

HeartDisease_Model

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Logistic Model

```
#Grabbing Saved Csv file created from python
hd.df <- read.csv('HeartDisease_clean.csv', stringsAsFactors = T)

#Checking to make sure everything is how it's supposed to be
#str(hd.df)
#dim(hd.df)

set.seed(42)
train.index <- sample(c(1:dim(hd.df)[1]), dim(hd.df)[1]*0.6)
train.df <- hd.df[train.index, ]
valid.df <- hd.df[-train.index, ]

# run logistic regression
# use glm() (generalized linear model) with family = "binomial" to fit a logistic
# regression.
logit.reg <- glm(HeartDisease ~ ., data = train.df, family = "binomial")
summary(logit.reg)

##
## Call:
## glm(formula = HeartDisease ~ ., family = "binomial", data = train.df)
##
## Deviance Residuals:
##      Min        1Q     Median        3Q       Max
## -2.2047   -0.4185   -0.2613   -0.1475    3.4689
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -5.982182  0.078556 -76.152 < 2e-16 ***
## BMI          0.013502  0.001453   9.291 < 2e-16 ***
## Smoking       0.457013  0.018204  25.106 < 2e-16 ***
## AlcoholDrinking -0.289324  0.043552  -6.643 3.07e-11 ***
## Stroke         1.147333  0.028887  39.717 < 2e-16 ***
## PhysicalHealth  0.022282  0.000966  23.067 < 2e-16 ***
## MentalHealth    0.009787  0.001121   8.730 < 2e-16 ***
## DiffWalking     0.407066  0.022986  17.709 < 2e-16 ***
## Sex            0.736602  0.018545  39.719 < 2e-16 ***
```

```

## AgeCategory      0.282363   0.003858   73.196 < 2e-16 ***
## Race            0.024226   0.008183   2.960 0.003072 **
## Diabetic        0.299656   0.010320   29.036 < 2e-16 ***
## PhysicalActivity -0.077089  0.020493  -3.762 0.000169 ***
## GenHealth       -0.030193  0.006577  -4.590 4.42e-06 ***
## SleepTime        -0.031416  0.005579  -5.631 1.79e-08 ***
## Asthma          0.347512   0.024620   14.115 < 2e-16 ***
## KidneyDisease    0.744684   0.030978   24.039 < 2e-16 ***
## SkinCancer       0.129114   0.024820   5.202 1.97e-07 ***
##
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 112665  on 191876  degrees of freedom
## Residual deviance: 89577  on 191859  degrees of freedom
## AIC: 89613
##
## Number of Fisher Scoring iterations: 6

```

Logistic Regression Assumptions

```
library(car)
```

```
## Loading required package: carData
```

```
car::vif(logit.reg) # really good in terms of multicolinearity because nothing is above 2
```

	BMI	Smoking	AlcoholDrinking	Stroke
##	1.164010	1.035150	1.018863	1.030259
##	PhysicalHealth	MentalHealth	DiffWalking	Sex
##	1.395021	1.220200	1.424225	1.068930
##	AgeCategory	Race	Diabetic	PhysicalActivity
##	1.239205	1.055830	1.118845	1.171042
##	GenHealth	SleepTime	Asthma	KidneyDisease
##	1.010863	1.040068	1.056930	1.043661
##	SkinCancer			
##	1.075697			

```
library(arm)
```

