

# Appendix S2: Extinction risk status of saproxylic beetles reflects the ecological degradation of forests in Europe

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## Abstract

We describe a linear mixed effects model with correlated random effects and details of model fitting and model inference.

*Keywords:* linear mixed proportional odds model.

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## 1. Linear Mixed Proportional Odds Model

Let  $Y_i$  denote the extinction risk category of species  $i$  and  $\mathbf{x}_i$  the traits for this species. We analysed the data using the linear mixed proportional odds model with correlated random intercepts:

$$\begin{aligned}\mathbb{P}(Y_i \leq k) &= \text{logit}^{-1}(\vartheta_k - \mathbf{x}_i^\top \boldsymbol{\beta} - \gamma_i) \\ \boldsymbol{\gamma} &= (\gamma_1, \dots, \gamma_n) \sim \mathcal{N}_n(0, \tau^2 \mathbf{C}).\end{aligned}$$

The  $n \times n$  correlation matrix  $\mathbf{C}$  was obtained from the phylogenetic tree.

The model was fitted using function `c1mm()` from package **ordinal**. Since this function only allow fitting of models with uncorrelated random intercepts, we modified the linear predictor in the model as follows. With  $\mathbf{C} = \mathbf{R}\mathbf{R}^\top$  denoting the Cholesky decomposition of the correlation matrix, we can rewrite the linear predictor of the model as

$$\begin{aligned}-\eta_i &:= \mathbf{x}_i^\top \boldsymbol{\beta} + \gamma_i \\ -\boldsymbol{\eta} &= -(\eta_1, \dots, \eta_n) = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\gamma} \\ &= \mathbf{X}\boldsymbol{\beta} + \mathbf{I}_n \boldsymbol{\gamma} \\ &= \mathbf{X}\boldsymbol{\beta} + \mathbf{I}_n \mathbf{R}\mathbf{R}^{-1} \boldsymbol{\gamma} \\ &= \mathbf{X}\boldsymbol{\beta} + \mathbf{R}\tilde{\boldsymbol{\gamma}}.\end{aligned}$$

The distribution of the new random effects  $\tilde{\boldsymbol{\gamma}}$  with random effects design matrix  $\mathbf{R}$  is now  $\tilde{\boldsymbol{\gamma}} = \mathbf{R}^{-1} \boldsymbol{\gamma} \sim \mathcal{N}_n(0, \tau^2 \mathbf{I}_n)$  and we only had to change the design matrix for the species-specific random effects from the unit matrix  $\mathbf{I}_n$  to the Cholesky factor  $\mathbf{R}$ .

### 1.1. Model Inference

Because the correlation between species is taken into account via the correlation matrix  $\mathbf{C}$  the Bayesian covariance matrix of the fixed effects can be assumed to be a close approximation of the variability of the estimated fixed effects. Standard asymptotic theory establishes convergence of the estimated fixed effects distribution to the normal distribution and we therefore use normal approximations to the standard  $z$ -statistics for model inference.

### 1.2. Model Predictions

For a species with unknown extinction risk level  $Y_i$ , we can predict the density of the extinction risk levels based on the trait values  $\mathbf{x}_i$  and the phylogenetic correlations the species the model was fitted to. The predicted extinction risk density was computed from the estimated model parameters  $\boldsymbol{\beta}$  and  $\tilde{\boldsymbol{\gamma}}$  via

$$\begin{aligned}\mathbb{P}(Y_i = 1) &= \mathbb{P}(Y_i \leq 1) = \text{logit}^{-1}(\vartheta_1 - \mathbf{x}_i^\top \boldsymbol{\beta} - \mathbf{r}_i \tilde{\boldsymbol{\gamma}}) \\ \mathbb{P}(Y_i = k) &= \mathbb{P}(Y_i \leq k) - \mathbb{P}(Y_i \leq k-1) \\ &= \text{logit}^{-1}(\vartheta_k - \mathbf{x}_i^\top \boldsymbol{\beta} - \mathbf{r}_i \tilde{\boldsymbol{\gamma}}) - \text{logit}^{-1}(\vartheta_{k-1} - \mathbf{x}_i^\top \boldsymbol{\beta} - \mathbf{r}_i \tilde{\boldsymbol{\gamma}}), k = 2, \dots, (K-1) \\ \mathbb{P}(Y_i = K) &= 1 - \mathbb{P}(Y_i \leq K-1) = 1 - \text{logit}^{-1}(\vartheta_{K-1} - \mathbf{x}_i^\top \boldsymbol{\beta} - \mathbf{r}_i \tilde{\boldsymbol{\gamma}})\end{aligned}$$

with  $\mathbf{r}_i$  corresponding to the  $i$ th row and all columns corresponding to species in the training sample of the Cholesky decomposition of the complete correlation matrix.

