HW4B: Stochastic Gradient Descent and Lipschitz Extensions

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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/HW4b/HW4b_Bhaven_Patel.ipynb).

Problem 1

(a)

$G = \mathbb{R}^n$, $H = [a, b]^n$, $x \sim x'$ differ on one row, $f(x) = \frac{1}{n} \sum_{i=1}^{n} x_i$

(i)
The global sensitivity $GS_f(x) = \infty$ because we can change any value in the dataset x from to ∞ (or some arbitrarily large number) to get a neighboring dataset x'. Thus, this would change the mean by ∞.

(ii)
The minimum local sensitivity $\min_{x \in G} LS_f(x) = \infty$ because the best case dataset x would be a one-value dataset/array $x = [x_1]$, where x_1 is any value. The worst case neighboring dataset x' would be a one-value dataset/array $x' = [x'_1]$, where $x'_1 = \infty$ (or some very large number). Thus, the difference between $f(x)$ and $f(x')$ would be infinite like the global sensitivity case.

(iii)
The restricted sensitivity of $RS_f^H = \frac{b-a}{n}$ because in the worst case we have a dataset $x = [a]^n$ and a neighboring dataset $x' = [a, \ldots, a, b]$, so the difference between $f(x)$ and $f(x')$ would be $\frac{b-a}{n}$, which is much less than the global sensitivity or the minimum local sensitivity.

Lipschitz entension
A Lipschitz entension of f would be

$$f'(x) = \frac{1}{n} \sum_{i=1}^{n} [x_i]_a^b$$

where each x_i is clipped to be between a and b.

This obeys the first condition of a Lipschitz entension that $f'(x)$ agrees with $f(x)$ on H because any datasets $x \in H$ are already clipped so the elements x_i are between a and b, so $f'(x) = f(x)$.

$f'(x)$ also obeys the second condition of a Lipschitz entension that $GS_{f'} = RS_{f'}^H$ because the $GS_{f'} = \dfrac{b-a}{n}$ because all the values in the datasets x and x' will be clipped to be between a and b, so the worst case difference between $f'(x)$ and $f'(x')$ is $\dfrac{b-a}{n}$. $RS_{f'}^H = \dfrac{b-a}{n}$ too because $x \in H$ means all the values in the dataset x will be clipped to be between a and b, so the worst case difference between $f'(x)$ and $f'(x')$, where $x,\ x' \in H$, is also $\dfrac{b-a}{n}$.

Thus, $f'(x)$ is a Lipschitz entension of f.

(b)

$G = \mathbb{R}^n$, $H = [a,b]^n$, $x \sim x'$ differ on one row, $f(x) = \text{median}(x_1, \ldots, x_n)$

(i)

The global sensitivity $GS_f(x) = \infty$ because say the dataset x is composed of 0s and ∞s (or some arbitrarily large numbers), where there is 1 more 0 than ∞ so $f(x) = 0$. In the worst case, a neighboring dataset x' would have one of the 0s changed to an ∞, so $f(x') = \infty$. Thus, the median has changed by ∞, so $GS_f(x) = \infty$.

(ii)

The minimum local sensitivity $\min_{x \in G} LS_f(x) = \infty$ because the best case dataset x would be a one-row dataset $x = [0]$, so $f(x) = 0$. The worst case neighboring dataset x' would be dataset $x' = [\infty]$, and $f(x') = \infty$. Thus, the difference between $f(x)$ and $f(x')$ would be ∞.

(iii)

The restricted sensitivity of $RS_f^H = b - a$ because in the worst case we have a dataset x composed of as and bs, where there is 1 more a than b so $f(x) = a$. In the worst case, a neighboring dataset x' would have one of the as changed to a b, so $f(x') = b$. Thus, the median has changed by $b - a$, so $RS_f^H = b - a$.

(c)

$G =$ the set of undirected graphs,
$H =$ the set of graphs in G in which every vertex has degree at most $d,\ 2 \leq d \leq n-1$,
$x \sim x'$ differ on one node/vertex, $f(x) = \#$ of isolated vertices

(i)

The global sensitivity $GS_f(x) = n$, where n is the number of nodes/vertices in graph x. In the worst case, the graph $x \in G$ can be composed of n isolated vertices, $f(x) = n$. A neighboring graph x' is the same as x except for an additional vertex that shares an edge with every other node, making $f(x') = 0$. Thus, difference between $f(x)$ and $f(x')$ is at maximum n.

