MUNI

HABILITATION THESIS REVIEWER'S REPORT

Masaryk University

Applicant	Mgr. David Bednář, Ph.D.
Habilitation thesis	Computational Tools for Analysis and Design of Proteins
Reviewer	doc. RNDr. David Šafránek, Ph.D.
Reviewer's home unit, institution	Faculty of Informatics, Masaryk University

Dr. Bednář presents a habilitation thesis in the field of Environmental Health Sciences. In particular, the thesis targets development of nine complex software tools. These tools with the original methods behind them make all together a significant research contribution to the enormously important field of protein engineering representing one of the fundamental pillars of biotechnology and pharmacology.

The thesis makes a representative of a methodological research based at the borders of biology, chemistry, and informatics. It has the form of a collection of nine manuscripts published in highly impacted journals during the last five years – *Nucleic Acid Research* (5x), *Bioinformatics* (3x), and *Briefings in Bioinformatics* (1x). Each of these journals plays an important role in some non-singleton subset of the mentioned disciplines. An important attribute of the presented research is evidently its multi-disciplinarity. This attribute is crucial for current needs of environmental and health sciences. It also goes hand in hand with the complexity of the research tasks that are necessary for successful development of the non-trivial algorithmics that needs to target the exact needs of users based in life-science communities.

An important step that precedes the success of the software is that the state-of-the-art bioinformatics technology must be brought close to the users in settings accenting the simplicity of the use. I am happy to see that Dr. Bednář masters his bioinformatics research and succeeds in this complex challenge. The presented tools (described in the collected manuscripts) show 742 citations in total (taken from Google Scholar in the time of writing this review). This is a clear marker of the high impact of Dr. Bednář's research contribution.

The text of the thesis is organised in four chapters consequently exploring the following research questions: (i) identification of novel enzymes from public databases, (ii) prediction of proteins solubility, (iii) prediction of protein stability, and finally, (iv) ligand pathways analysis methodology. Each of the chapters gives a brief introduction to the state-of-the-art behind the problem which is followed with an overview of the individual contributions. In most of the cases, the presented outcomes have a form of the specific software. Details of the algorithmics are accessible in the attached papers. In my point of view, the algorithmics makes the fundamental

base of this research contribution. After getting familiar with details on the algorithmics and software architectures available in the papers, I am happy to conclude that Dr. Bednář has played a crucial role in development of the tools. On one end, he is the author of the key theoretical ideas and methodological concepts that create the main essence of the entire software tools line. On the other end, in most cases he also plays the important role as a designer of graphical user interfaces. This is an important step that drives the tools towards the end-user community.

Dr. Bednář is by now 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. He makes a valuable member of the excellent research team, and he has very good abilities to motivate and tutor talented students. These all are the characteristics that make the pillar of his success.

In conclusion, Dr. Bednář has shown in his habilitation thesis the excellent skills of a researcher in bioinformatics, and his ability to contribute to multi-disciplinary international research of a high quality. His scientific achievements certainly match the criteria expected of a successful habilitation at Masaryk University.

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

Q1: Most of the presented tools are running on the web but some of them also have desktop versions. From my own experience it is quite a difficult task to manage the life cycle of such complex software packages. My question therefore targets the methodology you employ to keep the track of quite a large set of non-trivial software builds. Does it make still some good reason to develop and support desktop applications or do you see the near future of protein bioinformatics to be based entirely on web technologies?

Q2: I have found out that some of the older tools (2017-2018) you present in the thesis have quite significantly different numbers of citations (e.g., CaverAnalyst published in 2018 has twice more citations than FireProt published in 2017). Is the reason for that lying in a narrower user-base of the more specific tool or is that more about marketing in the area? Can you comment on how you propagate your tools to the end users (besides the well-impacted publications)?

Conclusion

The habilitation thesis entitled "Computational Tools for Analysis and Design of Proteins" by David Bednář **fulfils** requirements expected of a habilitation thesis in the field of Environmental Health Sciences.

Date: 28.2.2023   Signature: