

R Notebook

First, we load the dataset and get every package we need ready.

```
df = read.csv('rehosp.csv')
test = read.csv("test_rehosp.csv")

library(gbm)
```

```
## Loaded gbm 2.1.5
```

Then we use the gbm function to build a boosting method model. We name it "bm".

```
bm = gbm(hospital ~ ., data = df, distribution = 'adaboost',
         n.trees = 500, interaction.depth = 2, shrinkage = 0.01, verbose = F)
```

Now let's see how well it performed.

```
pdtn = predict(bm, newdata = test, n.trees = 500)
sqrt(mean((pdtn - test$hospital)^2))
```

```
## [1] 1.33946
```