Wildlife Biology

WLB-00416

Porteus, T. A., Reynolds, J. C. and McAllister, M. K. 2018. Quantifying the rate of replacement by immigration during restricted-area control of red fox in different landscapes. – Wildlife Biology 2018: wlb.00416

Appendix 1

Supplementary Figures

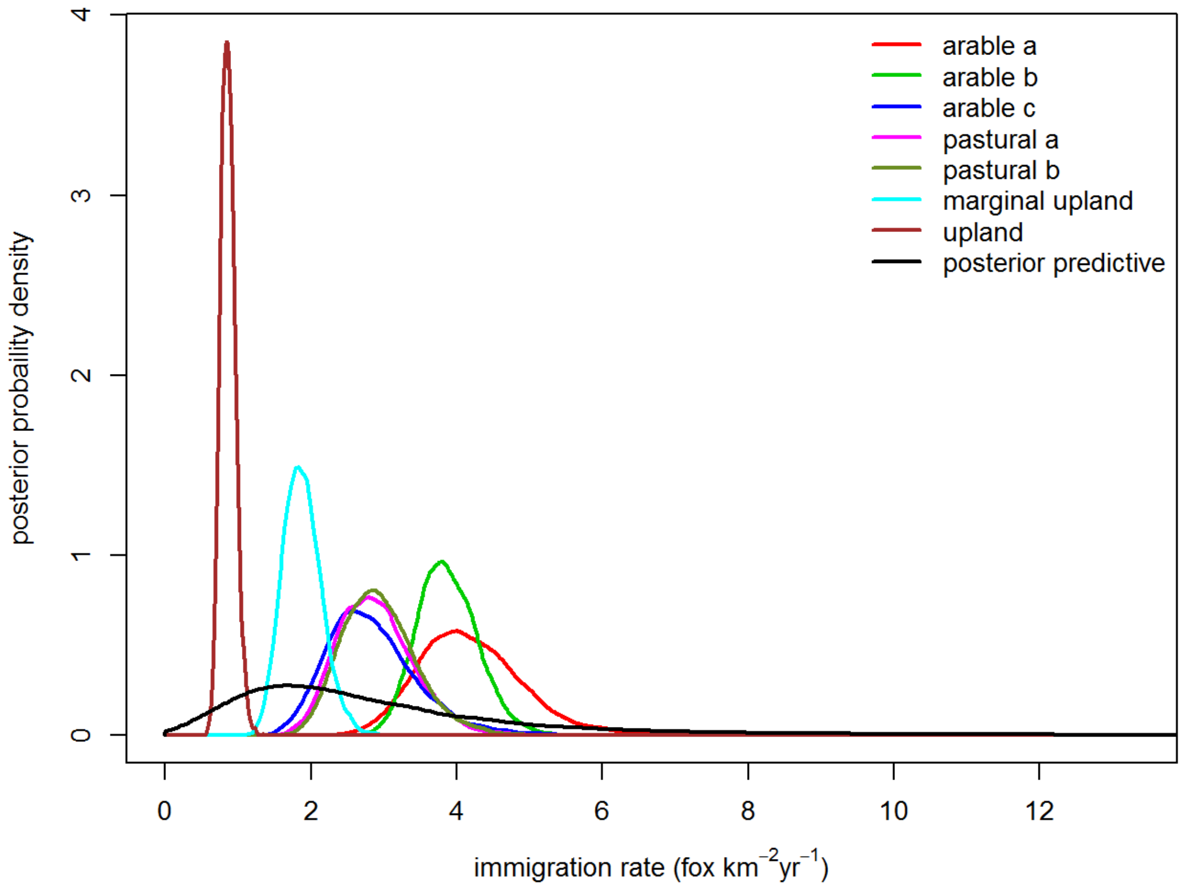

Figure A1.1. Posterior probability density functions for immigration rate in each landscape category. The posterior predictive density function was determined by the hyper-parameters of the hierarchical model.

