cs208 HW 3

Anthony Rentsch 4/2/2019

Note: I include the code I wrote directly in line for some questions that ask only to implement a method. For other questions, my code can be found in the Appendix and on Github. I worked with Bhaven Patel and Lipika Ramaswamy for this assignment.

Question 1

(a) To prove that this mechanism is ϵ -DP, I will show that (i) the percentile trimming transformation is 1-Lipschitz, (ii) that the Laplace noise injection mechanism is ϵ -DP, and (iii) that this implies that the entire mechanism M(x) is $(1 * \epsilon)$ -DP.

(i) A mapping T from dataset to dataset is c-Lipschitz iff $\forall x, x' \ d(T(x), T(x')) \le c * d(x, x')$. Here let's consider that x and x' only differ on one element. It follows that d(x, x') = 1.

Now consider the percentile trimming transformation in this mechanism. It again follows that d(T(x), T(x')) = 1 since the maximum number of rows that these two datasets will differ on is 1. Returning the inequality in the definition of a Lipschitz constant, we see that this transformation is 1-Lipschitz.

(ii) First, we observe that

$$\frac{1}{.9n} \sum_{P_{.05} \le x \le P_{0.95}} x_i$$

is simply an estimator for the mean of x after trimming the bottom and top 5% of the data. For simplicity, replace .9n with n' and call this mechanism M'. Note that the global sensitivity of this query is $GS_q = D/n'$. Since the Laplace noise is scaled by $\frac{GS_q}{\epsilon}$, M' is ϵ -DP.

(iii) In class, we discussed a lemma that states that if M is ϵ -DP and T is c-Lipschitz, then $M \circ T$ is $(c * \epsilon)$ -DP. Following from (i) and (ii), we then have that $M = M' \circ T$ is $(1 * \epsilon)$ -DP.

Below is the implementation of this mechanism.

```
sgn <- function(x) {</pre>
                           # 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</pre>
  draws <- mu - b * sgn(p) * log(1 - 2 * abs(p))
  return(draws)
}
trimmedMean <- function(x, n, d, epsilon) {</pre>
  scale <- d/(epsilon*0.9*n)</pre>
  quants \leftarrow quantile(x, c(0.05,0.95))
  x_trimmed <- x[x>quants[1] & x<quants[2]]</pre>
  mean_trimmed <- (1/(0.9*n))*sum(x_trimmed)</pre>
  mean_release <- mean_trimmed + rlap(mu=0,b=scale,size=1)</pre>
  return(mean_release)
}
```

(b) Let's first consider d(x, x') for two neighboring datasets $x \sim x'$. Under the change model, d(x, x') = 1. In the worst case we could move the value at the 5^{th} percentile above the 95^{th} percentile, which shifts (a) a value inside the middle 90^{th} percentile to the place of the 5^{th} percentile and (b) a value from the top 5^{th} percentile to place of the 95^{th} percentile. However, we can view (a) as a change, so there is only one element that differs.

Let's now consider d(T(x),T(x')) for $T(x)=[x]_{P_{05}}^{P_{95}}$. T(x) simply changes $\frac{1}{10}^{th}$ of the data, thus d(T(x),T(x'))=0.1n. By the lemma discussed in part (a), this transformation is 0.1n-Lipschitz. Further, since we are considering the composition of an ϵ -DP mechanism with a 0.1n-Lipschitz transformation, the resulting mechanism is $0.1n*\epsilon$ -DP and **not** ϵ -DP for n>10.

(c) In this mechanism, I first bin each data value into a bin and sort those bins. Then, for each bin, I calculate the utility function value for that bin, where the utility function is defined as

$$u = - \mid n * t - \#below \mid$$

where n is the number of observations, $t \in [0, 100]$ is the percentile, and #below is the number of observations with values less than or equal to the value of the current bin. The value of this utility function is close to 0 for bins that are close to the true percentile and is increasingly negative for bins that are further away from the true percentile.

These utility values are then turned into likelihoods using the exponential mechanism $\frac{e^{\epsilon u}}{2}$ and are further weighted by the number of values between any two successive bins. The resulting bin width-weighted likelihoods are turned into probabilities of being the actual percentile.

To produce our noisy estimate of the percentile, we randomly sample a number from the standard uniform distribution and consider the first bin for which the cumulative sum of the probabilities is greater than this random number as the target true bin. For the final step, a number is sampled from the interval between this number and the next largest number and returned as the DP estimate of the true percentile.

