Annex No. 10 to the MU Directive on Habilitation Procedures and Professor Appointment Procedures

HABILITATION THESIS REVIEWER'S REPORT

Masaryk University	
Applicant	Matej Lexa, Doctor of Philosophy
Habilitation thesis	Algorithmic approaches to biological sequence analysis generate new tools for the study of genome structure and function
Reviewer	**Ass. Prof. Sarah Berkemer**
Reviewer's home unit, institution	Department of Computer Science, Ecole Polytechnique, France

The habilitation thesis submitted by Matej Lexa describes his scientific work during his career. The work shows his steps from projects in applied bioinformatics towards the development and implementation of tools to conduct important analyses of data sets appearing in the research areas of biology and bioinformatics.
By presenting work from six different publications, the thesis shows Dr. Lexa's ability to work in a highly interdisciplinary field and provide useful new insights as well as accessible software tools for the research community.

After a short introduction and the list of included papers, the habilitation thesis is divided into single chapters where each chapter shortly describes the content of the paper and relates it to Dr. Lexa's career steps. Thus, it nicely summarizes Matej Lexa's path that he went through in order to shape his career in research.

I am not familiar with the rules for writing a habilitation thesis at Masaryk University, however, I want to mention a few points of Dr. Lexa's habilitation thesis that significantly differ from other habilitation theses I have seen before.

- In most of the papers in the thesis, Matej Lexa is the first author, and only once he took the role as last author. To me, a habilitation reflects seniority in research, thus I would have expected more last and less first authorships.
- Another important point for me regarding a habilitation is the ability to communicate own research to a wide audience including students. Dr. Matej's CV states that he is actively teaching bioinformatics courses at the university, however, I would have expected to get a more detailed introduction to the topics in his habilitation defense with explanaroty figures and examples.
- The conclusion is really short, I would have expected more future perspectives. A habilitation opens the possibility to become full professor or PI, thus I would have expected to read about Dr. Lexa's future plans and research projects that he plans to do in his next career steps.

Reviewer's questions for the habilitation thesis defence (number of questions up to the reviewer)

1. In the description of the pqsfinder tool, G4s are only mentioned regarding DNA sequences. However, G4s also exist in RNA. Would it be possible to extend the algorithm such that it could be applied to RNA sequences?
2. In the same light as above, would the triplex algorithm also work for RNA sequences?
3. As there is no description of future plans in the thesis, my question would be what his future direction in research will look like. Do you have any plans for PhD topics or larger projects including several researchers?

Conclusion

The habilitation thesis entitled "Algorithmic approaches to biological sequence analysis generate new tools for the study of genome structure and function" by Matej Lexa, Doctor of Philosophy, **fulfils** the requirements expected of a habilitation thesis in the field of Informatics.

Date: 26/04/2023 Signature: