Select-Best_Features

November 8, 2021

1 Atividade Prática.

2 Prazo: 08/Novembro

- Base: Diabetes Diagnostic
- Link: https://www.kaggle.com/houcembenmansour/predict-diabetes-based-on-diagnostic-measures

3 Data Analysis

[1]:
```
import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)
import seaborn as sns # data visualization library
import matplotlib.pyplot as plt
import time
from subprocess import check_output
import warnings
from imblearn.over_sampling import SMOTE
warnings.filterwarnings("ignore", category=FutureWarning)
```

[2]:
```
data = pd.read_csv('./base/diabetes.csv')
```

Before making anything like feature selection, feature extraction and classification, we start with basic data analysis. Lets look at features of data.

[3]:
```
display(data)  # head method shows only first 5 rows
```

	patient_number	cholesterol	glucose	hdl_chol	chol_hdl_ratio	age	\
0	1	193	77	49	3,9	19	
1	2	146	79	41	3,6	19	
2	3	217	75	54	4	20	
3	4	226	97	70	3,2	20	
4	5	164	91	67	2,4	20	
..	...	...	...	...	...	...	
385	386	227	105	44	5,2	83	
386	387	226	279	52	4,3	84	
387	388	301	90	118	2,6	89	
388	389	232	184	114	2	91	

```
389            390          165       94        69            2,4   92

     gender  height  weight   bmi  systolic_bp  diastolic_bp  waist  hip  \
0    female      61     119  22,5          118            70     32   38
1    female      60     135  26,4          108            58     33   40
2    female      67     187  29,3          110            72     40   45
3    female      64     114  19,6          122            64     31   39
4    female      70     141  20,2          122            86     32   39
..      ...     ...     ...   ...          ...           ...    ...  ...
385  female      59     125  25,2          150            90     35   40
386  female      60     192  37,5          144            88     41   48
387  female      61     115  21,7          218            90     31   41
388  female      61     127    24          170            82     35   38
389  female      62     217  39,7          160            82     51   51

    waist_hip_ratio     diabetes
0              0,84  No diabetes
1              0,83  No diabetes
2              0,89  No diabetes
3              0,79  No diabetes
4              0,82  No diabetes
..              ...          ...
385            0,88  No diabetes
386            0,85     Diabetes
387            0,76  No diabetes
388            0,92     Diabetes
389               1  No diabetes

[390 rows x 16 columns]
```

4 Vamos fazer uma cópia do Dataframe

[4]:
```
df = data.copy()
```

[5]:
```
df.head()
```

[5]:
```
   patient_number  cholesterol  glucose  hdl_chol chol_hdl_ratio  age  gender  \
0               1          193       77        49            3,9   19  female
1               2          146       79        41            3,6   19  female
2               3          217       75        54              4   20  female
3               4          226       97        70            3,2   20  female
4               5          164       91        67            2,4   20  female

   height  weight   bmi  systolic_bp  diastolic_bp  waist  hip  \
0      61     119  22,5          118            70     32   38
1      60     135  26,4          108            58     33   40
```

```
2      67     187  29,3          110            72     40   45
3      64     114  19,6          122            64     31   39
4      70     141  20,2          122            86     32   39

  waist_hip_ratio     diabetes
0            0,84  No diabetes
1            0,83  No diabetes
2            0,89  No diabetes
3            0,79  No diabetes
4            0,82  No diabetes
```

5 Vamos converter a classe para número

[6]:
```
#Mas antes vamos ver a distribuição
df['diabetes'].value_counts()
```

[6]:
```
No diabetes    330
Diabetes        60
Name: diabetes, dtype: int64
```

[7]:
```
dicionario = {'No diabetes':0, 'Diabetes':1}
df['diabetes'] = df['diabetes'].map(dicionario)
```

[8]:
```
df.head()
```

[8]:
```
   patient_number  cholesterol  glucose  hdl_chol chol_hdl_ratio  age  gender  \
0               1          193       77        49            3,9   19  female
1               2          146       79        41            3,6   19  female
2               3          217       75        54              4   20  female
3               4          226       97        70            3,2   20  female
4               5          164       91        67            2,4   20  female

   height  weight   bmi  systolic_bp  diastolic_bp  waist  hip  \
0      61     119  22,5          118            70     32   38
1      60     135  26,4          108            58     33   40
2      67     187  29,3          110            72     40   45
3      64     114  19,6          122            64     31   39
4      70     141  20,2          122            86     32   39

  waist_hip_ratio  diabetes
0            0,84         0
1            0,83         0
2            0,89         0
3            0,79         0
4            0,82         0
```

6 Vamos converter o Gênero

[9]:
```
df = pd.concat([df,pd.get_dummies(df['gender'], prefix='gender')],axis=1)
df.drop(['gender'],axis=1, inplace=True)
```

[10]:
```
df.head()
```

[10]:

	patient_number	cholesterol	glucose	hdl_chol	chol_hdl_ratio	age	height	\
0	1	193	77	49	3,9	19	61	
1	2	146	79	41	3,6	19	60	
2	3	217	75	54	4	20	67	
3	4	226	97	70	3,2	20	64	
4	5	164	91	67	2,4	20	70	

	weight	bmi	systolic_bp	diastolic_bp	waist	hip	waist_hip_ratio	\
0	119	22,5	118	70	32	38	0,84	
1	135	26,4	108	58	33	40	0,83	
2	187	29,3	110	72	40	45	0,89	
3	114	19,6	122	64	31	39	0,79	
4	141	20,2	122	86	32	39	0,82	

	diabetes	gender_female	gender_male
0	0	1	0
1	0	1	0
2	0	1	0
3	0	1	0
4	0	1	0

7 Converter a vírgula pelo ponto

[11]:
```
df['chol_hdl_ratio'] = df['chol_hdl_ratio'].str.replace(',', '.')
```

[12]:
```
df['bmi'] = df['bmi'].str.replace(',', '.')
```

[13]:
```
df['waist_hip_ratio'] = df['waist_hip_ratio'].str.replace(',','.')
```

[14]:
```
df.head()
```

[14]:

	patient_number	cholesterol	glucose	hdl_chol	chol_hdl_ratio	age	height	\
0	1	193	77	49	3.9	19	61	
1	2	146	79	41	3.6	19	60	
2	3	217	75	54	4	20	67	
3	4	226	97	70	3.2	20	64	
4	5	164	91	67	2.4	20	70	

	weight	bmi	systolic_bp	diastolic_bp	waist	hip	waist_hip_ratio	\
0	119	22.5	118	70	32	38	0.84	

```
1     135  26.4          108           58     33   40           0.83
2     187  29.3          110           72     40   45           0.89
3     114  19.6          122           64     31   39           0.79
4     141  20.2          122           86     32   39           0.82

   diabetes  gender_female  gender_male
0         0              1            0
1         0              1            0
2         0              1            0
3         0              1            0
4         0              1            0
```

7.1 Remoção de atributos irrelevantes

[15]:
```
# feature names as an Index (panda object including a list of column names and dtype)
col = df.columns       # .columns gives columns names in data
print(col)
```

```
Index(['patient_number', 'cholesterol', 'glucose', 'hdl_chol',
       'chol_hdl_ratio', 'age', 'height', 'weight', 'bmi', 'systolic_bp',
       'diastolic_bp', 'waist', 'hip', 'waist_hip_ratio', 'diabetes',
       'gender_female', 'gender_male'],
      dtype='object')
```

[16]:
```
df.columns
```

[16]:
```
Index(['patient_number', 'cholesterol', 'glucose', 'hdl_chol',
       'chol_hdl_ratio', 'age', 'height', 'weight', 'bmi', 'systolic_bp',
       'diastolic_bp', 'waist', 'hip', 'waist_hip_ratio', 'diabetes',
       'gender_female', 'gender_male'],
      dtype='object')
```

[17]:
```
X = df.drop(['patient_number','diabetes'],axis = 1)
y = df['diabetes']
```

[18]:
```
y.head()
```

[18]:
```
0    0
1    0
2    0
3    0
4    0
Name: diabetes, dtype: int64
```

[19]:
```
X
```

[19]:
```
     cholesterol  glucose  hdl_chol chol_hdl_ratio  age  height  weight   bmi  \
0            193       77        49            3.9   19      61     119  22.5
1            146       79        41            3.6   19      60     135  26.4
2            217       75        54              4   20      67     187  29.3
3            226       97        70            3.2   20      64     114  19.6
4            164       91        67            2.4   20      70     141  20.2
..           ...      ...       ...            ...  ...     ...     ...   ...
385          227      105        44            5.2   83      59     125  25.2
386          226      279        52            4.3   84      60     192  37.5
387          301       90       118            2.6   89      61     115  21.7
388          232      184       114              2   91      61     127    24
389          165       94        69            2.4   92      62     217  39.7

     systolic_bp  diastolic_bp  waist  hip waist_hip_ratio  gender_female  \
0            118            70     32   38            0.84              1
1            108            58     33   40            0.83              1
2            110            72     40   45            0.89              1
3            122            64     31   39            0.79              1
4            122            86     32   39            0.82              1
..           ...           ...    ...  ...             ...            ...
385          150            90     35   40            0.88              1
386          144            88     41   48            0.85              1
387          218            90     31   41            0.76              1
388          170            82     35   38            0.92              1
389          160            82     51   51               1              1

     gender_male
0              0
1              0
2              0
3              0
4              0
..           ...
385            0
386            0
387            0
388            0
389            0

[390 rows x 15 columns]
```

