Summer school on Advanced Bayesian Methods

12-16 September 2022

1st announcement

Interuniversity Institute for Biostatistics
and statistical Bioinformatics

The Interuniversity Institute for Biostatistics and statistical Bioinformatics can **finally** organize for the 4th time the summer school on Bayesian methods. After two years that the pandemic ruled the world and blocked our initiative, we are glad that we can restart our summer school on *Advanced Bayesian methods*. As before, the focus is on novel Bayesian methods relevant for the applied statistician.

In the third edition of the summer school, the following two courses will be organized in Leuven from **12 to 16 September 2022**:

- **Three-day course (12-14 September) on Bayesian analysis of infectious disease outbreak data** by Dr. Philip O'Neill (University of Nottingham, UK)
- **Two-day course (15-16 September) on Bayesian inference in latent variable models** by Dr. Paul Gustafson (University of British Columbia, Canada)

The target audience of the summer school are statisticians and/or epidemiologists with a sound background in statistics, but also with background in Bayesian methodology. In both courses, practical sessions are organized, so participants are asked to bring along their laptop with the appropriate software (to be announced) pre-installed.

The registration costs for the courses are:

Two-day course		Three-day course	
I-Biostat member	€ 50	I-Biostat member:	€ 50
PhD student	€ 200	PhD student:	€ 250
Quetelet member	€ 200	Quetelet member	€ 250
Academic	€ 300	Academic:	€ 400
ISBA member	€ 300	ISBA member:	€ 400
Research institute	€ 300	Research institute:	€ 400
Industry	€ 900	Industry:	€ 1200

Note that one is registered to the course, **ONLY when the registration costs have been paid**. The **deadline for registration is July 31, 2022**.

More information about the courses and practicalities (registration, location, transportation, etc.) can be found in due time on https://ibiostat.be.
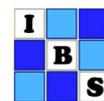
Please reserve already this week in September 2022!

For additional questions, please contact Kirsten Verhaegen (kirsten.verhaegen@kuleuven.be).

Supported by

Bayesian analysis of infectious disease outbreak data

by Professor Philip O'Neill (University of Nottingham, UK)

This course introduces methods for Bayesian analysis of data taken from outbreaks of infectious disease. The specific focus is on stochastic models of disease transmission that are defined at the level of individuals in the at-risk population, and on methods for fitting such models to data. The course will cover the basics of disease transmission models, including definitions and key concepts, as well as fitting methods involving data augmentation and Markov chain Monte Carlo methods. Applications to several different pathogens and data sets will be covered, including nosocomial infections, influenza, and whole-genome-sequence data on pathogens.

Bayesian inference in latent variable models

By Professor Paul Gustafson (University of British Columbia, Vancouver, Canada)

Statistical models involving latent variables are ubiquitous. They arise very naturally in many health-science applications, with examples of latent variables being true disease status when only an imperfect diagnostic test is available, true exposure status when the exposure assessment scheme is noisy, and true infection status for an untested individual. Bayesian routes to inference in latent variable models are very popular, with hierarchical model specifications in standard Bayesian software (based on Markov Chain Monte Carlo computational methods) being quite straightforward.

This course will explore Bayesian latent variable models in some depth, with particular reference to the applications like those mentioned above. There will be a mix of applied and conceptual material. The first part of the course will be more applied in nature. We will work through examples of specifying and fitting Bayesian models in contexts such diagnostic testing and adjusting for exposure measurement error.

The second part of the course will be more conceptual in nature. We will discuss topic such as partial identification, where we dig in to the question of how the sharpness of our inferences is driven by the extent of our knowledge about the relationship between latent variables and observables. And we will touch on how the decision-theoretic optimality of Bayesian procedures plays out in the sorts of models we have been discussing.

Bio sketches of the course instructors

Philip O'Neill (University of Nottingham, UK)

Professor Philip O'Neill is Professor of Applied Probability in the School of Mathematical Sciences at the University of Nottingham, UK. He received his doctoral degree from the University of Nottingham in 1993. His research focuses on the analysis and application of stochastic epidemic models. He has been instrumental in developing Bayesian methods for the analysis of data on infectious disease outbreaks and has authored over 50 publications. He is a former Associate Editor of the Journal of the Royal Statistical Society, Series B.

Paul Gustafson (University of British Columbia, Vancouver, Canada)

Paul Gustafson is Professor and Head in the Department of Statistics at the University of British Columbia, Vancouver.   He received his doctoral degree from Carnegie Mellon University in 1994.   His interests focus on Bayesian methods in biostatistical and epidemiological applications.   He is the author of a 2004 research monograph on Bayesian methods for measurement error problems, and a 2015 research monograph on Bayesian approaches to partially identified problems.   He is a former Editor-in-Chief of the Canadian Journal of Statistics.   He currently serves as an Associate Editor for Biometrics and as the Special Editor, Statistical Methods, for Epidemiology. He received the CRM-SSC prize in 2008, was named a Fellow of the American Statistical Association in 2011, and received the SSC Gold Medal in 2020.