HW4A: The Local Model

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4/17/2019

I worked with Anthony Rentsch, Lipika Ramaswamy, and Karina Huang on this homework.

My code can be found on my Github (https://github.com/bhavenp/cs208/blob/master/homework/HW4/HW4_Bhaven_Patel.ipynb).

Problem 1: Learning Conjunctions in the SQ Model

(a)

Centralized Version of SQ Model

For the centralized version of the SQ model, I chose to calculate $p_j = P[x[j] = 0 \ \wedge \ y = 1]$ for $j = 1, \ldots, d$. To do this, I create a "conjunction matrix" where the element at the i-th row ($i = 1, \ldots, n$) and the j-th column ($j = 1, \ldots, d$) contains an indicator as to whether $x_{ij} = 0 \wedge y_i = 1$ in the original dataset. p_j is just the mean of the j-th column in the conjunction matrix.

Then, laplace noise is added to p_j with a scale equal to $\frac{GS}{\tilde{\epsilon}}$, where the global sensitivity $GS = \frac{1}{n}$ and $\tilde{\epsilon} = \frac{\epsilon}{d}$. The $GS = \frac{1}{n}$ because changing one value ($0 \rightarrow 1$ or $1 \rightarrow 0$) in the column j changes p_j by $\frac{1}{n}$. Thus, every p_j has a differentially private release $\hat{p}_j$

$$\hat{p}_j = p_j + Lap\left(\frac{d}{n\tilde{\epsilon}}\right)$$

Each $\hat{p}_j$ is compared to a threshold t to determine if the feature j should be included in the set $\hat{S}$ that is returned.

Below are the helper functions we generally use.

In [1]:
```
rm(list=ls())       # Remove any objects in memory

# Random draw from Laplace distribution
#
# mu numeric, center of the distribution
# b numeric, spread
# size integer, number of draws
#
# return Random draws from Laplace distribution
# example:
#
# rlap(size=1000)

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

# Sign function
#
# Function to determine what the sign of the passed values should be.
#
# x numeric, value or vector or values
# return The sign of passed values
# example:
#
# sgn(rnorm(10))

sgn <- function(x) {
    return(ifelse(x < 0, -1, 1))
}
```

In [2]:
```
##function to create the matrix that holds an indicator if x_j==0 & y==1
createConjunctionMat <- function(xData, yData){
    #create matrix to hold indicator if x_j==0 & y==1
    result_matrix = matrix(0, nrow=nrow(xData), ncol=ncol(xData));
    for(i in 1:nrow(xData)){
        if(yData[i] == 1){ #only need to consider row if y=1
            result_matrix[i, ] <- (xData[i, ] == 0); #check if x_j == 0
        }
    }
    return(result_matrix);
}

#function to calculate DP-releases for each probability
probRelease <- function(xMat, epsilon=1.0){
    probs <- colMeans(xMat); #calculate true probabilities
    sensitivity <- 1 / nrow(xMat); #sensitivity is 1/n
    scale <- sensitivity / epsilon;
    dpProbs <- probs + rlap(mu=0, b=scale, size=length(probs)); #add laplac

    return(list(release=dpProbs, true=probs) );
}

#function that ties together the different parts for doing a DP release of
## xData: matrix of {0,1}
## yData: vector of {0,1}, same length as number of rows in xData
## epsilon: total privacy-loss parameter. This will get split up by the num
##          we must release probabilities for
## returns a list containing a vector of the indices corresponding to the c
## a vector of the DP released probabilities calculated for each column, ar

centrlDP_SQAlg <- function(xData, yData, totEpsilon=1.0, threshold=1e-4){
    pMatrix <- createConjunctionMat(xData=xData, yData=yData); #create conj

    dpRelease <- probRelease(pMatrix, epsilon = totEpsilon/ncol(xData) ); #
    indices <- which(dpRelease$release < threshold); #get indices with prob
    return(list(indices=indices, dpProbs=dpRelease$release, trueProbs=dpRel
}
```

Below I show that my centralized version of the SQ algorithm works for the *hw4testdata.csv* file.

In [3]:
```
#read in the test data
mydata <- read.csv('../../data/hw4testdata.csv');
# mydata[0:10, ]

#get set of features to use as predictors
set.seed(42);
centrlDP_SQAlg(xData = mydata[, 1:10], yData = mydata[['y']], totEpsilon =
```

$indices

1 2 3

$dpProbs

0.00017696776001586 0.000207267112552507 -5.58128522710643e-05
0.0620781446228576 0.0605533364523468 0.0611838940326656 0.0616140889946548
0.061668819397531 0.0608976855174546 0.0610927852373104

$trueProbs

0 0 0 0.06197 0.06052 0.06118 0.06155 0.0618 0.06086 0.06104

Local Model

For the local model implementation of the SQ algorithm, I begin by creating a "conjunction matrix" where the element in the i-th row ($i = 1, \ldots, n$) and the j-th column ($j = 1, \ldots, d$) contains an indicator $\hat{x}_{ij}$ as to whether $x_{ij} = 0 \wedge y_i = 1$ in the original dataset. This is the same step I took for the centralized DP version of the SQ algorithm.

