

# Homework 7, STA 360

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Total points: 10 (reproducibility) + 30 (Q1) = 40 points.

**General instructions for homeworks:** Please follow the uploading file instructions according to the syllabus. You will give the commands to answer each question in its own code block, which will also produce plots that will be automatically embedded in the output file. Each answer must be supported by written statements as well as any code used. Your code must be completely reproducible and must compile. Syllabus: (<https://github.com/resteorts/modern-bayes/blob/master/syllabus/syllabus-sta602-spring19.pdf>)

**Advice:** Start early on the homeworks and it is advised that you not wait until the day of. While the professor and the TA's check emails, they will be answered in the order they are received and last minute help will not be given unless we happen to be free.

**Commenting code** Code should be commented. See the Google style guide for questions regarding commenting or how to write code <https://google.github.io/styleguide/Rguide.xml>. No late homework's will be accepted.

Please look over the homework before lab this week. TA's will answer questions on the homework this week regarding these two problems below. I recommend that you work through them as much as possible before lab this week.

1. Multivariate Normal, 30 points, 10 points each) Hoff exercise 7.3 (Australian crab data).
2. Imputation, 50 points, 10 points each) Hoff 7.4 (Marriage data) (This is left as an optional exercise that will not be graded.)

**7.3 Australian crab data:** The files `bluecrab.dat` and `orangecrab.dat` contain measurements of body depth (Y1) and rear width (Y2), in millimeters, made on 50 male crabs from each of two species, blue and orange. We will model these data using a bivariate normal distribution.

```
library(plyr)
library(ggplot2)
library(dplyr)
library(xtable)
library(reshape)
library(tidyverse)
library(ggrepel)
library(MASS)
```

a) (10 points) For each of the two species, obtain posterior distributions of the population mean  $\theta$  and covariance matrix  $\Sigma$  as follows: Using the semiconjugate prior distributions for  $\theta$  and  $\Sigma$ , set  $\mu_0$  equal to the sample mean of the data, (caret) 0 and  $S_0$  equal to the sample covariance matrix and (caret)  $\nu_0 = 4$ . Obtain 10,000 posterior samples of  $\theta$  and  $\Sigma$ . Note that this “prior” distribution loosely centers the parameters around empirical estimates based on the observed data (and is very similar to the unit information prior described in the previous exercise). It cannot be considered as our true prior distribution, as it was derived from the observed data. However, it can be roughly considered as the prior distribution of someone with weak but unbiased information.

```
blueC = as.matrix(read.table("data/bluecrab.dat"))
orangeC = as.matrix(read.table("data/orangecrab.dat"))
set.seed(123)
crab.mcmc = lapply(list('blueC' = blueC, 'orangeC' = orangeC), function(crab) {
  c = ncol(crab)
  r = nrow(crab)
  ybar = colMeans(crab)

  mu_0 = ybar
  lambda_0 = s_0 = cov(crab)
  nu_0 = 4

  num = 10000
  theta_2 = matrix(nrow = num, ncol = c)
  sigma_2 = array(dim = c(c, c, num))

  sigma = s_0

  inv = solve

  for (n in 1:num)
  {
    lambda_n = inv(inv(lambda_0) + r * inv(sigma))
    mu_n = lambda_n %*% (inv(lambda_0) %*% mu_0 + r * inv(sigma) %*% ybar)
    theta = mvrnorm(n = 1, mu_n, lambda_n)

    resid = t(crab) - c(theta)
    s_theta = resid %*% t(resid)
    s_n = s_0 + s_theta
    sigma = inv(rWishart(1, nu_0 + r, inv(s_n))[, , 1])

    theta_2[n, ] = theta
    sigma_2[, , n] = sigma
  }

  list(theta = theta_2, sigma = sigma_2)
})
```

