ISBE

2010

13TH INTERNATIONAL
B E H A V I O R A L
ECOLOGY CONGRESS

Program
Abstracts
List of
Participants

Post Congress Symposia

Program & Abstracts

How can sexual selection be measured?	**Meeting Room 1**
Statistical tools for behavioural ecologists	**Meeting Room 2**
Why behavioural ecologists should care	**Meeting Room 3**
Integrating nutritional and behavioural ecology	**Meeting Room 7**
The ecology of sex roles	**Meeting Room 8**
Impact of symbionts on behaviour	**Meeting Room 11**
Are Humans cooperative breeders?	**Meeting Room 12**

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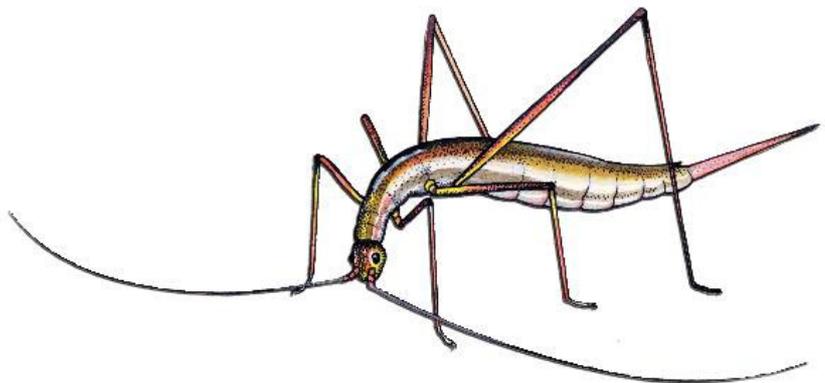
Statistical tools for Behavioral Ecologists

Meeting Room 2

Organisers
László Zsolt Garamszegi
Shinichi Nakagawa

Program

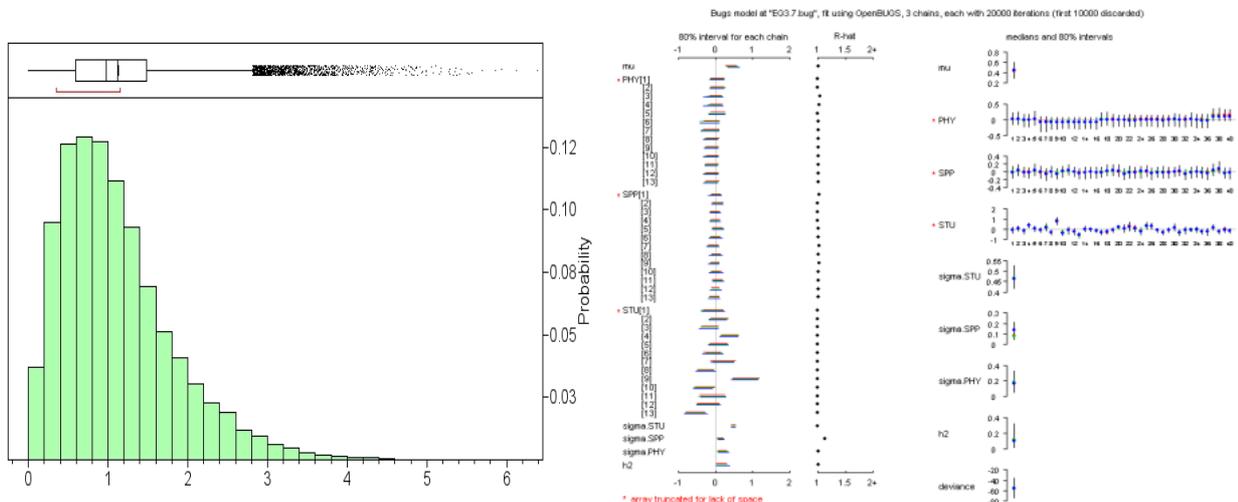09.00-09.10 – General introduction (Garamszegi)

