

A decorative graphic on the left side of the slide, consisting of a network of white lines and small circles on a blue gradient background, resembling a circuit board or a neural network.

FINAL PROJECT - DS48

MAXIMILIAN KLIMKO

09.11.2021

DATASET – HEART DISEASE

- 918 observations
- 5 different countries
- Sourced from University hospitals and Medical Institutes
- Taken from Kaggle
- Originally 5 datasets

<https://www.kaggle.com/fedesoriano/heart-failure-prediction>

WHAT DOES THE DATA SHOW?

- - Age
- - Sex
- - CPT: Angina Type
- - RBP: Resting Blood Pressure
- - CTL: Serum Cholesterol
- - FBS: Fasted Blood Sugar
- - ECG: Electrocardiogram Results
- - MHR: Max Heart Rate
- - ExA: Exercise-induced Angina
- - Old: ST [Numeric value measured in depression, implies restriction of bloodflow to tissue]
- - STS: ST segment slope during peak exercise

	Age	Sex	CPT	RBP	CTL	FBS	ECG	MHR	ExA	Old	STS	HD
0	40	M	ATA	140	289	0	Normal	172	N	0.0	Up	0
1	49	F	NAP	160	180	0	Normal	156	N	1.0	Flat	1
2	37	M	ATA	130	283	0	ST	98	N	0.0	Up	0
3	48	F	ASY	138	214	0	Normal	108	Y	1.5	Flat	1
4	54	M	NAP	150	195	0	Normal	122	N	0.0	Up	0

Which of these can be used to predict whether a person will suffer heart failure?

FEATURE IMPORTANCE

- Simple decision tree
- Assessment of feature importance

```
from sklearn.tree import export_graphviz
from sklearn.tree import DecisionTreeClassifier

treeclf = DecisionTreeClassifier(max_depth=3, random_state=50)

feature_cols = ['Age', 'RBP', 'CTL', 'FBS', 'MHR']

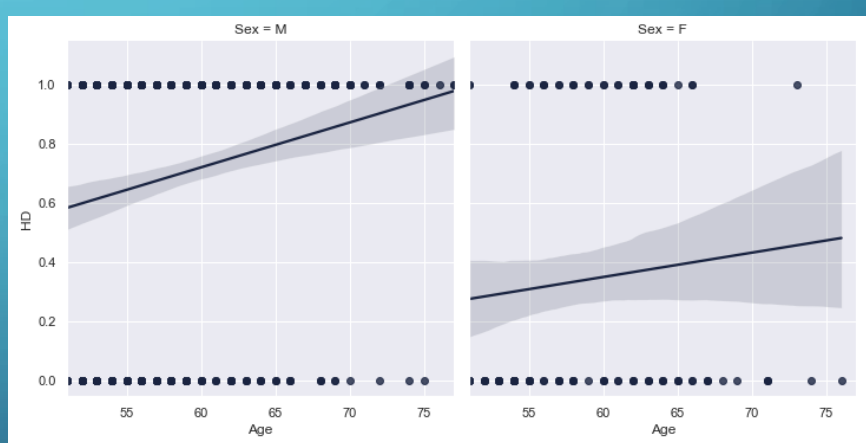
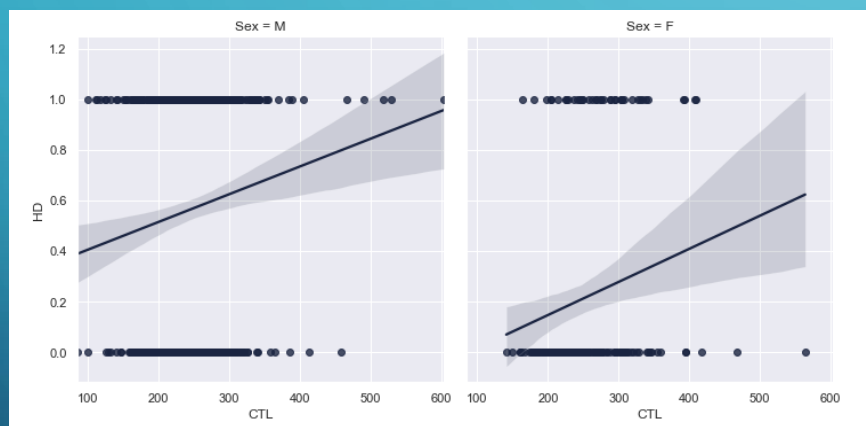
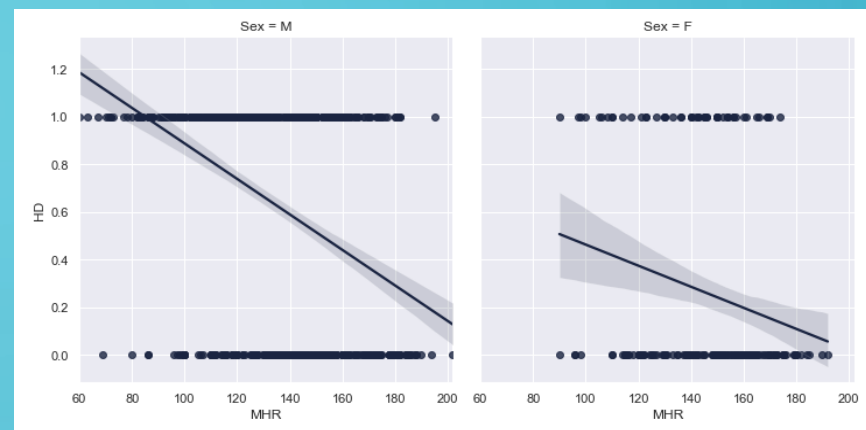
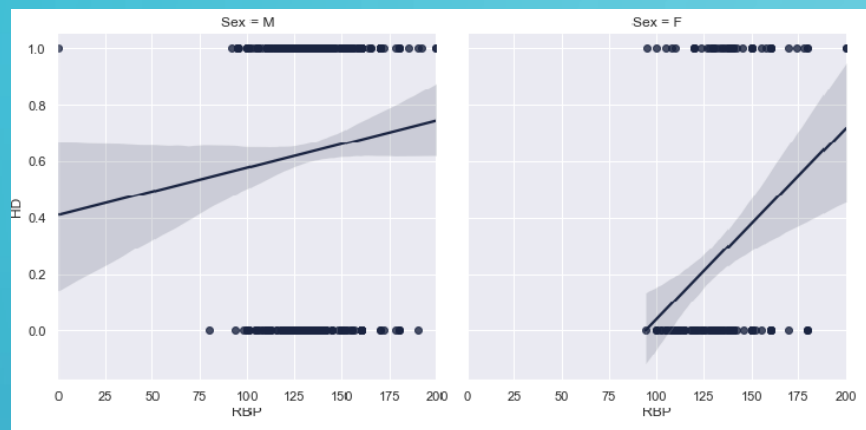
X = heartdataclean[feature_cols]
y = heartdataclean.HD

treeclf.fit(X, y)

DecisionTreeClassifier(max_depth=3, random_state=50)

pd.DataFrame(
    {'feature':feature_cols, 'importance':treeclf.feature_importances_}
).sort_values("importance", ascending=False)
```