7.2 Distruição das amostras entre as classes

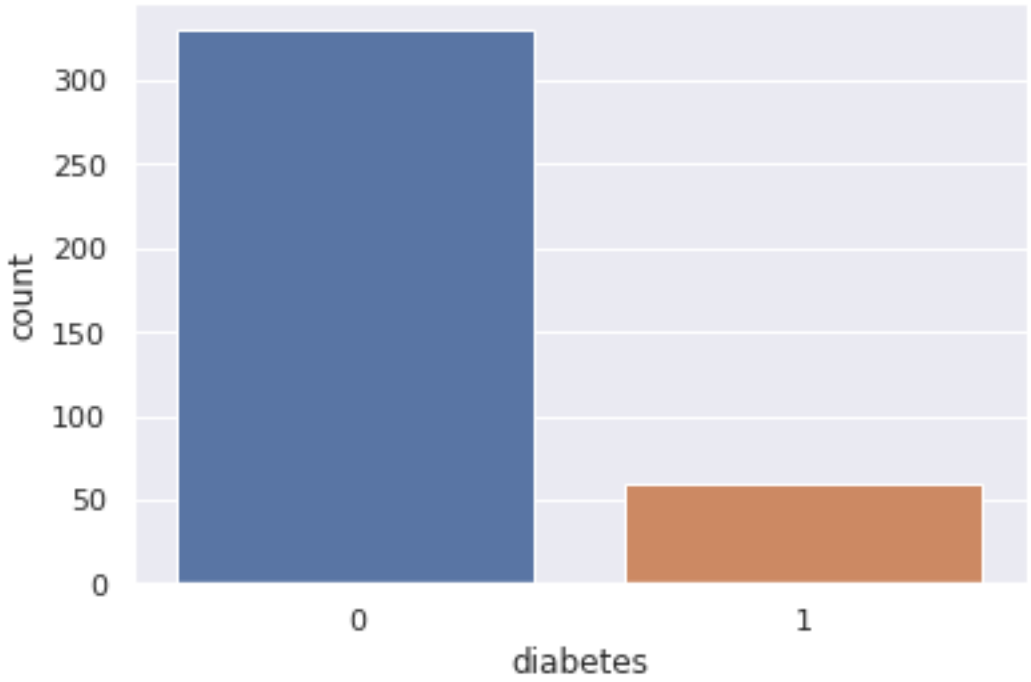
[20]:
```
y.value_counts()
```

[20]:
```
0    330
1     60
```

```
Name: diabetes, dtype: int64
```

[21]:
```
sns.set(style="darkgrid")
ax = sns.countplot(x = y)       # M = 212, B = 357
N, S = y.value_counts(sort=True) #sort=True (default) in order to be sure B, M␣
 ↪are in the right order (alphabetical)
print('No Diabetes: ',N)
print('Diabetes : ',S)
```

```
No Diabetes:  330
Diabetes :  60
```



8 Balancemaneto das classes

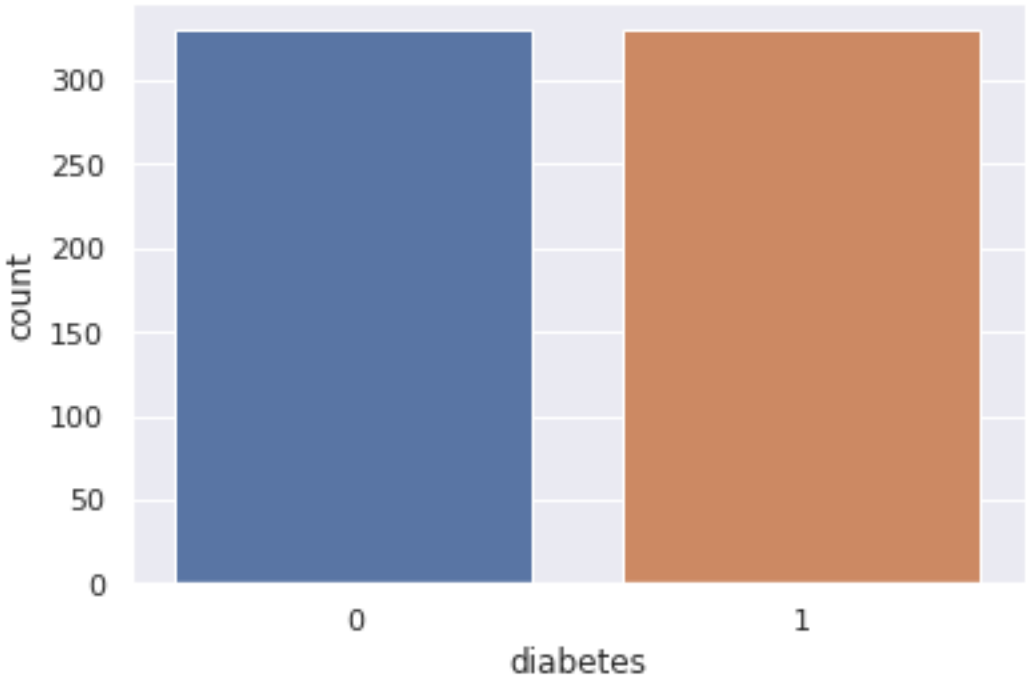
[22]:
```
smt = SMOTE()
X,y = smt.fit_resample(X,y)
```

9 Rever a distruição das amostras entre as classes

[23]:
```
sns.set(style="darkgrid")
ax = sns.countplot(x = y)       # M = 212, B = 357
N, S = y.value_counts(sort=True) #sort=True (default) in order to be sure B, M␣
 ↪are in the right order (alphabetical)
```

```
print('No Diabetes: ',N)
print('Diabetes : ',S)
```

```
No Diabetes:  330
Diabetes :  330
```



9.0.1 Verifica se há dados faltantes

[24]:
```
#check if there is a NaN value in our data frame x, a False indicates there are␣
 ↪no missing values
X.isnull().values.any()
```

[24]:
```
False
```

Let's now use the describe function in order to look at our features :

[25]:
```
X
```

[25]:
```
      cholesterol  glucose  hdl_chol chol_hdl_ratio  age  height  weight  \
0             193       77        49            3.9   19      61     119
1             146       79        41            3.6   19      60     135
2             217       75        54            4.0   20      67     187
3             226       97        70            3.2   20      64     114
4             164       91        67            2.4   20      70     141
..            ...      ...       ...            ...  ...     ...     ...
```

```
655          271      353        40       6.690464   65      68      194
656          270      129        36       7.552358   44      59      206
657          245      119        31       8.165698   40      64      169
658          261      208        47       5.581888   68      65      160
659          248      197        44       5.620365   64      63      159

            bmi  systolic_bp  diastolic_bp  waist  hip waist_hip_ratio  \
0          22.5           118            70     32   38            0.84
1          26.4           108            58     33   40            0.83
2          29.3           110            72     40   45            0.89
3          19.6           122            64     31   39            0.79
4          20.2           122            86     32   39            0.82
..          ...           ...           ...    ...  ...             ...
655  29.217936           145            89     40   42        0.946474
656  41.497979           119            70     41   48        0.864899
657  28.382389           146            95     36   40        0.887963
658  26.871236           156            86     34   41        0.844292
659   28.22746           150            84     33   41        0.800275

     gender_female  gender_male
0                1            0
1                1            0
2                1            0
3                1            0
4                1            0
..             ...          ...
655              0            1
656              1            0
657              0            0
658              0            0
659              1            0

[660 rows x 15 columns]
```

[26]:
```
X.shape
```

[26]:
```
(660, 15)
```

9.1 Normalização dos dados

[27]:
```
from sklearn.preprocessing import MinMaxScaler

# create a scaler object
scaler = MinMaxScaler()
# fit and transform the data
data_normal = pd.DataFrame(scaler.fit_transform(X), columns=X.columns)
```

[28]:
```
data_normal
```

[28]:

	cholesterol	glucose	hdl_chol	chol_hdl_ratio	age	height	\
0	0.315068	0.086053	0.342593	0.134831	0.000000	0.375000	
1	0.186301	0.091988	0.268519	0.117978	0.000000	0.333333	
2	0.380822	0.080119	0.388889	0.140449	0.013699	0.625000	
3	0.405479	0.145401	0.537037	0.095506	0.013699	0.500000	
4	0.235616	0.127596	0.509259	0.050562	0.013699	0.750000	
..	...	...	...	...	...	...	
655	0.528767	0.905045	0.259259	0.291599	0.630137	0.666667	
656	0.526027	0.240356	0.222222	0.340020	0.342466	0.291667	
657	0.457534	0.210682	0.175926	0.374477	0.287671	0.500000	
658	0.501370	0.474777	0.324074	0.229320	0.671233	0.541667	
659	0.465753	0.442136	0.296296	0.231481	0.616438	0.458333	

	weight	bmi	systolic_bp	diastolic_bp	waist	hip	\
0	0.088496	0.179803	0.17500	0.289474	0.200000	0.235294	
1	0.159292	0.275862	0.11250	0.131579	0.233333	0.294118	
2	0.389381	0.347291	0.12500	0.315789	0.466667	0.441176	
3	0.066372	0.108374	0.20000	0.210526	0.166667	0.264706	
4	0.185841	0.123153	0.20000	0.500000	0.200000	0.264706	
..	...	...	...	...	...	...	
655	0.420354	0.345269	0.34375	0.539474	0.466667	0.352941	
656	0.473451	0.647733	0.18125	0.289474	0.500000	0.529412	
657	0.309735	0.324689	0.35000	0.618421	0.333333	0.294118	
658	0.269912	0.287469	0.41250	0.500000	0.266667	0.323529	
659	0.265487	0.320873	0.37500	0.473684	0.233333	0.323529	

	waist_hip_ratio	gender_female	gender_male
0	0.347826	1.0	0.0
1	0.326087	1.0	0.0
2	0.456522	1.0	0.0
3	0.239130	1.0	0.0
4	0.304348	1.0	0.0
..	...	...	...
655	0.579292	0.0	1.0
656	0.401954	1.0	0.0
657	0.452094	0.0	0.0
658	0.357157	0.0	0.0
659	0.261467	1.0	0.0

