LIST OF PUBLICATIONS

Papers Published in International Conference Proceedings

- "Decision Tree Based Model for the Classification of Pathogenic Gene Sequences Causing ASD", International Conference on Smart Trends for Information Technology and Computer Communications, SmartCom 2017 conducted during 18-19 August 2017, Communications in Computer and Information Science, vol. 876. pp 201-212, Springer, Singapore **(Scopus indexed)**
- "Machine Learning-Based Model for Identification of Syndromic Autism Spectrum Disorder", International Conference on Integrated Intelligent Computing, Communication and Security, conducted during 24 - 25 Jan 2018, Studies in Computational Intelligence, vol. 771. pp. 141-148, Springer, Singapore **(Scopus indexed)**

Papers Published / Accepted in International Journals

- "Identification of Autism Spectrum Disorder using a Multi-Label Approach", Journal of Advanced Research and Dynamical Control Systems, Vol. 11, Issue – 2, pp. 134-141, 2019, **(Scopus indexed)**
- "Bidirectional Recurrent Neural Network based Model to identify ASD" – Accepted for publication in the Journal of Advances in Modelling and Analysis A. **(Scopus indexed)**

Papers in Review - International Journals

- "Codon Encoding of Gene Sequences for Deep Learning Based Prediction of Autism Spectrum Disorder" in the Journal of Computer Science
- "Long Short Term Memory Recurrrent Neural Networks for Autism Spectrum Disorder Prediction using Codon Encoding" in the Turkish Journal of Electrical Engineering and Computer Sciences
- "Gated Recurrent Neural Network for ASD Gene Prediction using Codon encoding" in the Periodicals of Engineering and Natural Science
- 'Efficient Prediction of Gene Susceptibility to Autism Spectrum Disorder using Deep Architectures" in the International Journal of Advanced Intelligence Paradigms (IJAIP)
- "Recurrent Neural Network Based Models to predict Autism Spectrum Disorder Causative Genes" in the Arabian Journal for Science and Engineering

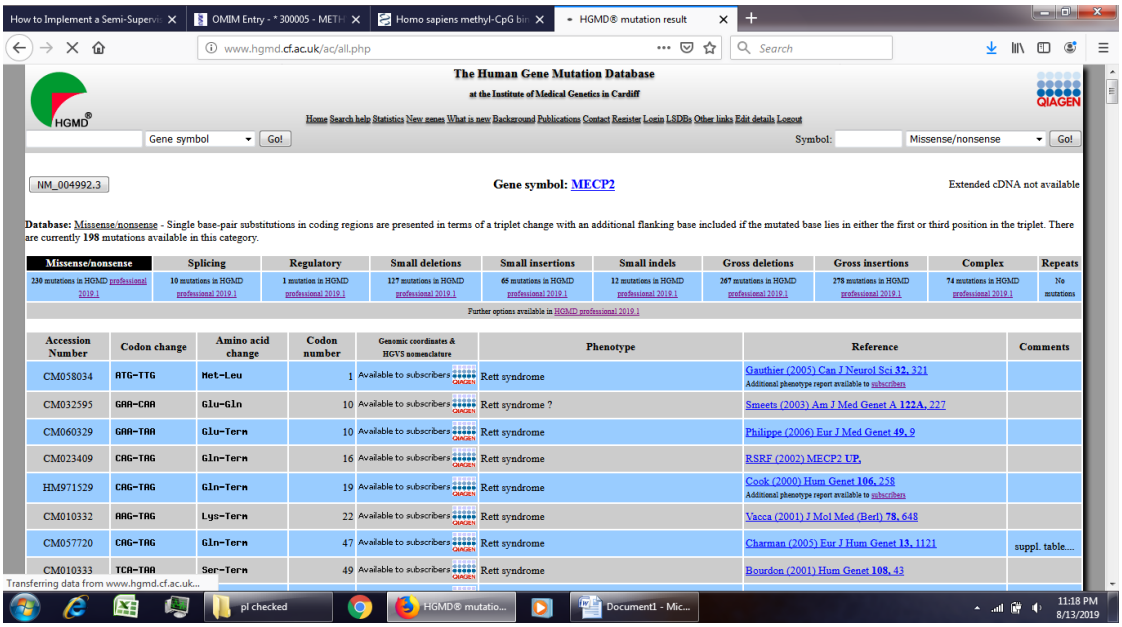
APPENDIX A - DATASETS

cDNA Sequence of MECP2 Gene

>NM_004992.3 Homo sapiens methyl-CpG binding protein 2 (MECP2), transcript variant 1, mRNA

ATGGTAGCTGGGATGTTAGGGCTCAGGGAAGAAAAGTCAGAAGACCAGGACCTCCAGGGCCTCAAGG
ACAAACCCCTCAAGTTTAAAAAGGTGAAGAAAGATAAGAAAGAAGAGAAAGAGGGCAAGCATGAGCC
CGTGCAGCCATCAGCCCACCACTCTGCTGAGCCCGCAGAGGCAGGCAAAGCAGAGACATCAGAAGGGT
CAGGCTCCGCCCCGGCTGTGCCGGAAGCTTCTGCCTCCCCCAAACAGCGGCGCTCCATCATCCGTGACC
GGGGACCCATGTATGATGACCCCACCCTGCCTGAAGGCTGGACACGGAAGCTTAAGCAAAGGAAATCT
GGCCGCTCTGCTGGGAAGTATGATGTGTATTTGATCAATCCCCAGGGAAAAGCCTTTAGCTCTAAAGTG
GAGTTGATTGCGTACTTCGAAAAGGTAGGCGACACATCCCTGGACCCTAATGATTTTGACTTCACGGTAA
CTGGGAGAGGGAGCCCCTCCCGGCGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCA
GGAACTGGCAGAGGCCGGGGACGCCCCAAAGGGAGCGGCACCACGAGACCCAAGGCGGCCACGTCAG
AGGGTGTGCAGGTGAAAAGGGTCCTGGAGAAAAGTCCTGGGAAGCTCCTTGTCAAGATGCCTTTTCAA
ACTTCGCCAGGGGGCAAGGCTGAGGGGGGTGGGGCCACCACATCCACCCAGGTCATGGTGATCAAACG
CCCCGGCAGGAAGCGAAAAGCTGAGGCCGACCCTCAGGCCATTCCCAAGAAACGGGGCCGAAAGCCG
GGGAGTGTGGTGGCAGCCGCTGCCGCCGAGGCCAAAAAGAAAGCCGTGAAGGAGTCTTCTATCCGATC
TGTGCAGGAGACCGTACTCCCCATCAAGAAGCGCAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGG
AAGTGGTGAAGCCCCTGCTGGTGTCCACCCTCGGTGAGAAGAGCGGGAAAGGACTGAAGACCTGTAAG
AGCCCTGGGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGCGCCTCCTCACCCCCCAA

