

HW7_anova and INLA

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Purpose:

The purpose of this markdown document is to work through Homework 7 in Dr. Babcock's Bayesian Statistics Course at the University of Miami. Homework 7 deals with ANOVA and INLA

General Start to Code

```
rm(list = ls())

#####github#####
#note, only needed after 90 days from 1/16/2024

# usethis::create_github_token()
# gitcreds::gitcreds_set()

#####check for r updates#####
#note, updateing may take some time so plan accordingly

#require(installr)

#check.for.updates.R()

#updateR() #only if needed

#####check for package updates#####
#note, updateing may take some time so plan accordingly

#old.packages()

# update.packages() #make the decision to the update the packages
```

Load packages

```
library(INLAutils)
library(INLA)
library(tidyverse)
library(R2jags)
```

```
library(rstan)
library(ggmcmc)
library(purrr)
library(magrittr)
library(here)
library(loo)
library(DHARMA)
theme_set(theme_bw(base_size=15))
options(mc.cores = parallel::detectCores())
rstan_options(auto_write = TRUE)
```

Data

The moth data will be used in the problem 1, and it contains three variables (Moth, Location, Bait). Moth is the number of spruce moths caught in a trap in 48 hours, Location is the location of the trap in the trees (Ground, Lower, Middle, Top), and Bait is the bait used (Chemical, Scent, Sugar).

The football data is the weight in lbs of randomly selected football players from randomly selected teams (coded as 1 to 5).

###problem 1 data

```
moth.data <- read_csv(here("data","moth.csv")) |>
  mutate(LocationNum = as.numeric(as.factor(Location)),
         BaitNum = as.numeric(as.factor(Bait)))
```

```
## Rows: 60 Columns: 3
## -- Column specification -----
## Delimiter: ","
## chr (2): Location, Bait
## dbl (1): Moths
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
head(moth.data)
```

###problem 2 data

```
football.data <- read_csv(here("data","football.csv"))
```

```
## Rows: 85 Columns: 2
## -- Column specification -----
## Delimiter: ","
## dbl (2): Team, Weight
##
## i Use 'spec()' to retrieve the full column specification for this data.
## i Specify the column types or set 'show_col_types = FALSE' to quiet this message.
```

```
head(football.data)
```

Problem 1: Fixed effects 2-way ANOVA JAGS

A) Fit an ANOVA model in JAGS to predict number of moths caught (y) as a function of the categorical (x) variables LocationNum and BaitNum. Do not include an interaction. Assume the error is normally distributed and all the factors are fixed effects. Use Chemical and Ground as the reference levels and estimate the differences from that reference level for the other levels of each factor. Use uninformative priors. Give the summary statistics. Which coefficients appear to be different from zero based on their credible intervals? table of contrasts

	BAIT Period		
	1	2	3
Location 1	-ref	-ref+Bait[2]	-ref+Bait[3]
Location 2	-ref+loc[2]	-ref+loc[2]+Bait[2]	-ref+Loc[2]+Bait[3]
Location 3	-ref+loc[3]	-ref+loc[3]+Bait[2]	-ref+Loc[3]+Bait[3]
Location 4	-ref+loc[4]	-ref+loc[4]+Bait[2]	-ref+Loc[4]+Bait[3]

