

Carnegie Mellon University in Qatar
AI for Medicine
15-182/282 - Spring 2022
Assignment 2

Name: _____

Andrew ID: _____

Due on: February 15, 2022 by Midnight

Instructions:

- This assignment spans 4 pages and has 3 problems with maximum scores of 100 points for 15-282 and 50 points for 15-182.
- You should submit your answers through Gradescope.

Problem	Points	Your Score
1	30	
2	20	
3	50	

Problem 1: Reading and Analyzing a Research Paper for an AI application in Medicine (30 Points)

Read the paper “Avey: An Accurate AI Algorithm for Self-Diagnosis” (available on the course website at: <https://web2.qatar.cmu.edu/~mhhammou/15282-s22/resources.html>) and answer the following questions:

- a) Write a 1-page summary of the paper.
- b) Discuss at least 3 strengths of the paper.
- c) Discuss at least 3 weaknesses of the paper.
- d) How do you foresee the future of medical diagnosis as AI evolves further? Explain and justify your opinion (e.g., you can read and cite papers that discuss this topic).

Problem 2: Comparing Two AI Medical Diagnostic Algorithms (20 Points)

In this problem you will compare the performance of two AI medical diagnostic algorithms using standard accuracy metrics.

Consider 3 gold-standard vignettes, each with a differential diagnosis as shown in Table 1. The letters, A, B, C, D, and E refer to diseases and the disease at the top of each differential list is considered as the main diagnosis in the list. Each disease in a differential list is assigned a relevance score as illustrated in the table. The higher the relevance of a disease, the more probable it is to be the right diagnosis.

Gold-standard					
Vignette 1		Vignette 2		Vignette 3	
Disease	Relevance	Disease	Relevance	Disease	Relevance
A	5	F	3	A	1
B	4	E	2		
C	3	C	1		
D	2				
E	1				

Table 1

Assume there are two AI medical diagnostic algorithms named *SuperMD* and *DigitalMD*. The 3 vignettes given in Table 1 were tested on *SuperMD* and *DigitalMD*, after which results were collected and demonstrated in Table 2 and Table 3, respectively.

<i>SuperMD</i> Results		
Vignette 1	Vignette 2	Vignette 3
B	F	A
E		

Table 2

<i>DigitalMD</i> Results		
Vignette 1	Vignette 2	Vignette 3
E	C	A
B		

Table 3

- a) Calculate and plot in a bar chart the average M1, average M2, average M3, average recall, average precision, average F1-measure, and average NDCG of *SuperMD* and *DigitalMD*.
- b) Which algorithm, *SuperMD* or *DigitalMD*, is better in your opinion. Explain.

Problem 3: Developing a Classifier in Python (50 Points)

Note: This problem is only for students who are taking 15-282.

In this problem you will develop a perceptron classifier using Python to classify whether a given Pribnow sequence is a true-site or a non-site.

Consider the following 3 Pribnow sequences (i.e., S1, S2, and S3), which are true sites of promoters on DNA for transcription to occur in bacteria:

S1: TACGAT
 S2: TATAAT
 S3: GATACT

Moreover, consider the following 2 sequences (i.e., S4 and S5), which are not Pribnow sequences (i.e., non-sites):

S4: AATTCC
 S5: GGTAA

- a) Assume that any sequence can be represented as a matrix of 4 x 6 elements, with the following characteristics:
 - i. Rows 0, 1, 2, and 3 refer to DNA bases A, C, G, and T, respectively
 - ii. Each column refers to a base in a given sequence
 - iii. Each cell at row i and column j is either 0 or 1, indicating the absence or presence of the base at row i in the sequence at position j

Show how S1 will look like based on the above suggested representation.

- b) Assume the following:
 - i. A true-site and a non-site can be represented as +1 and -1, respectively

- ii. Threshold $\theta = 0$
- iii. Learning-rate $\alpha = 0.5$
- iv. A weight matrix of 4 x 4 elements, each initialized to a random number between -1 and +1, inclusive

Show how the weight matrix will look like after running the perceptron algorithm for one full round over the given 5 sequences (*you should submit an excel sheet that shows your work for this part*).

- c) Write a Python program that runs the perceptron algorithm for either 10 rounds or until it converges over the given 5 sequences. You can assume that the perceptron has converged when the number of misclassified training sequences stops changing. Show below the final weight matrix generated by your program (*you should submit your Python program for this part*).
- d) Based on the weight matrix that you learnt in part (c), what will be the class of the sequence TATGTT? Show your work.