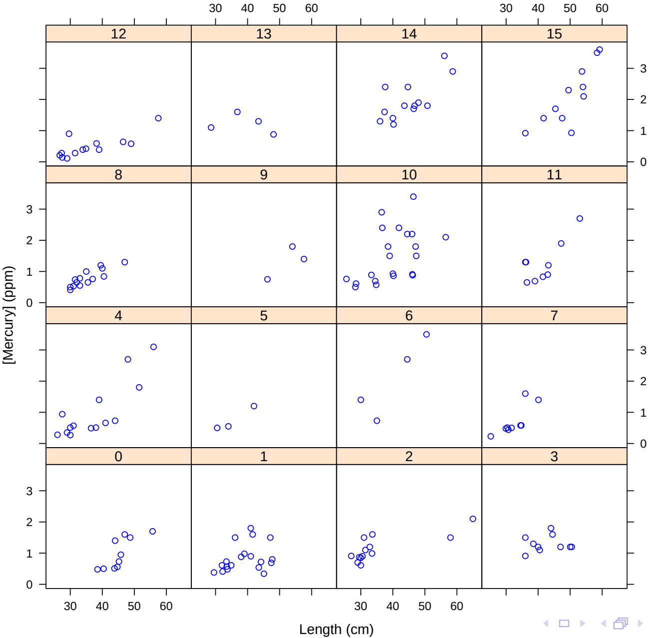
Hierarchical Regression Models

Hoff Chapter 11

November 12, 2015

NC Mercury in Fish data



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Use ANOVA to compare the 3 models

Fitting Models with Categorical Predictors in R

```
fish$S = factor(fish$STATION) # convert to categorical
fish.com = lm(log(MERCURY) ~ 1 + log(LENGTH), data=fish)
fish.par = lm(log(MERCURY) ~ S + log(LENGTH), data=fish)
fish.dif = lm(log(MERCURY) ~ S*log(LENGTH), data=fish)

anova(fish.com, fish.par, fish.dif)
Analysis of Variance Table

Model 1: log(MERCURY) ~ 1 + log(LENGTH)
Model 2: log(MERCURY) ~ S + log(LENGTH)
Model 3: log(MERCURY) ~ S * log(LENGTH)
  Res.Df    RSS  Df Sum of Sq      F    Pr(>F)
1    169 41.621
2    154 23.974  15    17.648 8.1515 5.051e-13 ***
3    139 20.062  15     3.912 1.8070   0.03918 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 '
```

Model Comparison: ANOVA Extra Sum-of-Squares F test

Under all models the MSE = RSS/df under model (3) is an estimate of σ^2. If one of the simpler models is true (say model (2)), then we expect that the difference in RSS between model (2) and (3) will be small relative to the extra degrees of freedom.

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- reject model (2) in favor of (3) at the $\alpha = 0.05$ level, but not at the 0.01 level
- reject model (1) at any $\alpha > 5.05 \times 10^{-13}$

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How can we use these models to predict MERCURY levels for other locations? View STATION as a random sample of locations

and build a hierarchical model

JAGS/BUGS Model - Non-Centered

```
for (n in 1:N){
 muj[n] <- alpha[station[n]]+beta[station[n]]*X[n]
 Y[n] ~ dnorm(muj[n], phi)
}

for (j in 1:J) {
  alpha[j] ~ dnorm(alpha.mu, alpha.phi)
  beta[j] ~ dnorm(beta.mu,  beta.phi)
}
phi ~ dgamma(.001, .001)
alpha.mu ~ dnorm(0.0, 1.0E-6)
alpha.sigma ~ dunif(0, 100)
alpha.phi <-1/(alpha.sigma*alpha.sigma)
beta.mu ~ dnorm(0.0, 1.0E-6)
beta.phi <- pow(beta.sigma, -2)
beta.sigma ~ dunif(0, 100)
```

