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 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 $GS_{f'} = RS^H_{f'}$ because the $GS_{f'} = \frac{b-a}{n}$ 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 $\frac{b-a}{n}$. $RS^H_{f'} = \frac{b-a}{n}$ too because $x \in H$ means all the values in the dataset x will be between a and b, so the worst case difference between $f'(x)$ and $f'(x')$, where $x,\ x' \in H$, is also $\frac{b-a}{n}$.

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 $RS^H_f = b - a$ 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 $RS^H_f = b - a$.

(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, so $f(x) = n$. 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.

For a given batch S_t, the noisy gradients from each subject/observation are averaged, and then the average is used to update the θs/parameters based on the specified learning rate.

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)
}
```

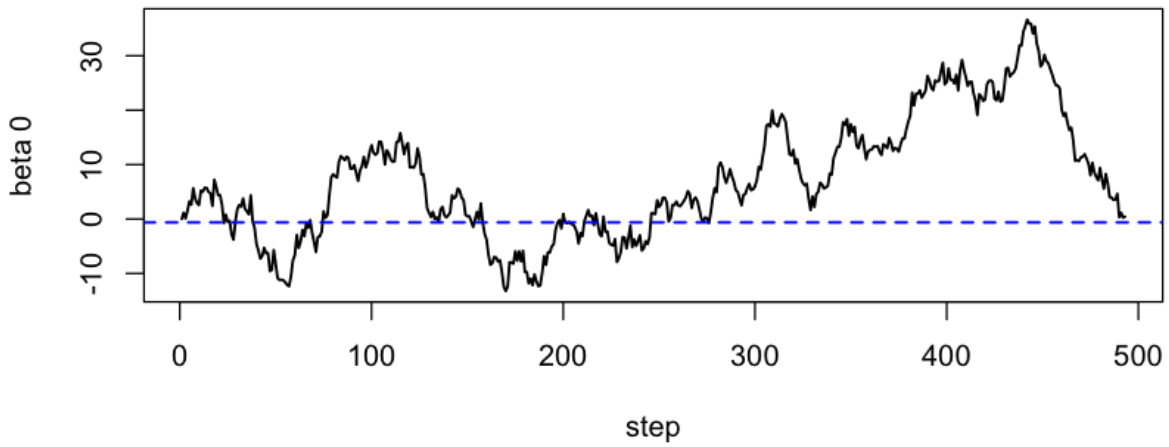
In [2]:
```
#load the Massachusetts PUMS data
library("foreign");
PUMSdata <- read.csv(file="https://raw.githubusercontent.com/privacytoolspr

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

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

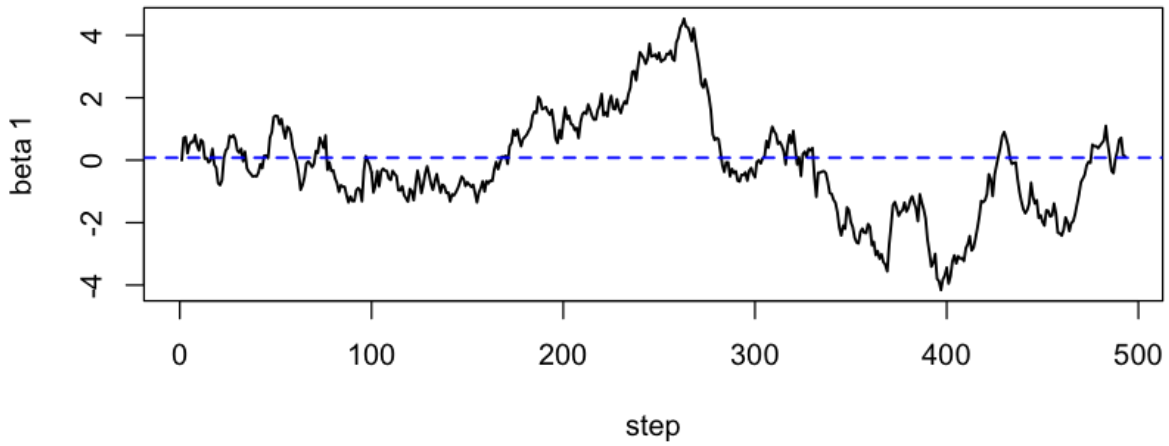
In [3]:
```
# Calculate the gradient at a point in the parameter space
calcgradient_localRelease <- function(row, C, thetas, fun, noise_sigma){
    dx <- 0.0001
    #using numerical approximation of gradient for each theta. Assuming two
    out1 <- eval(fun(b=thetas, data=row))
    out2 <- eval(fun(b=thetas + 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;
        thetas <- thetas - (nu * ave_gradient);   #theta^(l+1) = theta^(l)

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

    return(history);
}
```

In [ ]:
```
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
```

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

    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.

