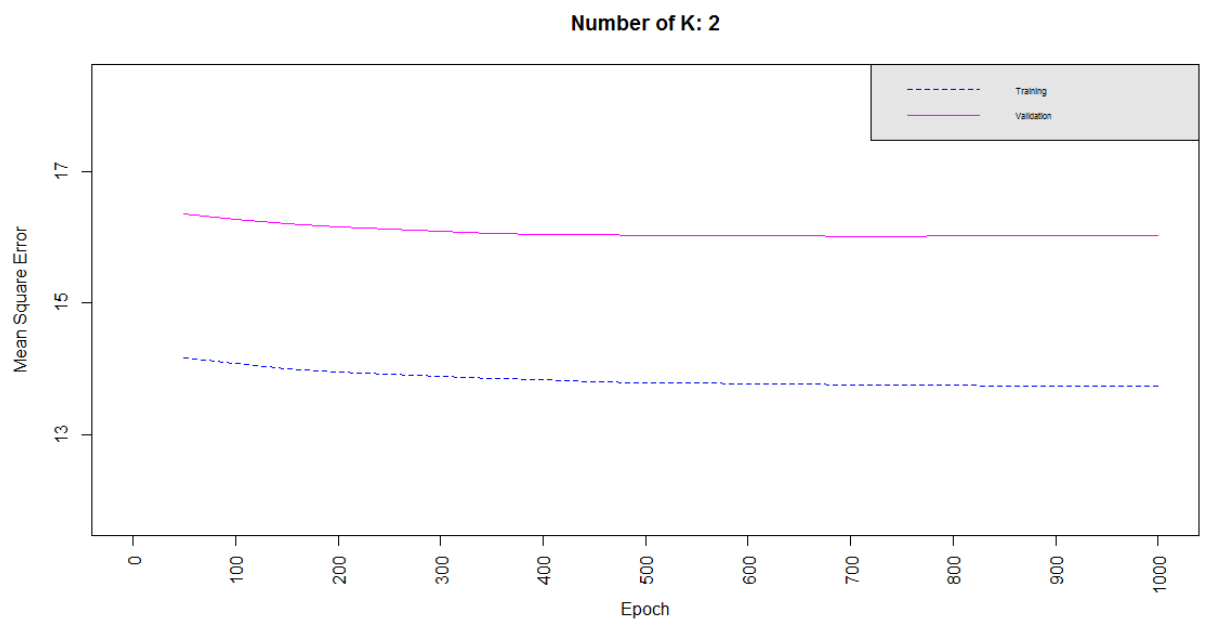
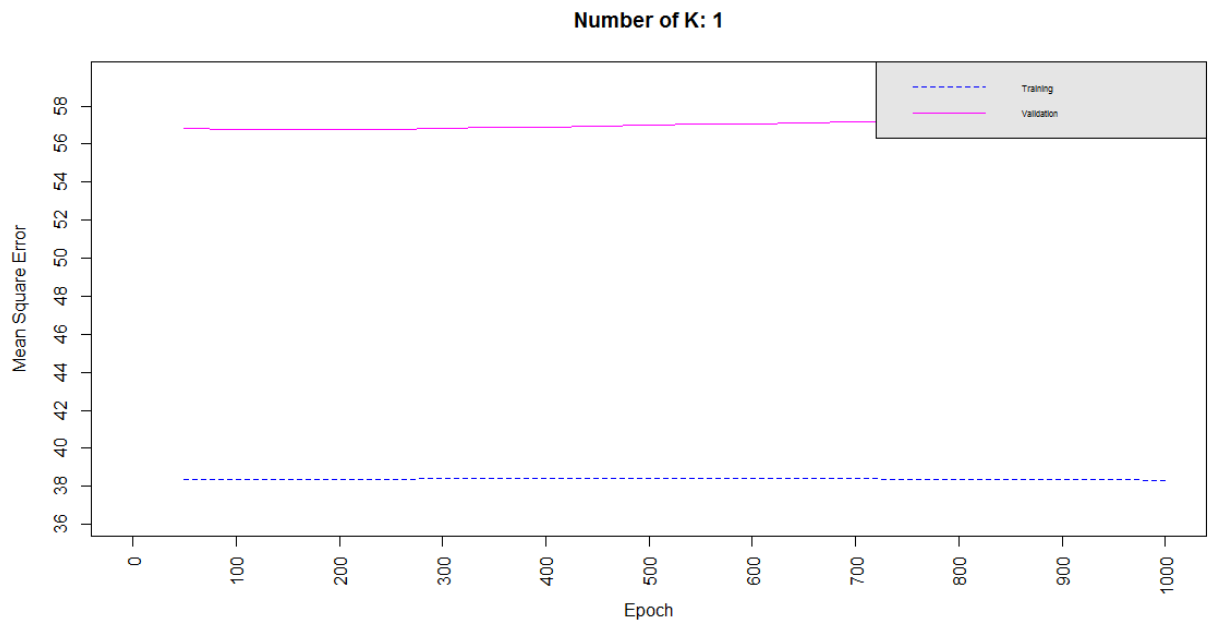
For Single Perceptron step, I first calculated perceptive field values, using centroid and spread values which are outputs of K-means process. For each K value (from 1 to 10), I applied basic single perceptron algorithm using epoch as 1000 and learning rate as 0.2 whose seem to be enough for every K value.

Results of RBF network are plotted and listed in the following section.