(ii)

The minimum local sensitivity $\min_{x \in G} LS_f(x) = 1$ because the best case graph x would have 0 isolated vertices, so $f(x) = 0$. The worst case neighboring graph x' would be x plus an isolated vertex, so $f(x') = 1$. Thus, difference between $f(x)$ and $f(x')$ is at maximum 1, which is the same for the global sensitivity.

(iii)

The restricted sensitivity of $RS_f^H = d$ because in the worst case, a graph $x \in H$ consists of n vertices where all the vertices are unconnected. For the graph x, $f(x) = n$. Then, we could have a neighboring graph x' in which the single vertex with d edges is added to x. Thus, $f(x') = n - d$, so the difference between $f(x)$ and $f(x')$ is d.

Problem 2

Local model for DP-SGD

Below is my implementation of the local model for DP-SGD. I changed it from the centralized model for DP-SGD because for every subject i in my batch S_t, I compute a noisy gradient for the current θs/parameters by calculating the actual gradient and then adding noise sampled from the Gaussian distribution $N(0, \tau^2 I)$, where

$$\tau = \left(\frac{C}{\epsilon_0/2}\right) \cdot \sqrt{T \cdot \frac{L}{n} \cdot \log\left(\frac{1}{\delta}\right)}$$

C is the clipping parameter. ϵ_0 is our total privacy-loss parameter specified by the user; we divide it by two because we are releasing two θs/parameters. δ is our also our user-specified parameter for (ϵ, δ)-DP. T is the number of steps, L is the batch size, and n is the number of training points.

In [1]:

```
## Here is the likelihood function for a Logit. 'b' is array of betas
calcllik<-function(b,data){
    y<-data[,1]
    x<-data[,2]

    pi<- 1/(1+exp(-b[1] - b[2]*x)) # Here is the systematic component
    if(pi == 1.0){ #probability of 1.0 causes NaNs, so change to 0.99999
        pi <- 0.99999;
    }
    if(pi == 0.0){ #probability of 0.0 causes NaNs and infinities, so chang
        pi <- 0.00001;
    }

    llik <- y * log(pi) + (1-y) * log(1-pi) # Here is the stocastic compone

    return(-llik)
}


## Bound/Censor/Clip a variable to a range
clip <- function(x, lower, upper){
    x.clipped <- x
    x.clipped[x.clipped<lower] <- lower
    x.clipped[x.clipped>upper] <- upper
    return(x.clipped)
}
```

In [2]:

```
#load the Massachusetts PUMS data
library("foreign");
PUMSdata <- read.csv(file="https://raw.githubusercontent.com/privacytoolspr

marg_educ_data <- PUMSdata[c("married","educ")]; #get married and education

#predict are you married {0,1} based on education
output <- glm(married ~ educ, family="binomial", data=marg_educ_data)
```

