

## 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

**Prof. Daniel Svozil, Ph.D.**

#### Reviewer's home unit, institution

Department of Informatics and Chemistry, UCT Prague

In his habilitation thesis, Dr. Lexa discusses his work in the field of biological sequence analysis, which began with combining a mathematical model of DNA synthesis with a sequence mining approach using a string matching algorithm. This led to the development of variety of efficient and practical tools and algorithms for analysing biological data. The author's contributions to the field are demonstrated through six attached publications, each with its own chapter and commentary. I particularly appreciate not only the high-quality English, but above all the very readable chapters that charmingly guide us through the author's entire scientific career. The attached publications provide further details on the author's work and its application to pressing or interesting biological problems at the time. The developed methods are state-of-the-art and seem correctly implemented. The evaluation of the novel approaches is of high quality. The tools were tested against known data and compared to existing tools.

Overall, the thesis demonstrates Dr. Lexa's expertise in various research fields and bioinformatics approaches for DNA sequence analysis. Dr. Lexa is definitely a mature researcher, with a solid research agenda. He is very successful in his results, especially, in making the whole line of research starting with the primary idea and finishing with a standalone software that implements it.

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

1. Can you elaborate on the specific areas in bioinformatics research that you identified as needing further exploration while working on the G4 pattern matching transposable element studies?
2. Which of his projects does Dr. Lexa consider to be more promising, and in which direction does he plan to proceed in his further scientific career?
3. Associate Professor is not only a scientific personality, but also a teacher and mentor. In the habilitation thesis, I found no description of Dr. Lexa's future plans on how to transfer his expertise to his students. I attribute this to various conventions regarding the content of habilitation works at different universities. Nevertheless, I would like to hear from Dr. Lexa about his ideas concerning his pedagogical and educational activities.

## 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: 18. 4. 2023

Signature: