

Supplementary Material S1: Description of Survey Data

For *Monadenia churchi*, the dataset was that used in Dunk et al. (2004). A stratified-random sampling design (each of the four National Forests as strata) was used to select 308 plots to be surveyed from the set of 1,101 FIA plots within these National Forests. (Model predictions were made for the 1,062 of the 1,101 plots for which environmental data was available). Most plots were sampled during spring of 1999-2000. Each FIA plot was sampled for mollusks twice, with a minimum of 10 days between surveys. Surveys were conducted only if the daytime temperature was $>5^{\circ}$ C and soil was moist as determined by touch. Surveys began with crews walking through the 1-ha plot and identifying structural features that were likely to provide mollusk habitat (e.g., downed wood), after which two types of focused searches were conducted. Area searches targeted the most likely mollusk habitat by thoroughly inspecting a feature (e.g., downed wood, rocks, ferns) and the area likely to contain mollusks within a 5 m radius surrounding that feature. One 20-person-minute time-constrained area search was conducted. Point searches were 40-minute time-constrained searches in which surveyors visited many locations within the plot, spending a maximum of 3 minute at any location before moving on. Thus, each plot was sampled twice, for 1 hour each time (Dunk et al. 2004).

For *Arborimus longicaudus*, the dataset was that used in Dunk and Hawley (2009). A stratified random sampling scheme was used to select 365 FIA plots from the 1,008 plots on National Forests within the range of *A. longicaudus*. Plots were stratified based on habitat and reserve status. Surveys were conducted between October 2001 and October 2004. At least 4 two trained observers conducted visual searches along four transects, spaced 25 m apart within each 1-ha plot, and recorded presence (at least 1 nest, occupied or not) or absence of *A. longicaudus* nests. Surveyors identified nest structures and conducted ground searches below nests for

evidence of the species. All potential nest trees, as well as five random trees, were climbed. Random trees were climbed on plots where no potential nest structures were detected from the ground, yet trees >61 cm dbh existed or the entire canopy was not visible (Dunk and Hawley 2009).

For *Martes pennanti pacifica*, the dataset was that used in Davis et al. (2007) with the addition of non-systematic surveys from coastal California (Carroll 2005) and more recent systematic surveys from northcentral California (S. Yeager, USFWS, unpubl. data). Systematic fisher surveys were conducted between 1991 and 2006. Field survey locations were arrayed in a systematic-cluster design aligned with the FIA grid. Fisher survey crews surveyed alternate FIA plots separated by approximately 11 km (Zielinski et al. 2005). Each of the sample units consisted of six enclosed carbon-blackened aluminum track-plate stations and 1-2 remotely triggered cameras. A track-plate station located at the FIA plot was surrounded by five additional track-plate stations equally spaced around the circumference of a 500 m radius circle centered on the plot. All stations were checked and rebaited every other day for eight visits over a 16-day survey. Presence-absence data for the fisher was also available from surveys conducted before the Northwest Forest Plan without reference to a systematic sampling design but with otherwise similar survey protocol (Carroll et al. 1999, Carroll 2005). This data was incorporated here to broaden geographic representation of sampled sites to private lands. In all, 993 of the 7813 FIA hexagons within the species' California range held one or more survey locations.

Supplementary Material S2: Results of comparison of alternate candidate models

Table S2a. Model selection results expressed as mean squared predictive error (MSPE) values for *Monadenia churchi* occurrence in southern Oregon and northern California. A neighborhood radius of 6 km was used in the spatial models. Sample size is 308 surveyed, 1062 total plots. Variables followed by 2 are present in the model in quadratic form. The metric used for calculating MSPE differs between species with point-level and landscape-level models so is not directly comparable between species.