set up and run JAGS model

```
write("model
{ # two-way ANOVA with interaction term, using reference classes

  #set up contrast priors

  base ~ dnorm(0, 1.0E-6)
  a[1] <- 0 #reference location
  a[2] ~ dnorm(0.0, 1.0E-6)
  a[3] ~ dnorm(0.0, 1.0E-6)
  a[4] ~ dnorm(0.0, 1.0E-6)
  b[1] <- 0 #reference bait
  b[2] ~ dnorm(0.0, 1.0E-6)
  b[3] ~ dnorm(0.0, 1.0E-6)

  tau ~ dgamma(0.001, 0.001) # uninformative precision

  for (i in 1:N) # for each of the samples
  {
    ymean[i] <- base + a[X1[i]] + b[X2[i]]
    Y[i] ~ dnorm(ymean[i], tau)
    LL[i] <- -0.5*log(2*3.14159)+0.5*log(tau)-0.5*tau*(Y[i]-ymean[i])*(Y[i]-ymean[i])
  }
}
",file=here("JAGS_mods","HW7-1A-ANOVA-2way-noint.txt"))

moth.list <- list(Y = moth.data$Moths,
                  X1 = moth.data$LocationNum,
                  X2 = moth.data$BaitNum,
                  N = length(moth.data$Moths))

jags.anova.2way.noint <- jags(data = moth.list,
  model.file=here("JAGS_mods","HW7-1A-ANOVA-2way-noint.txt"),
  parameters.to.save=c("base", "a", "b", "tau", "LL"), n.chains=2, n.iter=110000, n.burnin=10000, n.thin=10)

## Compiling model graph
##   Resolving undeclared variables
##   Allocating nodes
```

```
## Graph information:
##   Observed stochastic nodes: 60
##   Unobserved stochastic nodes: 7
##   Total graph size: 393
##
## Initializing model
##
##   |
```

output summary

```
round(jags.anova.2way.noint$BUGSoutput$summary,2)
```

##		mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
##	LL[1]	-3.38	0.28	-4.06	-3.54	-3.34	-3.18	-2.97	1	20000
##	LL[2]	-3.06	0.15	-3.42	-3.14	-3.04	-2.96	-2.82	1	20000
##	LL[3]	-3.97	0.45	-5.01	-4.24	-3.92	-3.64	-3.26	1	20000
##	LL[4]	-3.36	0.28	-4.02	-3.52	-3.32	-3.16	-2.96	1	20000
##	LL[5]	-3.62	0.36	-4.45	-3.82	-3.57	-3.36	-3.08	1	20000
##	LL[6]	-3.86	0.42	-4.84	-4.11	-3.80	-3.55	-3.20	1	8800
##	LL[7]	-5.50	0.80	-7.25	-6.00	-5.43	-4.92	-4.15	1	20000
##	LL[8]	-4.45	0.57	-5.73	-4.79	-4.38	-4.04	-3.53	1	8200
##	LL[9]	-3.15	0.19	-3.62	-3.25	-3.12	-3.02	-2.87	1	15000
##	LL[10]	-3.57	0.34	-4.35	-3.76	-3.52	-3.32	-3.05	1	16000
##	LL[11]	-4.37	0.55	-5.60	-4.71	-4.31	-3.97	-3.47	1	3900
##	LL[12]	-3.94	0.45	-4.98	-4.20	-3.88	-3.61	-3.24	1	8300
##	LL[13]	-3.38	0.28	-4.05	-3.55	-3.34	-3.18	-2.96	1	4200
##	LL[14]	-3.01	0.12	-3.28	-3.09	-3.00	-2.93	-2.81	1	20000
##	LL[15]	-3.06	0.15	-3.42	-3.14	-3.04	-2.96	-2.83	1	15000
##	LL[16]	-3.01	0.12	-3.27	-3.08	-3.00	-2.93	-2.81	1	20000
##	LL[17]	-3.24	0.23	-3.79	-3.36	-3.20	-3.07	-2.90	1	6700
##	LL[18]	-3.30	0.26	-3.92	-3.44	-3.26	-3.12	-2.93	1	4000
##	LL[19]	-3.04	0.14	-3.36	-3.11	-3.02	-2.95	-2.81	1	11000
##	LL[20]	-3.10	0.17	-3.50	-3.18	-3.07	-2.98	-2.84	1	9400
##	LL[21]	-3.96	0.44	-4.97	-4.23	-3.90	-3.63	-3.26	1	20000
##	LL[22]	-3.06	0.15	-3.43	-3.14	-3.04	-2.96	-2.82	1	20000
##	LL[23]	-3.63	0.36	-4.46	-3.84	-3.58	-3.37	-3.09	1	20000
##	LL[24]	-3.11	0.18	-3.55	-3.20	-3.09	-2.99	-2.85	1	20000
##	LL[25]	-3.49	0.32	-4.23	-3.67	-3.44	-3.26	-3.02	1	17000
##	LL[26]	-3.14	0.19	-3.60	-3.24	-3.11	-3.01	-2.86	1	20000
##	LL[27]	-3.31	0.26	-3.93	-3.45	-3.26	-3.12	-2.93	1	20000
##	LL[28]	-4.22	0.52	-5.39	-4.53	-4.16	-3.85	-3.40	1	20000
##	LL[29]	-3.24	0.23	-3.78	-3.36	-3.19	-3.07	-2.90	1	20000
##	LL[30]	-3.89	0.43	-4.87	-4.14	-3.83	-3.57	-3.21	1	20000
##	LL[31]	-3.50	0.32	-4.24	-3.68	-3.45	-3.27	-3.02	1	18000
##	LL[32]	-5.63	0.84	-7.48	-6.14	-5.55	-5.03	-4.22	1	20000
##	LL[33]	-3.11	0.18	-3.55	-3.20	-3.08	-2.99	-2.85	1	11000
##	LL[34]	-3.27	0.24	-3.85	-3.39	-3.22	-3.09	-2.92	1	12000
##	LL[35]	-3.07	0.15	-3.43	-3.15	-3.04	-2.96	-2.83	1	20000
##	LL[36]	-3.05	0.15	-3.40	-3.13	-3.03	-2.96	-2.82	1	5800
##	LL[37]	-3.41	0.29	-4.12	-3.57	-3.36	-3.19	-2.98	1	20000
##	LL[38]	-3.24	0.23	-3.81	-3.37	-3.20	-3.08	-2.90	1	6800
##	LL[39]	-3.67	0.38	-4.57	-3.89	-3.62	-3.40	-3.11	1	17000

