

Third Semester Report

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Statistical Physics, Biological Physics
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Thesis title: Developing next-generation phylogenetic methods

January 30, 2023

Introduction

Phylogenetics studies the evolutionary relationships between organisms by reconstructing their tree of descendants, called a phylogeny. During my doctoral studies, I am developing new methods and applications as described in the first semester's report.

Description of research work carried out in current semester

During this semester the manuscript describing our results in the project *New method to detect and ameliorate long branch attraction (LBA) artefacts: CAT-PMSF* was going through a second round of revision (first revision was sent in in August, second round of reviews were received in November, and the second revision was sent in in December) at the journal *Systematic Biology*. The review process has prolonged more than we were expecting, but has greatly improved our manuscript and as of writing this report we are waiting for the decision of the Editor in Chief.

The implementation of *Horizontal gene transfer highways* was continued, the code was refractored in Python, various unit tests were made, but unfortunately due to personal reasons no significant progress could be made after November.

The *Date the tree of fungi* project has moved on during the semester with great pace, we were able to determine a dated tree using fossil calibrations and using `McmcDate` (<https://github.com/dschrempf/mcmc-date> developed by one of our research group members, Dominik Schrempf. Having only two maximum calibrations has made the inference less conclusive as we were hoping for and during investigating the results with our collaborators (see Conferences section), one of the maximum calibrations proved to be unreliable which may turn this project to completely new tracks and an exciting publication is to be expected.

Connected to the *Date the tree of bacteria* project, a manuscript was prepared with our collaborators (involved in the original paper Coleman et al. (2021)) explaining the methods and controversies when working with deep phylogenies. Expected to be published during 2023.

Publications

The manuscript for the project *New method to detect and ameliorate long branch attraction (LBA) artefacts: CAT-PMSF* is waiting for the decision of the Editor in Chief at the journal Systematic Biology after sending in the second revision in December, 2022.

Studies in current semester

I have enrolled to the following classes:

FIZ/3/017E Physics of environmental flows (Jánosi Imre Miklós)

BIO/02/03E Human ethology (Kubinyi Enikő Dr.)

Both courses were graded with 5.

Conferences in current semester

I have attended the conference of Moore-Simons Project on the Origin of the Eukaryotic Cell Annual Meeting between 10th and 12th of October through Zoom.

I have participated on the Ecological Days conference between 13th and 14th of October in Vácrátót, presenting a 10 minutes talk about the paper “A rooted phylogeny resolves early bacterial evolution” Coleman et al. (2021).

On 19th of October we have visited our collaborators on the *Date the tree of fungi* project at BRC (Szeged Biological Research Center) where various people have held talks about their projects relevant to our common research.

Professional activities

I have maintained the research group’s high performance computing (HPC) cluster.

I have helped to maintain the university’s high performance computing (HPC) cluster which service is provided by the ELTE IIG.

References

Coleman, G. A., Davín, A. A., Mahendrarajah, T. A., **Szánthó, Lénárd L.**, Spang, A., Hugenholtz, P., Szöllősi, G. J., and Williams, T. A. (2021). A rooted phylogeny resolves early bacterial evolution. *Science*, 372(6542):eabe0511.