Then, I perform a randomized response on each row of the conjunction matrix. My ϵ is split into $\tilde{\epsilon} = \frac{\epsilon}{d}$, and each indicator variable $\hat{x}_{ij}$ in the row is returned as follows

$$Q(\hat{x}_{ij}) = \begin{cases} \hat{x}_{ij}, & w.p. \quad \frac{e^{\tilde{\epsilon}}}{1 + e^{\tilde{\epsilon}}} \\ 1 - \hat{x}_{ij}, & w.p. \quad \frac{1}{1 + e^{\tilde{\epsilon}}} \end{cases}$$

Using the randomized responses on the "conjunction matrix", I can calculate $\hat{p}_j$ by taking the mean of each column j in the randomized-response matrix. However, we need to calculate the correction factor to apply to the $\hat{p}_j$s because want $E[\hat{p}_j] = p_j$. We can begin with:

$$E[\hat{p}_j] = p_j$$

$$E\left[\frac{1}{n}\sum_{i=1}^{n} Q(\hat{x}_{ij})\right] = \frac{1}{n}\sum_{i=1}^{n} \hat{x}_{ij}$$

$$\frac{1}{n}\sum_{i=1}^{n} E\left[Q(\hat{x}_{ij})\right] = \frac{1}{n}\sum_{i=1}^{n} \hat{x}_{ij}$$

$$\sum_{i=1}^{n} E\left[Q(\hat{x}_{ij})\right] = \sum_{i=1}^{n} \hat{x}_{ij}$$

From the definition of $Q(\hat{x}_{ij})$ above, we can calculate $E\left[Q(\hat{x}_{ij})\right]$:

$$\begin{aligned} E\left[Q(\hat{x}_{ij})\right] &= \hat{x}_{ij}\frac{e^{\tilde{\epsilon}}}{1+e^{\tilde{\epsilon}}} + (1-\hat{x}_{ij})\frac{1}{1+e^{\tilde{\epsilon}}} \\ &= \hat{x}_{ij}\frac{e^{\tilde{\epsilon}}-1}{1+e^{\tilde{\epsilon}}} + \frac{1}{1+e^{\tilde{\epsilon}}} \end{aligned}$$

We can substitute this result in to get

$$\sum_{i=1}^{n} E\left[Q(\hat{x}_{ij})\right] = \sum_{i=1}^{n} \hat{x}_{ij}$$

$$\sum_{i=1}^{n}\left(\hat{x}_{ij}\frac{e^{\tilde{\epsilon}}-1}{1+e^{\tilde{\epsilon}}} + \frac{1}{1+e^{\tilde{\epsilon}}}\right) = \sum_{i=1}^{n} \hat{x}_{ij}$$

$$\frac{n}{1+e^{\tilde{\epsilon}}} + \frac{e^{\tilde{\epsilon}}-1}{1+e^{\tilde{\epsilon}}}\sum_{i=1}^{n} \hat{x}_{ij} = \sum_{i=1}^{n} \hat{x}_{ij}$$

From this result, we see that we need to multiply the left side by some factor c and add a quantity d so that it is equivalent to the right side.

$$d + c\cdot\left(\frac{n}{1+e^{\tilde{\epsilon}}} + \frac{e^{\tilde{\epsilon}}-1}{1+e^{\tilde{\epsilon}}}\sum_{i=1}^{n} \hat{x}_{ij}\right) = \sum_{i=1}^{n} \hat{x}_{ij}$$

If $c = \frac{1+e^{\tilde{\epsilon}}}{e^{\tilde{\epsilon}}-1}$ and $d = \frac{-n}{e^{\tilde{\epsilon}}-1}$, then the two sides of the equation are equivalent. Thus, we find that we must correct the sum $\sum_{i=1}^{n} \hat{x}_{ij}$ of each column j by multiplying the sum by $\frac{1+e^{\tilde{\epsilon}}}{e^{\tilde{\epsilon}}-1}$ and adding a factor $\frac{-n}{e^{\tilde{\epsilon}}-1}$. We can then divide each of these corrected sums by n to get our $\hat{p}_j$s.

Each $\hat{p}_j$ is compared to a threshold t to determine if the feature j should be included in the set $\hat{S}$ that is returned.