## LL[40]	-3.16	0.20	-3.65	-3.27	-3.13	-3.02	-2.87	1	6200
## LL[41]	-3.54	0.33	-4.32	-3.73	-3.49	-3.29	-3.04	1	11000
## LL[42]	-3.21	0.22	-3.75	-3.33	-3.17	-3.06	-2.89	1	9300
## LL[43]	-3.58	0.34	-4.38	-3.78	-3.53	-3.33	-3.06	1	9200
## LL[44]	-3.34	0.27	-3.97	-3.48	-3.29	-3.14	-2.95	1	11000
## LL[45]	-3.16	0.20	-3.64	-3.26	-3.13	-3.02	-2.87	1	18000
## LL[46]	-3.24	0.23	-3.81	-3.37	-3.20	-3.08	-2.91	1	20000
## LL[47]	-3.59	0.35	-4.41	-3.78	-3.54	-3.33	-3.07	1	20000
## LL[48]	-4.64	0.61	-6.01	-5.02	-4.58	-4.20	-3.62	1	20000
## LL[49]	-3.13	0.19	-3.59	-3.23	-3.10	-3.00	-2.86	1	20000
## LL[50]	-3.16	0.20	-3.66	-3.26	-3.13	-3.02	-2.87	1	20000
## LL[51]	-3.02	0.12	-3.30	-3.09	-3.01	-2.93	-2.81	1	20000
## LL[52]	-3.21	0.22	-3.75	-3.33	-3.18	-3.06	-2.89	1	20000
## LL[53]	-3.41	0.29	-4.11	-3.58	-3.37	-3.20	-2.98	1	20000
## LL[54]	-3.10	0.17	-3.51	-3.18	-3.07	-2.98	-2.84	1	14000
## LL[55]	-3.01	0.12	-3.27	-3.08	-3.00	-2.93	-2.81	1	18000
## LL[56]	-3.05	0.14	-3.39	-3.12	-3.03	-2.95	-2.82	1	20000
## LL[57]	-3.23	0.23	-3.79	-3.35	-3.19	-3.07	-2.90	1	20000
## LL[58]	-3.31	0.26	-3.93	-3.45	-3.27	-3.12	-2.93	1	12000
## LL[59]	-3.14	0.19	-3.61	-3.24	-3.11	-3.01	-2.86	1	8900
## LL[60]	-3.02	0.12	-3.29	-3.09	-3.01	-2.93	-2.81	1	7800
## a[1]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1	1
## a[2]	14.25	2.83	8.67	12.36	14.25	16.13	19.80	1	20000
## a[3]	11.90	2.85	6.23	10.02	11.92	13.79	17.45	1	20000
## a[4]	4.27	2.81	-1.29	2.38	4.28	6.18	9.76	1	6000
## b[1]	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1	1
## b[2]	-2.75	2.48	-7.70	-4.41	-2.77	-1.11	2.13	1	6900
## b[3]	0.31	2.46	-4.51	-1.32	0.32	1.95	5.16	1	20000
## base	19.90	2.45	15.04	18.28	19.90	21.55	24.77	1	20000
## deviance	415.30	3.93	409.66	412.40	414.64	417.49	424.60	1	20000
## tau	0.02	0.00	0.01	0.01	0.02	0.02	0.02	1	20000

