

Multivariate analysis using Additive Bayesian Networks

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Participants: 25

Analysing animal health data is challenging, as the health status of individuals or groups of animals might depend on many inter-related variables. Such complexity can be underestimated by traditional multivariable regression models, such as linear or generalized linear models, where one variable is designated as a single response variable and all the remaining variables as predictors. Therefore, a holistic, multidimensional approach may be preferable when conducting epidemiological analyses of complex biological data.

The goal of the workshop is to provide participants the tools to understand, perform and critically interpret additive Bayesian network modelling of animal health data.

Workshop outline:

1. Brief theoretical introduction on graphical modelling, Bayesian Networks, and structure discovery.
2. Hands-on exercise: setting up an additive Bayesian network model using the R package `abn`. Participants will be walked through a step-by-step procedure including data preparation, variable selection, structure search, bootstrapping and visualization and interpretation of results.
3. Brief demonstration of further options (heuristic searches, random effects, ...).
4. Wrap-up and discussion of advantages and limitations of the approach.

Learning outcomes

1. To understand the basic theory behind structure discovery and additive Bayesian networks;
2. To learn how to set up and interpret an additive Bayesian network model for multivariate analysis of animal health data using the R package “`abn`”.

Pre-workshop competences and knowledge

Basic statistics and basic knowledge of R. No prior knowledge about graph theory or Bayesian statistics is needed.

The workshop will be mostly practical and participants will work on their own laptops.

Basics of molecular epidemiology: phylogenetic trees and transmission trees

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Participants: 25

Molecular epidemiology of pathogens is a fascinating field within veterinary epidemiology. High quality sequence data is more and more accessible, and such sequence data open up many new opportunities for answering epidemiological questions.

With pathogen sequences, a first step is often to make a phylogenetic tree, which is a description and visualisation of the likely evolutionary relationship between the sequences. It can give information about the likely origin of sequences and to see if there are clusters or subpopulations, possibly with specific characteristics such as virulence factors. However, sequence data can also be used to learn about transmission and to reconstruct transmission trees.

This workshop is the use of pathogen sequence data to learn about transmission. It first covers the basics of phylogenetic trees. We will explain the terminology and evolutionary interpretation of phylogenetic trees, we will cover several methods to construct them, and we will explain how to interpret these trees in the context of pathogen transmission.

Then, we will continue with transmission trees. We will explain how they are different from phylogenetic trees, and we will cover two methods for direct reconstruction of transmission trees (who infected whom) by use of sequence data, both of which are available as R packages.

Participants will make and inspect phylogenetic trees and transmission trees on their own computer using several software packages and R/RStudio, using a real published dataset, in guided tutorials.

Learning outcomes

1. To provide you with a good basic understanding of phylogenetic and transmission trees;
2. To provide you with software and R-code that gives you a good starting point to analyse your own data.

We look forward to welcome you in our workshop!

Pre-workshop competences and knowledge

- Basic knowledge of what DNA is and what sequencing means is required.
- Participants use their own laptop during this workshop;
- Participants will be asked to install the required software prior to the workshop;
- Participants are expected to have a basic understanding of DNA and sequencing.

EMULSION: an expert-friendly language for designing and exploring mechanistic epidemiological models

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Participants: 30



Complex mechanistic epidemiological models are powerful methods to understand and predict pathogen spread at multiple scales. Yet, model development is a long and difficult task, often resulting in a frozen simulation code not easily accessible to non-computer scientists, either to check that the model was properly implemented, or to modify the model itself.

To help design such models, Artificial Intelligence (AI) provides powerful methods. Within this workshop, we aim to introduce EMULSION, an innovative AI-based tool intended to foster explicit model description via an user-friendly language, to revise/explore assumptions on model structure, on parameter values, and on disease management, and to facilitate scale change (e.g. from within- to between-herd scale).

The goal of this workshop is to demonstrate how to rapidly change models in response to revised hypotheses, including back and forth between one scale and another, and transforming a compartmental model into an individual-based one, without code implementation. After a short overview of EMULSION principles, participants will be guided through a set of gradual exercises based on realistic situations encountered in animal health. An already implemented model will be used and updated.

Hands-on work will be done in small groups (2-3 people) to foster interactivity. Participants are expected to work using their own laptop, for which installation instructions will be provided prior to the workshop.

Learning outcomes

1. To be able to use EMULSION modelling language to describe their models
2. To become familiar with the software commands to run their own simulations.

Pre-workshop competences and knowledge

- Experience in mechanistic epidemiological modelling. Programming skills not required.

Syndromic surveillance on routinely collected data: do's and don'ts

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Participants: 30

This workshop aims to provide researchers and other professionals in the field of veterinary epidemiology guidance in the development and practical implementation of a syndromic surveillance system in animal health using routinely collected data.