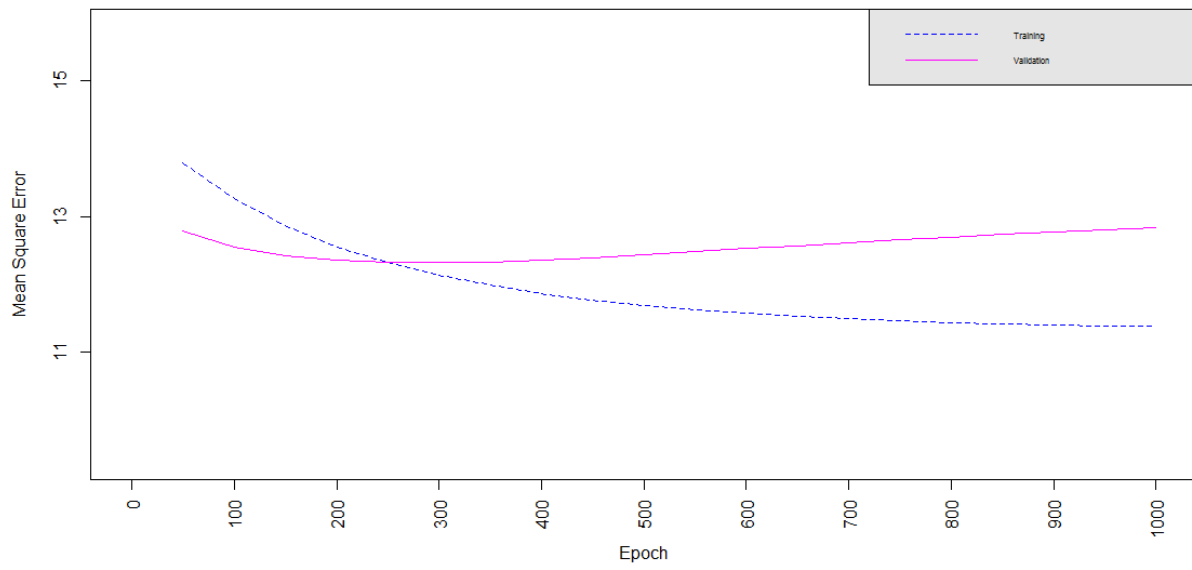
3. Plots

In this section, there are 3 types of plots; training and validation mean squared errors, training input and RBF network outputs, training data and network output together.

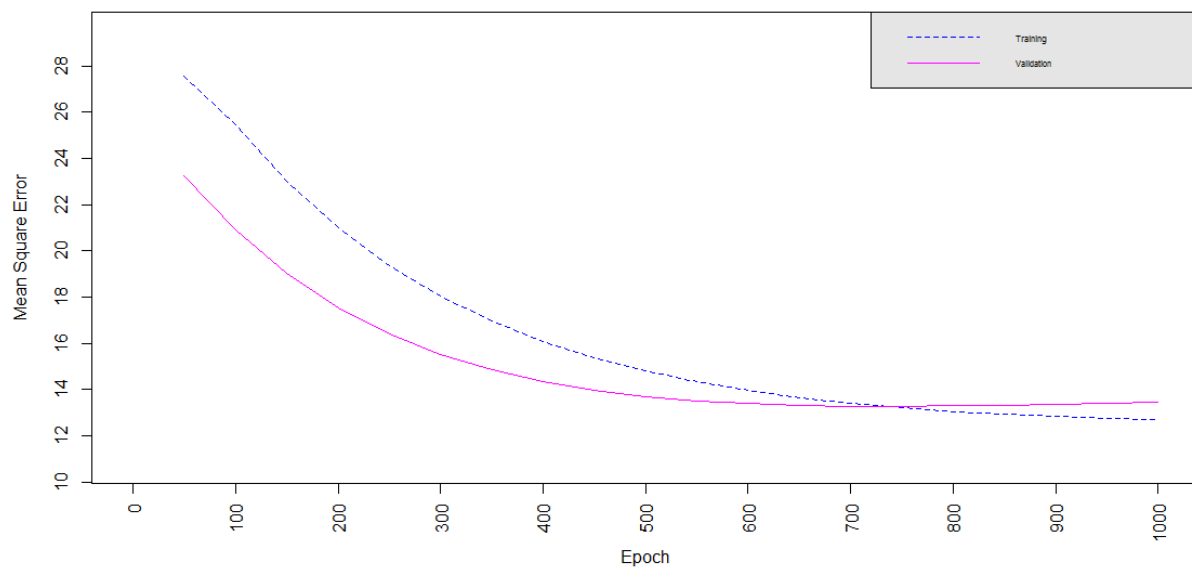
3.1 Training and Validation Mean Squared Errors