B) Now add the 2-way interaction between location and bait to your model. Give the summary statistics. Which coefficients appear to be different from zero based on their credible intervals?

contrasts

	BAIT Period		
	1	2	3
Location 1	-ref	ref+Bait[2]	ref+Bait[3]
Location 2	-ref+loc[2]	ref+loc[2]+Bait[2]+int[2,2]	-ref+Loc[2]+Bait[3]+int[2,3]
Location 3	-ref+loc[3]	ref+loc[3]+Bait[2]+int[3,2]	-ref+Loc[3]+Bait[3]+int[3,3]
Location 4	-ref+loc[4]	ref+loc[4]+Bait[2]+int[4,2]	-ref+Loc[4]+Bait[3]+int[4,3]

set up and run JAGS model

```
write("model
{ # two-way ANOVA with interaction term, using reference classes

  #set up contrast priors- noninteractions

  base ~ dnorm(0, 1.0E-6)
  a[1] <- 0 #reference location
  a[2] ~ dnorm(0.0, 1.0E-6)
  a[3] ~ dnorm(0.0, 1.0E-6)
```

```

a[4] ~ dnorm(0.0, 1.0E-6)
b[1] <- 0 #reference bait
b[2] ~ dnorm(0.0, 1.0E-6)
b[3] ~ dnorm(0.0, 1.0E-6)

#set up contrast priors- interactions
int[1,1] <- 0
int[2,1] <- 0
int[3,1] <- 0
int[4,1] <- 0
int[1,2] <- 0
int[2,2] ~ dnorm(0.0, 1.0E-6)
int[3,2] ~ dnorm(0.0, 1.0E-6)
int[4,2] ~ dnorm(0.0, 1.0E-6)
int[1,3] <- 0
int[2,3] ~ dnorm(0.0, 1.0E-6)
int[3,3] ~ dnorm(0.0, 1.0E-6)
int[4,3] ~ dnorm(0.0, 1.0E-6)

tau ~ dgamma(0.001, 0.001) # uninformative precision

#model

for (i in 1:N) # for each of the samples
{
  ymean[i] <- base + a[X1[i]] + b[X2[i]] + int[X1[i],X2[i]]
  Y[i] ~ dnorm(ymean[i], tau)
  LL[i] <- -0.5*log(2*3.14159)+0.5*log(tau)-0.5*tau*(Y[i]-ymean[i])*(Y[i]-ymean[i])
}
",file=here("JAGS_mods","HW7-1B-ANOVA-2way-int.txt"))

moth.list <- list(Y = moth.data$Moths,
                  X1 = moth.data$LocationNum,
                  X2 = moth.data$BaitNum,
                  N = length(moth.data$Moths))

jags.anova.2way.int <-jags(data = moth.list,
  model.file=here("JAGS_mods","HW7-1B-ANOVA-2way-int.txt"),
  parameters.to.save=c("base","a","b","int","tau","LL"),n.chains=2,n.iter=110000,n.burnin=10000,n.thin=

## Compiling model graph
##   Resolving undeclared variables
##   Allocating nodes
## Graph information:
##   Observed stochastic nodes: 60
##   Unobserved stochastic nodes: 13
##   Total graph size: 399
##
## Initializing model
##
##   |

