

## **Recolonisation of rabbit warrens following coordinated ripping programs in Victoria, south-eastern Australia**

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**Appendix S1.** JAGS code used for the discrete-time Weibull survival analysis with Gibbs variable selection (GVS).

```

# data step to populate the full warren x time event history matrix y[,]
# from event summaries. The time[] variable contains the last time of
# event or censoring for each warren and d[] is the censoring indicator
# (1 - event; 0 - censoring)
data {
  for(i in 1:N) {
    y[i,time[i]] <- d[i]
    for (j in 1:time[i]-1) {y[i,j] <- 0}
  }
}

Model {
# Warren level model. Discrete-time Weibull
  for (i in 1:N) {
    for (j in 1:time[i]) {y[i,j] ~ dbern(q[i,j])}
    cloglog(q[i,j]) <- a0[sites[i]] + Kappa * log(j) +
      beta[1]*NW[i] +
      beta[2]*AE[i] +
      beta[3]*IE[i] +
      beta[4]*K[i] +
      beta[5]*TH[i] +
      beta[6]*U[i]
  }
}

# Site level model
  for(j in 1:Nsite) {
    a0[j] ~ dnorm(eta[j], tau.0)
    eta[j]<- beta0 + beta[7]*RA[j] + beta[8]*MT[j] + beta[9]*MC[j]
  }

# Gibbs variable selection. gam[] is the indicator for each covariate

  for(j in 1:p) {
    gam[j] ~ dbern(0.5)
    betaG[j] ~ dnorm(0, tau.b)
    beta[j]<- gam[j]*betaG[j]
  }

  beta0 ~ dnorm(0, 0.001)
  tau.0<- 1/(sig.0*sig.0)
  sig.0 ~ dunif(0,100)
  tau.b<- 1/(sig.b*sig.b)
  sig.b ~ dunif(0,20)
  Kappa ~ dnorm(0, 0.01)

# Model indices
  for (j in 1:p){mindex[j] <- pow(2,j)}
  modl <- 1 + inprod(gam, mindex)
}

```