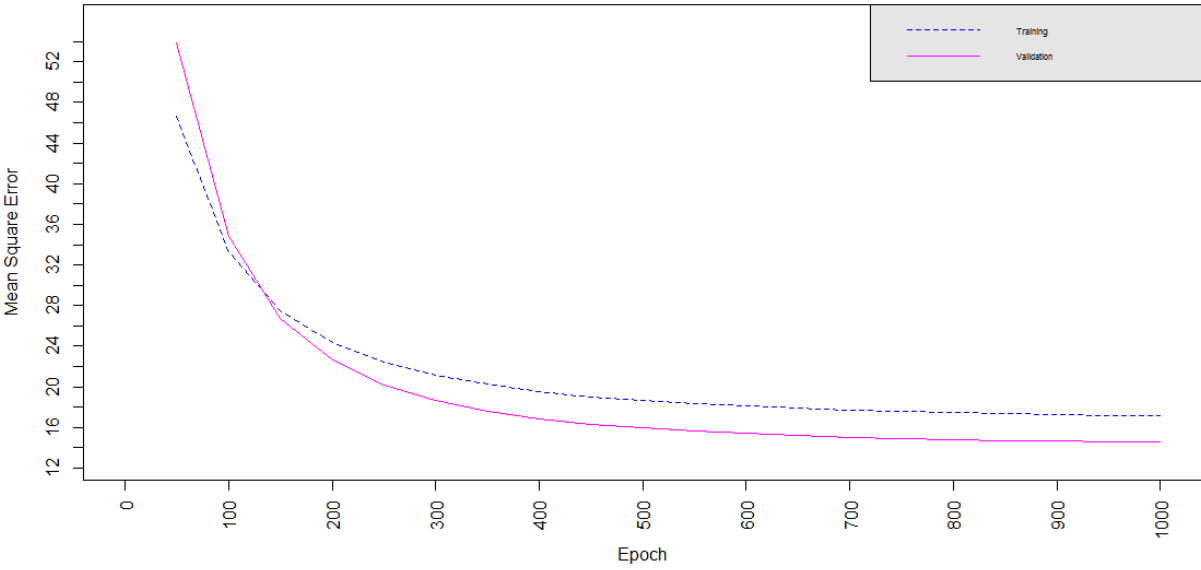
Number of K: 3



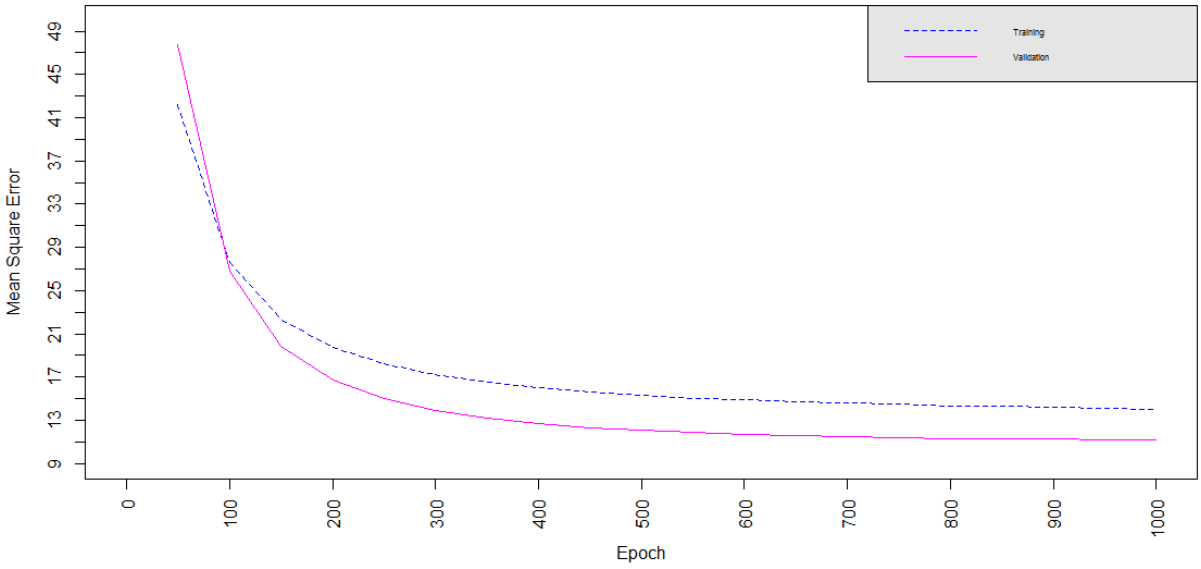
Number of K: 4



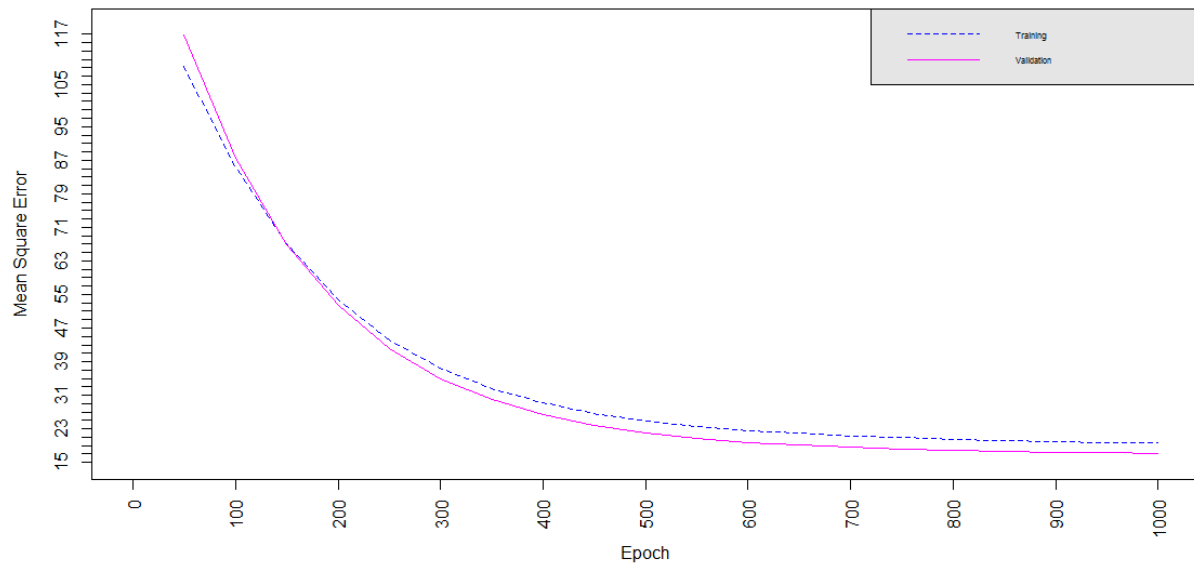
