

ds-and-health

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0.1 Vignette: asking and answering a predictive question

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```
[2]: import numpy as np
import pandas as pd
from sklearn.compose import ColumnTransformer
from sklearn.ensemble import RandomForestClassifier
from sklearn.linear_model import LogisticRegression, LogisticRegressionCV
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import OneHotEncoder, StandardScaler
from sklearn.tree import DecisionTreeClassifier

from sklearn.dummy import DummyClassifier

# Preprocessing and pipeline
from sklearn.impute import SimpleImputer

# train test split and cross validation
from sklearn.model_selection import (
    GridSearchCV,
    cross_val_score,
    cross_validate,
    train_test_split,
)
from sklearn.pipeline import FeatureUnion, Pipeline, make_pipeline
from sklearn.preprocessing import (
    FunctionTransformer,
    Normalizer,
    OneHotEncoder,
    StandardScaler,
    normalize,
    scale,
)
from sklearn.svm import SVC
from sklearn.tree import DecisionTreeClassifier
```

```
from sklearn.datasets import load_breast_cancer
```

Task: Predicting the presence or absence of heart disease (the target) based on a set of 13 different biophysical measures (the features).

Dataset: from UCI Machine Learning Repository: <https://archive.ics.uci.edu/ml/datasets/Heart+Disease>

```
[3]: heart_df = pd.read_csv("heart_disease.csv", index_col=0)
```

```
[4]: df_train, df_test = train_test_split(heart_df, random_state=123)
```

```
[5]: df_train
```

```
[5]:
```

	age	sex	chest_pain_type	resting_blood_pressure	\
patient_id					
36	54	female	non-anginal pain	135	
148	44	male	non-anginal pain	120	
21	44	male	non-anginal pain	130	
187	54	male	angina	124	
161	55	female	non-anginal pain	132	
...	
106	69	male	non-anginal pain	160	
83	52	male	non-anginal pain	152	
17	66	female	non-anginal pain	150	
230	47	male	non-anginal pain	108	
98	43	male	non-anginal pain	130	

	cholesterol	fasting_blood_sugar	rest_ecg	\
patient_id				
36	304	greater than 120mg/ml	abnormal	
148	226	lower than 120mg/ml	abnormal	
21	233	lower than 120mg/ml	abnormal	
187	266	lower than 120mg/ml	normal	
161	342	lower than 120mg/ml	abnormal	
...	
106	234	greater than 120mg/ml	normal	
83	298	greater than 120mg/ml	abnormal	
17	226	lower than 120mg/ml	abnormal	
230	243	lower than 120mg/ml	abnormal	
98	315	lower than 120mg/ml	abnormal	

	max_heart_rate_achieved	exercise_induced_angina	st_depression	\
patient_id				
36	170	no	0.0	
148	169	no	0.0	
21	179	yes	0.4	
187	109	yes	2.2	

161	166	no	1.2
...
106	131	no	0.1
83	178	no	1.2
17	114	no	2.6
230	152	no	0.0
98	162	no	1.9

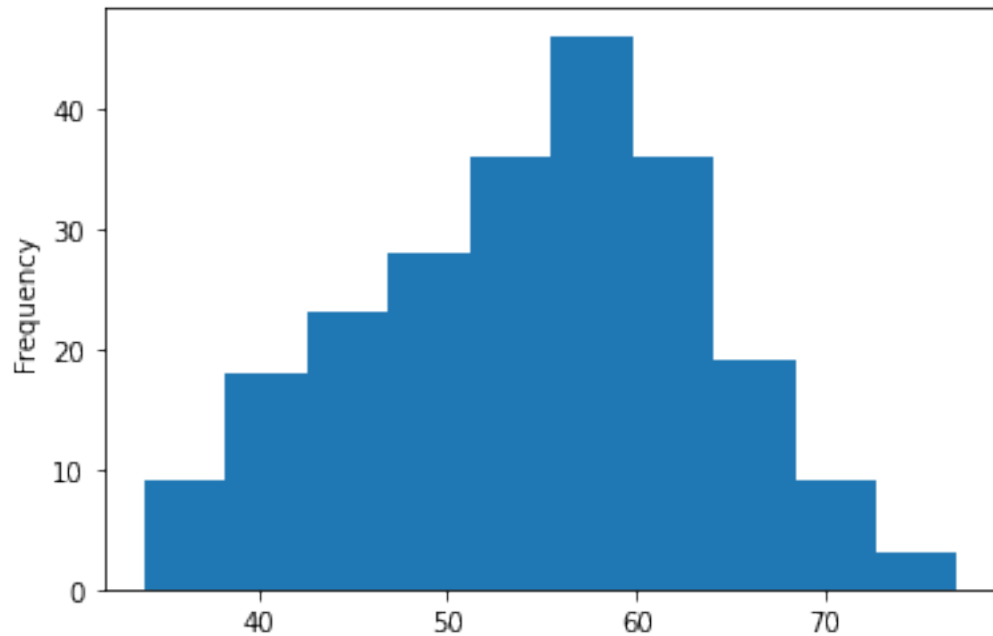
	st_slope	num_major_vessels	thalassemia	target
patient_id				
36	downsloping	0	normal	1
148	downsloping	0	normal	1
21	downsloping	0	normal	1
187	flat	1	abnormal	0
161	downsloping	0	normal	1
...
106	flat	1	normal	1
83	flat	0	abnormal	1
17	upsloping	0	normal	1
230	downsloping	0	normal	0
98	downsloping	1	normal	1

[227 rows x 14 columns]

