

# BAYES 20

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# @LUND17

A mini-conference in Bayesian analysis at Lund University  
Room MA4, in the Maths Annex building, Sölvegatan 20,  
Lund  
20 April 2017

<http://maths.lu.se/bayeslund2017>

Sponsored by BECC and COMPUTE

<http://www.becc.lu.se/>

<http://cbbp.thep.lu.se/compute/>

## 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 MA4, 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	<b>Keynote talk:</b> Darren Wilkinson	
10.05-10.30	<i>coffee break</i>	
<b>Bayesian Analysis I</b>		
10.30-10.55	Stefan Wiens	
10.55-11.20	Martin Stjernman	
11.20-11.45	Shravan Vasishth	
11.45-13.05	<i>lunch break (not included in the registration)</i>	
13.05-14.00	<b>Keynote talk:</b> Richard McElreath	
<b>Decisions and Teaching</b>		
14.00-14.25	Judith Bütepage	
14.25-14.50	Mark Andrews	
14.50-15.10	<i>coffee break</i>	
<b>Parallel Sessions</b>		
15.10-15.35	<b>Bayesian Analysis II (room MA4)</b> Thomas Hamelrick	<b>Teaching Bayes (room MA6)</b> Richard Torkar
	15.35-16.00 Junpeng Lao	Bertil Wegmann
<b>Bayesian Analysis III (room MA4)</b>		
16.05-16.30	Erik Lindström	
16.30-16.55	Ullrika Sahlin	

# Keynote lectures

## Hierarchical modelling of genetic interaction in budding yeast

**DARREN J. WILKINSON**

*School of Mathematics and Statistics, Newcastle University, UK, darren.wilkinson@ncl.ac.uk*

*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**

*Max Planck Institute for Evolutionary Anthropology, Germany, richard\_mcelreath@eva.mpg.de*

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

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

**STEFAN WIENS**

*Gösta Ekman Laboratory, Department of Psychology, Stockholm University, sws@psychology.su.se*

**MATS E. NILSSON**

*Gösta Ekman Laboratory, Department of Psychology, Stockholm University*

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](https://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?

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

**MARTIN STJERNMAN**

*Department of Biology, Lund University, martin.stjernman@zooekol.lu.se*

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**

*University of Potsdam and CEREMADE Universite-Paris, vasisht@uni-potsdam.de*

**NICOLAS CHOPIN** *ENSAE, Paris*

**ROBIN RYDER** *CEREMADE Universite-Paris, Dauphine*

**BRUNO NICENBOIM** *University of Potsdam*

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**

*Robotics, Perception and Learning Lab, CSC, KTH, butepage@kth.se*

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, mark.andrews@ntu.ac.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**

*Bioinformatics Centre, Department of Biology & Image Group, Department of Computer Science, University of Copenhagen, Denmark, thamelry@binf.ku.dk*

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**

*Chalmers and the University of Gothenburg, richard.torkar@chalmers.se*

**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**

*Eye and Brain Mapping Laboratory (iBMLab), Department of Psychology, University of Fribourg, Fribourg, Switzerland, junpeng.lao@unifr.ch*

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**

*Statistik och maskininlärning (STIMA), institutionen för datavetenskap (IDA) Linköpings Universitet, bertil.wegmann@liu.se*

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.

# Multilevel Monte Carlo methods for inference in multivariate diffusions

**ERIK LINDSTRÖM**

*Centre for Mathematical Sciences, Lund University, Sweden, erikl@maths.lth.se*

Stochastic differential equations is a class of stochastic processes well suited for inclusion of prior knowledge on the model structure. That makes them well suited for a wide range of applications in science as well as in finance.

The main obstacle when using these models has been the computational demands. The reason for this is that the likelihood function often is unknown, and has to be approximation using some numerical methods. We show, using theory on Multi Level Monte Carlo methods, how a substantial reduction of the computational complexity can be obtained compared to standard Monte Carlo methods. Finally, we illustrate how posterior estimates are computed using the PMMH algorithm.