<u>Model</u>	<u>Spatial</u>	<u>Non-spatial</u>
1 CDBH2, HC2, CVPRE2, SMRT2	0.0007631	0.001657
2 CDBH, HC2, CVPRE2, SMRT2	0.0007631	0.001695
3 CDBH2, HC, CVPRE2, SMRT2	0.0007704	0.001660
4 CDBH2, HC2, CVPRE, SMRT2	0.0007670	0.001657
5 CDBH2, HC2, CVPRE2, SMRT	0.0007650	0.001674
6 CDBH	0.0008330	0.001897
7 HC	0.0008091	0.001759
8 CVPRE	0.0008735	0.001820
9 SMRT	0.0008533	0.001831
10 CDBH2, HC2, CVPRE, SMRT	0.0007754	0.001675
11 CDBH, HC, CVPRE, SMRT	0.0007625	0.001720
12 CDBH2, HC, CVPRE, SMRT	0.0007781	0.001682

13 CDBH, HC2, CVPRE, SMRT	0.0007593	0.001712
14 CDBH2, HC2, CVPRE	0.0007870	0.001675
15 CDBH2, HC2, SMRT	0.0007667	0.001701

Table S2b. Model selection results expressed as mean squared predictive error (MSPE) values for *Arborimus longicaudus* occurrence in southern Oregon and northern California. A neighborhood radius of 8 km was used in the spatial models. Sample size is 365 surveyed, 1008 total plots.

Model	Spatial	Non-spatial
1 SLOPE2, BAREA2, SDDBH2, MAXDBH2	0.001028	0.001588
2 SLOPE, BAREA2, SDDBH2, MAXDBH2	0.001050	0.001589
3 SLOPE2, BAREA, SDDBH2, MAXDBH2	0.001039	0.001622
4 SLOPE2, BAREA2, SDDBH, MAXDBH2	0.001030	0.001596
5 SLOPE2, BAREA2, SDDBH2, MAXDBH	0.001024	0.001619
6 SLOPE, BAREA2, SDDBH, MAXDBH2	0.001046	0.001598
7 SLOPE, BAREA, SDDBH, MAXDBH2	0.001036	0.001638
8 SLOPE2, BAREA, SDDBH, MAXDBH	0.001039	0.001653
9 SLOPE, BAREA, SDDBH, MAXDBH	0.001053	0.001654
10 SLOPE	0.001316	0.002081
11 BAREA	0.001319	0.002105
12 SDDBH	0.001187	0.001804
13 MAXDBH	0.001234	0.001716

14 SLOPE, BAREA2, SDDBH2, MAXDBH

0.001046

0.001619

Table S2c. Model selection results expressed as mean squared predictive error (MSPE) values for *Martes pennanti pacifica* occurrence in California. A neighborhood radius of 8 km was used in the spatial models. Sample size is 993 surveyed, 7813 total cells.

<u>Model</u>	<u>Spatial</u>	<u>Non-spatial</u>
1 SIZ, GRN, TRI, SNOW2	0.1023	0.2258
2 DEN, GRN, TRI, SNOW2	0.1022	0.2227
3 DEN, GRN, TRI, SNOW	0.1023	0.2226
4 DEN, GRN, TRI	0.1025	0.2240
5 GRN, TRI, SNOW	0.1026	0.2261
6 DEN, GRN, SNOW	0.1024	0.2323
7 DEN, TRI, SNOW	0.1029	0.2292
8 DEN, TRI	0.1030	0.2361
9 DEN	0.1028	0.2448
10 TRI	0.1039	0.2627
11 DEN, TRI, WHR2	0.1024	0.2342
12 DEN, TRI, PPT	0.1029	0.2360
13 DEN, TRI, WHR1	0.1027	0.2324

Supplementary Material S3. Example WinBUGS and OpenBUGS code for ICAR and CAR models of species occurrence and abundance and R function for creating neighborhood weights used in CAR models of species occurrence.

