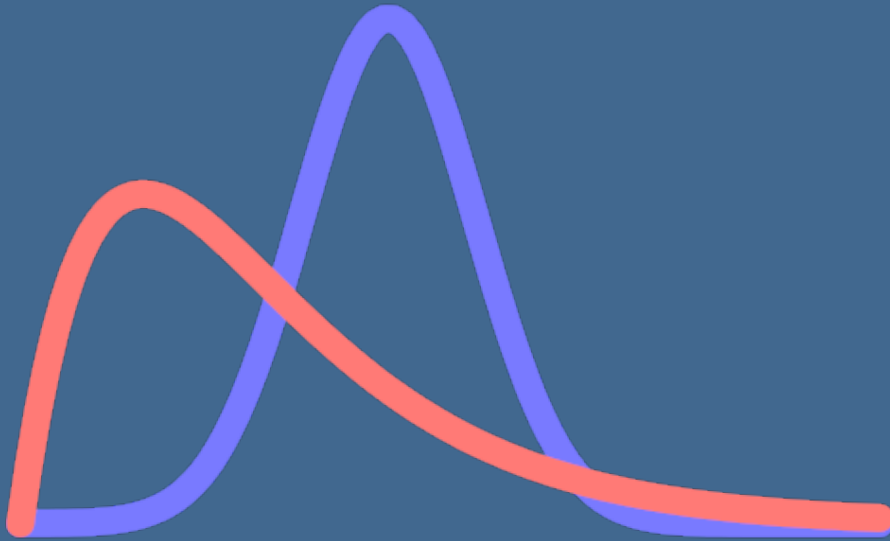


Bayesian Biostatistics



January 25-27, 2016, Symbiosis, Interim II at iDiv

Abstract

This course is an introduction to modern applied Bayesian statistics. It approaches statistics as a modular kit in which several simple blocks can be used to analyse problems of any complexity. The course emphasizes practical advantages of Bayesian statistics over theoretical or philosophical ones.

Participants will learn to specify, fit and evaluate basic models in BUGS language (OpenBUGS, JAGS). The course assumes elementary knowledge of R (i.e. "I can launch R, load data into R, I can do a simple regression model" and so on). Any programming skills are advantageous.

We will use ecological examples, but the methods are applicable throughout biology. All materials will be provided online. The course is 3 days long, with 4-5 hours per day. Everything is in English.

Taught by **Petr Keil**
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Syllabus & timeline

Day 1 – 25 Jan 2016, Symbiosis, Interim II

10:00-12:00

- Introduction: Course contents, pros and cons of Bayes, necessary skills.
- Basics of likelihood: Introducing likelihood and deviance on the Normal example.

13:00-15:30

- Poisson distribution: The didactic simplicity of Poisson and its likelihood. Likelihood maximization. Probability mass function.
- Calculating posterior probability. The principle of MCMC sampling.

Day 2 – 26 Jan 2016, Symbiosis, Interim II

10:00-12:00

- Generalized linear models - linear regression, logistic regression, Poisson regression, ANOVA etc., all that in BUGS.

13:00-15:30

- Hierarchical (mixed-effect, multilevel) models, random effects vs. fixed effects, latent variables, complex models, informative vs. non-informative priors.

Day 3 – 26 Jan 2016, Symbiosis, Interim II

10:00-12:00

- Exercise the stuff from Days 1 and 2 – participants work on their own with Petr's supervision.
- Time series analysis, autocorrelation function, density dependence, random walks (theme will be chosen based on participants' preferences).

13:00-15:30

- Models for spatial data, spatial autocorrelation, GeoBUGS module in OpenBUGS.
- Model selection, model evaluation, information theory criteria, handling uncertainty, Bayesian credible intervals, prediction intervals.

What should you bring?

- Your own **laptop** with **R** and **JAGS** installed.
- **How to install JAGS?**
 - Windows and OS X users download the installers at: <http://goo.gl/tbw7Lt>
 - Ubuntu users: `sudo apt-get install jags`
- JAGS is not part of R, it's a stand-alone application, but we will command it from R. For this you will need to **install a few extra R packages** by typing (in R):
`install.packages(c("R2jags", "rjags", "coda"))`
- It will be advantageous to have at least a **basic familiarity with R**: You should know how to set a working directory, how to import and export data, you should know how R works with array indexing (the square brackets `[,]`), and you should be familiar with the following types of objects: `vector`, `data.frame`, and `list`.

Is there an exam?

No, students will be credited for attendance and for performing a simple Bayesian analysis.

Literature

- Kéry M. (2010) *Introduction to WinBUGS for Ecologists: Bayesian approach to regression, ANOVA, mixed models and related analyses*. Academic Press.
- McCarthy M.A. (2007) *Bayesian Methods for Ecology*. Cambridge Univ. Press.
- Clark J.S. (2007) *Models for Ecological Data*. Princeton Univ. Press.
- Gelman A., Carlin J.B., Stern H.S. & Rubin D.B. (2004) *Bayesian Data Analysis*. Chapman & Hall.
- Bolker B.M. (2008) *Ecological Models and Data in R*. Princeton Univ. Press.
- *OpenBUGS user manual*: www.openbugs.info