# Using expert's knowledge in Bayesian analysis

**ULLRIKA SAHLIN**

*Centre for Environmental and Climate Research, Lund University, ullrika.sahlin@cec.lu.se*

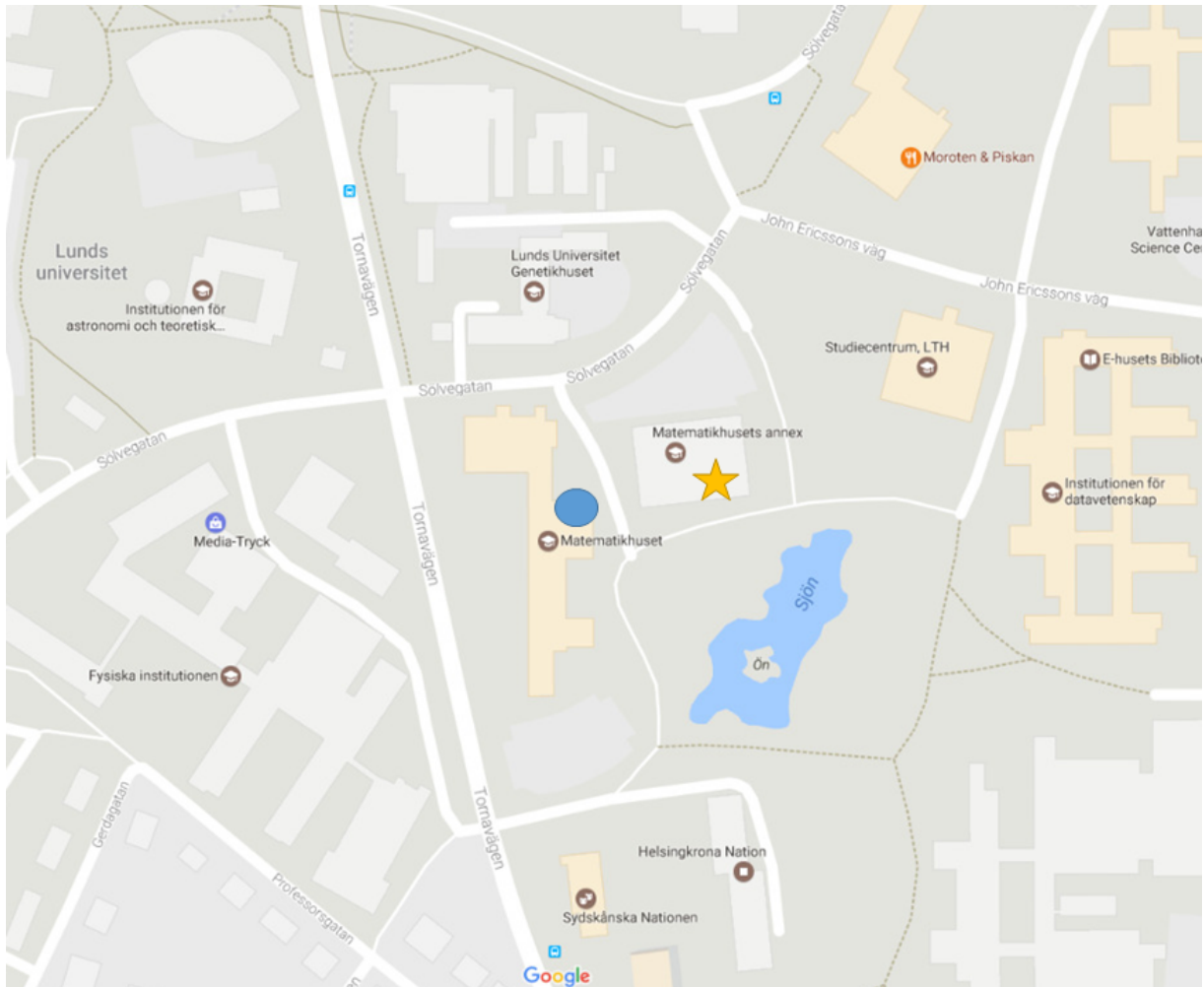
An advantage with the Bayesian framework is that it allows us to integrate data and expert's knowledge for learning and forecasting. In particular, it is possible to build informative priors or predictions based on expert's knowledge. Trained in different fields and traditions, we are more or less comfortable 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.



## Maps

The conference starts in room MA4 in the Matematikhusets Annex, marked with a yellow ★ (Sölvegatan 20, Lund).