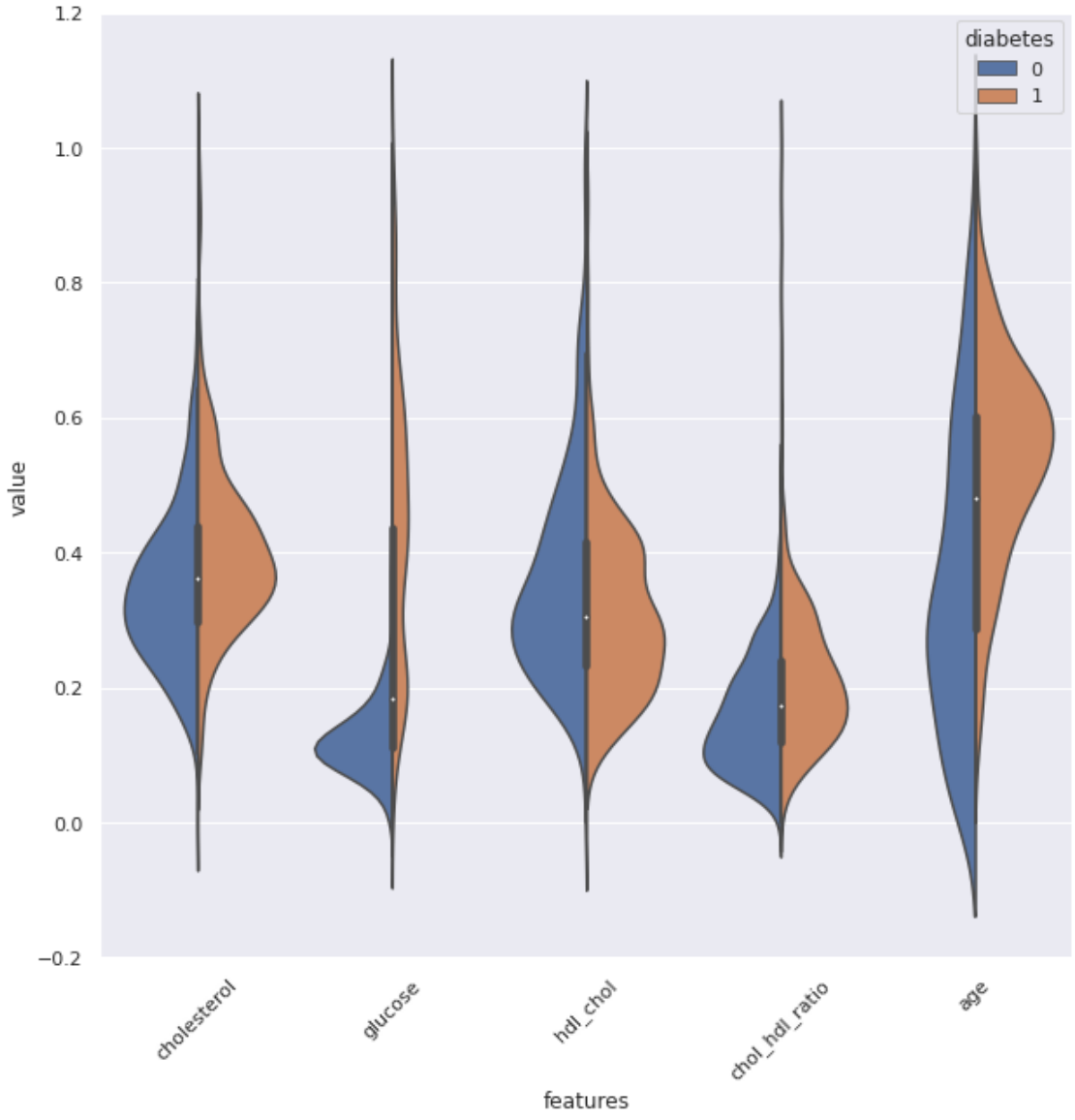
[660 rows x 15 columns]

10 Visualização

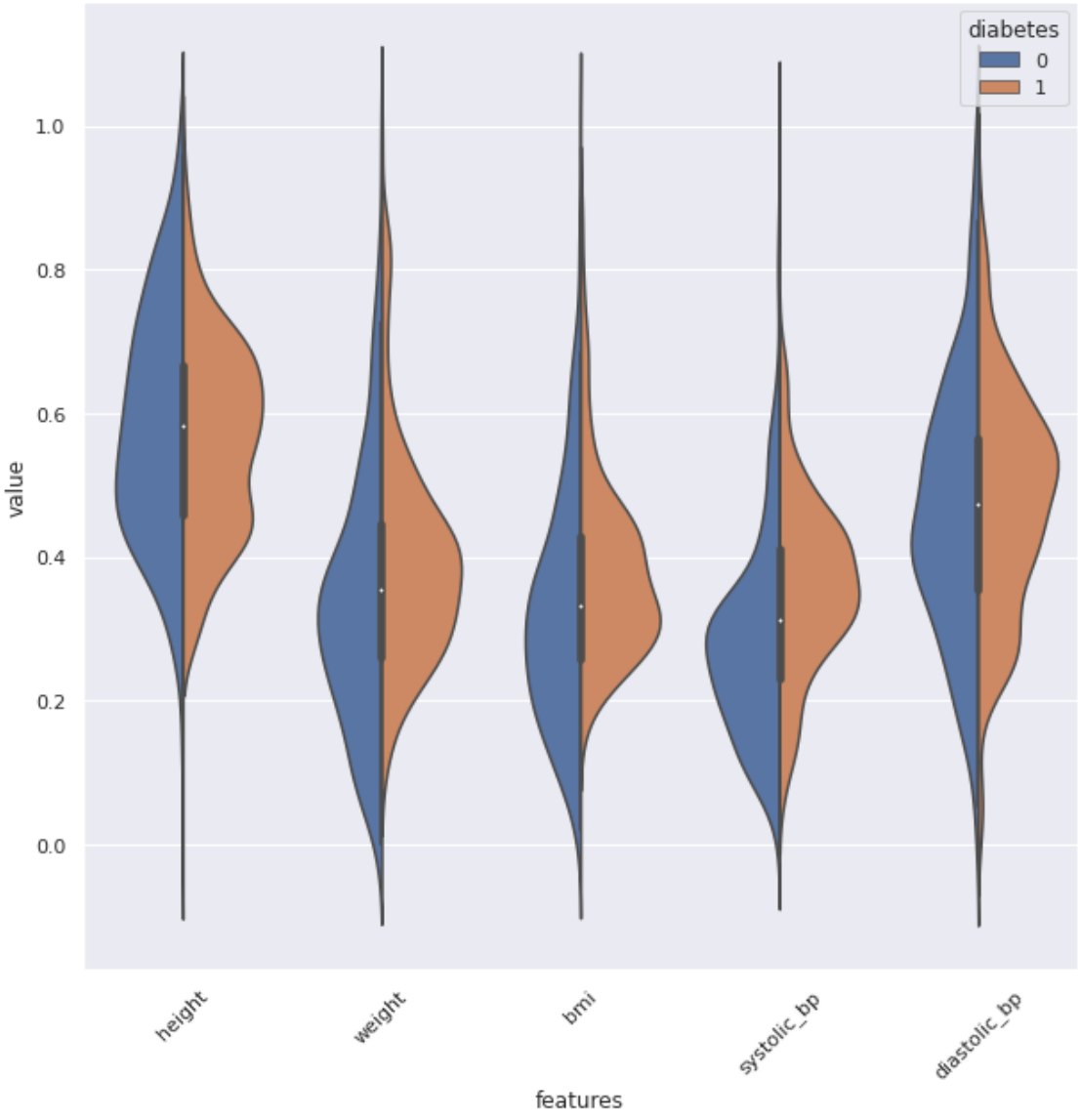
– https://mode.com/blog/violin-plot-examples/

[29]:
```
def violin_plot(beginning,end):
    dados = pd.concat([y,data_normal.iloc[:,beginning:end]],axis=1)
    dados = pd.melt(dados, id_vars='diabetes', var_name="features",␣
 ↪value_name='value')
    plt.figure(figsize=(10,10))
    sns.violinplot(x='features', y='value', hue='diabetes', data=dados,␣
 ↪split=True, inner="box")
    plt.xticks(rotation=45)
```

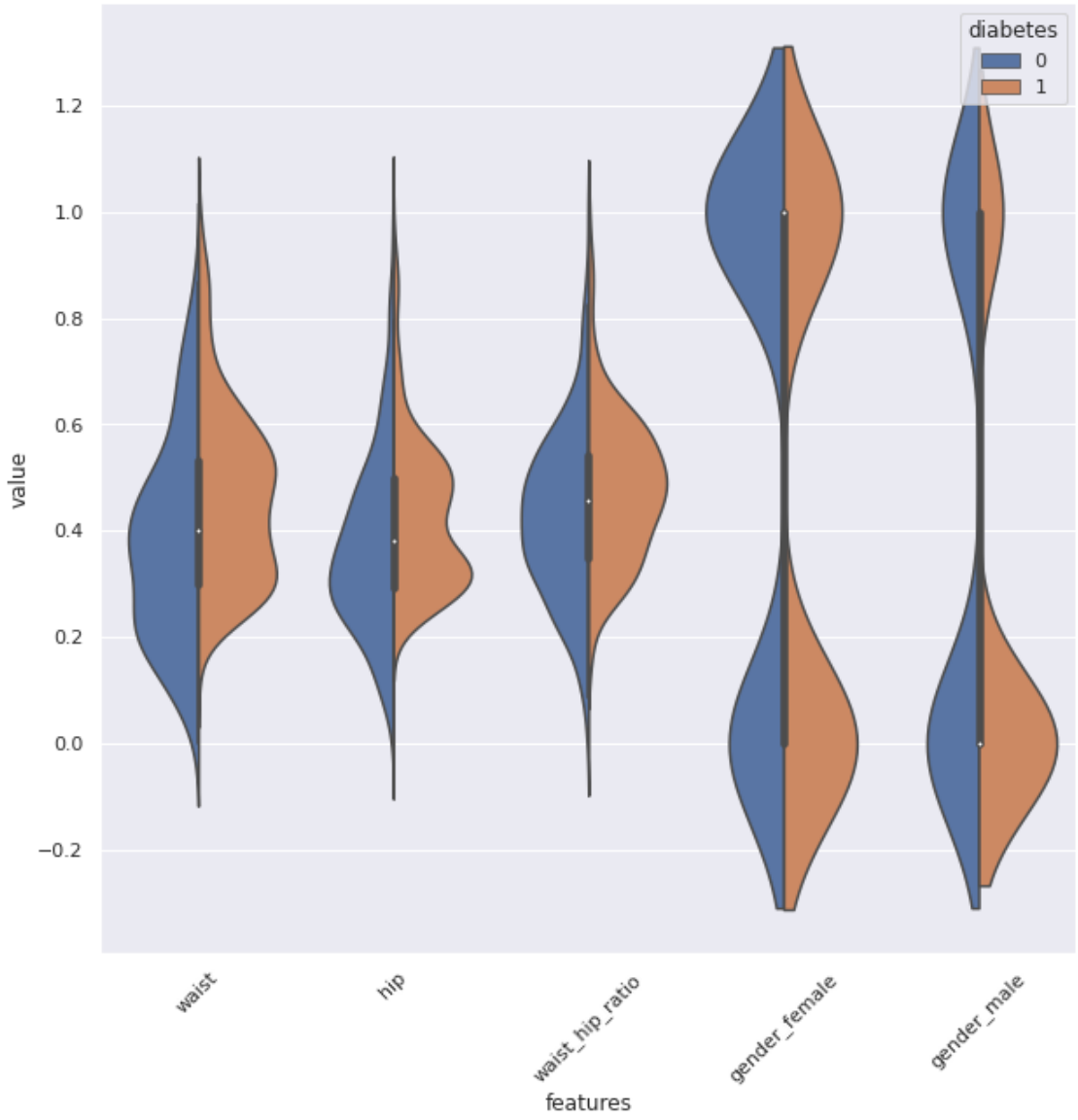
[30]:
```
# first ten features
violin_plot(0,5)
```