In [3]:
```
#local release mechanism works for x as a vector. Adjusted from J. Honaker'
##
## x: vector of {0,1} for which local release must be performed
## values: vector of length two containing the possible values in vector 'x
## epsilon: privacy-loss parameter to use for flipping values in 'x'
## returns a vector

localReleaseVec <- function(x, values=c(0,1), epsilon){
    draws <- runif(n=length(x), min=0, max=1); #get number of draws equal t
    cutoff <- 1/(1+exp(epsilon));
    release <- x; #make a copy of the vector x
    for(i in 1:length(x)){
        if(draws[i] < cutoff){ #we are going to flip the our value
            release[i] <- values[ !values %in% x[i] ] ; #create flag with (
        }
    }
    return(release);
}


#function that ties together the different parts for doing a DP release of
## xData: matrix of {0,1}
## yData: vector of {0,1}, same length as number of rows in xData
## epsilon: total privacy-loss parameter. This will get split up by the num
##          we must release probabilities for
## returns a list containing a vector of the indices corresponding to the c
## and a vector of the DP released probabilities calculated for each columr

localDP_SQAlg <- function(xData, yData, totEpsilon=1.0, threshold=1e-4){
    cjMatrix <- createConjunctionMat(xData=xData, yData=yData);#create conj
    trueProbs <- colMeans(cjMatrix); #calculate the true probabilities for
    epsSplit <- totEpsilon / ncol(xData); #divide the total epsilon by the

    #perform local release of conjunction matrix
    lrMatrix <- cjMatrix; #create a copy of the conjunction matrix
    for(r in 1:nrow(cjMatrix)){
        lrMatrix[r, ] <- localReleaseVec(x=cjMatrix[r, ], values = c(0,1),
    }

    dpSums <- colSums(lrMatrix); #get sums of the local release of the conj
    #perform correction
    inflation <- (exp(epsSplit) + 1) / (exp(epsSplit) - 1); #coefficient to
    n <- nrow(xData); #get number of rows
    additive <- -n / (exp(epsSplit) - 1); #additive factor to apply for bec

    dpProbs <- (dpSums * inflation + additive) / n;

    indices <- which(dpProbs < threshold); #get indices with probability le
    return(list(indices=indices, dpProbs=dpProbs, trueProbs=trueProbs));
}
```

Below I show that my local version of the SQ algorithm works for the *hw4testdata.csv* file.

In [5]:
```
set.seed(42);
mydata <- read.csv('../../data/hw4testdata.csv');
localDP_SQAlg(xData = mydata[, 1:10], yData = mydata[['y']], totEpsilon = 1
```

$indices

1 2 3

$dpProbs

-0.0102247625446308 -0.0560629228517006 -0.0114257623780041 0.0420187302070949 0.049424895846229 0.0452213964294235 0.0600337277076906 0.0822522246250906 0.0648377270411828 0.0372147308736027

$trueProbs

0 0 0 0.06197 0.06052 0.06118 0.06155 0.0618 0.06086 0.06104

(b)

Centralized DP version of SQ algorithm

I will refer to the d columns in each dataset x_i as features.
$P[\hat{S} \not\supseteq S]$ is the probability that set S contains a feature j that $\hat{S}$ does not. This equivalent to determining the probability that at least one of the features $j \in S$ has DP-released $\hat{p}_j$ that is greater than the threshold t we specify. Thus, we get

$$P[\hat{S} \not\supseteq S] = \sum_{j \in S} P[\hat{p}_j > t]$$

For the centralized DP SQ algorithm, I chose $\hat{p}_j = p_j + Lap\left(\frac{d}{n\tilde{\epsilon}}\right)$. Additionally, we know that for each $j \in S$, we have $p_j = 0$. Thus, we get

$$P[\hat{S} \not\supseteq S] = \sum_{j \in S} P[p_j + Lap\left(\frac{d}{n\tilde{\epsilon}}\right) > t]$$

$$= \sum_{j \in S} P[0 + Lap\left(\frac{d}{n\tilde{\epsilon}}\right) > t]$$

This can be equation can be expanded to be in terms of t, n, ϵ, and $|S|$ because we can expand the probability that a value chosen from the Laplace distribution is greater than t and $\sum_{j \in S} = |S|$:

$$= \sum_{j \in S} P[0 + Lap\left(\frac{d}{n\tilde{\epsilon}}\right) > t]$$

$$= |S| \cdot \int_t^{\infty} \frac{e^{(-|y| \cdot n\epsilon/d)} \cdot n\epsilon}{2d} dy$$

Now, if we say that $P[\hat{S} \not\supseteq S] \leq 0.1$, we can find an upper bound on what the threshold t should be:

$$P[\hat{S} \not\supseteq S] \leq 0.1$$

$$|S| \cdot \int_t^{\infty} \frac{e^{(-|y| \cdot n\epsilon/d)} \cdot n\epsilon}{2d} dy \leq 0.1$$

$$|S| \frac{n\epsilon}{2d} \cdot \int_t^{\infty} e^{(-|y| \cdot n\epsilon/d)} dy \leq 0.1$$

$$\int_t^{\infty} e^{(-|y| \cdot n\epsilon/d)} dy \leq \frac{(0.1) \cdot 2d}{|S| n\epsilon}$$

$$\left[\frac{-d}{n\epsilon} e^{(-y \cdot n\epsilon/d)} \right]_t^{\infty} \leq \frac{(0.1) \cdot 2d}{|S| n\epsilon}$$

$$\frac{-d}{n\epsilon} \left[e^{(-\infty \cdot n\epsilon/d)} - e^{(-t \cdot n\epsilon/d)} \right] \leq \frac{(0.1) \cdot 2d}{|S| n\epsilon}$$

$$-1 \left[0 - e^{(-t \cdot n\epsilon/d)} \right] \leq \frac{(0.2)}{|S|}$$

$$e^{(-t \cdot n\epsilon/d)} \leq \frac{(0.2)}{|S|}$$

$$-t \geq \frac{d}{n\epsilon} \log\left(\frac{(0.2)}{|S|} \right)$$

$$t \leq \frac{-d}{n\epsilon} \log\left(\frac{(0.2)}{|S|} \right)$$

Thus, for the centralized DP SQ algorithm, we find that $t \leq \frac{-d}{n\epsilon} \log\left(\frac{(0.2)}{|S|} \right)$ if we want $P[\hat{S} \not\supseteq S] \leq 0.1$.