Mutational information for MECP2 Gene from HGMD



Missense Mutated MECP2 Gene

>NM_004992.3 Homo sapiens methyl-CpG binding protein 2 (MECP2), transcript variant 1, mRNA

TTGGTAGCTGGGATGTTAGGGCTCAGGGAAGAAAAGTCAGAAGACCAGGACCTCCAGGGCCTCAAGGA
CAAACCCCTCAAGTTTAAAAAGGTGAAGAAAGATAAGAAAGAAGAGAAAGAGGGCAAGCATGAGCCC
GTGCAGCCATCAGCCCACCACTCTGCTGAGCCCGCAGAGGCAGGCAAAGCAGAGACATCAGAAGGGTC
AGGCTCCGCCCCGGCTGTGCCGGAAGCTTCTGCCTCCCCCAAACAGCGGCGCTCCATCATCCGTGACCG
GGGACCCATGTATGATGACCCCACCCTGCCTGAAGGCTGGACACGGAAGCTTAAGCAAAGGAAATCTG
GCCGCTCTGCTGGGAAGTATGATGTGTATTTGATCAATCCCCAGGGAAAAGCCTTTAGCTCTAAAGTGG
AGTTGATTGCGTACTTCGAAAAGGTAGGCGACACATCCCTGGACCCTAATGATTTTGACTTCACGGTAAC
TGGGAGAGGGAGCCCCTCCCGGCGAGAGCAGAAACCACCTAAGAAGCCCAAATCTCCCAAAGCTCCAG
GAACTGGCAGAGGCCGGGGACGCCCCAAAGGGAGCGGCACCACGAGACCCAAGGCGGCCACGTCAGA
GGGTGTGCAGGTGAAAAGGGTCCTGGAGAAAAGTCCTGGGAAGCTCCTTGTCAAGATGCCTTTTCAAA
CTTCGCCAGGGGGCAAGGCTGAGGGGGGTGGGGCCACCACATCCACCCAGGTCATGGTGATCAAACGC
CCCGGCAGGAAGCGAAAAGCTGAGGCCGACCCTCAGGCCATTCCCAAGAAACGGGGCCGAAAGCCGG
GGAGTGTGGTGGCAGCCGCTGCCGCCGAGGCCAAAAAGAAAGCCGTGAAGGAGTCTTCTATCCGATCT
GTGCAGGAGACCGTACTCCCCATCAAGAAGCGCAAGACCCGGGAGACGGTCAGCATCGAGGTCAAGGA
AGTGGTGAAGCCCCTGCTGGTGTCCACCCTCGGTGAGAAGAGCGGGAAAGGACTGAAGACCTGTAAGA
GCCCTGGGCGGAAAAGCAAGGAGAGCAGCCCCAAGGGGCGCAGCAGCAGCGCCTCCTCACCCCCCAA

SAMPLE OF CMDS DATASET

1256	2521	2211	1125	0.67	1.04	0.84	1.27	0.78	1.14	1.11	0.68	1.21
1.06	1	1.07	0.79	0.51	0.92	1.28	1.17	0.75	-4.75	7.1	-3.72	4.16
5.27	-13.4	5.8	1.5	0.19	2.54	-5.1	-8.32	-2.15	6.91	2.77	13130	
2	15	13	0.149	1.003								
1258	2521	2211	1125	0.67	1.06	0.92	1.26	0.8	1.16	1.11	0.69	1.27
1.06	1.01	1.07	0.79	0.51	0.92	1.28	1.17	0.75	-4.75	7.1	-3.72	4.16
5.27	-13.4	5.8	1.5	0.19	2.54	-5.1	-8.32	-2.15	6.91	2.77	13130	
2	15	12	0.149	1.004								
1079	1030	988	889	0.76	2.04	0.84	2.27	0.78	2.15	2.5	0.72	2.20
1.04	1.02	1.06	0.77	0.51	0.92	1.28	1.17	0.75	-1.71	7.4	-3.72	4.16
5.25	-13.4	5.8	1.4	0.2	2.54	-5.3	-8.32	-2.15	6.91	2.75	7374	
1	15	13	0.15	1.002								
393	437	439	192	0.55	1.15	0.6	0.84	1.39	0.7	1.01	1.3	1.13
0.72	2.20	1.04	1.02	1.06	0.77	0.51	0.92	1.28	1.17	0.75	-4.75	7.4
-3.72	4.16	5.25	-13.4	5.8	1.4	0.2	2.54	-8.32	-2.15	6.91	2693	
1	15	13	0.15	1.002								
2211	1866	1940	1729	0.33	1.03	0.8	0.4	0.9	0.47	0.1	1.3	1.13
0.2	2.20	2.04	1.02	1.06	0.78	0.51	0.2	1.23	1.18	0.65	-2.75	7.4
1.72	4.16	5.25	-13.4	5.8	1.4	0.2	2.54	-5.3	-8.32	-2.15	6.91	
14299	1	11	17	0.12	1.02							
2211	1867	1940	1729	0.36	1.07	0.9	0.5	0.6	0.67	0.1	1.7	1.13
0.2	2.20	2.04	1.02	1.06	0.78	0.51	0.8	1.23	1.18	0.65	-2.75	7.4
1.72	4.16	5.25	-13.4	5.8	1.4	0.2	2.54	-8.32	-2.15	6.91	2.7	14299
1	11	17	0.12	1.02								
686	557	467	438	0.49	1.04	0.98	0.2	1.39	1.27	0.41	0.3	1.6
0.72	2.24	1.04	1.02	1.06	0.77	0.51	0.92	1.28	1.17	0.75	-4.75	7.4
-3.72	4.16	5.25	-13.4	5.8	1.4	0.2	2.54	-5.3	-8.32	-2.15	2.7	2621
1	1	1	0.15	1.002								

