

# DecisionTree\_1 (1)

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```
[1]: import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

```
[2]: data = pd.read_csv('horse.csv')
data.head()
```

```
[2]:  surgery    age  hospital_number  rectal_temp  pulse  respiratory_rate  \
0      no  adult         530101         38.5    66.0             28.0
1      yes  adult         534817         39.2    88.0             20.0
2      no  adult         530334         38.3    40.0             24.0
3      yes  young        5290409         39.1   164.0             84.0
4      no  adult         530255         37.3   104.0             35.0

    temp_of_extremities  peripheral_pulse  mucous_membrane  capillary_refill_time  \
0                cool          reduced              NaN          more_3_sec
1                NaN              NaN  pale_cyanotic          less_3_sec
2              normal          normal          pale_pink          less_3_sec
3                cold          normal  dark_cyanotic          more_3_sec
4                NaN              NaN  dark_cyanotic          more_3_sec

    ...  packed_cell_volume  total_protein  abdomo_appearance  abdomo_protein  \
0  ...              45.0              8.4              NaN              NaN
1  ...              50.0             85.0             cloudy              2.0
2  ...              33.0              6.7              NaN              NaN
3  ...              48.0              7.2      serosanguinous              5.3
4  ...              74.0              7.4              NaN              NaN

    outcome  surgical_lesion  lesion_1  lesion_2  lesion_3  cp_data
0      died              no     11300         0         0       no
1  euthanized              no      2208         0         0       no
2      lived              no         0         0         0      yes
3      died              yes      2208         0         0      yes
4      died              no      4300         0         0       no
```

[5 rows x 28 columns]

```
[3]: data.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 299 entries, 0 to 298
Data columns (total 28 columns):
#   Column                Non-Null Count  Dtype
---  -
0   surgery               299 non-null    object
1   age                   299 non-null    object
2   hospital_number       299 non-null    int64
3   rectal_temp           239 non-null    float64
4   pulse                 275 non-null    float64
5   respiratory_rate       241 non-null    float64
6   temp_of_extremities    243 non-null    object
7   peripheral_pulse       230 non-null    object
8   mucous_membrane       252 non-null    object
9   capillary_refill_time  267 non-null    object
10  pain                  244 non-null    object
11  peristalsis           255 non-null    object
12  abdominal_distention  243 non-null    object
13  nasogastric_tube      195 non-null    object
14  nasogastric_reflux     193 non-null    object
15  nasogastric_reflux_ph  53 non-null     float64
16  rectal_exam_feces     197 non-null    object
17  abdomen               181 non-null    object
18  packed_cell_volume     270 non-null    float64
19  total_protein          266 non-null    float64
20  abdomo_appearance     134 non-null    object
21  abdomo_protein         101 non-null    float64
22  outcome               299 non-null    object
23  surgical_lesion       299 non-null    object
24  lesion_1              299 non-null    int64
25  lesion_2              299 non-null    int64
26  lesion_3              299 non-null    int64
27  cp_data               299 non-null    object
dtypes: float64(7), int64(4), object(17)
memory usage: 65.5+ KB
```

```
[4]: data.isna().sum()
```

```
[4]: surgery          0
     age             0
     hospital_number  0
     rectal_temp      60
     pulse            24
     respiratory_rate  58
     temp_of_extremities 56
```

peripheral_pulse	69
mucous_membrane	47
capillary_refill_time	32
pain	55
peristalsis	44
abdominal_distention	56
nasogastric_tube	104
nasogastric_reflux	106
nasogastric_reflux_ph	246
rectal_exam_feces	102
abdomen	118
packed_cell_volume	29
total_protein	33
abdomo_appearance	165
abdomo_protein	198
outcome	0
surgical_lesion	0
lesion_1	0
lesion_2	0
lesion_3	0
cp_data	0

dtype: int64

```
[5]: data.outcome.value_counts()
```

```
[5]: lived      178
     died       77
     euthanized  44
     Name: outcome, dtype: int64
```

```
[6]: features = data.drop(['outcome'], axis = 1)
     target = data[['outcome']]
```

```
[7]: features.shape, target.shape
```

```
[7]: ((299, 27), (299, 1))
```

```
[8]: features.dtypes
```

```
[8]: surgery      object
     age          object
     hospital_number  int64
     rectal_temp   float64
     pulse         float64
     respiratory_rate float64
     temp_of_extremities object
     peripheral_pulse object
```

mucous_membrane	object
capillary_refill_time	object
pain	object
peristalsis	object
abdominal_distention	object
nasogastric_tube	object
nasogastric_reflux	object
nasogastric_reflux_ph	float64
rectal_exam_feces	object
abdomen	object
packed_cell_volume	float64
total_protein	float64
abdomo_appearance	object
abdomo_protein	float64
surgical_lesion	object
lesion_1	int64
lesion_2	int64
lesion_3	int64
cp_data	object
dtype:	object

```
[9]: features_transformed = pd.get_dummies(features)
```

```
[10]: from sklearn.model_selection import train_test_split
      from sklearn.tree import DecisionTreeClassifier
      from sklearn.ensemble import RandomForestClassifier
```

```
[11]: X_train , X_test, y_train, y_test = train_test_split(features_transformed,
      ↪target, random_state = 10)
```

```
[12]: print(X_train.shape)
      print(X_test.shape)
      print(y_train.shape)
      print(y_test.shape)
```

```
(224, 67)
(75, 67)
(224, 1)
(75, 1)
```

```
[13]: from sklearn.impute import SimpleImputer
```

```
[14]: imputer = SimpleImputer(missing_values=np.nan, strategy='most_frequent')
```

```
[15]: X_train = imputer.fit_transform(X_train)
      X_test = imputer.fit_transform(X_test)
```