Local DP version of SQ algorithm

I will refer to the d columns in each dataset x_i as features.
$P[\hat{S} \not\supseteq S]$ is the probability that set S contains a feature j that $\hat{S}$ does not. This equivalent to determining the probability that at least one of the features $j \in S$ has DP-released $\hat{p}_j$ that is greater than the threshold t we specify. Thus, we get

$$P[\hat{S} \not\supseteq S] = \sum_{j \in S} P[\hat{p}_j > t]$$

In the local DP version of the SQ algorithm, $\hat{p}_j$ is calculated from the randomized-response "conjunction matrix". Thus, $\hat{p}_j = \frac{1}{n}\sum_{i=1}^{n} \hat{x}_{ij}$, where $\hat{x}_{ij}$ is the value in the i-th row and j-th column of the in the randomized-response "conjunction matrix". So we can expand $P[\hat{p}_j > t]$ as follows

$$\sum_{j \in S} P[\hat{p}_j > t] = \sum_{j \in S} P\left[\frac{1}{n}\sum_{i=1}^{n} \hat{x}_{ij} > t\right]$$

$$= \sum_{j \in S} P\left[\sum_{i=1}^{n} \hat{x}_{ij} > nt\right]$$

Because $j \in S$, in the original "conjunction matrix" the entire column j would be zeroes. However after randomized-response, the zero values in column j may have been flipped to 1s, so

$$P[\hat{x}_{ij} = 1] \sim \text{Bernoulli}\left(\frac{1}{1+e^{\epsilon}}\right)$$

$$\sum_{i=1}^{n} \hat{x}_{ij} \sim \text{Bin}\left(n, \frac{1}{1+e^{\epsilon}}\right)$$

We can approximate the Binomial distribution using a normal distribution with the mean and the variance of the Binomial distribution:

$$\sum_{i=1}^{n} \hat{x}_{ij} \sim N(n\left(\frac{1}{1+e^{\epsilon}}\right), n\left(\frac{1}{1+e^{\epsilon}}\right)\left(\frac{e^{\epsilon}}{1+e^{\epsilon}}\right))$$

We can now standardize $P\left[\sum_{i=1}^{n} \hat{x}_{ij} > nt\right]$ using the normal distribution:

$$P\left[\frac{\sum_{i=1}^{n} \hat{x}_{ij} - \frac{n}{1+e^{\epsilon}}}{\sqrt{\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}}} > \frac{nt - \frac{n}{1+e^{\epsilon}}}{\sqrt{\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}}}\right] = P\left[Z > \frac{nt - \frac{n}{1+e^{\epsilon}}}{\sqrt{\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}}}\right]$$

So we now have

$$\sum_{j \in S} P\left[\sum_{i=1}^{n} \hat{x}_{ij} > nt\right] = \sum_{j \in S} P\left[Z > \frac{nt - \frac{n}{1+e^{\epsilon}}}{\sqrt{\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}}}\right]$$

$$= |S| \cdot \Phi\left(\frac{nt - \frac{n}{1+e^{\epsilon}}}{\sqrt{\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}}}\right)$$

Thus for the local DP version of the SQ algorithm $P[\hat{S} \not\supseteq S] = |S| \cdot \Phi\left(\frac{nt - \frac{n}{1+e^{\epsilon}}}{\sqrt{\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}}}\right)$.

Now, if we say that $P[\hat{S} \not\supseteq S] \leq 0.1$, we can find an upper bound on what the threshold t should be:

$$P[\hat{S} \not\supseteq S] \leq 0.1$$

$$|S| \cdot \Phi\left(\frac{nt - \frac{n}{1+e^{\epsilon}}}{\sqrt{\frac{ne^{\epsilon}}{(1+e^{\epsilon})^2}}}\right) \leq 0.1$$

$$|S| \cdot \Phi\left(\frac{\sqrt{n}t(1+e^{\epsilon}) - \sqrt{n}}{\sqrt{e^{\epsilon}}}\right) \leq 0.1$$

$|S| \leq d$ so we get

$$d \cdot \Phi\left(\frac{\sqrt{n}t(1+e^{\epsilon}) - \sqrt{n}}{\sqrt{e^{\epsilon}}}\right) \leq 0.1$$

$$\Phi\left(\frac{\sqrt{n}t(1+e^{\epsilon}) - \sqrt{n}}{\sqrt{e^{\epsilon}}}\right) \leq \frac{0.1}{d}$$

$$\frac{\sqrt{n}t(1+e^{\epsilon}) - \sqrt{n}}{\sqrt{e^{\epsilon}}} \leq \Phi^{-1}\left(\frac{0.1}{d}\right)$$

$$\sqrt{n}t(1+e^{\epsilon}) \leq \sqrt{e^{\epsilon}}\Phi^{-1}\left(\frac{0.1}{d}\right) + \sqrt{n}$$

$$t \leq \frac{\sqrt{e^{\epsilon}}\Phi^{-1}\left(\frac{0.1}{d}\right) + \sqrt{n}}{\sqrt{n}(1+e^{\epsilon})}$$

Thus, for the local DP version of the SQ algorithm, we find that $t \leq \frac{\sqrt{e^{\epsilon}}\Phi^{-1}\left(\frac{0.1}{d}\right) + \sqrt{n}}{\sqrt{n}(1+e^{\epsilon})}$ if we want $P[\hat{S} \not\supseteq S] \leq 0.1$.