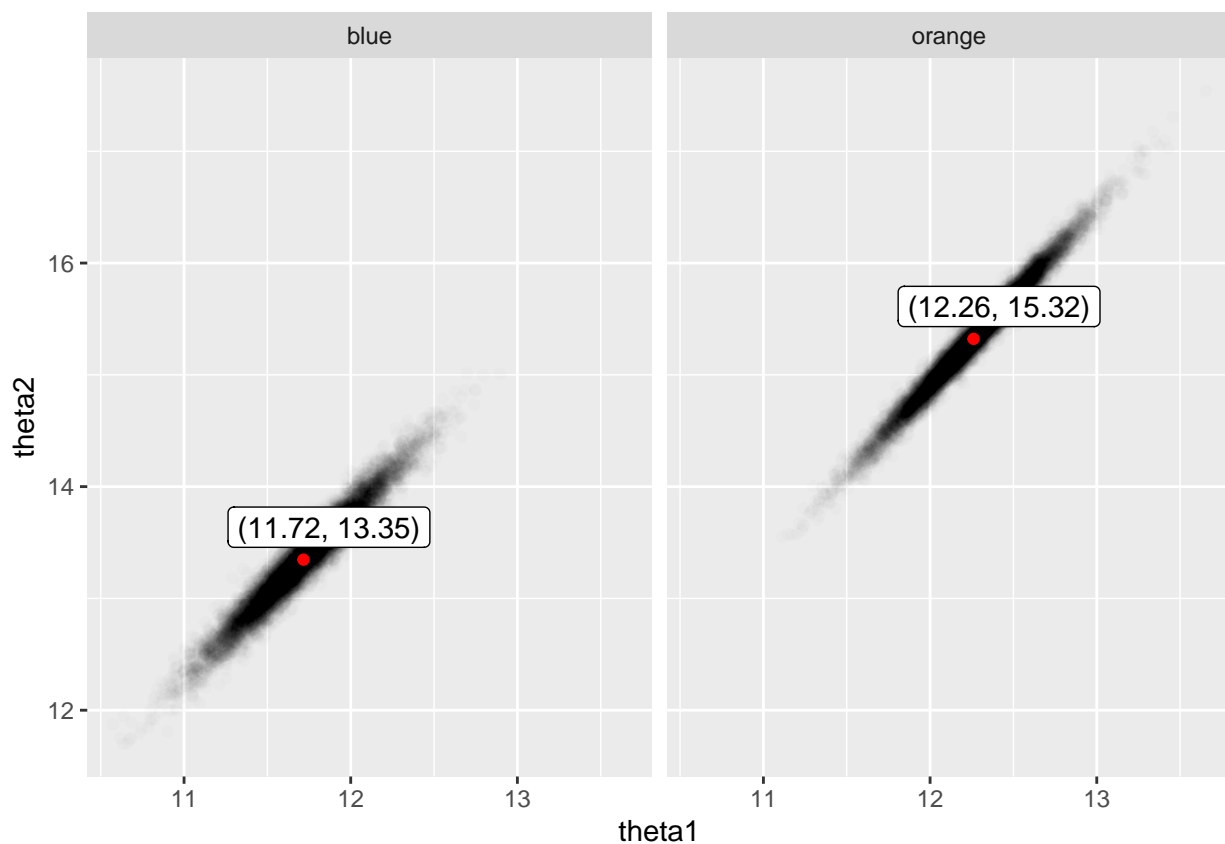
b) (10 points) Plot values of  $\theta = (\theta_1, \theta_2)$  for each group and compare. Describe any size differences between the two groups.

```
set.seed(123)
blueC.df = data.frame(crab.mcmc$blueC$theta, species = 'blue')
orangeC.df = data.frame(crab.mcmc$orangeC$theta, species = 'orange')

colnames(blueC.df) = colnames(orangeC.df) = c('theta1', 'theta2', 'species')
crab.df = rbind(blueC.df, orangeC.df)
blueC.means = as.data.frame(t(as.matrix(colMeans(blueC.df[, c('theta1', 'theta2')]))))
orangeC.means = as.data.frame(t(as.matrix(colMeans(orangeC.df[, c('theta1', 'theta2')]))))
blueC.means$species = 'blue'
orangeC.means$species = 'orange'

crab.means = rbind(blueC.means, orangeC.means)

ggplot(crab.df, aes(x = theta1, y = theta2)) +
  geom_point(alpha = 0.01) +
  geom_point(data = crab.means, color = 'red') +
  geom_label_repel(data = crab.means, aes(label = paste0("(", round(theta1, 2), ", ", round(theta2, 2), ")")),
    facet_wrap(~ species)
```



Looking at the plots of  $\theta_1$  and  $\theta_2$ , we can see that on average, orange crabs seem to have a larger  $\theta_1$  value than blue crabs ( $12.26 > 11.72$ ), and on average, orange crabs seem to have a larger  $\theta_2$  value than blue crabs ( $15.32 > 13.35$ ).

```
set.seed(123)
mean(orangeC.df$theta1 > blueC.df$theta1)
```

```
## [1] 0.8996
```

```
mean(orangeC.df$theta2 > blueC.df$theta2)
```

