

JAGS Examples from Kery's book Introduction to WinBugs

Code in Kery's book can be downloaded from here:

[http://www.mbr/-
pwr.usgs.gov/software/kerybook/R/_WB/_code.txt](http://www.mbr/-pwr.usgs.gov/software/kerybook/R/_WB/_code.txt)

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Most of the code will run, with a few modifications, using JAGS. In particular, we have to add `BUGSoutput` when referencing any of the output from JAGS.

- In Kery's book: `plot (out$mean$predicted, out$mean$residual)`
- We need to use:
`plot (out$BUGSoutput$mean$predicted, out$BUGSoutput$mean$residual).`

Trends in Wallcreeper Counts



- Proportion of sample quadrats where the bird is observed
- Assume deviations from a linear trend are normally distributed

Ch 8: Linear regression

Prior and likelihood is very similar to what we have already seen.

```
linreg<-function() {  
  
  # Priors  
  alpha ~ dnorm(0,0.001)  
  beta ~ dnorm(0,0.001)  
  sigma ~ dunif(0, 100)  
  
  # Likelihood  
  for (i in 1:n) {  
    y[i] ~ dnorm(mu[i], tau)  
    mu[i] <- alpha + beta*x[i]  
  }  
}
```

Derived quantities

```
# Derived quantities  
tau <- 1/ (sigma * sigma)  
p.decline <- 1-step(beta)      # Probability of decline
```

Step() = 1 if what is in the “()” is > 0 (and 0 otherwise). So, this calculates the probability that $\beta < 0$.

Residuals

```
for (i in 1:n) {  
  residual[i] <- y[i]-mu[i]      # Residuals for observed data  
  predicted[i] <- mu[i]         # Predicted values  
  sq[i] <- pow(residual[i], 2)  # Squared residuals for observed data  
}
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Residual: $r[i] = y_i - (\alpha + \beta * x[i])$.

We generate n_{MCMC} values of α and β , so n_{MCMC} values of $r[i]$!

Bayesian p-value

- Generate new (“ideal”) data: $y_{\text{new}}[i] \sim \text{dnorm}(\mu[i], \tau)$
 - Using the assumed model
 - Using parameters drawn from the posterior distribution (accounts for parameter uncertainty)

Bayesian p-value

- Generate new (“ideal”) data: $y_{\text{new}}[i] \sim \text{dnorm}(\mu[i], \tau)$
 - Using the assumed model
 - Using parameters drawn from the posterior distribution (accounts for parameter uncertainty)
- Calculate measure of “fit” (or lack of fit) for the observed data and simulated data
 - `fit <- sum(sq[])` sum of squared residuals for the observed data
 - `fit.new <- sum(sq.new[])` (same for simulated data)

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- test = 1 if $SS(\text{simulated data}) > SS(\text{observed data})$, i.e., the model fits the observed data better than the simulated data.
- `bpvalue <- mean(test)` (how often does the model fit observed data better than the simulated data)
- Want bpvalue to be large (can't conclude there is a lack of fit).

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We have $n_{MCMC} = \text{n.chains}(\text{n.iter} - \text{n.burn})$ draws from the posterior distribution of (α, β, σ) .

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For each value of $X = x$ (loop), he generates n_{MCMC} predictions.

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for(i in 1:length(x)){  
  predictions[i,] <- out$BUGSoutput$sims.list$alpha +  
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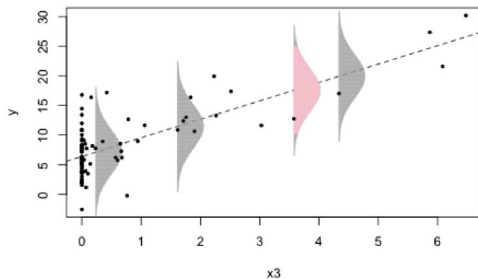
- Gives us n_{MCMC} draws of $E[Y|X = x] = \alpha + x\beta$. What does this tell us?
- This is the posterior distribution of the fitted line (tells us about the line and its uncertainty)

Prediction Intervals

What about prediction intervals? Intervals that are likely to contain a new observation, if collected?

Prediction Intervals

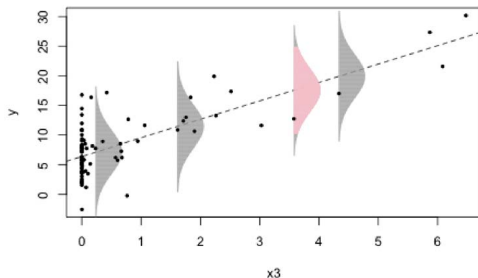
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- Requires we also consider the variability about the line
- This variability is described by the errors $\sim N(0, \sigma^2)$.

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- gives us the posterior of $Y_{new}|X$ (rather than $E[Y|X]$)
- Try to modify Kery's code to do this! Hint: to figure out n_{MCMC} , inspect the dimension of `out$BUGSoutput$sims.list$alpha`

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We could have just added `y.new` to our “parameters.to.save” vector and then summarized the quantiles of the jags output to get the prediction intervals.

Exercise 2: Prediction Intervals (frequentist)

For linear models fit in R, we can generate confidence and prediction intervals using the `predict` function, and more specifically, `predict.lm`

- Look up the help file for `predict.lm` and examples at bottom
- Calculate these intervals for the fitted linear model.
- Plot these intervals using the `lines` function along with Bayesian prediction intervals

Chapter 11: ANCOVA model (importance of priors and scaling)

Relationship between Body Mass and Body Length



- Asp viper's from 3 populations (Pyrenees, Massif Central, Jura Mountains) in Switzerland
- Interested in population-specific differences in the body-mass relationship

Linear regression model

$$y_i = \alpha_0 + \beta_1 x_i + \epsilon_i$$

- y_i = body mass of individual i
- x_i = body length of snake i

How do we capture “population-specific differences in the body-mass relationship”?

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How do we capture “population-specific differences in the body-mass relationship”?

Include interactions!

Example CH 11.2

Effects parameterization:

$$y_i = \alpha_{pyr} + \beta_1 I_{MC,i} + \beta_2 I_{Jura,i} + \beta_3 x_i + \beta_4 x_i I_{MC,i} + \beta_5 x_i I_{Jur,i} + \epsilon_i$$

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Identify the parameters used in the simulation:

- Effects model (α and $\beta_1 - \beta_5$)
- Means model (α and β) for each population.

Parameters

Effects parameterization

- $\alpha = -250$
- $\beta_1 = 150$
- $\beta_2 = 200$
- $\beta_3 = 6$
- $\beta_4 = -3$
- $\beta_5 = -4$

Means parameterization

- Pyrenees: $\alpha = -250, \beta = 6$
- Massif: $\alpha = -100, \beta = 3$
- Jura: $\alpha = -50, \beta = 2$

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```
curve(dnorm(x, 0, sqrt(1/0.001)), from=-250, to=250)
```

