```
import pandas as pd
import numpy as np
import seaborn as sb
import matplotlib.pyplot as plt
import scipy as spy
import keras
from sklearn.metrics import accuracy_score, recall_score, confusion_matrix
from sklearn.model_selection import train_test_split
from keras.models import Sequential
from keras.layers import Dense, Dropout, Input
from keras.optimizers import Adam, RMSprop
df = pd.read_csv('winequality-white.csv')
2021-08-11 12:11:24.330688: W tensorflow/stream_executor/platform/default/dso_loader.cc:6
4] Could not load dynamic library 'libcudart.so.11.0'; dlerror: libcudart.so.11.0: cannot
```

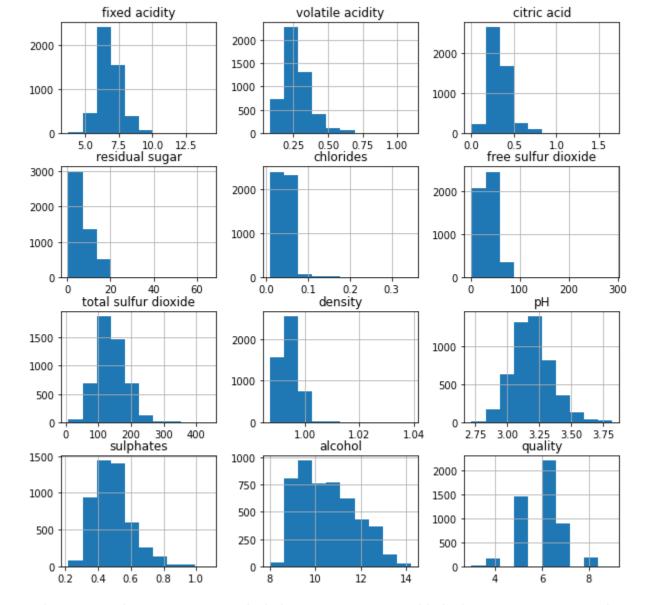
2021-08-11 12:11:24.330688: W tensorflow/stream_executor/platform/default/dso_loader.cc:6
4] Could not load dynamic library 'libcudart.so.11.0'; dlerror: libcudart.so.11.0: cannot open shared object file: No such file or directory
2021-08-11 12:11:24.330706: I tensorflow/stream_executor/cuda/cudart_stub.cc:29] Ignore ab ove cudart dlerror if you do not have a GPU set up on your machine.

Olhando abaixo, não temos nenhum valor N/A, então não precisamos tratar isso.

```
In [2]:
         df.isna().sum()
Out[2]: fixed acidity
                                  0
        volatile acidity
                                  0
        citric acid
                                  0
        residual sugar
                                  0
        chlorides
                                  0
        free sulfur dioxide
        total sulfur dioxide
                                  0
        density
        рН
                                  0
        sulphates
                                  0
        alcohol
                                  0
        quality
                                  0
        dtype: int64
In [3]:
         print(len(df))
         df
         4898
```

ut[3]:		fixed acidity	volatile acidity	citric acid	residual sugar	chlorides	free sulfur dioxide	total sulfur dioxide	density	рН	sulphates	alcohol	quality
	0	7.0	0.27	0.36	20.7	0.045	45.0	170.0	1.00100	3.00	0.45	8.8	6
	1	6.3	0.30	0.34	1.6	0.049	14.0	132.0	0.99400	3.30	0.49	9.5	6
	2	8.1	0.28	0.40	6.9	0.050	30.0	97.0	0.99510	3.26	0.44	10.1	6
	3	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.99560	3.19	0.40	9.9	6
	4	7.2	0.23	0.32	8.5	0.058	47.0	186.0	0.99560	3.19	0.40	9.9	6
	4893	6.2	0.21	0.29	1.6	0.039	24.0	92.0	0.99114	3.27	0.50	11.2	6
	4894	6.6	0.32	0.36	8.0	0.047	57.0	168.0	0.99490	3.15	0.46	9.6	5
	4895	6.5	0.24	0.19	1.2	0.041	30.0	111.0	0.99254	2.99	0.46	9.4	6
	4896	5.5	0.29	0.30	1.1	0.022	20.0	110.0	0.98869	3.34	0.38	12.8	7
	4897	6.0	0.21	0.38	0.8	0.020	22.0	98.0	0.98941	3.26	0.32	11.8	6

```
In [4]:
         df['quality'].value_counts()
             2198
Out[4]:
        5
             1457
        7
              880
        8
              175
        4
              163
        3
               20
        9
                5
        Name: quality, dtype: int64
In [5]:
         df.hist(figsize = (10, 10))
        array([[<AxesSubplot:title={'center':'fixed acidity'}>,
Out[5]:
                <AxesSubplot:title={'center':'volatile acidity'}>,
                <AxesSubplot:title={'center':'citric acid'}>],
                [<AxesSubplot:title={'center':'residual sugar'}>,
                <AxesSubplot:title={'center':'chlorides'}>,
                <AxesSubplot:title={'center':'free sulfur dioxide'}>],
                [<AxesSubplot:title={'center':'total sulfur dioxide'}>,
                <AxesSubplot:title={'center':'density'}>,
                <AxesSubplot:title={'center':'pH'}>],
                [<AxesSubplot:title={'center':'sulphates'}>,
                <AxesSubplot:title={'center':'alcohol'}>,
                <AxesSubplot:title={'center':'quality'}>]], dtype=object)
```



Podemos ver acima que temos um desbalancemaneto na quantidade de amostras. Temos muitas regulares e poucas ruins e ótimas. Vamos usar uma técnica chamada SMOTE que consiste em fazer o oversampling das amostras minoritárias, deixando assim o dataset balanceado. Essa técnica foi descrita no artigo.

```
In [6]:
         X=df.drop(columns=['quality'])
         y=df['quality']
In [7]:
         from imblearn.over_sampling import SMOTE
         oversample = SMOTE(k_neighbors=4)
         X, y = oversample.fit_resample(X, y)
In [8]:
         print(y.dtypes)
         print(y.count())
         y.value_counts()
        int64
        15386
              2198
Out[8]:
        5
              2198
        7
              2198
        8
              2198
        4
              2198
        3
              2198
```

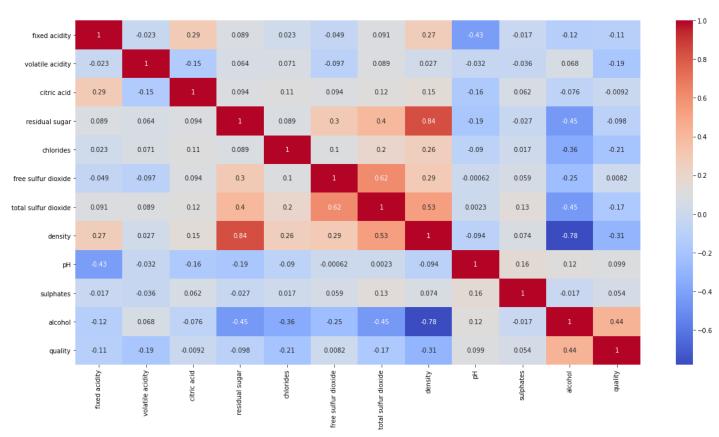
```
9 2198
Name: quality, dtype: int64
```

Pronto, agora temos todas as amostras em quantias iguais.

mapa de correlação:

```
corr=df.corr()
plt.figure(figsize=(20,10))
sb.heatmap(corr,annot=True, cmap='coolwarm')
```

Out[9]: <AxesSubplot:>



Também quero codificar essas qualidades numericamente:

```
In [10]:
          X_train, X_test, y_train, y_test = train_test_split(X,y,test_size=0.20,random_state=21)
          print('Formato do dataset de treinamento Xs:{}'.format(X_train.shape))
          print('Formato do datasett de teste Xs:{}'.format(X_test.shape))
          print('Formato do dataset de treino y:{}'.format(y_train.shape))
          print('Formato do dataset de test y:{}'.format(y_test.shape))
          y_train
         Formato do dataset de treinamento Xs:(12308, 11)
         Formato do datasett de teste Xs:(3078, 11)
         Formato do dataset de treino y:(12308,)
         Formato do dataset de test y:(3078,)
         12509
                  8
Out[10]:
         14261
                  9
                  9
         13650
         7263
                  4
         2851
                  5
         48
                  6
         8964
                  4
         5944
                  3
                  3
         5327
```

```
Name: quality, Length: 12308, dtype: int64
        Escalando o dataset
In [11]:
          from sklearn.preprocessing import StandardScaler
          sc=StandardScaler()
          X_train =sc.fit_transform(X_train)
          X_test=sc.fit_transform(X_test)
          X_train
         array([[-0.22741558, -1.0639914 , -0.38458136, ..., 0.00307363,
Out[11]:
                 -0.12161052, 0.06661161],
                [-0.16436717, 0.57646457,
                                            0.01817661, ..., 0.50304968,
                 -1.14134359, 1.42526059],
                [-0.13978815, 0.48381
                                            0.16594051, ..., 0.55187255,
                 -1.11749413, 1.44325812],
                . . . ,
                [ 1.04942297, 0.19851959, 0.8274273 , ..., 0.16877131,
                 -1.44675857, 1.13961914],
                [ 0.87318938, -0.4188991 , -1.07750024, ..., -0.04315277,
                  0.59747948, -0.92846942],
                [ 0.16432647, -0.45375517, 1.04106329, ..., 0.89852317,
                 -0.39543528, 1.47342487]])
In [12]:
          from sklearn.ensemble import RandomForestClassifier
          forest=RandomForestClassifier(n_estimators=10, criterion = 'entropy', random_state=0)
          forest.fit(X_train,y_train)
         RandomForestClassifier(criterion='entropy', n_estimators=10, random_state=0)
Out[12]:
        Outros testes com outro método
        avaliação do resultado:
```

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