SAMPLE OF MDS DATASET

898	898	1	7113	0	-1	-6	-0.4	-3	-4	-2.2	2	5
7.23	-2.76											
3032	3032	1	7113	0	-2	-6	-2.3	-5	-2	-3.3	8	20
4.21	-2.9											
4328	4328	1	7113	0	0	-1	0.6	-1	-1	-0.6	13	17
5.23	-2.7											
203	203	1	7113	0	0	-5	-0.2	-3	-3	-2.3	11	15
7.22	-2.7											
1214	1214	1	1461	0	0	-5	-0.2	-3	-3	-2.3	15	11
1.97	1.67											
410	410	1	1461	0	-2	-4	0.5	-2	-1	-0.8	7	8
1.98	4.78											
1339	1340	2	7114	1	-1	0	0.8	0	1	0.5	1	8
7.56	1.13											
925	926	2	7111	2	-1	-4	-0.1	-3	-4	-1	2	8
9.08	-4.1											
2971	2986	16	7130	3	0	-3	-1.3	-2	-1	-0.9	15	2
7.76	-5.03											
3728	3728	1	7114	3	4	7	2.5	5	3	2.4	1	1
7.88	1.51											

SAMPLE OF PMDS DATASET

393 437 439 192 0.55 1.15 0.6 0.84 1.39 0.7 1.01 1.3 1.13
0.72 2.20 1.04 1.02 1.06 0.77 0.51 0.92 1.28 1.17 0.75 -4.75 7.4
-3.72 4.16 5.25 -13.4 5.8 1.4 0.2 2.54 -8.32 -2.15 6.91 2693 1
5 13 0.15 1.002 925 926 2 4310 2 -1 -4 -0.1 -3
-4 -1 2 8 9.08 -4.1

1079 1030 988 889 0.76 2.04 0.84 2.27 0.78 2.15 2.5 0.72 2.20 1.04
1.02 1.06 0.77 0.51 0.92 1.28 1.17 0.75 -4.75 7.4 -3.72 4.16 5.25
-13.4 5.8 1.4 0.2 2.54 -5.3 -8.32 -2.15 6.91 2.75 7374 1 15
13 0.15 1.002 410 410 1 2861 0 -2 -4 0.5 -2 -1
-0.8 7 8 1.98 4.78

1256 2521 2211 1125 0.67 1.04 0.84 1.27 0.78 1.14 1.11 0.68 1.21
1.06 1 1.07 0.79 0.51 0.92 1.28 1.17 0.75 -4.75 7.1 -3.72
4.16 5.27 -13.4 5.8 1.5 0.19 2.54 -5.1 -8.32 -2.15 6.91 2.77
13130 2 15 13 0.149 1.003 898 898 1 2861 0 -1 -6
-0.4 -3 -4 -2.2 2 5 7.23 -2.76

2211 1866 1940 1729 0.33 1.03 0.8 0.4 0.9 0.47 0.1 1.3 1.13
0.2 2.20 2.04 1.02 1.06 0.78 0.51 0.2 1.23 1.18 0.65 -2.75 7.4
1.72 4.16 5.25 -13.4 5.8 1.4 0.2 2.54 -5.3 -8.32 -2.15 6.91
14299 1 11 17 0.12 1.02 1339 1340 2 7114 1 -1 0
0.8 0 1 0.5 1

1258 2520 2210 1125 0.67 1.06 0.92 1.26 0.8 1.16 1.11 0.69 1.27
1.06 1.01 1.07 0.79 0.51 0.92 1.28 1.17 0.75 -4.75 7.1-3.72 4.16
5.27 -13.4 5.8 1.5 0.19 2.54 -5.1 -8.32 -2.15 6.91 2.77 13130
2 15 12 0.149 1.004 3032 3032 1 2861 0 -2-6 -2.3 -
5-2 -3.3 8 20 7.21 -2.9

2210 1867 1940 1729 0.36 1.03 0.9 0.7 1.4 0.55 0.1 1.3 2.13
0.2 2.20 2.04 1.02 1.06 0.78 0.51 0.2 1.23 1.18 0.65 -2.75 7.4
1.72 4.16 5.25 -13.4 5.8 1.4 0.2 2.54 -5.3 -8.32 -2.15 6.91
14299 1 11 17 0.12 1.02 1339 1340 2 7114 1 -1 0
0.8 0 1 0.5 1

SAMPLE OF GSDS DATASET

122	2	1731	1	8	20	1	2	3	-1	-6	-0.4
-3	-4	-2.2	5.66E-08		2.94E-04		4	1	1	1	1
0	1	1	1883.4								
85	5	1130	2	5	8	1	3	2	-1	-4	1.1
-3	-4	-2.2	5.66E-08		0	3	1	0	1	1	0
1	0	1234.9									
43	1	770	2	6	10	1	2	2	-1	-3	-0.6
-3	-4	-2.2	0	5.71E-04		3	0	1	0	1	0
1	1	830.20									
66	2	131	1	5	7	1	1	1	-1	-1	-0.13
-3	-4	-2.2	0	5.71E-04		4	1	1	1	1	0
1	1	213.6									
110	1	1731	1	6	8	1	1	3	-1	-6	-0.2
-3	-4	-2.2	5.66E-08		2.94E-04		4	1	1	1	1
0	1	0	1854.6								
122	5	1731	1	8	10	1	2	2	-1	-2	0.17
-3	-4	-2.2	5.66E-08		2.94E-04		4	1	1	1	1
0	0	1	1878.97								
21	2	1731	1	5	11	1	2	1	-1	-4	0.5
-3	-4	-2.2	5.66E-08		2.94E-04		4	0	1	1	1
0	0	1	1769.3								

