homework1

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1 Homework 1

1.0.1 Objectives

- Basic numpy operations to access data
- Basic plotting of subsets of data
- Simple descriptive statistics
- Do not save work within the ml_practices folder
  - create a folder in your home directory for assignments, and copy the temples there

1.0.2 General References

- Sci-kit Learn Breast Cancer Dataset
- Numpy Reference
- Summary of matplotlib
  - Plot
  - Boxplots
  - Histograms
  - Scatter plots
  - Colormap Plots

[1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.datasets import load_breast_cancer
```

2 LOAD BREAST CANCER DATA SET

[2]:
```
"""
Load the dataset into the bc_dataset variable, by calling the
load_breast_cancer() function imported from sklearn.datasets.
Then display the bc_dataset object's list of keys. bc_dataset
is a dictionary object.
"""
```

```
bc_dataset = load_breast_cancer() # TODO
bc_dataset.keys()
```

[2]:
```
dict_keys(['data', 'target', 'target_names', 'DESCR', 'feature_names',
'filename'])
```

2.0.1 Dataset Details

The `bc_dataset` variable is a dictionary with multiple fields: * `data` : m by n numpy array of the n observed feature values, for each of the m samples
* `target` : m by 1 numpy array of samples' classification as either malignant (i.e. 0) or benign (i.e. 1)
* `target_names` : 2 by 1 numpy array of the possible tumor classifications
* `DESCR` : string containing a detailed description of the dataset
* `feature_names` : n by 1 numpy array of the names of the feature variables
* `filename` : string containing the absolute path to where the file containing all the data information is located on the local system

[3]:
```
""" TODO
Print out the description of the data, by accessing the
'DESCR' field
"""

print(bc_dataset['DESCR'])
```

```
.. _breast_cancer_dataset:

Breast cancer wisconsin (diagnostic) dataset
--------------------------------------------

**Data Set Characteristics:**

    :Number of Instances: 569

    :Number of Attributes: 30 numeric, predictive attributes and the class

    :Attribute Information:
        - radius (mean of distances from center to points on the perimeter)
        - texture (standard deviation of gray-scale values)
        - perimeter
        - area
        - smoothness (local variation in radius lengths)
        - compactness (perimeter^2 / area - 1.0)
        - concavity (severity of concave portions of the contour)
        - concave points (number of concave portions of the contour)
        - symmetry
        - fractal dimension ("coastline approximation" - 1)
        The mean, standard error, and "worst" or largest (mean of the three
        largest values) of these features were computed for each image,
        resulting in 30 features.  For instance, field 3 is Mean Radius, field
        13 is Radius SE, field 23 is Worst Radius.

        - class:
                - WDBC-Malignant
                - WDBC-Benign

    :Summary Statistics:

    ===================================== ====== ======
                                           Min    Max
    ===================================== ====== ======
    radius (mean):                        6.981  28.11
    texture (mean):                       9.71   39.28
    perimeter (mean):                     43.79  188.5
    area (mean):                          143.5  2501.0
    smoothness (mean):                    0.053  0.163
    compactness (mean):                   0.019  0.345
    concavity (mean):                     0.0    0.427
    concave points (mean):                0.0    0.201
    symmetry (mean):                      0.106  0.304
    fractal dimension (mean):             0.05   0.097
    radius (standard error):              0.112  2.873
    texture (standard error):             0.36   4.885
    perimeter (standard error):           0.757  21.98
    area (standard error):                6.802  542.2
    smoothness (standard error):          0.002  0.031
    compactness (standard error):         0.002  0.135
    concavity (standard error):           0.0    0.396
    concave points (standard error):      0.0    0.053
    symmetry (standard error):            0.008  0.079
    fractal dimension (standard error):   0.001  0.03
    radius (worst):                       7.93   36.04
    texture (worst):                      12.02  49.54
    perimeter (worst):                    50.41  251.2
    area (worst):                         185.2  4254.0
    smoothness (worst):                   0.071  0.223
    compactness (worst):                  0.027  1.058
    concavity (worst):                    0.0    1.252
    concave points (worst):               0.0    0.291
    symmetry (worst):                     0.156  0.664
    fractal dimension (worst):            0.055  0.208
    ===================================== ====== ======

    :Missing Attribute Values: None
```

```
    :Class Distribution: 212 - Malignant, 357 - Benign

    :Creator:  Dr. William H. Wolberg, W. Nick Street, Olvi L. Mangasarian

    :Donor: Nick Street

    :Date: November, 1995

This is a copy of UCI ML Breast Cancer Wisconsin (Diagnostic) datasets.
https://goo.gl/U2Uwz2

Features are computed from a digitized image of a fine needle
aspirate (FNA) of a breast mass.  They describe
characteristics of the cell nuclei present in the image.

Separating plane described above was obtained using
Multisurface Method-Tree (MSM-T) [K. P. Bennett, "Decision Tree
Construction Via Linear Programming." Proceedings of the 4th
Midwest Artificial Intelligence and Cognitive Science Society,
pp. 97-101, 1992], a classification method which uses linear
programming to construct a decision tree.  Relevant features
were selected using an exhaustive search in the space of 1-4
features and 1-3 separating planes.

The actual linear program used to obtain the separating plane
in the 3-dimensional space is that described in:
[K. P. Bennett and O. L. Mangasarian: "Robust Linear
Programming Discrimination of Two Linearly Inseparable Sets",
Optimization Methods and Software 1, 1992, 23-34].