Code for the mechanism is below.

```
exponentialPercentile <- function(x, t, d, epsilon){</pre>
  t <- t/100
  bins <- sort(c(x,d))
  nbins = length(bins)
  likelihoods <- rep(NA, nbins)
  for(i in 1:nbins){
    quality \leftarrow -1 * abs(nbins*t - i)
    if(i < nbins) { bin_width <- bins[i]-bins[i+1]+1 }</pre>
    else { bin_width <- 1 }</pre>
    likelihoods[i] <- (exp(epsilon * quality) / 2)*(bin width)</pre>
  }
  probabilities <- likelihoods/sum(likelihoods)</pre>
  flag <- runif(n=1, min=0, max=1) < cumsum(probabilities)</pre>
  bin_low_ind = which(flag)[1]
  bin_high_ind = bin_low_ind + 1
  DPrelease <- runif(n=1, min=bins[bin_low_ind], max=bins[bin_high_ind])</pre>
  return(DPrelease)
}
(d)
```

```
e3trimmedMean <- function(x, epsilon, n, d, tile_low=5, tile_high=95) {
   tile_low_value <- exponentialPercentile(x, t=tile_low, d=d, epsilon=epsilon/3)
   tile_high_value <- exponentialPercentile(x, t=tile_high, d=d, epsilon=epsilon/3)
   x_trimmed <- x[x>tile_low_value & x<tile_high_value]
   mean_trimmed <- (1/(0.9*n))*sum(x_trimmed)

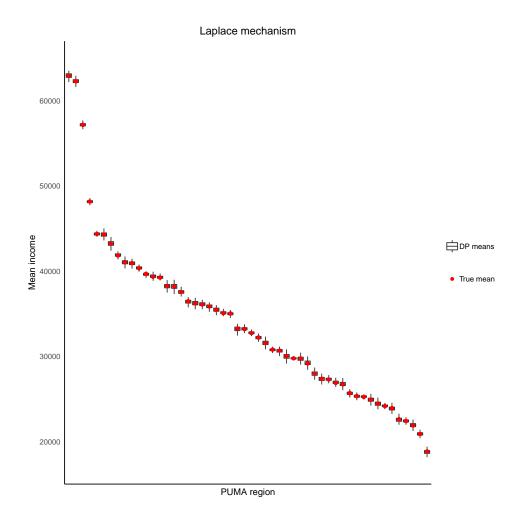
   scale <- (3*(tile_high_value-tile_low_value))/(0.9*epsilon*n)
   mean_release <- mean_trimmed + rlap(mu=0,b=scale,size=1)
   return(mean_release)
}</pre>
```

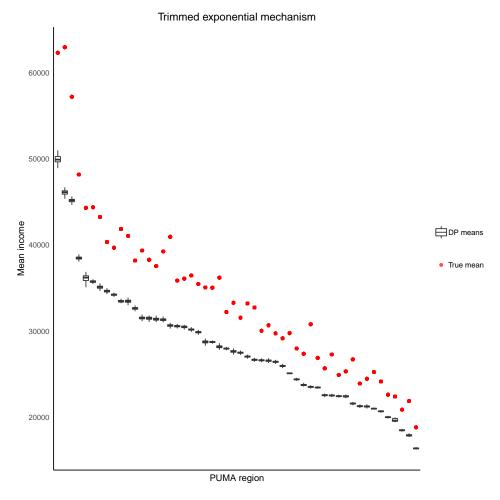
- (e) My intuition is that this mechanism is ϵ -DP. First, since we are combining the results of three $\frac{\epsilon}{3}$ -DP mechanisms, we can say that the resulting mechanism is ϵ -DP. Second, the scale of the Laplace noise is appropriate here, as the sensitivity of our data is proportional to the range of our data $(GS_q = \frac{\hat{P}_{.95} \hat{P}_{.05}}{n})$ once we clamp to the estimated percentiles. Finally, the mechanism in (b) failed to meet DP because we composed a mechanism that was ϵ -DP with a transformation that leaked information about the underlying data. In this mechanism, the Winsorization step is not leaking information in the same way since the percentiles are being estimated in a DP fashion.
- (f) As the plots below show, the Laplace mechanism gives unbiased results for the actual mean while the trimmed exponential mechanism means are downwardly biased. In this case, it appears pretty obvious that the ordinary Laplace mechanism provides better performance. That is likely because the data is heavily right-skewed so that the ordinary Laplace mechanism (which only trims the data to a range based on the user's knowledge of the data domain) does not remove much of the data before computing a noisy estimate while the trimmed exponential mechanism clamps data to the 5^{th} and 95^{th} percentile, which will by design push the right tail of the income distribution downward, which will downwardly bias the estimate of the mean. In general, I would expect that the Laplace mechanism would perform better than the trimmed exponential mechanism for heavily skewed data like the PUMS income data.

