cs208 HW 4a

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Question 1

(a)

The centralized version of the SQ algorithm simply takes in a conjunction matrix - a matrix with a conjunction of x_j and y in each column - computes an estimate of p_j for $j \in \{1, ..., d\}$ and then adds Laplace noise with scale factor $\frac{d}{n\epsilon}$ to each of the d estimates. For each $\hat{p_j} < t$ for some threshold t, j is returned.

In the localized version, I perform randomized response on each row of the conjunction matrix with the local randomizer defined as follows:

$$Q(x_i) = \begin{cases} x_i & w.p. \frac{e^{\epsilon/d}}{e^{\epsilon/d}+1} \\ 1 - x_i & w.p. \frac{1}{e^{\epsilon/d}+1} \end{cases}$$

From here, we are left with a new conjunction matrix $\hat{x}$ with each row the result of a randomized response process. We can then calculate the estimate of p_j for each column of the new conjunction matrix. However, we will have to correct the output of this, as it will be biased in expectation. I'll consider correcting the numerator of the estimate of p_j and in my implementation I'll divide this by the number rows to get the appropriate estimate of the probability.

$$\begin{aligned} E\left[\hat{p_j}_{numerator}\right] &= E\left[\sum_{i=1}^{n} \hat{x_i}[j]\right] \\ &= \sum_{i=1}^{n} E[\hat{x_i}[j]] \\ &= \sum_{i=1}^{n} \left[x_i \frac{e^\epsilon}{e^\epsilon + 1} + (1 - x_i)\frac{1}{e^\epsilon + 1}\right] \\ &= \sum_{i=1}^{n} \left[x_i \frac{e^\epsilon - 1}{e^\epsilon + 1} + \frac{1}{e^\epsilon + 1}\right] \\ &= n x_i \frac{e^\epsilon - 1}{e^\epsilon + 1} + \frac{n}{e^\epsilon - 1} \end{aligned}$$

Thus, our correction will need a multiplicative and an additive term. The appropriate terms are

$$\begin{aligned} c &= \frac{e^\epsilon + 1}{e^\epsilon - 1} \\ d &= \frac{-n}{e^\epsilon - 1} \\ E[c * \hat{p_j}_{numerator} + d] &= \frac{e^\epsilon + 1}{e^\epsilon - 1}\left[n x_i \frac{e^\epsilon - 1}{e^\epsilon + 1} + \frac{n}{e^\epsilon - 1}\right] - \frac{n}{e^\epsilon - 1} \\ &= n x_i + \frac{n}{e^\epsilon - 1} - \frac{n}{e^\epsilon - 1} \\ &= n x_i \end{aligned}$$

As I did in the centralized version, j is returned if $\hat{p_j} > t$ for some threshold t.

For the implmentation of these algorithms, see the Appendix. Note that the algorithm that I implement simply considers the conjunction of x_j and y when both are equal to 1. Since the coding of features can be done arbitrarily, a more complete version of this algorithm would consider the reverse coding of each x_j as well. Furthermore, a more complete version may also consider derived attributes based on conjunctions of predictors, such as $x_a \wedge x_b$. I did not implement those here because I was able to detect what the true conjunction was after close inspection of the dataset and a manual recoding of one feature.

(b)

Centralized

$$\begin{aligned}
P[\hat{S} \not\supset S] &= \sum_{j \in S} P[\hat{p_j} > t] \\
&= \sum_{j \in S} P\left[Lap\left(\frac{d}{n\epsilon}\right) > t\right] \\
&= |S| \int_t^\infty \frac{e^{-|y|n\epsilon/d} * n\epsilon}{2d} dy \\
&= |S| \frac{n\epsilon}{2d} \frac{-d}{n\epsilon} \left[e^{-yn\epsilon/d}\right]_t^\infty \\
&= \frac{|S|}{2} e^{-tn\epsilon/d}
\end{aligned}$$

Now consider that $P[\hat{S} \not\supset S] \leq 0.1$.

$$\begin{aligned}
\frac{|S|}{2} e^{-tn\epsilon/d} &\leq 0.1 \\
-\frac{tn\epsilon}{d} &\geq log\left(\frac{0.2}{|S|}\right) \\
t &\leq -\frac{d\epsilon}{n} log\left(\frac{0.2}{|S|}\right) \\
t &\leq -\frac{d\epsilon}{n} log\left(\frac{0.2}{d}\right) \quad (|S| \leq d)
\end{aligned}$$

