exercise_06_v2

December 18, 2023

1 Exercise 6

1.1 Recall

Basics: List four typical methods applied in the context of Knowledge Discovery from Databases (KDD) applications and briefly describe them!

Basics: List and describe the 6 phases of the CRISP-DM model!

Basics: What should happen during the evaluation phase?

Evaluation: Define the accuracy measure.

Evaluation: What is class imbalance and why can it cause a high accuracy even though the classifier is bad? Give an example.

Evaluation: In what applications is precision more important than recall, and in which applications is recall more important than precision?

Evaluation: What is grouped cross validation and when should you use it? Come up with an example and iterate all splits.

Statistics: Multiple hypothesis comparison

1) Explain what the multiple hypothesis comparison is and why it is a problem (refer to p-values in the process).
2) What is a way to correct for multiple hypothesis comparison. Give a concrete example.
3) What is the difference between an α-value and a p-value?

1.2 Univariate analysis

1.2.1 Load the data

[2]:
```
# imports
import numpy as np
import pandas as pd

from sklearn.model_selection import train_test_split, cross_validate,␣
 ↪StratifiedKFold, RepeatedStratifiedKFold

from sklearn.pipeline import make_pipeline

from sklearn.impute import SimpleImputer
from sklearn.preprocessing import StandardScaler

from sklearn.linear_model import LogisticRegression
from sklearn.ensemble import RandomForestClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.svm import LinearSVC

import matplotlib.pyplot as plt
import seaborn as sns
```

[3]:

```
# load data
data_titanic = pd.read_csv("exercise_01_intro-to-python_titanic.csv",␣
 ↪index_col="PassengerId")
```

[4]:

```
def extract_features(data):
    """Extract features from existing variables"""

    data_extract = data.copy()

    # name
    name_only = data_extract["Name"].str.replace(r"\(.*\)", "", regex=True)
    first_name = name_only.str.split(", ", expand=True).iloc[:,1]
    title = first_name.str.split(".", expand=True).iloc[:,0]
    data_extract["Title"] = title

    # ticket

    # ...

    return data_extract

data_extract = extract_features(data_titanic)
```

[5]:

```
def preprocess(data):
    """Convert features into numeric variables readable by our models."""

    data_preprocessed = data.copy()

    # Sex

    data_preprocessed = pd.get_dummies(data_preprocessed, columns=["Sex"],␣
 ↪drop_first=True)

    # Embarked

    data_preprocessed = pd.get_dummies(data_preprocessed, columns=["Embarked"],␣
 ↪dummy_na=True)
```

```
    # Title
    title = data_preprocessed["Title"]
    title_counts = title.value_counts()
    higher_titles = title_counts[title_counts < 50]
    title_groups = ["higher" if t in higher_titles else t for t in title]
    data_preprocessed["Title"] = title_groups
    data_preprocessed = pd.get_dummies(data_preprocessed, columns=["Title"])

    # drop the rest
    data_preprocessed.drop(columns=["Name", "Cabin", "Ticket"], inplace=True)

    return data_preprocessed

data_preprocessed = preprocess(data_extract)
```

[6]:

```
# before inspecting the data, selecting and building models, etc.
# FIRST split data into train and test data (we set the test data size to 30%)

X = data_preprocessed.drop(columns="Survived")
y = data_preprocessed["Survived"]
```

[7]:

```
X.head(3)
```

[7]:

```
             Pclass   Age  SibSp  Parch     Fare  Sex_male  Embarked_C  \
PassengerId
1                 3  22.0      1      0   7.2500      True       False
2                 1  38.0      1      0  71.2833     False        True
3                 3  26.0      0      0   7.9250     False       False

             Embarked_Q  Embarked_S  Embarked_nan  Title_Miss  Title_Mr  \
PassengerId
1                 False        True         False       False      True
2                 False       False         False       False     False
3                 False        True         False        True     False

             Title_Mrs  Title_higher
PassengerId
1                False         False
2                 True         False
3                False         False
```

1.2.2 Univariate comparison

[8]:

```
from scipy.stats import spearmanr, mannwhitneyu, ranksums
```

[9]:

```
# for each feature calculate whether there is a statistical difference between survivors (1) and victims (0)
tests = {}
for c in X.columns:
    # TODO: fill this in by computing the test statistic for each feature columns!
    # tests[c] = mannwhitneyu()
    pass
tests
```

[9]:

```
{}
```

Which is the feature most associated with surviving?

