Sistemas de Información y Telemedicina. *

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Listings

1 Preámbulo

```
1  import numpy as np
2  from   scipy import stats
3
4  #  names of variables
5  labels = ['age', 'leptin', 'bmi', 'adiponectin', 'glucose',
6          'resistin', 'insulin', 'MCP1', 'HOMA']
7
8  #  loads data
9  data = np.loadtxt (open (r'../../data.csv', 'rb'), delimiter = ',')
10
11 #  rewrites data as all the rows of data w/out nan cells
12 data = data [~np.isnan (data).any (axis=1)]
13
14 #  separates parameters into matrix x
15 x    = np.array ([list (data [x][:-1])    for x in range (len (data))])
16
17 #  and class (1, 2) into vector y
18 y    = np.array ([int  (data [x][ -1])    for x in range (len (data))])
19
20 #  removes outliers
21 data_no = data [(np.abs (stats.zscore (data)) < 3).all (axis = 1)]
22 #    ↑ = No Outliers
23
24 x_no = np.array ([list (data_no [x][:-1]) for x in range (len (data_no))])
25 y_no = np.array ([int  (data_no [x][ -1]) for x in range (len (data_no))])
```

Listing 1: Importaciones iniciales y preparacion de datos.

2 Histogramas

En este apartado dibujamos los histogramas comparativos.