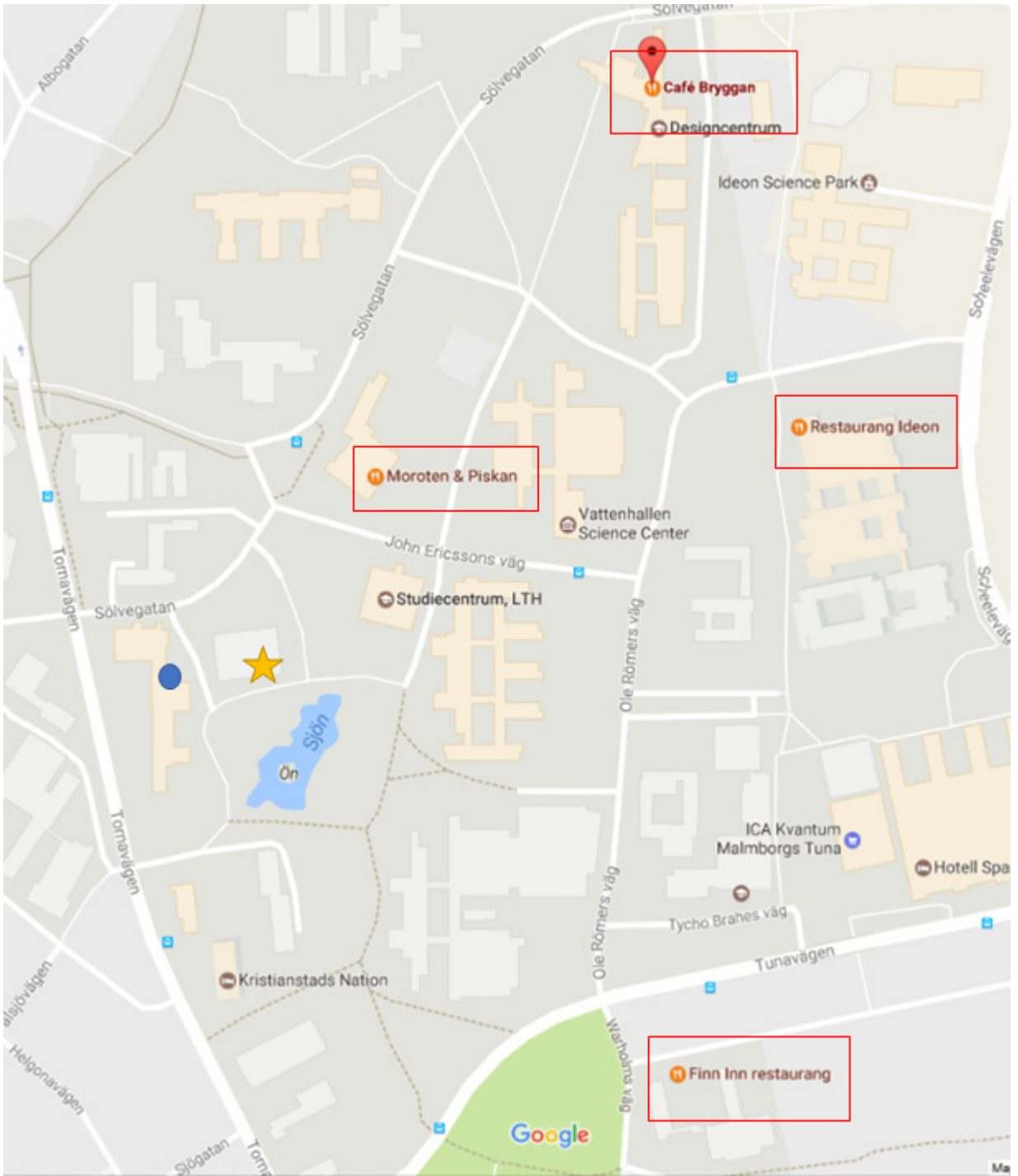
The tutorial on 19 April is in room MH:C in Matematikhuset, marked with a blue ●.



## Lunch options

Lunches are not included in the registration.

Please consider the restaurant options at next page, all within 5-10 minutes walk from the conference venue denoted with a yellow ★.



## 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.

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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.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/>.