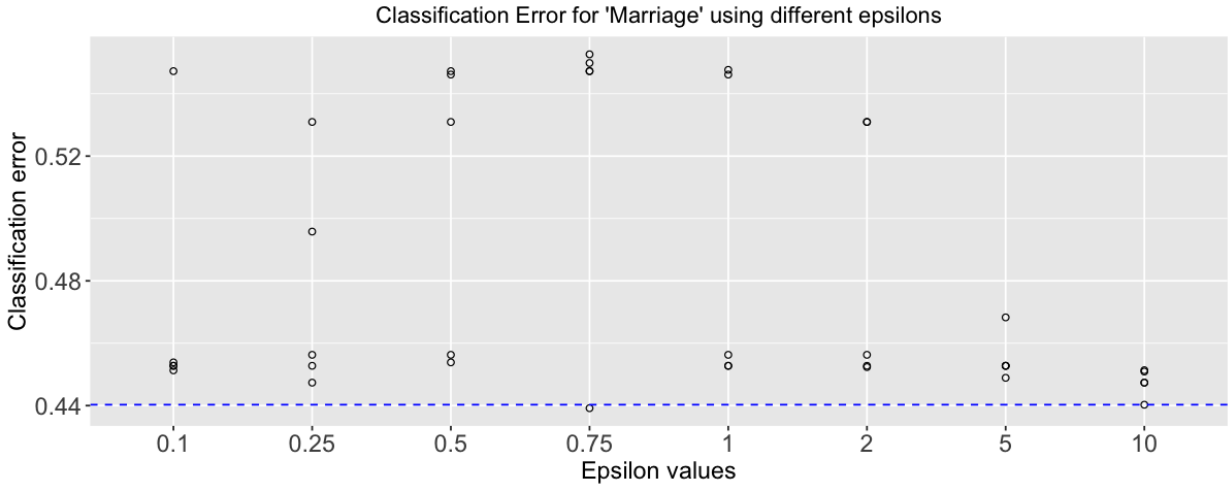
In [4]:
```
#get actual beta0 and beta1
PUMSdata <- read.csv(file="https://raw.githubusercontent.com/privacytoolspr
marg_educ_data <- PUMSdata[c("married","educ")]; #get married and educatior

#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$Epsilon == eps, ];
    theta0_rmse <- calc_rmse(theta_preds = eps_thetas[['Theta0']],
                             true_theta = output$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
```

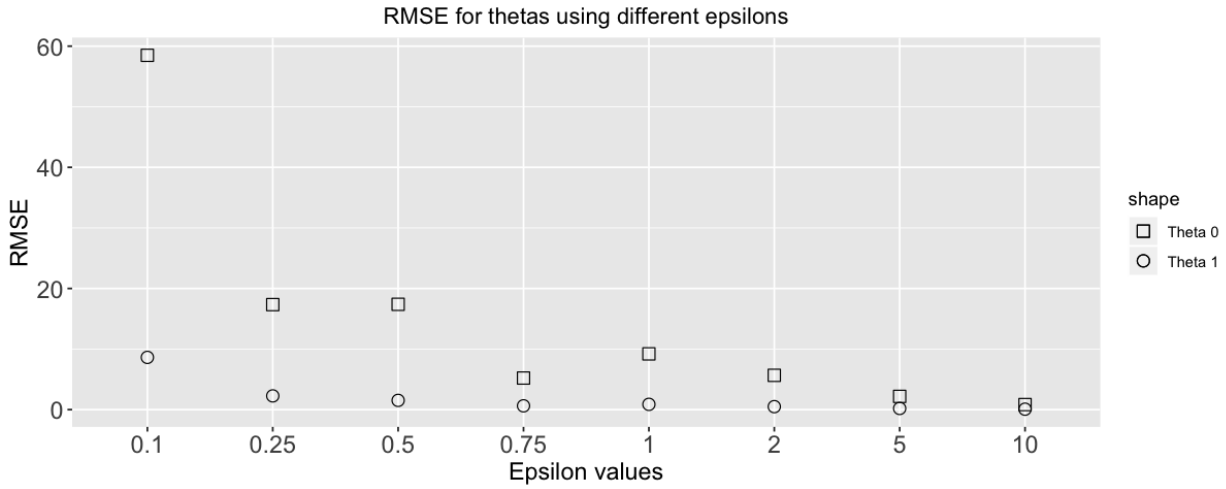
Epsilon	Theta0_RMSE	Theta1_RMSE
0.10	58.4897664	8.62586692
0.25	17.3367477	2.26721362
0.50	17.3861059	1.52739047
0.75	5.2143182	0.62752650
1.00	9.2045759	0.87378240
2.00	5.6627062	0.49357280
5.00	2.1886716	0.19687928
10.00	0.8359723	0.07511608

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. I ran this simulation a few times, and the classification error rates at low values of ϵ jump around between 0.44 and 0.56 randomly, which might be due to the fact that we are only using one predictor for classifying "Marriage" status. 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 $\epsilon = 0.1$ leads to a larger standard deviation for the Normal distribution from which we draw noise. 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 during SGD. The DP-released θ_0 values are also generally an order of magnitude greater than their accompanying θ_1 values, leading to the larger RMSE.