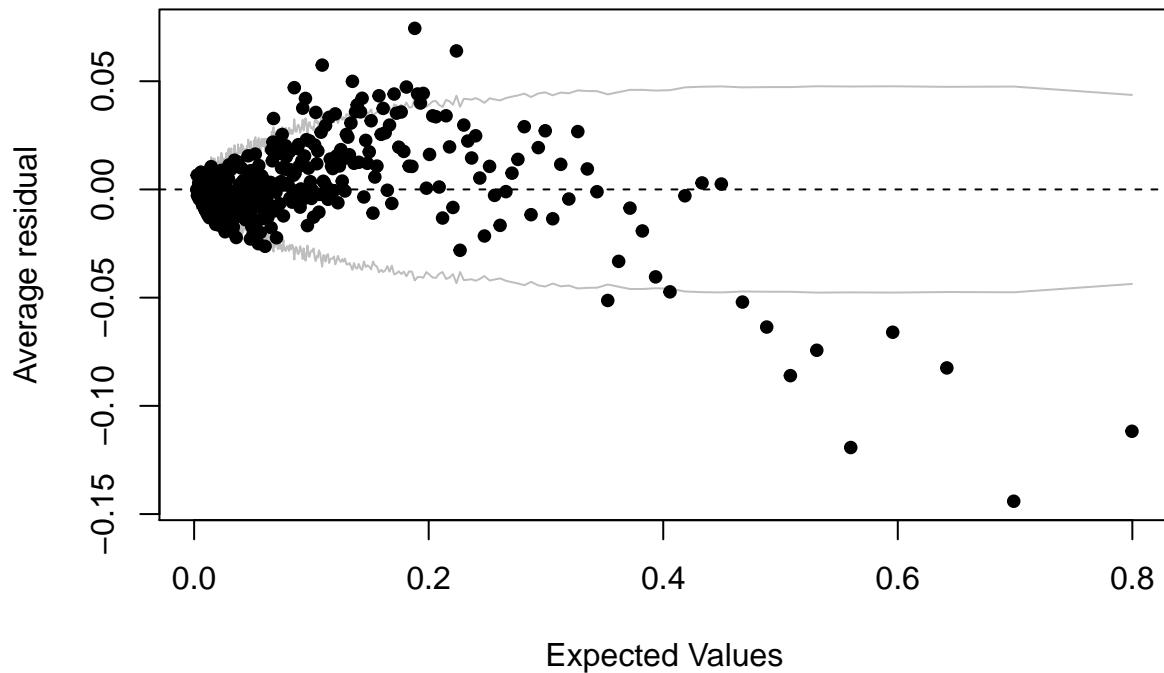
```
## Loading required package: MASS
```

```
## Loading required package: Matrix
```

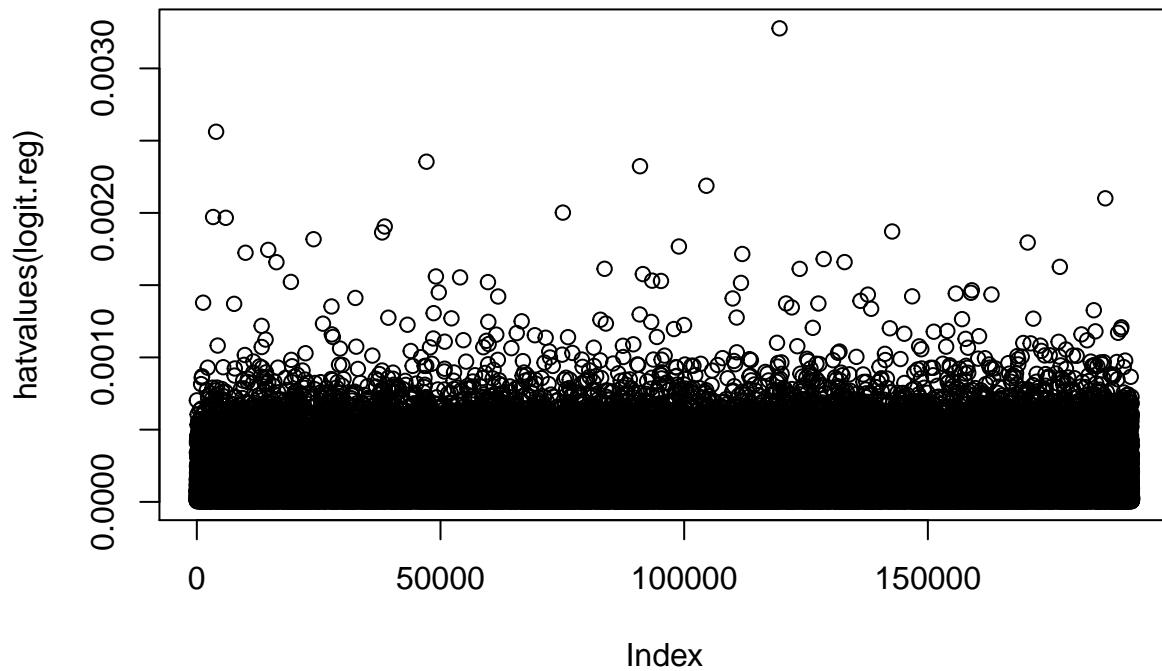
```
## Loading required package: lme4
```

```
## Registered S3 methods overwritten by 'lme4':  
##   method           from  
##   cooks.distance.influence.merMod car  
##   influence.merMod            car  
##   dfbeta.influence.merMod    car  
##   dfbetas.influence.merMod   car  
  
##  
## arm (Version 1.12-2, built: 2021-10-15)  
  
## Working directory is /Users/kevintroncoso/Desktop/Internships  
  
##  
## Attaching package: 'arm'  
  
## The following object is masked from 'package:car':  
##  
##   logit  
  
binnedplot(fitted(logit.reg),  
            residuals(logit.reg, type = "response"),  
            nclass = NULL,  
            xlab = "Expected Values",  
            ylab = "Average residual",  
            main = "Binned residual plot",  
            cex.pts = 0.8,  
            col.pts = 1,  
            col.int = "gray")
```

Binned residual plot



```
log.pred<-predict(logit.reg, valid.df, type = "response")
#plot(log.pred, which = 5)
plot(hatvalues(logit.reg))
```



Measure of accuracy and Rmse

```
#Produce the confusion matrix with cutoff=0.5, through trial and error we see its the best one.
yhat<-ifelse(log.pred > 0.5, 1,0)
y<-valid.df$HeartDisease
con.matrix<-table(yhat, y)
con.matrix

##      y
## yhat      0      1
##   0 116116  9827
##   1    963  1012

#Classification Rate: one measure of accuracy
class.rate = (con.matrix[1]+con.matrix[4])/(sum(con.matrix))
class.rate

## [1] 0.9156491

#Produce ROC
library(pROC)
```

```

## Type 'citation("pROC")' for a citation.

##
## Attaching package: 'pROC'

## The following objects are masked from 'package:stats':
## cov, smooth, var

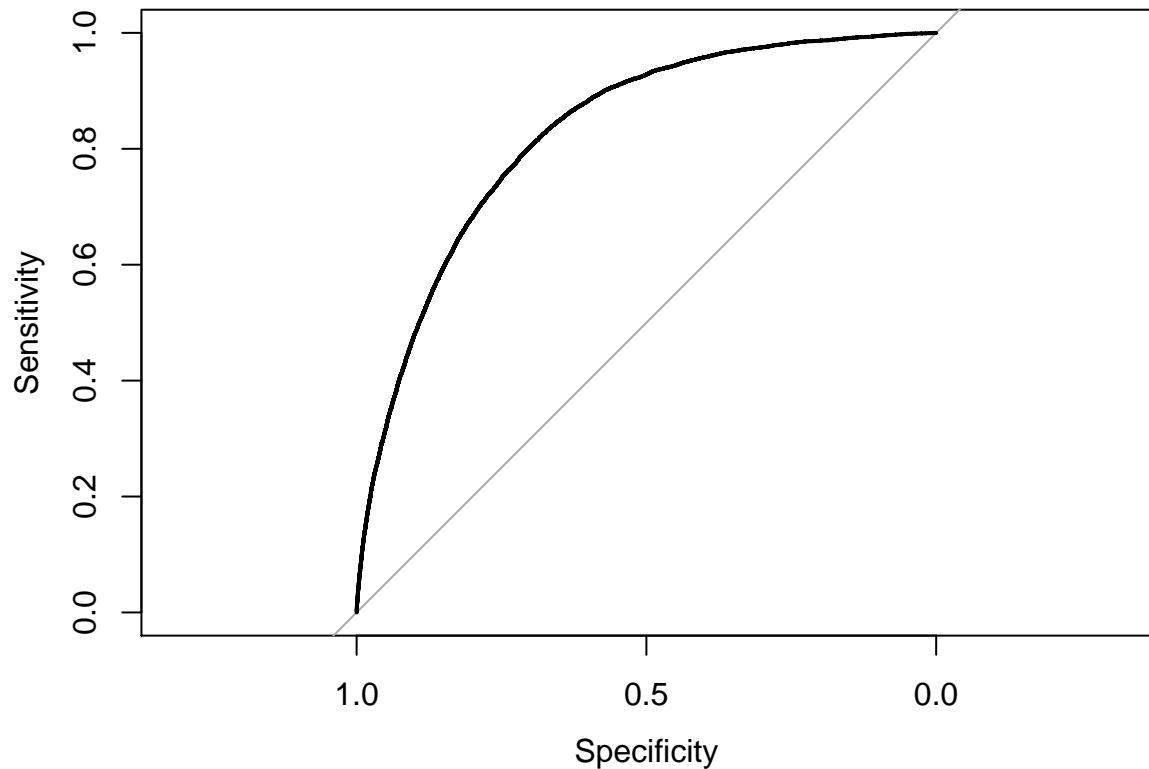
log.r<-roc(y,log.pred)

## Setting levels: control = 0, case = 1

## Setting direction: controls < cases

plot.roc(log.r)

