



**Workshop**  
**EPONGE**  
Epidemiology meets POpulation GENetics

**Date:** 2 -6<sup>th</sup> September, 2019  
**Venue:** Universidad Nacional de San Agustín de Arequipa  
Campus Biomédicas, Faculty of Medicine  
Av. Virgen del Pilar 1713  
Arequipa, Peru

**Workshop organizing team:**

- Global Health Institute-**University of Antwerp** (Belgium)
- **Universidad Nacional de San Agustín de Arequipa** (Peru)
- Malaria Laboratory/Instituto de Medicina Tropical Alexander von Humboldt-**Universidad Peruana Cayetano Heredia** (Peru)
- **Universidad Nacional de Amazonia Peruana** (Peru)

**Expenses**

Attendance to the EPONGE has no cost for selected participants. Travel costs or accommodation are not covered.

EPONGE is organized within the VLIR Joint project “Improved infectious diseases control in Peru through sustainable capacity building for bioinformatics and genome sequencing”.

**Sponsors**

VLIR-UOS (JOINT project PE2019JOI018A102, Belgium) and Fogarty (2D43TW007120-11A1, NIH-USA)

**Website:** [www.uantwerp.be/eponge](http://www.uantwerp.be/eponge)  
[twitter.com/EPONGE 2019](https://twitter.com/EPONGE_2019)



## Epidemiology meets population genetics

Within the framework of infectious diseases, the interface between epidemiology and population genetics allows scientists to uncover relevant parameters that influence the dynamics of a disease. Currently this interface is exploited to:

- Identify routes of transmission of infectious agents and their vectors.
- Model the risk, origin and spread of drug resistance.
- Assess the efficacy of drug treatments, diagnostics or vaccines.
- Assess the impact of prevention, control and elimination programs.

## EPONGE workshop

The EPONGE<sup>□</sup> workshop will provide a series of theoretical and practical lectures directed to shed light into the interface between epidemiology and population genetics and its relevance for the better understanding of the dynamics and evolution of infectious diseases.

Basic and advanced concepts on epidemiology and population genetics will be delivered and complemented by hands-on practices on genetic multivariate analyses. Population genetics

Open-source computer packages will be used to provide the basis on population genetics analysis ([GenAlEx](#), [LIAN](#), [Structure](#), [PHYLOViZ](#) and [Bottleneck](#)) by exploring genetic diversity, differentiation and population structure. Moreover, an introduction to phylogenetics and Linux for bioinformatics will be provided by [Dr. Conor Meehan](#) (University of Bradford, UK).

Noteworthy, the formulation and Bayesian inference of migration models (gene flow patterns) will be taught by [Prof. Peter Beerli](#) (FSU, USA), developer of the program [MIGRATE-N](#), through lectures and hands-on tutorials.

Within the EPONGE workshop experts from different international research institutions have been invited to present through teleconferences how they approach population genetics within the scope of the epidemiology of infectious diseases.

**All the lectures and talks will be taught in English.**

<sup>□</sup>EPONGE is translated from French to sponge. We anticipate that you will become a sponge during the workshop and 'absorb' as much as possible!

## EPONGE lecturers

- [Jean-Pierre Van Geertruyden](#), MD PhD (University of Antwerp, Belgium)
- [Dionicia Gamboa Vilela](#), PhD (Universidad Peruana Cayetano Heredia, Peru)
- [Christopher Delgado-Ratto](#), PhD (University of Antwerp, Belgium)
- [Peter Beerli](#), PhD (Florida State University, USA.)
- [Conor Meehan](#), PhD (University of Bradford, UK)
- [Anna Rosanas-Urgell, PhD](#) (Institute of Tropical Medicine, Antwerp, Belgium)
- [Tim Downing](#), PhD (Dublin City University, Ireland)
- [Arun Decano, PhDc](#) (Dublin City University, Ireland)
- [Jan Conn, PhD](#) (State University of New York)
- [Kirstyn Bruner](#), PhD (University of Glasgow, Scotland)
- [Alexander Berry](#), PhD (University of Pennsylvania, USA)

## How to apply

The EPONGE workshop is aimed to graduate students, postdoctoral researchers and faculty members at Universities and academic institutions from Peru.

All lectures/talks will be given in English therefore good knowledge of English is compulsory.

Register online at [www.uantwerp.be/eponge](http://www.uantwerp.be/eponge) filling the online application form and submitting a CV resume and support letter of your supervisor.