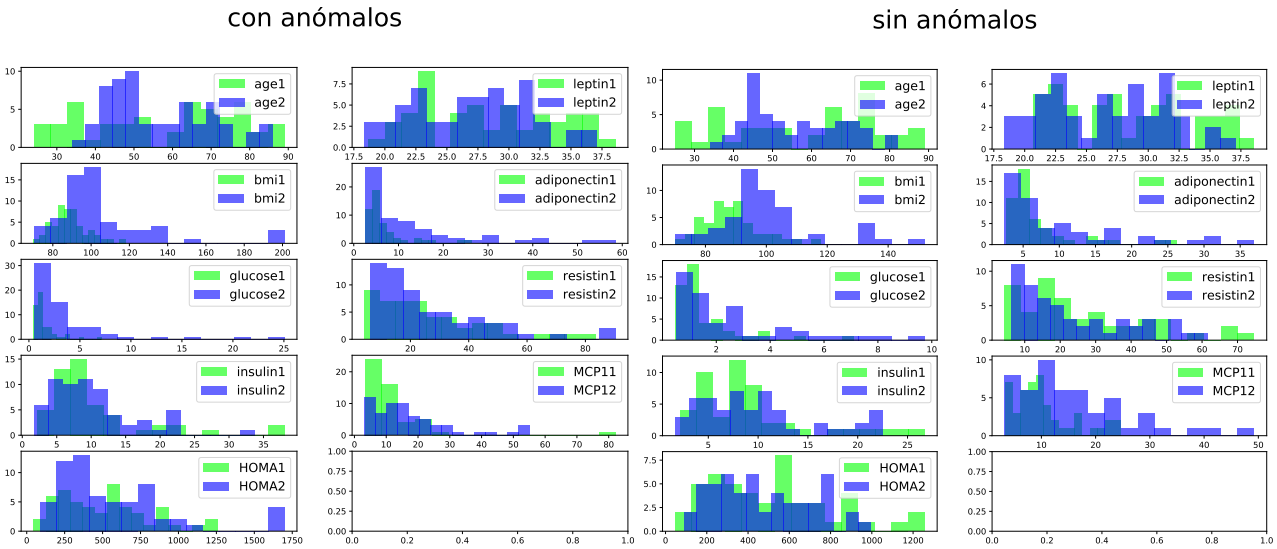

Fig. 1: Histogramas para datos con y sin anomalias.

```
1  import matplotlib as mpl
2  import matplotlib.pyplot as plt
3
4  #  load preprocessed data, x and y are raw, x_no and y_no contain no outliers
5  from preprocessing import x, y, x_no, y_no, labels
6
7  #  colours for the histograms
8  fc = [(), (0, 1, 0, 0.6), (0, 0, 1, 0.6)]
9  #          (R, G, B,  α )← transparency
10
11 fig, ax = plt.subplots (nrows = 5, ncols = 2, figsize = (13, 10))
12 ax = ax.flatten ()
13
14 #  draws each of the histograms, two for each variable
15 for i in range (0, 9):
16     for j in [1, 2]:
17         ax[i].hist (x [y == j, i], bins = 15, fc = fc [j], label = labels [i] + str ↘
               (j))
18         ax[i].legend (loc = 1, prop={'size': 15})
19
20 fig.suptitle ('con anómalos', fontsize = 30)
21 fig.savefig  ('../images/hist.pdf', bbox_inches = 'tight', pad_inches = 0)
```

Listing 2: Código generador de los histogramas con datos anómalos.

3 Kernel Density

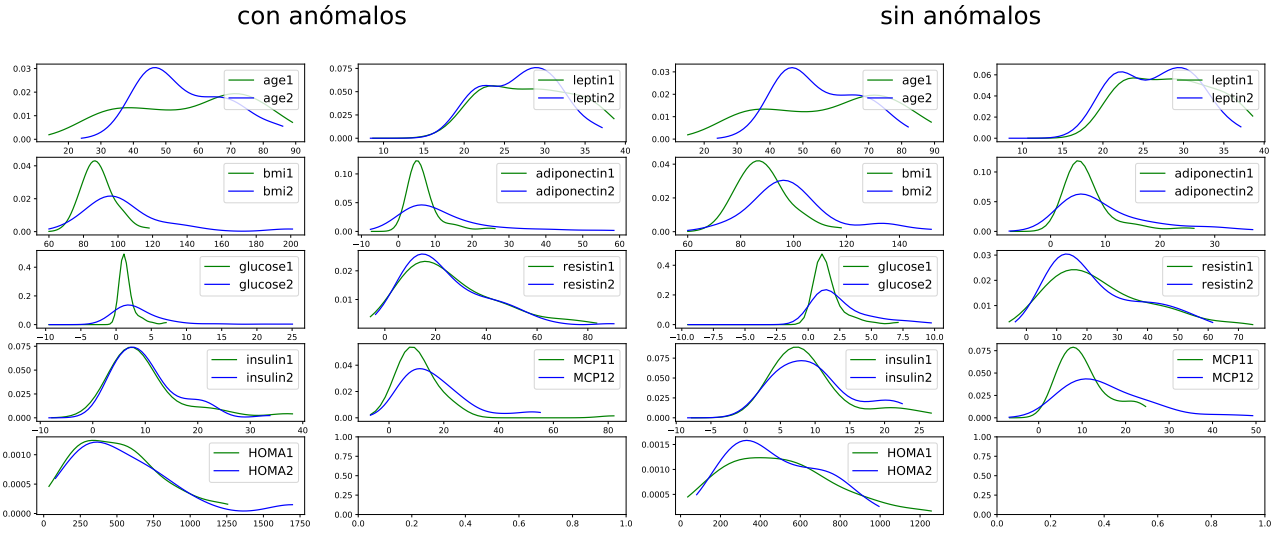

Fig. 2: Kernel Density para datos con y sin anomalias.

```
import matplotlib as mpl
import matplotlib.pyplot as plt
import numpy as np
from scipy.stats import gaussian_kde

#  load preprocessed data, x and y are raw, x_no and y_no contain no outliers
from preprocessing import x, y, x_no, y_no, labels

#  colours
fc = ['', 'green', 'blue']

fig, ax = plt.subplots (nrows = 5, ncols = 2, figsize = (13, 10))
ax = ax.flatten ()

#  same loop in principle as before
for i in range (0, 9):
    for j in [1, 2]:
        kde = gaussian_kde (x_ := x [y == j, i])
        xs = np.linspace(np.min (x_) - 10, np.max (x_), num=len (x_))
        ax[i].plot (xs, kde(xs), c = fc[j], label = labels [i] + str (j))
        ax[i].legend (loc = 1, prop={'size': 15})

fig.suptitle ('con anómalos', fontsize = 30)
fig.savefig  ('../images/kden.pdf', bbox_inches = 'tight', pad_inches = 0)
```

Listing 3: Código generador de los kernel density plots con datos anómalos.