(c)

Centralized DP version SQ algorithm

From part (b), we know that the upper bound on the threshold t is $t \leq \frac{-d}{n\epsilon}\log\left(\frac{(0.2)}{|S|}\right)$. For the *CaPUMS5full.csv* data, we can calculate the upper bound using $n = 1223992$, $d = 10$, $\epsilon = 1.0$, and $|S| = d = 10$.

$$\begin{aligned} t &= \frac{-d}{n\epsilon}\log\left(\frac{(0.2)}{|S|}\right) \\ &= \frac{10}{(1223992)(1.0)}\log\left(\frac{(0.2)}{10}\right) \\ &= 3.20 \cdot 10^{-5} \end{aligned}$$

Thus for the *CaPUMS5full.csv* dataset, the upper bound on the threshold t is $3.20 \cdot 10^{-5}$. I will use this threshold to show that my centralized DP SQ algorithm works on the *CaPUMS5full.csv* dataset.

In [4]:
```
#read in the test data
caPUMS <- read.csv('../../data/CaPUMS5full.csv');
print(paste(nrow(caPUMS), " rows in CA PUMS"));
caPUMS[1:3, ]
```

```
[1] "1223992  rows in CA PUMS"
```

sex	married	black	asian	collegedegree	employed	militaryservice	uscitizen	disability	englishab
1	1	0	0	0	1	0	1	0	
1	1	0	0	0	0	0	1	0	
0	1	0	0	0	0	1	1	0	

In [8]:
```
#get set of features to use as predictors
cDPInd <- centrlDP_SQAlg(xData = caPUMS[, 1:10], yData = caPUMS[['targetted
print(cDPInd$indices) #print the indices chosen as predictors for targetted
print(colnames(caPUMS)[cDPInd$indices]) #print the colnames from the origin
```

```
[1]  6  8 10
[1] "employed"       "uscitizen"      "englishability"
```

In [10]:
```
#get the true probabilities of the chosen features
print("True")
cDPInd$trueProbs[cDPInd$indices]
```

```
0 0 0
```

In [5]:
```
#test on blackfemale as target column
bfInd <- centrlDP_SQAlg(xData = caPUMS[, 1:10], yData = caPUMS[['blackfemale
bfInd
```

$indices

1 3

$dpProbs

-2.91780939154774e-07 0.0223343102285882 1.80795049632527e-06
0.0329113644604611 0.025055623044478 0.0154311989676051 0.0314126361800656
0.00129763163275449 0.0232001460585942 0.000450896465560159

$trueProbs

0 0.022335930300198 0 0.0329095288204498 0.0250573533160347
0.0154412773939699 0.0314127870116798 0.001307198086262 0.0232019490323466
0.000448532343348649

Using the threshold t I calculated, we see that the columns **employed**, **uscitizen**, and **englishability** are the columns chosen for the set $\hat{S}$ and these same columns/features have a true $p_j = 0$. However if you look at the first row of the dataset (displayed in an output above), the

conjunction of these columns do not perfectly predict **targetted**. Thus, there must be another column/demographic that the advertisers used in defining their targetted population.

Thus after some sleuthing, I found that the **sex** column is coded as 1s for "female" and 0s for "males". I will try to make the opposite of all the demographics to see if one of the "opposite"/"not" demographics is the missing feature in the conjunction defining the targeted audience.

In [10]:
```
#creat new PUMS dataset with not columns
newCAPUMS <- caPUMS[, 1:10]; #get initial features
for(col in colnames(newCAPUMS)){
    newColName <- paste("not_",col);
    newCAPUMS[, newColName] <- 1 - newCAPUMS[, col];
}
newCAPUMS$targetted <- caPUMS$targetted; #add targetted column to new datas
newCAPUMS[1:5, ]
```

ıilitaryservice	uscitizen	disability	englishability	⋯	not_ married	not_ black	not_ asian	not_ collegedegree	not_ employed
0	1	0	1	⋯	0	1	1	1	0
0	1	0	1	⋯	0	1	1	1	1
1	1	0	1	⋯	0	1	1	1	1
0	1	1	1	⋯	1	1	1	1	1
0	1	0	1	⋯	0	1	1	1	1