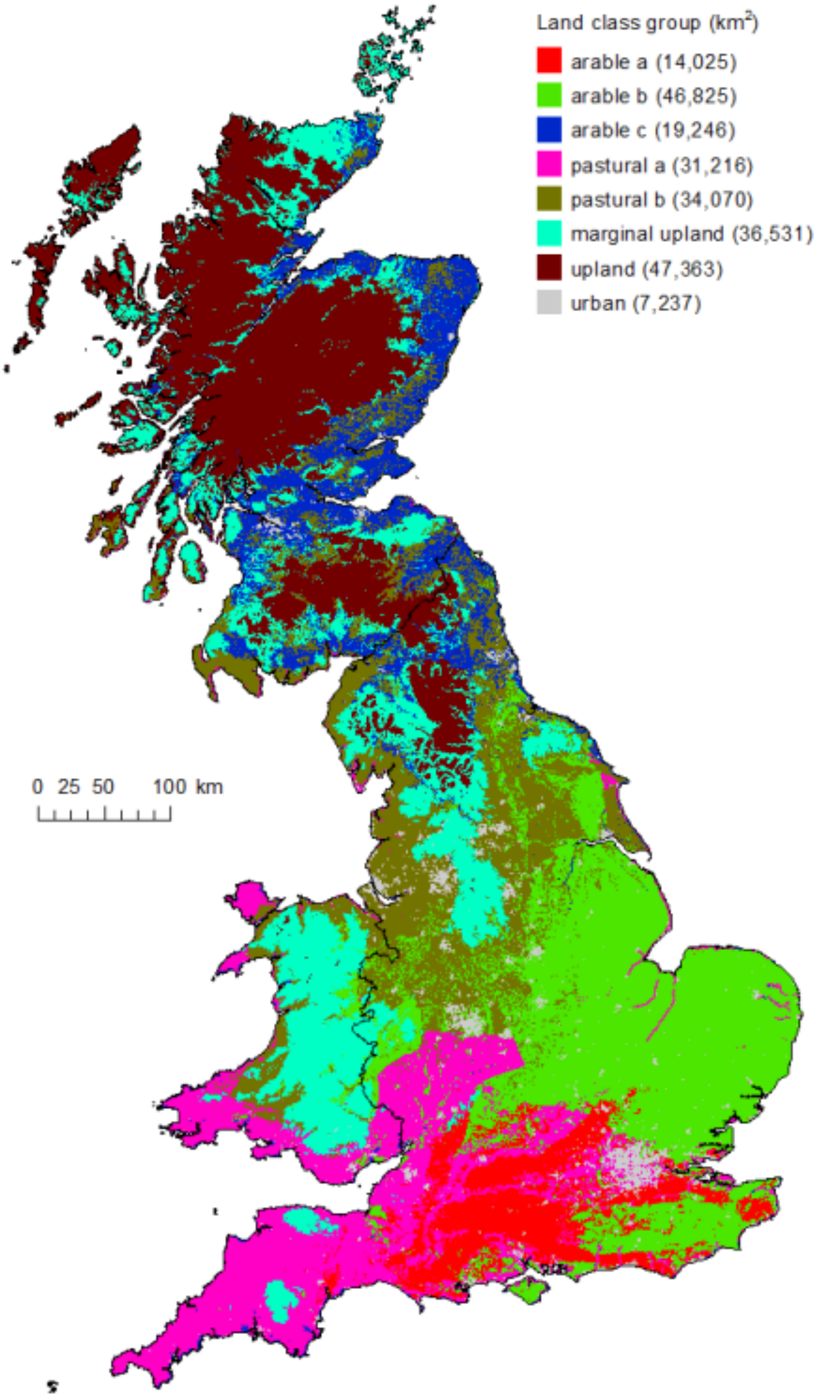

Figure A1.2. Map of Britain showing the landscape categories obtained from land class grouping.

