

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. The combination of molecular and spatial tools can also add great value to surveillance programmes by providing high resolution answers to epidemiological problems.

What do I need to bring along?

Participants will need to bring their own laptop

Venue

University of Sydney, Camperdown Campus

Registration

AUS\$ 600 (full)
AUS\$400 (student)

Registration includes:
Lunch as well as morning and afternoon tea
Course material (Printed course notes and workshop CD)

Registration can be done through the [GEOVET 2010 website](#)
Deadline for registration is October 31ST 2010

Contact

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