Geophysical Research Abstracts Vol. 19, EGU2017-17530, 2017 EGU General Assembly 2017 © Author(s) 2017. CC Attribution 3.0 License.



## **BUMPER:** the Bayesian User-friendly Model for Palaeo-Environmental Reconstruction

Phil Holden (1), John Birks (2), Steve Brooks (3), Mark Bush (4), Grace Hwang (5), Frazer Matthews-Bird (4), Bryan Valencia (4), and Robert van Woesik (4)

(1) Open University, Earth Environmental and Ecosystems, Milton Keynes, United Kingdom (philip.holden@open.ac.uk), (2) Department of Biology, Universty of Bergen, PO Box 7803, N-5020 Bergen, Norway, (3) Department of Entomology, Natural History Museum, Cromwell Road, London SW7 5BD, UK, (4) Department of Biological Sciences, Florida Institute of Technology, 150 West University Boulevard, Melbourne, FL 32901, USA, (5) The Johns Hopkins University Applied Physics Laboratory, 11000 Johns Hopkins Road, Laurel, MD 20723, USA

We describe the Bayesian User-friendly Model for Palaeo-Environmental Reconstruction (BUMPER), a Bayesian transfer function for inferring past climate and other environmental variables from microfossil assemblages.

The principal motivation for a Bayesian approach is that the palaeoenvironment is treated probabilistically, and can be updated as additional data become available. Bayesian approaches therefore provide a reconstruction-specific quantification of the uncertainty in the data and in the model parameters.

BUMPER is fully self-calibrating, straightforward to apply, and computationally fast, requiring  $\sim$ 2 seconds to build a 100-taxon model from a 100-site training-set on a standard personal computer.

We apply the model's probabilistic framework to generate thousands of artificial training-sets under ideal assumptions. We then use these to demonstrate both the general applicability of the model and the sensitivity of reconstructions to the characteristics of the training-set, considering assemblage richness, taxon tolerances, and the number of training sites. We demonstrate general applicability to real data, considering three different organism types (chironomids, diatoms, pollen) and different reconstructed variables.

In all of these applications an identically configured model is used, the only change being the input files that provide the training-set environment and taxon-count data.