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title: STAT 457 Homework 05
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date: 2019-11-16
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$set(echo=FALSE, fig.width = 10, fig.height = 4)
decimal <- function(x, k) trimws(format(round(x, k), nsmall=k))</pre>
dec <- 5
#knitr::opts chunk$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
```

y.psi <- 2

```
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} \psing
the normal approximation.
$$
p \left(\ln \left[\frac{ \pi}{1 - \pi} \right] > \ln \left[
\frac{ \psi}{1 - \psi} \right] \mid \text{data} \right)
p \left(\ln \left[\frac{ \pi}{1 - \pi} \right] - \ln \left[
\frac{\psi}{1 - psi} \pright] > 0 \mid \text{data} \pright)
$$
\begin{aligned}
p(\pi) & \sim \text{Beta}(\alpha 0, \beta 0) \\
p(\psi) & \sim \text{Beta}(\alpha 0, \beta 0) \\
p(\pi \mid Y) & \sim \text{Beta}(y {\pi}+ \alpha 0, \ n {\pi} -
y {\pi} +\beta 0) \stackrel{\text{def}}{=} \text{Beta}(\alpha,
\beta) \\
p(\pi \mid Y) & \sim \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{Normal Approx Variance} & = \frac{1}{\alpha} + \frac{1}
{\beta} + \frac{1}{\gamma} + \frac{1}{\delta} \\
\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
```

```
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")
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") %>%
```

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Problem 1d
Is deliquency releated to birth order?
```{r 1d-counts}
alpha <- c(127, 123, 93, 17)/360 #most delinquent
gamma \leftarrow c(345, 209, 158, 65)/777 #least delinquent
parameters <- rbind(alpha, gamma)</pre>
total <- c(sum(alpha), sum(gamma))</pre>
table.count <- decimal(cbind(parameters, total), dec)</pre>
rownames(table.count) <- c("Most Delinquent", "Least Delinquent")
colnames(table.count) <- c("Oldest", "In-between", "Youngest",</pre>
"Only Child", "Total")
knitr::kable(table.count, booktabs=TRUE, 'latex', 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>
diff <- cbind(#most - least</pre>
 prop[,1] - prop[,5] #diff for Oldest
 ,prop[,2] - prop[,6] #diff for in-between
```

```
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)
응>응
  kableExtra::kable styling(latex options="hold position" )
. . .
There is evidence that birth order has an effect on deliquency
rates.
```

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Problem 2

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

```
\\[1ex]
\frac{ \overline{x}}{\overline{y}} & \stackrel{\mathcal{D}}{\to}
\mathcal{N} \left(
\frac{\theta}{\phi}, \
\frac{ 1}{\phi^2} - \frac{ \sigma^2}{\phi^4}
\right)
\end{aligned}
$$
\newpage
## Problem 4
197 animals are distributed into four categories: $Y = (y 1, y 2,
y 3, y 4)$ according to the genetic linkage model $\left( \frac{2}{}
+ \theta}{4}, \frac{1 - \theta}{4}, \frac{1- \theta}{4}, \frac{
\theta}{4} \right)$. In HW#4 you derived the likelihood for the
data \$Y = (125, 18, 20, 34)\$ and you derived the likelihood for
the data \$Y = (14, 0, 1, 15)\$. In that homework, you also used
Newton-Raphson algorithm to obtain the MLE ($\hat{\theta}$) of $
\theta$ and the standard error of $\hat{\theta}$.
$$
\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 - \theta}{4} \right)^{y} 2
\left( \frac{1 - \theta}{4} \right)^{y} 3
\left( \frac{4}{4} \right)^{9}
& \propto (2+ \theta)^{y 1} \cdot (1 - \theta)^{y 2 + y 3} \cdot (2 + \theta)^{y 1}
(\theta)^{y} 4
\\[1ex]
y 3) \log(1 - \theta) + y 4 \log(\theta)
\[.5ex]
- \frac{y 2 + y 3}{1 - \theta} + \frac{y 4}{\theta}
\frac{2 + \frac{2}{2} e^2}{\frac{2}{2}} = -\frac{1}{2}
\theta^2 - \frac{y^2 + y^3}{(1 - \theta^2)^2} - \frac{y^4}{(1 - \theta^2)^2}
{\theta^2}
\\[.5ex]
\theta^{(i+1)} &= \theta^{(i)} -
\frac{
\frac{y 1}{2 + \theta^{(i)}} - \frac{y 2 + y 3}{1 - \theta^{(i)}}
```

```
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] <- 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>
 secondderiv \leftarrow -(yval[1] / (2 + theta.mle)^2) - ((yval[2] +
```

```
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 \leftarrow function(x) { yval[1]*log(2+x) + (yval[2] +
yval[3])*log(1 - x) + yval[4]*log(x) }
 #-nh (theta)
func 1st.nh <- function(x) { yval[1]/(2+x)-(yval[2]+yval[3])/(1-x)
+yval[4]/x
 #d(-nh(theta))/d theta- first derivative
```

```
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)\}
 \#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)</pre>
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</pre>
for Y=(", print.yval, ")")
knitr::kable(table, booktabs=T, 'latex', caption=name) %>%
 kableExtra::kable styling(latex options="hold position")
$$
\begin{aligned}
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)
```
```