Is the association with `Survived` positive or negative?

[12]:

```
# calculate the spearman correlation between all features
tests = {}
for c1 in X.columns:
    for c2 in X.columns:
        # TODO: fill this on
        # tests[(c1, c2)] = spearmanr()
        pass
tests
```

[12]:

```
{}
```

[14]:

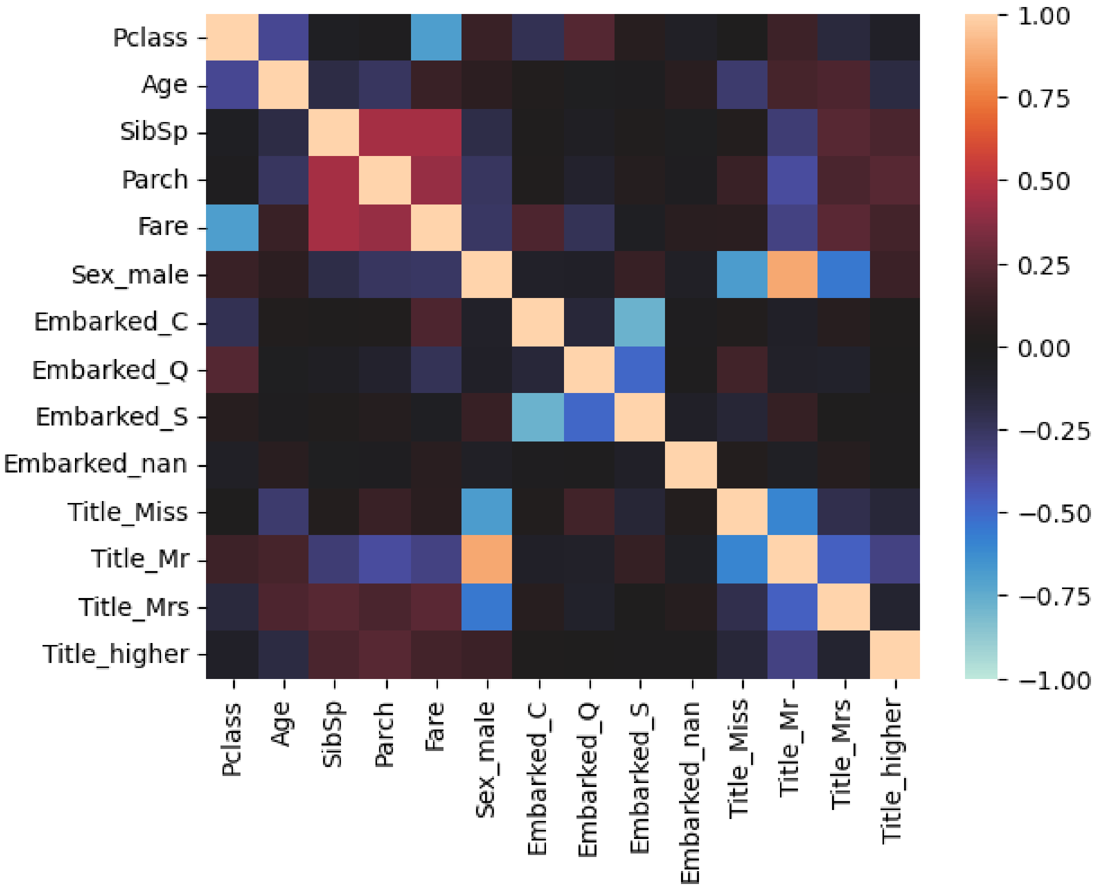
```
# we can do the same with a pandas function:
corr = X.corr(method="spearman")
```

[15]:

```
# and plot it
sns.heatmap(corr, center=0, vmin=-1, vmax=1)
```

[15]:

```
<Axes: >
```



What is the maximum and minimum value of the Spearman correlation coefficient and what do they mean?

Answer: -1 (strong negative correlation) and 1 (strong positive correlation)

What is the strongest correlation of all feature pairs?

Answer: Check `tests`

1.3 BONUS:

Plot a scatter plot with each point representing a feature (e.g., using t-SNE for dimensionality reduction), the size represention the assciation to `Survived`, the color corresponding to the direction of the association, and ines between the features if their absolute correlation exceeds 0.5.

```
[ ]:
```