4 Boxplot

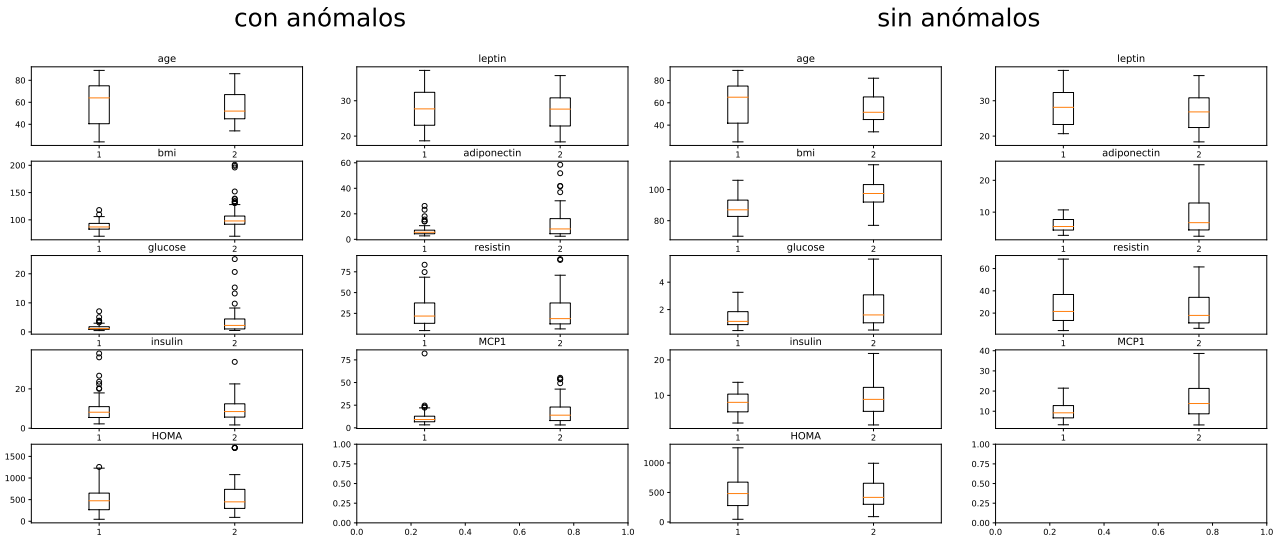

Fig. 3: Boxplots para datos con y sin anomalias.

```
1  import matplotlib as mpl
2  import matplotlib.pyplot as plt
3
4  #  load preprocessed data, x and y are raw, x_no and y_no contain no outliers
5  from preprocessing import x, y, x_no, y_no, labels
6
7  fig, ax = plt.subplots (nrows = 5, ncols = 2, figsize = (13, 10))
8  ax = ax.flatten ()
9
10 for i in range (0, 9):
11     ax[i].boxplot ([x [y == 1, i], x [y == 2, i]])
12     ax[i].title.set_text (labels [i])
13
14 fig.suptitle ('con anómalos', fontsize = 30)
15 fig.savefig  ('../images/boxp.pdf', bbox_inches = 'tight', pad_inches = 0)
```

Listing 4: Código generador de los boxplots con datos anómalos.

