Sistemas de Información y Telemedicina. *

Marta Girones Sanguesa

Silvia Marset Gomis

Ignacio Amat Hernández

Sofía Gutiérrez Santamaría

November 11, 2019

1 Preámbulo

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

Listing 1: Importaciones iniciales y preparacion de datos.

^{*}Grado en Ingeniería Biomédica, Escuela Técnica Superior de Ingenieros Industriales, Valencia, España.

2 Histogramas

En este apartado dibujamos los histogramas comparativos.

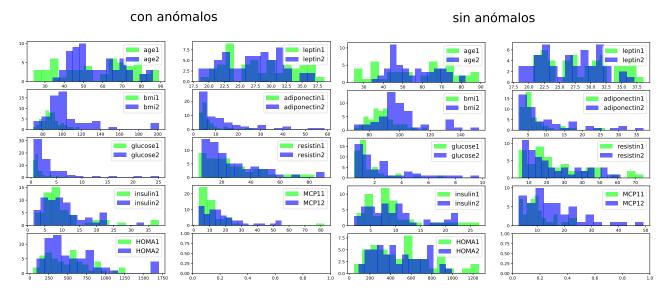


Fig. 1: Histogramas para datos con y sin anomalias.

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

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

```
fig_no, ax_no = plt.subplots (nrows = 5, ncols = 2, figsize = (13, 10))
1
2
  ax_no = ax_no.flatten ()
3
  \# faster, less readable way of coding the loop, they both do exactly SAME thing
4
  [(ax_no[i].hist (x_no [y_no == j, i], bins = 15, fc = fc [j], label = labels [i] + \sqrt{}
5
      str (j)),
    ax_no[i].legend (loc = 1, prop={'size': 15})) for i in range (0, 9) for j in range (1)
         (1,3)]
7
  fig_no.suptitle ('sin anómalos', fontsize = 30)
8
  fig_no.savefig ('../images/hist1.pdf', bbox_inches = 'tight', pad_inches = 0)
```

Listing 3: Código generador de los histogramas sin datos anómalos.