[31]:
```
# Second ten features
violin_plot(5,10)
```



[32]:
```
# Third ten features
violin_plot(10,15)
```



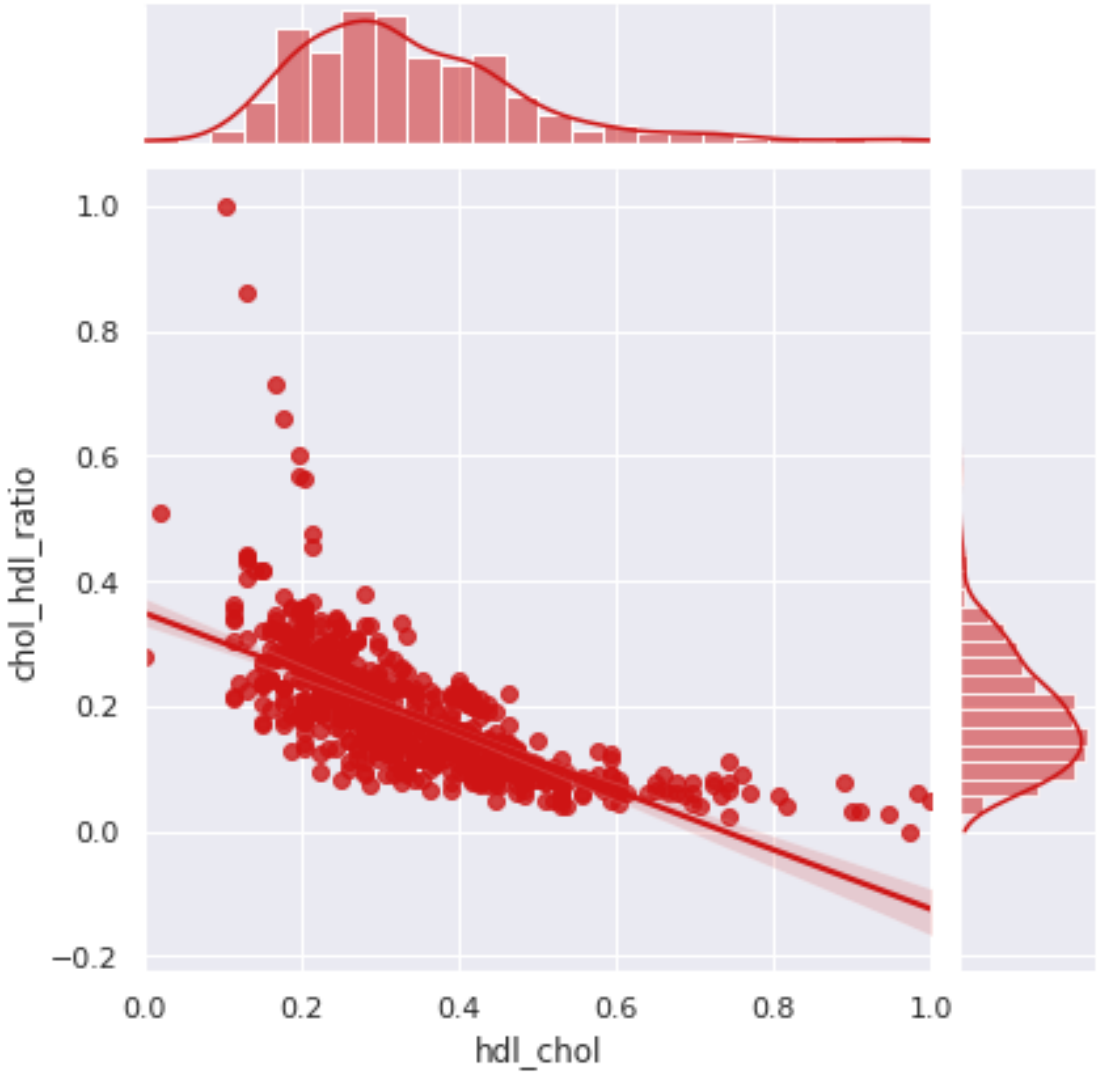
[33]:
```
data_normal.columns
```

[33]:
```
Index(['cholesterol', 'glucose', 'hdl_chol', 'chol_hdl_ratio', 'age', 'height',
       'weight', 'bmi', 'systolic_bp', 'diastolic_bp', 'waist', 'hip',
       'waist_hip_ratio', 'gender_female', 'gender_male'],
      dtype='object')
```

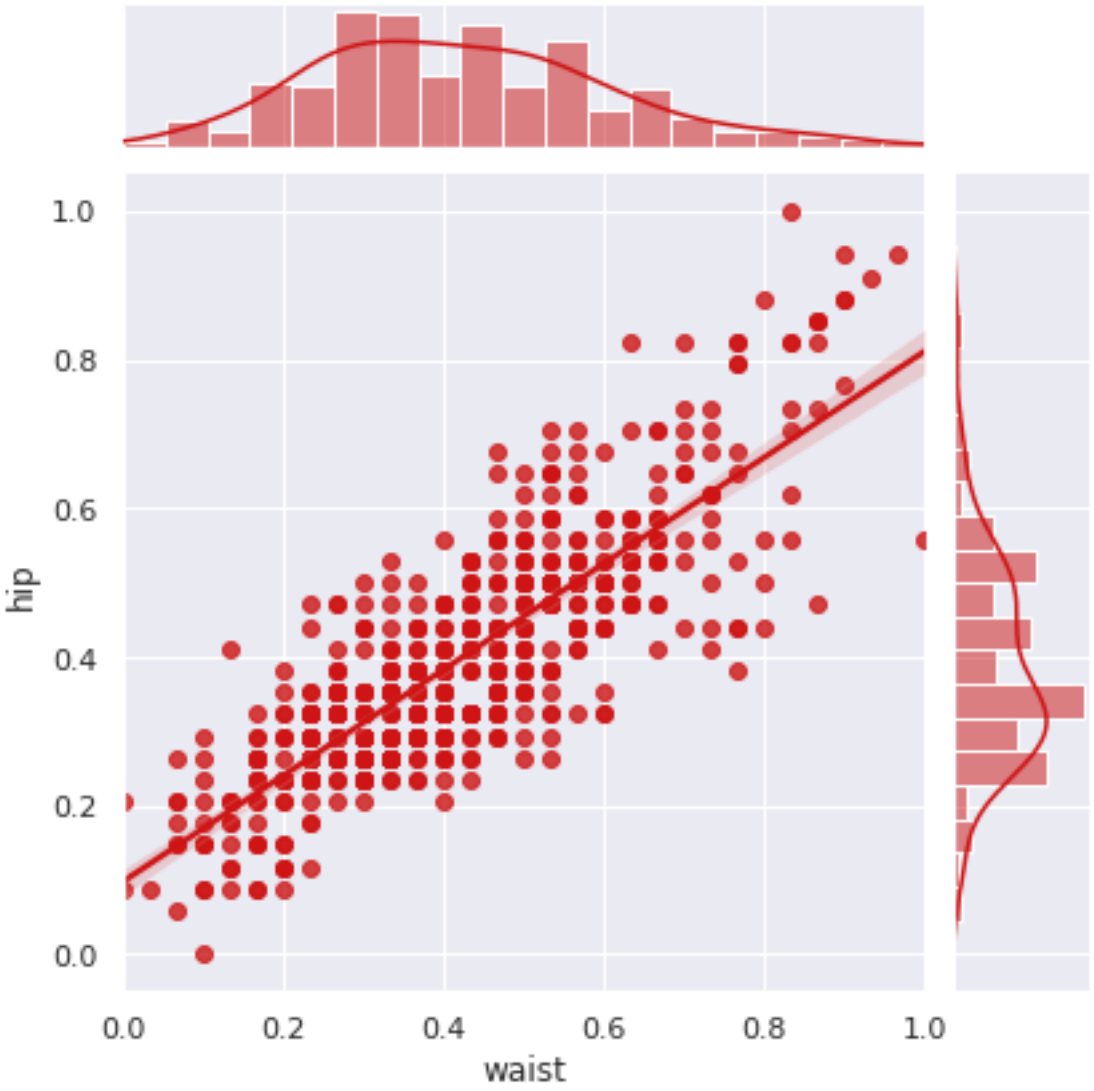
11 Aqui, acho que questão de atualização de pacotes no meu não funcionou o regg com dois g.

[34]:
```
def joint_plot(feature1, feature2):
    """ I have a FutureWarning on this function, anyone knows how to get rid of␣
 ↪it ?"""
    sns.jointplot(data_normal.loc[:,feature1], data_normal.loc[:,feature2],␣
 ↪kind="reg", color="#ce1414")
```

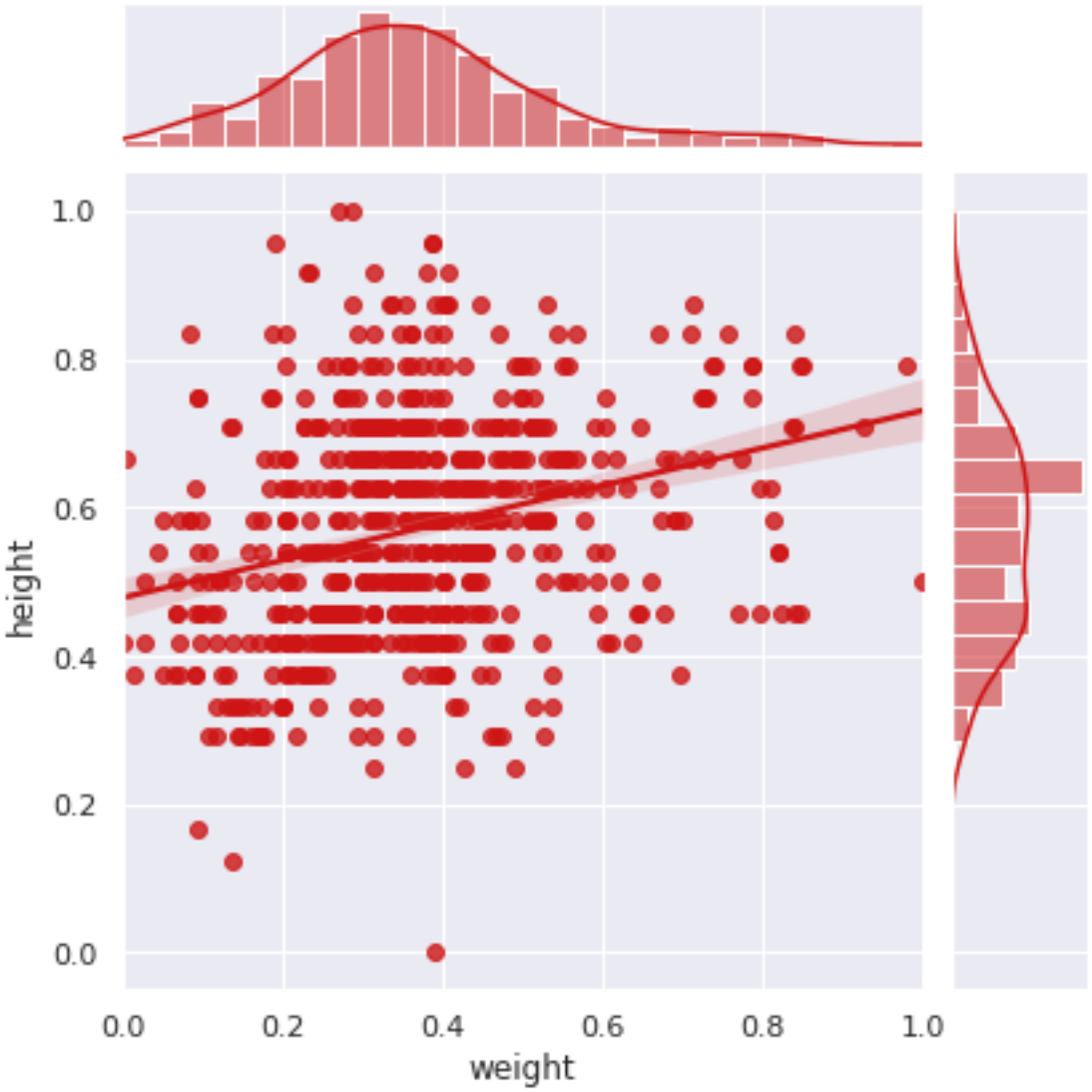
[35]:
```
joint_plot('hdl_chol','chol_hdl_ratio')
#joint_plot("radius_worst","smoothness_worst")
```