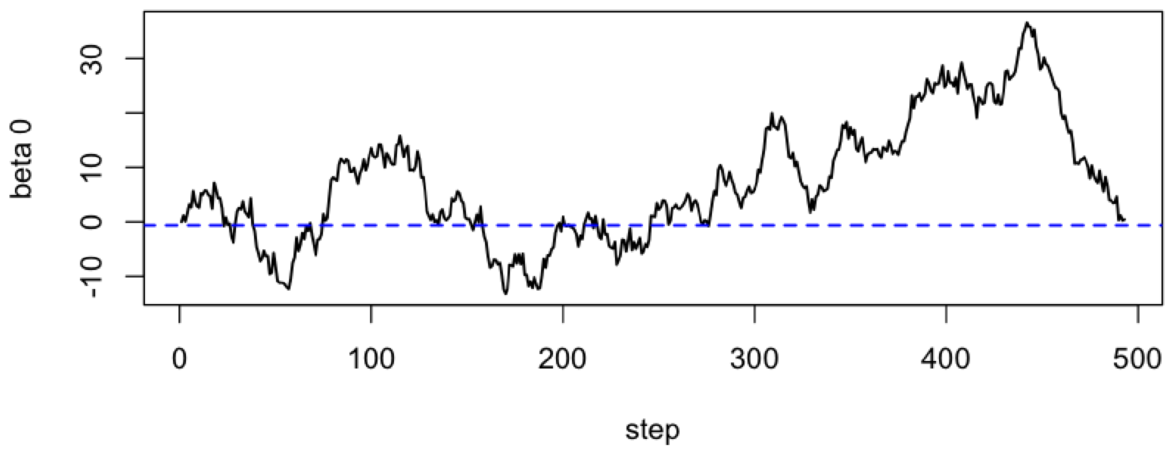
In [3]:
```
# Calculate the gradient at a point in the parameter space
calcgradient_localRelease <- function(row, C, thetas, fun, noise_sigma){
    dx <- 0.0001
    #using numerical approximation of gradient for each theta. Assuming two
    out1 <- eval(fun(b=thetas, data=row))
    out2 <- eval(fun(b=thetas + c(0,dx), data=row))
    out3 <- eval(fun(b=thetas + c(dx,0), data=row))

    #calculate clipped gradient for theta1
    theta1_grad <- (out3 - out1) / dx;
    theta1_grad <- clip(theta1_grad, lower=-C, upper=C);

    #calculate clipped gradient for theta2
    theta2_grad <- (out2 - out1) / dx;
    theta2_grad <- clip(theta2_grad, lower=-C, upper=C);

    #add Gaussian noise to gradients
    thetas_grad <- c(theta1_grad, theta2_grad) + rnorm(n=length(thetas), me

    return(thetas_grad);
}
```

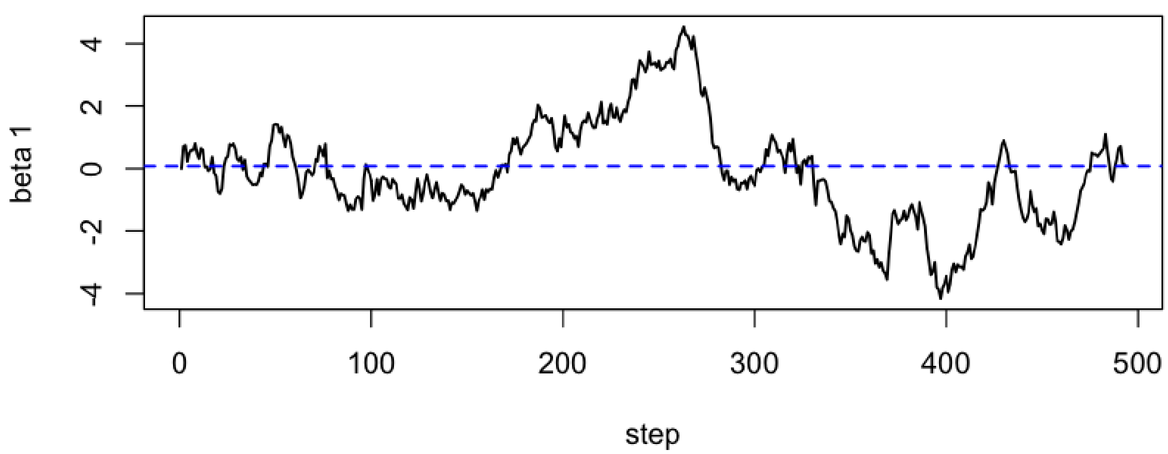
In [4]:
```
# ##function to perform local model for SGD
# ##
# ## data: 2-column dataframe where first
# ## N: number of training data points
# ## batch_size: number of training points to be considered in each step
# ## steps: number of iterations to perform local SGD for
# ## C: clipping parameter for gradient
# ## epsilon: privacy-loss parameter
# ## delta: privacy-loss parameter
localSGD <- function(data, N, batch_size, steps, C, epsilon, delta=1e-6){

    thetas <- c(0,0)   # Starting parameters
    nu <- c(0.05, 0.01); #c(1,0.01)   # Learning speeds for each theta
    history <- matrix(NA, nrow=steps+1, ncol=2);
    history[1,] <- thetas;

    # Iterate one step of SGD
    for(i in 1:steps){

        #Generate our batch for this step
        startB <- ((i-1)*batch_size+1) #beginning index for our batch
        if(i<batch_size){#get end index for our batch
            stopB <- i*batch_size;
        }else{
            stopB <- nrow(data)
        }
        B <- data[startB:stopB, ]; #get rows for this batch

        #calculate gradient separately for each point
        tot_gradient <- c(0,0);
        sigma = C / (epsilon/2) * sqrt( steps*batch_size/N * log(1/delta) )

        for(b in 1:nrow(B)){
            single_row <- B[b, ]; #get row from the data
            #calculate the gradient for this data point
            # 'C' is the clipping parameter. 'thetas' are our parameters to
            # 'noise_sigma' is the standard deviation for the normal with w
            grad_i <- calcgradient_localRelease(single_row, C, thetas, fun=
            tot_gradient <- tot_gradient + grad_i;
        }

        ave_gradient <- tot_gradient / batch_size;
    #   cat("Del:  ",Del,"\n")
        thetas <- thetas - (nu * ave_gradient);   #theta^(l+1) = theta^(l)
    #   cat("Theta:",theta, "\n")

        history[i+1,] <- thetas;
    }

    return(history);
}
```