SAMPLE OF CODON ENCODED GENE SEQUENCE

10	46	5	41	6	12	11	54	3	22	18
35	21	44	39	10	15	17	21	14	11	12
4	41	60	24	28	13	19	11	8	35	41
9	26	6	41	6	38	11	54	26	22	18
15	20	4	39	10	15	18	21	8	11	24
4	57	48	25	39	12	20	16	62	35	49
10	46	5	41	6	15	11	54	3	22	18
35	21	44	39	10	15	17	21	14	11	2
4	41	36	24	28	12	19	11	8	35	41
3	26	16	41	6	24	11	54	26	22	18
15	20	23	39	10	15	18	21	8	11	24
4	57	60	25	39	12	20	16	62	35	4
12	26	32	8	6	17	11	54	26	22	18
15	20	23	39	10	15	19	21	8	11	24
4	57	60	25	39	12	20	16	61	35	60

APPENDIX B – CODING

R Code for Inducing Mutations and Extracting Features

```
require(stringi)
require(seqinr)
lines <- readLines('SHANK3.txt')
bdy2 <- paste(lines, collapse=",")
x<-stri_replace_all_charclass(bdy2, "\\p{WHITE_SPACE}", "")
x2<-gsub('[0-9]+', '', x)
x3<- gsub('[[:punct:]]', '', x2)
// Replace  character in codon and convert to data frame
Posn= (Codon_number-1)* i +1  // i is position of character in a codon to be replaced
x4<-subcharT(x3, Posn)
 x5<-data.frame(x4)
write.fasta(sequences=x5,names="",file.out="E://out1.fasta")
 // Function  select according to variation
subcharT <- function(string, pos, char="T") {
 for(i in pos) { string <- gsub(paste("^(.{", i-1, "}).", sep=""), "\\1T", string, perl=TRUE)  }
string  }
subcharG <- function(string, pos, char="G") {
 for(i in pos) { string <- gsub(paste("^(.{", i-1, "}).", sep=""), "\\1G", string, perl=TRUE) }
 string  }
subcharA <- function(string, pos, char="A") {
 for(i in pos) { string <- gsub(paste("^(.{", i-1, "}).", sep=""), "\\1A", string, perl=TRUE) }
 string  }
subcharC<- function(string, pos, char="C") {
 for(i in pos) { string <- gsub(paste("^(.{", i-1, "}).", sep=""), "\\1C", string, perl=TRUE) }
 string  }
 // Extract Features From Modified Fasta
require(seqinr)
sh <- read.fasta(file = "E://out1.fasta")
shseq<-sh[[1]]
extract_feature(shseq)
// Function to extract features
extract_feature<-function(sequence)
{
T<-table(shseq)
G<-GC(shseq)
R<-round(rho(shseq, wordsize=2),2)
```

```
Z<-round(zscore(shseq, modele='base'),2)
 Y<- count(shseq, wordsize=3)
p<-c2s(shseq)
globalAligns1s2 <- pairwiseAlignment(x3, x4, substitutionMatrix = sigma, gapOpening = -2,
gapExtension = -8, scoreOnly = FALSE)
print(T)
print(G)
print(R)
print(Z)
print(Y)
print(globalAligns1s2)
}
// To normalize
sample=read.csv("E:\\out2.csv")
  // formula is normalized = (x-min(x))/(max(x)-min(x))
normalized = (sample-min(sample))/(max(sample)-min(sample))
write.csv(normalized, "E:\\out3.csv")
```

Code to Predict ASD Gene Type

```
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler
from sklearn.neural_network import MLPClassifier
from sklearn.metrics import classification_report,confusion_matrix
from sklearn.metrics import accuracy_score
df=pd.read_csv('E:\cmds.csv')
print(df)
x=df.values[:,0:43]
y=df.values[:,43]
x_train,x_test,y_train,y_test=train_test_split(x,y)
scaler=StandardScaler()
scaler.fit(x_train)
StandardScaler(copy=True,with_mean=True,with_std=True)
x_train=scaler.transform(x_train)
x_test=scaler.transform(x_test)
mlp=MLPClassifier(hidden_layer_sizes=(8,8,8),max_iter=500)
mlp.fit(x_train,y_train)
# BUILD MODEL
MLPClassifier()
```

```
predictions=mlp.predict(x_test)
print(confusion_matrix(y_test,predictions))
print(classification_report(y_test,predictions))
# ACCURACY_SCORE
print ("Accuracy is",accuracy_score(y_test,predictions)*100)
```

Code to Predict ASD Causing Mutations

```
from sklearn.tree import DecisionTreeClassifier
from sklearn import metrics
from sklearn.cross_validation import train_test_split
from sklearn.metrics import accuracy_score
df=pd.read_csv('E:\mds.csv')
print(df)
x=df.values[:,0:15]
y=df.values[:,15]
x_train,x_test,y_train,y_test=train_test_split(x,y,test_size=3,random_state=100)
model=DecisionTreeClassifier()
model.fit(x_train,y_train)
y_pred=model.predict(x_test)
y_pred
# ACCURACY
print "Accuracy using DecisionTreeClassifier is",accuracy_score(y_test,y_pred)*100
print(metrics.classification_report(expected,predicted))
print(metrics.classification_report(y_test,y_pred))
```