Localized

$$\begin{aligned}
P[\hat{S} \not\supset S] &= \sum_{j \in S} P[\hat{p_j} > t] \\
&= \sum_{j \in S} P\left[\frac{1}{n} \sum_{i=1}^n \hat{x_i}[j] > t\right]
\end{aligned}$$

Since $\hat{x_i}[j] \sim Bernoulli\left(\frac{1}{e^\epsilon + 1}\right)$, this implies that $\sum_{i=1}^n \hat{x_i}[j] \sim Binomial\left(n, \frac{1}{e^\epsilon + 1}\right)$.

$$\begin{aligned}
\sum_{i=1}^n \hat{x_i}[j] &\sim Binomial\left(n, \frac{1}{e^\epsilon + 1}\right) \\
&\sim N\left(n\left(\frac{1}{e^\epsilon + 1}\right), n\left(\frac{1}{e^\epsilon + 1}\right)\left(\frac{e^\epsilon}{e^\epsilon + 1}\right)\right) \\
&\sim N\left(\frac{n}{e^\epsilon + 1}, \frac{ne^\epsilon}{(e^\epsilon + 1)^2}\right)
\end{aligned}$$

where ϕ is the cumulative distribution function for the normal distribution. Thus, the probability is

$$|S|\phi\left(\frac{nt-\frac{n}{1+e^{\epsilon}}}{\left(\left(\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}\right)^{1/2}\right)}\right)$$

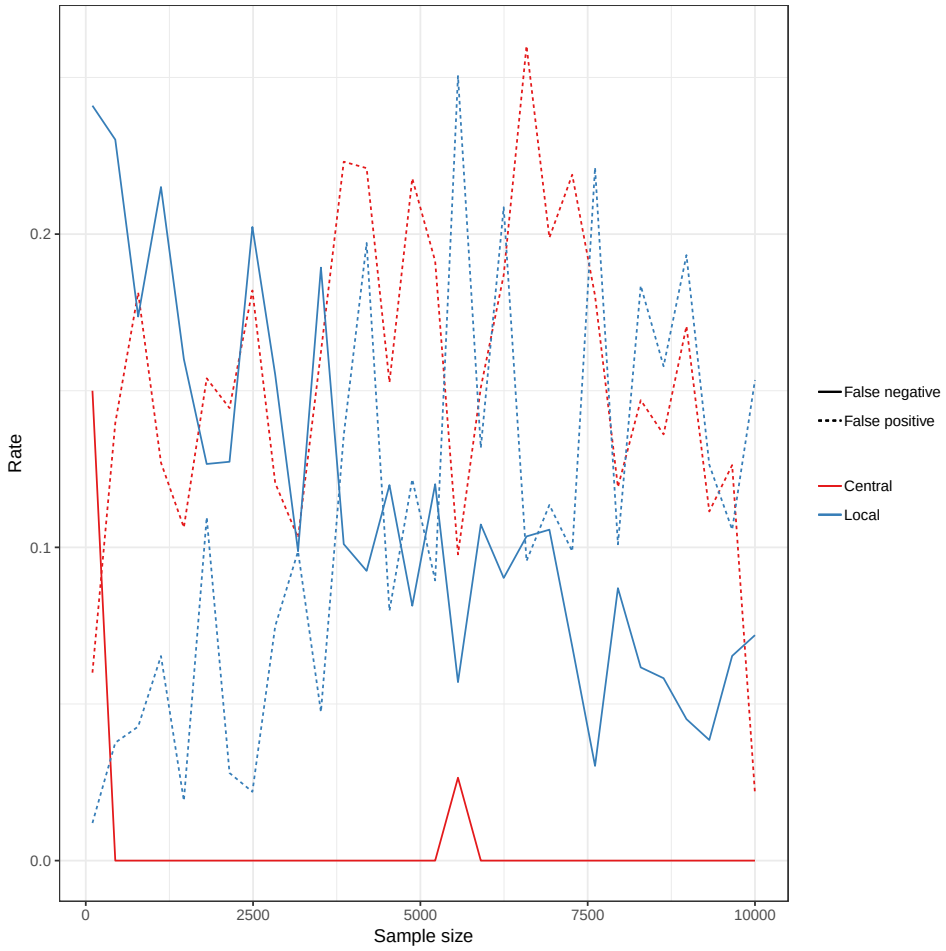
$$\begin{aligned}
|d|\phi\left(\frac{nt-\frac{n}{1+e^{\epsilon}}}{\left(\left(\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}\right)^{1/2}\right)}\right) &\leq 0.1 \\
\phi\left(\frac{nt(1+e^{\epsilon})-n}{\sqrt{ne^{\epsilon}}}\right) &\leq \frac{0.1}{d} \\
\frac{nt(1+e^{\epsilon})-n}{\sqrt{ne^{\epsilon}}} &\leq \phi^{-1}\left(\frac{0.1}{d}\right) \\
t &\leq \frac{\sqrt{e^{\epsilon}}\phi^{-1}(\frac{0.1}{d})+\sqrt{n}}{\sqrt{n}(1+e^{\epsilon})}
\end{aligned}$$