On the other hand, I would expect the opposite to be true if the data was normally distributed but the user provided clip values were not symmetric around the mean of the distribution so the mean estimate would be biased in the direction in which the user's data domain varied from the empirical data range. By design, the percentiles that the trimmed exponential mechanism clamps to will be more symmetric around the center so the estimates of the means from that mechanism will be unbiased.

One further observation: in the the ordinary Laplace mechanism, we add noise proportional to the user provided value of D, i.e., the maximum value of the data domain. As such, if we increase D we will add more noise to the released mean and would observe much more variance between our estimates and the true means for each PUMA. Changing the value of D does not affect the noise added by the trimmed exponential mechanism in the same way, so increasing D for this mechanism will not affect the variance of our results.

Thinking about the utility of the trimmed exponential mechanism for this dataset, if we took the log of the income variable, we would expect the mechanism to produce much more unbiased results since this transformation would remove the skew that led to the downwardly biased results.





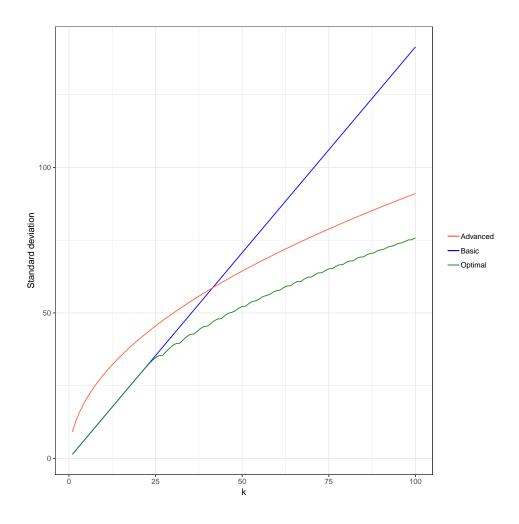
Below is a table with the average RMSE from both mechanisms for each PUMA region. In general, RMSE values are much lower for the exponential mechanism than for the ordinary Laplace mechanism, which is supported by my analysis of the skewed nature of the PUMS income data above.

PUMA Region	Average RMSE from Laplace	Average RMSE from exponential
100	201.41762	4757.708
200	96.43064	4662.124
300	199.57360	3423.130
400	269.36341	6171.545
500	166.58453	5452.784
600	242.78767	2604.331
700	171.35101	7264.007
800	218.93572	7809.378
900	222.07640	6287.309
1000	247.81285	6803.281
1100	184.56191	7906.431
1200	219.24006	3108.631
1300	204.28659	5709.944
1400	244.22946	12289.516
1500	228.59527	5592.113
1600	266.94429	5122.327
1700	225.09186	2628.419
1800	272.99281	3570.783

PUMA Region	Average RMSE from Laplace	Average RMSE from exponential
1900	207.26280	2388.282
2000	293.69294	5635.852
2100	239.79814	3303.858
2200	231.88797	5590.211
2300	167.56098	3452.322
2400	264.97385	8144.962
2500	262.76689	7603.388
2600	276.92916	16863.435
2700	141.88965	8618.011
2800	285.77781	8151.286
2900	272.77687	3210.070
3000	265.51085	3207.903
3100	240.76374	3608.770
3200	265.05926	8010.977
3301	256.26174	3971.552
3302	219.55111	10291.362
3303	262.61158	2440.315
3304	230.89783	2900.297
3305	223.37613	4105.401
3400	196.99428	12029.469
3500	244.37049	9701.943
3600	299.01899	5552.113
3700	256.16577	5295.376
3800	240.03737	6316.291
3900	210.59690	8397.562
4000	251.43058	2468.830
4100	178.66542	4245.715
4200	317.01122	3420.228
4300	262.04722	4073.000
4400	196.19946	2733.223
4500	132.79131	4252.374
4600	175.22269	6308.186
4700	192.01704	6160.371
4800	171.88171	6063.544

Question 2

The "optimal" composition theorem strictly improves upon the standard deviation of the injected noise from the basic composition theorem when $k \geq 17$ and advanced composition strictly improves upon basic composition when $k \geq 42$. Up to k = 17, basic and "optimal" composition correspond to roughly the same standard deviation. The standard deviation from advanced composition is strictly larger than the standard deviation from "optimal" composition, but the ratio between the two appears to remain constant as $k \to \infty$.