```
[6]: df_train['target'].value_counts()
```

```
[6]: 1    128
      0     99
      Name: target, dtype: int64
```

```
[7]: df_train['age'].plot.hist();
```



```
[8]: numeric_features = [  
    "age",  
    "resting_blood_pressure",  
    "cholesterol",  
    "max_heart_rate_achieved",  
    "st_depression",  
    "num_major_vessels",  
]  
categorical_features = [  
    "sex",  
    "chest_pain_type",  
    "fasting_blood_sugar",  
    "rest_ecg",  
    "exercise_induced_angina",  
    "st_slope",  
    "thalassemia",  
]
```

```
[9]: X_train = df_train.drop(columns=["target"])  
y_train = df_train["target"]  
  
X_test = df_test.drop(columns=["target"])  
y_test = df_test["target"]
```

```
[10]: df_train["st_slope"]
```

```
[10]: patient_id
      36      downsloping
      148     downsloping
      21      downsloping
      187         flat
      161     downsloping

      ...
      106         flat
      83         flat
      17      upsloping
      230     downsloping
      98      downsloping
      Name: st_slope, Length: 227, dtype: object
```

```
[11]: preprocessor = ColumnTransformer([
      ("scale", StandardScaler(), numeric_features),
      ("ohe", OneHotEncoder(), categorical_features),
    ])
preprocessor.fit(X_train)
new_columns = numeric_features + list(preprocessor.named_transformers_["ohe"].
    ↳get_feature_names(categorical_features))
X_train_enc = pd.DataFrame(preprocessor.transform(X_train),
    ↳columns=new_columns, index=X_train.index)
X_train_enc
```

