ADVANCED BAYESIAN MODELING

JAGS Analysis: First Attempt

 y_{ijk} = number of damage incidents to ships in category (i, j, k) t_{ijk} = total months of service represented by category (i, j, k)

i: type of ship j: era of construction k: period of operation

Loglinear Rate Model

$$y_{ijk} \mid \beta, t_{ijk} \sim \text{indep. Poisson}(\lambda_{ijk})$$
 $\lambda_{ijk} = t_{ijk} r_{ijk}$

$$\log \lambda_{ijk} = \log(t_{ijk} r_{ijk}) = \log t_{ijk} + \beta^0 + \beta^t_i + \beta^e_j + \beta^p_k$$

$$\beta^t_i \mid \sigma^2_t \sim \text{iid N}(0, \sigma^2_t) \quad \beta^e_j \mid \sigma^2_e \sim \text{iid N}(0, \sigma^2_e) \quad \beta^p_k \mid \sigma^2_p \sim \text{iid N}(0, \sigma^2_p)$$

$$\beta^0 \sim \text{N}(0, 100^2) \quad \sigma_t, \sigma_e, \sigma_p \sim \text{iid U}(0, 100)$$

In file ships1.bug:

Anticipating posterior predictive checking, we define replicated data incidentsrep.

```
beta0 ~ dnorm(0, 0.0001)
for (i in 1:max(type)) {
  beta.t[i] ~ dnorm(0, 1/sigma.t^2)
for (j in 1:max(era)) {
  beta.e[j] ~ dnorm(0, 1/sigma.e^2)
for (k in 1:max(period)) {
  beta.p[k] ~ dnorm(0, 1/sigma.p^2)
sigma.t ~ dunif(0, 100)
sigma.e ~ dunif(0, 100)
sigma.p ~ dunif(0, 100)
```

Set up data and initializations for four chains:

Recall unclass produces the integer codes of a factor.

```
> library(rjags)
. . .
> m1 <- jags.model("ships1.bug", d1, inits1, n.chains=4, n.adapt=1000)
. . .
> update(m1, 1000) # burn-in
 > x1 <- coda.samples(m1, c("beta0","sigma.t","sigma.e","sigma.p"), n.iter=2000)</pre>
```

Note: For checking convergence, we monitor only the top-level nodes.

> gelman.diag(x1, autoburnin=FALSE) Potential scale reduction factors:

	Point est.	Upper C.I.
beta0	90.57	196.05
sigma.e	1.35	1.89
sigma.p	1.02	1.06
sigma.t	1.17	1.46

Multivariate psrf

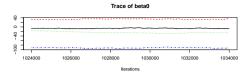
74

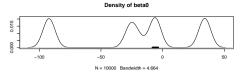
I tried repeatedly running the chains and checking for convergence, doubling the number of iterations each time.

Even after over a million iterations, there was still no convergence.

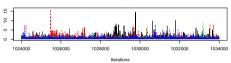
Trace plots suggest why:

> plot(x1, smooth=FALSE)

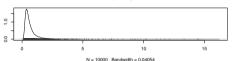




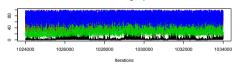




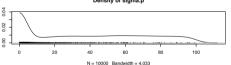




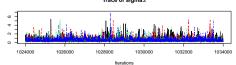
Trace of sigma.p



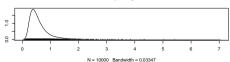
Density of sigma.p



Trace of sigma.t



Density of sigma.t



The chain shows dramatically slow mixing for β^0 and σ_p , and some chains have σ_p values near the arbitrary upper bound of 100.

Since the data has only two periods of operation (k=1,2), it is possible that σ_p^2 is poorly defined – it is the variance of only two random effects.

An improved model might treat β_1^p and β_2^p as fixed effects instead.