Number of K: 5



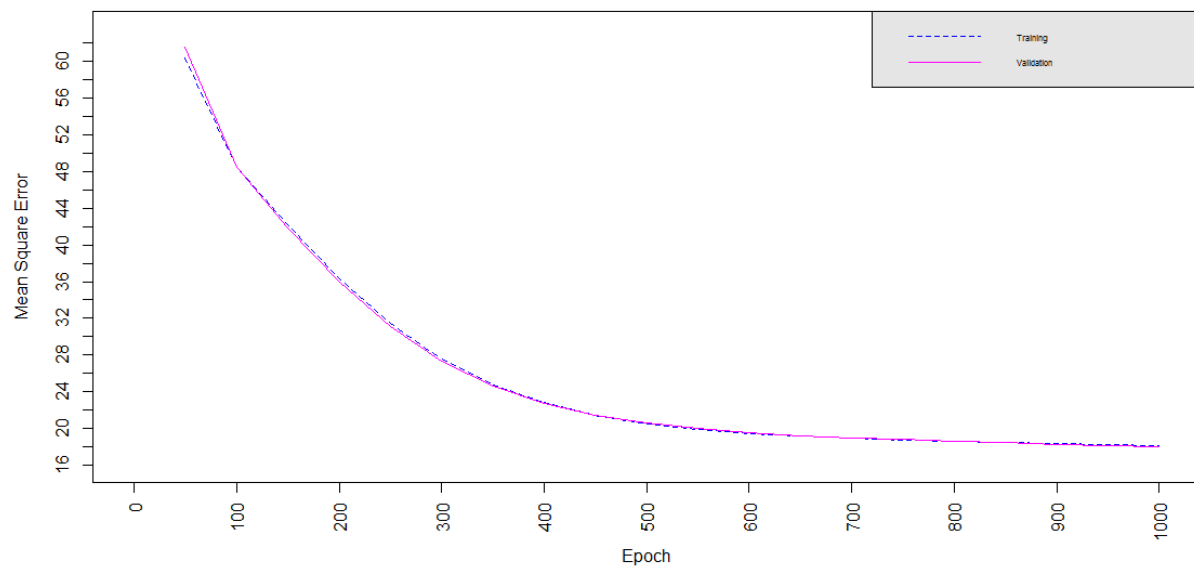
Number of K: 6

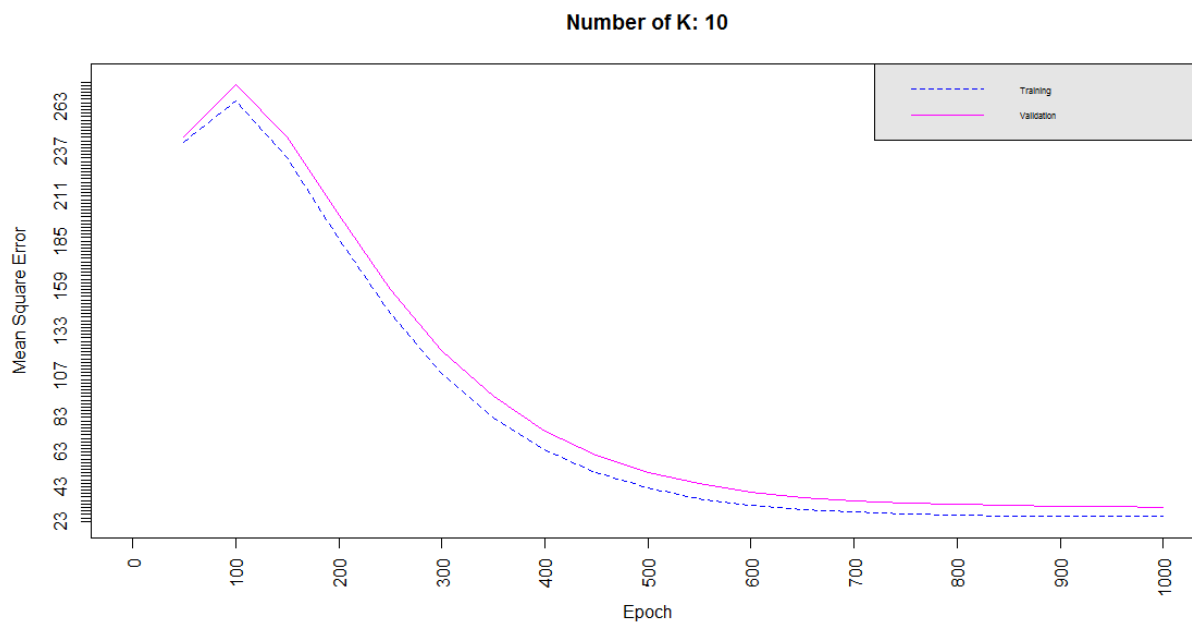
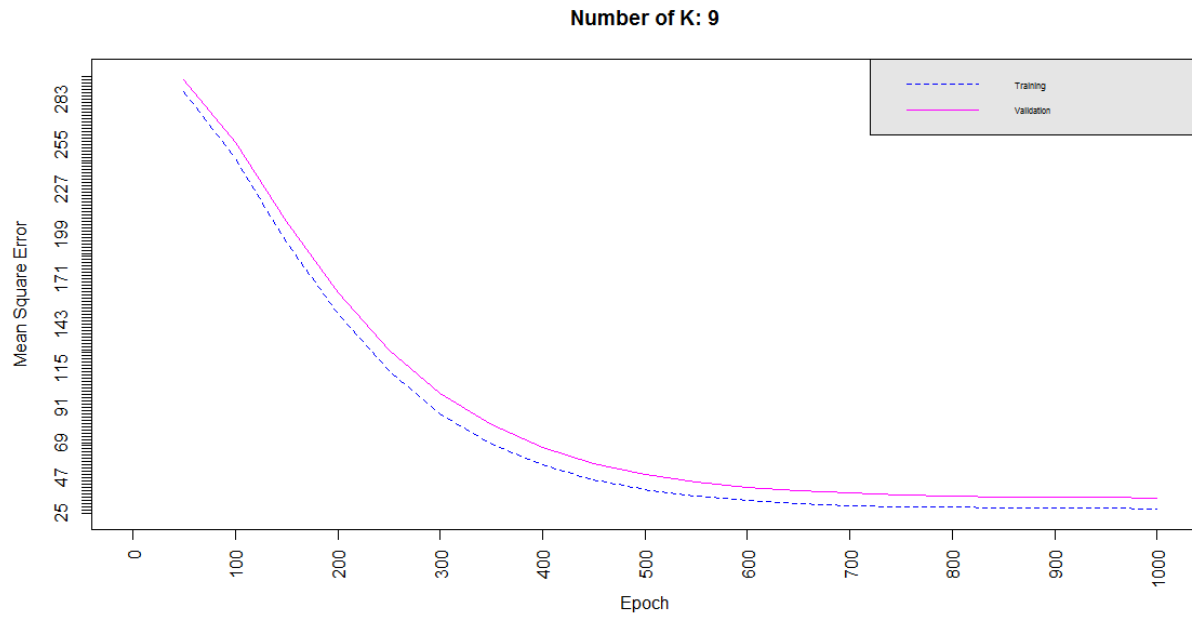