Question 3

Here, I examine the utility of synthetic data generated using the DP histogram approach. To do this, I (1) generate synthetic data by adding Laplace distributed noise to the age x education x income bin counts for the PUMS data, (2) sample 10,000 synthetic observations based on these bin counts, (3) estimate a regression model relating age and education to income, and (4) compute the mean squared error, squared bias, and variance of the coefficient estimates for age, education, and the intercept. To get a sense of the expected behavior of this procedure, I repeat this process 10 times (performing it many more times was too computationally expensive).

As a pre-process to this whole procedure, I clip the income variable to 1 so that I can work with the log of the income. I then use the log of the clipped income for the remainder of the problem, i.e., to compute the sensitive regression on the entire dataset and to produce the histogram release and corresponding synthetic data.

The table below summarizes my results. The MSE from running the regression on synthetic data is slightly larger than the MSE from running the regression on bootstrapped data, which suggests that the synthetic data approach I implement here only adds slightly more noise than we would expect to be added due to sampling. It is very likely that this DP-added error would go down even further if I binned income into more than 10 bins (I chose 10 because it made computation time reasonable).

Decomposing the MSE of the DP release itself, the bias is contributing much more to the introduced error than variance. This implies that our method will be stable while at the same time there is room to improve

upon the bias, i.e., binning variables (like income) with more granularity.

Metric	Intercept	Education	Age
DP MSE	0.2181647	0.0000379	0.0004556
DP Variance	0.0067352	0.0000010	0.0000758
DP Bias^2	0.2114295	0.0000370	0.0003797
Sampling MSE	0.2174255	0.0000242	0.0010317

BONUS

One possible idea would be to include a full example tutorial for the interface. For instance, a potential user could be walked through, step-by-step how to carry out an analysis for an example dataset (like the California Census data). Right now the interface does a nice job of explaining what is happening to users and requiring that they input domain knowledge and specify their privacy budget beforehand (with the option of adjusting things after they begin their analysis). I find that a full tutorial is often helpful for me when transitioning over to new services.

This semester I am taking a class on the science of behavior change (aka behavioral economics). We talk a lot about choice architecture and I definitely see some of the principles we talk about in practice here, like requiring forced choice, anchoring people's choice of ϵ with information about what type of data requires what approximate value of ϵ , and adding friction when users try to do undesirable things (like set $\epsilon >> 1$). I think forced choice makes sense here because you want to force users to be really thoughtful about what they want to do.but However, it might be worthwhile to also set defaults that are skewed toward preserving privacy, since default options tend to be very sticky.

People like Todd Rogers at the Harvard Kennedy School might be good resources for further development of the tool from a behavioral user design perspective.

Appendix

I put the code for all of my analyses here. You can also find it on Github.

```
# Set up
require(plyr); require(dplyr); require(ggplot2)
pums <- read.csv("MaPUMS5full.csv")</pre>
```