5 QQplot

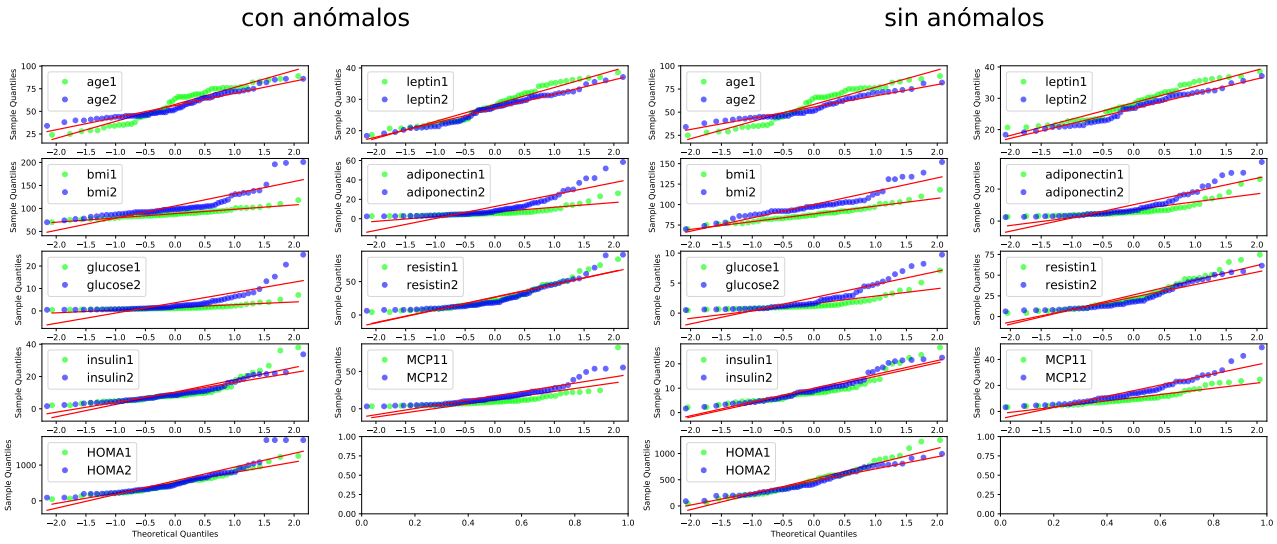

Fig. 4: QQplots para datos con y sin anomalias.

```
import matplotlib as mpl
import matplotlib.pyplot as plt

#  load preprocessed data, x and y are raw, x_no and y_no contain no outliers
from preprocessing import x, y, x_no, y_no, labels
import statsmodels.api as sm

fc = [(), (0, 1, 0, 0.6), (0, 0, 1, 0.6)]

fig, ax = plt.subplots (nrows = 5, ncols = 2, figsize = (13, 10))
ax = ax.flatten ()

for i in range (0, 9):
    for j in [1, 2]:
        sm.qqplot (x [y == j, i], ax = ax[i], c = fc[j],
                line = 's', label = labels [i] + str (j))
        ax[i].legend (loc = 2, prop={'size': 15})

fig.suptitle ('con anómalos', fontsize = 30)
fig.savefig  ('../images/qqp.pdf', bbox_inches = 'tight', pad_inches = 0)
```

Listing 5: Código generador de los QQplots con datos anómalos.

6 Corrplot

```
dataframe = pd.DataFrame.from_records(x)
sns.pairplot(dataframe, kind = 'reg')
plt.suptitle ('con anómalos', fontsize = 30)
plt.savefig  ('../images/corrp.pdf', bbox_inches = 'tight', pad_inches = 0)
```

Listing 6: Código generador de los corrplots con datos anómalos.

