Wulfing_HW05
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Learn by breaking a model. Provide three errors from a JAGS model (just copy and paste them) and then briefly explain why each one occurred and/or how you fixed it.

Error 1:

```
Error in jags.model(model.file, data = data, inits = init.values, n.chains =
n.chains,  :
  RUNTIME ERROR:
Compilation error on line 16.
Index out of range taking subset of  alpha
```

This one I got because I was categorizing my parameters like this:

```
for(i in 1:nrow(bonus_hares)){
        if(bonus_hares$landuse[i] == "arable"){
                bonus_hares$x[i] <- 0
        }
        else{ # if(bonus_hares$landuse[i] == "grass")
                bonus_hares$x[i] <- 1
        }
}
```

Where I used 1's and 0's to distinguish the two categories. However, we have to change alpha using the inputs of x as the index, and R starts at 1 instead of 0 when indexing. My original solution was to go through the jags code and add (x[i] + 1) to all of the times that x was used for double bracketing (which actually worked, shockingly) but then you mentioned in class that if you just categorize x starting at 1 instead of zero like this:

```
for(i in 1:nrow(bonus_hares)){
        if(bonus_hares$landuse[i] == "arable"){
                bonus_hares$x[i] <- 1
        }
        else{ # if(bonus_hares$landuse[i] == "grass")
                bonus_hares$x[i] <- 2
        }
}
```

That's a way better solution. Which is also why this is my new favorite error because I get it all the time now

Error 2:

```
Error in jags.model(model.file, data = data, inits = init.values, n.chains =
n.chains,  :
  RUNTIME ERROR:
Unable to resolve the following parameters:
elevation[562] (line 16)
elevation[563] (line 16)
```

That error went on for a while. Basically Jags just doesn't like having NA's in your data. I removed them with this:

```
hares <- hares_data %>% drop_na(elevation) %>% drop_na(mean.density)
```

And that way jags is able to run through your data just fine

Error 3:

```
cat("model {

     # Priors
     beta0 ~ dnorm(0,0.01)
     beta1 ~ dnorm(0,0.01)
     precision <- 1 / variance
     variance <- sigma^2
     sigma ~ dunif(0,15)

     # Likelihood
     for(i in 1:nobs){
     mean.density[i] ~ dnorm(mu[i], precision)

     mu[i] <- beta0 + beta1 * elevation[i]

     }

     } # end of the model.
     ",fill=TRUE)
sink()

# Bundle data
win.data <- list(y = y,
                 x = x,
                 n = n)
Error: object 'y' not found
```

Or sometimes I do this:

```
win.data <- list(mean.density = hares$mean.density,
                 nobs = nrow(hares))
Error in jags.model(model.file, data = data, inits = init.values, n.chains =
n.chains,  :
  RUNTIME ERROR:
Compilation error on line 16.
Unknown variable elevation
Either supply values for this variable with the data
or define it  on the left hand side of a relation.
```

These are kind of dumb ones but basically I get them from forgetting to update the bundle data line when I'm transferring your code to my assignment. It just yells at you because you define stuff in the jags code which you don't read in from data in the R part so jags tries to make a model with nothing. For this model, this would be the correct code:

```
win.data <- list(mean.density = hares$mean.density,
                 elevation = hares$elevation,
                 nobs = nrow(hares))
```