**Problem One**

A) Feature set <number of friends, number of photos, number of videos, number of statuses>

This feature set consists of a variety of indicative features that can be measured using real numbers. Number of friends, number of photos, number of posts, and number of videos can all be measured using any integer greater than or equal to 0. This feature set is useful is gauging what type of Facebook user it is as it clearly represents user activity and engagement.

B) Given the above feature set, a metric could be the total number of likes the profile has. This measurable could be clearly compared across profiles, and would be a good indicator of how popular a given user is. If a user receives more likes than another user when taking into account pictures, videos, and posts, then this is a holistic view of general online popularity.

C) No it does not make sense to put people in a Euclidean 3-space. I would place the most weight on number of hairs on head. This metric is not dependent on gender, because no matter what it is likely that a child has more hair than an elderly person; this trend is clear across gender lines. That being said, the distribution would definitely be more extreme for the male gender. I would then weigh height and weight at the next tier, as they are less indicative of age. While it is true a shorter, lighter person is probably a child, this is not as clear of a pattern and is a bit more difficult to discern across gender.

D) As explained in the paper, one could assess the distance between strings based on how many edits are necessary to make them identical. The three different means to edit a given string are insertion, deletion, and replacement. Weighted equally, these methods can determine the distance between two strings by counting how many times each needs to be applied. This metric could also be used to discern the distance between two DNA strands. Because DNA strands are encoded with 4 bases, each represented with a letter, their representations take the same format as a standard string. Because of this, the method described in the paper could be used as it stands to determine the distance between two DNA strands. In order to see how two DNA strands’ bases compare, this algorithm could assess the distance between their two string representations.

**Problem 3**

A) Because the wikipediatypo.txt file is extremely long, 4223 lines, I took sample sets of the file to determine how long it would take to check the entire file. I first created a test.txt document that consisted of 10 lines of the original wikipediatypo.txt document. Using the time function, it took 12.2094750404 seconds to run measure\_error on the 10 lines with the entire 3esl dictionary. Then, I edited the text.txt file to have 20 lines of the original wikipediatypo.txt file. Using the time function, it took 26.0232889652 seconds to run measure\_error on the 20 lines with the entire 3esl dictionary. Through these two calculations, one can extrapolate that the file’s size (lines) and the time it takes to measure error is relatively linear. With this information, I did the following math calculation.

4223 / 10 = 422.3 sample sets of size ten within the entire file

(422.3 sets) \* (12.2094750404 sec) = 5,156.0613096 seconds

5,156.0613096 seconds / 60 = 85.93435516 minutes

85.93435516 min / 60 = 1.4322392527 hours

Thus, it would take approximately 1.4 hours to run measure\_error on the entire wikipediatypo.txt file using the 3esl dictionary.

A variation on this process would be testing how long it takes to run all 64 parameter combinations for insertion, deletion and substitution costs among the values in the set {0, 1, 2, 4}. Because the above calculation represents running measure\_error using one possible combination within this value set, this process would take approximately 64 times longer.

1.4322392527 hr \* 64 = 91.663312173 hours

91.663312173 hr / 24 = 3.8193046739 days

Thus, it would take approximately 3.8 days to run measure\_error on wikipediatypo.txt using the entire 3esl dictionary, and testing all 64 parameter combinations.

Another variation of this process would be testing how long is takes to run 10-fold cross validation on the wikipediatypo.txt file and testing all 64 parameter combinations. Using this method, you would divide the wikipediatypo.txt file into 10 equal sections. Then, you would run measure\_error using all 64 combinations on 90% of the file to determine the best parameter combination. After, you would measure\_error on the remaining 10% of the file using the chosen best parameter combination. This process would repeat 10 times, cycling through each 10% of the file. Given this method, I did the follow math computation to determine approximately how long it would take.

4223 \* .10 = 422.3 lines (10% of the file)

4223 lines \*.90 = 3,800.7 lines (90% of the file)

3,800.7 lines \* (12.2094750404 sec / 10 lines) = 4,640.4551786 seconds

4,640.4551786 seconds \* 64 combos = 296,989.13143 seconds

422.3 lines \* (12.2094750404 sec / 10 lines) = 515.60613094 seconds

296,989.13143 sec+ 515.60613096 sec = 297,504.73756096 seconds

297,504.73756096 sec \* 10 = 2,975,047.3756 seconds

2,975,047.3756 sec / 60 = 49,584.122927 minutes

49,584.122927 min / 60 = 8,264.0204878 hours

8,264.0204878 hrs / 24 = 344.33418699 days

Cross-validation would take much longer, but it would provide more accurate data because the training data and testing data are separated. That being said, a way to expedite this process would be to divide wikipediatypo.txt alphabetically, and test it against a subset of the dictionary that corresponds to the given set’s alphabetical order. This would be quicker because it would iterate through a smaller dictionary, but it would compromise the test results because it is not fully testing our model.