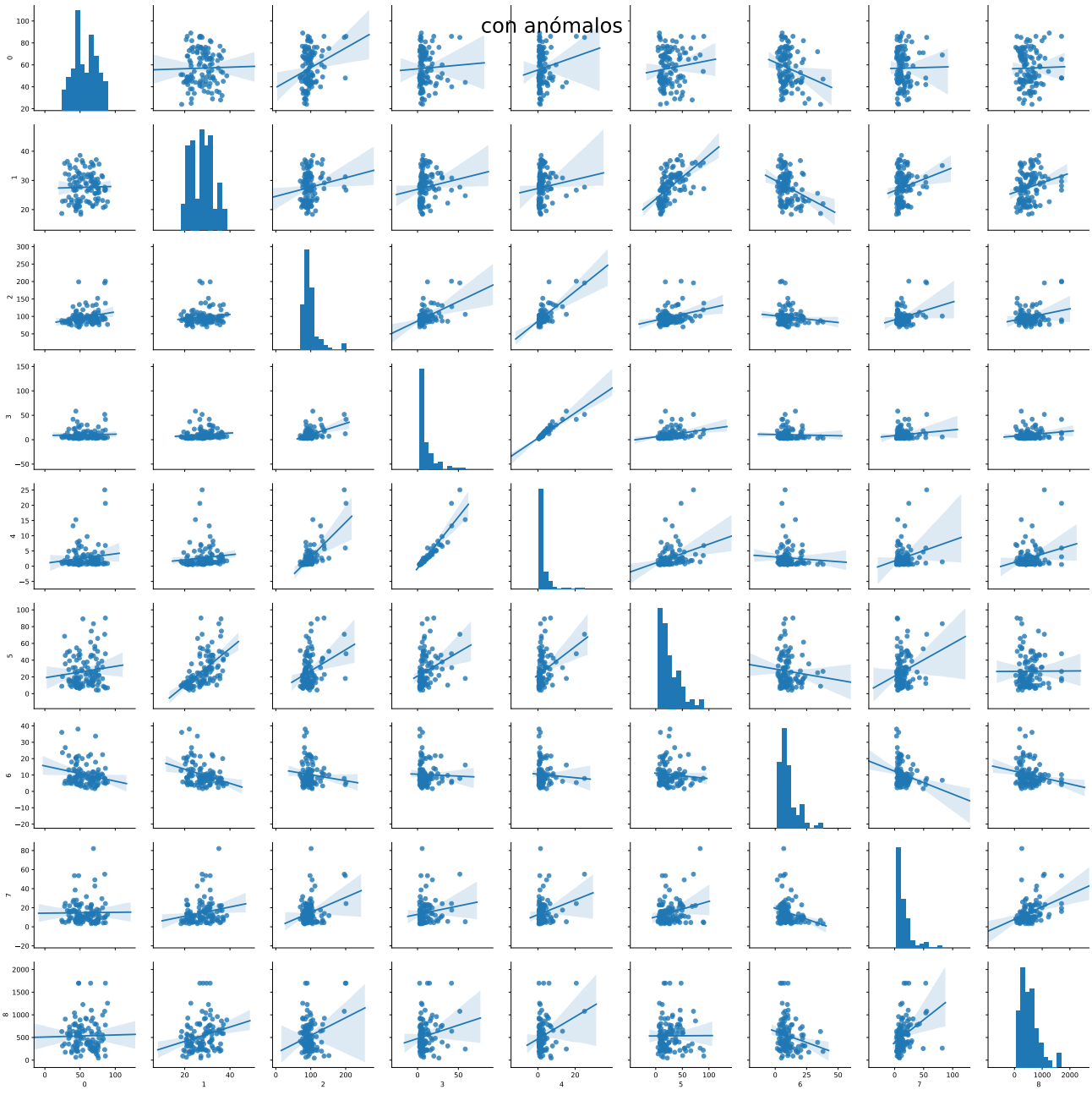

Fig. 5: Corrplot para datos con anomalias.