Number of K: 7



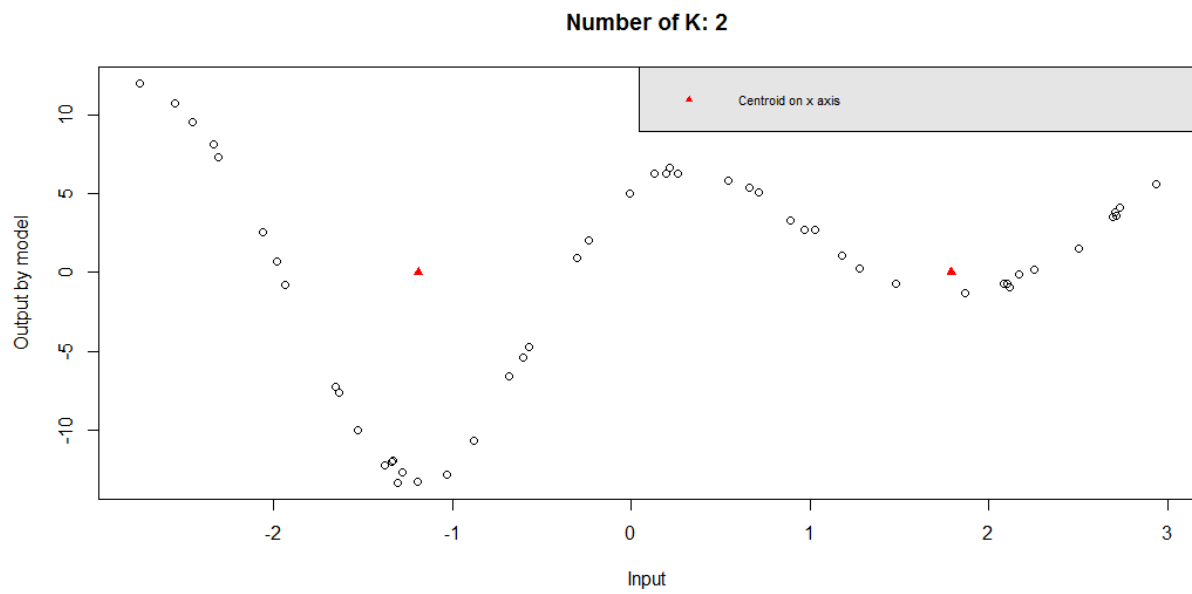
Number of K: 8



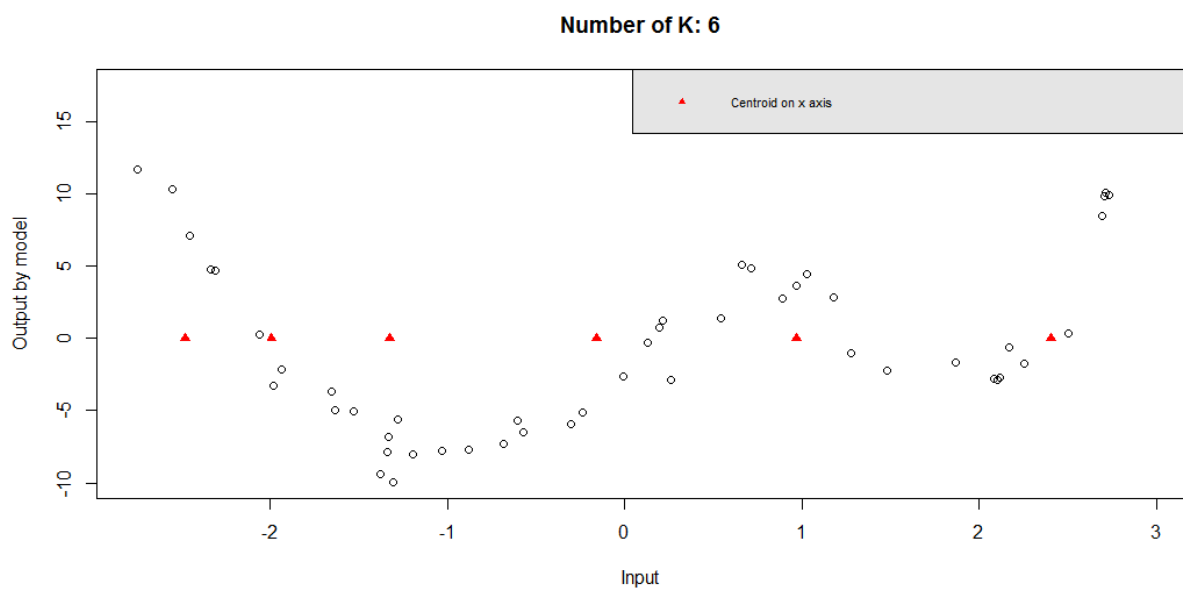


3.2 Training Input and RBF Network Output

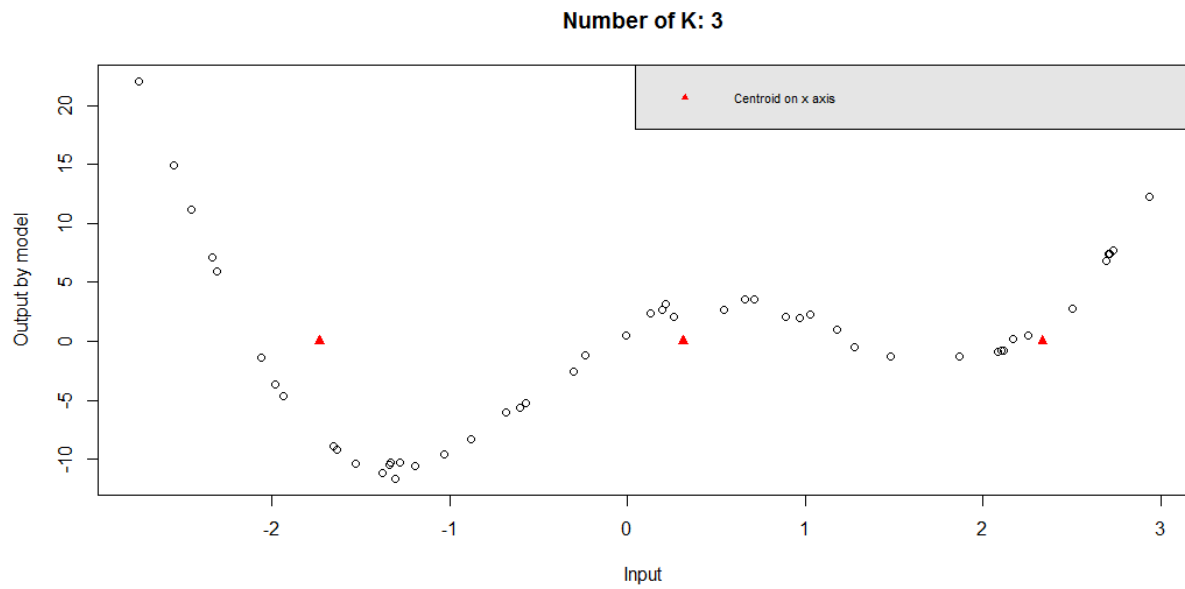
A. For underfitting



B. For good fit

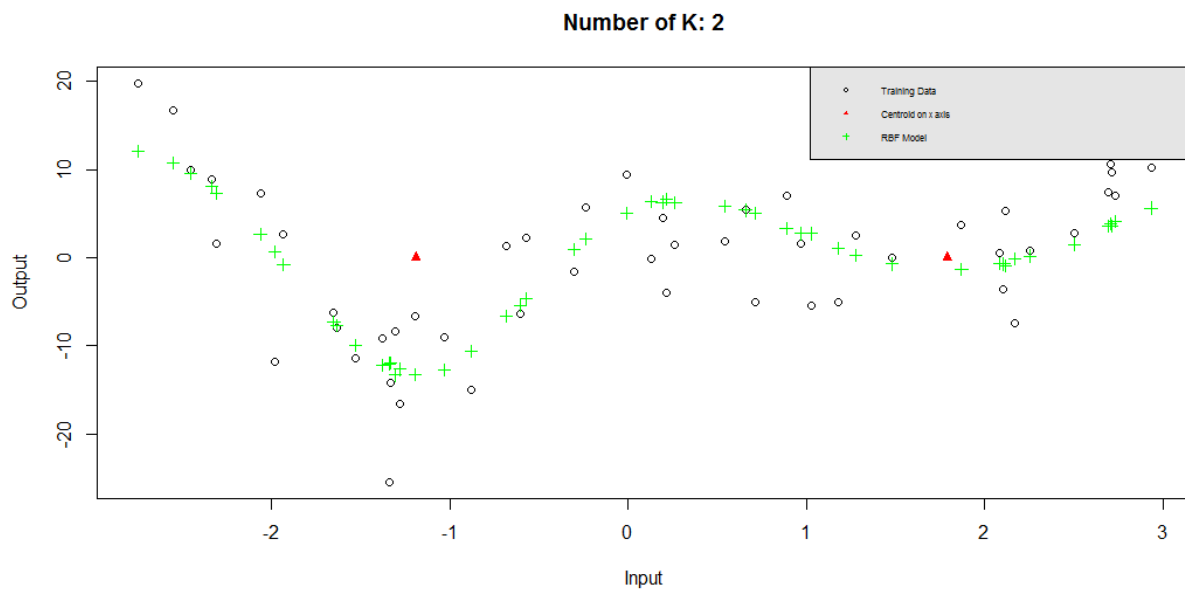


C. For overfitting

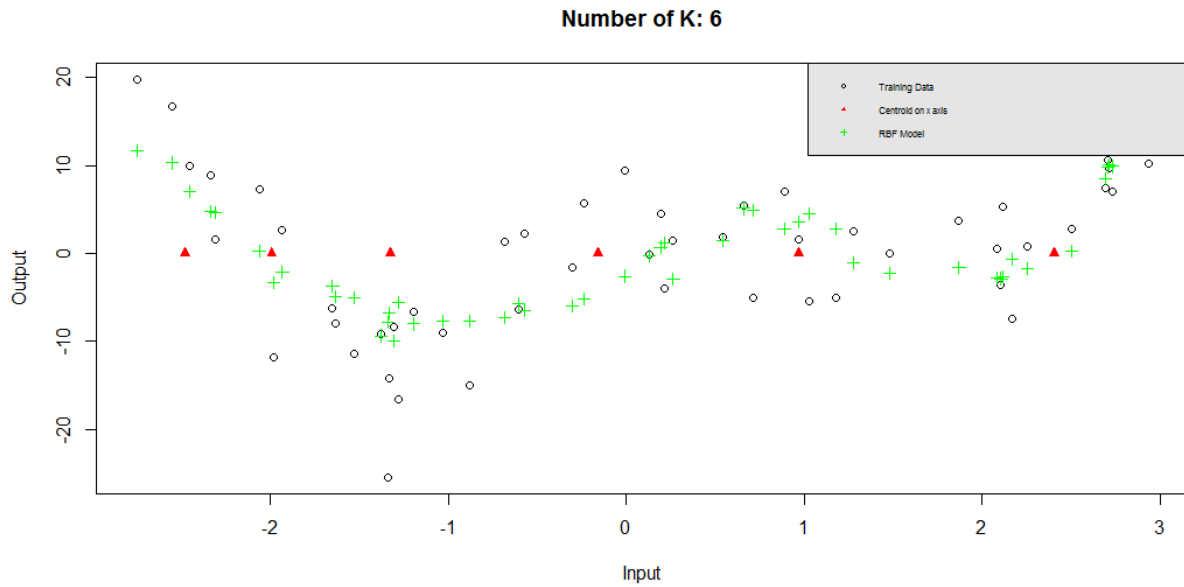


3.3 Training Data and RBF Values

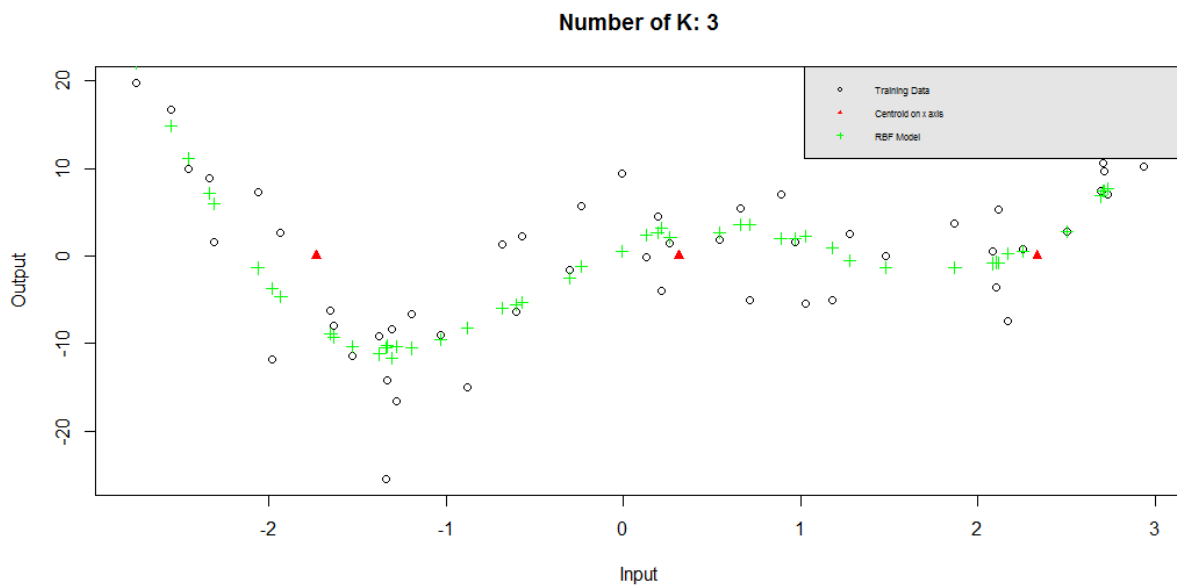
A. For Underfitting



B. For Good Fit



C. For Overfitting



4. Conclusion

As a result of implementation of RBF network for regression, I can say that training and validation error decrease until K (number of clusters) value around 6, 7. Network fits best in K value 6 or 7. When K is increased more than 7, error tends to start again. But, these results highly depends on K-means centroid which are initialized randomly which can give a different result in every execution. These given results are general characteristics of data in RBF network.

Execution time of the training the network is quite fast. It takes 10 seconds average to finish for almost every K value (number of cluster).

Samet Yazak
1604262

5. Source Code

You can find the copied source code below. Source code and other material (data, plots, report) for this assignment is also available on github; <https://github.com/yazaksamet/RBF> .

```
#setwd("C:/Users/sametyazak/Desktop/ynwa/bau/2017 - Spring/ann/Assignment2")
```

```
#### hyper parameters
```