(c)

My centralized algorithm produces `sex` (after recoded to 0 = male and 1 = female), `employed`, `uscitizen`, and `englishability` every time for a reasonably low threshold ($t = 0.01$), while the localized model does not produce a consistent set of predictors for the same threshold (some runs it does produce the exact same set as the centralized, while other runs output other predictors or miss one of these four).

I also test my algorithms to predict `targetted` and compute the false positive and false negative rates as a function of the size of the dataset used to train the algorithm. For each n, I set the optimal upper bound of the threshold for each model using the expressions derived in (b) and then obtain 10 bootstrapped samples, compute my releases, and calculate the false positive and negative rates. Since I compute the optimal upper bound for both models, I also choose to scale the threshold I use by 0.1. In practice, this leads to plots that match my expectations for the results for this problem.

I would expect that the false positive rates converge to 0 fairly quickly, as for any $\hat{S} \supset S$ the false positive rate should be 0. On the other hand, the false negative rate should converge to $\sum_{j \in \hat{S}} p_{ij}$. The false positive rate for the central converges to 0 very quickly while the false positive rate of the local model converges to 0 less quickly. The false negative rate for both models jitters between roughly 0.05 and 0.2.



Appendix

Question 1

```
test_data <- read.csv("hw4testdata.csv")
pums <- read.csv("CAPUMS5full.csv")
pums$sex <- 1-pums$sex

# a
## general ##
get_conjunction_matrix <- function(x, y, negative_val=0, positive_val=1){
  n <- nrow(x)
  d <- ncol(x)
  conjunction <- matrix(NA, nrow=n, ncol=d)
  for(j in 1:d) {
    conjunction[,j] <- as.integer(x[,j]==negative_val & y==positive_val)
  }
  return(conjunction)
}

calc_pj <- function(conjunction, epsilon, type) {
```

```
  if(type=="c"){
    # centralized - add Laplace noise
    scale <- 1/(epsilon*length(conjunction))
    pj <- mean(conjunction) + rlap(mu=0, b=scale, size=1)
  }
  else if(type=="l"){
    # localized - bias correction for RR
    pj <- correction(release=conjunction, epsilon=epsilon)
  }
  else{
    print("Type not supported.")
  }
  return(pj)
}

## centralized ##
sgn <- function(x) {     # function borrowed from class
  return(ifelse(x < 0, -1, 1))
}

rlap = function(mu=0, b=1, size=1) {     # function borrowed from class
  p <- runif(size) - 0.5
  draws <- mu - b * sgn(p) * log(1 - 2 * abs(p))
  return(draws)
}

SQcentralized <- function(conjunction, t, epsilon=1) {
  d <- ncol(conjunction)
  attributes <- c()
  for(j in 1:d) {
    cur_pj <- calc_pj(conjunction=conjunction[,j], epsilon=epsilon/d, type="c")
    if(cur_pj < t) {
      attributes <- c(attributes, j)
    }
  }
  return(attributes)
}

## localized ##
localRelease <- function(x, values=c(0,1), epsilon){     # function borrowed from class
  draw <- runif(n=1, min=0, max=1)
  cutoff <- 1/(1+exp(epsilon))
  if(draw < cutoff){
    return_val <- values[!values %in% x]
  }
  else{
    return_val <- x
  }
  return(return_val)
}

correction <- function(release, epsilon){     # function updated from class
  n <- length(release)
  mulitiplicative <- (exp(epsilon) + 1)/(exp(epsilon) - 1)
```

```
  additive <- -n/(exp(epsilon) - 1)
  expectation <- (sum(release)*mulitiplicative + additive)/n
  return(expectation)
}

SQlocalized <- function(conjunction, t, epsilon=1, negative_val=0, positive_val=1) {
  n <- nrow(conjunction)
  d <- ncol(conjunction)
  new_conjunction <- matrix(NA, nrow=n, ncol=d)
  attributes <- c()

  # RR
  for(j in 1:d){
    for(i in 1:n){
