

Homework 7

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For this assignment, your task is simple: The researchers want to know which seed type, cultivar, and/or seed type by cultivar has the best yield.

Use JAGS or Stan to perform this analysis. You will be graded on your ability to perform a complete analysis.

This is a classic split plot, with a potential interaction affect. Since we are interested in whether seed type, cultivar, or a combination affects yield, I assumed that any affects introduced by differences between fields were not interesting.

```
model1 <- "  
model {  
  for (i in 1:24) {  
    yield[i] ~ dnorm(mu[i], 1/s2error)  
    mu[i] <- alpha0 + field[i] + seed[type[i]] + food[cultivar[i]] + interax[type[i], cultivar[i]]  
  }  
  alpha0 ~ dnorm(0, 0.000001)  
  for (i in 1:4) {  
    field[i] ~ dnorm(0, 0.01)  
  }  
  
  for (i in 1:2) {  
    seed[i] ~ dnorm(30, 1/s2seed)  
  }  
  
  for (i in 1:3) {  
    food[i] ~ dnorm(0, 1/s2cult)  
  }  
  
  for (i in 1:2) {  
    for (j in 1:3) {  
      interax[i,j] ~ dnorm(0, 0.001)  
    }  
  }  
  s2error ~ dgamma(1.1, 0.05)  
  s2cult ~ dgamma(1.1, 0.05)  
  s2seed ~ dgamma(1.1, 0.05)  
}  
"  
  
writeLines(model1, 'hw7model.txt')  
  
field <- cult$field  
type <- cult$type
```

```

cultivar <- cult$cultivar
yield <- cult$yield

data.jags <- c('field', 'type', 'cultivar', 'yield')
parms <- c('seed', 'food', 'interax', 's2error', 's2cult', 's2seed', 'alpha0')

cult.sim <- jags(model.file = 'hw7model.txt', data = data.jags, parameters.to.save = parms,
               n.iter = 5000, n.burnin = 1000, n.chains = 4, n.thin = 1, inits = NULL)

```

```
## module glm loaded
```

```

## Compiling model graph
##   Resolving undeclared variables
##   Allocating nodes
## Graph information:
##   Observed stochastic nodes: 28
##   Unobserved stochastic nodes: 15
##   Total graph size: 146
##
## Initializing model

```

```
cult.sim
```

```

## Inference for Bugs model at "hw7model.txt", fit using jags,
## 4 chains, each with 5000 iterations (first 1000 discarded)
## n.sims = 16000 iterations saved
##
##      mu.vect sd.vect   2.5%   25%   50%   75%  97.5%  Rhat
## alpha0      -2.108  13.533 -28.677 -11.104 -2.097   7.018 24.464 1.001
## food[1]      -0.100   4.532  -9.770  -2.417 -0.061   2.260  9.110 1.001
## food[2]      -0.100   4.486  -9.763  -2.422 -0.026   2.273  9.168 1.001
## food[3]       0.093   4.541  -9.458  -2.222  0.034   2.434  9.872 1.001
## interax[1,1] -2.390  13.799 -30.066 -11.460 -2.378   6.809 24.276 1.001
## interax[2,1] -2.252  13.785 -29.086 -11.506 -2.257   6.958 24.744 1.001
## interax[1,2] -1.025  13.737 -28.409 -10.069 -0.964   8.244 25.562 1.001
## interax[2,2]  0.350  13.684 -26.361  -8.983  0.321   9.646 27.096 1.001
## interax[1,3]  2.681  13.792 -24.822  -6.505  2.728  11.990 29.147 1.001
## interax[2,3]  3.025  13.739 -23.993  -6.167  2.933  12.277 29.906 1.001
## s2cult       21.551  20.066   0.815   6.909 15.620 30.005 75.550 1.003
## s2error       8.375   3.051   4.261   6.230  7.743   9.848 16.077 1.001
## s2seed       21.241  20.728   0.670   6.551 15.083 29.276 75.590 1.003
## seed[1]      29.992   4.470  20.666  27.716 29.997 32.274 39.526 1.001
## seed[2]      29.997   4.518  20.503  27.764 29.996 32.232 39.695 1.001
## deviance    142.214   4.577 135.660 138.822 141.421 144.744 153.061 1.001
##
##      n.eff
## alpha0    16000
## food[1]    16000
## food[2]    16000
## food[3]    16000
## interax[1,1] 16000
## interax[2,1] 16000
## interax[1,2] 16000
## interax[2,2] 16000

