

## Response to van der Lans

Chris Holmes\* and Leonhard Held†

We wish to thank Ralf van der Lans for pointing out corrections to part of the pseudo-code in Appendix A.5 provided in Holmes and Held (2006) concerning the polychotomous regression. The pseudo-code was inconsistent, and we have highlighted below the required corrections in a compact fashion making clear the extent of the necessary changes. It is also important to note that the theory and methods presented in the paper are correct.

Regarding correction 1, two comment lines on the bottom of page 166 should have read

```
% % Hence, C records the sum of the Q - 1 terms, exp(X[j,]β[, t, i]),
% % for, t ∈ {1, ..., q - 1, q + 1, ..., Q},
```

with our corrections in bold face, but we stress that the preceding coding line,

$$C \leftarrow \text{sum}(\exp(\mathbf{X}[j,]\boldsymbol{\beta}[-q, i])) \quad (1)$$

is correct. “Correction 1” of van der Lans is equivalent, but in conflict with the notation used in our paper. In particular, as is common, we defined  $\beta_Q \equiv 0$  in our paper and the subscript  $-q$  refers to “all sets other than the  $q$ ’th”.

Regarding correction 2, we apologise that an offset term is missing from two lines of pseudo-code in Appendix A.5 involving the updates to  $\beta[, q, i]$  and  $\Lambda[j, j, q]$ , which should read

$$\begin{aligned} B &\leftarrow VX'\Lambda[:, q]^{-1}(Z[, q] + \log C[]) \\ R &\leftarrow (Z[j, q] - m + \log C[j]), \end{aligned}$$

again with our changes in bold face. Note that the vector  $C[]$  with elements  $C[j]$  from (1) can be calculated outside the “FOR  $j = 1$  to number of observations” loop.

For convenience we have replicated Appendix A.5 with these corrections, highlighting in bold the required changes. We apologise for any problems resulting from this.

**A5: Procedure for sampling the Bayesian polychotomous model,  $\beta \sim \pi(\beta|Y, X, v)$ , using joint update to  $\{Z, \lambda\}$ .**

```
% % Let, Y[i][j] denote the category indicator variable, Y[i][j] = 1 if the
% % ith observation is of class j, j ∈ {1, ..., Q}, Y[i][j] = 0 otherwise.
```

\*Department of Statistics & The Oxford-Man Institute, University of Oxford, Oxford, U.K., <http://www.stats.ox.ac.uk/~cholmes/>

†Institute of Social and Preventive Medicine, Division of Biostatistics, University of Zurich, Zurich, Switzerland, <mailto:leonhard.held@ifspm.uzh.ch>

```

%% % Initialise mixing weights,  $\Lambda[:, q]$  for each category to the  $(n \times n)$ 
identity matrix
FOR q=1 to Q-1
     $\Lambda[:, q] \leftarrow I_n$ 
    %% % draw  $Z$  from truncated logistic
     $Z[:, q] \sim Lo(0, 1)Ind(Y[:, q], Z[:, q])$ 
END
FOR i = 1 to number of MCMC iterations
    FOR q=1 to Q-1
         $C[] \leftarrow \text{sum}(\exp(X[:, ]\beta[:, -q, i]))$ 
        %% % Hence, C records the sum of the Q-1 terms,  $\exp(X[:, ]\beta[:, t, i])$ ,
        %% % for,  $t \in \{1, \dots, q-1, q+1, \dots, Q\}$ ;
         $V \leftarrow (X^T \Lambda[:, q]^{-1} X + v^{-1})^{-1}$ 
        %% % note that  $\Lambda^{-1}$  is a diagonal matrix and hence simple to invert
         $L \leftarrow \text{Chol}(V)$ 
        %% % So L stores the lower triangular Cholesky factorisation of V
         $B \leftarrow V X^T \Lambda[:, q]^{-1} (Z[:, q] + \log C[])$ 
         $T \sim N(0, I_p)$ 
         $\beta[:, q, i] \leftarrow B + LT$ 
        %% % Now update  $\{Z, \Lambda\}$ 
        FOR j=1 to number of observations
             $m \leftarrow X[j, ]\beta[:, q, i]$ 
            %% % Now draw  $Z[j, q]$  from truncated logistic
             $Z[j, q] \sim Lo(m - \log C[j], 1)Ind(Y[j, q], Z[j, q])$ 
            %% % now draw new value for mixing variance
             $R \leftarrow (Z[j, q] - m + \log C[j])$ 
             $\Lambda[j, j, q] \sim \pi(\lambda | R^2)$ 
        %% % See program A4.
        END
    END
END MCMC iterations; RETURN  $\beta$ 

```