	feature	importance
4	MHR	0.640681
0	Age	0.272739
1	RBP	0.067089
2	CTL	0.019491
3	FBS	0.000000



LOGISTIC REGRESSION

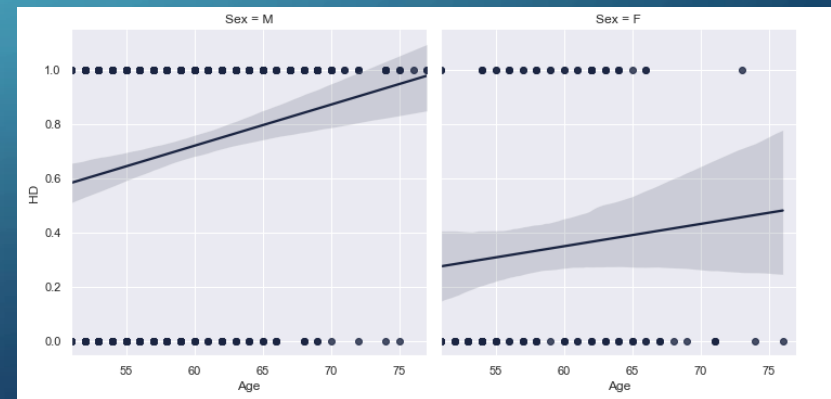
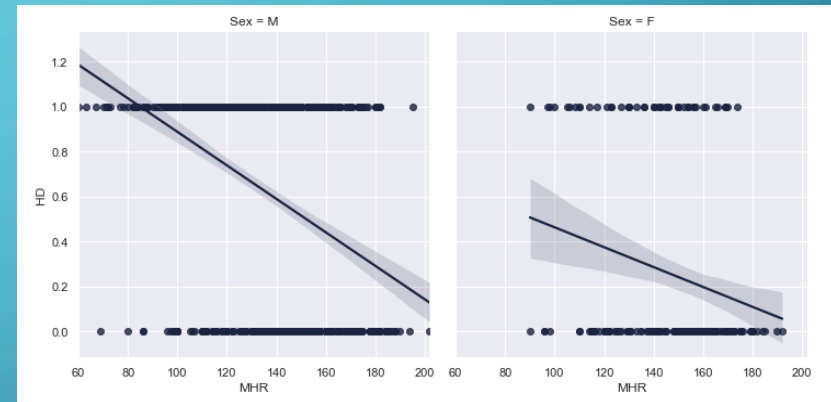
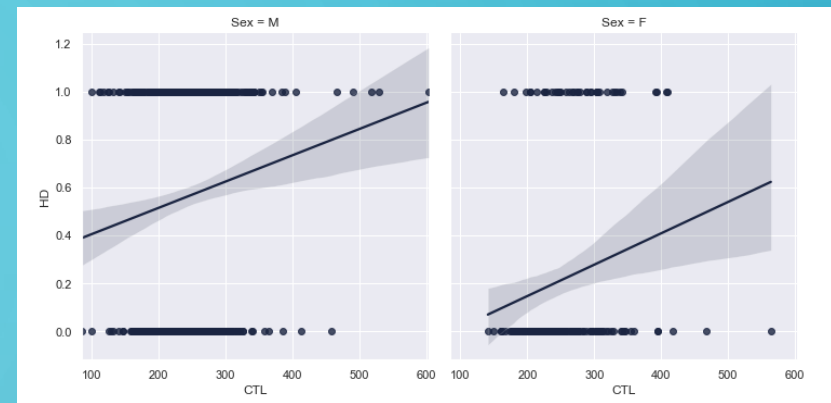
- Small dataset
- Target is a class (0 or 1)
- CTL / MHR / Age

```
#there are 172 0 values for CTL in this dataset so I filtered them and saved the result as a new dataframe
print(heartdata[["CTL"]].value_counts())
heartdataclean = heartdata[(heartdata.CTL > 0)]
```

```
CTL
0      172
254    11
223    10
220    10
211     9
...
117     1
123     1
131     1
293     1
603     1
Length: 222, dtype: int64
```

```
heartdataclean.CTL.value_counts().sort_values()
```

```
603     1
407     1
529     1
409     1
518     1
..
204     9
230     9
220    10
223    10
254    11
Name: CTL, Length: 221, dtype: int64
```



CONFUSION MATRIX

TN: 63 FP: 23

FN: 40 TP: 61

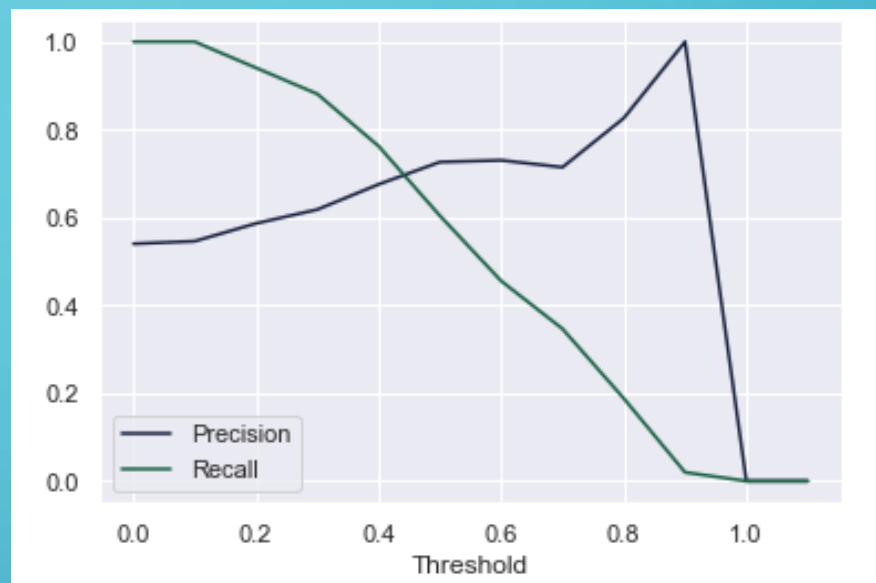
Accuracy – 0.69

Precision – 0.72

Recall – 0.60

False Positive rate – 0.25


F1 – 0.65



Lowering the threshold to 0.4 or even 0.3 would be justifiable as higher recall would mean less FN



PERSONAL TAKEAWAYS

- Learned about heart disease predictors
 - Could have picked a larger dataset
 - Or a different problem entirely
 - I realized there is much more to learn about ML
 - And that I wish to continue studying it
- 
- 