```
title: STAT 457 Homework 05
author: Martha Eichlersmith
date: 2019-11-19
output:
 pdf document:
    fig caption: yes
header-includes:
 - \usepackage{color}
  - \usepackage{mathtools}
  - \usepackage{amsbsy} #bold in mathmode
  - \usepackage{nicefrac} # for nice fracs
  - \usepackage{booktabs}
  - \usepackage{geometry}
  - \usepackage{caption} #to remove automatic table name and
number - \captionsetup[table]{labelformat=empty}, put code under
geometry: "left=1.75cm, right=1.75cm, top=1.5cm, bottom=2cm"
\captionsetup[table]{labelformat=empty}
```{r setup, echo=FALSE, results="hide", warning=FALSE,
message=FALSE}
library(ggplot2) #ggplot
library(readr) #import CSV
library(gridExtra) #organize plots
library(grid) #organize plots
library(latex2exp) #latex in ggplot titles
library(matlib) \#A = matrix, inv(A) = A^{-1}
library(numDeriv) #calculate numerical first and second order
derivatives
library(gtable) #for tablegrob functions
#library(kableExtra) #for kable functions
library(dplyr) #for piping
library (MCMCpack) #for dirichelt
knitr::opts chunk$set(echo=FALSE, fig.width = 10, fig.height = 4)
decimal <- function(x, k) trimws(format(round(x, k), nsmall=k))</pre>
#knitr::opts chunk$set(echo=FALSE) #using knitr for this option
but don't have to load
Problem 1
Consider two urns each containing an unknown mixture of blue and
```

```
Problem 1a
Let π denote the proportion of blue marbles in urn #1 and let
ψ denote the corresponding proportion in urn #2. Under the
(i) Haldane, (ii) flat and (iii) non-informative priors, compute
$p \left(\ln \left[\frac{ \pi}{1 - \pi} \right] > \ln \left[
\frac{\psi}{1 - psi} \right] \mid \text{data} \psis{using}
the normal approximation.
$$
p \left(\ln \left[\frac{ \pi}{1 - \pi} \right] > \ln \left[
\frac{ \psi}{1 - \psi} \right] \mid \text{data} \right)
p \left(\ln \left[\frac{ \pi}{1 - \pi} \right] - \ln \left[
\frac{\proof \proof \proo
$$
$$
\begin{aligned}
p(\pi) & \sim \text{Beta}(\alpha 0, \beta 0) \\
p(\psi) & \sim \text{Beta}(\alpha 0, \beta 0) \\
p(\pi Y) = m Y & \sim \text{Beta}(y {\pi}+ \alpha 0, \ n {\pi} -
y {\pi} +\beta 0) \stackrel{\text{def}}{=} \text{Beta}(\alpha,
\beta) \\
p(\pi Y) \in \mathbb{Y} (y is im \text{Beta}(y {\pi}+ \alpha 0, \ n {\pi} -
y {\pi} +\beta 0) \stackrel{\text{def}}{=} \text{Beta}(\gamma,
\delta)\\
\text{Normal Approx Mean} & = \ln \left(\frac{ \alpha \cdot
\delta}{ \beta \cdot \gamma} \right) \\
\text{Variance} & = \frac{1}{\lambda} + \frac{1}{\lambda}
{\beta + \frac{1}{\gamma} + \frac{1}{\gamma} + \frac{1}{\gamma} + \frac{1}{\gamma} }
\text{Normal Approx} & \sim \mathcal{N} \left(\ln \left(\frac{
\sqrt{
\frac{1}{\lambda} + \frac{1}{\lambda} + \frac{1}{\lambda} + \frac{1}{\lambda} + \frac{1}{\lambda}
{\delta}
} \
\right)
\end{aligned}
 ```{r pla, warning=FALSE}
n.pi <- 18
n.psi <- 6
y.pi <- 14
y.psi <- 2
```

```
Repeat (1a) by drawing deviates from the appropriate beta
distributions. Quantify the Monte Carlo error in your value.
```{r plb, warning=FALSE}
set.seed(050101)
n.pi <- 18
n.psi <- 6
y.pi <- 14
y.psi <- 2
func pval <- function(it, a0, b0){</pre>
a0 <- 0
b0 <- 0
alpha <- y.pi + a0
gamma <- y.psi + a0</pre>
beta <- n.pi - y.pi + b0
delta <- n.psi - y.psi + b0
post.pi <- rbeta(it, alpha, beta)</pre>
post.psi <- rbeta(it, gamma, delta)</pre>
inside.log <-(post.pi/(1 - post.pi))/(post.psi/(1 - post.psi))</pre>
#inside.log <- (alpha*delta) / (beta*gamma)</pre>
difflogodds <- log(inside.log)</pre>
se <- sd(difflogodds)/sqrt(it)</pre>
pval <- 1 - pnorm(0, mean(difflogodds), sd(difflogodds))</pre>
results <- c(pval, se)
func logdiff <- function(it.vec, a0, b0){</pre>
a0.vec <- rep(a0, length(it.vec))</pre>
b0.vec <- rep(b0, length(it.vec))</pre>
pvals <- mapply(func pval, it.vec, a0.vec, b0.vec)</pre>
table <- rbind(it.vec, decimal(pvals, dec))</pre>
rownames(table) <- c("Iterations", "p-value", "Standard Error")</pre>
table
it.vec < c(1e+04, 1e+05, 1e+06)
dt <- cbind(func logdiff(it.vec, 0, 0), func logdiff(it.vec, 1,</pre>
1), func logdiff(it.vec, .5, .5))
knitr::kable(dt, booktabs=T, 'latex', caption="Probability that
the log differences are greater than 0") %>%
```

```
\newpage
Problem 1d
Is delinquency related to birth order?
```{r 1d-props}
alpha <- c(127, 123, 93, 17)/360 #most delinquent
gamma <- c(345, 209, 158, 65)/777 #least delinquent
parameters <- rbind(alpha, gamma)</pre>
total <- c(sum(alpha), sum(gamma))</pre>
diff <- .5*c(alpha-gamma, sum(alpha-gamma))</pre>
table <- rbind( cbind(parameters, total), diff)</pre>
rownames(table) <- c("Most Delinquent", "Least Delinquent",
"(1/2)Difference (Most - Least)")
colnames(table) <- c("Oldest", "In-between", "Youngest", "Only</pre>
Child", "Total")
knitr::kable(table, booktabs=TRUE, 'latex', digits=dec,
caption="Row Proportion") %>%
 kableExtra::kable styling(latex options="hold position" )
```{r 1d-function}
func diff <- function(matrix){</pre>
diff.matrix <- cbind(#most - least</pre>
 matrix[,1] - matrix[,5] #diff for Oldest
 , matrix[,2] - matrix[,6] #diff for in-between
 , matrix[, 3] - matrix[, 7] #diff for youngest
 , matrix[,4] - matrix[,8] #diff for only-child
)
diff.matrix
}
func values <- function(vec) {</pre>
 it <- length(vec)</pre>
 CI.val <- decimal(quantile(vec, c(0.025, 0.975)), dec)
 CI.95 <- paste("(", paste(CI.val, collapse=", "), ")")</pre>
 mean <- decimal(mean(vec), dec)</pre>
 pval <- length(vec[vec > 0])/it
 vec <- c(it, mean, CI.95, pval)</pre>
 vec
func deling <- function(it) {</pre>
set.seed(050104)
prop <- rdirichlet(it, t(parameters))</pre>
```

```
```{r 1d-tables}
func table <- function(i, name) {</pre>
table <- cbind(it.1[,i], it.2[,i], it.3[,i])