The workshop will be organized as follows. First, the relevance and added value of syndromic surveillance next to existing monitoring components will be discussed. Then, by means of an interactive brainstorm, participants will identify which applications of syndromic surveillance could be relevant and can be applied in their own region or country. Also, requirements for data sources to be suitable for implementation in a syndromic surveillance system will be handled, as well as which practical issues need to be dealt with when setting up such a system. Then, an introduction will be given on analytical methods that are commonly used in syndromic surveillance (e.g. time-series analyses, space- and/or time cluster detection methods). In addition, a number of examples of syndromic surveillance that are currently operative for cattle health in the Netherlands (including examples that failed to be successful and why) will be discussed. The workshop will be finished by a group-wise practical in which participants get acquainted with a real-life example of a syndromic surveillance analysis using SaTScan™.

Learning outcomes

1. To understand the added value of syndromic surveillance in animal health;
2. To identify practical requirements that data sources need to meet to be used for syndromic surveillance;
3. To identify issues that may arise when implementing syndromic surveillance in practice in terms of data quality, logistics, privacy issues and follow-up of signals;
4. To comprehend commonly used statistical methods used for syndromic surveillance.

Pre-workshop competences and knowledge

Familiarity with basic summary statistics and linear regression.

Assessment of Confounding and Effect Modification during Data Analysis: The need for causal thinking

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Participants: 30

At SVEPM 2018, we hosted a workshop on the use of directed acyclic graphs (DAGs) for confounder identification. In this sequential workshop, we introduce tools to assess confounding and effect modification given explicitly stated causal assumptions. Unlike model selection procedures based on statistical significance, the approach to be presented, leads to coherency between causal assumptions and final statistical models.

Part I: We will give an overview of confounding and effect modification based on currently accepted epidemiologic theory and thinking (i. e. the use of DAGs and the counterfactual model of causation). Emphasis will be placed on the theoretical basis for treating confounding and effect modification as distinct phenomena.

Part II: We will then jointly do interactive exercises on assessing confounding and effect modification using stratification and multivariable regression within the framework of causal models introduced in Part I.

Learning outcomes

1. To recognise the importance of causal assumptions to the assessment confounding and effect modification.
2. To explain how confounders and effect modifiers influence effect estimates.
3. To apply sound analytical approaches to model confounders and effect modifiers and select appropriate effect estimates for interpretation.

Pre-workshop competences and knowledge

- Participants should be familiar with:
- Commonly used epidemiological effect measures
- Contingency table analysis and multiple logistic regression

Self-determination theory in practice: how to motivate your students?

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Participants: 12 (very limited availability!!)

Who doesn't recognize the student who is unmotivated in class? Worse when it is a whole group of students. The causes differ from student related factors (fatigue, not seeing the point of it all), the content, the manner of teaching etc.

How can a teacher influence the motivation of students? In this workshop we will practice influencing motivation, both during teaching and in the design of education. As theoretical framework we will use the "Self-determination theory" by Deci and Ryan, which describes how student can be moved from extrinsic motivation to more intrinsic forms of motivation.

Pre-workshop competences and knowledge

Experience in teaching

Bayesian tools for the estimation of the true disease prevalence

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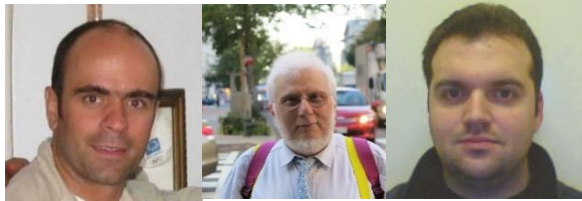
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Participants: 25



Countries, depending on their needs and animal population characteristics, collect data using different sampling schemes and diagnostic methods, especially for non-regulated diseases. Thus, the resulting apparent prevalence estimates are not directly comparable, which is an issue often highlighted in reports from EU institutions like EFSA. The objective of this workshop is to provide training in Bayesian tools for the estimation of true prevalence of disease. Such estimates can be more robustly compared between different diagnostic tests, sampling schemes and among regions/countries.

Learning outcomes

1. To be able to perform Bayesian estimation of true prevalence of disease/infection
2. To be able to perform Bayesian estimation of true prevalence of disease/infection for hierarchically structured data
3. To present an interactive user-friendly website for prevalence estimation

Pre-workshop competences and knowledge

- Basic knowledge of Bayesian analysis principles and some previous experience working with OpenBUGS or JAGS is required. Experience with R is recommended but not necessary for this workshop unless choosing to work with JAGS.
- Participants need laptops with either (1) OpenBUGS or (2) JAGS, R and the R packages rjags and runjags installed.
- Example code and additional material will be disseminated to the registered participants prior to the workshop.