In [10]:
```
N <- nrow(marg_educ_data);
L <- round(sqrt(N));      # This is the recommended batch size- sqrt(# of tr
# set.seed(24);
steps <- L; #number of iterations for SGD is same as the number of batches

## Shuffle the data
index <- sample(1:nrow(marg_educ_data), replace=FALSE); #shuffle because we
marg_educ_data <- marg_educ_data[index,];
epsilon = 0.1;
delta = 1e-6;
C <- 10;               # Interval to clip over

history <- localSGD(data=marg_educ_data, N=N, batch_size=L, steps=steps, C=
                    epsilon=epsilon, delta=1e-6);

history
```

0.00000000	0.000000000
1.14315834	0.714910003
0.09071891	0.745191032
1.53889885	0.224617753
3.24127378	0.492825849
2.62331115	0.591141451
5.64571983	0.580655562
3.75142509	0.804210150
2.89119127	0.472479052
2.56410473	0.311100252
5.23543482	0.650424595
5.00780169	0.590312072
5.74613548	0.052310917

In [11]:
```
par(mfcol=c(2,1))

all.ylim<-c( min(c(history[,1],output$coef[1] )), max(c(history[,1],output$
plot(history[,1], type="l", ylim=all.ylim, ylab="beta 0", xlab="step", lwd=
abline(h=output$coef[1], lty=2, col="blue", lwd=1.5)


all.ylim<-c( min(c(history[,2],output$coef[2] )), max(c(history[,2],output$
plot(history[,2], type="l", ylim=all.ylim, ylab="beta 1", xlab="step", lwd=
abline(h=output$coef[2], lty=2, col="blue", lwd=1.5)

# dev.copy2pdf(file="./dpSGD.pdf")
```





As the plots above show, my `localSGD` function provides a DP-release of θ_0 and θ_1 that are close to true, non-DP θ values when I use an $\epsilon = 1$. We observe much more jitteriness in the values of the θs because we are adding much more noise in the local model. I tuned my learning rate parameters until I got good results using an $epsilon = 1$.

Evaluate performance of the local model of DP-SGD

Below, I evaluate the performance of the local model of DP-SGD by performing DP-releases for θ_0 and θ_1 for ϵs in ranging from 0.1 to 10. For each ϵ, I perform 5 DP-releases, so that I can calculate a range of classification errors for each ϵ and calculate the RMSE of the DP-released parameters compared to the non-DP released parameters.

In [3]:
```
#function to calculate the classification error given the data and thetas f
calc_classf_error <- function(data, thetas){
    preds <- 1 / (1+ exp(-thetas[1] - thetas[2] * data[,2]) ); #perform lin
    preds[preds >= 0.5] <- 1; #convert probabilities >= 0.5 to 1s
    preds[preds < 0.5] <- 0; #convert probabilities < 0.5 to 0s
#     cat(sum(preds))

    y_true = data[[1]]; #get the true classifications
    comparison <- (preds == y_true); #compare the predictions to true label
    error <- 1 - mean(comparison); #mean of comparison vector is accuracy.
    return(error);

}
```

