

GeoVet 2023 Workshop Proposal

Workshop title:

Applied introduction of phylodynamic methods for genomic surveillance of infectious diseases

Instructor:

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Workshop's learning outcomes:

Gain an understanding and develop basic skills in the phylodynamic analysis of genomic data of rapidly evolving pathogens under a Bayesian statistical framework.

Background and skills workshop attendees:

Everyone with interest to get basic hands-on skills in phylodynamic analysis using a collection of open-source software such as TempEst, BEAST 1.10.4, and Spread3. Existing experience in the sequence alignment and construction of phylogenetic trees using classical methods, such as maximum likelihood approaches, would be beneficial to grasp the essential concepts of the workshop in full but not required.

The history of the workshop: Yes [X] No []:

Part of this workshop was conducted in the GeoVet 2019 pre-conference workshop entitled "Application of molecular tools to spatial epidemiology", which was led by Prof. Andres Perez from the University of Minnesota and Dr Julio Alvarez from the University of Marid. The workshop was held at the University of California Davis and was attended by approximately 12 participants. The instructor conducted similar workshops at the University of Minnesota, Kuwait Institute for Scientific Research, and Kuwait University.

Workshop specifications

- Do you prefer to organize a pre- or post-workshop? Pre [X] Post [] Either []
- What's the minimum and max number of attendees for the workshop? Min [8] Max [10]
- What's the duration (days) of the workshop: [2 days]
- Additional material / accessories needed: N/A
- What is the proposed cost (EUR) of the workshop for the participants: [500 EUR full, 300 EUR student].

Workshop contents and schedule

The course will run from 9am – 5pm on one of the two days. I will teach using an interactive combination of presentations, hands-on tutorials, and group discussions.

Why this course?

In the past few decades, molecular analysis of rapidly evolving pathogens has become integral to animal and human disease surveillance systems worldwide. However, most molecular surveillance systems of infectious disease pathogens depend on classical epidemiological and phylogenetic methods such as neighbour-joining, and maximum likelihood approaches to either genotype or assess tree topologies relationships while ignoring uncertainties associated with estimates of phylogenetic relationships, host, temporal, and spatial factors. Furthermore, they investigated spatio-temporal, and evolutionary dynamics of the virus isolates in a disjointed analytical framework and made joint conclusions from both analytical approaches. Bayesian phylodynamic methods, borrowed from the field of evolutionary biology, have become a powerful tool for exploring the evolutionary epidemiology of infectious pathogens. During the last two decades, the rapid growth of pathogens' genetic data and computational resources increased the applications of phylodynamic methods in animal and human disease surveillance. Using a single Bayesian statistical framework, these methods can account for uncertainties and uniquely integrate complex epidemiological and evolutionary processes in populations. Therefore, this innovative quantitative integration improved disease investigation by untangling novel epidemiological questions about the evolutionary history, spatiotemporal origins, within and between-host transmission, and environmental risk factors for rapidly evolving pathogens. In fact, during the last decade, phylodynamic models have become well-established tools for studying the evolution of animal and human viral diseases especially SARS-CoV-2, influenza, and Foot-mouth disease. These approaches will provide a robust platform for guiding the allocation of resources within a surveillance system, for example targeting emerging strains with higher evolutionary rates or hosts at high risk of generating new strains, which subsequently will reduce the economic costs of sampling, control, and prevention activities. Phylodynamic methods are implemented in many open-source statistical software packages, while the most popular user-friendly software package is formally known as Bayesian evolutionary analysis by sampling tree (BEAST). In this workshop, we will demonstrate basic principles for building a phylodynamic analytical pipeline, illustrate examples of the impact of gene segment and prior selection on posterior evolutionary inferences, and highlight the prospects of the methods in improving infectious disease surveillance.

What do I need to bring along?

Participants must bring their laptops that support Java-based applications such as BEAST 1.10.4.

Venue

TBA

Registration

EUR € 500 (full)

EUR € 300 (Student)

Participants must register on-line <https://geovet2023.izs.it> using the registration link that will be active on TBA.

Registration includes:

Lunch as well as coffee breaks

Course material (downloadable material through web-link)

Registration can be done through the GEOVET 2019 website

Deadline for registration is TBA

Day	Time	Topic	Format
1	8:30 – 9:00 am	Welcome	
	9:00 - 10:30 am	Introduction to evolutionary epidemiology of rapidly evolving infectious diseases	Lecture
	10:30 - 11:00 am	Coffee break	
	11:00 - 12:30 pm	Preliminary phylogenetic analysis of sequence data	Guided tutorial software installation and illustration
	12:30 - 1:30 pm	Lunch	
	1:30 - 3:00 pm	Exploring the suitability of sequence data for molecular clock analysis using TempEst	Lecture and hands-on tutorial
	3:00 - 3:30 pm	Coffee break	
	3:00 - 5:00 pm	Exploring best-fitting substitution models for sequence data	Lecture and hands-on tutorial
2	9:00 - 10:30 am	Introduction to Bayesian Phylodynamic methods using BEAST (demographic reconstruction modeling of sequence data)	Lecture and hands-on tutorial
	10:30 - 11:00 am	Coffee break	
	11:00 - 12:30 pm	Ancestral-state reconstruction using BEAST (Phylogeographic diffusion in discrete space)	hands-on tutorial
	12:30 - 1:30 pm	Lunch	
	1:30 - 3:00 pm	Examples of published phylodynamic studies by the instructor	Lecture
	3:00 - 3:30 pm	Coffee break	
	3:00 - 5:00 pm	Software trouble shooting tips, brainstorming session and discussion	Open table