SYMPOSIUM

From Molecules to Millennia

Advances & Challenges in Phylogenetic Dating

23–25 April 2024

LOCATION

The symposium is hosted by the Max Planck Instiute for Evolutionary Anthropology, Leipzig.

ORGANISER

Organised by the tide research group at the Max Planck Insitute of Geoanthropology.

23.4.2024 PRE-SYMPOSIUM INTRODUCTION
24.4.2024 LECTURES BY INVITED SPEAKERS
25.4.2024 FOCUS SESSIONS

tide

Symposium 23-25 April, 2024

From Molecules to Millennia: Advances and Challenges in Phylogenetic Dating

As high-throughput sequencing techniques continue to advance, an increasing amount of genetic information across all branches of the tree of life is being generated. With the introduction of the molecular clock hypothesis, we are now capable not only of making inferences about genetic divergence based on the number of differing mutations between sequences but also of estimating divergence in terms of absolute time units. Since then, numerous conceptual and methodological advancements have facilitated bridging the gap between genetic data and temporal divergence, jumping from molecules to millennia. Nevertheless, many challenges still remain that need to be addressed to form a more comprehensive understanding of evolution as a function of time.

Dates

Tuesday 23 – Thursday 25 April, 2024

More information

If you have any further questions, please contact organisers at tide-seminars@gea.mpg.de

Organiser

'tide' research group

Location

Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, 04103 Leipzig, Germany

Registration link

https://shh-cloud.gnz.mpg.de/index.php/apps/forms/s/xnCxg9mWKQWyFgFR6LyYwq6Z

Registration closes 16 April 2024
Please note that on Thursday 25th the maximum number of participants is 30 and registration is required.

Preliminary schedule, all times are subject to change.

Tuesday, April 23rd, Large seminar room (H4.10)

14:00 – 17:00	**Journal club**	Literature: Bromham et al. (2017) Bayesian molecular dating: opening up the black box. *Biological Reviews* 93:1165–1191 https://doi.org/10.1111/brv.12390
17:00 – 18:00	**Dinner for organisers and speakers**	Location: Umaii Ramen
18:00 – 19:00	**Collection of discussion points for focus sessions I–III**	Location: MPI-EVA

Wednesday, April 24th, Lecture hall

09:15 – 09:30	**Opening remarks**	tide group
09:30 – 10:00	**Dr. Kirsten Bos**	Title: TBA Affiliation: MPI-EVA
10:00 – 10:30	**Dr. Alexander Herbig**	Title: Prehistoric Disease and Evolution of Human Pathogens Affiliation: MPI-EVA
10:30 – 11:00	**Coffee break**	
11:00 – 12:00	**Prof. Rachel Warnock**	Title: The fossilised birth-death process as a framework for unifying evidence in paleobiology Affiliation: FAU Erlangen-Nürnberg, Germany
12:00 – 13:00	**Lunch break**	
13:00 – 14:00	**Dr. Sebastián Duchêne**	Title: Dating with uncertainty: untangling temporal signal and the molecular clock of microbial genome data Affiliation: Institut Pasteur, France
14:00 – 14:30	**Coffee break**	
14:30 – 15:30	**Dr. Mahan Ghafari**	Title: Beyond standard molecular clocks: developing the next generation of methods for reconstructing the evolutionary history of viruses Affiliation: University of Oxford, UK
15:30 – 16:00	**Coffee break**	
16:00 – 17:00	**Yaniv Swiel**	Title: Reference bias in the human Y chromosome phylogeny Affiliation: MPI-EVA
17:00 – 18:00	**Discussion round**	Plenum
18:00 – 19:00	**Symposium dinner**	Location: Thüringer Hof

28 Participants

19:00 – 20:00	**Collection of discussion points for focus sessions I–III**	Location: MPI-EVA

Thursday, April 25th

09:15 - 09:30	**Opening remarks** *Lecture Hall*	tide group
09:30 – 10:30	**Focus sessions I–III** *ABI seminar room (B6.21), Container seminar rooms (X 1.09 / X 0.10)*	Parallel focus sessions (session descriptions below)
10:30 – 11:00	**Coffee break**	
11:00 – 12:00	**Focus sessions I–III cont.** *ABI seminar room, Container seminar rooms (X 1.09 / X 0.10)*	Parallel focus sessions (session descriptions below)
12:00 – 13:00	**Lunch break**	Lunch provided for people who have registered
13:00 – 14:00	**Focus exchange** *Large seminar room*	In plenum discussion of results from focus sessions I–III
14:00 – 14:30	**Coffee break**	
14:30 – 15:30	**Best practice guidelines** *Large seminar room*	Plenum
15:30 – 16:00	**Closing remarks** *Large seminar room*	Plenum

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Thursday 25 April, 2024

Focus Session I: Scientific motivation and data requirements

In recent years, inferring evolutionary timescales has increasingly become a standard practice in most phylogenetic studies. These inferences, however, require enough information on the absolute timing as input data. As highlighted in Session III, many potential biases exist that can further complicate them. Often these global timescales are used to draw binary conclusions about the timing of specific events represented in the phylogenetic tree. Since such conclusions do not always rely on the global dating of the phylogeny, certain biases can be readily mitigated through different study setups.

Our objective here is to collect the various scientific motivations for inferring time-scaled phylogenies. We also want to discuss the criteria that the data must meet to provide the requisite information for phylogenetic dating, along with the methods available for achieving this. This discussion will, e.g., include different approaches to evaluate the amount of information concerning absolute time scales in the data (referred to as 'temporal signal'), as well as alternatives to dating of the global phylogeny.

Focus Session II: Integration of different data sources

Traditionally, phylogenetic analyses rely solely on time-stamped genomic data. In many instances, however, we also have other sources of valuable information available. Particularly in Bayesian inference, these can be incorporated into the phylogenetic analysis through prior probability distributions.

Together we want to compile a list of the various data types that inform our analyses and the methodologies for integrating multiple sources of information. We will discuss the distinctions and similarities among different genetic datasets, ranging from viral genomic data to eukaryotic SNP sequences, and which additional data types they entail or would necessitate. We will explore various ways for jointly analysing all available data, including temporal or geographical calibrations on internal nodes, as well as model-based likelihood approaches.

Focus Session III: Sensitivity of evolutionary timescale estimates

Phylogenetic models are built upon numerous assumptions regarding the phylogenetic and temporal structure of the data, yet it is often unclear to what extent our data deviates from these assumptions. However, the accurate estimation of evolutionary timescales from time-structured data relies on precise assessment of evolutionary rates, which in turn is influenced by various factors. These include, for instance, rate heterogeneity among lineages, time-dependency, demographic model assumptions, and the presence of population substructure. Furthermore, different molecular dating methods have shown to be subject to varying degrees of systematic biases when inferring evolutionary rate estimates under diverse biologically realistic scenarios.

During this session, we aim to compile guidelines for conducting sensitivity analyses aimed at assessing potential biases arising from data structure or the chosen method of inference. Additionally, we will discuss our level of familiarity with method specific sensitivities concerning the aforementioned factors.