



Heart Disease Causes Analysis

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Introduction



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UNDERSTANDING

TRANSFORMATION

DATA MINING

EVALUATION

- Heart Disease Data Set
 - Abstract: 4 databases: Cleveland, Hungary, Switzerland, and the VA Long Beach
 - Number of Instances: 303
 - Attribute Characteristics: Categorical, Integer, Real
 - Database contains 76 attributes, but the published experiment dataset refer to using a subset of 14 of them.
- Through the 14 attributes, we decide the predicted attribute, target value from 0 and 1.

- Backward Stepwise Processing
 - Determine relevant independent variables from the data.

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Conclusion

- Logistic Regression
 - Accuracy of the data
- KNN
 - Performance and Error rate
- LDA
 - Percentage of Correctness

- According to the evaluations
 - Find the meaningful result
 - Interpret the result
 - Prediction accuracy
 - Correctness Implications(From LDA)

Data Description

303 observations

13 factors: age, sex, chest pain type, resting blood pressure, serum cholesterol, fasting blood sugar, resting electrocardiographic results, max heart rate, exercise induced angina, oldpeak, the slope of the peak exercise, number of major vessels, thal

1: disease 0: healthy

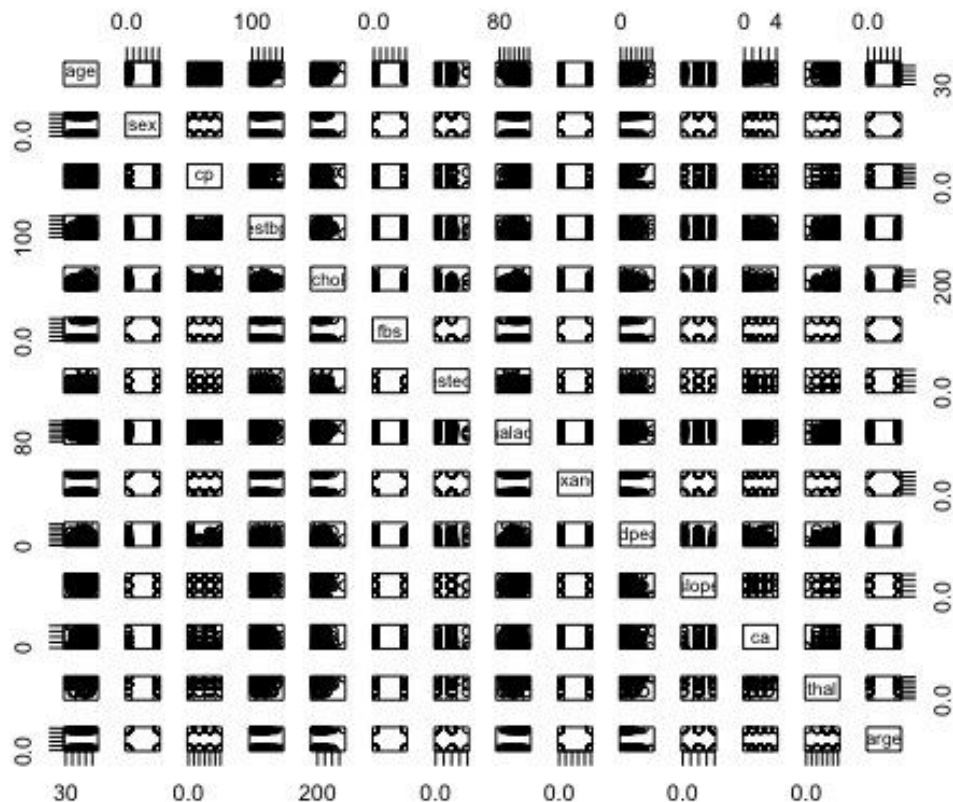
	age	sex	cp	trestbps	chol	fb	restecg	thalach	exang	oldpeak	slope	ca	thal	target
1	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
2	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
3	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
4	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
5	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1
6	57	1	0	140	192	0	1	148	0	0.4	1	0	1	1
7	56	0	1	140	294	0	0	153	0	1.3	1	0	2	1
8	44	1	1	120	263	0	1	173	0	0.0	2	0	3	1
9	52	1	2	172	199	1	1	162	0	0.5	2	0	3	1
10	57	1	2	150	168	0	1	174	0	1.6	2	0	2	1
11	54	1	0	140	239	0	1	160	0	1.2	2	0	2	1
12	48	0	2	130	275	0	1	139	0	0.2	2	0	2	1
13	49	1	1	130	266	0	1	171	0	0.6	2	0	2	1
14	64	1	3	110	211	0	0	144	1	1.8	1	0	2	1
15	58	0	3	150	283	1	0	162	0	1.0	2	0	2	1
16	50	0	2	120	219	0	1	158	0	1.6	1	0	2	1
17	58	0	2	120	340	0	1	172	0	0.0	2	0	2	1
18	66	0	3	150	226	0	1	114	0	2.6	0	0	2	1
19	43	1	0	150	247	0	1	171	0	1.5	2	0	2	1
20	69	0	3	140	239	0	1	151	0	1.8	2	2	2	1
21	59	1	0	135	234	0	1	161	0	0.5	1	0	3	1
22	44	1	2	130	233	0	1	179	1	0.4	2	0	2	1
23	42	1	0	140	226	0	1	178	0	0.0	2	0	2	1
24	61	1	2	150	243	1	1	137	1	1.0	1	0	2	1