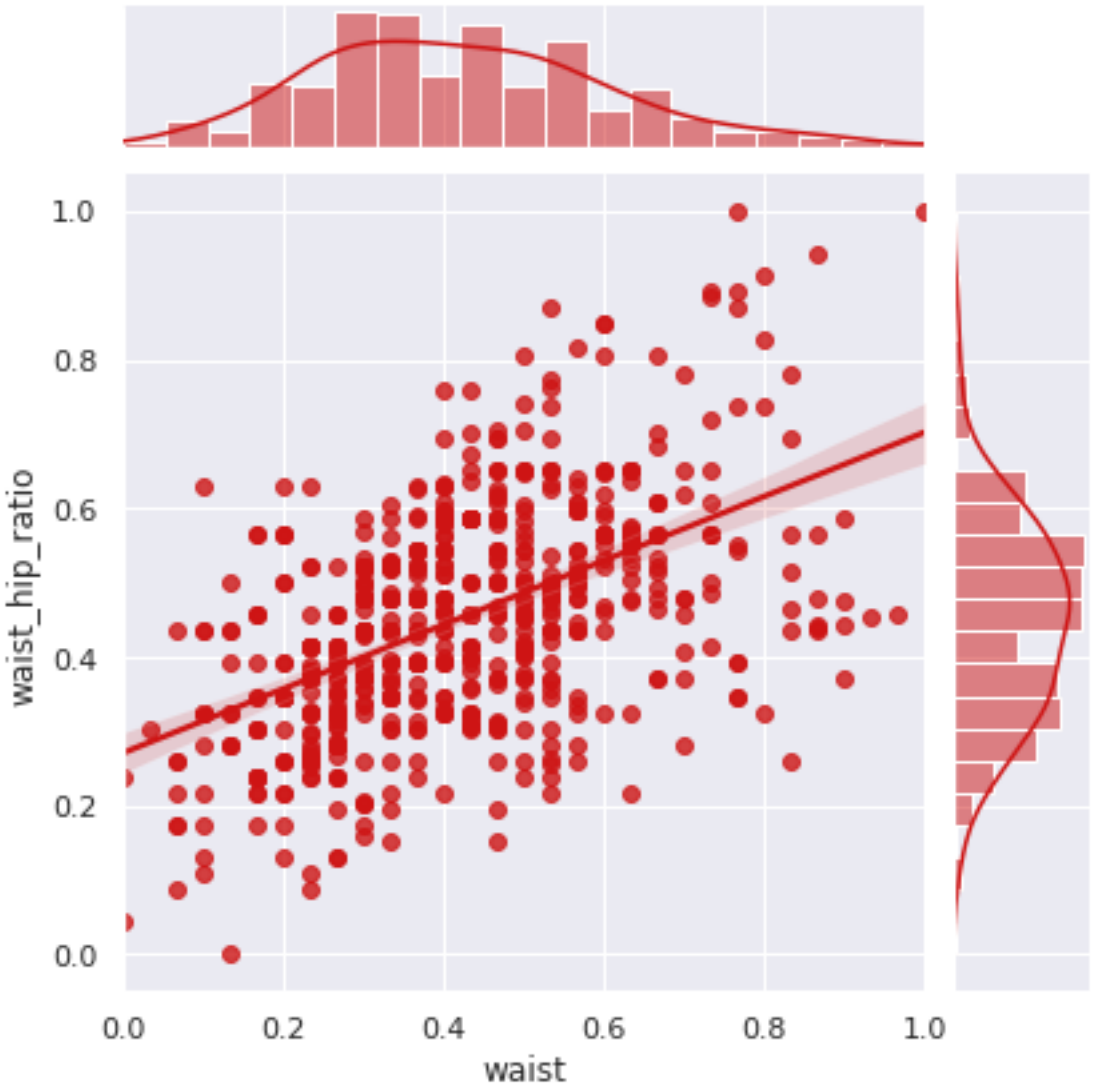
[36]:
```
joint_plot("waist","hip")
```



[37]:
```
joint_plot('weight','height')
```

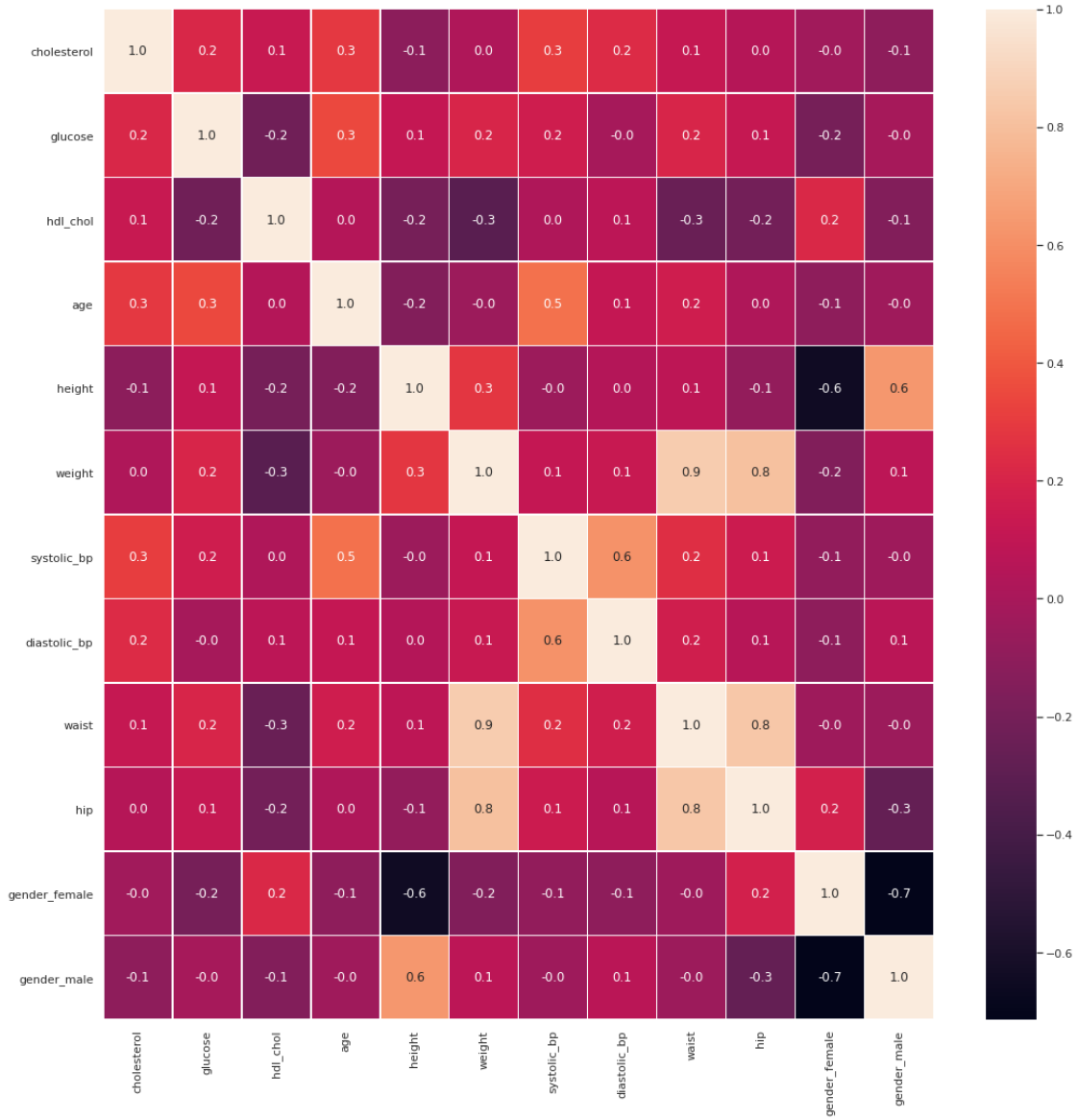


[38]:
```
joint_plot('waist','waist_hip_ratio')
```



11.1 Mapa de calor com a correlação entre os atributos

[39]:
```
#correlation map
f,ax = plt.subplots(figsize=(18, 18))
ax = sns.heatmap(X.corr(), annot=True, linewidths=.5, fmt= '.1f',ax=ax)
```



