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Analysis of ordered categorical data via a structural heteroscedastic threshold model with random effects.

Analysis of discrete ordinal outcomes is an important issue in biomedical studies. An appealing model for the analysis of such traits is the so-called threshold model. The aim of this Winbugs/Openbugs programme is to propose a flexible threshold model in which subpopulations differ not only in location of the underlying variable but also in dispersion (scaling) parameters. Heterogeneity of variances is described via a structural mixed model and a loglink function involving continuous and discrete covariates. Current software is generally unable to run such models or, if it can, the approximated likelihood based procedures on which it is based (Liu et al., 2006; Rigby and Stasinopoulos , 2005; Lee and Nelder, 2006) might lead to severely biased estimators of both fixed and random effects (Meza et al., 2008). This highlights the obvious interest of an "exact" procedure such as the Bayesian one chosen here.
The Winbugs/Openbugs code provided is quite general and can be applied both to elementary and grouped data. Although a probit model was applied in the example presented, the proposed heterogeneous model can be used with any other link function, such as the logit model. Several choices of priors on the variances of random effects (inverse gamma, lognormal, half Cauchy, uniform) have also been made available to the user.

Reference
Foulley J-.L., Jaffrézic F., Modelling and estimating heterogeneous variances in threshold models for ordinal discrete data via Winbugs Openbugs, *Computer Methods and Programs in Biomedicine*, (2009) submitted.