Workshop title:
The application of molecular tools to spatial epidemiology

Instructor(s):

- Prof. Andres Perez (DVM, PhD). aperez@umn.edu. College of Veterinary Medicine, University of Minnesota, USA
- Dr. Julio Alvarez (DVM, PhD). jalvarez@ucm.es. Centro de Vigilancia Sanitaria Veterinaria (VISAVET) and Departamento de Sanidad Animal, Facultad de Veterinaria, Universidad Complutense, Madrid, Spain
- Dr. Moh Alkhamis (DVM, PhD). m.alkhamis@hsc.edu.kw. Faculty of Public Health, Health Sciences Center, Kuwait University
- Dr. Catalina Picasso (DVM, PhD). picas001@umn.edu. College of Veterinary Medicine, University of MInnesota, USA
- Dr. Kaushi Kanankege (DVM, PhD). kanan009@umn.edu. College of Veterinary Medicine, University of MInnesota, USA

Workshop's learning outcomes:
Gain understanding and develop skills in the interface between molecular epidemiology and spatial analysis

Background and skills workshop attendees:
Everyone with an interest to get a basic understanding of molecular epidemiology and to learn how molecular tools can complement spatial studies of infectious disease. Existing experience would be beneficial but is not essential.

The history of the workshop: Yes [X] No [ ].
This workshop series was initiated more than 10 years ago by Dr. Petra Muellner, and some of us have collaborated with her in teaching this course at different locations. For example, a version of this workshop was offered in GeoVet 2010 during 29th - 30th November by Drs. Andres Perez, Petra Müllner, Peter Durr, and Nigel French. The workshop was held at the University of Sydney and it was attended by approximately 20 participants.

Workshop specifications

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

Workshop contents and schedule

The course will run from 9am – 5pm on each of the two days. We will teach using an Interactive combination of presentations, exercises and group discussions.

Why this course?

The availability of modern typing tools has greatly advanced our understanding of several infectious diseases. Correctly applied and interpreted, molecular approaches offer unique opportunities to advance the field of epidemiology, from addressing a herd health problem to understanding the global spread of a disease. In general, the pathogenesis and epidemiology of diseases can differ both between and within species of viruses, bacteria and parasites. Therefore, epidemiological studies may need to consider information at the subspecies level to understand pathogen evolution, host association, sources of infection, and transmission mechanisms. Molecular measures, as techniques of refinement, can for example offer high-resolution answers to questions of disease causation or transmission. For infectious diseases, these measures can provide insight that is not available with traditional culture methods or species-level identification. However, despite their increasing availability, molecular methods are often not completely understood, and in consequence inefficiently applied. Studies that combine population genetic data with spatial analysis present new opportunities for the development of surveillance tools and for improving our understanding of the epidemiology and control of infectious disease. For example constraints that landscape features impose on the distribution, relation, and movement of animals and their diseases have a direct impact on the movement of individuals, their diseases, (and their genes!) in different environments. With concepts borrowed from ecology, statistics, geography, genetics and veterinary medicine, the combined application of molecular and spatial analysis has important implications for the prevention and control of animal and human diseases. Spatial analysis may be applied, for example, to identify spatial relationships between and among groups of pathogens that are genetically related, to quantify transmission and spread of diseases at a molecular level, or to characterize the spatial heterogeneity of the sensitivity and specificity of a molecular test. Furthermore, modern phylogeographic approaches, borrowed from the field of evolutionary biology, have recently become popular as they provide a powerful platform to explore and identify origins and dispersal patterns of infectious pathogens on different geographical scales. Thus, the combination of molecular and spatial tools can also add great value to surveillance programs by providing high resolution answers to epidemiological problems.

What do I need to bring along?

Participants will need to bring their own laptop

Venue

UC Davis Conference Center or the Gladys Valley Hall

Registration

US$ 500 (full)
US$ 300 (student)
Participants must register on-line https://geovet2019.ucdavis.edu using the registration link that will be active on March 1st 2019.

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 September 31st 2019

Day	Time	Topic	Presenter	Format
1	8.30 – 9.00am	Welcome		
	9.00 – 10.30am	Introduction to molecular epidemiology of viruses	Andres	
	10.30 –11.00am	Coffee break		
	11.00 – 12.30pm	Examples of epidemiological studies	Andres & Kaushi	
	12.30 – 1.30pm	Lunch		
	1.30 – 3.00pm	Introduction to molecular epidemiology of bacteria	Julio	
	3.00 – 3.30pm	Coffee break		
	3.30 – 5.00pm	Examples of epidemiological studies	Julio & Cata	
2	9.00 – 10.00am	Introduction to Bayesian Phylodynamic methods using BEAST	Moh	
	10.30 –11.00am	Coffee break		
	11.00 – 12.30pm	Phylogeographic diffusion in discrete space using BEAST 1.10.4 (examples studies, and quick tutorial)	Moh, Kaushi & Cata	
	12.30 – 1.30pm	Lunch		
	1.30 – 3.00pm	Small group discussions/an activity	All	
	3.00 – 3.30pm	Coffee break		
	3.30 – 5.00pm	Brainstorming and discussion	All	