In [12]:
```
#get set of features to use as predictors
cDPInd <- centrlDP_SQAlg(xData = newCAPUMS[, 1:20], yData = newCAPUMS[['tar
                         totEpsilon = 1.0, threshold = 3.2e-5);
print(cDPInd) #print the indices chosen as predictors for targetted
print(colnames(newCAPUMS)[cDPInd$indices]) #print the colnames from the ori
```

```
$indices
[1]  6 10 11

$dpProbs
 [1]  2.538813e-01  1.049174e-01  2.383391e-01  2.297780e-01  1.482202e-0
1
 [6] -3.539269e-05  1.913699e-01  3.264775e-05  2.163959e-01  2.405709e-0
5
[11] -4.422795e-06  1.489794e-01  1.557758e-02  2.419174e-02  1.056648e-0
1
[16]  2.538953e-01  6.248138e-02  2.538914e-01  3.745450e-02  2.538643e-0
1

$trueProbs
 [1] 0.25389463 0.10493124 0.23833898 0.22978418 0.14821666 0.00000000
 [7] 0.19141547 0.00000000 0.21644504 0.00000000 0.00000000 0.14896339
[13] 0.01555566 0.02411045 0.10567798 0.25389463 0.06247917 0.25389463
[19] 0.03744959 0.25389463

[1] "employed"       "englishability" "not_ sex"
```

Although my centralized model does not output **uscitizen** as a predictor in this run, we can see that **not_sex** is now included as a predictor to include in the conjunction. Another run of the centralized model may produce **uscitizen** as a predictor or possibly increasing my threshold (which is the upper-bound for t when $d = 10$ and now we have $d = 20$) could allow us to uncover **uscitizen** as well.

From the true probabilities, we see that **employed**, **uscitizen**, **englishability** and **not_sex** all have $p_j = 0$, so the conjunction of these predictors should predict the **targetted** column perfectly, as I have shown below. Thus, the centralized model does pretty well in identifying the proper predictor columns.

In [16]:
```
#show that the four columns predict
targeted <- newCAPUMS[newCAPUMS$targetted == 1, ];
targeted[1:5, c(6,8,10,11,21)]
```

	employed	uscitizen	englishability	not_ sex	targetted
7	1	1	1	1	1
9	1	1	1	1	1
11	1	1	1	1	1
14	1	1	1	1	1
16	1	1	1	1	1

Local DP version of SQ algorithm

From part (b), we know that the upper bound on the threshold t is $t \leq \dfrac{\sqrt{e^{\epsilon}}\Phi^{-1}\left(\dfrac{0.1}{d}\right) + \sqrt{n}}{\sqrt{n}(1 + e^{\epsilon})}$.

For the *CaPUMS5full.csv* data, we can calculate the upper bound using $n = 1223992$, $d = 10$, $\epsilon = 1.0$, and $|S| = d = 10$.

$$t = \frac{\sqrt{e^{1}}\Phi^{-1}\left(\dfrac{0.1}{10}\right) + \sqrt{1223992}}{\sqrt{1223992}(1 + e^{1})}$$
$$= 0.268$$

Thus for the *CaPUMS5full.csv* dataset, the upper bound on the threshold t is 0.268. I will use this threshold to show that my local DP version of the SQ algorithm works on the *CaPUMS5full.csv* dataset.

In [18]:
```
#perform local DP release for SQ algorithm
lDPInd <- localDP_SQAlg(xData = newCAPUMS[, 1:20], yData = newCAPUMS[['targ
                              totEpsilon = 1.0, threshold = 0.1*0.268);
print(lDPInd$indices) #print the indices chosen as predictors for targetted
print(colnames(newCAPUMS)[lDPInd$indices]) #print the colnames from the dat
```

```
[1]  6  8 10 11 13 14
[1] "employed"       "uscitizen"      "englishability" "not_ sex"
[5] "not_ black"     "not_ asian"
```

The local DP version of the SQ algorithm was able to identify all four columns that perfectly predict **targetted** in addition to **not_black** and **not_asian**. This is most likely due to the increased noise added with the local model implementation.

Compare mechanisms

Now, I will compare the false positive and false negative rate as a function of n for the two versions of my SQ algorithms. My ns will range from 100 to 500,000. For each n, I will generate 5 bootstrapped samples and a produce a centralized and local DP release for the set of features $\hat{S}$ that predict **targetted=1**; I will calculate a false positive rate and false negative rate by predicting the value of **targetted** for the rows included in the bootstrap using the conjunction of the features included in $\hat{S}$ for each of the 5 DP releases.

For my dataset, I am using my augmented version of the *CaPUMS5full.csv dataset* in which I added the opposite/"not" columns.

