



Course and Workshop

Bayesian Data Analyses Using Linear Models with and WinBUGS

8. – 12. September 2014, Basel, Switzerland

Bayesian data analysis becomes more and more standard in the analyses of biological data. Bayesian methods are the only methods that provide exact estimates of the standard errors in non-normal, hierarchical and more complex models (see e.g. Bolker et al. 2008, TREE 24:127-135). They allow fitting models that are too complex to be fitted easily using frequentist methods, e.g. hierarchical ecological models. Furthermore, existing knowledge about a parameter can formally be used when analysing the data, and the results have a natural interpretation such as the probability of a meaningful hypothesis.

The course introduces the principles of Bayesian data analyses together with a sound training in applying linear models. Today, life scientists, especially ecologists, are expected to be familiar with **normal linear models** (LM), **linear mixed models** (LME), **generalised linear models** (GLM), and **generalised linear mixed models** (GLMM). These four types of models form the basis for a variety of more complicated models, such hierarchical ecological models of which the occupancy, the point count model and the Cormack-Jolly-Seber model will be introduced using the free software WinBUGS.

Participants will apply linear models including LM, LME, GLM, and GLMM using Bayesian methods with the free statistical software R (www.r-project.org). The course follows Gelman & Hill 2007, Data Analysis Using Regression and Multilevel/Hierarchical Models, Cambridge University Press.

Worked examples will include:

- graphical data exploration (various plotting functions)
- fit of the model to data (R-Functions *lm*, *lmer*, *glm*, *glmer*)
- assessment of model fit and model assumptions (diagnostic plots of residuals)
- visualization of the results and drawing conclusions (*summary*, *anova*, *predict*, *sim*)

During the last day of the course, participants analyse their own data.

Date: 8. – 12. September 2014

Location: Evolutionary Biology, Zoological Institute, University of Basel,
Vesalgasse 1, 4051 Basel

Teachers: Fränzi Korner-Nievergelt, oikostat GmbH, Ettiswil (oikostat.ch)
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Contents: Day 1: Short introduction to R (optional)
Introduction to Bayesian statistics
Overview frequentist and Bayesian statistics
Normal linear model (LM): ANOVA, ANCOVA, regression

Day 2: Model selection
Linear mixed effects model (LME)
Generalised linear model (GLM): logistic regression

Day 3: Generalised linear model (GLM): binomial and Poisson-model
Generalised linear mixed model (GLMM)

Day 4: Extensions of GLMMs
Introduction to WinBUGS, introduction to Cormack-Jolly-Seber
models and point count/occupancy models.

Day 5: Participants work on their own (or example) data and give short
presentations

Course form: Lectures and exercises
The number of participants is limited to 20.
Participants are expected to bring their own laptop with R installed

Course hours: 9 00 to 17 30 including two coffee breaks and a one hour lunch break.

Prerequisite: Make sure you are familiar with the following terms: mean,
standard deviation, standard error, and t-test (e.g. chapter 5 in
Dalgaard 2008, Introductory Statistics with R, Springer).
Basic knowledge in R programming
(e.g. chapters 1, 2, and 4 in Dalgaard 2008,
or chapters 1-5 in Crawley 2007, The R-book, Wiley,)

Costs: Student price CHF. 850.-/ regular price CHF 1050.-

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