In [13]:
```
### SET-UP PARAMETERS
eps_vals <- c(0.1, 0.25, 0.5, 0.75, 1.0, 2.0, 5.0, 10.0);
num_sims <- 5;
N <- nrow(marg_educ_data);
L <- round(sqrt(N));      # This is the recommended batch size- sqrt(# of tr
steps <- L; #number of iterations for SGD is same as the number of batches
delta = 1e-6;
C <- 10;               # Interval to clip over

#shuffle because we worry the data may have been sorted in some way
index <- sample(1:nrow(marg_educ_data), replace=FALSE);
marg_educ_data <- marg_educ_data[index,];

thetas_history <- matrix(0, nrow=length(eps_vals)*num_sims, ncol=4);

row = 1;
for(eps in eps_vals){
    #printing for diagnostic purposes
    cat("Beginning simulations for epsilon= ", eps, '\n');
    cat(format(Sys.time(), "%a %b %d %X %Y"), '\n')

    for(l in 1:num_sims){
        #get a DP release of the thetas for the given epsilon
        history <- localSGD(data=marg_educ_data, N=N, batch_size=L, steps=s
        dp_thetas <- history[L+1, ];
        #calculate classificaiton error for this DP-release of thetas
        clsf_error <- calc_classf_error(data = marg_educ_data, thetas=dp_th
        #save the thetas and classification error
        thetas_history[row, ] <- c(eps, dp_thetas, clsf_error);
        row <- row + 1;
    }
}
```

```
Beginning simulations for epsilon=  0.1
Sun Apr 28 18:36:08 2019
Beginning simulations for epsilon=  0.25
Sun Apr 28 18:38:53 2019
Beginning simulations for epsilon=  0.5
Sun Apr 28 18:41:40 2019
Beginning simulations for epsilon=  0.75
Sun Apr 28 18:44:26 2019
Beginning simulations for epsilon=  1
Sun Apr 28 18:47:12 2019
Beginning simulations for epsilon=  2
Sun Apr 28 18:49:56 2019
Beginning simulations for epsilon=  5
Sun Apr 28 18:52:37 2019
Beginning simulations for epsilon=  10
Sun Apr 28 18:55:21 2019
```

In [14]:
```
#create dataframe from history matrix
thetas_history_df <- as.data.frame(thetas_history);
colnames(thetas_history_df) <- c("Epsilon", "Theta0", "Theta1", "Classifica
#save the dataframe to analyze later
write.csv(thetas_history_df, './theta_vals.csv')
```

Below, I load the DP-releases of the theta values for different values of ϵ.

In [1]:
```
thetas_history_df <- read.csv("./theta_vals.csv");

thetas_history_df
```

X	Epsilon	Theta0	Theta1	Classification_Error
1	0.10	-1.478539e+01	5.933797e+00	0.4513088
2	0.10	1.164043e+01	1.309560e+00	0.4527602
3	0.10	7.005811e-01	-2.380979e+00	0.5472398
4	0.10	-5.554668e+01	5.776009e+00	0.4538601
5	0.10	6.548709e+00	3.789757e-01	0.4527602
6	0.25	3.355382e+00	-1.911276e-01	0.4527602
7	0.25	-1.403541e+01	2.121839e+00	0.4473639
8	0.25	3.470551e+00	-2.720917e-01	0.5309515
9	0.25	-9.081222e+00	8.912470e-01	0.4562833
10	0.25	3.437159e+00	-2.501663e-01	0.4957946
11	0.50	-5.764790e-01	1.327062e-02	0.5472398
12	0.50	1.322441e+01	-1.041727e+00	0.5309515

Calculate the true values for β_0 and β_1. Also calculate the classification error for these values.