Question 1

```
# a
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)
}

trimmedMean <- function(x, n, d, epsilon) {
  scale <- d/(epsilon*0.9*n)
  quants <- quantile(x, c(0.05,0.95))</pre>
```

```
x trimmed <- x[x>quants[1] & x<quants[2]]</pre>
  mean_trimmed <- (1/(0.9*n))*sum(x_trimmed)</pre>
  mean_release <- mean_trimmed + rlap(mu=0,b=scale,size=1)</pre>
  return(mean_release)
}
exponentialPercentile <- function(x, t, d, epsilon){</pre>
  t <- t/100
  bins <- sort(c(x,d))
  nbins = length(bins)
  likelihoods <- rep(NA, nbins)</pre>
  for(i in 1:nbins){
    quality <- -1 * abs(nbins*t - i)
    if(i < nbins) { bin_width <- bins[i]-bins[i+1]+1 }</pre>
    else { bin_width <- 1 }</pre>
    likelihoods[i] <- (exp(epsilon * quality) / 2)*(bin_width)</pre>
  }
  probabilities <- likelihoods/sum(likelihoods)</pre>
  flag <- runif(n=1, min=0, max=1) < cumsum(probabilities)</pre>
  bin_low_ind = which(flag)[1]
  bin_high_ind = bin_low_ind + 1
  DPrelease <- runif(n=1, min=bins[bin_low_ind], max=bins[bin_high_ind])
  return(DPrelease)
}
# d
e3trimmedMean <- function(x, epsilon, n, d, tile_low=5, tile_high=95) {
  tile_low_value <- exponentialPercentile(x, t=tile_low, d=d, epsilon=epsilon/3)
  tile_high_value <- exponentialPercentile(x, t=tile_high, d=d, epsilon=epsilon/3)
  x_trimmed <- x[x>tile_low_value & x<tile_high_value]</pre>
  mean trimmed \langle (1/(0.9*n)) \rangle \times (x \text{ trimmed})
  scale <- (3*(tile_high_value-tile_low_value))/(0.9*epsilon*n)</pre>
  mean_release <- mean_trimmed + rlap(mu=0,b=scale,size=1)</pre>
  return(mean release)
}
clip <- function(x, lower, upper){</pre>
                                           # borrowed from class
  x.clipped \leftarrow x
  x.clipped[x.clipped<lower] <- lower</pre>
  x.clipped[x.clipped>upper] <- upper</pre>
  return(x.clipped)
}
rmse <- function(pred, true) {</pre>
  val <- sqrt(mean((pred-true)^2))</pre>
  return(val)
```

```
}
laplaceMeanRelease <- function(x, lower, upper, epsilon){</pre>
                                                                 # borrowed from class
  n <- length(x)
  sensitivity <- (upper - lower)/n
  scale <- sensitivity / epsilon</pre>
  x.clipped <- clip(x, lower, upper)</pre>
  DPrelease <- mean(x.clipped) + rlap(mu=0, b=scale, size=1)</pre>
  return(DPrelease)
}
### simulations
pumas <- unique(pums$puma)</pre>
n_pumas <- length(pumas)</pre>
n_reps <- 100
means_mat <- matrix(NA, nrow=n_pumas*n_reps, ncol=6)</pre>
row ind <- 1
for(i in 1:n_pumas){
  print(i)
  puma_region <- pumas[i]</pre>
  dat <- pums$income[pums$puma==puma_region]</pre>
  true_mean <- mean(dat)</pre>
  for(j in 1:n_reps){
    laplace_noise <- laplaceMeanRelease(x=dat, lower=0, upper=1000000 , epsilon=1)</pre>
    e3_trimmed <- e3trimmedMean(x=dat, epsilon=1, n=length(dat), d=1000000)
    means_mat[row_ind,1] <- puma_region</pre>
    means_mat[row_ind,2] <- true_mean</pre>
    means_mat[row_ind,3] <- laplace_noise</pre>
    means_mat[row_ind,4] <- e3_trimmed</pre>
    means_mat[row_ind,5] <- rmse(laplace_noise, true_mean)</pre>
    means_mat[row_ind,6] <- rmse(e3_trimmed, true_mean)</pre>
    row ind <- row ind + 1
  }
}
means_df <- data.frame(means_mat)</pre>
names(means_df) <- c("puma","true_mean","laplace_mean","exponential_mean","rmse_laplace","rmse_exponent
### results
q1_results <- means_df %>% group_by(puma) %>% summarise(avg_lap=mean(rmse_laplace),
                                             avg_exp=mean(rmse_exponential))
write.csv(q1_results, "q1_results.csv")
q1_plot1 <- ggplot(data=means_df, aes(x=reorder(factor(puma), -laplace_mean))) +
  geom_boxplot(aes(y=laplace_mean, shape="DP means"), outlier.shape=NA, alpha=0.7) +
  geom_point(aes(y=true_mean, colour="True mean")) +
  scale_colour_manual(values=c("red")) +
  labs(x="PUMA region", y="Mean income", title="Laplace mechanism") +
```

```
theme bw() +
  theme(axis.text.x=element_blank(), axis.ticks.x=element_blank(), axis.ticks.y=element_blank(),
        axis.line = element line(colour = "black"), panel.grid.major = element blank(),