Code for Gene Susceptibility Prediction

```
import numpy as np
import matplotlib.pyplot as plt
from itertools import cycle
import pandas as pd
from sklearn import svm, datasets
from sklearn.metrics import roc_curve, auc
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import label_binarize
from sklearn.multiclass import OneVsRestClassifier
from scipy import interp
# Import some data to play with
dd=pd.read_csv("E:/genesuscept.csv")
X=dd.values[:,0:25]
```

```
y=dd.values[:,25]
# Binarize the output
y = label_binarize(y, classes=[0, 1, 2])
n_classes = y.shape[1]
# shuffle and split training and test sets
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=.5,
random_state = 0)
# Learn to predict each class against the other
classifier = OneVsRestClassifier(svm.SVC(kernel='linear', probability=True,
random_state=random_state))
y_score = classifier.fit(X_train, y_train).decision_function(X_test)
Y_pred =model.predict(X_test)
Y_pred
#ACCURACY SCORE
print "Accuracy is",accuracy_score(Y_test,Y_pred)*100
#CONFUSION MATRIX
print "confusion matrix",confusion_matrix(y_test,Y_pred)
#CLASSIFICATION REPORT
print "report:",classification_report(y_test,Y_pred)
# Compute ROC curve and ROC area for each class
fpr = dict()
tpr = dict()
roc_auc = dict()
for i in range(n_classes):
    fpr[i], tpr[i], _ = roc_curve(y_test[:, i], y_score[:, i])
    roc_auc[i] = auc(fpr[i], tpr[i])
# Compute micro-average ROC curve and ROC area
fpr["micro"], tpr["micro"], _ = roc_curve(y_test.ravel(), y_score.ravel())
roc_auc["micro"] = auc(fpr["micro"], tpr["micro"])
all_fpr = np.unique(np.concatenate([fpr[i] for i in range(n_classes)]))
lw=2
# Then interpolate all ROC curves at this points
mean_tpr = np.zeros_like(all_fpr)
for i in range(n_classes):
    mean_tpr += interp(all_fpr, fpr[i], tpr[i])
# Finally average it and compute AUC
mean_tpr /= n_classes
fpr["macro"] = all_fpr
tpr["macro"] = mean_tpr
roc_auc["macro"] = auc(fpr["macro"], tpr["macro"])
```

```
# Plot all ROC curves
plt.figure()
plt.plot(fpr["micro"], tpr["micro"],
        label='micro-average ROC curve (area = {0:0.2f})'
              ".format(roc_auc["micro"]),
        color='deeppink', linestyle=':', linewidth=4)
plt.plot(fpr["macro"], tpr["macro"],
        label='macro-average ROC curve (area = {0:0.2f})'
              ".format(roc_auc["macro"]),
        color='navy', linestyle=':', linewidth=4)
colors = cycle(['aqua', 'darkorange', 'cornflowerblue'])
for i, color in zip(range(n_classes), colors):
    plt.plot(fpr[i], tpr[i], color=color, lw=lw,
             label='ROC curve of class {0} (area = {1:0.2f})'
             ".format(i, roc_auc[i]))
plt.plot([0, 1], [0, 1], 'k--', lw=lw)
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.legend(loc="lower right")
plt.show()
```

Codon Encoding

```
rep_val={"AAA":1, "ATA":2, "AGA":3, "ACA":4, "AAT":5, "ATT":6, "AGT":7, "ACT":8,
"AAG":9, "ATG":10, "AGG":11, "ACG":12, "AAC":13, "ATC":14, "AGC":15, "ACC":16,
"TAA":17, "TTA":18,  "TGA":19, "TCA":20, "TAT":21,  "TTT":22, "TGT":23,  "TCT":24,
"TAG":25,  "TTG":26, "TGG":27, "TCG":28, "TAC":29, "TTC":30, "TGC":31, "TCC":32,
"GAA":33, "GTA":34, "GGA":35, "GCA":36, "GAT":37, "GTT":38, "GGT":39, "GCT":40,
"GAG":41,  "GTG":42, "GGG":43, "GCG":44, "GAC":45, "GTC":46,"GGC":47, "GCC":48,
"CAA":49,  "CTA":50,  "CGA":51, "CCA":52, "CAT":53, "CTT":54, "CGT":55,  "CCT":56,
"CAG":57, "CTG":58, "CGG":59, "CCG":60, "CAC":61, "CTC":62,  "CGC":63, "CCC":64}
dataframe = pandas.read_csv("D:\\New folder\\New folder\\sample\\data1.csv", header=None)
dataframe.replace(rep_val, inplace=True)
dataframe.head()
dataframe.to_csv("D:\\out3.csv")
```

Code for Bidirectional RNN Based Gene Prediction

```
import keras
```

```
import tensorflow as tf
from keras.models import Sequential
from keras.layers.wrappers import Bidirectional
from keras.layers import Dense
from keras.layers import SimpleRNN
from keras.layers import Dropout
from sklearn.model_selection import StratifiedKFold
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from keras.wrappers.scikit_learn import KerasClassifier
import numpy as np
from sklearn.preprocessing import LabelEncoder
from keras.utils import np_utils
import pandas
data_dim = 1
timesteps = 2582
num_classes = 10
np.random.seed=7
opt = tf.train.AdamOptimizer(learning_rate=0.01)
dataframe = pandas.read_csv("D:\\geneid.csv", header=None)
dataset = dataframe.values
X = dataset[:,0:2582].astype(float)
Y = dataset[:,2582]
encoder = LabelEncoder()
```

```
encoder.fit(Y)

encoded_Y = encoder.transform(Y)

# convert integers to dummy variables (i.e. one hot encoded)

dummy_y = np_utils.to_categorical(encoded_Y)

model = Sequential()

model.add(Masking(mask_value=0., input_shape=(timesteps,data_dim)))

model.add(Bidirectional(SimpleRNN(8, return_sequences=False,input_shape=(timesteps,
data_dim))))

model.add(Dropout(0.3))

model.add(Dense(10, activation='softmax'))

model.compile(loss='categorical_crossentropy', optimizer=opt, metrics=['accuracy'])

from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, dummy_y, test_size = 0.2, random_state = 0)

from sklearn.preprocessing import StandardScaler

X_train = X_train.reshape((len(X_train), timesteps, data_dim))

X_test = X_test.reshape((len(X_test), timesteps, data_dim))

model.fit(X_train, y_train, epochs=50, batch_size=200)

loss, accuracy = model.evaluate(X_test,y_test, verbose=0)

print('Accuracy: %f' % (accuracy))

print('Loss: %f' % (loss))

y_pred = model.predict_classes(X_test)

#print(y_pred)

ycat_pred = np_utils.to_categorical(y_pred, num_classes=10)

#print(ycat_pred)

from sklearn.metrics import precision_score
```

```
print(precision_score(y_test, ycat_pred, average='micro'))

from sklearn.metrics import recall_score

print(recall_score(y_test, ycat_pred, average='micro'))

from sklearn.metrics import classification_report

target_names = ['class 0', 'class 1', 'class 2','class 3', 'class 4', 'class 5','class 6', 'class 7', 'class 8','class 9']

print(classification_report(y_test, ycat_pred, target_names=target_names))
```