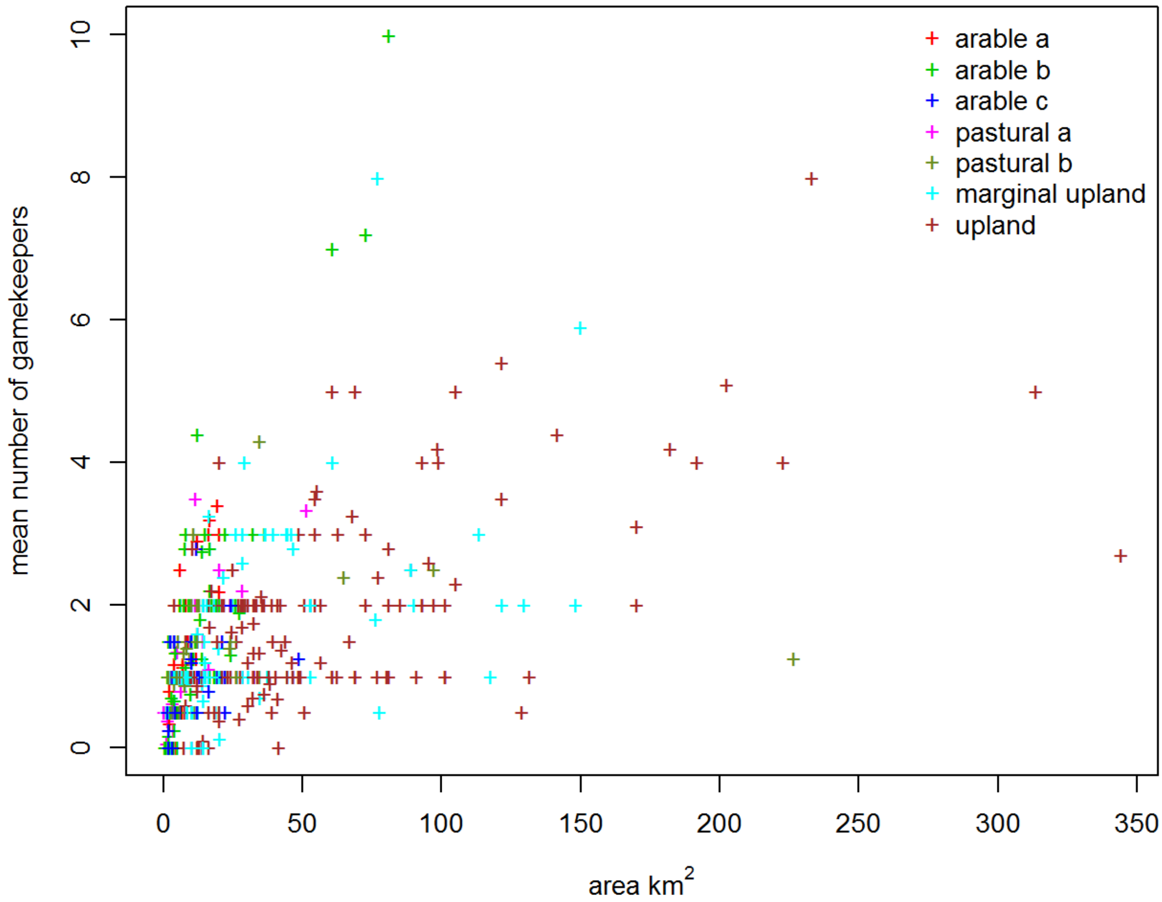

Figure A1.3. Relationship between the number of active gamekeepers (represented as a mean number across years) and estate area in each landscape category from those NGC estates contributing data on fox bags for the period 1996–2000.