Note on choice of priors: The priors used in these models can be characterized as weakly informative. This is due to the fact that

1) Priors for beta are expressed on the logit scale, that when expressed on the scale of the response are weakly informative. For the prior on $[\text{beta}[i] \sim \text{dnorm}(0, 0.4)]$, 0.4 represents the precision, so variance = 2.5, and SD = 1.58, resulting in a nearly flat distribution once transformed by the inverse logit.

2) The prior used in defining the distribution of spatial random effect $[\text{gamma}_z \sim \text{dbeta}(9,1)]$ results in the mass of the distribution lying close to 1. This is due to the fact that distributions that appear uninformative (e.g., uniform (0,1) are actually informative in suggesting no spatial effect in this context (Ferreira, M. A. R. and De Oliveira, V. 2007. Bayesian reference analysis for Gaussian Markov random fields. *Journal of Multivariate Analysis* 98:789-812).

#Binomial ICAR model for *Martes pennanti pacifica* (Model 2: DEN, GRN, TRI, SNOW²).
 #As in Latimer et al. (2006), N_LOC = total number of cells, N_sampled = number of
 #cells with response data (termed N_nonzeroy in Latimer et al. 2006), and ind = index of those cells.
 #PCC (percent correct classification) = 100 * (1 - (pmc/N_sampled))

```

model
{
  # likelihood
  for (i in 1 : N_sampled) {
    y[ind[i]] ~ dbin(p[ind[i]], n[ind[i]])
    residind[i]<-log(y.rep[i]+0.00000001)-log(y[ind[i]]+0.00000001)
    residind2[i]<-abs(y.rep[i]-y[ind[i]])/n[ind[i]]
    p.rep[i] <- cut(p[ind[i]])
    y.rep[i] ~ dbin(p.rep[i], n[ind[i]])
  }
  for(i in 1:N_LOC){

    logit(p[i]) <- rho[i]+xbeta[i]+mu
    xbeta[i]<-beta[1]*den[i]+beta[2]*grn[i]+beta[3]*tri[i]+beta[4]*snow[i]+beta5*snow[i]*snow[i]
  }

  # CAR prior distribution for spatial random effects:
  rho[1:N_LOC] ~ car.normal(adj[], weights[], num[], tau)

temp<-whr2[1]+prec[1]+whr1[1]+rd[1]+siz[1]

# other priors
mu ~ dflat()
for ( i in 1:4) { beta[i] ~ dnorm(0, 0.4) }
beta5 ~ dunif(-.1, .1)
vrho ~ dnorm(0, 0.2) l(0,)
tau <- 1/vrho

```

```

#Model Choice using Gelfand and Ghosh (1998) Criteria
#divisor=N_sampled(N_sampled+1)/2, here 493521
MSPEa <- inprod(residind[],residind[])/493521
pmc <- sum(residind2[])
}

```

#Bernoulli CAR point-level model for *Arborimus longicaudus* (Model 5: SLOPE², BAREA², SDDBH², MAXDBH).
N_LOC = total number of points, N_sampled = number of points with response data (termed N_nonzeroy in Latimer et al. 2006), and ind = index of those cells.

```

model
{
  # likelihood
  for (i in 1 : N_sampled) {
    y[ind[i]] ~ dbern(p[ind[i]])
    residindB[i]<-abs(y.rep[i]-y[ind[i]])
    p.rep[i] <- cut(p[ind[i]])
    y.rep[i] ~ dbern(p.rep[i])
  }
  for(i in 1:N_LOC){

    logit(p[i]) <- sig*z[i]+xbeta[i]+mu
    xbeta[i]<-beta[1]*slope[i]+beta[2]*slope[i]*slope[i]+beta[3]*barea[i]+beta[4]*barea[i]*barea[i]
    +beta[5]*sddbh[i]+beta[6]*sddbh[i]*sddbh[i]+beta[7]*maxdbh[i]
    mu.z[i]<-0
  }

  # CAR prior distribution for spatial random effects:
  z[1:N_LOC] ~ car.proper(mu.z[], C[], adj[],num[], M[], 1, gamma)

  #temp<-barea[1]+sddbh[1]+maxdbh[1]

