

Hong Kong, 22 - 27 October 2018

# C3BI Courses: Introduction to Molecular Phylogenetics

At HKU-Pasteur Research Pole  
HKJC Building for Interdisciplinary Research  
5 Sassoon Road, Pokfulam, Hong Kong

**Deadline for applications August 7**

This introductory course aims to give the **basic theoretical and practical concepts**, best practices, and software necessary to start working on **molecular phylogenetics** and its applications to **epidemiology**. The course will have theoretical morning sessions followed by small groups practice for a few selected students with their own data.

## FACULTY

**Chair: Olivier GASCUEL**, C3BI, Institut Pasteur (France)

**Veronika BOSKOVA**, ETH Zürich (Switzerland)

**Sebastian DUCHENE**, University of Melbourne (Australia)

**Julien GUGLIELMINI**, C3BI, Institut Pasteur (France)

**Tommy LAM**, The University of Hong Kong (Hong Kong)

**Frédéric LEMOINE**, C3BI, Institut Pasteur (France)

**Hein Min TUN**, The University of Hong Kong (Hong Kong)

**Tim VAUGHAN**, ETH Zürich (Switzerland)

**Anna ZHUKOVA**, C3BI, Institut Pasteur (France)

## Course dates:

Monday, October 22<sup>nd</sup> to  
Saturday, October 27<sup>th</sup>, 2018

## Pre-requisites:

- Basic knowledge on how to use sequence databanks
- Basic knowledge using Blast and multiple alignments software
- Basic knowledge on statistics (tests, distributions, parameter estimation)

## Applications:

Open to postgraduate students, MD, DVM, postdoctoral fellows and young scientists from Hong Kong and overseas.

The course fees are **500HK** for the theory sessions and **1000HK** for the full course. Students coming from the **Institut Pasteur international Network** will have the fees waived

Please fill in the following application form before **August 7<sup>st</sup> Midnight (HK time):**

<https://goo.gl/forms/CKvFipX016OyGebV2>



## TOPICS

- Introduction to phylogeny: general principles for the inference, interpretation of trees, and application to infectious diseases;
- Introduction to the math behind the trees and evolutionary models;
- Distance and parsimony methods;
- Maximum likelihood methods;
- Bayesian methods, phylodynamics;
- Branch supports, bootstrapping;
- How to select the best method and evolutionary model;
- Tree dating, reconstructing and using character evolution;
- Molecular epidemiology