## 0.1 Decision Tree

```
[36]: my_DT_model = DecisionTreeClassifier(max_depth=7)
```

```
[37]: my_DT_model.fit(X_train,y_train)
```

```
[37]: DecisionTreeClassifier(max_depth=7)
```

```
[38]: my_preds = my_DT_model.predict(X_test)
```

```
[39]: from sklearn.metrics import accuracy_score, confusion_matrix, \
      ↪ classification_report
```

```
[40]: accuracy_score(y_test, my_preds)
```

```
[40]: 0.6266666666666667
```

```
[41]: print(confusion_matrix(y_test, my_preds))
```

```
[[ 6  3  6]
 [ 5  4  2]
 [ 4  8 37]]
```

```
[42]: print(classification_report(y_test, my_preds))
```

	precision	recall	f1-score	support
died	0.40	0.40	0.40	15
euthanized	0.27	0.36	0.31	11
lived	0.82	0.76	0.79	49
accuracy			0.63	75
macro avg	0.50	0.51	0.50	75
weighted avg	0.66	0.63	0.64	75

```
[50]: features.columns
```

```
[50]: Index(['surgery', 'age', 'hospital_number', 'rectal_temp', 'pulse',
          'respiratory_rate', 'temp_of_extremities', 'peripheral_pulse',
          'mucous_membrane', 'capillary_refill_time', 'pain', 'peristalsis',
          'abdominal_distention', 'nasogastric_tube', 'nasogastric_reflux',
          'nasogastric_reflux_ph', 'rectal_exam_feces', 'abdomen',
          'packed_cell_volume', 'total_protein', 'abdomo_appearance',
          'abdomo_protein', 'surgical_lesion', 'lesion_1', 'lesion_2', 'lesion_3',
          'cp_data'],
          dtype='object')
```

```
[53]: import operator
sorted(list(zip(features.columns,my_DT_model.feature_importances_)),
      ↪key=operator.itemgetter(1), reverse=True)
```

```
[53]: [('respiratory_rate', 0.15811606733352418),
      ('mucous_membrane', 0.14269762191554108),
      ('temp_of_extremities', 0.13328172362507973),
      ('cp_data', 0.07225624381928748),
      ('hospital_number', 0.06361554996427964),
      ('rectal_exam_feces', 0.05922435066217908),
      ('rectal_temp', 0.0462423438344502),
      ('nasogastric_reflux_ph', 0.04267256707100241),
      ('surgical_lesion', 0.030073999650039797),
      ('surgery', 0.0297961156153894),
      ('peripheral_pulse', 0.029238610770872014),
      ('nasogastric_reflux', 0.027432364545644412),
      ('abdomen', 0.008223264663320757),
      ('age', 0.0),
      ('pulse', 0.0),
      ('capillary_refill_time', 0.0),
      ('pain', 0.0),
      ('peristalsis', 0.0),
      ('abdominal_distention', 0.0),
      ('nasogastric_tube', 0.0),
      ('packed_cell_volume', 0.0),
      ('total_protein', 0.0),
      ('abdomo_appearance', 0.0),
      ('abdomo_protein', 0.0),
      ('lesion_1', 0.0),
      ('lesion_2', 0.0),
      ('lesion_3', 0.0)]
```

### 0.1.1 Voting Classifier

```
[43]: from sklearn.ensemble import VotingClassifier, BaggingClassifier,
      ↪RandomForestClassifier
from sklearn.linear_model import LogisticRegression
from sklearn.svm import SVC
```

```
[44]: my_logreg_clf = LogisticRegression()
rf_clf = RandomForestClassifier()
svm_clf = SVC()
```

```
[45]: my_vt_clf = VotingClassifier(estimators=[('lr', my_logreg_clf), ('rf', rf_clf),
      ↪('svc', svm_clf)])
```

```
[46]: my_vt_clf.fit(X_train, y_train)
```

```
/usr/local/lib/python3.7/site-packages/sklearn/utils/validation.py:63:  
DataConversionWarning: A column-vector y was passed when a 1d array was  
expected. Please change the shape of y to (n_samples, ), for example using  
ravel().  
    return f(*args, **kwargs)  
/usr/local/lib/python3.7/site-packages/sklearn/linear_model/_logistic.py:765:  
ConvergenceWarning: lbfgs failed to converge (status=1):  
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.
```

```
Increase the number of iterations (max_iter) or scale the data as shown in:  
    https://scikit-learn.org/stable/modules/preprocessing.html  
Please also refer to the documentation for alternative solver options:  
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-  
regression  
    extra_warning_msg=_LOGISTIC_SOLVER_CONVERGENCE_MSG)
```

```
[46]: VotingClassifier(estimators=[('lr', LogisticRegression()),  
                                   ('rf', RandomForestClassifier()), ('svc', SVC())])
```

```
[47]: y_pred = my_vt_clf.predict(X_test)  
      accuracy_score(y_test, y_pred)
```

```
[47]: 0.6533333333333333
```

```
[ ]:
```