## 2. Results

### 2.1. clmm() for Correlated Observations

We redefine the `clmm` model in order to take phylogenetic correlations, specified via a correlation matrix `CORR`, into account:

```
> set.seed(29)
> library("ordinal", lib = "../lib")
> stopifnot(packageVersion("ordinal") == "2012.9.11")
> attach(asNamespace("ordinal"))
> phylo_clmm <-
+   function(formula, data, weights, start, subset,
+             na.action, contrasts, Hess = TRUE, model = TRUE,
+             link = c("logit", "probit", "cloglog", "loglog",
+                     "cauchit"), ##, "Aranda-Ordaz", "log-gamma"), ## lambda,
+             doFit = TRUE, control = list(), nAGQ = 1L,
+             threshold = c("flexible", "symmetric", "equidistant"), CORR, ...)
+ {
+   mc <- match.call(expand.dots = FALSE)
+   link <- match.arg(link)
+   threshold <- match.arg(threshold)
+   if(missing(formula)) stop("Model needs a formula")
```

```

+   if(missing(contrasts)) contrasts <- NULL
+   ## set control parameters:
+   control <- getCtrlArgs(control, list(...))
+   nAGQ <- as.integer(round(nAGQ))
+   ## Extract y, X, Zt, offset (off), weights (wts):
+   frames <- clmm.model.frame(mc, contrasts)
+   if(control$method == "model.frame") return(frames)
+   ## Test rank deficiency and possibly drop some parameters:
+   ## X is guarantied to have an intercept at this point.
+   frames$X <- drop.coef(frames$X, silent=FALSE)
+   ## Compute the transpose of the Jacobian for the threshold function,
+   ## tJac and the names of the threshold parameters, alpha.names:
+   ths <- makeThresholds(frames$y, threshold)
+
+   ## Set rho environment:
+   rho <- with(frames, {
+     clm.newRho(parent.frame(), y=y, X=X, weights=wts,
+       offset=off, tJac=ths$tJac) })
+
+   nbeta <- rho$nbeta <- ncol(frames$X) - 1 ## no. fixef parameters
+   nalpha <- rho$nalpha <- ths$nalpha ## no. threshold parameters
+   ntau <- rho$ntau <- length(frames$grList) ## no. variance parameters
+
+   ## Set inverse link function and its two first derivatives (pfun,
+   ## dfun and gfun) in rho:
+   setLinks(rho, link)
+
+   ## Set starting values for the parameters:
+   if(missing(start)) start <- clmm.start(frames, link, threshold)
+   stopifnot(is.numeric(start) &&
+     length(start) == (nalpha + nbeta + ntau))
+   rho$par <- start
+
+   Zt <- frames$Zt
+   stopifnot(all(rownames(Zt) == rownames(CORR)))
+   if (!is.null(CORR)) {
+     R <- as(t(chol(CORR)), class(Zt))
+     Zt <- t(crossprod(Zt, R))
+   }
+   rho.clm2clmm(rho=rho, Zt=Zt, grList=frames$grList,
+     ctrl=control$ctrl)
+
+   ## Possibly return the environment, rho without fitting:
+   if(!doFit) return(rho)
+
+   ## Fit the clmm:
+   fit <- clmm.fit.env(rho, control = control$optCtrl, Hess)