Data Description

```
> pairs(heart)
```

```
> dim(heart)
```

```
[1] 303 14
```



Data Description

```
disease_data <- heart[1:165,]
```

```
summary(disease_data)
```

```
> summary(disease_data)
```

age	sex	cp	trestbps	chol	fbs
Min. :29.0	Min. :0.0000	Min. :0.000	Min. : 94.0	Min. :126.0	Min. :0.0000
1st Qu.:44.0	1st Qu.:0.0000	1st Qu.:1.000	1st Qu.:120.0	1st Qu.:208.0	1st Qu.:0.0000
Median :52.0	Median :1.0000	Median :2.000	Median :130.0	Median :234.0	Median :0.0000
Mean :52.5	Mean :0.5636	Mean :1.376	Mean :129.3	Mean :242.2	Mean :0.1394
3rd Qu.:59.0	3rd Qu.:1.0000	3rd Qu.:2.000	3rd Qu.:140.0	3rd Qu.:267.0	3rd Qu.:0.0000
Max. :76.0	Max. :1.0000	Max. :3.000	Max. :180.0	Max. :564.0	Max. :1.0000

restecg	thalach	exang	oldpeak	slope
Min. :0.0000	Min. : 96.0	Min. :0.0000	Min. :0.000	Min. :0.000
1st Qu.:0.0000	1st Qu.:149.0	1st Qu.:0.0000	1st Qu.:0.000	1st Qu.:1.000
Median :1.0000	Median :161.0	Median :0.0000	Median :0.200	Median :2.000
Mean :0.5939	Mean :158.5	Mean :0.1394	Mean :0.583	Mean :1.594
3rd Qu.:1.0000	3rd Qu.:172.0	3rd Qu.:0.0000	3rd Qu.:1.000	3rd Qu.:2.000
Max. :2.0000	Max. :202.0	Max. :1.0000	Max. :4.200	Max. :2.000

ca	thal	target
Min. :0.0000	Min. :0.000	Min. :1
1st Qu.:0.0000	1st Qu.:2.000	1st Qu.:1
Median :0.0000	Median :2.000	Median :1
Mean :0.3636	Mean :2.121	Mean :1
3rd Qu.:0.0000	3rd Qu.:2.000	3rd Qu.:1
Max. :4.0000	Max. :3.000	Max. :1

Data Description

```
healthy_data <- heart[166:303,]
```

```
summary(healthy_data)
```

```
> summary(healthy_data)
```