Appendix 2

Examination of results for possible effects of spurious correlation

The possibility of spurious correlations influencing the results was examined in two ways. First, the correlation coefficients between cull and area within each landscape were calculated and compared to the correlation coefficients between cull density and area. Second, randomisation testing (Edgington 1995) was used to compare the intercept and slope parameter values for each landscape with the distribution of intercept and slope values derived from randomised cull and area data. The expected distributions for each landscape were obtained by randomly sampling the cull and area data without replacement to give 9999 datasets to compare to the observed dataset (thus giving a total of 10 000 datasets). The cull density was calculated for each dataset and a non-hierarchical version of the model in Eq. 3 was then fitted using maximum likelihood estimation. The resulting intercept and slope values were summarised in frequency histograms and compared to the values estimated from the observed data in the same way. Because there was a priori an expectation that spurious correlation would result in a change in slope and intercept values in one direction, a one-tailed test was applied to determine the statistical significance of the observed data estimates to the randomised distribution.

Using a log-linear model, randomisation tests indicated the intercept and slope parameter values estimated from the observed data were lower and higher, respectively, than those expected under random association (Fig. A2.1). These differences were all significant ($p < 0.05$, one-tailed test). We conclude that our analysis using cull density was not appreciably affected by spurious correlations. The use of ratios for data standardisation is prevalent in ecology, e.g. to remove study area or body size effects from variables of interest (Jackson and Somers 1991). Pearson (1897) documented the problem of spurious correlations in ratio variables over a century ago and, despite several reminders (Kenney 1982, Jackson and Somers 1991, Brett 2004), it is still not widely appreciated and can be the cause of erroneous conclusions. Had there been no relationship between cull and area in these NGC data, performing the analysis would have resulted in estimates of immigration rate that were artificially high. Evaluation of the results from use of ratios using randomisation testing is therefore an important step in ensuring that conclusions are not erroneous (Jackson and Somers 1991).