rownames(table) <- c("Iterations", "Mean", "95% CI", "P(diff>0)")
title <- paste("Difference in Proportion for", name, ": Most
Delinquent - Least Delinquent")
knitr::kable(table, booktabs=T, 'latex', caption=title) %>%
  kableExtra::kable styling(latex options="hold position" ) #hold
table in place
func table(1, "Oldest")
func table(2, "In-Between")
func table(3, "Youngest")
func table(4, "Only")
```{r 1d-chisqtest}
func pval.chisq <- function(pvals) {</pre>
 x <- -2*sum(log(as.numeric(pvals)))</pre>
 combined.pval <- pnorm(x, 2*length(pvals))</pre>
}
pvals.vec <- cbind(it.1[4,], pval.2 <- it.2[4,], pval.3 <- it.</pre>
3[4,])
combined <- apply(pvals.vec, 2, func pval.chisq)</pre>
combined.pvals <- rbind(it.vec, decimal(combined, dec))</pre>
rownames(combined.pvals) <- c("Iterations", "Combined p-value")</pre>
title <- paste("Combined p-values:","$X = -2 \times {i=1}^4 (p i)
\sim \\chi^2 {df=8}$")
knitr::kable(combined.pvals, booktabs=T, 'latex', caption=title)
 kableExtra::kable styling(latex options="hold position")
There is evidence that birth order has an effect on delinquency
rates. There may be an argument that younger brothers are more
delinquent, but my younger brother is not a delinquent (anecdotal
evidence!).
```

```
g(\hat{p}) & \stackrel{\mathcal{D}}{\to} \mathcal{N} \left(
g(\hat{p}), \ \frac{1}{n} \right)
\\
2\sin^{-1}\sgrt{\hat{p}} & \stackrel{\mathcal{D}}{\to}
\mathcal{N} \left(2 \sin^{-1} \sqrt{p} \right) / \left(2 \sin^{-1} \right)
\end{aligned}
$$
Problem 3
Let x 1, cdots, x n be an iid sample from mathcal{N}(theta)
1)$ and let $y 1, \cdots , y n$ be an independent iid sample from
\mathcal{N}(\phi, 1). Derive the distribution of \varphi
/ \overline{y}$ (where $\overline{y} \neq 0$) via the delta
method.
$$
\begin{aligned}
\operatorname{N} \left(\sum_{x \in \mathbb{N}} \left(\sum_{x \in \mathbb{N}} \right) \right)
\overline{y} & \sim \mathcal{N}(\phi, \nicefrac{1}{n})
//
\text{text}\{\text{Let }\}\ h(x, y) \& = x / y \neq \text{text}\{\text{so}\} \neq h(B) = 0
\operatorname{verline}\{x\} / \operatorname{verline}\{y\} \operatorname{text}\{and\} \operatorname{duad} h(\operatorname{beta}) =
\theta / \phi
//
\left(h(B) - h(\beta) \right) &
\stackrel{\mathcal{D}}{\to} \mathcal{N} \left(0, \nabla h
(\beta)^T \cdot \Sigma \cdot \nabla h(\beta) \right)
\delta = \left[\left(\frac{matrix}{1/n \& 0} \right) & 1/n \right]
\right]
\[0.5ex]
\nabla h (\beta)^T & = \left[\begin{matrix}
\frac{ \partial h}{ \partial x} &
\frac{ \partial h}{ \partial y}
\end{matrix} \right] {\theta, \phi}
\left[\begin{matrix}
\frac{1}{y} &
- \frac{x}{y^2}
\end{matrix} \right] {\theta, \phi}
\left[\begin{matrix}
\frac{1}{\phi} &
- \frac{\theta}{\phi^2}
\end{matrix} \right]