```

output summary

```
round(jags.anova.2way.int$BUGSoutput$summary,2)
```

##	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
## LL[1]	-3.45	0.40	-4.47	-3.65	-3.36	-3.16	-2.95	1	4500
## LL[2]	-3.15	0.22	-3.72	-3.23	-3.10	-3.01	-2.86	1	4100
## LL[3]	-4.00	0.62	-5.49	-4.35	-3.89	-3.53	-3.12	1	3000
## LL[4]	-3.42	0.39	-4.41	-3.61	-3.33	-3.14	-2.93	1	3600
## LL[5]	-3.66	0.49	-4.86	-3.92	-3.56	-3.29	-3.00	1	4100
## LL[6]	-4.10	0.66	-5.68	-4.48	-3.99	-3.61	-3.15	1	20000
## LL[7]	-5.07	0.95	-7.22	-5.63	-4.96	-4.38	-3.58	1	20000
## LL[8]	-4.71	0.85	-6.68	-5.21	-4.58	-4.09	-3.39	1	20000
## LL[9]	-3.17	0.23	-3.78	-3.25	-3.12	-3.01	-2.86	1	5900
## LL[10]	-3.47	0.41	-4.52	-3.67	-3.38	-3.17	-2.94	1	20000
## LL[11]	-4.10	0.66	-5.69	-4.48	-3.99	-3.61	-3.15	1	8200
## LL[12]	-4.20	0.69	-5.86	-4.59	-4.09	-3.68	-3.19	1	19000
## LL[13]	-3.32	0.34	-4.19	-3.47	-3.24	-3.09	-2.91	1	20000
## LL[14]	-3.11	0.18	-3.57	-3.19	-3.08	-2.99	-2.85	1	7600
## LL[15]	-3.22	0.27	-3.94	-3.32	-3.15	-3.04	-2.88	1	6100
## LL[16]	-3.10	0.18	-3.55	-3.18	-3.07	-2.99	-2.85	1	20000
## LL[17]	-3.30	0.32	-4.16	-3.44	-3.22	-3.08	-2.90	1	20000
## LL[18]	-3.39	0.37	-4.36	-3.57	-3.30	-3.13	-2.92	1	17000
## LL[19]	-3.14	0.21	-3.68	-3.22	-3.10	-3.00	-2.86	1	20000
## LL[20]	-3.17	0.24	-3.81	-3.27	-3.12	-3.02	-2.87	1	20000
## LL[21]	-3.80	0.55	-5.16	-4.09	-3.70	-3.39	-3.05	1	20000
## LL[22]	-3.20	0.26	-3.87	-3.31	-3.14	-3.03	-2.87	1	20000
## LL[23]	-3.54	0.44	-4.65	-3.76	-3.44	-3.21	-2.97	1	20000
## LL[24]	-3.27	0.30	-4.05	-3.40	-3.19	-3.06	-2.89	1	20000
## LL[25]	-3.68	0.50	-4.92	-3.96	-3.59	-3.31	-3.01	1	15000
## LL[26]	-3.16	0.23	-3.75	-3.25	-3.11	-3.01	-2.86	1	3700
## LL[27]	-3.27	0.31	-4.07	-3.40	-3.20	-3.06	-2.89	1	5200
## LL[28]	-4.00	0.63	-5.49	-4.35	-3.89	-3.53	-3.11	1	17000
## LL[29]	-3.43	0.39	-4.42	-3.62	-3.33	-3.14	-2.94	1	20000
## LL[30]	-4.13	0.68	-5.74	-4.52	-4.02	-3.63	-3.16	1	18000
## LL[31]	-4.02	0.63	-5.55	-4.38	-3.91	-3.56	-3.13	1	13000
## LL[32]	-4.70	0.84	-6.62	-5.18	-4.58	-4.09	-3.41	1	20000
## LL[33]	-3.10	0.18	-3.54	-3.18	-3.07	-2.99	-2.85	1	20000
## LL[34]	-3.14	0.21	-3.69	-3.23	-3.10	-3.00	-2.86	1	20000
## LL[35]	-3.37	0.36	-4.29	-3.53	-3.28	-3.11	-2.92	1	20000
## LL[36]	-3.18	0.24	-3.80	-3.27	-3.12	-3.02	-2.87	1	20000
## LL[37]	-3.39	0.37	-4.35	-3.56	-3.30	-3.12	-2.92	1	20000
## LL[38]	-3.39	0.37	-4.34	-3.56	-3.30	-3.13	-2.93	1	20000
## LL[39]	-3.61	0.47	-4.79	-3.86	-3.51	-3.26	-2.99	1	20000
## LL[40]	-3.30	0.32	-4.14	-3.44	-3.22	-3.08	-2.90	1	20000
## LL[41]	-3.74	0.52	-5.03	-4.02	-3.64	-3.35	-3.04	1	20000
## LL[42]	-3.39	0.37	-4.32	-3.56	-3.30	-3.12	-2.92	1	20000
## LL[43]	-3.49	0.42	-4.53	-3.70	-3.39	-3.18	-2.95	1	20000
## LL[44]	-3.30	0.32	-4.12	-3.45	-3.22	-3.08	-2.90	1	20000
## LL[45]	-3.17	0.24	-3.79	-3.27	-3.12	-3.02	-2.87	1	20000
## LL[46]	-3.32	0.33	-4.18	-3.46	-3.23	-3.08	-2.91	1	20000
## LL[47]	-3.64	0.49	-4.82	-3.89	-3.54	-3.27	-3.00	1	20000
## LL[48]	-4.61	0.81	-6.50	-5.08	-4.49	-4.01	-3.36	1	20000
## LL[49]	-3.22	0.27	-3.92	-3.33	-3.15	-3.04	-2.88	1	20000

```