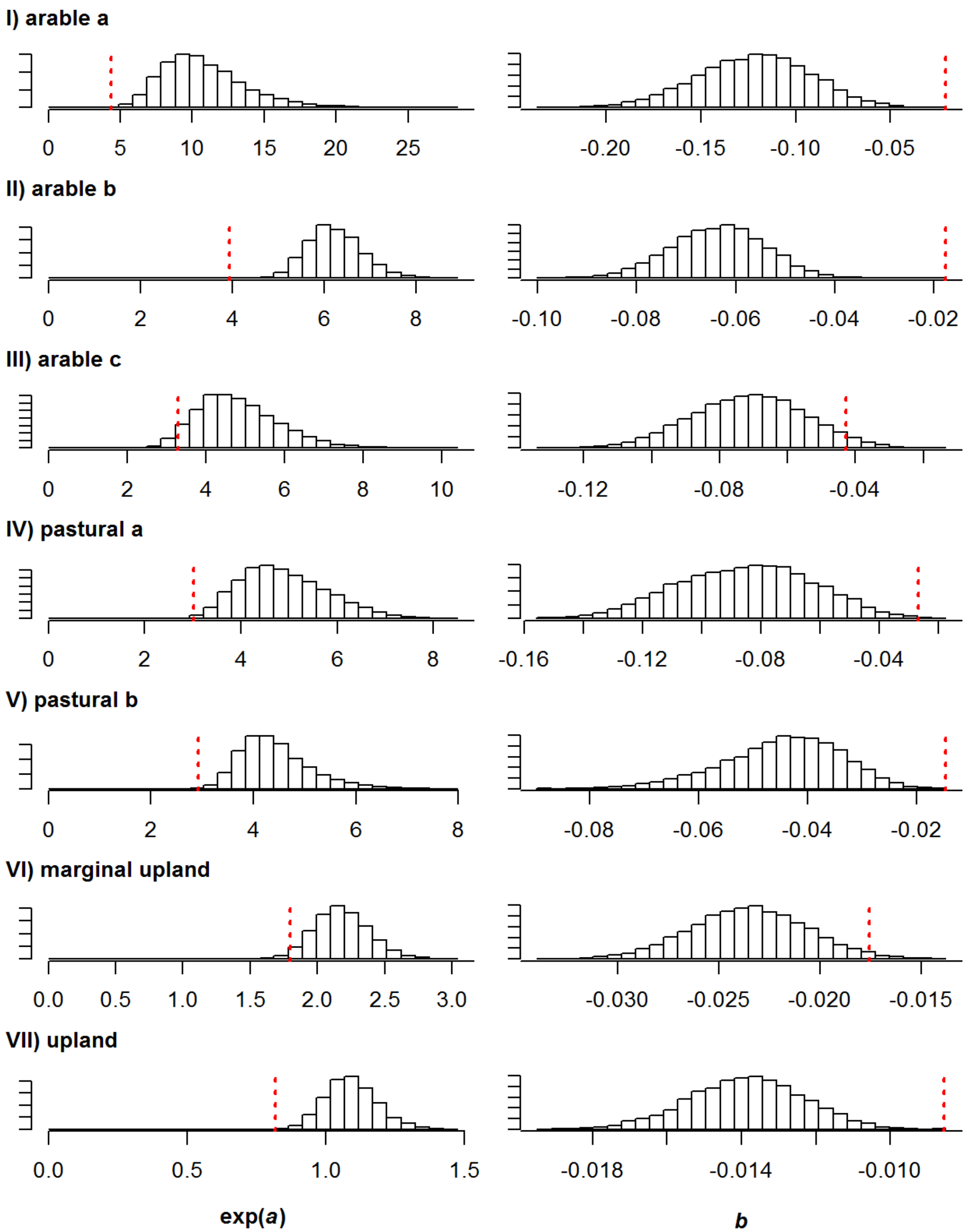

Figure A2.1. Frequency histograms for each landscape category showing intercept (exp(a)) and slope (b) estimates from a randomisation test of the cull density and area relationship. Locations of empirically estimated values are shown by the vertical dashed lines. Note that the vertical scales of each plot are not the same and the y-axes are not labelled for clarity.

Appendix 3

WinBUGS Script

```
model

{

    ###LIKELIHOOD###

    for (i in 1:NData) {

        ln.pred[i] <- a[group[i]] + b[group[i]] * area.km2[i]

        ln.cullD[i] ~ dnorm(ln.pred[i], tau.obs)

    }

    ###PRIORS###

    sd.obs ~ dunif(0, 10)

    tau.obs <- 1/(sd.obs * sd.obs)

    for (i in 1:NGroup) {

        a[i] ~ dnorm(mu.a, tau.a) #intercept for group i (on a

                                  #log scale)

        b[i] ~ dnorm(mu.b, tau.b) #slope for group i

        v[i] <- exp(a[i]) #prediction of immigration rate as

                          #fox km-2 yr-1.  MCMC samples from

                          #the posterior give unbiased

                          #estimates of the mean and variance

    }

    ###HYPERPARAMETERS###

    mu.a ~ dnorm(0, 1.0E-06) #global mean of intercepts

    mu.b ~ dnorm(0, 1.0E-06) #global mean of slopes
```

```
    sigma.a ~ dunif(0, 10) #s.d. of all intercepts

    tau.a <- 1/(sigma.a * sigma.a)

    sigma.b ~ dunif(0, 10) #s.d. of all slopes

    tau.b <- 1/(sigma.b * sigma.b)

    ###POSTERIOR PREDICTIVE DISTRIBUTIONS###

    a.pred ~ dnorm(mu.a, tau.a)

    b.pred ~ dnorm(mu.b, tau.b)

    v.pred <- exp(a.pred)

}
```

References used in the Appendices

Brett, M. T. 2004. When is a correlation between non-independent variables “spurious”? – Oikos 105: 647–656.

Edgington, E. S. 1995. Randomization tests. – Marcel Dekker, Inc.

Jackson, D. A. and Somers, K. M. 1991. The spectre of ‘spurious’ correlations. – Oecologia 86: 147–151.

Kenney, B. C. 1982. Beware of spurious self-correlations! – Water Resour. Res. 18: 1041–1048.

Pearson, K. 1897. Mathematical contributions to the theory of evolution. On a form of spurious correlation which may arise when indices are used in the measurement of organs. – Proc. R. Soc. B 60: 489–498.