```
numberOfClusters = 10
```

```
epoch = 1000
```

```
larningRateDefault = 0.2
```

```
epochLogNumber = 50
```

```
## read data
```

```
trainingData = read.table("d_reg_tra.txt")
```

```
trainingData = data.frame(trainingData, 0, 0)
```

```
colnames(trainingData) <- c("Input", "Output", "ClusterIndex", "ModelOutput")
```

```
testData = read.table("d_reg_val.txt")
```

```
testData = data.frame(testData, 0)
```

```
colnames(testData) <- c("Input", "Output", "ClusterIndex")
```

```
trainingDataPlot = data.frame(trainingData$Input, trainingData$Output)
```

```
#plot(trainingDataPlot)
```

```
clusterCentroids = matrix(sample(c(0:0), numberOfClusters, TRUE), 1, numberOfClusters)
```

```
clusterSpreads = matrix(sample(c(0:0), numberOfClusters, TRUE), 1, numberOfClusters)
```

```
## assign initial centroids for K-means randomly
```

Samet Yazak
1604262

```
for (c in 1:numberOfClusters) {  
  randomCentroidIndex = sample(1:dim(trainingData)[1], 1);  
  clusterCentroids[1,c] = trainingData[randomCentroidIndex,1]  
}  
  
numberOfClusterChanges = 0  
kmeansIterationCount = 0  
  
# iterate until no cluster changes or 10 iterations  
while (kmeansIterationCount == 0 || (numberOfClusterChanges > 0 && kmeansIterationCount < 10))  
{  
  kmeansIterationCount = kmeansIterationCount + 1  
  ## assign training data to clusters  
  
  numberOfClusterChanges = 0  
  
  clusterCentroidTotals = matrix(sample(c(0:0), numberOfClusters, TRUE), numberOfClusters, 2)  
  