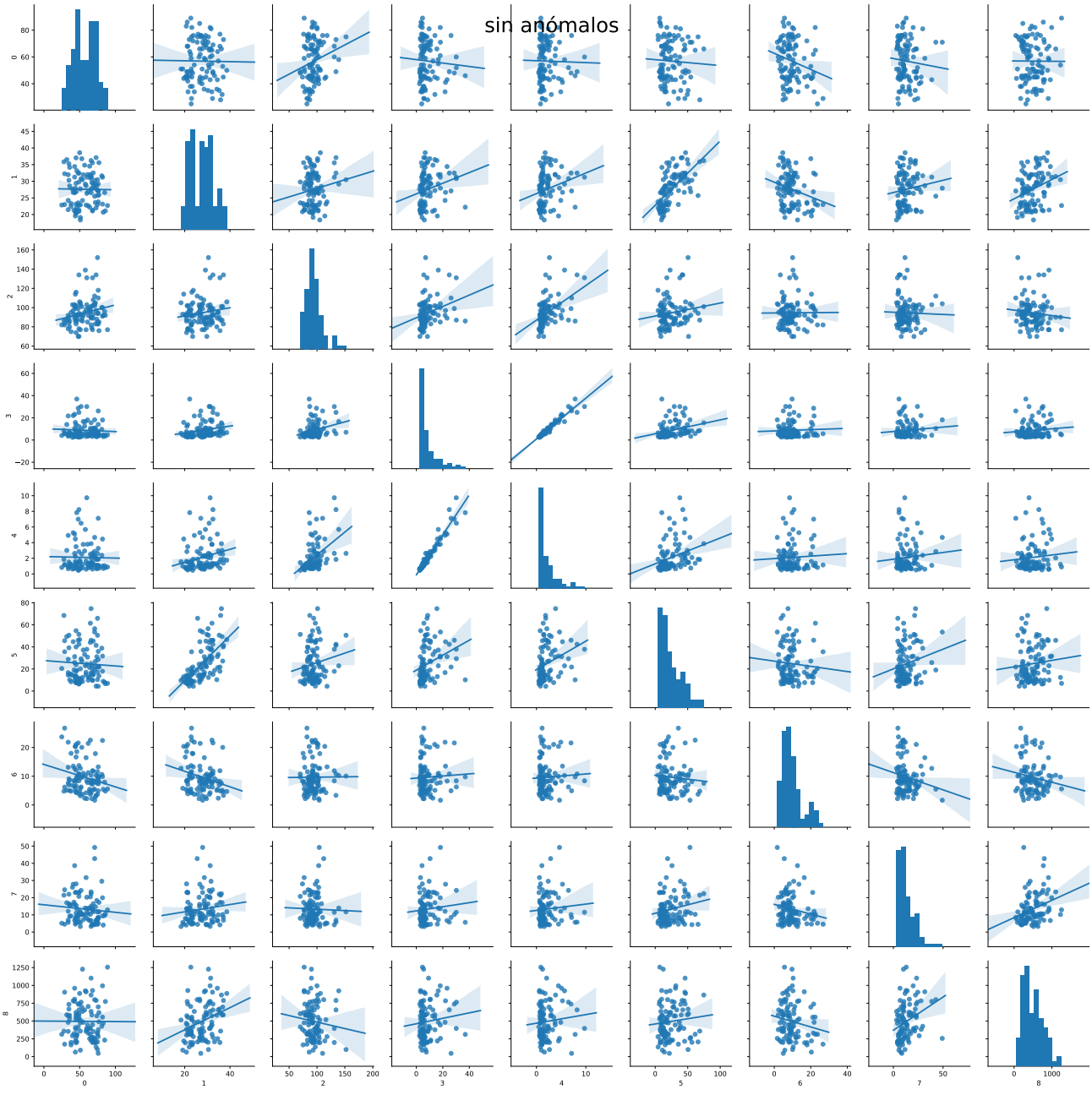

Fig. 6: Corrplot para datos sin anomalias.

7 Filter Methods

```
#  Filter Methods
import sklearn.feature_selection as sk

Fscore, pval = sk.f_classif (x_no, y_no)
r1 = Fscore.argsort().argsort() #  fscore rank
print (r1+1)

import ReliefF as rl

r2 = rl.ReliefF (n_neighbors = 1) #  relieff rank
r2.fit(x_no, y_no)
r2 = r2.top_features
print (r2+1)

diferencias = abs (r1-r2)
media = np.mean (diferencias)
```

Listing 7: Aplicación métodos *filter* de selección características.

```
[4 5 9 6 7 3 1 8 2] -> fscore
[1 9 8 7 6 5 4 2 3] -> relieff
[3 4 1 1 1 2 3 6 1] -> diferencias
2.4444444444444446  -> media
```

Listing 8: Ranking de variables según los métodos filter.