```
[11]:
```

	age	resting_blood_pressure	cholesterol	\
patient_id				
36	-0.057019	0.213311	1.033292	
148	-1.163276	-0.706088	-0.414936	
21	-1.163276	-0.093155	-0.284967	
187	-0.057019	-0.460915	0.327745	
161	0.053607	0.029432	1.738839	
...	
106	1.602368	1.745644	-0.266400	
83	-0.278270	1.255298	0.921890	
17	1.270490	1.132711	-0.414936	
230	-0.831399	-1.441608	-0.099297	
98	-1.273902	-0.093155	1.237529	
	max_heart_rate_achieved	st_depression	num_major_vessels	\
patient_id				
36	0.861754	-0.900071	-0.715888	
148	0.818128	-0.900071	-0.715888	
21	1.254386	-0.525523	-0.715888	
187	-1.799420	1.159945	0.293470	
161	0.687250	0.223574	-0.715888	
...	

106	-0.839652	-0.806434	0.293470
83	1.210760	0.223574	-0.715888
17	-1.581291	1.534493	-0.715888
230	0.076489	-0.900071	-0.715888
98	0.512747	0.879034	0.293470

	sex_female	sex_male	chest_pain_type_angina	\
patient_id				
36	1.0	0.0		0.0
148	0.0	1.0		0.0
21	0.0	1.0		0.0
187	0.0	1.0		1.0
161	1.0	0.0		0.0
...	
106	0.0	1.0		0.0
83	0.0	1.0		0.0
17	1.0	0.0		0.0
230	0.0	1.0		0.0
98	0.0	1.0		0.0

	chest_pain_type_non-anginal	pain	...	\
patient_id				
36		1.0	...	
148		1.0	...	
21		1.0	...	
187		0.0	...	
161		1.0	...	
...		
106		1.0	...	
83		1.0	...	
17		1.0	...	
230		1.0	...	
98		1.0	...	

	fasting_blood_sugar_lower than 120mg/ml	rest_ecg_abnormal	\
patient_id			
36	0.0	1.0	
148	1.0	1.0	
21	1.0	1.0	
187	1.0	0.0	
161	1.0	1.0	
...	
106	0.0	0.0	
83	0.0	1.0	
17	1.0	1.0	
230	1.0	1.0	
98	1.0	1.0	

	rest_ecg_normal	exercise_induced_angina_no \
patient_id		
36	0.0	1.0
148	0.0	1.0
21	0.0	0.0
187	1.0	0.0
161	0.0	1.0
...
106	1.0	1.0
83	0.0	1.0
17	0.0	1.0
230	0.0	1.0
98	0.0	1.0

	exercise_induced_angina_yes	st_slope_downsloping	st_slope_flat \
patient_id			
36	0.0	1.0	0.0
148	0.0	1.0	0.0
21	1.0	1.0	0.0
187	1.0	0.0	1.0
161	0.0	1.0	0.0
...
106	0.0	0.0	1.0
83	0.0	0.0	1.0
17	0.0	0.0	0.0
230	0.0	1.0	0.0
98	0.0	1.0	0.0

	st_slope_upsloping	thalassemia_abnormal	thalassemia_normal
patient_id			
36	0.0	0.0	1.0
148	0.0	0.0	1.0
21	0.0	0.0	1.0
187	0.0	1.0	0.0
161	0.0	0.0	1.0
...
106	0.0	0.0	1.0
83	0.0	1.0	0.0
17	1.0	0.0	1.0
230	0.0	0.0	1.0
98	0.0	0.0	1.0

[227 rows x 21 columns]

```
[12]: pipe = make_pipeline(preprocessor, LogisticRegressionCV())
```

```
[13]: cross_val_score(pipe, X_train, y_train, cv=20).mean()
```

```
[13]: 0.868560606060606
```

```
[15]: pipe.fit(X_train, y_train);
```

```
[17]: X_test[:1]
```

```
[17]:      age      sex  chest_pain_type  resting_blood_pressure  \
patient_id
11      48  female  non-anginal pain                130

      cholesterol  fasting_blood_sugar  rest_ecg  \
patient_id
11              275  lower than 120mg/ml  abnormal

      max_heart_rate_achieved  exercise_induced_angina  st_depression  \
patient_id
11                                139                        no          0.2

      st_slope  num_major_vessels  thalassemia
patient_id
11      downsloping                0      normal
```

```
[18]: pipe.predict(X_test[:1])
```

```
[18]: array([1])
```

```
[19]: pipe.predict_proba(X_test[:1])
```

```
[19]: array([[0.10810309, 0.89189691]])
```

```
[20]: y_test[:1]
```

```
[20]: patient_id
11      1
Name: target, dtype: int64
```

```
[21]: pipe.score(X_test, y_test)
```

```
[21]: 0.8026315789473685
```

```
[ ]:
```

```
[ ]:
```

```
[ ]:
```


0.2 Challenges

Type of data:

- Images
- Videos
- Text
- Time series
- Censored data (survival analysis)
- ...

Data quality:

- Missing data
- Incorrect data
- Outliers
- ...

Data quantity:

- Need lots of data to get this to work
- For this type of analysis, need **labeled** data

Computational issues:

- Code may take a long time to run?
- Do we need distributed / cloud computing?
- Are the tools actively maintained?
- ...

Error metrics:

- False positive vs. false negatives (sensitivity vs. specificity)
- ...

Ethical challenges:

- How confident are we really in our results?
- Can we trust it if we don't understand it?
- Relevant article: <https://medium.com/@jrzech/what-are-radiological-deep-learning-models-actually-learning-f97a546c5b98>
- Is our model biased?

0.3 Where to learn more data science at UBC?

- <https://extendedlearning.ubc.ca/programs/key-capabilities-data-science> and <https://prolearn.mds.ubc.ca/en>
- <https://masterdatascience.ubc.ca/>
- DSCI 100, CPSC 330
- Upcoming undergraduate courses

[]: