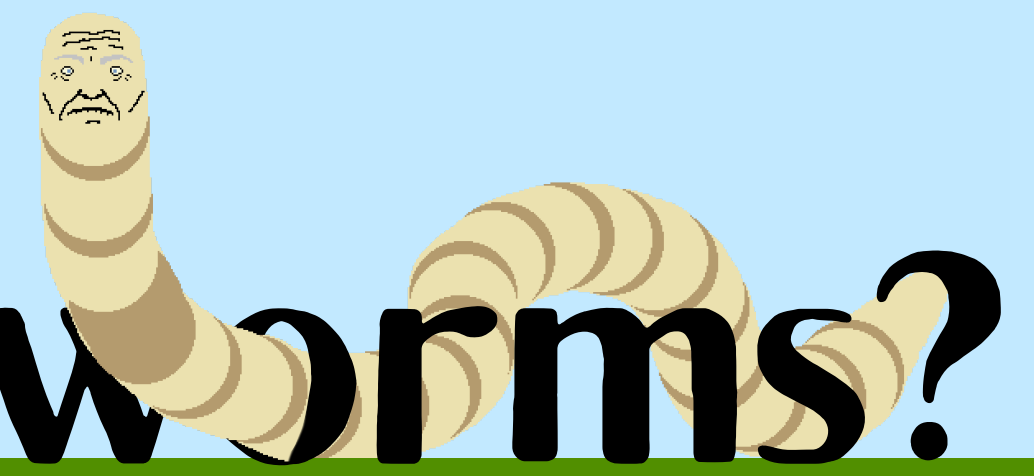


How old are these worms?



Molecular dating of the annelid tree of life

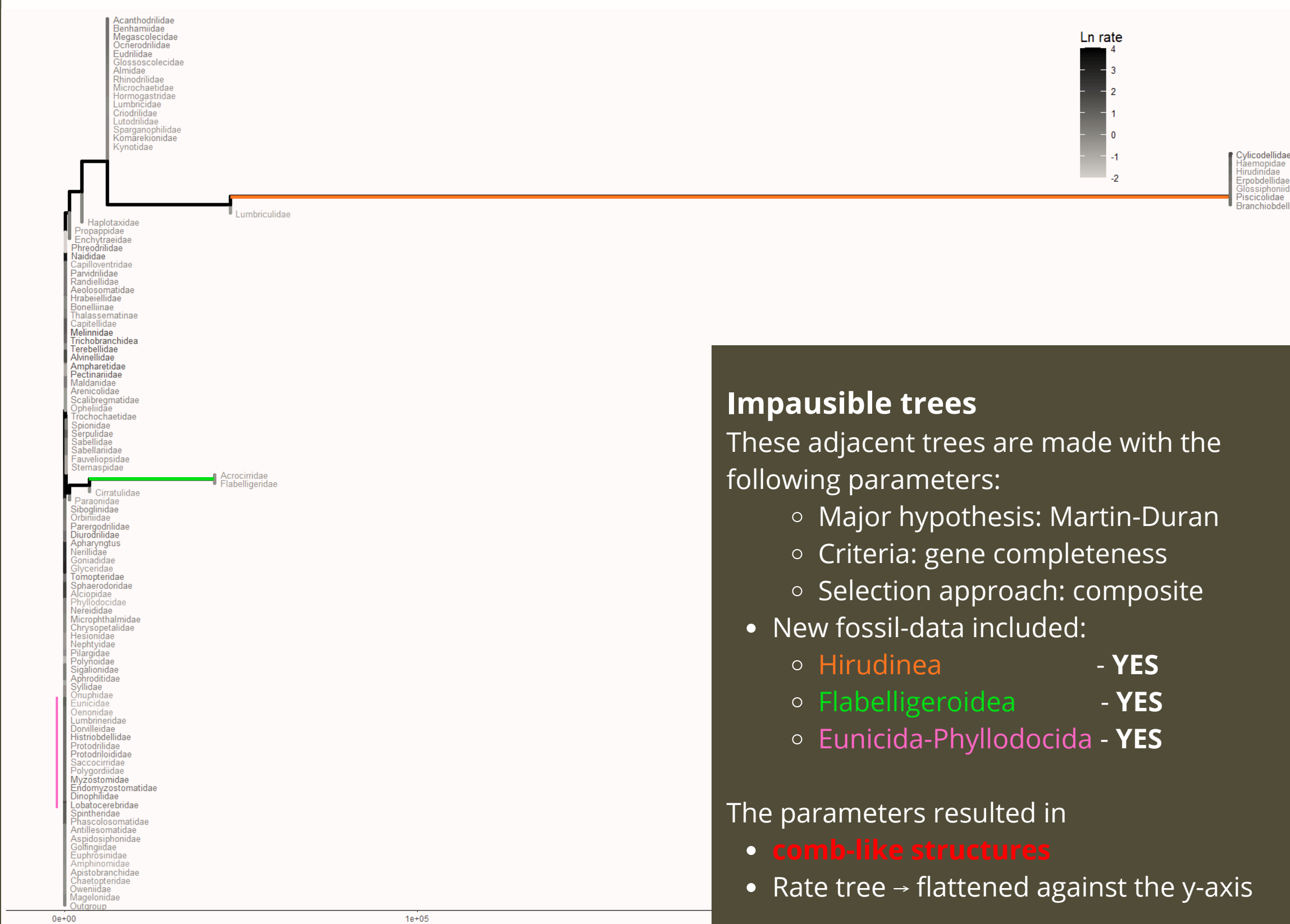
Aim and Background

Annelida is the phylum of the segmented worms. It is a diverse group containing over 22000 living species on land and in the sea. With modern science and technology we can say a lot about the worms that are around today, but there is still much that is uncertain about how they got here. Dates for major events in the Annelid tree of life are lacking. This project aims to address this gap in knowledge by combining genetic and fossil data to construct phylogenetic trees using modern software. This project builds upon a previous masters project from 2021. Much of the data collection and programming was done then. Since then here have been found new fossils of annelida that are claimed to be members of Eunicida-Phyllodocida (EP), Flabelligeroidea, and Hirudinea. And they are millions of years older than the representatives of those groups used in the project in 2021. It was necessary to update the project by introducing this new fossil data, and seeing what effect this would have on the annelid tree of life.

What I did

- Used the RelTime dating method in MEGA X and R-scripts to create many theoretical phylogenetic trees for annelida.
- I then went through all the trees looking for clues as to which ones were the most plausible.
- For the **MEGA X trees** I did the following:
 - Checked for **comb-like structures** (see figure) in
 - Sedentaria (Flabelleigeridae)
 - Clitellata (Hirudinea)
 - EP
 - Recorded:
 - the age of the "comb-ridge"
 - the range of ages
 - the age of the root
- For the **rate trees** Recorded the rough relative rate of the branch leading to Flabelleigeridae and the one to Hirudinea and other branches where it seemed important

Rate trees illustrate the rate at which the molecular clock ticks. I introduced different combinations of the new fossil-data.



Implausible trees

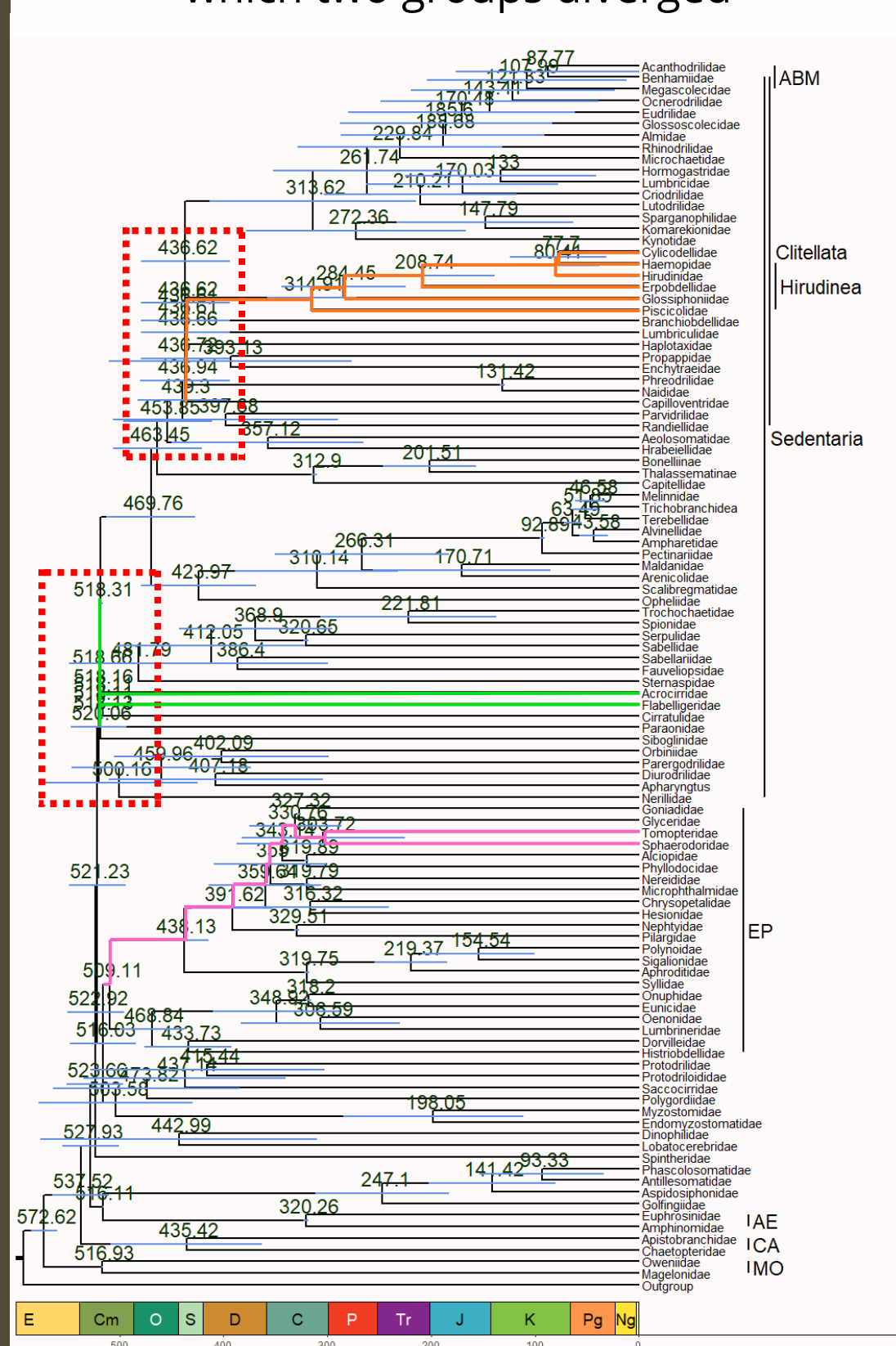
These adjacent trees are made with the following parameters:

- Major hypothesis: Martin-Duran
- Criteria: gene completeness
- Selection approach: composite
- New fossil-data included:
 - Hirudinea - YES
 - Flabelligeroidea - YES
 - Eunicida-Phyllodocida - YES