age		sex	cp	trestbps	chol	fb	
Min.	:35.0	Min.	:0.0000	Min.	:100.0	Min.	:0.0000
1st Qu.	:52.0	1st Qu.	:1.0000	1st Qu.	:120.0	1st Qu.	:0.0000
Median	:58.0	Median	:1.0000	Median	:130.0	Median	:0.0000
Mean	:56.6	Mean	:0.8261	Mean	:134.4	Mean	:0.1594
3rd Qu.	:62.0	3rd Qu.	:1.0000	3rd Qu.	:144.8	3rd Qu.	:0.0000
Max.	:77.0	Max.	:1.0000	Max.	:200.0	Max.	:1.0000
restecg		thalach	exang	oldpeak	slope	ca	
Min.	:0.0000	Min.	:71.0	Min.	:0.0000	Min.	:0.0000
1st Qu.	:0.0000	1st Qu.	:125.0	1st Qu.	:0.600	1st Qu.	:0.000
Median	:0.0000	Median	:142.0	Median	:1.400	Median	:1.000
Mean	:0.4493	Mean	:139.1	Mean	:1.586	Mean	:1.167
3rd Qu.	:1.0000	3rd Qu.	:156.0	3rd Qu.	:2.500	3rd Qu.	:2.000
Max.	:2.0000	Max.	:195.0	Max.	:6.200	Max.	:4.000
thal		target					
Min.	:0.000	Min.	:0				
1st Qu.	:2.000	1st Qu.	:0				
Median	:3.000	Median	:0				
Mean	:2.543	Mean	:0				
3rd Qu.	:3.000	3rd Qu.	:0				
Max.	:3.000	Max.	:0				

Data Description

Splitting the data into training and testing:

```
sampladata <- sample(c(1:303),280,replace = FALSE, prob = NULL)
```

```
Train <- heart[c(sampladata),]
```

```
Test <- heart[-c(sampladata),]
```


Logistic Regression

```
> glm.fit1 = glm(target~age+sex+cp+trestbps+chol+fbs+restecg+thalach+exang+oldpeak+slope+ca+thal,  
data=Train, family = binomial)
```

```
>step(glm.fit1, direction = "backward", trace=FALSE )
```

#we get final model of glm as target ~ sex + cp + trestbps + exang + oldpeak + slope + ca + thal

```
>glm.final <- glm(formula = target ~ sex + cp + trestbps + exang + oldpeak + slope + ca + thal, family =  
binomial, data = Train)
```

#AIC = 208.8

```
> step(glm.fit1, direction = "backward", trace=FALSE )
```

```
Call:  glm(formula = target ~ sex + cp + trestbps + exang + oldpeak +  
slope + ca + thal, family = binomial, data = Train)
```

Coefficients:

(Intercept)	sex1	cp1	cp2	cp3	trestbps	exang1
2.99345	-1.46281	1.00504	2.35756	2.61850	-0.01996	-0.88295
oldpeak	slope1	slope2	ca1	ca2	ca3	ca4
-0.51022	-1.04114	0.66226	-2.25023	-3.20611	-1.57761	1.36727
thal1	thal2	thal3				
2.20579	2.35923	0.80404				

```
Degrees of Freedom: 279 Total (i.e. Null); 263 Residual
```

```
Null Deviance: 386.7
```

```
Residual Deviance: 174.8
```

```
AIC: 208.8
```

Logistic Regression

- > From the result, the model is 86.94% correct overall
- > The model has 95.35% accuracy for identifying people with disease
- > The model has 76% accuracy for identifying people without disease

```
> table(pred_class,Test_class)
      Test_class
pred_class  0   1
      0   6   1
      1   2  14
> prop.table(table(pred_class,Test_class))
      Test_class
pred_class      0      1
      0 0.26086957 0.04347826
      1 0.08695652 0.60869565
> |
```

KNN

Step 1: Selecting significant variables using Backward selection

```
Call: glm(formula = target ~ sex + cp + trestbps + exang + oldpeak +  
      slope + ca + thal, family = binomial, data = heart)
```

Coefficients:

(Intercept)	sex0	sex1	cp0	cp1
6.22978	1.63154	NA	-2.55944	-1.52887
cp2	cp3	trestbps	exang0	exang1
-0.33929	NA	-0.02211	0.85234	NA
oldpeak	slope0	slope1	slope2	ca0
-0.47970	-0.70078	-1.60752	NA	-1.23217
ca1	ca2	ca3	ca4	thal0
-3.58731	-4.34156	-3.49973	NA	-0.91673
thal1	thal2	thal3		
1.70736	1.44627	NA		

KNN



Step 2: Find the best K

Outer Loop: for (k in c(1:floor(0.8*nrow(heart))))

Inner Loop: repeat l times

Choose a new training and testing set, Fit a knn model with $k = k$

Calculate error rate/

Calculate average error rate for each k/

Best K obtained is 21

KNN

How well the model perform?