```



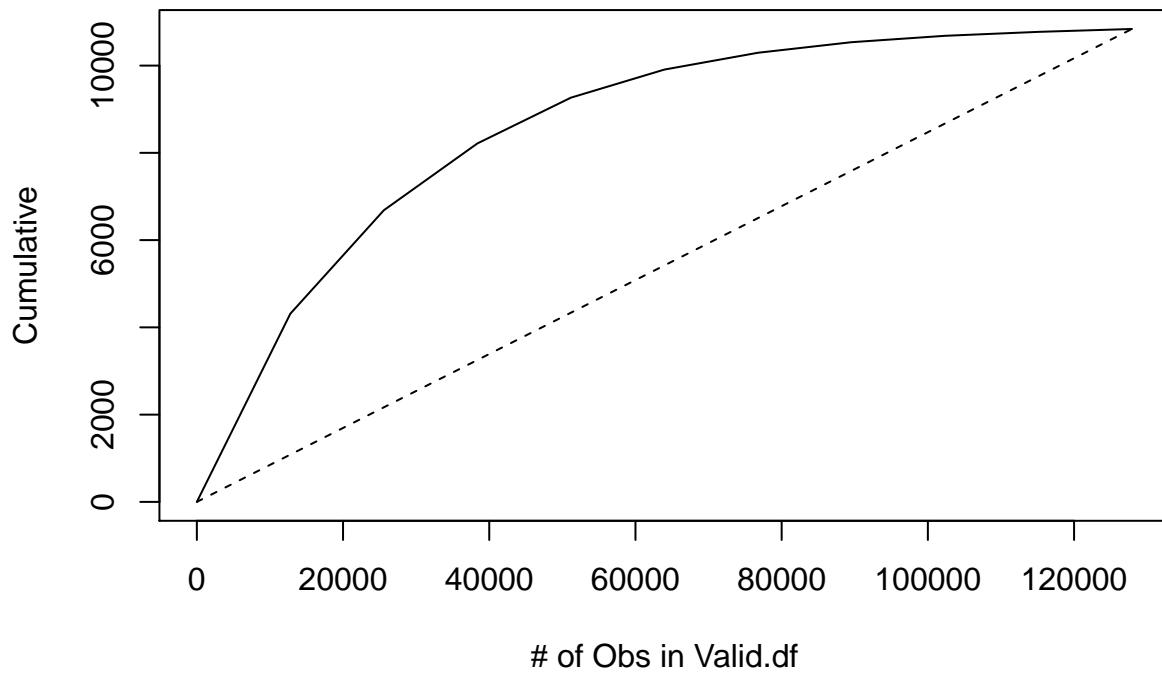
```

#better than baseline model
log.auc<-auc(log.r) # 0.8273 is a really good score
log.auc

## Area under the curve: 0.8273

```

```
#Producing a lift curve
library(gains)
gain <- gains(y, log.pred, groups=10)
plot(c(0,gain$cume.pct.of.total*sum(y))~c(0,gain$cume.obs),
     xlab="# of Obs in Valid.df", ylab="Cumulative", main="", type="l")
lines(c(0,sum(y))~c(0, dim(valid.df)[1])), lty=2)
```



```
gain
```

## Depth		Cume	Mean	Cume	Cume Pct	Lift	Cume	Mean
## of		N	Resp	Mean	of Total	Index	Lift	Model
## File		N	Resp	Resp	Resp		Lift	Score
##	---							
## 10	12791	12791	0.34	0.34	39.8%	398	398	0.36
## 20	12792	25583	0.19	0.26	61.7%	219	308	0.17
## 30	12792	38375	0.12	0.21	75.8%	141	253	0.11
## 40	12792	51167	0.08	0.18	85.5%	97	214	0.07
## 50	12792	63959	0.05	0.15	91.4%	59	183	0.05
## 60	12791	76750	0.03	0.13	95.0%	36	158	0.04
## 70	12792	89542	0.02	0.12	97.2%	22	139	0.03
## 80	12792	102334	0.01	0.10	98.6%	14	123	0.02
## 90	12792	115126	0.01	0.09	99.4%	8	110	0.01
## 100	12792	127918	0.01	0.08	100.0%	6	100	0.01

Lift Index = 308 in the output of gains() means that the top 39.8% of
of the data ranked by the logistic regression identifies 3.98 times
as many successful individuals with heart disease as would a random selection of 39.8% of the data