

Stat 341 – Homework 06

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```
data(foxes)
foxes <- na.omit(foxes)
glimpse(foxes)
```

```
## Rows: 116
## Columns: 5
## $ group    <int> 1, 1, 2, 2, 3, 3, 4, 4, 5, 5, 5, 6, 6, 6, 7, 7, 7, 8, 8, 8, ~
## $ avgfood  <dbl> 0.37, 0.37, 0.53, 0.53, 0.49, 0.49, 0.45, 0.45, 0.74, 0.74, ~
## $ groupsize <int> 2, 2, 2, 2, 2, 2, 2, 2, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, ~
## $ area     <dbl> 1.09, 1.09, 2.05, 2.05, 2.12, 2.12, 1.29, 1.29, 3.78, 3.78, ~
## $ weight   <dbl> 5.02, 2.84, 5.33, 6.07, 5.85, 3.25, 4.53, 4.09, 6.13, 5.59, ~
```

Interested in the affect of avgfood, groupsize on weight, avgfood on groupsize, and area on avgfood.

```
foxes <- foxes |>
  mutate(avgfood_scaled = as.numeric(scale(avgfood))) |>
  mutate(groupsize_scaled = as.numeric(scale(groupsize))) |>
  mutate(area_scaled = as.numeric(scale(area))) |>
  mutate(weight_scaled = as.numeric(scale(weight)))
```

```
model_descrip <- alist(
  # note variable name has to match actual data variable name
  weight_scaled ~ dnorm(mu, sigma),
  mu ~ beta0 + beta1 * avgfood_scaled + beta2 * groupsize_scaled + beta3 * area_scaled,
  beta0 ~ dnorm(mean = 0, sd = 1),
  beta1 ~ dnorm(mean = 0, sd = 1),
  beta2 ~ dnorm(mean = 0, sd = 1),
  beta3 ~ dnorm(mean = 0, sd = 1),
  sigma ~ dnorm(mean = 0, sd = 1)
)
```

```
model_descrip2 <- alist(
  # note variable name has to match actual data variable name
  weight_scaled ~ dnorm(mu, sigma),
  mu ~ beta0 + beta1 * avgfood_scaled + beta2 * groupsize_scaled,
  beta0 ~ dnorm(mean = 0, sd = 1),
  beta1 ~ dnorm(mean = 0, sd = 1),
  beta2 ~ dnorm(mean = 0, sd = 1),
  sigma ~ dnorm(mean = 0, sd = 1)
)
```

```
model_descrip3 <- alist(
  # note variable name has to match actual data variable name
  weight_scaled ~ dnorm(mu, sigma),
```

```

mu ~ beta0 + beta1 * avgfood_scaled,
beta0 ~ dnorm(mean = 0, sd = 1),
beta1 ~ dnorm(mean = 0, sd = 1),
sigma ~ dnorm(mean = 0, sd = 1)
)

```

```

quap_fox_model <- quap(flist = model_descrip,
                      data = foxes)

```

```

quap_fox_model2 <- quap(flist = model_descrip2,
                      data = foxes)

```

```

quap_fox_model3 <- quap(flist = model_descrip3,
                      data = foxes)

```

```

compare(quap_fox_model, quap_fox_model2 ,quap_fox_model3, func=WAIC )

```

```

##              WAIC      SE      dWAIC      dSE      pWAIC      weight
## quap_fox_model  323.6525 16.76479  0.0000000      NA  5.330908  0.532471281
## quap_fox_model2 323.9269 16.61470  0.2743365  3.879595  4.071367  0.464220985
## quap_fox_model3 333.8150 13.76236 10.1625307  8.269259  2.589541  0.003307735

```

The WAIC are also pretty close to one another but the initial normal model with 3 different parameters has the lowest score and thus has the lowest penalty in results. I had a third model with a WAIC score of 333.9 but I wasn't able to knit the file so I am still trouble shooting. It may be it this new knit file.