## LL[50]    -3.24 0.29 -4.00 -3.36 -3.17 -3.05 -2.89    1 20000
## LL[51]    -3.11 0.18 -3.56 -3.19 -3.08 -2.99 -2.85    1 20000
## LL[52]    -3.17 0.23 -3.79 -3.27 -3.12 -3.02 -2.87    1 14000
## LL[53]    -3.30 0.32 -4.13 -3.44 -3.22 -3.08 -2.90    1 10000
## LL[54]    -3.30 0.32 -4.13 -3.44 -3.22 -3.08 -2.90    1 20000
## LL[55]    -3.13 0.20 -3.66 -3.22 -3.09 -3.00 -2.85    1 20000
## LL[56]    -3.16 0.23 -3.76 -3.25 -3.12 -3.02 -2.86    1 20000
## LL[57]    -3.37 0.35 -4.29 -3.53 -3.28 -3.11 -2.92    1 20000
## LL[58]    -3.32 0.33 -4.18 -3.47 -3.23 -3.09 -2.90    1  8200
## LL[59]    -3.18 0.25 -3.83 -3.28 -3.13 -3.02 -2.87    1  6200
## LL[60]    -3.10 0.18 -3.55 -3.18 -3.07 -2.99 -2.85    1  7500
## a[1]      0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## a[2]     16.77 5.10  6.72 13.43 16.75 20.18 26.91    1 20000
## a[3]     12.55 5.12  2.49  9.10 12.53 16.00 22.53    1 18000
## a[4]      3.77 5.12 -6.33  0.35  3.78  7.19 13.82    1 20000
## b[1]      0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## b[2]     -2.25 5.13 -12.31 -5.65 -2.25  1.16  7.94    1 20000
## b[3]      1.76 5.16 -8.49 -1.68  1.80  5.23 11.80    1 10000
## base     19.24 3.63 12.09 16.82 19.23 21.68 26.34    1 16000
## deviance 420.40 5.79 411.25 416.24 419.65 423.83 433.69    1 20000
## int[1,1]  0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## int[2,1]  0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## int[3,1]  0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## int[4,1]  0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## int[1,2]  0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## int[2,2] -1.00 7.29 -15.56 -5.85 -0.96  3.90 13.23    1 20000
## int[3,2] -1.77 7.23 -16.06 -6.55 -1.78  2.96 12.37    1 20000
## int[4,2]  0.60 7.26 -13.66 -4.24  0.70  5.33 14.93    1 16000
## int[1,3]  0.00 0.00  0.00  0.00  0.00  0.00  0.00    1     1
## int[2,3] -6.56 7.24 -20.79 -11.38 -6.53 -1.80  7.80    1 20000
## int[3,3] -0.16 7.31 -14.45 -5.08 -0.19  4.69 14.40    1 20000
## int[4,3]  0.82 7.32 -13.48 -4.07  0.73  5.65 15.37    1 20000
## tau      0.02 0.00  0.01  0.01  0.02  0.02  0.02    1  5800
```

```
LLs <- paste0("LL[",1:moth.list$N,"]")

WAIC.table <- tibble(model = c("2way-Anova-noint", "2way-Anova-int"),
  model.ls = c(list(jags.anova.2way.noint), list(jags.anova.2way.int)),
  LL.ls = c(list(jags.anova.2way.noint$BUGSoutput$sims.matrix[,LLs]),
    list(jags.anova.2way.int$BUGSoutput$sims.matrix[,LLs]))) |>
  mutate(WAIC.ls = map(LL.ls, waic),
    elpd_waic = map_dbl(WAIC.ls,c(1,1)),
    p_waic = map_dbl(WAIC.ls,c(1,2)),
    waic = map_dbl(WAIC.ls,c(1,3)),
    deltaWAIC = waic - min(waic),
    weight = round(exp(-2*deltaWAIC)/sum(exp(-2*deltaWAIC)),digits = 5))
```