        panel.grid.minor = element_blank(), panel.border = element_blank(),
        panel.background = element_blank(), legend.title = element_blank(),
        plot.title = element text(hjust = 0.5))
pdf("plots/q1_plot1.pdf", width=8, height=8)
q1 plot1
dev.off()
q1_plot2 <- ggplot(data=means_df, aes(x=reorder(factor(puma), -exponential_mean))) +
  geom_boxplot(aes(y=exponential_mean, shape="DP means"), outlier.shape=NA, alpha=0.7) +
  geom_point(aes(y=true_mean, colour="True mean"), alpha=0.7) +
  scale_colour_manual(values=c("red")) +
  labs(x="PUMA region", y="Mean income", title="Trimmed exponential mechanism") +
  theme_bw() +
  theme(axis.text.x=element_blank(), axis.ticks.x=element_blank(), axis.ticks.y=element_blank(),
        axis.line = element_line(colour = "black"), panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(), panel.border = element_blank(),
        panel.background = element_blank(), legend.title = element_blank(),
        plot.title = element_text(hjust = 0.5))
pdf("plots/q1_plot2.pdf", width=8, height=8)
q1 plot2
dev.off()
Question 2
# parameters
global_epsilon = 1
global_delta = 10^{-9}
global_sens = 1
max_k = 100
# Laplace sd
laplaceSD <- function(epsilon) { return((sqrt(2)/epsilon)) }</pre>
# basic
basicComposition <- function(epsilon, k) { return(epsilon/k) }</pre>
advancedComposition <- function(epsilon, k, delta) { return(epsilon/sqrt(2*k*log(1/delta))) }
# optimal
# use PSIlence:::update_parameters
# compute sds
sds <- matrix(NA, nrow=100, ncol=4)</pre>
for (k in 1:max_k) {
  epsilon_comp <- basicComposition(global_epsilon, k)</pre>
  epsilon_adv <- advancedComposition(global_epsilon, k, global_delta)</pre>
  init \leftarrow rep(c(1/k, 0), k)
```

```
params <- matrix(init, nrow=k, ncol=2, byrow=TRUE)</pre>
  inverse <- PSIlence:::update_parameters(params, hold=0, eps=global_epsilon, del=global_delta)</pre>
  epsilon_opt <- max(inverse[,1])</pre>
  sds[k,1] <- laplaceSD(epsilon_comp)</pre>
  sds[k,2] <- laplaceSD(epsilon adv)</pre>
  sds[k,3] <- laplaceSD(epsilon_opt)</pre>
  sds[k,4] \leftarrow k
sds_df <- data.frame(sds)</pre>
names(sds_df) <- c("basic", "advanced", "optimal", "k")</pre>
q2_plot <- ggplot(sds_df) + geom_line(aes(x=k, y=basic, colour="Basic")) +
  geom_line(aes(x=k, y=advanced, colour="Advanced")) +
  geom_line(aes(x=k, y=optimal, colour="Optimal")) +
  labs(x="k", y="Standard deviation") +
  scale_colour_manual(values=c("#FF6347", "#0000FF", "#228B22")) +
  theme_bw() +
  theme(legend.title = element blank())
pdf("plots/q2_plot.pdf", width=8, height=8)
q2 plot
dev.off()
# when do advanced/optimal beat basic?
paste0("Advanced: ", min(sds_df$k[sds_df$advanced < sds_df$basic]))</pre>
paste0("Optimal: ", min(sds_df$k[sds_df$optimal < sds_df$basic]))</pre>
Question 3
sgn <- function(x) {  # borrowed from class</pre>
  return(ifelse(x < 0, -1, 1))
rlap = function(mu=0, b=1, size=1) {  # borrowed from class
  p <- runif(size) - 0.5
  draws <- mu - b * sgn(p) * log(1 - 2 * abs(p))
  return(draws)
clip <- function(x, lower, upper){</pre>
                                      # borrowed from class
  x.clipped \leftarrow x
  x.clipped[x.clipped<lower] <- lower</pre>
  x.clipped[x.clipped>upper] <- upper</pre>
  return(x.clipped)
}
bootstrap <- function(x, y=NULL, n){</pre>
                                          # borrowed from class
  index <- sample(x=1:length(x), size=n, replace=TRUE)</pre>
  if(is.null(y)){
    return(x[index])
  }else{
```

```
return(list(x=x[index], y=y[index]))
  }
}
normalize <- function(x){</pre>
                              # borrowed from class
  x[x<0] <- 0
  x <- x/sum(x)
  return(x)
mse <- function(pred, true) {</pre>
  mse = mean((pred-true)^2)
  return(mse)
}
xyzHistogramRelease <- function(x, y, z, xlower, xupper, ylower, yupper, zlower, zupper, xnbins=0, ynbi
  if(xnbins==0){
    xlower <- floor(xlower)</pre>
    xupper <- ceiling(xupper)</pre>
    xbins <- xlower:(xupper+1)</pre>