  for (i in 1:dim(trainingData)[1]) {  
    ## find closest cluster  
  
    innerClusterIndex = 0  
    inputValue = trainingData[i,1]  
    bestDistance = -1  
  
    for (c2 in 1:numberOfClusters) {  
      clusterDistance = abs(inputValue - clusterCentroids[1,c2])  
  
      if (bestDistance == -1 || clusterDistance < bestDistance) {  
        innerClusterIndex = c2  
        bestDistance = clusterDistance  
      }  
    }  
  }  
}
```

Samet Yazak
1604262

```
# assign found cluster
if (trainingData[i,3] != innerClusterIndex) {
  trainingData[i,3] = innerClusterIndex
  numberOfClusterChanges = numberOfClusterChanges + 1
}

clusterCentroidTotals[innerClusterIndex,1] = clusterCentroidTotals[innerClusterIndex,1] +
inputValue
clusterCentroidTotals[innerClusterIndex,2] = clusterCentroidTotals[innerClusterIndex,2] + 1

# calculate most distant instance for spread
if (abs(inputValue - clusterCentroids[1,innerClusterIndex]) > clusterSpreads[1,innerClusterIndex]) {
  clusterSpreads[1,innerClusterIndex] = abs(inputValue - clusterCentroids[1,innerClusterIndex])
}

}

## re-calculate centroid values
for (c3 in 1:numberOfClusters) {
  if (clusterCentroidTotals[c3,2] != 0) {
    clusterCentroids[1,c3] = clusterCentroidTotals[c3,1] / clusterCentroidTotals[c3,2]
  }
  else {
    clusterCentroids[1,c3] = 0
  }
}

}

## calculate cluster spreads

clusterSpreads = clusterSpreads / 2
```

