BAYES 20
@LUND 17

A mini-conference in Bayesian analysis at Lund University
Room MA7, in the Maths annex building, Sölvegatan 20,
Lund
20 April 2017

http://maths.lu.se/bayeslund2017

Program, 20 April

Welcome to the fourth edition of Bayes@Lund!

Here is the program for the conference day on 20 April. The conference starts in auditorium MA7, Mathematics annex building, Sölvegatan 20, Lund.

For full information, including options for accommodation, please see `http://www.maths.lu.se/bayeslund2017/`.

[For the tutorial on Bayesian analysis held on 19 April, see http://www.maths.lu.se/bayeslund2017/tutorial/]

time	
08.30-9.00	registration
09.00-9.10	Welcome and an overview of Bayesian activities in Lund: Umberto Picchini and Ullrika Sahlin
9.10-10.05	**Keynote talk:** Darren Wilkinson
10.05-10.30	*coffee break*
Bayesian Analysis I	
10.30-10.55	Måns Magnusson
10.55-11.20	Martin Stjernman
11.20-11.45	Shravan Vasishth
11.45-13.05	*lunch break*
13.05-14.00	**Keynote talk:** Richard McElreath
Decisions and Teaching	
14.00-14.25	Judith Bütepage
14.25-14.50	Mark Andrews
14.50-15.10	*coffee break*
Parallel Sessions	
	Bayesian Analysis II (room MA7) / **Teaching Bayes (room MA6)**
15.10-15.35	Thomas Hamelrick / Richard Torkar
15.35-16.00	Junpeng Lao / Bertil Wegmann
Bayesian Analysis III (room MA7)	
16.05-16.30	Stefan Wiens
16.30-16.55	Ullrika Sahlin

Keynote lectures

Hierarchical modelling of genetic interaction in budding yeast

DARREN J. WILKINSON

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Saccharomyces cerevisiae (often known as budding yeast, or brewers yeast) is a single-celled micro-organism that is easy to grow and genetically manipulate. As it has a cellular organisation that has much in common with the cells of humans, it is often used as a model organism for studying genetics. High-throughput robotic genetic technologies can be used to study the fitness of many thousands of genetic mutant strains of yeast, and the resulting data can be used to identify novel genetic interactions relevant to a target area of biology. The processed data consists of tens of thousands of growth curves with a complex hierarchical structure requiring sophisticated statistical modelling of genetic independence, genetic interaction (epistasis), and variation at multiple levels of the hierarchy. Starting from simple modelling of individual growth curves, a Bayesian hierarchical model can be built with variable selection indicators for inferring pairs of genes that genetically interact. The methods will be applied to data from experiments designed to highlight networks of genetic interactions relevant to telomere biology.

Understanding Bayesian statistics without frequentist language

RICHARD MCELREATH

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Most scholars encounter Bayesian statistics after learning classical, or Frequentist, statistics. As a result, Bayesian concepts and models are nearly always explained using Frequentist language. This can result in lasting confusion about the Bayesian approach, even among those who use it routinely. To advance this argument, I examine two cases of Frequentist language in widespread use in Bayesian statistics and reexplain the underlying concepts using new terms. The first case is the replacement of Frequentist "parameters" and "data" with Bayesian "variables", both latent and observed. The second case is the replacement of both "likelihood" and "prior" with "state of information". It is probably too late to change statistical terminology, but appreciating the friction created by using Frequentist terms in Bayesian contexts can help to avoid mistakes in both design and interpretation.

Contributed Talks

Probabilistic modeling of political perspectives in multi-party systems

Måns Magnusson
Linköping University, mons.magnusson@gmail.com
Richard Öhrvall *Linköping University*
Katarina Barrling *Uppsala University*
David Mimno *Cornell University*

During the last decade topic models have become more and more popular as an approach to model textual data using probabilistic methods. We introduce a probabilistic topic model that tries to capture political ideology based on parliamentary speeches in a multi-party parliamentary situation. We also include prior seeding of topics to a priori specify certain topics of interest. This model is used to analyze the debates on immigration and how these debates change after the Swedish democrats enter the parliament as well as after the refugee crisis in 2015-2016. The data used is all parliamentary speeches of the Swedish parliament during the period 1994 - 2016, a total of approximately 280 000 speeches and almost 50 million word tokens.

Joint species modelling – beautiful in theory, tricky in practice.

Martin Stjernman
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Farmland birds are declining and authorities are looking for remedies. To help in this endeavour, researchers are developing predictive habitat association models that can be used to evaluate alternative measures of landuse management. These models need to be able to propagate uncertainty as well as to allow simultaneous modelling of a group of species such that information can be gained at both individual species and group level. Theoretically, joint species modelling in a Bayesian framework would serve this purpose well. However, to a simple empiricist like myself, what looked beautiful in theory turned out to be slightly more complicated in practice. I will describe my modelling and the stumbles and pitfalls that turned up but hopefully also some interesting and useful results.