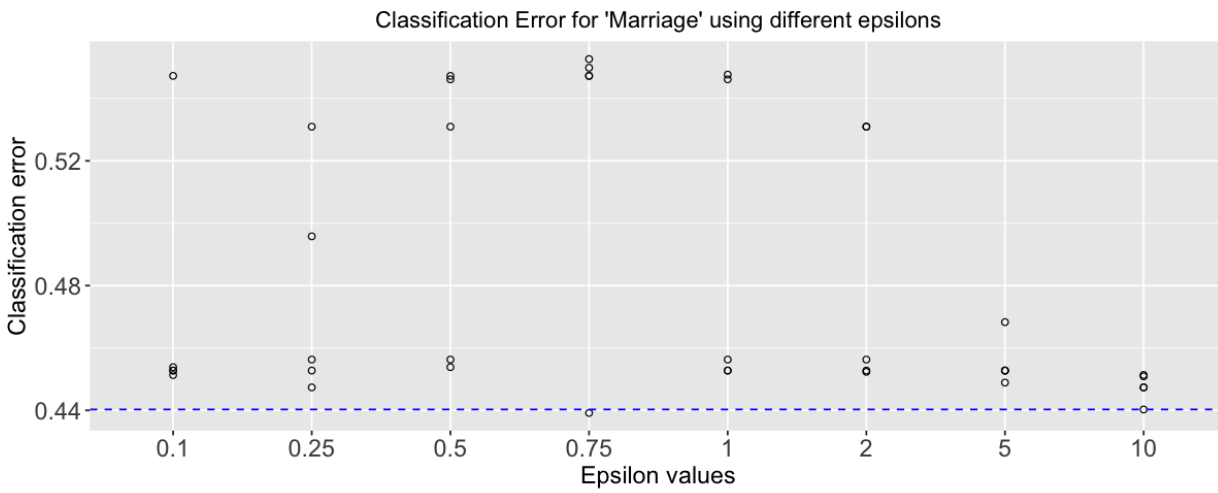
In [4]:
```
#get actual beta0 and beta1
PUMSdata <- read.csv(file="https://raw.githubusercontent.com/privacytoolspr
marg_educ_data <- PUMSdata[c("married","educ")]; #get married and educatior

#predict are you married {0,1} based on education
output <- glm(married ~ educ, family="binomial", data=marg_educ_data);

#calculate classification error for non-DP thetas
nondp_error <- calc_classf_error(data = marg_educ_data, thetas=output$coeff
nondp_error
```

0.440280362237936

In [5]:
```
#function to calculate the RMSE of DP-released thetas compared to true thet
calc_rmse <- function(theta_preds, true_theta){
    square_sum <- sum( (theta_preds - true_theta)^2 );
    rmse <- sqrt(square_sum);
    return(rmse);
}

#calculate RMSE values for thetas
unq_eps <- unique(thetas_history_df$Epsilon); #get unique epsilon values
rmse_matrix <- matrix(data = 0, nrow = length(unq_eps), ncol = 3);

row_counter = 1;
for(eps in unq_eps){
    eps_thetas <- thetas_history_df[thetas_history_df$Epsilon == eps, ];
    eps_thetas[['Theta0']]
    theta0_rmse <- calc_rmse(theta_preds = eps_thetas[['Theta0']],
                             true_theta = output$coefficients[1]);
    theta1_rmse <- calc_rmse(theta_preds = eps_thetas[['Theta1']],
                         true_theta = output$coefficients[2]);

    rmse_matrix[row_counter, ] <- c(eps, theta0_rmse, theta1_rmse);
    row_counter = row_counter + 1;
}

rmse_matrix_df <- as.data.frame(rmse_matrix);
colnames(rmse_matrix_df) <- c("Epsilon", "Theta0_RMSE", "Theta1_RMSE");
rmse_matrix_df
```

