Review of: "NER Sequence Embedding of Unified Medical Corpora to Incorporate Semantic Intelligence in Big Data Healthcare Diagnostics"

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1. Analysis of the results is missing in the paper. There is a big gap between the results and the conclusion. There should be a result analysis between these two sections. After comparing the methods, you have to be able to analyze the results and relate them to the structure of all algorithms. It would be interesting to have your thoughts on why the method works that way.

2. How do you ensure that the comparison between the ML algorithms is fair?

3. You can also link the findings to the hypotheses of the paper. Long story short, this paper requires a very deep analysis from different perspectives

4. To have an unbiased view of the paper, there should be some discussions on the limitations proposed Deep model, check these manuscripts https://doi.org/10.32604/cmc.2022.022901, https://doi.org/10.1016/j.chemolab.2020.104056, https://doi.org/10.3934/math.2023840.

5. The author needs to discuss some technical points in the pre-training, training, testing, and independent testing phase.

6. Lastly, add future work i.e. parallel computing for big data For example, you can use parallel deep learning techniques. The following references are recommended for possible consideration. i.e. https://doi.org/10.1109/ACCESS.2020.3011508 and https://doi.org/10.3390/app13127059