8 Wrapper Methods

```
from sklearn.linear_model import LinearRegression
from sklearn.neighbors import KNeighborsClassifier
from mlxtend.feature_selection import SequentialFeatureSelector

knn = KNeighborsClassifier (n_neighbors = 50)

sfs = SequentialFeatureSelector (knn,
                k_features = 4,
                forward = True,
                scoring = 'accuracy',
                cv = 10)

sfs.fit (x_no, y_no, custom_feature_names = labels)
print (sfs.k_score_)
print ('Sequential Forward  Selection', sfs.k_feature_names_, end = '\n\n')

sfs.forward = False

sfs.fit (x_no, y_no, custom_feature_names = labels)
print (sfs.k_score_)
print ('Sequential Backward Selection', sfs.k_feature_names_, end = '\n\n')
```

Listing 9: Aplicación métodos *wrapper* de selección características.

```
0.7054545454545454
Sequential Forward  Selection ('leptin', 'bmi', 'glucose', 'MCP1')

0.7094949494949495
Sequential Backward Selection ('leptin', 'bmi', 'glucose', 'insulin')
```

Listing 10: Resultados del filtrado mediante wrappers.

9 PCA

```
from sklearn.preprocessing import StandardScaler
x_no = StandardScaler ().fit_transform (x_no) #  typify

from sklearn.decomposition import PCA
pca = PCA (n_components = 9)
principalComponents = pca.fit_transform(x_no)
evr = pca.explained_variance_ratio_
```

Listing 11: *Principal Component Analysis*

9.1 Pareto

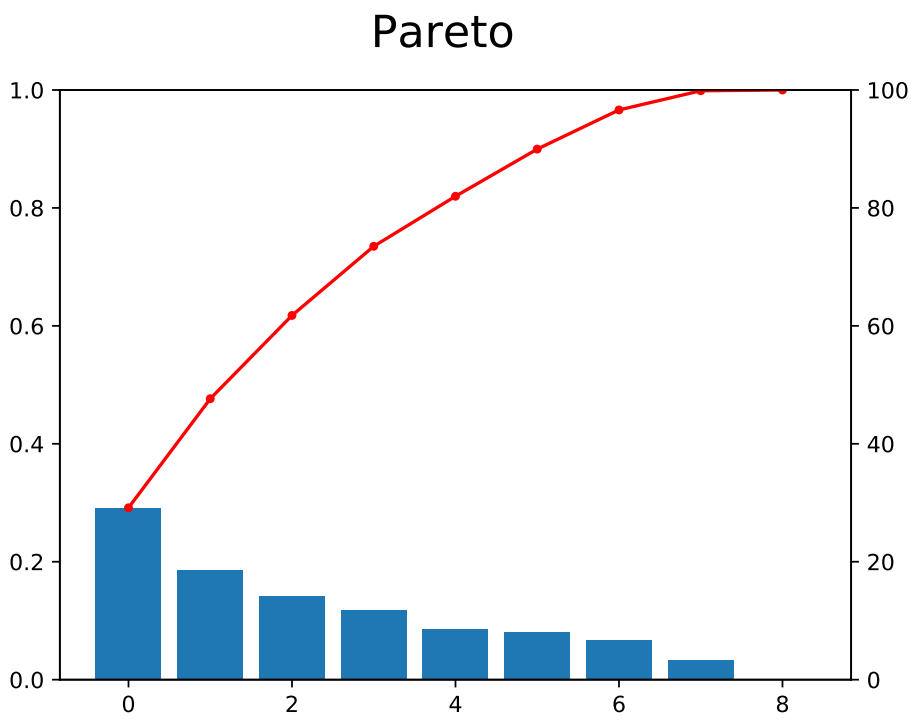

Fig. 7: Diagrama de Pareto.

```
fig, ax = plt.subplots ()
ax.bar (range (len (evr)), evr)
ax.set_ylim (top=1)

ax1 = ax.twinx ()
ax1.set_ylim (top=100)
ax1.plot (range (len (evr)), np.cumsum (evr)*100, marker = '.', color = 'red')

fig.suptitle ('Pareto', fontsize = 20)
fig.savefig  ('../images/pareto.pdf', bbox_inches = 'tight', pad_inches = 0)
```

Listing 12: Código generador del diagrama de Pareto