```

```
\ \left\{ \mathbb{N} \right\}
\left(\frac{1}{\phi^2} - \frac{\theta^2}{\phi^4} \right)
\right)
\\[1ex]
\frac{ \overline{x}}{\overline{y}} & \stackrel{\mathcal{D}}{\to}
\mathcal{N} \left(
\frac{\theta}{\phi}, \
\frac{1}{n} \left(\frac{1}{\phi^2} - \frac{1}{\phi^2} - \frac{1}{\phi^4} \right)
\right)
\right)
\end{aligned}
\newpage
Problem 4
197 animals are distributed into four categories: $Y = (y 1, y 2,
y 3, y 4)$ according to the genetic linkage model $\left(\frac{2}
+ \hat{4}, \frac{1 - \hat{4}}{4}, \frac{1 - \hat{4}}{4}, \frac{4}{4}, \frac{4}{4},
\theta}{4} \right)$. In HW#4 you derived the likelihood for the
data \$Y = (125, 18, 20, 34)\$ and you derived the likelihood for
the data \$Y = (14, 0, 1, 15)\$. In that homework, you also used
Newton-Raphson algorithm to obtain the MLE ($\hat{\theta}$) of $
\theta \ and the standard error of \theta \
$$
\begin{aligned}
L(\theta \in \mathbb{Y}) \& =
\frac{(y_1 + y_2 + y_3 + y_4)!}{(y_1! y_2!y_2! y_4!)}
\left(\frac{2 + \theta}{4} \right)^{y} 1
\left(\frac{1 - \left(1 - \frac{4}{4}\right)^{2}}{\right)}
\left(\frac{1 - \theta}{4} \right)^{y} 3
\left(\frac{\theta}{4}
 \right)^{y 4}
\label{local_section} \
& \propto (2 + \theta)^{y 1} \cdot (1 - \theta)^{y 2 + y 3} \cdot (1 - \theta)^{y 2 + y 3} \cdot (1 - \theta)^{y 2 + y 3} \cdot (1 - \theta)^{y 3 + \theta}
(\theta)^{y}
\\[1ex]
\left(\left(\mathbf{Y} \right) \right) & \propto y 1 \log(2 + \theta) + (y 2 +
y 3) \log(1 - \theta) + y 4 \log(\theta)
\[.5ex]
- \frac{y 2 + y 3}{1 - \theta} + \frac{y 4}{\theta}
\[.5ex]
\frac{2 + \frac{2}{2} \& = - \frac{y 1}{(2 + \frac{2}{2})}}{\frac{2 + \frac{2}{2}}}
\theta^2 - \frac{y^2 + y_3}{(1 - \theta^2)^2} - \frac{y_4}
{\theta^2}
```

```
print.yval <- paste(yval, collapse=", ")</pre>
name <- paste("Normal Likelihood and Normal Approximation for
Y=(", print.yval, ")")
table <- data.frame("Statistic"=c("MLE", "Standard Error")</pre>
 , "Value"=decimal(c(theta.mle, se), dec))
tg <- tableGrob(table)</pre>
x < - seq(0, 1, 0.001)
df <- data.frame("X"=x)</pre>
ggplot(data=df, aes(x=X)) +
 norm.like+normal.approx+
 ggtitle(paste(name))+
 theme(axis.title.x = element blank())+
 scale colour manual("", values = c(colors[1], colors[2])) +
 #theme(legend.position = "bottom")+
 annotation custom(tg, xmin=.0, ymin=.25, xmax=0.5, ymax=1)
```{r p4-netwonraphson}
func newton.raphson <- function(f, start, it, tol){</pre>
 x0 <- start
  k <- c()
  for (i in 1:it) {
    x1 <- x0 - f(x0) #calcualte next value x1
    k[i] \leftarrow x1 \#store x1
    root.approx <- tail(k, n=1)</pre>
    it.completed <- length(k)</pre>
    # Once the difference between x0 and x1 becomes sufficiently
small, output the results.