JAGS/BUGS Model - Centered

```
for (n in 1:N){
 muj[n] <- alpha[station[n]]+beta[station[n]]*(X[n]-xbar)
 Y[n] ~ dnorm(muj[n], phi)
}

for (j in 1:J) {
  alpha[j] ~ dnorm(alpha.mu, alpha.phi)
  beta[j] ~ dnorm(beta.mu,  beta.phi)
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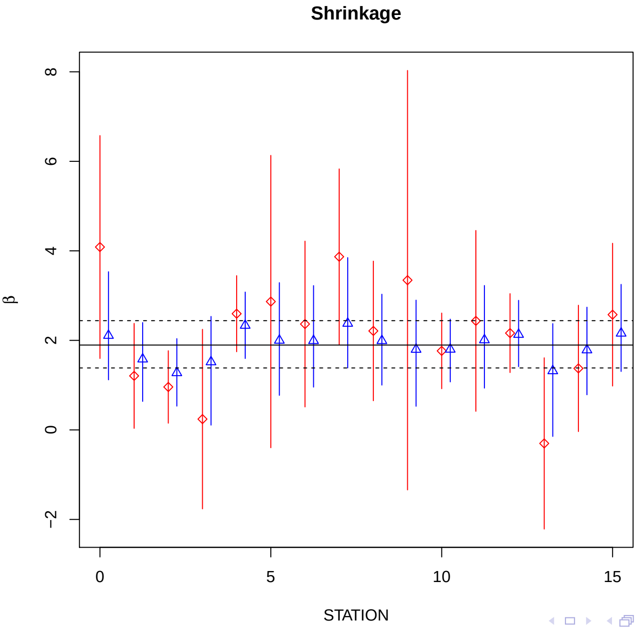
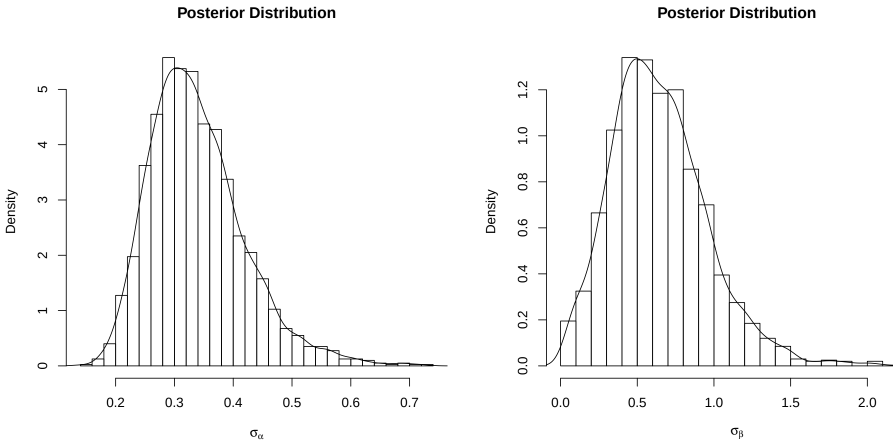
Shrinkage

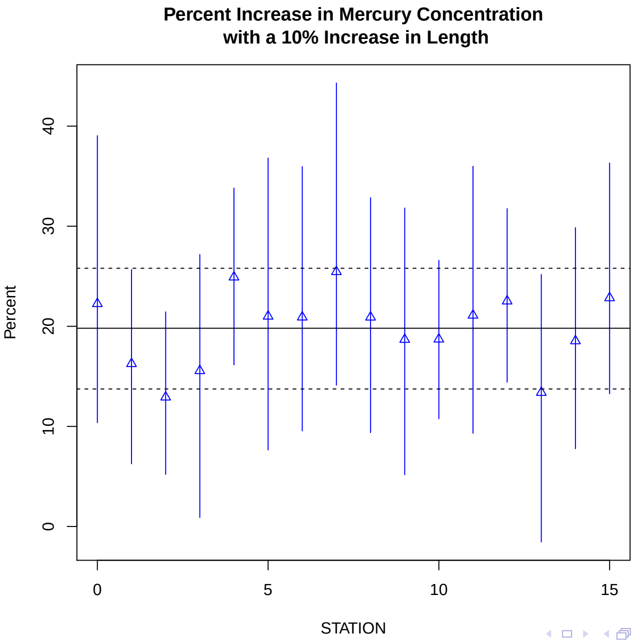


Variance Components



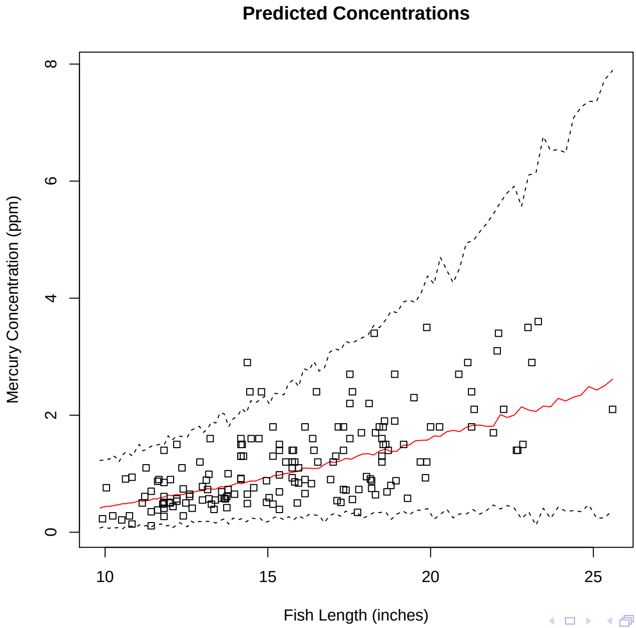
Interpretation of Coefficients

Percent Increase

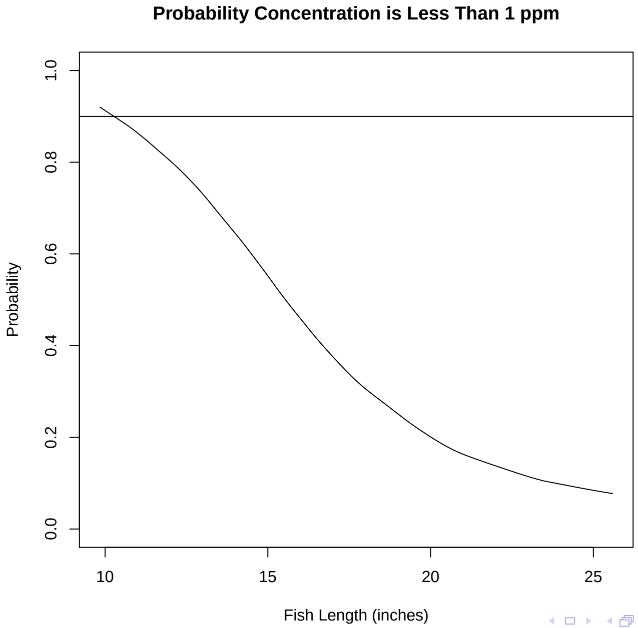


Predicting at a New Location

Predictions for a Random Location



Probability Concentration Does not Exceed 1ppm



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