Code for LSTM Based Gene Prediction

```
import keras
from keras.models import Sequential
from keras.layers import LSTM, Dense
import numpy as np
data_dim = 1
timesteps = 2582
num_classes = 10
model = Sequential()
model.add(LSTM(8, return_sequences=True,
               input_shape=(timesteps, data_dim)))  # returns a sequence of vectors of dimension 32
model.add(LSTM(8))  # return a single vector of dimension 32
model.add(Dense(11, activation='softmax'))
import pandas
from sklearn.preprocessing import LabelEncoder
from keras.utils import np_utils
model.compile(loss='categorical_crossentropy',              optimizer='adam',
metrics=['accuracy'])
dataframe = pandas.read_csv("D:\\RESULTS\\out2.csv", header=None)
dataset = dataframe.values
X = dataset[:,0:2582].astype(float)
Y = dataset[:,2582]
X = X.reshape((len(X), timesteps, data_dim))
encoder = LabelEncoder()
encoder.fit(Y)
encoded_Y = encoder.transform(Y)
# convert integers to dummy variables (i.e. one hot encoded)
dummy_y = np_utils.to_categorical(encoded_Y)
```

```
y_new = dummy_y.reshape((len(X), num_classes))
estimator= model.fit(X, y_new, epochs=1, batch_size=2)
```

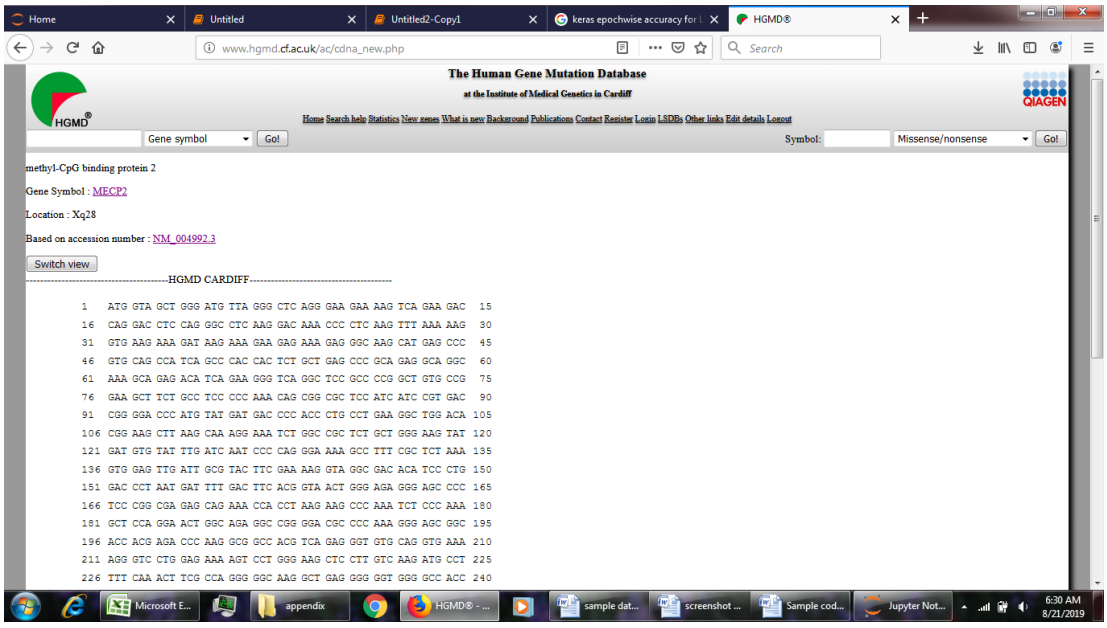
Code for GRU Based Gene Prediction

```
from keras.utils import plot_model
from keras.models import Model
from keras.layers import Input
from keras.layers import Dense
from keras.layers.recurrent import LSTM
from keras.layers.merge import concatenate
# define input
visible = Input(shape=(2582,1))
# feature extraction
extract1 = GRU(8)(visible)
# first interpretation model
interp1 = Dense(8, activation='relu')(extract1)
# second interpretation model
interp11 = Dense(8, activation='relu')(extract1)
interp12 = Dense(8, activation='relu')(interp11)
interp13 = Dense(8, activation='relu')(interp12)
# merge interpretation
merge = concatenate([interp1, interp13])
# output
output = Dense(10, activation='sigmoid')(merge)
model = Model(inputs=visible, outputs=output)
# summarize layers
import keras
import tensorflow as tf
from keras.models import Sequential
from keras.layers import GRU, Dense
from keras.layers import SimpleRNN
from keras.layers import Masking
from keras.layers import Dropout
from sklearn.model_selection import StratifiedKFold
from sklearn.model_selection import KFold
from sklearn.model_selection import cross_val_score
from keras.wrappers.scikit_learn import KerasClassifier
import numpy as np
from sklearn.preprocessing import LabelEncoder
```

