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**Bayesian analysis of split sex ratios:
methods and application to the ant *Aphaenogaster rudis***

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Appendices are posted at <http://evolutionary-ecology.com/data/2506.pdf>

APPENDICES

Appendix A. OpenBugs code for analysis of sex ratios.

Model 1. Model including treatment (TRE), the number of reproductive offspring (S), the number of workers (WOR), presence or absence of a queen (QU), and the site (SITE) as independent variables. No random error term is included in this model. # denotes a comment line.

```

model {for (i in 1:N)
  {
logit(p[i]) <- alpha + betaTRE*tre[i] + betaS*s[i] + betaWOR*wor[i] + betaQU*qu[i] +
betaSITE*site[i]
f[i] ~ dbin(p[i],s[i])
  }
  alpha ~ dnorm(0,0.001)
  betaS ~ dnorm(0,0.001)
  betaTRE ~ dnorm(0,0.001)
  betaWOR ~ dnorm(0,0.001)
  betaQU ~ dnorm(0,0.001)
  betaSITE ~ dnorm(0,0.001)
}

```

#initial values, Model 1. These provide the starting values for the Markov chain.

```

list( alpha = 0, betaTRE = 0, betaS = 0, betaWOR = 0, betaQU = 0, betaSITE = 0
)

```

Model 2. Model including the independent variables in Model 1 plus a random error term. # denotes a comment line.

```
#specification of the model
model {for (i in 1:N)
  {
logit(p[i]) <- nu[i]
nu[i] ~ dnorm(mu[i], tau)
mu[i] <- alpha + betaTRE*tre[i] + betaS*s[i] + betaWOR*wor[i] + betaQU*qu[i] +
betaSITE*site[i]
f[i] ~ dbin(p[i],s[i])
  }

  alpha ~ dnorm(0,0.001)
  betaS ~ dnorm(0,0.001)
  betaTRE ~ dnorm(0,0.001)
  betaWOR ~ dnorm(0,0.001)
  betaQU ~ dnorm(0,0.001)
  betaSITE ~ dnorm(0,0.001)
  tau <- pow(sigma,-2)
  sigma ~ dunif(0,10)
}

#initial values, Model 2.

list( alpha = 0, betaTRE = 0, betaS = 0, betaWOR = 0, betaQU = 0, betaSITE = 0, sigma
= 1,
```


Appendix B: Code for posterior prediction of the number of colonies with all-male or all-female broods.

```

model {for (i in 1:N){

    f[i] ~ dbin(p[i],s[i])
    logit(p[i]) <- nu[i]
    nu[i] ~ dnorm(mu[i], tau)
    mu[i] <- alpha + betaS*s[i]

    # posterior predictions
    fz[i] ~ dbin(pz[i], s[i])
    logit(pz[i]) <- nuz[i]
    nuz[i] ~ dnorm(muz[i], tau)
    muz[i] <- alpha + betaS*s[i]

    # sum the number of broods predicted to be all of one sex
    allfem[i] <- step((fz[i]/s[i] - 0.999999))
    allmale[i] <- step(0.000001 - fz[i])
    allsame[i] <- max(allfem[i],allmale[i])

    #store the number of females separately for colonies with big broods (>100)
    #the next stores 0 if the colony has a brood size <100, otherwise the predicted #
of females
    bigf[i] <- step(s[i]-100)*fz[i]
}

# mean sex ratio (weighted) for the 11 colonies with more than 100 in the brood
bigratio <- sum(bigf[])/1726

```


Appendix C. OpenBUGS code for estimating the population sex ratio under the accepted model.*

#preferred model, which includes brood size and the random error term. Parameter values for some terms of this model were used in the simulation model that follows.

```
model {for (i in 1:N){
      s[i] ~ dpois(lambda[i])
      lambda[i] ~ dgamma(shape,rScale)
      logit(p[i]) <- nu[i]
      nu[i] ~ dnorm(mu[i], tau)
      mu[i] <- alpha + betaS*s[i]
      f[i] ~ dbin(p[i],s[i])
    }
```

Simulation model used to determine the number of females, numerical sex ratio and investment sex ratio for 100,000 samples from posterior probability distributions.

```
for (j in 1:1000){
      lambdaZ[j] ~ dgamma(shape,rScale)
      sZ[j] ~ dpois(lambdaZ[j])
      epsZ[j] ~ dnorm(0,tau)
      Z[j] <- alpha + betaS*sZ[j] + epsZ[j]
      prZ[j] <- 1/(1+exp(-Z[j]))
      fZ[j] ~ dbin(prZ[j],sZ[j])
      fInv[j] <- fZ[j]*5.3007
      TotInv[j] <- fInv[j] + (sZ[j]-fZ[j])
    }

sumf <- sum(fZ[])
```


Appendix C. *continued*

#Data

```
list(f=c(28,20,47,23,46,9,41,13,9,19,51,17,15,11,12,47,15,27,0,17,9,32,39,7,13,0,8,1,45,1
8,43,0,26,7,61,0,0,9,24,31,31,26,0,12,15,18,25,53,5,0),
s=c(28,20,177,190,82,11,44,13,41,20,82,17,17,134,15,120,50,50,1,123,9,46,39,7,13,46,5
9,1,45,164,126,51,167,26,61,19,1,23,136,31,49,43,69,65,15,164,25,225,6,27), N=49))
```

* Posterior predictions for other models listed in Table 4 were carried out with similar coding. The logistic regression model and the associated sampling model that yielded values of $Z[j]$ were modified according to the model being used. To provide values for the simulation procedure the terms Queen presence, site, and treatment were described as binomial distributions with a $p = 0.5$ and $n = 1$. The “number-of-workers” values were generated from a random distribution with a mean = 622 and tau = .0038, both of which were determined from the data.