```

```

+
+   ## Modify and return results:
+   fit$nAGQ <- nAGQ
+   fit$link <- link
+   fit$start <- start
+   fit$threshold <- threshold
+   fit$call <- match.call()
+   fit$formula <- frames$formula
+   fit$tJac <- ths$tJac
+   fit$contrasts <- attr(frames$X, "contrasts")
+   fit$na.action <- attr(frames$mf, "na.action")
+   fit$terms <- frames$terms
+   fit$xlevels <- .getXlevels(fit$terms, frames$mf)
+   fit$y.levels <- levels(frames$y)
+   res <- clmm.finalize(fit=fit, frames=frames,
+                        alpha.names=ths$alpha.names)
+
+   ## add model.frame to results list?
+   if(model) res$model <- frames$mf
+
+   return(res)
+ }

```

## 2.2. Model Fitting

We fit the linear mixed proportional odds model with correlated species-specific random intercepts

```

> load("Seibold_ESM_App3.rda")
> if (!file.exists("clmm_model.Rda")) {
+   mod <- phylo_clmm(RL ~ mean_body_size + mean_elev + distribution +
+                     niche_diam + niche_canopy + niche_decay + flowers +
+                     tree + habitat + feeding + (1 | species) ,
+                     data = bmodel, CORR = phylo_corr)
+   save(mod, file = "clmm_model.Rda")
+ } else {
+   load("clmm_model.Rda")
+ }

```

## 2.3. Model Inference

We first fit a conventional proportional odds model to the data (ignoring species-specific random effects) as a benchmark model

```

> library("MASS")
> library("multcomp")

```

```

> ### use polr model to set-up X and K
> pmod <- polr(RL ~ mean_body_size + mean_elev + distribution +
+             niche_diam + niche_canopy + niche_decay + flowers +
+             tree + habitat + feeding,
+             data = bmodel)
> X <- model.matrix(pmod)
> Xnew <- model.matrix(delete.response(formula(pmod)), data = bpred)
> pmod <- update(pmod, Hess = TRUE)
> K1 <- glht(pmod, linfct = mcp(tree = "Tukey"))$linfct
> K2 <- glht(pmod, linfct = mcp(habitat = "Tukey"))$linfct
> K <- rbind(K1, K2)
> i <- c(1:5, 20)

```

Output of proportional odds model without random intercepts

```
> cftest(pmod)
```

#### Simultaneous Tests for General Linear Hypotheses

```
Fit: polr(formula = RL ~ mean_body_size + mean_elev + distribution +
      niche_diam + niche_canopy + niche_decay + flowers + tree +
      habitat + feeding, data = bmodel, Hess = TRUE)
```

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z )
mean_body_size == 0	0.06826	0.01392	4.902	9.46e-07 ***
mean_elev == 0	-0.44097	0.16615	-2.654	0.007955 **
distribution == 0	-0.31193	0.01759	-17.729	< 2e-16 ***
niche_diam == 0	0.94609	0.12887	7.342	2.11e-13 ***
niche_canopy == 0	-0.77925	0.22401	-3.479	0.000504 ***
niche_decay == 0	0.12498	0.12663	0.987	0.323640
flowers == 0	-0.51084	0.20774	-2.459	0.013930 *
treel == 0	0.66209	0.28245	2.344	0.019072 *
treen == 0	-1.23574	0.36354	-3.399	0.000676 ***
habitatWood and bark == 0	-0.54668	0.32882	-1.663	0.096401 .
habitatFungi == 0	-0.02653	0.42053	-0.063	0.949704
feedingd == 0	0.57437	0.51082	1.124	0.260842
feedingm == 0	-0.03120	0.32407	-0.096	0.923299
feedingx == 0	0.86899	0.22095	3.933	8.39e-05 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Univariate p values reported)

Output of mixed proportional odds model with species-specific correlated random intercepts

```
> summary(mod)
```

Cumulative Link Mixed Model fitted with the Laplace approximation

```
formula: RL ~ mean_body_size + mean_elev + distribution + niche_diam +
        niche_canopy + niche_decay + flowers + tree + habitat + feeding +
        (1 | species)
data:    bmodel
```

```
link threshold nobs logLik AIC      niter    max.grad cond.H
logit flexible 1025 -837.16 1714.32 35(5406) 2.42e-06 1.6e+04
```