Finite Mixture Modeling: A Case Study involving Retrieval Processes in Sentence Comprehension

SHRAVAN VASISHTH

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NICOLAS CHOPIN *CEREMADE Universite-Paris, Dauphine*
ROBIN RYDER *University of Potsdam*
BRUNO NICENBOIM *ENSAE, Paris*

In sentence comprehension, it is widely assumed (e.g., Lewis & Vasishth, 2005) that the distance between linguistic co-dependents affects the latency of dependency resolution: the longer the distance, the longer the retrieval time. By reanalyzing two published data-sets on Chinese relative clauses, we show that the effect of increasing dependency distance on retrieval time is better characterized in terms of a mixture process, better known as the direct-access model (McElree et al., 2003). This model assumes that retrieval times are a mixture of two distributions: one distribution represents successful retrieval and the other represents an initial failure to retrieve the correct dependent, followed by a reanalysis that leads to successful retrieval. Successful retrievals take constant time regardless of dependency distance, but reanalyses cost extra time, and the proportion of failures increases with increasing dependency distance. We implement several hierarchical Bayesian models and show that the data support the direct-access model's predictions.

Learning to make decisions under uncertainty

JUDITH BÜTEPAGE

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Agents can be defined to be intelligent if they make rational decisions under uncertainty. Commonly, reinforcement learning is employed to estimate parametric value and policy functions for optimal decision making. However, assumptions about the structure of these functions can be highly limiting in an ever-changing environment. In this talk, we introduce a Bayesian approach by modelling both the system dynamics and the value function with Gaussian Processes. Gaussian Processes are of advantage as they adapt to noise and novel samples and return an estimate of uncertainty. We show how this method can be used by a robot to learn sensorimotor correlations in a physical human-robot collaboration task and how these patterns can guide optimal action selection in this scenario.

Related publications: https://arxiv.org/pdf/1601.00852.pdf
https://arxiv.org/pdf/1607.07939.pdf

Teaching Bayesian Data Analysis to Social Scientists

MARK ANDREWS

Department of Psychology, Nottingham Trent University, UK ,
THOM BAGULEY *Department of Psychology, Nottingham Trent University, UK*

For the past three years, we have been sponsored by the UK's Economic and Social Research Council (ESRC) to teach Bayesian data analysis to a diverse group of social scientists. We have done so through a series of day-long workshops held throughout the year (see http://www.priorexposure.org.uk).

These workshops progress from introductory topics, e.g. the nature of Bayesian inference and how Bayesian methods differ from their classical counterparts, to advanced topics, e.g. hierarchical generalized linear models, nonlinear regression, and latent variable modelling. In each workshop, we focus heavily on the practice of Bayesian data analysis using R and probabilistic modelling languages such as JAGS. In this talk, we will describe our experiences with these workshops and the lessons we have learned about how to effectively teach Bayesian data analysis to social scientists. We will also describe the diversity of backgrounds, perspectives, and motivations amongst our students, and what topics and content proved to be most (and least) popular or well received.

Potentials of mean force for protein structure prediction: from hack to math

THOMAS HAMELRYCK

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Accurate and efficient prediction of the three-dimensional structure of proteins from their amino acid sequence is one of the great open problems in science. Many protein structure prediction methods make use of so-called "potentials of mean force" (PMFs). These PMFs are interpreted as physical energies whose parameters are estimated from the collection of known protein structures. However, for many decades the validity of these potentials has been widely disputed. I will explain how these potentials arise as the result of well-justified Bayesian reasoning. Specifically, PMFs result from the application of Jeffrey's rule or probability kinematics, which allows Bayesian updating in the light of updated information on the probabilities of the elements of a partition of the event space. This explanation validates PMFs and opens the way to a full Bayesian treatment of the protein structure prediction problem.

Convincing Researchers to Transition to Bayesian Statistics - the Case of Software Engineering

RICHARD TORKAR

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ROBERT FELDT

Chalmers and the University of Gothenburg

Many researchers, even in empirically focused scientific areas, are not experts in statistics and often use only standard, typically frequentist, statistical tests when analysing their research results. Even though a trend in recent years have been to propose and use alternative, non-parametric statistics that rely less on assumptions of normality this has had only limited effect on practice. However, we are convinced that transitioning to bayesian statistics would have many advantages and are developing a data-driven argument to change the current state of affairs.

