

### **Supervisor statement – Nikolas Tolar**

Nikolas approached me in his first year of Bioinformatics studies and described himself as unexperienced programmer who knew nothing about biology. I was therefore originally hesitant, however, Mrs. Vohnoutová described him as exceptionally talented and hardworking, so we started working together. I deliberately used words working together, as with Nikolas I never felt that he was working as a student under my supervision of a more experienced scientist, but instead it was like working with an equal colleague, a programmer.

I can therefore confirm that Nikolas is exceptionally talented, hardworking, self-motivated, and has a very nice and easy-going personality, making our collaboration pleasant and smooth. Since spring 2019, he independently developed a number of Python scripts (not included in his thesis) for various projects in the laboratory including several collaborative projects, mostly processing gtf annotation files, fasta sequence files, and extracting and merging information from large tables. In coming years, he will therefore be a co-author of several publications, which is a great achievement for an undergraduate student. Thanks to his programming skills, the ability to self-study to extend his knowledge and skills and the ability to critically evaluate the results, he could easily be a Ph.D. student. I think it is fair to say his programming abilities are much more advanced than biological knowledge, but this was considerably improved during the course of his studies, especially from the point of view of the application of programming to solve biological problems.

Nikolas worked on his thesis project in the last year of his undergraduate studies. We recently started research on naked mole rats, extraordinarily long-lived rodents which are relatively resistant to age-associated diseases. As epigenetic alterations are one of the hallmarks of aging, we would like to study longevity in these animals from the epigenetics perspective. The aim of Nikolas therefore was to develop a software to identify sequence changes in the epigenetic modifier proteins that could have a functional impact on the protein, compared to mouse and human which have well annotated proteins, and their functional sites, regions and domains. He saved hours, or more likely weeks of painful work of a Biology student, identifying candidate proteins that will be further studied for their potential role in securing epigenetic stability leading to longevity and healthy aging. His results form a basis of future studies in our laboratory. As a direct follow up, Nikolas will broaden the program in order to develop protein sequence comparison software for whole scientific community, applicable to any species of interest with available sequences which can be compared to well-annotated model organisms.

Nikolas produced a very high quality first draft of his thesis which required almost zero changes and comments from my side, with the exception of few subchapters of background dealing with biology, for example epigenetics of aging, where I commented that they have to be completely rewritten because of poor quality. These were considerably improved in the second draft. Quite unusually, Nikolas included basic information about genetic code, DNA, RNA and proteins in his theoretical background which would not be appropriate for a thesis of Biology student, but he justified it by telling me that he wanted his thesis to be easily understood also by pure informaticians without strong biology knowledge.

I can conclude that I was more than happy with Nikolas's work and I am looking forward to our collaboration in the future.

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