12 Executando o Random Forest com todos os atributos

[40]:
```
display(data_normal)
```

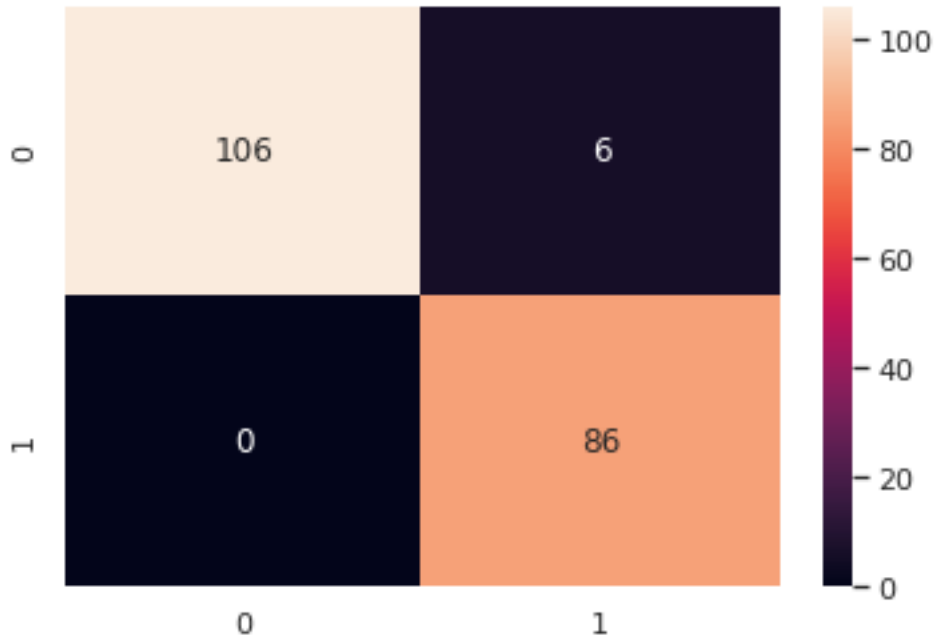
```
     cholesterol   glucose  hdl_chol  chol_hdl_ratio       age    height  \
0       0.315068  0.086053  0.342593        0.134831  0.000000  0.375000
1       0.186301  0.091988  0.268519        0.117978  0.000000  0.333333
2       0.380822  0.080119  0.388889        0.140449  0.013699  0.625000
3       0.405479  0.145401  0.537037        0.095506  0.013699  0.500000
4       0.235616  0.127596  0.509259        0.050562  0.013699  0.750000
..           ...       ...       ...             ...       ...       ...
```

```
655     0.528767  0.905045  0.259259         0.291599  0.630137  0.666667
656     0.526027  0.240356  0.222222         0.340020  0.342466  0.291667
657     0.457534  0.210682  0.175926         0.374477  0.287671  0.500000
658     0.501370  0.474777  0.324074         0.229320  0.671233  0.541667
659     0.465753  0.442136  0.296296         0.231481  0.616438  0.458333

       weight       bmi  systolic_bp  diastolic_bp     waist       hip  \
0    0.088496  0.179803      0.17500      0.289474  0.200000  0.235294
1    0.159292  0.275862      0.11250      0.131579  0.233333  0.294118
2    0.389381  0.347291      0.12500      0.315789  0.466667  0.441176
3    0.066372  0.108374      0.20000      0.210526  0.166667  0.264706
4    0.185841  0.123153      0.20000      0.500000  0.200000  0.264706
..        ...       ...          ...           ...       ...       ...
655  0.420354  0.345269      0.34375      0.539474  0.466667  0.352941
656  0.473451  0.647733      0.18125      0.289474  0.500000  0.529412
657  0.309735  0.324689      0.35000      0.618421  0.333333  0.294118
658  0.269912  0.287469      0.41250      0.500000  0.266667  0.323529
659  0.265487  0.320873      0.37500      0.473684  0.233333  0.323529

     waist_hip_ratio  gender_female  gender_male
0           0.347826            1.0          0.0
1           0.326087            1.0          0.0
2           0.456522            1.0          0.0
3           0.239130            1.0          0.0
4           0.304348            1.0          0.0
..               ...            ...          ...
655         0.579292            0.0          1.0
656         0.401954            1.0          0.0
657         0.452094            0.0          0.0
658         0.357157            0.0          0.0
659         0.261467            1.0          0.0

[660 rows x 15 columns]
```

[41]:
```python
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import f1_score, confusion_matrix
from sklearn.metrics import accuracy_score, recall_score,classification_report
from sklearn.preprocessing import LabelEncoder

#Binary format, with B=0 and M=1
#y = y.replace("B", 0)
#y = y.replace("M", 1)

# Para obter as classes como inteiros, utilizamos
# a classe LabelEncoder da scikit-learn
```

```
# split data train 70 % and test 30 %
x_train, x_test, y_train, y_test = train_test_split(data_normal, y, test_size=0.
↪3, random_state=42)

#random forest classifier with n_estimators=10 (default)
clf_rf = RandomForestClassifier(random_state=43)
clr_rf = clf_rf.fit(x_train,y_train)

recall = recall_score(y_test,clf_rf.predict(x_test))
print('Recall is: ', recall)
accuracy = accuracy_score(y_test,clf_rf.predict(x_test))
print('Accuracy is: ', accuracy)
f1 = f1_score(y_test,clf_rf.predict(x_test))
print('F1 score is: ', f1)
cm = confusion_matrix(y_test,clf_rf.predict(x_test))
ax = sns.heatmap(cm,annot=True,fmt="d")
```

```
Recall is:  1.0
Accuracy is:  0.9696969696969697
F1 score is:  0.9662921348314606
```



[42]:
```
#Eu inseri esse
#print(classification_report(y_test, y_pred_class))
print(classification_report(y_test, clf_rf.predict(x_test)))
```

```
              precision    recall  f1-score   support
```

```
              0       1.00      0.95      0.97       112
              1       0.93      1.00      0.97        86

    accuracy                            0.97       198
   macro avg       0.97      0.97      0.97       198
weighted avg       0.97      0.97      0.97       198
```

13 Seleção de características e Aprendizado de Máquina

Nesta seção, selecionaremos recursos com métodos diferentes que são seleção de recursos com correlação, eliminação de recurso recursivo (RFE) e eliminação de recurso recursivo com validação cruzada (RFECV). Usaremos a classificação Random Forest para treinar nosso modelo.

13.1 1) Feature Selection with correlation and Random Forest classification

height,waist e hib are correlated -> I choose **height**. **hdl_chol,chol_hdl_ratio** are correlated negative -> I choose **chol_hdl_ratio**.

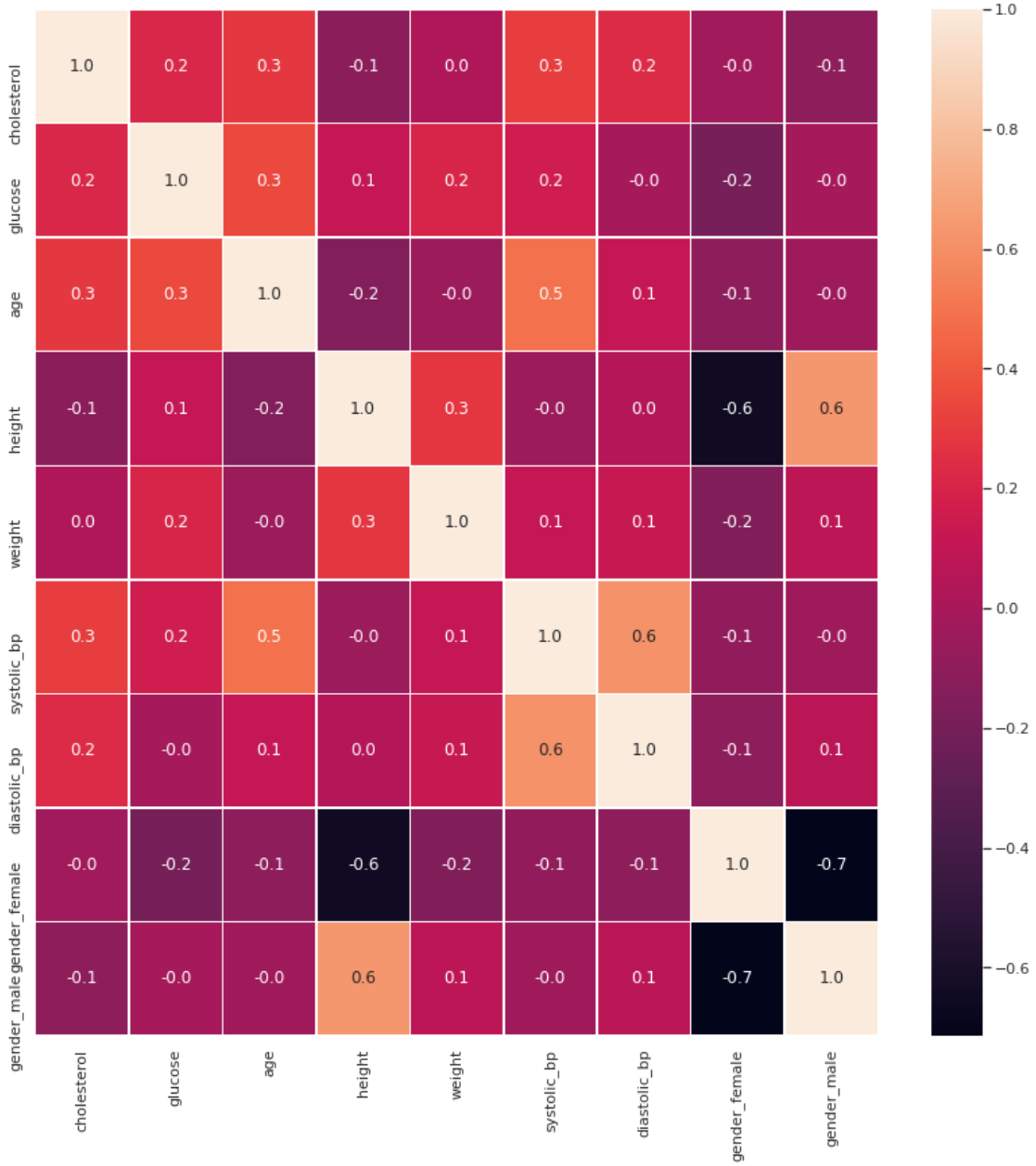
[43]:
```
drop_list = ['waist','hip','hdl_chol']
x_1 = X.drop(drop_list,axis = 1 )        # do not modify x, we will use it later
x_1.head()
```

[43]:

	cholesterol	glucose	chol_hdl_ratio	age	height	weight	bmi	\
0	193	77	3.9	19	61	119	22.5	
1	146	79	3.6	19	60	135	26.4	
2	217	75	4.0	20	67	187	29.3	
3	226	97	3.2	20	64	114	19.6	
4	164	91	2.4	20	70	141	20.2	

	systolic_bp	diastolic_bp	waist_hip_ratio	gender_female	gender_male
0	118	70	0.84	1	0
1	108	58	0.83	1	0
2	110	72	0.89	1	0
3	122	64	0.79	1	0
4	122	86	0.82	1	0