Samet Yazak
1604262

calculate ph values

+ 1 means bias unit

```
trainingDataPerceptives = matrix(sample(c(0:0), numberOfClusters + 1, TRUE), dim(trainingData)[1],  
numberOfClusters + 1)
```

```
testDataPerceptives = matrix(sample(c(0:0), numberOfClusters + 1, TRUE), dim(testData)[1],  
numberOfClusters + 1)
```

assign bias unit

```
trainingDataPerceptives[,1] = 1
```

```
testDataPerceptives[,1] = 1
```

```
for (pi in 1:dim(trainingData)[1]) {  
  for (ph in 1:numberOfClusters) {  
    pht = exp(-((abs(trainingData[pi,1] - clusterCentroids[1,ph]))^2 / 2*(clusterSpreads[1,ph])^2))  
    trainingDataPerceptives[pi,ph+1] = pht  
  }  
}
```

```
for (pi in 1:dim(testData)[1]) {  
  for (ph in 1:numberOfClusters) {  
    pht = exp(-((abs(testData[pi,1] - clusterCentroids[1,ph]))^2 / 2*(clusterSpreads[1,ph])^2))  
    testDataPerceptives[pi,ph+1] = pht  
  }  
}
```

train single layer perceptron

weight initialization

```
inputWeight = matrix(sample(c(-100:100), numberOfClusters + 1, TRUE) / 10000, 1,  
numberOfClusters + 1)
```

Samet Yazak
1604262

```
errorMatrix = matrix(0, ncol = 4, nrow = ((epoch / epochLogNumber)))  
errorSet = data.frame(errorMatrix)  
colnames(errorSet) <- c("K", "epoch", "trainingMSE", "validationSME")
```

```
# run epochs
```

```
learningRate = lerningRateDefault
```

```
for (e in 1:epoch){  
  for(x in 1:dim(trainingData)[1]) {  
    y = sum(inputWeight[1,] * trainingDataPerceptives[x,])  
    r = trainingData[x,2]  
  
    deltaWeight = learningRate*(r-y)*trainingDataPerceptives[x,]  
    inputWeight = inputWeight + deltaWeight  
  
    trainingData[x,4] = y  
  }  
}
```

```
if (e %% epochLogNumber == 0) {  
  trainingErrorSum = 0  
  validationErrorSum = 0
```

```
  # calculate training data  
  for(x in 1:dim(trainingData)[1]) {  
    y = sum(inputWeight[1,] * trainingDataPerceptives[x,])  
    r = trainingData[x,2]  
  
    trainingErrorSum = trainingErrorSum + 0.5 * (r-y)^2  
  }
```

Samet Yazak
1604262

```
# mean square error
trainingMSE = trainingErrorSum / dim(trainingData)[1]

for(x in 1:dim(testData)[1]) {
  y = sum(inputWeight[1,] * testDataPerceptives[x,])
  r = testData[x,2]

  validationErrorSum = validationErrorSum + 0.5 * (r-y)^2
}

# mean square error
validationMSE = validationErrorSum / dim(testData)[1]

# log error
epochLogIndex = (e / epochLogNumber)
errorSet[epochLogIndex,1] = numberOfClusters
errorSet[epochLogIndex,2] = e
errorSet[epochLogIndex,3] = trainingMSE
errorSet[epochLogIndex,4] = validationMSE
}

learningRate = learningRate * 0.998
print(paste0("K: ", numberOfClusters, ", epoch:", e))
}

## plot validation and training error

subErrorSet = errorSet
subTrainingError = data.frame(subErrorSet$epoch, subErrorSet$trainingMSE)
subValidationError = data.frame(subErrorSet$epoch, subErrorSet$validationSME)

maxValidationError = max(subValidationError[,2])
minValidationError = min(subValidationError[,2])
```

Samet Yazak
1604262

```
maxTrainingError = max(subTrainingError[,2])
```

```
minTrainingError = min(subTrainingError[,2])
```

```
minError = min(minValidationError,minTrainingError) - 2
```

```
maxError = max(maxTrainingError,maxValidationError) + 2
```

```
plot(subTrainingError,type="l",col=4, lty = 2, xlab="Epoch", ylab="Mean Square Error",
```

```
      xlim=c(0,epoch),
```

```
      ylim=c(minError, maxError),
```

```
      axes = FALSE)
```

```
axis(1, xaxp=c(0, epoch, (epoch/(epochLogNumber*2))), las=2)
```

```
axis(side = 2, at = seq(as.integer(minError), as.integer(maxError), by = 2))
```

```
#axis(2, xaxp=c(10, 1000, 10), las=2)
```

```
lines(subValidationError,col=6,lty = 1, pch = 4)
```

```
title(paste0("Number of K: ", numberOfClusters))
```

```
legend("topright", c("Training", "Validation"), col = c(4, 6),
```

```
      text.col = "black", lty = c(2,1),
```

```
      bg = "gray90", cex = 0.5)
```

```
box()
```

```
## plot input and model output for training data
```

```
trainingDataPlot = data.frame(trainingData$Input, trainingData$ModelOutput)
```

```
clusterCentroidsPlot = matrix(sample(c(0:0), numberOfClusters, TRUE), numberOfClusters, 2)
```

```
clusterCentroidsPlot[,1] = t(clusterCentroids)
```

```
plot(trainingDataPlot, xlab="Input", ylab="Output by model")
```

```
points(clusterCentroidsPlot, col="red", pch=17)
```

```
title(paste0("Number of K: ", numberOfClusters))
```

```
legend("topright", c("Centroid on x axis"), col = c("red"),
```

```
      text.col = "black", pch=17,
```

```
      bg = "gray90", cex = 0.7)
```


Samet Yazak
1604262

```
## plot both training data and model output
```

```
trainingDataPlot2 = data.frame(trainingData$Input, trainingData$Output)
```

```
plot(trainingDataPlot2, xlab="Input", ylab="Output")
```

```
points(clusterCentroidsPlot, col="red", pch=17)
```

```
points(trainingDataPlot, col="green", pch=3)
```

```
title(paste0("Number of K: ", numberOfClusters))
```

```
legend("topright", c("Training Data", "Centroid on x axis", "RBF Model"), col = c("black", "red",  
"green"),
```

```
text.col = "black", pch= c(1,17,3),
```

```
bg = "gray90", cex = 0.5)
```