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*All the programs are written in python 2.7*.

(Should have numpy, matplotlib and glob module installed in the system)

Do not tamper with the location of program files, they are inter-connected.

Some part of code is commented out which is used to get different output files.

1. Main\_File\_4.py has P-value and Super-Information functions to give primarily results and importing F3 function from F3.py to get F3 value too.

2. F3.py has a function module which gives the F3 value for a given DNA file.

3. Main\_ML.py program gives the output file which generates the data-sets to be used in WEKA and Tensorflow.

4. DNA folder has all the DNA file and gff3 files of respective DNA and also the resultant plots from Main\_File\_4.py

5. WEKA folder includes screenshots of results obtained and input file (.arff) for WEKA.

6. The ML folder contains two files load.py and learn.py. The load.py file is used to extract and load the data-sets into pythonic variables and creates the training data-set and test data-set. The learn.py file is used to execute the ML training and evaluation. The training part takes ~5 mins to execute. The system should have tensorflow module in order to execute learn.py.