In [20]:
```
##function to calculate false positive and false negative rates given true
##
## yTrue: vector of true values for targetted column
## yPreds: vector of predicted values for targetted column

calcFPandFN <- function(yTrue, yPreds){
    numPos <- sum(yTrue); #number of positive results is just sum of the ve
    numNeg <- length(yTrue) - numPos;

    #calculate the false negative
    posInd <- which(yTrue == 1); #get indices of positive results
    tps <- sum( yTrue[posInd] == yPreds[posInd]);
    fnRate <- 1 - tps/numPos; #FN-rate is 1 - TP-rate

    #calculate the false positive
    negInd <- which(yTrue == 0); #get indices of negative results
    tns <- sum( yTrue[negInd] == yPreds[negInd]);
    fpRate <- 1 - tns/numNeg; #FP-rate is 1 - TN-rate

    return(list(fp=fpRate, fn=fnRate));
}

## function to get an analytical calculation of the threshold for centraliz
## n: the number of rows in the dataset
## d: the number of predictors in the dataset
## epsilon: the total privacy-loss parameter
centralized_tCalculation <- function(n, d, epsilon){
    r <- log(0.2/d);
    r <- r * -d/ (n * epsilon);
    return(r);

}

## function to get an analytical calculation of the threshold for local DP
## n: the number of rows in the dataset
## d: the number of predictors in the dataset
## epsilon: the total privacy-loss parameter
local_tCalculation <- function(n, d, epsilon){
    numerator <- sqrt(exp(epsilon)) * qnorm(0.1/d) + sqrt(n);
    denom <- sqrt(n) * (1 + exp(epsilon));
    r <- numerator / denom;
    return(r);
}
```

In [21]:
```
# set.seed(24);
sampSizes <- c(1e2, 1e3, 5e3, 1e4, 5e4, 1e5, 5e5); #size of datasets
numSims <- 5; #number of simulations per bootstrap
eps <- 1.0; #total epsilong

numRows <- length(sampSizes) * numSims;
resultsMatrix <- matrix(NA, nrow = numRows, ncol = 7);

Sys.time()
r = 1; #row counter
for(sSize in sampSizes){

    for(i in 1:numSims){
        #sample the indices from the dataset
        sample_ind <- sample(x=1:nrow(newCAPUMS), size=sSize, replace=TRUE)
        bootstrap <- newCAPUMS[sample_ind, ]; #create a bootstrap sample

        ####Perform centralized release
        #calculate the threshold for the centralized release
        cThres <- centralized_tCalculation(n=sSize, d=20, epsilon=eps);
        cDPInd <- centrlDP_SQAlg(xData = bootstrap[, 1:20], yData = bootstr
                                 totEpsilon = eps, threshold = cThres);
        #check if no columns were selected, then the predictions should be
        if(length(cDPInd$indices) == 0){
            cent_yPreds <- rep(0, sSize); #create vector of zeroes that is
        }else{
            #get the predictors specified by the bootstrap
            bootstrapPreds <- bootstrap[, cDPInd$indices];
            if(length(cDPInd$indices) > 1){
                #get predictions for bootstrapped sample. If conjunction of
                #then prediction is 1.
                cent_yPreds <- (rowSums(bootstrapPreds) == length(cDPInd$in
            }else{ #handle case when there is just one predictor in set
                cent_yPreds <- bootstrapPreds;
            }
        }


        ####Perform local release
        #calculate the threshold for the centralized release
        lThres <- 0.1*local_tCalculation(n=sSize, d=20, epsilon=eps);
        lDPInd <- localDP_SQAlg(xData = bootstrap[, 1:20], yData = bootstra
                                 totEpsilon = eps, threshold = lThres);
        #check if no columns were selected
        if(length(lDPInd$indices) == 0){ #re-run release if feature set is
            local_yPreds <- rep(0, sSize); #create vector of zeroes that is
        }else{
             #get the predictors specified by the bootstrap
            bootstrapPreds <- bootstrap[, lDPInd$indices];
            if(length(lDPInd$indices) > 1){
                #get predictions for bootstrapped sample. If conjunction of
                #then prediction is 1.
                local_yPreds <- (rowSums(bootstrapPreds) == length(lDPInd$i
            }else{ #handle case when there is just one predictor in set
                local_yPreds <- bootstrapPreds;
            }
```

```
        }


        #get the FP and FN rates for centralized release
        cstats <- calcFPandFN(yTrue=bootstrap[['targetted']], yPreds=cent_y
        #get the FP and FN rates for local release
        lstats <- calcFPandFN(yTrue=bootstrap[['targetted']], yPreds=local_

        resultsMatrix[r, ] <- c(sSize, cstats$fp, cstats$fn, cThres, lstats
#         resultsMatrix[r, ] <- c(sSize, cstats$fp, cstats$fn, cThres, 0, 0
        r = r+1; #increment row counter
    }
}
Sys.time()
```

```
[1] "2019-04-17 16:02:18 EDT"
```

```
[1] "2019-04-17 16:13:37 EDT"
```