Random effects:

```
          Var Std.Dev
species 1.973   1.405
Number of groups: species 1025
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
mean_body_size	0.06890	0.02089	3.299	0.000971	***
mean_elev	-0.48472	0.18393	-2.635	0.008407	**
distribution	-0.36565	0.02484	-14.720	< 2e-16	***
niche_diam	1.10301	0.16367	6.739	1.59e-11	***
niche_canopy	-0.93708	0.27571	-3.399	0.000677	***
niche_decay	-0.07503	0.16736	-0.448	0.653932	
flowers	-0.42474	0.28106	-1.511	0.130736	
treel	0.65252	0.31429	2.076	0.037876	*
treen	-1.48398	0.41555	-3.571	0.000355	***
habitatWood and bark	-0.75184	0.38852	-1.935	0.052973	.
habitatFungi	-0.05600	0.54623	-0.103	0.918336	
feedingd	0.80689	0.76514	1.055	0.291623	
feedingm	-0.20641	0.48485	-0.426	0.670314	
feedingx	0.56817	0.36969	1.537	0.124322	

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Threshold coefficients:

	Estimate	Std. Error	z value
0 1	-4.1211	0.8805	-4.681
1 2	-3.5323	0.8667	-4.076
2 3	-1.9276	0.8587	-2.245
3 4	-0.4526	0.8579	-0.528
4 5	1.1508	0.8686	1.325

Post-hoc comparisons for the mixed proportional odds model

```
> set.seed(29)
> summary(glht(mod, linfct = K, coef = function(x) coef(x)[-i],
+          vcov = function(x) vcov(mod)[-i, -i]))
```

## Simultaneous Tests for General Linear Hypotheses

```
Fit: phylo_clmm(formula = RL ~ mean_body_size + mean_elev + distribution +
      niche_diam + niche_canopy + niche_decay + flowers + tree +
      habitat + feeding + (1 | species), data = bmodel, CORR = phylo_corr)
```

Linear Hypotheses:

	Estimate	Std. Error	z value	Pr(> z )
l - b == 0	0.6525	0.3143	2.076	0.17526
n - b == 0	-1.4840	0.4155	-3.571	0.00204 **
n - l == 0	-2.1365	0.3339	-6.398	< 1e-04 ***
Wood and bark - Hollow tree == 0	-0.7518	0.3885	-1.935	0.23453
Fungi - Hollow tree == 0	-0.0560	0.5462	-0.103	0.99996
Fungi - Wood and bark == 0	0.6958	0.4462	1.560	0.44835

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1  
(Adjusted p values reported -- single-step method)

## 2.4. Model Predictions and Uncertainty

For the species used to estimate the model, we compute the fitted extinction risk level density and corresponding most-probable categories

```
> ### fitted density and classes
> lp <- X[,-1] %*% coef(mod)[-i]
> th <- coef(mod)[1:5]
> p <- cbind(do.call("cbind", lapply(th, function(u)
+           plogis((u - (lp - mod$ranef[[1]]))))), 1)
> dens <- t(apply(p, 1, function(x) c(x[1], diff(x)))))
> cls <- apply(dens, 1, which.max)
> ## compare with response
> (x <- table(factor(cls, levels = 1:6, labels = 0:5), bmodel$RL))
```

	0	1	2	3	4	5
0	623	54	80	21	3	6
1	0	0	0	0	0	0
2	42	5	29	28	8	2
3	13	2	12	17	21	11
4	2	0	2	7	15	9
5	1	0	1	0	4	7

In order to assess the uncertainty of these predictions, we first construct simultaneous confidence intervals for  $\vartheta_k - \mathbf{x}_i^\top \boldsymbol{\beta}$  for all extinction risk categories and observations. Based on these confidence intervals, we reconstruct the conditional density of extinction risk categories for each observation and compute the lowest and highest extinction risk category in agreement with the model from these two densities. This gives us “prediction intervals” of extinction risk

categories for each observations. For the species used to estimate the model, we compare these prediction intervals with the observed extinction risk category. For the remaining species, we compare these prediction intervals with the predicted extinction risk category.