- Error rate in testing is 0.18

```
> knnPred<-predict(knnModel, data=datTest)
> knnConfusion<-table(datTest$target, knnPred)
> knnErrorRate<-
+   (knnConfusion[1,2]+knnConfusion[2,1])/sum(knnConfusion)
> cat("Total Error Rate is ", knnErrorRate)
Total Error Rate is  0.1803279
```

KNN



How we evaluate the result?

- $N \ll 2^d$, where $N = 303$, $d = 8$ \Rightarrow sample is not big enough
- The result of the best K is not always consistent

LDA

Step 1: Selecting significant variables using Backward selection

```
> model = glm (target~.,data=Train, family = binomial)
> step(model, direction = "backward", trace=FALSE )
```

```
Call: glm(formula = target ~ sex + cp + trestbps + chol + thalach +
      exang + oldpeak + slope + ca + thal, family = binomial, data = Train)
```

Coefficients:

(Intercept)	sex	cp	trestbps	chol	thalach	exang	oldpeak	slope	ca
4.091343	-1.942293	0.805186	-0.023130	-0.006724	0.024245	-0.980154	-0.450130	0.619040	-0.716137
thal									
-0.828633									

Degrees of Freedom: 279 Total (i.e. Null); 269 Residual

Null Deviance: 387

Residual Deviance: 199.4 AIC: 221.4

LDA

Step 2: Apply LDA

```
library(MASS)
```

```
> lda.fit1 <- lda(target~sex+cp+chol+fbs+exang+slope+ca+thal, data=Train)
```

```
> lda.fit1
```

```
call:
```

```
lda(target ~ sex + cp + chol + fbs + exang + slope + ca + thal,  
    data = Train)
```

Prior probabilities of groups:

	0	1
	0.4535714	0.5464286

Group means:

	sex1	cp1	cp2	cp3	chol	fbs	exang1	slope	ca1	ca2
0	0.8267717	0.06299213	0.1259843	0.04724409	253.0157	0.1417323	0.5748031	1.173228	0.3149606	0.22047244
1	0.5555556	0.24836601	0.4052288	0.10457516	241.2092	0.1437908	0.1372549	1.594771	0.1372549	0.04575163

	ca3	ca4	thal1	thal2	thal3
0	0.1338583	0.00000000	0.07874016	0.2519685	0.6614173
1	0.0130719	0.01960784	0.03921569	0.7843137	0.1699346

LDA

Step 2: Generate table and the result

```
> lda.pred <- predict(lda.fit1, Test)
> table(lda.pred$class, Test$target)
```

	0	1
0	6	2
1	5	10

```
> mean(lda.pred$class==Test$target)
[1] 0.6956522
```

- This suggests that LDA predictions are accurate around 69.57% of the time, which is much lower than the previous two model.
- The test error rate is 30.43%, which is too high among the heart disease tests
- These results are very different from those obtained with the logistic regression model.

Results



- Correctness Implications from each correctness scenarios in LDA result table
 - Percentage of correct predictions: 69.56%
 - The correctness of Target is right most of the time by 83.33%
 - The correctness of Target is wrong most of the time by 45.45%
 - Since the best correctness rate and the worst correctness rate have a big difference, we can conclude that this database model is not sufficient enough and LDA method is not the best result model among the types of methods we used.

Results

- Significant factors that may lead to heart disease (by backward selection)
 - sex, chest pain type, resting blood pressure, resting electrocardiographic, thalach, exercise induced angina, oldpeak, number of major vessels

Models	Accuracy	Comments
Logistic Regression	86.94%	Works well when response variable is Binary and sample size is small
KNN	82%	The small size of data would influence model accuracy
LDA	69.57%	LDA works better for normally distributed data

Conclusions



- Among the three machine learning methods
 - Logistic regression is so far presenting the most accurate data
 - quite satisfying to reach a classification percentage of 86%
- The classification percentage changes depend on the application in which data mining is used
 - Still, there are total of 75 attributes that can affect the target value
 - But, all published experiments refer to using a subset of 14 of them.
- Not enough data entries to predict more accurate result (303 entries)
 - To have a good model, the data entries need to be larger than 2^8

References



Data source: <https://www.kaggle.com/ronitf/heart-disease-uci>

<https://stats.stackexchange.com/questions/248812/when-does-logistic-regression-not-work-properly>