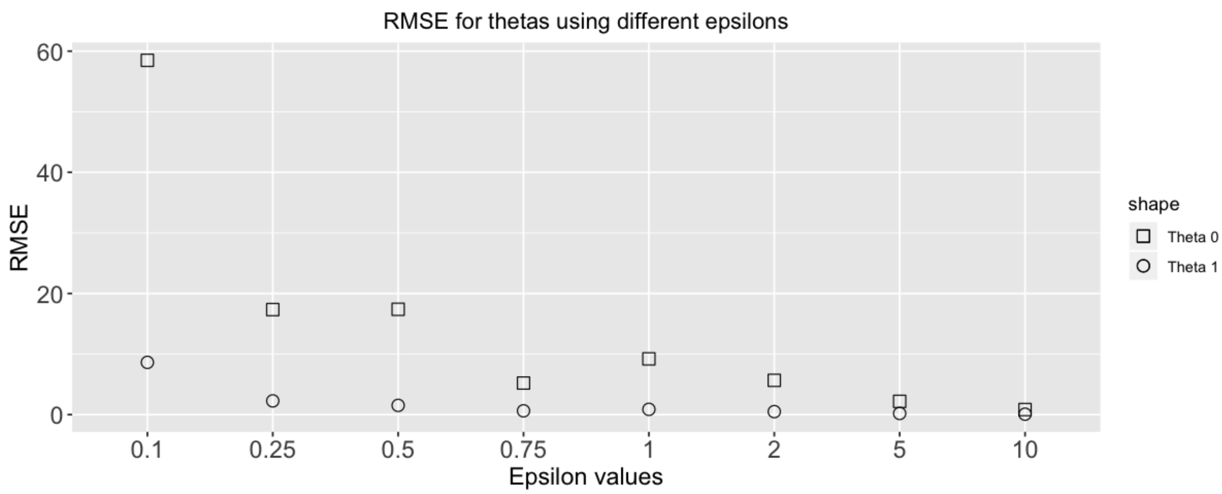
Epsilon	Theta0_RMSE	Theta1_RMSE
0.10	58.4897664	8.62586692
0.25	17.3367477	2.26721362
0.50	17.3861059	1.52739047
0.75	5.2143182	0.62752650
1.00	9.2045759	0.87378240
2.00	5.6627062	0.49357280
5.00	2.1886716	0.19687928
10.00	0.8359723	0.07511608

In [8]:
```
library(ggplot2)
# plot classification errors for different epsilon values
x_vals <- factor(thetas_history_df$Epsilon);
p1 <- ggplot(thetas_history_df) +
    geom_point(aes(x=x_vals, y=thetas_history_df$Classification_Error), sha
    geom_hline(yintercept=nondp_error, linetype="dashed", color = "blue");

p1 <- p1 + labs(x = "Epsilon values", y = 'Classification error', title =
        'Classification Error for \'Marriage\' using different epsilons') +
    theme(plot.title = element_text(hjust = 0.5),
          axis.text = element_text(size=14), axis.title = element_text(size

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



The dashed blue line represents the classification error of the non-DP released θ_0 and θ_1 when used to predict "Marriage" based on "Education".

In [7]:
```
library(ggplot2)
# plot classification errors for different epsilon values
x_vals <- factor(rmse_matrix_df$Epsilon);
p1 <- ggplot(rmse_matrix_df) +
    geom_point(aes(x=x_vals, y=rmse_matrix_df$Theta0_RMSE, shape='Theta 0')
    geom_point(aes(x=x_vals, y=rmse_matrix_df$Theta1_RMSE, shape='Theta 1')

p1 <- p1 + scale_shape_manual(values = c("Theta 0"=0, "Theta 1"=1));

p1 <- p1 + labs(x = "Epsilon values", y = 'RMSE', title =
        'RMSE for thetas using different epsilons') +
    theme(plot.title = element_text(hjust = 0.5),
          axis.text = element_text(size=14), axis.title = element_text(size

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



The first graph shows the relationship between ϵ and classification error rate. For the most part, lower values of ϵ lead to higher classification error rate, as can be seen with $\epsilon = 0.25, 0.5$, and 0.75. Unexpectedly, the classification error for $\epsilon = 0.1$ is near the true classification error rate for most of the 5 trials, which could be due to the low number of simulations (5) run or possibly the regularization effect of performing a differentially-private release of the θs; the noise added at $\epsilon = 0.1$ may help the model better predict on points that the non-DP model misclassifies. When $\epsilon > 1$, the classification error for most trials shrinks toward the classification error observed with the non-DP θs (blue line), which is expected because we add less noise to the gradients with greater values of ϵ.

The second graph displays the RMSE between the DP-released θs for a given value of ϵ and the non-DP released θs. Overall, as ϵ increases, we observe that the RMSE of the θs decreases, and at $\epsilon = 10$, the RMSEs are almost 0. Although the classification error rate for $\epsilon = 0.1$ was closer to baseline, the RMSE for the θs is the highest for $\epsilon = 0.1$, which is expected because an $\epsilon = 0.1$ causes a larger standard deviation for the Normal distribution from which we draw noise. As stated above, the noiser θs must be better at classifying some of the points that are misclassified as the $thetas$ approach the non-DP θs. For all values of ϵ, θ_1 has a lower RMSE than θ_0, which might be due to the larger learning rate for θ_1, causing it to jump around much more with each update to it.