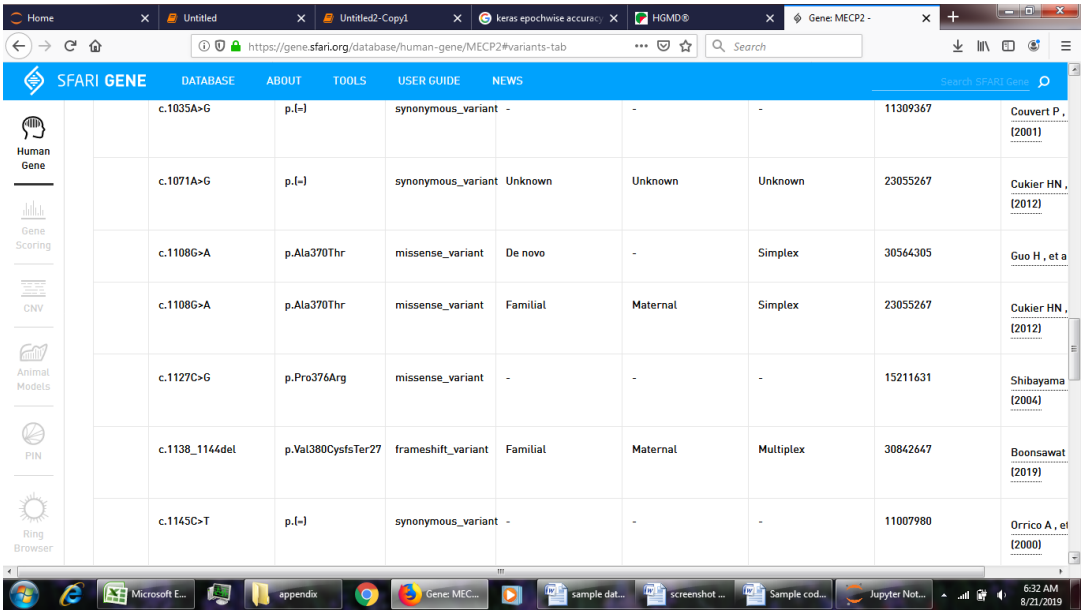
```
from keras.utils import np_utils
import pandas
data_dim = 1
timesteps = 2582
num_classes = 10
np.random.seed=7
opt = tf.train.AdamOptimizer(learning_rate=0.01)
dataframe = pandas.read_csv("D:\\new1.csv", header=None)
dataset = dataframe.values
X = dataset[:,0:2582].astype(float)
Y = dataset[:,2582]
encoder = LabelEncoder()
encoder.fit(Y)
encoded_Y = encoder.transform(Y)
# convert integers to dummy variables (i.e. one hot encoded)
dummy_y = np_utils.to_categorical(encoded_Y)
model.compile(loss='categorical_crossentropy', optimizer=opt, metrics=['accuracy'])
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, dummy_y, test_size = 0.2, random_state =
0)
from sklearn.preprocessing import StandardScaler
X_train = X_train.reshape((len(X_train), timesteps, data_dim))
X_test = X_test.reshape((len(X_test), timesteps, data_dim))
model.fit(X_train, y_train, epochs=60, batch_size=64)
```