    xnbins <- length(xbins)-1</pre>
    xgranularity <- 1
    xcodebook <- xbins[1:xnbins]</pre>
  } else {
    xbins <- seq(from=xlower, to=xupper, length=xnbins+1)</pre>
    xgranularity <- (xupper-xlower)/xnbins</pre>
    xbins[xnbins+1] <- xbins[xnbins+1] + xgranularity</pre>
    xcodebook <- xbins[1:xnbins] + 0.5*xgranularity</pre>
  }
  if(ynbins==0){
    ylower <- floor(ylower)</pre>
    yupper <- ceiling(yupper)</pre>
    ybins <- ylower:(yupper+1)</pre>
    ynbins <- length(ybins)-1</pre>
    ygranularity <- 1
    ycodebook <- ybins[1:ynbins]</pre>
  } else {
    ybins <- seq(from=ylower, to=yupper, length=ynbins+1)</pre>
    ygranularity <- (yupper-ylower)/ynbins</pre>
    ybins[ynbins+1] <- ybins[ynbins+1] + ygranularity</pre>
    ycodebook <- ybins[1:ynbins] + 0.5*ygranularity</pre>
  }
  if(znbins==0){
    zlower <- floor(zlower)</pre>
    zupper <- ceiling(zupper)</pre>
    zbins <- zlower:(zupper+1)</pre>
    znbins <- length(zbins)-1</pre>
    zgranularity <- 1
    zcodebook <- zbins[1:znbins]</pre>
  } else {
    zbins <- seq(from=zlower, to=zupper, length=znbins+1)</pre>
```

```
zgranularity <- (zupper-zlower)/znbins
    zbins[znbins+1] <- zbins[znbins+1] + zgranularity</pre>
    zcodebook <- zbins[1:znbins] + 0.5*zgranularity</pre>
  }
  x.clipped <- clip(x=x, lower=xlower, upper=xupper)</pre>
  y.clipped <- clip(x=y, lower=ylower, upper=yupper)</pre>
  z.clipped <- clip(x=z, lower=zlower, upper=zupper)</pre>
  sensitivity <- 2
  scale <- sensitivity / (epsilon)</pre>
  sensitiveValue <- DPrelease <- matrix(NA, nrow=xnbins*ynbins*znbins, ncol=4)
  row_ind <- 1</pre>
  for(i in 1:xnbins){
    for(j in 1:ynbins){
      for(k in 1:znbins){
        bin_count <- sum(x.clipped >= xbins[i] & x.clipped < xbins[i+1] & y.clipped >= ybins[j] & y.cli
        release_count <- bin_count + rlap(mu=0, b=scale, size=1)
        sensitiveValue[row_ind,] <- c(i,j,k,bin_count)</pre>
        DPrelease[row_ind,] <- c(i,j,k,release_count)</pre>
        row_ind = row_ind + 1
    }
  }
 return(list(release=DPrelease, true=sensitiveValue, xcodebook=xcodebook, ycodebook=ycodebook, zcodebo
# clip and log income
pums$log_income_clipped <- log(clip(x=pums$income, lower=1, upper=1000000))</pre>
log_income_low <- floor(log(1))</pre>
log_income_high <- ceiling(log(1000000))</pre>
# run histogram release
start = Sys.time()
res = xyzHistogramRelease(x=pums$educ, y=pums$age, z=pums$log_income_clipped,
                           xlower=1, xupper=16, ylower=18, yupper=100, zlower=log_income_low, zupper=log
                           xnbins=0, ynbins=0, znbins=10, epsilon=1)
end = Sys.time()
end-start
# private results
synthetic_n <- 10000
synthetic_bin_probs <- normalize(res$release[,4])</pre>
synthetic_inds <- sample(x=1:nrow(res$release), size=synthetic_n, replace=TRUE, prob=synthetic_bin_prob
synthetic_data <- res$release[synthetic_inds,1:3]</pre>
synthetic_data_df <- data.frame(synthetic_data)</pre>
names(synthetic_data_df) <- c("educ", "age", "log_income")</pre>
synthetic_data_df$educ <- plyr::mapvalues(synthetic_data_df$educ,</pre>
                                             from=sort(unique(synthetic_data_df$educ)),
```

```
to=res$xcodebook)
synthetic_data_df$age <- plyr::mapvalues(synthetic_data_df$age,</pre>
                                            from=sort(unique(synthetic_data_df$age)),
                                            to=res$ycodebook)
synthetic_data_df$log_income <- plyr::mapvalues(synthetic_data_df$log_income,
                                           from=sort(unique(synthetic data df$log income)),
                                           to=res$zcodebook)
synthetic_reg <- lm(log_income ~ age + educ, data = synthetic_data_df)</pre>
synthetic_slopes <- coef(synthetic_reg)[1:3]</pre>
# sensitive results
true_reg <- lm(log_income_clipped ~ age + educ, data = pums)</pre>
true_slopes <- coef(true_reg)[1:3]</pre>
# error
paste0("MSE for intercept: ", mse(synthetic_slopes[1], true_slopes[1]))
