

Mathematical and Epidemiological modeling of endemic infectious disease – a hands-on workshop

General information

This workshop is aimed at epidemiologists with an interest in combining analysis of field observations with mathematical modeling. The workshop uses methods and examples that are based on data from field studies and are all based on published materials. The objective of the workshop is to show the participants the connection between observations from the field and mathematical models. The workshop will be using the observational data and apply mathematical modeling to obtain a better understanding of the infection dynamics of endemic infectious diseases. Throughout the workshop, lectures and practicals will be used to communicate the key concepts. All practicals are available in either Modelmaker or Berkeley Madonna. Free versions of this software will be made available to all participants.

Workshop specifications

We do not have a preference for a pre or post-conference workshop

We would expect to have between 15 and 25 participants in the course. The minimum would be 15 the maximum would be 25.

The duration of the workshop will be three days. .

There are no specific needs for the workshop. We will be providing all the software and the data to work with. Participants are expected to bring their own laptop computer.

The workshop contents

Day 1 Introduction to mathematical modeling. The importance of modeling in analyzing field data. Basic examples of SIR models using field data. Application of models in modeling software. Conceptual development of mathematical models. Examples include BHV1 and Salmonella.

Day 2 Introduction of more advanced modeling concepts. The use of deterministic and stochastic models. Fitting stochastic models using basic modeling software. Examples of deterministic and stochastic models using field data. Examples include Salmonella and MAP infections.

Day 3 Use of mathematical modeling for different data collection levels. Models of the immune response using bacterial and immune cells. Application of field and experimental data to mathematical modeling. Examples includes Mastitis models and meta-population models of antimicrobial resistance.

The general schedule of the course will be:

08:30 - 09:00: Registration (Day 1 only)

09:00 - 10:30: Lesson 1

10:30 - 11:00: Coffee break

11:00 - 12:30: Practical 1

12:30 - 13:30: Lunch break

13:30 - 15:00: Lesson 2

15:00 - 15:30: Coffee break

15:30 - 17:00: Practical 2

Registration fee

Registration fee is set at 500 Euro per participant

History of the workshop

We have offered the workshop before at Cornell University in 2009, 2010 and 2011. We have offered the workshop at the University of Helsinki in 2009 and the University of Oslo on 2010. In each of these courses there were approximately 20 participants. The course has evolved throughout the year and contains more and more advanced materials. The course materials have substantially improved over time

Short biographies and contact information of all the workshop organizers

Contact information:

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Dr. Ynte Schukken (yhs2@cornell.edu) is a Professor of Epidemiology and Herd Health in the Department of Population Medicine and Diagnostic Sciences. He is also the director of Quality Milk Production Services at Cornell University. Dr. Schukken received his DVM from the University of Utrecht in 1985, his M.Sc. from Cornell University in 1987, and his Ph.D. in 1990 from the University of Utrecht. He has published widely in the field of veterinary epidemiology and herd health in dairy cattle. Dr Schukken's research interests include 1) udder health, food safety and milk quality in well managed dairy herds 2) understanding population dynamics of infectious diseases in animal populations, and 3) application of epidemiological, statistical and mathematical methods to animal disease research. The emphasis in his research is on a combination of statistical/mathematical approaches with strong biological and observational data.

Dr. Yrjö Gröhn (ytg1@cornell.edu) is a professor of epidemiology and the chair for the Department of Population Medicine and Diagnostic Sciences, Cornell University. His research interests have evolved from studies of basic metabolism in ruminants and genetics to veterinary epidemiology, economic modeling and food safety. The two main areas of investigations currently ongoing in his laboratory are: 1) optimizing dairy herd health and management decisions, and 2) mathematical modeling of zoonotic infectious diseases (such as *L. monocytogenes*, *E. coli*, MDR salmonella and paratuberculosis). Both of these areas of research also offer opportunities for training in epidemiological and mathematical modeling, genetic analysis and economic methods.

Dr. Rebecca Mitchell (rmm37@cornell.edu) is a post-doctoral researcher at the Department of Population Medicine and Diagnostic Sciences, Cornell University. She received her DVM and Ph.D. in Comparative Biomedical Sciences from Cornell University. Her research interests include transmission dynamics of infectious agents, and the effect of host and pathogen heterogeneity. Her post-doctoral research focuses on the effect of multi-strain infections of *Mycobacterium avium* subspecies paratuberculosis in dairy herds.

Dr. Zhao Lu (zhaolu@cornell.edu) is a research associate at the Department of Population Medicine and Diagnostic Sciences, Cornell University. He received his Ph.D. in physics from Kent State University. His research interests include the development and application of mathematical and epidemiological approaches to study dynamics and control of infectious diseases in animal and human populations. His research aims to understand the transmission dynamics and persistence of pathogens in host populations and to quantify the effect of control strategies. His current research projects include: (1) modeling the transmission dynamics of *Mycobacterium avium* subsp. paratuberculosis and evaluating the effectiveness of MAP control programs in dairy cattle, (2) *Salmonella* strain competition in a dairy farm.