```

```
## interax[1,3] 16000
## interax[2,3] 16000
## s2cult      1300
## s2error     6200
## s2seed      1100
## seed[1]     15000
## seed[2]     16000
## deviance    6100
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 10.5 and DIC = 152.7
## DIC is an estimate of expected predictive error (lower deviance is better).
```

It appears there is hardly a difference between seed one and two.

```
model2 <- "
model {
  for (i in 1:24) {
    yield[i] ~ dnorm(mu[i], 1/s2error)
    mu[i] <- alpha0 + field[i] + seed[type[i]] + food[cultivar[i]] + interax[type[i], cultivar[i]]
  }
  alpha0 ~ dnorm(30, 0.0001)
  for (i in 1:4) {
    field[i] ~ dnorm(0, 0.01)
  }

  for (i in 1:2) {
    seed[i] ~ dnorm(0, 1/s2seed)
  }

  for (i in 1:3) {
    food[i] ~ dnorm(0, 1/s2cult)
  }

  for (i in 1:2) {
    for (j in 1:3) {
      interax[i,j] ~ dnorm(0, 0.01)
    }
  }
  s2error ~ dgamma(1.1, 0.05)
  s2cult ~ dgamma(1.1, 0.05)
  s2seed ~ dgamma(1.1, 0.05)
}
"

writeLines(model2, 'hw7model2.txt')

cult.sim <- jags(model.file = 'hw7model2.txt', data = data.jags, parameters.to.save = parms,
  n.iter = 5000, n.burnin = 1000, n.chains = 4, n.thin = 1, inits = NULL)
```

```
## Compiling model graph
##   Resolving undeclared variables
##   Allocating nodes
## Graph information:
##   Observed stochastic nodes: 28
##   Unobserved stochastic nodes: 15
##   Total graph size: 145
##
## Initializing model
```

```
cult.sim
```

```
## Inference for Bugs model at "hw7model2.txt", fit using jags,
## 4 chains, each with 5000 iterations (first 1000 discarded)
## n.sims = 16000 iterations saved
##
```

	mu.vect	sd.vect	2.5%	25%	50%	75%	97.5%	Rhat
## alpha0	27.974	5.689	16.737	24.268	27.966	31.731	39.229	1.001
## food[1]	-0.599	3.729	-8.817	-2.571	-0.396	1.452	6.925	1.001
## food[2]	-0.135	3.722	-8.026	-2.116	-0.073	1.833	7.563	1.001
## food[3]	0.612	3.758	-6.983	-1.417	0.392	2.544	9.018	1.001
## interax[1,1]	-1.857	5.556	-12.677	-5.576	-1.914	1.841	9.240	1.001
## interax[2,1]	-1.919	5.588	-12.838	-5.731	-1.912	1.826	9.082	1.001
## interax[1,2]	-1.023	5.508	-11.741	-4.706	-1.066	2.601	10.002	1.001
## interax[2,2]	0.187	5.542	-10.802	-3.552	0.212	3.857	11.047	1.001
## interax[1,3]	2.070	5.525	-8.761	-1.617	2.116	5.704	13.070	1.001
## interax[2,3]	2.290	5.555	-8.640	-1.398	2.283	5.988	13.244	1.001
## s2cult	18.255	17.863	0.671	5.656	12.819	25.152	65.474	1.001
## s2error	8.445	3.217	4.244	6.226	7.778	9.897	16.618	1.001
## s2seed	19.425	19.107	0.632	5.975	13.518	26.791	70.587	1.003
## seed[1]	-0.057	3.875	-8.231	-2.057	-0.048	1.949	8.146	1.001
## seed[2]	0.107	3.820	-7.793	-1.933	0.029	2.149	8.159	1.001
## deviance	142.189	4.571	135.627	138.804	141.402	144.774	153.084	1.001

```
##
```

	n.eff
## alpha0	9600
## food[1]	16000
## food[2]	16000
## food[3]	13000
## interax[1,1]	16000
## interax[2,1]	16000
## interax[1,2]	7000
## interax[2,2]	12000
## interax[1,3]	7300
## interax[2,3]	8000
## s2cult	6000
## s2error	16000
## s2seed	1000
## seed[1]	7300
## seed[2]	6000
## deviance	13000

```
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
```

```
## pD = 10.4 and DIC = 152.6
```

```
## DIC is an estimate of expected predictive error (lower deviance is better).
```

Just based on what we are seeing so far, I would say that the best bet is to use seed type 2 with cultivation
3. So, type b, with liv as the food type.