paste0("MSE for age coefficient: ", mse(synthetic_slopes[2], true_slopes[2]))
paste0("MSE for education coefficient: ", mse(synthetic_slopes[3], true_slopes[3]))
# simulations to examine contribution to MSE of bias and variance
n sims <- 10
sim_history <- matrix(NA, nrow=n_sims, ncol=3)</pre>
if(run_sims_flag){
  for(i in 1:n_sims){
    print(i)
    res_sim = xyzHistogramRelease(x=pums$educ, y=pums$age, z=pums$log_income_clipped,
                                   xlower=1, xupper=16, ylower=18, yupper=100, zlower=log_income_low, zu
                                   xnbins=0, ynbins=0, znbins=10, epsilon=1)
    synthetic_bin_probs_sim <- normalize(res_sim$release[,4])</pre>
    synthetic_inds_sim <- sample(x=1:nrow(res_sim$release), size=synthetic_n, replace=TRUE, prob=synthe
    synthetic_data_sim <- res_sim$release[synthetic_inds_sim,1:3]</pre>
    synthetic_data_sim_df <- data.frame(synthetic_data_sim)</pre>
    names(synthetic_data_sim_df) <- c("educ", "age", "log_income")</pre>
    synthetic_data_sim_df$educ <- plyr::mapvalues(synthetic_data_sim_df$educ,
                                                    from=sort(unique(synthetic_data_sim_df$educ)),
                                                    to=res_sim$xcodebook)
    synthetic_data_sim_df$age <- plyr::mapvalues(synthetic_data_sim_df$age,
                                                   from=sort(unique(synthetic data sim df$age)),
                                                   to=res sim$ycodebook)
    synthetic_data_sim_df$log_income <- plyr::mapvalues(synthetic_data_sim_df$log_income,
                                                      from=sort(unique(synthetic_data_sim_df$log_income))
                                                      to=res_sim$zcodebook)
    synthetic_reg_sim <- lm(log_income ~ age + educ, data = synthetic_data_sim_df)
    synthetic_slopes_sim <- coef(synthetic_reg_sim)[1:3]</pre>
    sim_history[i,1] <- synthetic_slopes_sim[1]</pre>
    sim_history[i,2] <- synthetic_slopes_sim[2]</pre>
    sim_history[i,3] <- synthetic_slopes_sim[3]</pre>
  write.csv(sim_history, "sim_history.csv")
```

```
}
sim history <- read.csv("sim history.csv")</pre>
# bootstrap to examine sampling error
n boots <- 1000
boot size <- 1000
boot_history <- matrix(NA, nrow=n_boots, ncol=3)</pre>
for(i in 1:n_boots){
  boot_inds <- bootstrap(x=1:nrow(pums), n=boot_size)</pre>
  boot_data <- pums[boot_inds,]</pre>
  boot_reg <- lm(log_income_clipped ~ age + educ, data=boot_data)</pre>
  boot_slopes <- coef(boot_reg)[1:3]</pre>
  boot_history[i,1] <- boot_slopes[1]</pre>
  boot_history[i,2] <- boot_slopes[2]</pre>
  boot_history[i,3] <- boot_slopes[3]</pre>
}
# print results
mse_int <- mse(pred=sim_history[,2], true=true_slopes[1])</pre>
var_int <- var(sim_history[,2])</pre>
bias_sq_int <- mse_int - var_int</pre>
sampling_mse_int <- mse(boot_history[,1], true_slopes[1])</pre>
mse_age <- mse(pred=sim_history[,3], true=true_slopes[2])</pre>
var_age <- var(sim_history[,3])</pre>
bias_sq_age <- mse_age - var_age</pre>
sampling_mse_age <- mse(boot_history[,2], true_slopes[2])</pre>
mse_educ <- mse(pred=sim_history[,4], true=true_slopes[3])</pre>
var_educ <- var(sim_history[,4])</pre>
bias_sq_educ <- mse_educ-var_educ</pre>
sampling_mse_educ <- mse(boot_history[,3], true_slopes[3])</pre>
cat("Intercept","\nDP MSE: ", mse_int, "\nDP Variance: ", var_int, "\nDP Bias^2: ", bias_sq_int, "\nSam
cat("Age","\nDP MSE: ", mse_age, "\nDP Variance: ", var_age, "\nDP Bias^2: ", bias_sq_age, "\nSampling I
cat("Educ", "\nDP MSE: ", mse_educ, "\nDP Variance: ", var_educ, "\nDP Bias^2: ", bias_sq_educ, "\nSampl
# save results
q3 results <- data.frame("Metric"=c("DP MSE","DP Variance","DP Bias^2","Sampling MSE"),
                           "Intercept"=c(mse_int,var_int,bias_sq_int,sampling_mse_int),
                           "Education"=c(mse_age,var_age,bias_sq_age,sampling_mse_age),
                           "Age"=c(mse_educ,var_educ,bias_sq_educ,sampling_mse_educ))
write.csv(q3_results, "q3_results.csv")
```