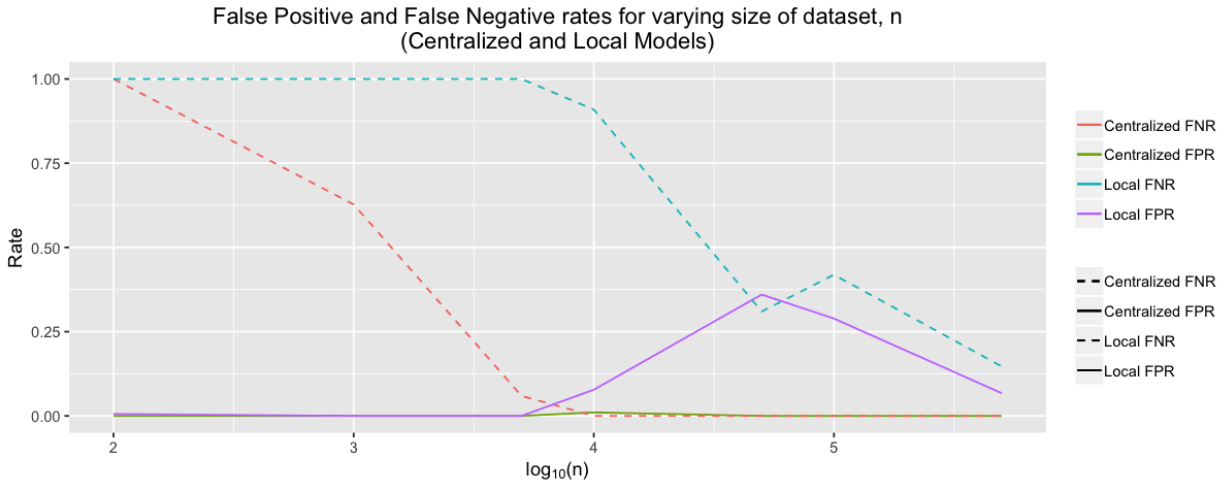
In [28]:
```
final_results <- as.data.frame(resultsMatrix);
colnames(final_results) <- c("n", "central_FPR", "central_FNR", "central_th
                             "local_FPR", "local_FNR", "local_thres");
# final_results
# write.csv(final_results, file='ctlDP_bootstrap.csv', row.names=FALSE);
```

In [29]:
```
agg_final_results <- aggregate(final_results, by = list(final_results$n), F
agg_final_results
```

Group.1	n	central_FPR	central_FNR	central_thres	local_FPR	local_FNR	local_thres
1e+02	1e+02	0.00000000	1.00000000	0.9210340372	0.005882353	1.0000000	0.01547267
1e+03	1e+03	0.00000000	0.62768499	0.0921034037	0.000000000	1.0000000	0.02328236
5e+03	5e+03	0.00000000	0.05928565	0.0184206807	0.000000000	1.0000000	0.02527890
1e+04	1e+04	0.01049119	0.00000000	0.0092103404	0.077753735	0.9091400	0.02575200
5e+04	5e+04	0.00000000	0.00000000	0.0018420681	0.360151591	0.3097664	0.02638336
1e+05	1e+05	0.00000000	0.00000000	0.0009210340	0.288927054	0.4188957	0.02653296
5e+05	5e+05	0.00000000	0.00000000	0.0001842068	0.067350927	0.1466811	0.02673262

In [30]:
```
library(ggplot2)
# plot FPRs and FNRs for both mechanisms
x_vals <- log10(agg_final_results$n);
p1 <- ggplot(agg_final_results) +
    geom_line(aes(x=x_vals, y=agg_final_results$central_FPR, color = "Centr
    geom_line(aes(x=x_vals, y=agg_final_results$central_FNR, color = "Centr
    geom_line(aes(x=x_vals, y=agg_final_results$local_FPR, color = "Local F
    geom_line(aes(x=x_vals, y=agg_final_results$local_FNR, color = "Local F
p1 <- p1 + scale_linetype_manual(values = c("Centralized FPR"="solid", "Cen
                                            "Local FPR" = "solid", "Local F
p1 <- p1 + labs(x = expression("log"[10]*"(n)"), y = 'Rate', title =
         'False Positive and False Negative rates for varying size of datase
    theme(plot.title = element_text(hjust = 0.5), legend.title = element_bl

options(repr.plot.width=10, repr.plot.height=4); #set plot dimensions
p1 #show plot
```



For the centralized DP version of the SQ algorithm, we see that the false-positive rate for the predictions essentially stays at zero as n increases and the false-negative rate decreases from 1.0 at $n = 100$ to 0 at $n = 10,000$. This is what I would expect because with smaller datasets, it is more difficult to find predictors that when in a conjunction accurately predict the **targetted** value because the global sensitivity ($\frac{1}{n}$) is higher, so the scale for the Laplace noise that is added is greater. So when n is small, the false-positive rate will be low because it is difficult to find predictors that when in conjunction will give **targetted=1**. As a result, all of the true **targetted=1** points are predicted as **targetted=0**, producing a high false-negative rate. As n increases, the false-negative rate decreases because the centralized model is able to output predictors that when in conjunction do predict the true **targetted=1** points correctly.

For the local DP version of the SQ algorithm, we see that false-positive rate stays close to 0 until $n = 5000$, where it begins to increase until $n = 50,000$, after which it decreases close to 0 at $n = 500,000$. This can be rationalized because again with smaller datasets (small n) it is difficult to find predictors that when in a conjunction accurately predict the **targetted** value because of the noise introduced by the randomized responses. So with small n, we predict everything to be **targetted=0**. As n increases, the false-positive rate picks up while the false-negative rate drops, which is expected because we are finding some subset of predictors that in conjunction accurately predict the true **targetted=1** points but also incorrectly predict some true **targetted=0** points as 1s. As n gets large ($n > 100,000$), the subset of predictors $\hat{S}$ better reflects the true subset S with

less false-positive predictors because the noise from the randomized responses is averaged out by the large n. Therefore, we see both the false-positive and false-negative rates go to zero as n increases.