APPENDIX C – SCREENSHOTS

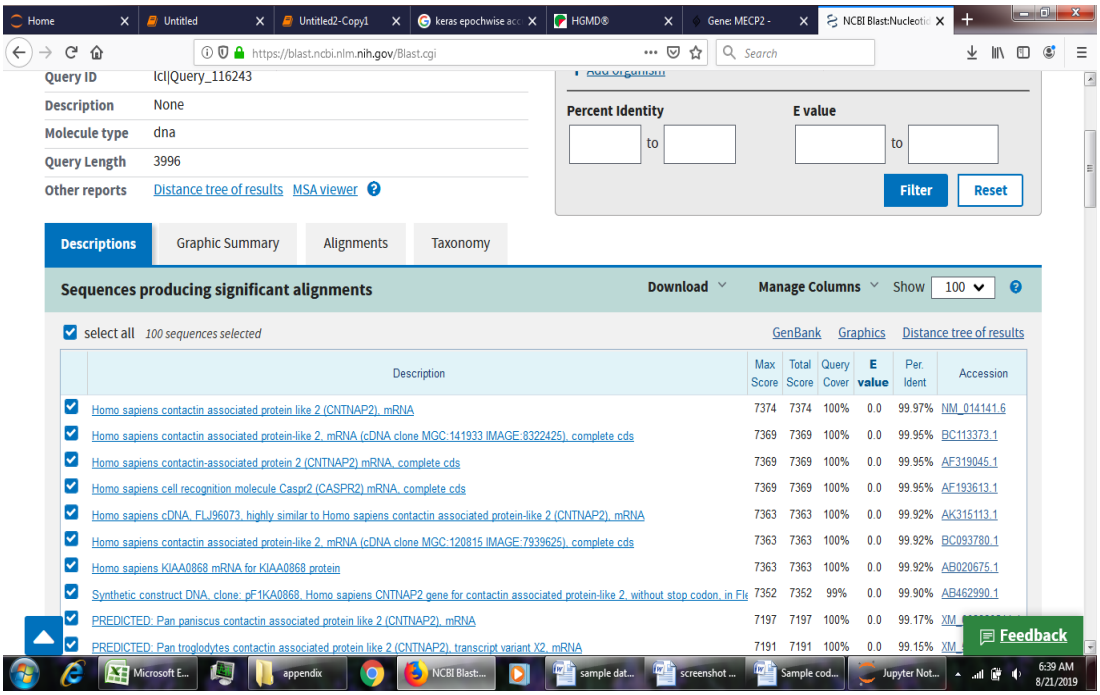
CDNA Gene Sequence for MECP2 gene



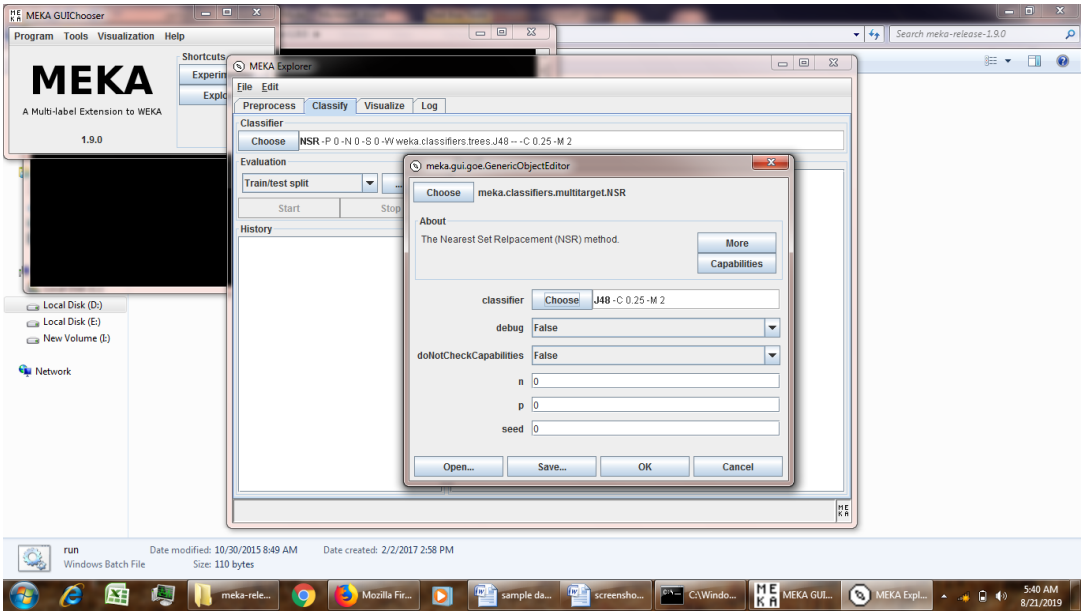
Mutational information from SFARI gene database for MECP2 gene



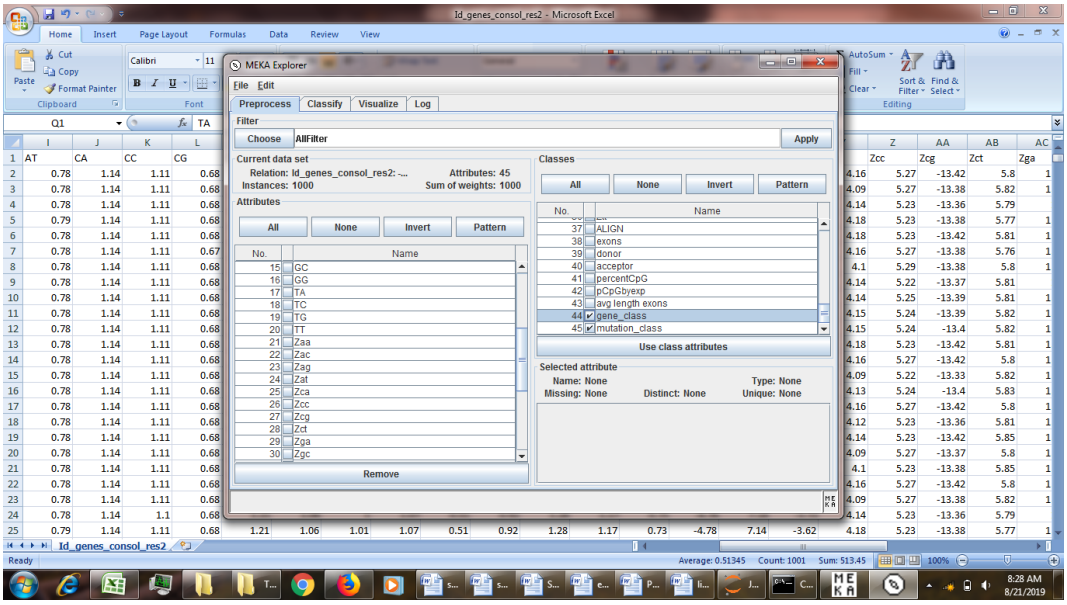
BLAST Alignment Results



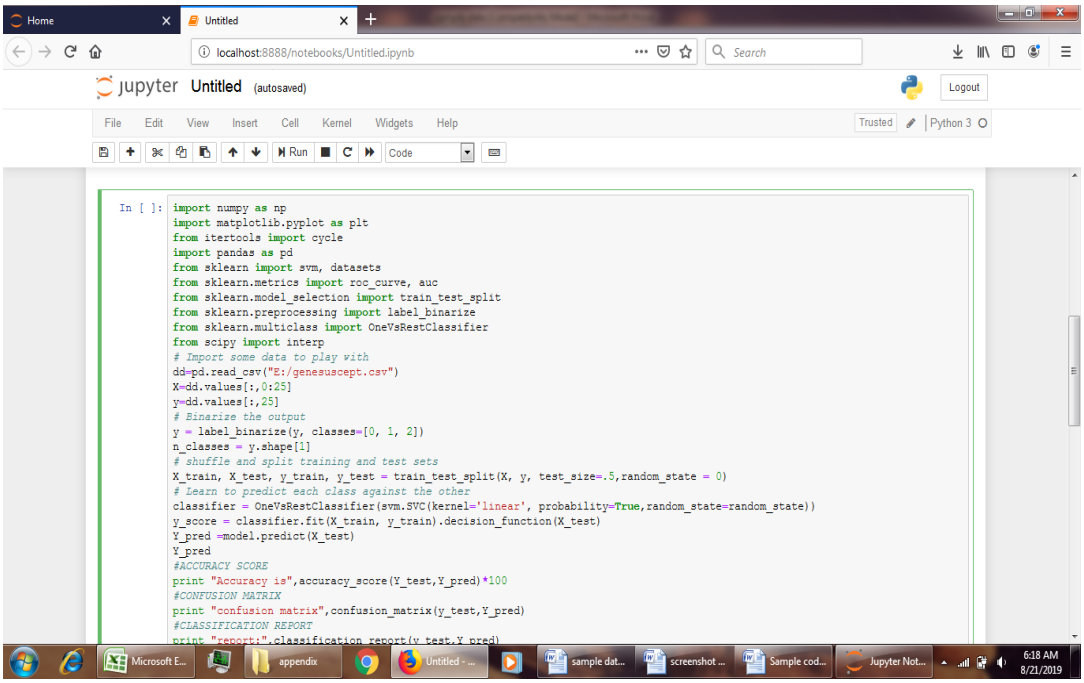
MEKA Environment



Input for Gene – Mutation Prediction in MEKA



Gene Susceptibility Prediction using Sci-kit learn



Output from Sci-kit learn Environment