**Deadline to submit applications: 26 July 2019**

Contact: [eponge@uantwerp.be](mailto:eponge@uantwerp.be)

## Tentative schedule (2-6 September 2019)

Venue: Campus Biomédicas, Faculty of Medicine - UNSA, Arequipa-Peru

| Time  | Topic  | Lecturer  | Location      |
|---|--|---|---------------|
| <b>Monday 02/09</b> (coffee break at 10.30 and 15:00)   |  |   |               |
| 8:00-08:15  | Registration   |   | Paraninfo     |
| 8:15-9:00   | Welcome and intro to the EPONGE workshop   | UNSA authorities,<br><a href="#">Christopher Delgado-Ratto</a> ,<br><a href="#">Renzo Salazar</a> | Paraninfo     |
| 9:00-12:00  | Introduction to Epidemiology/study design  | <a href="#">JP Van geertruyden</a>  | Paraninfo     |
| 13:00-15:00   | Molecular epidemiology of infectious diseases: examples, molecular markers and current genotyping techniques | <a href="#">Dionicia Gamboa</a>   | Paraninfo     |
| 15:15-17:00   | Epidemiology meets population genetics   | <a href="#">Christopher Delgado-Ratto</a>   | Paraninfo     |
| <b>Tuesday 03/09</b> (coffee break at 10.30 and 16:00)  |  |   |               |
| 8:30-12:00  | Intro to population genetics analysis  | <a href="#">Christopher Delgado-Ratto</a>   | Computer room |
| 13:00-16:00   | Intro to Phylogenetics   | <a href="#">Conor Meehan</a>  | Paraninfo     |
| 16:00-18:00   | Bioinformatics in Linux  | <a href="#">Conor Meehan</a>  | Computer room |
| <b>Wednesday 04/09</b> (coffee break at 10.00 and 16:00)  |  |   |               |
| 8:00-9:00   | Human population genetics for malaria research   | <a href="#">Anna Rosanas-Urgell</a>   | Paraninfo     |
| 9:00-10:00  | TB   | <a href="#">Conor Meehan</a>  | Paraninfo     |
| 10:15-13:00   | Coalescence theory   | <a href="#">Peter Beerli</a>  | Paraninfo     |
| 14:00-18:00   | Tutorial and discussion of improving estimates   | <a href="#">Peter Beerli</a>  | Computer room |
| <b>Thursday 05/09</b> (coffee break at 11.00 and 16:00)   |  |   |               |
| 9:00-13:00  | Bayes factors (assessing gene flow models)   | <a href="#">Peter Beerli</a>  | Paraninfo     |
| 14:00-18:00   | Tutorial in Bayes factors and model selection  | <a href="#">Peter Beerli</a>  | Computer room |
| <b>Friday 06/09</b> (coffee break at 10:50 and 16.30)   |  |   |               |
| <b>Population genetics/genomics for infectious diseases research (teleconferences &amp; oral presentations)</b> |  | 45-min presentations<br>+ 10-min questions  |               |
| 9:00-9:50   | Population genetics, evolutionary pangenomics and genomic epidemiology for Leishmania parasites              | <a href="#">Tim Downing</a>   |               |
| 10:00-10:50   | <i>Escherichia coli</i> ST131  | <a href="#">Arun Decano</a>   |               |
| 11:15-12:10   | Chagas   | <a href="#">Alexander Berry</a>   | Paraninfo     |
| 12:10-13:00   | Lunch  |   |               |
| 13:00-13:50   | Malaria parasite   | <a href="#">Anna Rosanas-Urgell</a>   |               |
| 14:00-14:50   | Malaria vector   | <a href="#">Jan Conn</a>  |               |
| 15:00-15:50   | Rabies   | <a href="#">Kirstyn Brunker</a>   |               |
| 16:00-17:00   | Closure - Certificates   | Christopher Delgado,<br>Renzo Salazar, UNSA<br>authority  |               |

## Organizing committee

- Christopher Delgado Ratto (UAntwerp)
- Renzo Salazar Sanchez (UNSA)
- Jorge Andres Ballón Echegaray (UNSA)
- Dionicia Gamboa Vilela (UPCH)
- Oscar Nolasco Cárdenas (UPCH)
- Carlos Fernández Miñope (UPCH)
- Berónica Infante García (UPCH)