    if (abs(x1 - x0) < tol & !is.na(abs(x1-x0)))
      { root.approx
      break}
    else if( it.completed == it) {print(paste("Start at", start,
": diverges"))}
    else{x0 <- x1}
  return(root.approx)
tol <- 1e-5
it <- 1000
func se <- function(theta.mle) {</pre>
```

```
}
theta.mle <- func newton.raphson(func a, 0.6, it, tol)
se <- func se(theta.mle)</pre>
func plots (yval, theta.mle, se)
### Problem 4b
Repeat (4a) for \$Y = (14, 0, 1, 5)\$
```{r p4b, warning=FALSE, fig.height=2.5}
yval < -c(14, 0, 1, 5)
func b<-function(x){</pre>
 (
 yval[1]/(2+x)-(yval[2]+yval[3])/(1-x)+yval[4]/x
) / (
 -yval[1]/(2+x)^2-(yval[2]+yval[3])/(1-x)^2-yval[4]/x^2
) #iterations of newton raphson = theta\{i + 1\} = theta\{i\} -
(1st deriv of log like) / (2nd deriv of log like)
theta.mle <- func newton.raphson(func b, 0.9, it, tol)
se <- func se(theta.mle)</pre>
func plots(yval, theta.mle, se)
\newpage
Problem 5
Use Laplace's method (second order) to compute the posterior mean
(under a flat prior) for the genetic linkage model for both data
sets.
```{r p5-LaplacePostMean}
func LaplacePostMean <- function(yval, start.hat, start.star) {</pre>
n <- sum(yval)</pre>
func nh <- function(x) { yval[1]*log(2+x) + (yval[2] +
yval[3])*log(1 - x) + yval[4]*log(x) }
  #-nh(theta)
func lst.nh \leftarrow function(x) \{ yval[1]/(2+x)-(yval[2]+yval[3])/(1-x) \}
+yval[4]/x
```

```
func theta.star <-function(x) { ( func 1st.nh.star(x) ) / (</pre>
func 2nd.nh.star(x) ) }
  #function for NR to find mle theta star for -nh*(theta)
  #iterations of newton raphson = theta^{i + 1} = theta^{i} -
(1st deriv of log like) / (2nd deriv of log like)
func sig.star <- function(x){1/sqrt(func 2nd.nh.star(x)/-n) }</pre>
    \#sigma.star = h''(theta.star) ^{-1/2}
theta.hat <- func newton.raphson(func theta.hat, start.hat, it,
theta.star <- func newton.raphson(func theta.star, start.star,
it, tol)
sig.hat <- func sig.hat(theta.hat)</pre>
sig.star <- func sig.star(theta.star)</pre>
post.mean <- (sig.star/sig.hat) *</pre>
(exp(func nh.star(theta.star)))/(exp(func nh(theta.hat)))
name <- c("theta.hat", "theta.star", "sigma.hat", "sigma.star",</pre>
"Posterior Mean")
values <- c(theta.hat, theta.star, sig.hat, sig.star, post.mean)
table <- data.frame("Statistic"=name, "Value"=decimal(values,
dec))
print.yval <- paste(yval, collapse=", ")</pre>
name <- paste("Laplace's Method (Second Order) of Posterior Mean
for Y=(", print.yval, ")")
knitr::kable(table, booktabs=T, 'latex', caption=name) %>%
 kableExtra::kable styling(latex options="hold position" )
$$
\begin{aligned}
L(\theta \ Mid Y) \& propto (2 + \theta)^{y 1} (1 - \theta)^{y 2 + \theta}
y 3} (\theta)^{y 4 }
\\
\ell (\theta \mid Y) & \propto y 1 \ln(2 + \theta) + (y 2 + y 3)
\ln (1 - \theta) + y 4 \ln (\theta)
```

```
```{r p5a}
yval <- c(125, 18, 20, 34)
func_LaplacePostMean(yval, 0.6, 0.6)
```{r p5b}
yval <- c(14, 0, 1, 5)
func_LaplacePostMean(yval, 0.9, 0.91)
```</pre>
```