The parameters resulted in

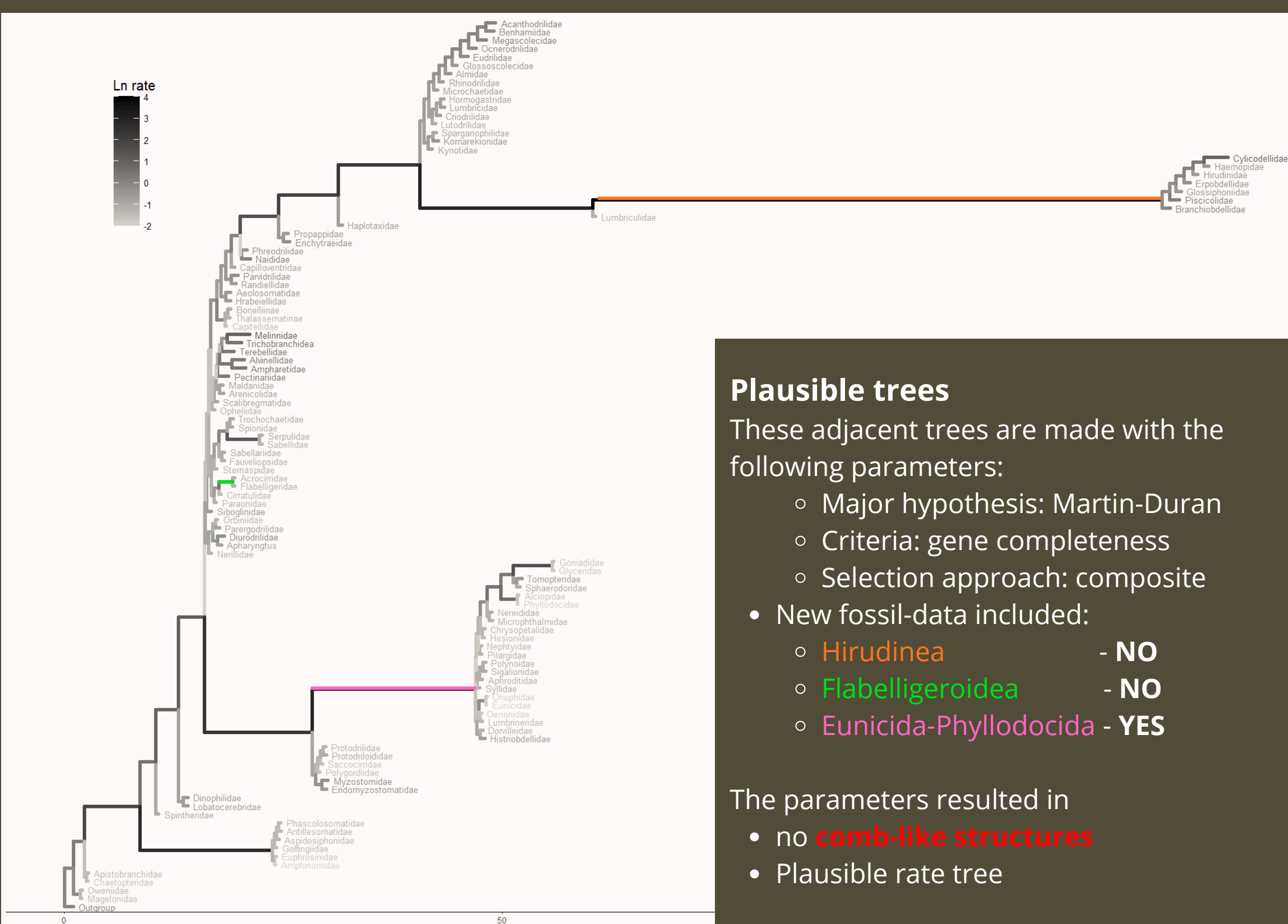
- comb-like structures
- Rate tree → flattened against the y-axis

MEGA X trees show the estimated date at which two groups diverged



Results

- Based on my analysis I concluded that the trees on the bottom were among the most plausible.
- Most of the trees were similar to the examples shown here. They all followed a similar pattern.
- Inclusion of the new Hirudinea- and Flabelligeroidea fossil data always led to the comb-like structures and flattened rate trees.
- Flattening is a result of the Hirudinea group having a rate of 300 000x to 200 000 000x, and the Flabelligeroidea group having one of 2 000x to 79 000x.



Plausible trees

These adjacent trees are made with the following parameters:

- Major hypothesis: Martin-Duran
- Criteria: gene completeness
- Selection approach: composite
- New fossil-data included:
 - Hirudinea - NO
 - Flabelligeroidea - NO
 - Eunicida-Phyllodocida - YES

The parameters resulted in

- no comb-like structures
- Plausible rate tree

Conclusion

The results indicate that the proposals for Hirudinea and Flabelligeroidea are likely not part of their respective subclass and crown group, but that the fossil proposed for Eunicida-Phyllodocida is in fact part of this order. It was however difficult to determine which trees were the best candidates for the annelid tree of life, as the patterns were mostly similar across the different parameters.

This poster was made by Eivind Mosesen. I was supervised by Dr. Dimitar Dimitrov at the UiB University Museum in collaboration with Dr. Torsten Struck from the Natural History Museum in Oslo (UiO). Stian Aleksander Helsem was responsible for much of the data collection and the tools used in this project.

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