```

```

# other priors
  mu ~ dflat()
  for ( i in 1:7) { beta[i] ~ dnorm(0, 0.4) }
  sig ~ dnorm(0,0.4)
  abs.sig <- abs(sig) # the standard deviation of the z[] process
  gammaz ~ dbeta(9,1)
  gamma.max <- max.bound(C[], adj[], num[], M[])
  gamma <- gammaz*gamma.max
  #Model Choice using Gelfand and Ghosh (1998) Criteria
  #divisor=N_sampled(N_sampled+1)/2, here 66795
  MSPEb <- inprod(residindB[],residindB[])/66795
  pmc <- sum(residindB[])
}
# R function for creating CAR weights
#'Four types of weighting schemes are available: RSW ('rs', exponential Cressie ('exp.cressie'),Cressie, and ICAR

data = read.table(file.choose(),sep=',',head=T)
data[,2:3]=data[,2:3]/1000 # Convert coordinates to km

nm = 'ANVO'

xcol=2
ycol=3
threshold=8
ndefLstRS = ndef.dist(data=data,xcol=xcol,ycol=ycol,threshold=threshold,type='rs')
ndefLstEC = ndef.dist(data=data,xcol=xcol,ycol=ycol,threshold=threshold,type='exp.cressie')
ndefLstCR = ndef.dist(data=data,xcol=xcol,ycol=ycol,threshold=threshold,type='cressie')

library(BRugs)
# DATA
bugsData(list(adj=ndefLstRS$adj, num=ndefLstRS$num, C=ndefLstRS$C, M=ndefLstRS$M),
  fileName=paste(nm,'_CAR_RowStandardized.txt'))
bugsData(list(adj=ndefLstEC$adj, num=ndefLstEC$num, C=ndefLstEC$C, M=ndefLstEC$M),

```

```
fileName=paste(nm,'_CAR_Exp_Cressie.txt')
bugsData(list(adj=ndefLstCR$adj, num=ndefLstCR$num, C=ndefLstCR$C, M=ndefLstCR$M),
  fileName=paste(nm,'_CAR_Cressie.txt'))
```

```
#####
# Weights Function
#####
```

```
ndef.dist <- function(data, xcol, ycol, threshold,
  type=c('rs','exp.cressie','cressie','icar'), phi) {
  thresh <- threshold
  distmat <- as.matrix(dist(cbind(data[,xcol], data[,ycol])))
  dist.ind <- (distmat <= thresh)*1.0
  diag(dist.ind) <- 0
  num <- as.vector(apply(dist.ind,1,sum))
  M <- 1/ifelse(num==0,1,num)
  if(type%in%c('exp.cressie','cressie'))
  {
    if(missing(phi))
    {
      if(type=='exp.cressie') phi <- thresh/3
      else phi <- 1
    }
    NC <- sqrt((1/num)%*%t(num))
    if(type=='exp.cressie') edist <- exp(-distmat/phi)*NC*dist.ind
    else edist <- (distmat^(-phi))*NC*dist.ind
    edist <- edist/max(edist[edist>0])
  }
  else if(type=='rs')
  {
```

```
  edist <- sweep(dist.ind,1,num, '/')
}
else edist <- dist.ind
n <- length(distmat[,1])
adj <- NULL
C <- NULL
for(i in 1:n) {
  neigh <- as.vector((1:n)*dist.ind[i,] )
  neigh <- neigh[neigh > 0]
  neigh.C <- as.vector(edist[i,neigh])
  adj <- as.vector(c(adj,neigh))
  C <- as.vector(c(C, neigh.C))
}
if(type %in% c('rs','cressie','exp.cressie'))
return(list(adj = adj, num = num, C=C, M=M))
else return(list(adj = adj, num = num, weights=C)) }
```