```
> if (file.exists("xt-in.rda")) {
+   load("xt-in.rda")
+ } else {
+   D <- diag(5)
+   est <- matrix(NA, nrow(X), ncol = 6)
+   lwr <- matrix(NA, nrow(X), ncol = 6)
+   upr <- matrix(NA, nrow(X), ncol = 6)
+   for (j in 1:nrow(X)) {
+     XD <- cbind(D, (-1) * X[j,-1,drop = FALSE][rep(1, 5),], 0)
+     ci <- confint(glht(mod, linfct = XD))$confint + mod$ranef[[1]][j]
+     est[j,] <- c(plogis(ci[, "Estimate"]), 1)
+     lwr[j,] <- c(plogis(ci[, "lwr"]), 1)
+     upr[j,] <- c(plogis(ci[, "upr"]), 1)
+   }
+
+   max(abs(p - est))
+
+   dest <- t(apply(est, 1, function(x) c(x[1], diff(x))))
+   dlwr <- t(apply(lwr, 1, function(x) c(x[1], diff(x))))
+   dupr <- t(apply(upr, 1, function(x) c(x[1], diff(x))))
+
+   clsest <- ordered(apply(dest, 1, which.max), levels = 1:6, labels = 0:5)
+   clslwr <- ordered(apply(dlwr, 1, which.max), levels = 1:6, labels = 0:5)
+   clsupr <- ordered(apply(dupr, 1, which.max), levels = 1:6, labels = 0:5)
+
+   x <- data.frame(clsupr, RL = bmodel$RL, clslwr)
+   save(x, file = "xt-in.rda")
+ }
> names(x) <- c("lower", "RL", "upper")
> xt <- xtabs(~ lower + upper + RL, data = x)
```

For 86% of the species, the true extinction risk category is between the predicted lowest and highest extinction risk category in agreement with the model. The length of these intervals is distributed as follows:

```
> table(with(x, (0:5)[upper] - (0:5)[lower]))
```

0	1	2	3	4
632	15	264	112	2

Table 1 summarizes the number of all possible interval combinations for each extinction risk category. The model is most accurate and confident for species with extinction risk category zero. For the remaining categories, the uncertainty can be judged from the number of species



whose extinction risk category is not contained in the interval. For example, we have 31 extinction risk 1 species where both the lowest and highest extinction risk category obtained from the model is zero. For 22 species, the model suggests a category between 0 and 2; and for 6 species between 0 and 3. For 2 species, the model “predicts” a extinction risk category between 2 and 4. The overall picture is similar for higher extinction risk categories.

Now we do the same for species with unknown extinction risk category

```
> ### predicted density and classes
> lp <- Xnew[,-1] %*% coef(mod)[-i]
> th <- coef(mod)[1:5]
> p <- cbind(do.call("cbind", lapply(th, function(u) plogis(u - lp))), 1)
> dens <- t(apply(p, 1, function(x) c(x[1], diff(x))))
> cls <- factor(apply(dens, 1, which.max), levels = 1:6, labels = 0:5)
> table(cls)

cls
 0  1  2  3  4  5
88  0 48 27 22  3

> if (file.exists("xt-out.rda")) {
+   load("xt-out.rda")
+ } else {
+   D <- diag(5)
+   est <- matrix(NA, nrow(Xnew), ncol = 6)
+   lwr <- matrix(NA, nrow(Xnew), ncol = 6)
+   upr <- matrix(NA, nrow(Xnew), ncol = 6)
+   for (j in 1:nrow(Xnew)) {
+     print(j)
+     XD <- cbind(D, (-1) * Xnew[j,-1,drop = FALSE][rep(1, 5),], 0)
+     ci <- confint(glht(mod, linfct = XD))$confint
+     est[j,] <- c(plogis(ci[, "Estimate"]), 1)
+     lwr[j,] <- c(plogis(ci[, "lwr"]), 1)
+     upr[j,] <- c(plogis(ci[, "upr"]), 1)
+   }
+
+   max(abs(p - est))
+
+   dest <- t(apply(est, 1, function(x) c(x[1], diff(x))))
+   dlwr <- t(apply(lwr, 1, function(x) c(x[1], diff(x))))
+   dupr <- t(apply(upr, 1, function(x) c(x[1], diff(x))))
+
+   clsest <- factor(apply(dest, 1, which.max), levels = 1:6, labels = 0:5)
+   clslwr <- factor(apply(dlwr, 1, which.max), levels = 1:6, labels = 0:5)
+   clsupr <- factor(apply(dupr, 1, which.max), levels = 1:6, labels = 0:5)
+
+   x <- data.frame(clsupr, clsest, clslwr)
+   save(x, file = "xt-out.rda")
}
```

upper		0	1	2	3	4	5
RL	lower						
0	0	549	0	80	35	0	0
	1	0	0	0	0	0	0
	2	0	0	0	1	10	4
	3	0	0	0	0	0	2
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
1	0	31	0	22	6	0	0
	1	0	0	0	0	0	0
	2	0	0	0	0	2	0
	3	0	0	0	0	0	0
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
2	0	44	0	43	18	0	0
	1	0	0	0	0	0	0
	2	0	0	0	3	10	3
	3	0	0	0	0	0	2
	4	0	0	0	0	0	1
	5	0	0	0	0	0	0
3	0	5	0	18	23	1	0
	1	0	0	0	0	0	0
	2	0	0	0	1	13	5
	3	0	0	0	0	0	7
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
4	0	0	0	4	5	1	0
	1	0	0	0	0	0	0
	2	0	0	0	1	18	4
	3	0	0	0	0	0	14
	4	0	0	0	0	0	3
	5	0	0	0	0	0	1
5	0	1	0	5	2	0	0
	1	0	0	0	0	0	0
	2	0	0	0	0	5	7
	3	0	0	0	0	0	9
	4	0	0	0	0	0	5
	5	0	0	0	0	0	1

Table 1: Summary of in-sample prediction confidence. **RL** is the extinction risk status, **lower** the lowest extinction risk category and **upper** to highest extinction risk category in agreement with the model. The numbers in the table give the number of species which fall in the corresponding categories.