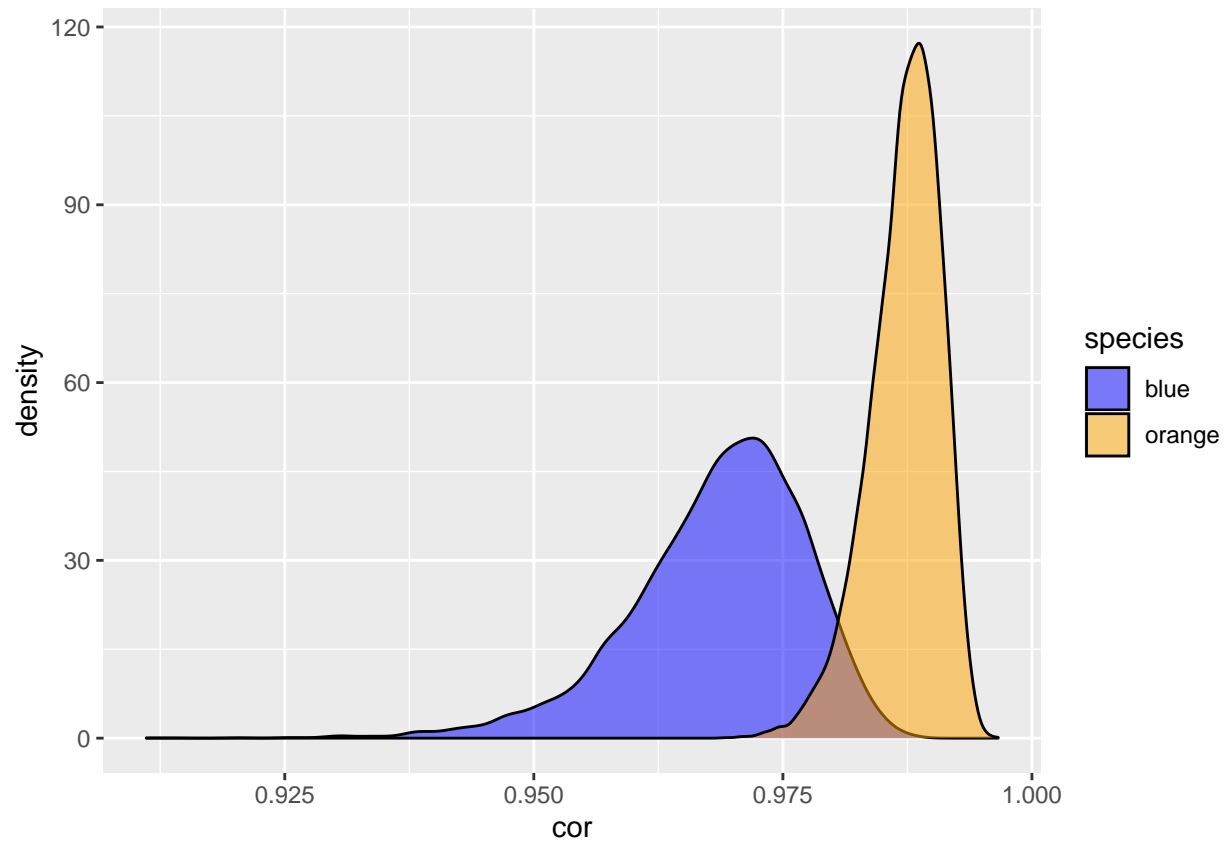
```
## [1] 0.9983
```

Looking at the plots of theta 1 and theta 2, we can see that on average, orange crabs seem to have a larger theta 1 value than blue crabs ( $12.26 > 11.72$ ), and on average, orange crabs seem to have a larger theta 2 value than blue crabs ( $15.32 > 13.35$ ). This is further shown by the looking at the probability that theta 1 is greater for orange crabs than blue crabs, which is 0.8996 and the probability that theta 2 is greater for orange crabs than blue crabs, which is 0.9983. This shows that 89.96% of the time theta 1 is greater for orange crabs compared to blue crabs for our sample, which is a large majority of the time, which means on average orange crabs have a larger theta 1. This also shows that 99.83% of the time theta 2 is greater for orange crabs compared to blue crabs, which is a large majority of the time, which means on average orange crabs have a larger theta 2.

c) (10 points) From each covariance matrix obtained from the Gibbs sampler, obtain the corresponding correlation coefficient. From these values, plot posterior densities of the correlations  $p\_blue$  and  $p\_orange$  for the two groups. Evaluate differences between the two species by comparing these posterior distributions. In particular, obtain an approximation to  $\Pr(p\_blue < p\_orange | y_{blue}, y_{orange})$ . What do the results suggest about differences between the two populations?

```
set.seed(123)
blueC.cor = apply(crab.mcmc$blueC$sigma, MARGIN = 3, FUN = function(covmat) {
  covmat[1, 2] / (sqrt(covmat[1, 1] * covmat[2, 2]))
})
orangeC.cor = apply(crab.mcmc$orangeC$sigma, MARGIN = 3, FUN = function(covmat) {
  covmat[1, 2] / (sqrt(covmat[1, 1] * covmat[2, 2]))
})
cor.df = data.frame(species = c(rep('blue', length(blueC.cor)), rep('orange', length(orangeC.cor))),
  cor = c(blueC.cor, orangeC.cor))

ggplot(cor.df, aes(x = cor, fill = species)) +
  geom_density(alpha = 0.5) +
  scale_fill_manual(values = c('blue', 'orange'))
```



```
mean(orangeC.cor > blueC.cor)
```

```
## [1] 0.9915
```

The Plot of the posterior densities of correlation coefficients are both somewhat normal distributed, and show that for orange and blue crabs on average, the correlation is higher for orange crabs than blue crabs, for both measurements of theta 1 and theta 2. Through our calculation of  $\Pr(p_{\text{blue}} < p_{\text{orange}} | y_{\text{blue}}, y_{\text{orange}}) = 0.9915$ , we can see that the probability that the correlation of orange crabs is greater than the correlation coefficient of blue crabs is 99.15%, which is a large majority of the time, which means on average orange crabs have a larger correlation.