In this talk, we present data from a survey analysing the top publication venues in software engineering with respect to level of empiricism, statistical approach (Bayesian, Frequentist (parametric and non-parametric)), type of statistical question asked and tests used, as well as types and availability of data. Based on our analysis we outline how we are developing guidelines and an argument for how our research area, software engineering, should evolve to use more bayesian statistical methods. We think such a transition would benefit the area which is typically characterised by disparate

types of data, small sample sizes and violations of assumptions of normality.

Statistical Inferences of Eye movement data using Bayesian smoothing

JUNPENG LAO

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Human observer performs rapid ballistic eye movements to sample visual information, with a combination of fixations and saccades. One of the challenges in the analysis of eye gaze is the sparseness of the data, as only one sample is observed at a given time point. One of the solutions is the usage of kernel smoothing. It is first applied as descriptive data representation (i.e., heat map), and later for statistical inference (e.g., iMap4, Lao et al., 2016). However, it is impossible to infer the smoothing parameters (e.g., kernel size), as they are mostly fixed and chosen arbitrarily. A more natural solution is to use Gaussian Process. Bayesian inference on the kernel length scale of the covariance function can capture the actual smooth spatial-temporal effect, whereas the uncertainty of the observed data points is naturally expressed as the kernel variance. Here, I demonstrate the advantage of this approach on an eye movement study using dynamic stimuli.

Experiences from teaching Bayesian inference to students familiar with frequentist statistics

BERTIL WEGMANN

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Teaching a first course on Bayesian inference can be challenging in different aspects. The audience might be very heterogeneous including people from not knowing anything about Statistics to people who are at least familiar with some statistical methods. Suitable teaching activities can also differ substantially with respect to previous background, mathematical background, pragmatic or idealistic view, or bachelor or master students. Regardless of audience, however, I believe that it is always important to address the philosophical view of Bayesian inference and visualize what consequences different choices of priors and models for data make on different types of Bayesian analyses. In my talk, I will mainly focus on challenges from teaching Bayesian inference to bachelor students who have a non-Bayesian two-year background in, especially, frequentist statistics.

Making the most of your ANOVAs: From NHST to Bayesian analyses

Stefan Wiens
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Mats E. Nilsson
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In many disciplines, factorial designs are analyzed with ANOVAs and interpreted in terms of p values and standardized effect sizes (e.g., partial eta squared). Contrast analysis may be more informative because it tests specific questions (see osf.io/gczhm). It weighs several means and combines them into a t test. The effect size is simply the difference between means. The confidence interval informs about direction, hypothesis exclusion, and the relevance of the effects of interest. However, any interpretation in terms of precision or likelihood requires the use of likelihood intervals or credible intervals (Bayesian). These intervals and a Bayesian t test can be obtained easily with free software. This tutorial reviews these methods to guide researchers in answering the following questions: When I analyze mean differences in factorial designs, where can I find the effects of central interest, and what can I learn about their effect sizes?

Using expert's knowledge in Bayesian analysis

Ullrika Sahlin
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An advantage with the Bayesian framework is that it allows us to integrate data and expert's knowledge for learning and forecasting. In particular, it is possible to build informative priors or predictions based on expert's knowledge. Trained in different fields and traditions, we are more or less comfortable using expert's knowledge. Using expert's knowledge raises questions challenging our view on uncertainty and its subjective dimension. Research on risk communication in combination with mathematics can help us to deal with bias and heuristics when humans are to make judgements. I will demonstrate the R-package "SHELF" (Tools to Support the Sheffield Elicitation Framework) developed for structured procedures to elicit expert's beliefs trying to avoid common biases and heuristics. I welcome more focus on expert knowledge in Bayesian analysis used in research and society. I exemplify with current developments on the treatment of uncertainty and use of expert's knowledge in scientific opinions in risk assessments at the European Food Safety Agency.

Lunch venues

TBA

Maps

TBA

Organizing Committee

- Umberto Picchini, Centre for Mathematical Sciences, Lund University.
- Ullrika Sahlin, Centre for Environmental and Climate Research, Lund University.

Scientific Committee

- Rasmus Bååth, King.com, Malmö.
- Johan Lindström, Centre for Mathematical Sciences, Lund University.
- Umberto Picchini, Centre for Mathematical Sciences, Lund University.
- Ullrika Sahlin, Centre for Environmental and Climate Research, Lund University.
- Jonas Wallin, Department of Statistics, Lund University.

Acknowledgements

Find out more at:

- http://www.becc.lu.se/
- http://cbbp.thep.lu.se/compute/

Bayesian email lists

For events related to Bayesian analysis happening in the neighbourhood of Lund subscribe the Bayes@Lund mail list at http://www.lucs.lu.se/bayes/ (this mail list is not formally connected to the conference).

More broadly, if you wish to get notified of events in the Nordic countries that relate to Bayesian analysis subscribe the Bayes Nordics mail list https://sites.google.com/site/bayesnordics/.