      new_conjunction[i,j] <- localRelease(conjunction[i,j], values=c(0,1), epsilon=epsilon/d)
    }
  }

  # pj calculation (bias correction happens inside here)
  for(j in 1:d) {
    cur_pj <- calc_pj(conjunction=new_conjunction[,j], epsilon=epsilon/d, type="l")
    if(cur_pj < t) {
      attributes <- c(attributes, j)
    }
  }
  return(attributes)
}

## test ##
test_conj_mat <- get_conjunction_matrix(x=test_data[,1:10], y=test_data[,11])
SQcentralized(test_conj_mat, t=0.01, epsilon=1)
SQlocalized(conjunction=test_conj_mat, t=0.01, epsilon=1)


# c
pums_x <- pums[,c("sex","married","black","asian","collegedegree","employed","militaryservice",
                  "uscitizen","disability","englishability")]
pums_y <- pums$targetted
pums_conj_mat <- get_conjunction_matrix(pums_x, pums_y)

names(pums[SQcentralized(conjunction=pums_conj_mat, t=0.01, epsilon=1)])
names(pums[SQlocalized(conjunction=pums_conj_mat, t=0.01, epsilon=1)])

bootstrap <- function(x, n){     # function updated from class
  index <- sample(x=1:nrow(x), size=n, replace=TRUE)
  return(x[index,])
}

return_rates <- function(predictors, y_true){
  d <- ncol(predictors)
  if(d == 0){
    y_pred <- rep(0, length(y_true))
  }
  else if(d > 1){
```

```
    y_pred <- ifelse(rowSums(predictors) == d, 1, 0)
  }
  else{
    y_pred <- ifelse(predictors == d, 1, 0)
  }
  fpr <- mean(y_pred==1 & y_true==0)
  fnr <- mean(y_pred==0 & y_true==1)
  return(list(fpr=fpr, fnr=fnr))
}

ns <- round(seq(from=100, to=10000, length.out=30))
num_boots <- 10
predictors <- c("sex","married","black","asian","collegedegree","employed","militaryservice",
                "uscitizen","disability","englishability")
eps <- 1

rates <- matrix(NA, nrow=length(ns), ncol=5)
i <- 1
for(n in ns){
  central_fprs <- c()
  central_fnrs <- c()
  local_fprs <- c()
  local_fnrs <- c()

  # optimal t calc
  thresh_central <- -1*(10*eps/n)*log(0.2/10)*0.1
  thresh_local <- (sqrt(exp(eps))*qnorm(0.1/10)+sqrt(n))/(sqrt(n)*(1+exp(eps)))*0.1

  for(boot in 1:num_boots){

    new_data <- bootstrap(x=pums, n=n)
    new_conj_mat <- get_conjunction_matrix(new_data[,predictors], new_data$targetted)

    central_res <- names(pums[SQcentralized(conjunction=new_conj_mat, t=thresh_central, epsilon=eps)])
    local_res <- names(pums[SQlocalized(conjunction=new_conj_mat, t=thresh_local, epsilon=eps)])

    central_predictor_mat <- as.matrix(new_data[,central_res])
    local_predictor_mat <- as.matrix(new_data[,local_res])
    central_rates <- return_rates(predictors=central_predictor_mat, y_true=new_data$targetted)
    local_rates <- return_rates(predictors=local_predictor_mat, y_true=new_data$targetted)

    central_fprs <- c(central_fprs, central_rates$fpr)
    central_fnrs <- c(central_fnrs, central_rates$fnr)
    local_fprs <- c(local_fprs, local_rates$fpr)
    local_fnrs <- c(local_fnrs, local_rates$fnr)
  }

  rates[i, 1] <- n
  rates[i, 2] <- mean(central_fprs)
  rates[i, 3] <- mean(central_fnrs)
  rates[i, 4] <- mean(local_fprs)
  rates[i, 5] <- mean(local_fnrs)
  i = i + 1
}
```

```
rates_df <- as.data.frame(rates)
names(rates_df) <- c("n", "central_fpr", "central_fnr", "local_fpr", "local_fnr")

q1_plot <- ggplot(rates_df) +
  geom_line(aes(x=n, y=central_fpr, colour="Central", lty="False positive")) +
  geom_line(aes(x=n, y=central_fnr, colour="Central", lty="False negative")) +
  geom_line(aes(x=n, y=local_fpr, colour="Local", lty="False positive")) +
  geom_line(aes(x=n, y=local_fnr, colour="Local", lty="False negative")) +
  scale_colour_brewer(palette="Set1") +
  theme_bw() +
  labs(x="Sample size", y="Rate") +
  theme(legend.title=element_blank())
pdf("plots/q1_plot.pdf", width=8, height=8)
q1_plot
dev.off()
```