Third peer review report (MMDF)

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1 Reproducibility

Running the code   Under the condition of the lack access to the data, we did not have opportunity to rerun the text features code. Based on the saved outputs and illustrations, that part of code is done. The code for corresponding modules is well structured. As for the ECG part, we managed to run the notebook, although with some changes in the code, so that access to the dataset works (renaming the data path). This part worked fine, we managed to produce the same results.

We did not manage to rerun the code in the notebooks on Vizualization, as there was no possibility to access the data.

In general, it is hard to judge whether results are reproducible, as we do not have the access to the datasets. The code for Vizualization is also well structured and documentation is present.

2 Recommendation to use the library

In general, the aim of the package is definitely important for the real-world application in medicine. As for vizualization part, the code structure is good, but inability to see the datasets makes it hard to understand further how to use this package for some other data. While some things are explained, it would be in general useful to explain how the input data should look like or how to change the code, in order to use our own data. Saved outputs from notebook allow us to judge that this code serves the purposes, described by the team. As for text features, it has examples of input data and therefore one can figure out how to use it. It can be used on the custom data one chooses to analyze with Brat. The usage of this is pretty straight-forward, as it allows to process medical text data and work on the processed features. The ECG part is working the best currently and is much easier understandable. However, more documentation and explanation on the tutorial and created features will be useful for a new user.

In general, there are some data access restrictions, which do not allow to fully evaluate the usefulness of the particular code for the problem. We

see that it serves its function for this particular data, however cannot judge whether it will be useful out-of-the box for other data structures. Although we understand, that this is inevitable under circumstances, it might be useful to find a workaround to explain in more detail how the data should look like and be structured, as the functionality this code bears is exceptionally useful for a very important medical tasks. Under the condition of more detail on the input data provided where required, we would recommend to use the library for similar tasks.