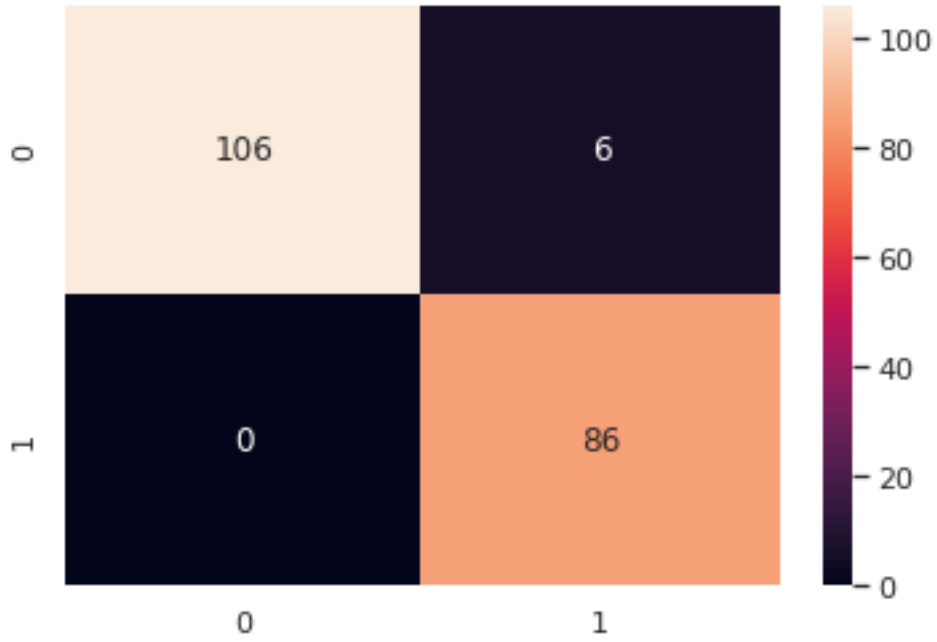
[44]:
```
#correlation map
f,ax = plt.subplots(figsize=(14, 14))
ax = sns.heatmap(x_1.corr(), annot=True, linewidths=.5, fmt= '.1f',ax=ax)
```



[45]:
```
x_train, x_test, y_train, y_test = train_test_split(x_1, y, test_size=0.3,␣
 ↪random_state=42)

#random forest classifier with n_estimators=10 (default)
clf_rf = RandomForestClassifier(random_state=42)
clr_rf = clf_rf.fit(x_train,y_train)

recall = recall_score(y_test,clf_rf.predict(x_test))
print('Recall is: ', recall)
```

```
accuracy = accuracy_score(y_test,clf_rf.predict(x_test))
print('Accuracy is: ', accuracy)
f1 = f1_score(y_test,clf_rf.predict(x_test))
print('F1 score is: ', f1)
cm = confusion_matrix(y_test,clf_rf.predict(x_test))
ax = sns.heatmap(cm,annot=True,fmt="d")
```

```
Recall is:  1.0
Accuracy is:  0.9696969696969697
F1 score is:  0.9662921348314606
```



13.2 2) Recursive feature elimination (RFE) with Random Forest

RFE usa um dos métodos de classificação (floresta aleatória) que atribui pesos a cada recurso. Os menores pesos são removidos do conjunto atual de recursos. Esse procedimento é repetido recursivamente no conjunto podado até que o número desejado de recursos seja alcançado.

[46]:
```
display(data_normal)
```

```
     cholesterol   glucose  hdl_chol  chol_hdl_ratio       age    height  \
0       0.315068  0.086053  0.342593        0.134831  0.000000  0.375000
1       0.186301  0.091988  0.268519        0.117978  0.000000  0.333333
2       0.380822  0.080119  0.388889        0.140449  0.013699  0.625000
3       0.405479  0.145401  0.537037        0.095506  0.013699  0.500000
4       0.235616  0.127596  0.509259        0.050562  0.013699  0.750000
..           ...       ...       ...             ...       ...       ...
655     0.528767  0.905045  0.259259        0.291599  0.630137  0.666667
```

```
656     0.526027  0.240356  0.222222         0.340020  0.342466  0.291667
657     0.457534  0.210682  0.175926         0.374477  0.287671  0.500000
658     0.501370  0.474777  0.324074         0.229320  0.671233  0.541667
659     0.465753  0.442136  0.296296         0.231481  0.616438  0.458333

       weight       bmi  systolic_bp  diastolic_bp     waist       hip  \
0    0.088496  0.179803      0.17500      0.289474  0.200000  0.235294
1    0.159292  0.275862      0.11250      0.131579  0.233333  0.294118
2    0.389381  0.347291      0.12500      0.315789  0.466667  0.441176
3    0.066372  0.108374      0.20000      0.210526  0.166667  0.264706
4    0.185841  0.123153      0.20000      0.500000  0.200000  0.264706
..        ...       ...          ...           ...       ...       ...
655  0.420354  0.345269      0.34375      0.539474  0.466667  0.352941
656  0.473451  0.647733      0.18125      0.289474  0.500000  0.529412
657  0.309735  0.324689      0.35000      0.618421  0.333333  0.294118
658  0.269912  0.287469      0.41250      0.500000  0.266667  0.323529
659  0.265487  0.320873      0.37500      0.473684  0.233333  0.323529

     waist_hip_ratio  gender_female  gender_male
0           0.347826            1.0          0.0
1           0.326087            1.0          0.0
2           0.456522            1.0          0.0
3           0.239130            1.0          0.0
4           0.304348            1.0          0.0
..               ...            ...          ...
655         0.579292            0.0          1.0
656         0.401954            1.0          0.0
657         0.452094            0.0          0.0
658         0.357157            0.0          0.0
659         0.261467            1.0          0.0

[660 rows x 15 columns]
```

[61]:
```
#Importando o modelo RFE -> (Wrapper)
from sklearn.feature_selection import RFE

# split data train 70 % and test 30, this time with x and not x_1 in order to␣
 ↪have all the features %
x_train, x_test, y_train, y_test = train_test_split(data_normal, y, test_size=0.
 ↪3, random_state=42)

# Create the RFE object and rank each pixel
clf_rf_2 = RandomForestClassifier(random_state=42)
rfe = RFE(estimator=clf_rf_2, n_features_to_select=4, step=1)
rfe = rfe.fit(x_train, y_train)
```

[62]:
```
print('Atributos abordagem rfe:',x_train.columns[rfe.support_])
```

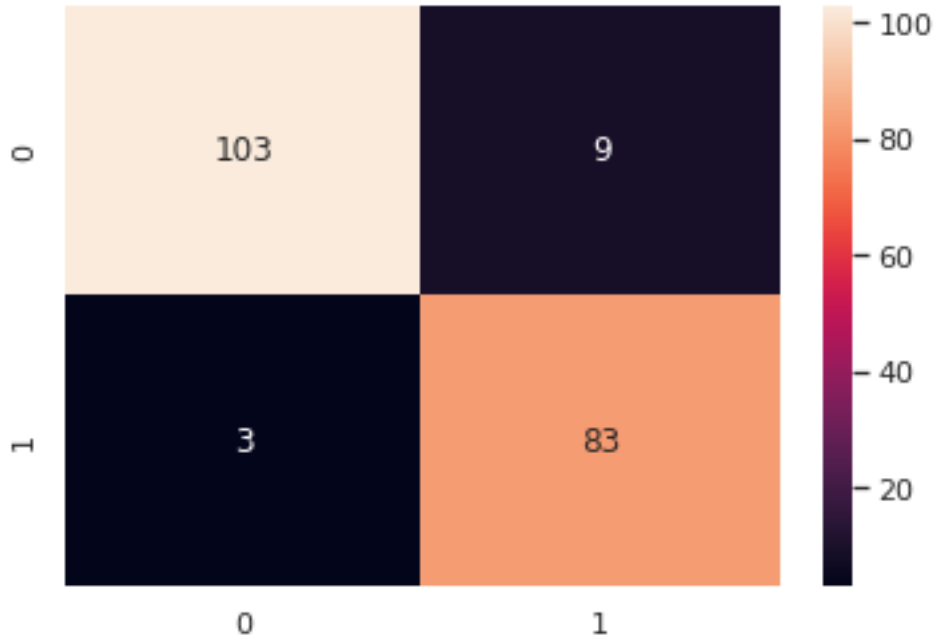
```
Atributos abordagem rfe: Index(['glucose', 'age', 'bmi', 'systolic_bp'],
dtype='object')
```

[63]:
```
type(x_train.columns[rfe.support_])
```

[63]:
```
pandas.core.indexes.base.Index
```

[64]:
```
recall = recall_score(y_test,rfe.predict(x_test))
print('Recall is: ', recall)
accuracy = accuracy_score(y_test,rfe.predict(x_test))
print('Accuracy is: ', accuracy)
f1 = f1_score(y_test,rfe.predict(x_test))
print('F1 score is: ', f1)
cm = confusion_matrix(y_test,rfe.predict(x_test))
ax = sns.heatmap(cm,annot=True,fmt="d")
```

```
Recall is:  0.9651162790697675
Accuracy is:  0.9393939393939394
F1 score is:  0.9325842696629213
```



13.3 3) Recursive feature elimination with cross validation and Random Forest classification