C) Calculate the delta-WAIC. Which of these two models is best? Is that consistent with what you would expect from looking at the credible intervals of the parameter estimates?

```
## Warning: There were 2 warnings in 'mutate()'.
```



```
## The first warning was:
## i In argument: 'WAIC.ls = map(LL.ls, waic)'.
## Caused by warning:
## !
## 2 (3.3%) p_waic estimates greater than 0.4. We recommend trying loo instead.
## i Run 'dplyr::last_dplyr_warnings()' to see the 1 remaining warning.
```

```
WAIC.table |> select(-model.ls, -LL.ls, -WAIC.ls) |> knitr::kable(caption = "WAIC Table")
```

Table 1: WAIC Table

model	elpd_waic	p_waic	waic	deltaWAIC	weight
2way-Anova-noint	-211.1404	6.348355	422.2807	0.00000	1
2way-Anova-int	-216.8741	11.450028	433.7482	11.46745	0

Problem 2: Mixed effects/ hierarchical models in JAGS or STAN

A) Treating team as a random effect, estimate the mean for each team, the grand mean, the standard deviation between teams and the standard deviation within teams (i.e. error sd). Assume the data are normally distributed. Assume the within group variance is the same for all groups. Use an exponential prior for the standard deviations. Show the summary statistics for all the parameters and use `ggs_caterpillar` to compare the means across teams.

B) Compare the CIs of the standard deviations within and between groups. Based on these results, do you think the location random effect is necessary in this model?

C) Now run the model without the location random effect, with only the grand mean (i.e a null model). Show the WAIC values for the models in part a and part c. Does the WAIC support including the random effect in the model?

D) When, if ever, would it make sense to model team as a fixed effect rather than a random effect? Explain your reasoning.

Problem 3: INLA

A) Repeat the moth models from part 1 in INLA along with a 3rd model with location only, using default priors, and print the results with `summary` and `autoplot`. Do you get similar coefficients to part 1 for the same models?

B) Calculate DIC and WAIC for all 3 models. Which model is preferred?

C) Plot the residuals vs. fitted values and `qqnormal` of the residuals from the WAIC best model for the moth data. Does the normal model seem to fit adequately?

D) Repeat the football models from part 2a and c in INLA, using default priors, and print the results with `summary` and `autoplot`. What did you get for the WAIC values and was the deltaWAIC result the same?