```
+ }
> names(x) <- c("lower", "predicted", "upper")
> xt <- xtabs(~ lower + upper + predicted, data = x)
```

The length of these intervals is distributed as follows for the species with unknown extinction risk status:

```
> table(with(x, (0:5)[upper] - (0:5)[lower]))
```

```
 0  1  2  3
44 13 92 39
```

Table 2 summarizes the number of all possible interval combinations for each extinction risk category.

upper		0	1	2	3	4	5
predicted	lower						
0	0	44	0	44	0	0	0
	1	0	0	0	0	0	0
	2	0	0	0	0	0	0
	3	0	0	0	0	0	0
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
1	0	0	0	0	0	0	0
	1	0	0	0	0	0	0
	2	0	0	0	0	0	0
	3	0	0	0	0	0	0
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
2	0	0	0	6	32	0	0
	1	0	0	0	0	0	0
	2	0	0	0	9	1	0
	3	0	0	0	0	0	0
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
3	0	0	0	0	0	0	0
	1	0	0	0	0	0	0
	2	0	0	0	1	21	5
	3	0	0	0	0	0	0
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
4	0	0	0	0	0	0	0
	1	0	0	0	0	0	0
	2	0	0	0	0	0	2
	3	0	0	0	0	0	20
	4	0	0	0	0	0	0
	5	0	0	0	0	0	0
5	0	0	0	0	0	0	0
	1	0	0	0	0	0	0
	2	0	0	0	0	0	0
	3	0	0	0	0	0	0
	4	0	0	0	0	0	3
	5	0	0	0	0	0	0

Table 2: Summary of out-of-sample prediction confidence. **predicted** is the predicted extinction risk status, **lower** the lowest extinction risk category and **upper** to highest extinction risk category in agreement with the model. The numbers in the table give the number of species which fall in the corresponding categories.

## Computational Details

The following computational environment was used to produce the above results:

```
> sessionInfo()
```

```
R version 3.1.1 (2014-07-10)
```

```
Platform: x86_64-unknown-linux-gnu (64-bit)
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

```
[1] splines    tools      stats      graphics  grDevices  utils      datasets
[8] methods    base
```

```
other attached packages:
```

```
[1] memisc_0.96-9      lattice_0.20-29    multcomp_1.3-5     TH.data_1.0-3
[5] survival_2.37-7    mvtnorm_1.0-0      ordinal_2012.09-11 Matrix_1.1-4
[9] ucminf_1.1-3       MASS_7.3-33
```

```
loaded via a namespace (and not attached):
```

```
[1] car_2.0-20          grid_3.1.1          nnet_7.3-8          numDeriv_2012.9-1
[5] sandwich_2.3-0      zoo_1.7-11
```

**Affiliation:**