Part I (chair: Garamszegi)

09.10-09.30	Squeezing maximum information from matrix data in behavioural ecology (speaker: Kutsukake)
09.30-09.50	The tolerance interval method for assessment of agreement in behavioral ecology studies with repeated measurements (speaker: Maurer)
09.50-10.10	Repeatability for binary, proportion and count data (speaker: Nakagawa)
10.10-10.30	Advances in meta-analysis in Behavioural Ecology (speaker: Santos)
10.30-11.00	coffee break
10.50-11.10	rangeMapper: A package for easy generation of biodiversity (species richness) or life-history traits maps using species geographical ranges (speaker: Dale)

Part II (chair: Nakagawa)

11.10-11.30	Not quite a piece of cake: problems encountered on a behavioural ecologist's honeymoon with Akaike's Information Criterion (speaker: Symonds)
11.30-11.50	Information-theoretic approaches to statistical analysis in behavioural ecology: an introduction to a special journal issue (speaker: Garamszegi)
11.50-12.10	Avoiding common pitfalls when applying 'animal' models to behaviour using Bayesian methods (speaker: Dugdale)
12.10-12.30	Women have relatively larger brains than men: a comment on the misuse of GLM in the study of sexual dimorphism (speaker: Forstmeier)
12.30-12.50	Using variance-covariance structures to incorporate data heterogeneity (speaker: Cleasby)
12.50-13.00	Conclusion & take home message (Nakagawa)
13.00	General discussion over lunch or beer

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INFORMATION-THEORETIC APPROACHES TO STATISTICAL ANALYSIS IN BEHAVIOURAL ECOLOGY: AN INTRODUCTION TO A SPECIAL JOURNAL ISSUE

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Scientific thinking may require the consideration of multiple hypotheses, which often call for complex statistical models at the level of data analysis. Complex models have traditionally been treated by model selection approaches using threshold-based removal of terms, i.e. stepwise selection. A recently introduced method for model selection applies an Information Theoretic (IT) approach, which has been increasingly propagated in the field of ecology. However, a literature survey shows that its spread in behavioural ecology has been much slower, and model simplification using stepwise selection is still more widespread than IT-based model selection. Why has the use of IT method in behavioural ecology lagged behind other disciplines? A special issue (SI) will soon appear in *Behavioral Ecology and Sociobiology* that examines the suitability of the IT method for analyzing data with multiple predictors. The volume brings together different viewpoints to aid behavioural ecologists in understanding the method. In my talk, I will provide a brief overview on the content of the SI by emphasizing the often-misinterpreted benefits and shortcomings of the IT tool and by pointing to avenues along which the evaluation of multiple hypotheses may develop.

AVOIDING COMMON PITFALLS WHEN APPLYING 'ANIMAL' MODELS TO BEHAVIOUR USING BAYESIAN METHODS

Hannah L Dugdale[1,2], David S Richardson[3], Jan Komdeur[1] and Terry Burke[2]

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For behaviour to evolve selection must act on behaviour; behaviour and variation in it must be heritable. In the past, behavioural ecologists have rarely tested whether behaviours are heritable, assuming instead that behaviours are flexible. This is primarily because elucidating heritability in the wild is difficult, requiring long-term study of individual behaviours and a multi-generation pedigree. As these data have become available, there has been a surge of interest in applying 'animal' models (mixed models that estimate how similar phenotypic traits are across related individuals) to behaviours. However, behaviours are often binary or rate measures, requiring non-Gaussian error structures and Bayesian techniques to assess the heritability of such behaviours have only recently become available. Furthermore, as relatives frequently not only share genes but also common environments, it is crucial to account for this in models. Using a long-term dataset and genetic pedigree of the Seychelles warbler, we demonstrate the application of 'animal' models to behaviour. We highlight how interpretation of whether helping behaviour is heritable is influenced by priors (the prior probability distribution of the unknown quantity of interest e.g. variance in helping). We therefore demonstrate the importance of using simulations to determine whether there is power to detect heritability.

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