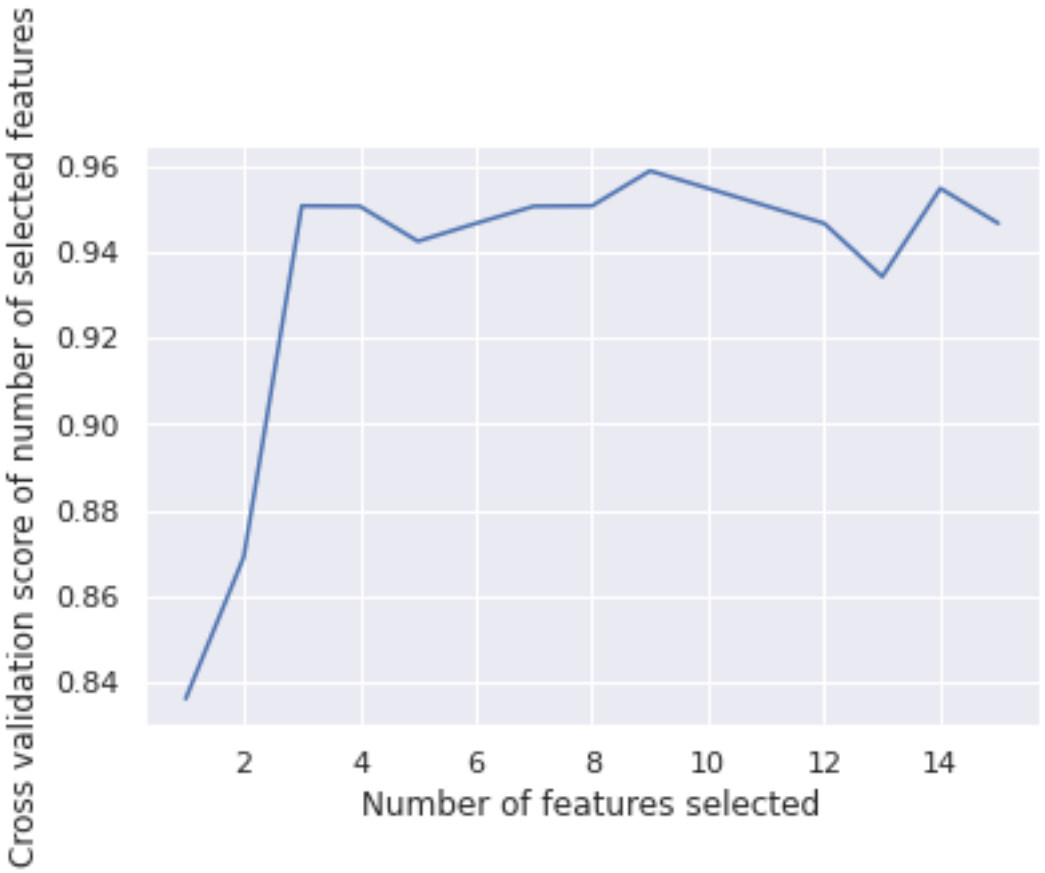
[65]:
```
from sklearn.feature_selection import RFECV

clf_rf_3 = RandomForestClassifier(random_state=42)
rfecv = RFECV(estimator=clf_rf_3, step=1, cv=5, scoring='recall')   #5-fold␣
 ↪cross-validation
rfecv = rfecv.fit(x_train, y_train)

print('Optimal number of features :', rfecv.n_features_)
print('Best features :', x_train.columns[rfecv.support_])
```

```
Optimal number of features : 9
Best features : Index(['cholesterol', 'glucose', 'chol_hdl_ratio', 'age',
'weight', 'bmi',
       'systolic_bp', 'waist', 'waist_hip_ratio'],
      dtype='object')
```

[66]:
```
type(x_train.columns[rfecv.support_])
```

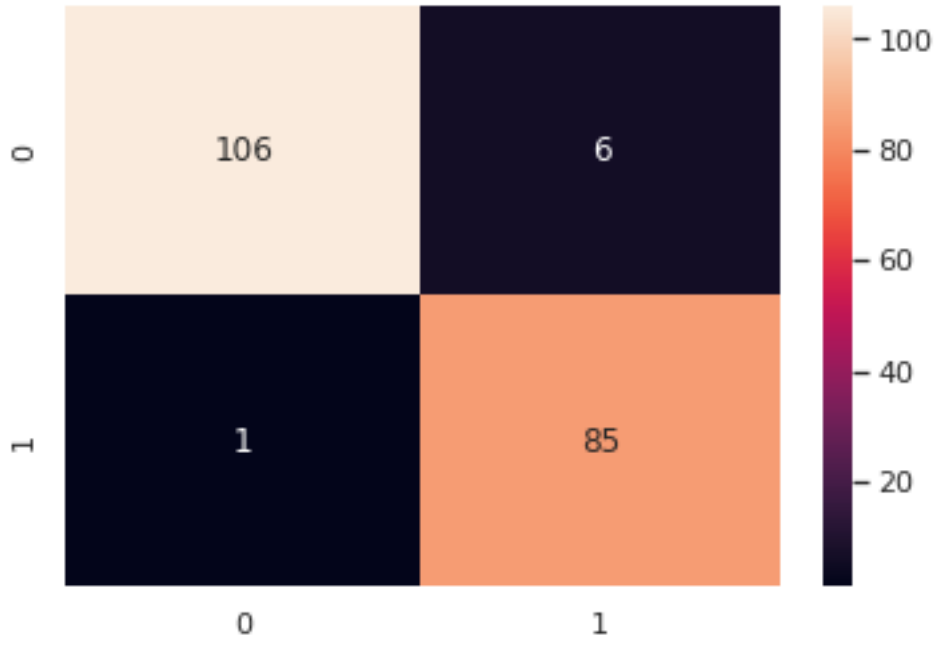
[66]:
```
pandas.core.indexes.base.Index
```

[67]:
```
# Plot number of features VS. cross-validation scores
import matplotlib.pyplot as plt
plt.figure()
plt.xlabel("Number of features selected")
plt.ylabel("Cross validation score of number of selected features")
plt.plot(range(1, len(rfecv.grid_scores_) + 1), rfecv.grid_scores_)
plt.show()
```



[68]:
```
recall = recall_score(y_test,rfecv.predict(x_test))
print('Recall is: ', recall)
accuracy = accuracy_score(y_test,rfecv.predict(x_test))
print('Accuracy is: ', accuracy)
f1 = f1_score(y_test,rfecv.predict(x_test))
print('F1 score is: ', f1)
cm = confusion_matrix(y_test,rfecv.predict(x_test))
ax = sns.heatmap(cm,annot=True,fmt="d")
```

```
Recall is:  0.9883720930232558
Accuracy is:  0.9646464646464646
F1 score is:  0.96045197740113
```



13.4 4) Utilizando abordagem Filtro

[55]:
```
# Import the necessary libraries first
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import chi2
```

[56]:
```
#Feature selection with Mutual Information
import numpy
import pandas
from pandas.plotting import scatter_matrix
from sklearn.feature_selection import chi2
from sklearn.feature_selection import SelectKBest
from sklearn.feature_selection import mutual_info_classif
from sklearn.feature_selection import f_classif

# split data train 70 % and test 30 %
#x_train, x_test, y_train, y_test = train_test_split(x_1, y, test_size=0.3,␣
 ↪random_state=42)
x_train, x_test, y_train, y_test = train_test_split(data_normal, y, test_size=0.
 ↪3, random_state=42)

#selector = SelectKBest(score_func=chi2, k=3)
selector = SelectKBest(score_func=mutual_info_classif, k=8)
#selector = SelectKBest(score_func=f_classif, k=42)
```

```
#selector.fit(data_normal, y)
selector.fit(x_train, y_train)

# Get columns to keep and create new dataframe with those only
cols = selector.get_support(indices=True)
print(cols)

# print the scores
#for i in range(len(selector.scores_)):
 #   print('Feature %d: %f' % (i, selector.scores_[i]))


# plot the scores
'''
plt.bar([i for i in range(len(fit.scores_))], fit.scores_)
plt.show()
'''
```

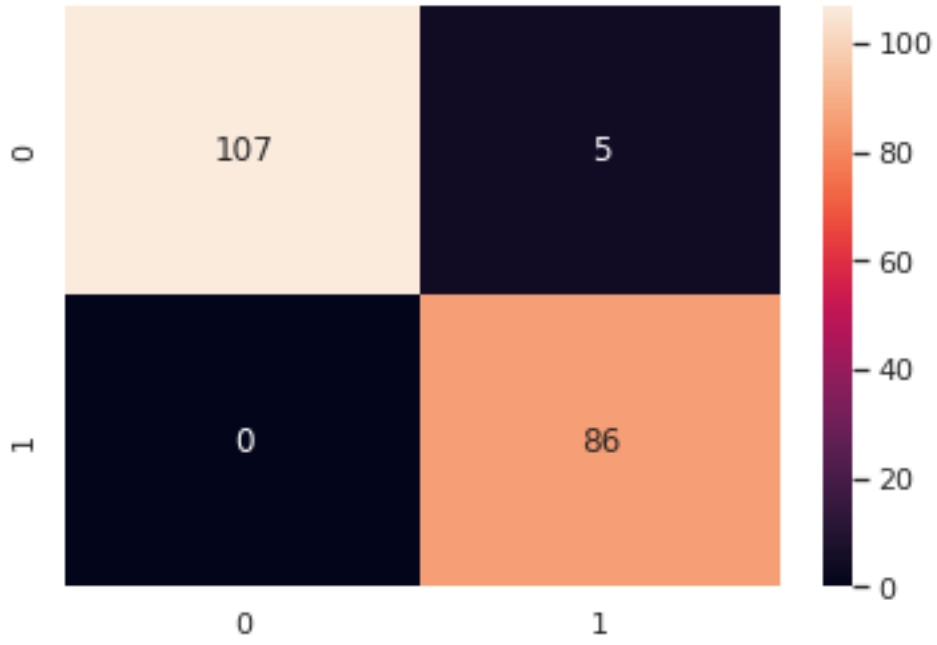
```
[ 1  3  4  7  8  9 11 12]
```

[56]:
```
'\nplt.bar([i for i in range(len(fit.scores_))], fit.scores_)\nplt.show()\n'
```

[57]:
```
# to remove the rest of the features:

x_train = selector.transform(x_train)
x_test = selector.transform(x_test)
```

[58]:
```
#random forest classifier with n_estimators=10 (default)
clf_rf = RandomForestClassifier(random_state=42)
clr_rf = clf_rf.fit(x_train,y_train)

recall = recall_score(y_test,clf_rf.predict(x_test))
print('Recall is: ', recall)
accuracy = accuracy_score(y_test,clf_rf.predict(x_test))
print('Accuracy is: ', accuracy)
f1 = f1_score(y_test,clf_rf.predict(x_test))
print('F1 score is: ', f1)
cm = confusion_matrix(y_test,clf_rf.predict(x_test))
ax = sns.heatmap(cm,annot=True,fmt="d")
```

```
Recall is:  1.0
Accuracy is:  0.9747474747474747
F1 score is:  0.9717514124293786
```



14 Resultados

14.1 Sem seleção dos atributos:

Recall is: 1.0
Accuracy is: 0.9696969696969697
F1 score is: 0.9662921348314606

14.2 Feature Selection with correlation and Random Forest classification:

Recall is: 1.0
Accuracy is: 0.9696969696969697
F1 score is: 0.9662921348314606

14.3 Recursive feature elimination (RFE) with Random Forest:

Recall is: 0.9651162790697675
Accuracy is: 0.9393939393939394
F1 score is: 0.9325842696629213

14.4 Recursive feature elimination with cross validation and Random Forest classification:

Recall is: 0.9883720930232558
Accuracy is: 0.9646464646464646
F1 score is: 0.96045197740113

14.5 Utilizando abordagem Filtro:

Recall is: 1.0
Accuracy is: 0.9747474747474747
F1 score is: 0.9717514124293786

14.6 Conclusão:

14.6.1 Analisando os dados, pode-se constatar que os melhores resultados para as métricas, recall, Accuray e F1-Score, foram obtidos pela abordagem filtro, seguido pela execução da base completa e correlação com remoção manual, tendo os mesmos valores. Vale destacar que foram usados os mesmas configurações para todos.