This database is also available through the UW CS ftp server:

ftp ftp.cs.wisc.edu
cd math-prog/cpo-dataset/machine-learn/WDBC/

.. topic:: References

   - W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction
     for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on
     Electronic Imaging: Science and Technology, volume 1905, pages 861-870,
     San Jose, CA, 1993.
   - O.L. Mangasarian, W.N. Street and W.H. Wolberg. Breast cancer diagnosis and
     prognosis via linear programming. Operations Research, 43(4), pages
570-577,
     July-August 1995.
   - W.H. Wolberg, W.N. Street, and O.L. Mangasarian. Machine learning
techniques
     to diagnose breast cancer from fine-needle aspirates. Cancer Letters 77
```

```
(1994)
     163-171.
```

2.1 SETUP USEFUL VARIABLES

[4]:
```
"""
Store the names of the features and the names
of the target classes, into the variables
feature_names and target_names respectively.
"""
feature_names = bc_dataset['feature_names']# TODO
target_names = bc_dataset['target']# TODO

""" TODO
Print the list of feature names and target names
"""
print(feature_names)
print(target_names)
```

```
['mean radius' 'mean texture' 'mean perimeter' 'mean area'
 'mean smoothness' 'mean compactness' 'mean concavity'
 'mean concave points' 'mean symmetry' 'mean fractal dimension'
 'radius error' 'texture error' 'perimeter error' 'area error'
 'smoothness error' 'compactness error' 'concavity error'
 'concave points error' 'symmetry error' 'fractal dimension error'
 'worst radius' 'worst texture' 'worst perimeter' 'worst area'
 'worst smoothness' 'worst compactness' 'worst concavity'
 'worst concave points' 'worst symmetry' 'worst fractal dimension']
[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
 1 0 0 0 0 0 0 0 0 1 0 1 1 1 1 1 0 0 1 0 0 1 1 1 1 0 1 0 0 1 1 1 1 0 1 0 0
 1 0 1 0 0 1 1 1 0 0 1 0 0 0 1 1 1 0 1 1 0 0 1 1 1 0 0 1 1 1 1 0 1 1 0 1 1
 1 1 1 1 1 1 0 0 0 1 0 0 1 1 1 0 0 1 0 1 0 0 1 0 0 1 1 0 1 1 0 1 1 1 1 0 1
 1 1 1 1 1 1 1 1 0 1 1 1 1 0 0 1 0 1 1 0 0 1 1 0 0 1 1 1 1 0 1 1 0 0 0 1 0
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 1 0 1 1 1 1 1 0 0 1 1 0 1 1 0 0 1 0 1 1 1 1 0 1 1 1 1 1 0 1 0 0 0 0 0 0 0
 0 0 0 0 0 0 0 1 1 1 1 1 1 0 1 0 1 1 0 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1
 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0 1 1 1 0 1 0 1 1 1 1 0 0 0 1 1
 1 1 0 1 0 1 0 1 1 1 0 1 1 1 1 1 1 1 0 0 0 1 1 1 1 1 1 1 1 1 1 1 0 0 1 0 0
 0 1 0 0 1 1 1 1 1 0 1 1 1 1 1 0 1 1 1 0 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1
 1 0 1 1 1 1 1 0 1 1 0 1 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 0 1 1 1 1 1 0 1 1
 0 1 0 1 1 0 1 0 1 1 1 1 1 1 1 1 0 0 1 1 1 1 1 1 0 1 1 1 1 1 1 1 1 1 1 0 1
 1 1 1 1 1 1 0 1 0 1 1 0 1 1 1 1 1 0 0 1 0 1 0 1 1 1 1 1 0 1 1 0 1 0 1 0 0
 1 1 1 0 1 1 1 1 1 1 1 1 1 1 1 0 1 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 1 1 1 1 1 1 1 0 0 0 0 0 0 1]
```

[5]:
```
"""
Create variables for the feature and target data
The X variable is a numy array containing the data measured
```

```
for each feature for each sample. Each column of X is a
different feature for all the samples. Each row of X is a
different sample with all its features.
The y variable is a numpy array containing the classification
for each sample. A sample tumor is either Benign or Malignant.
"""
X = bc_dataset['data']# TODO
y = target_names# TODO

""" TODO
Print the dimensions of the X and y variables respectively
"""
print('dimension of X: %s'%str(X.shape))
print('dimension of y: %s'%str(y.shape))
```

```
dimension of X: (569, 30)
dimension of y: (569,)
```

[6]:
```
"""
Store the number of samples and the number of features, by
accessing the values from the shape of X
"""
nsamples = X.shape[0]# TODO
nfeatures = X.shape[1]#TODO

""" TODO
Print the print the number of samples and numberof features respectively
"""
print('number of samples: %d; number of features: %d'%(nsamples, nfeatures))
```

```
number of samples: 569; number of features: 30
```

2.2 SELECT SUBSET OF FEATURES

Not all available data is necessary or useful for making predictions and classifying observations. There are numerous feature selection algorithms that exist, which will be discussed in more detail later within the cousre. For now we are going to arbitrarly select mean radius, mean area, mean concavity, and mean symmetry as our predictor variables. We will not yet be performing any predictions in this assignment; rather this term is used to conveniently distinuguish this subset of features from the full set of features.

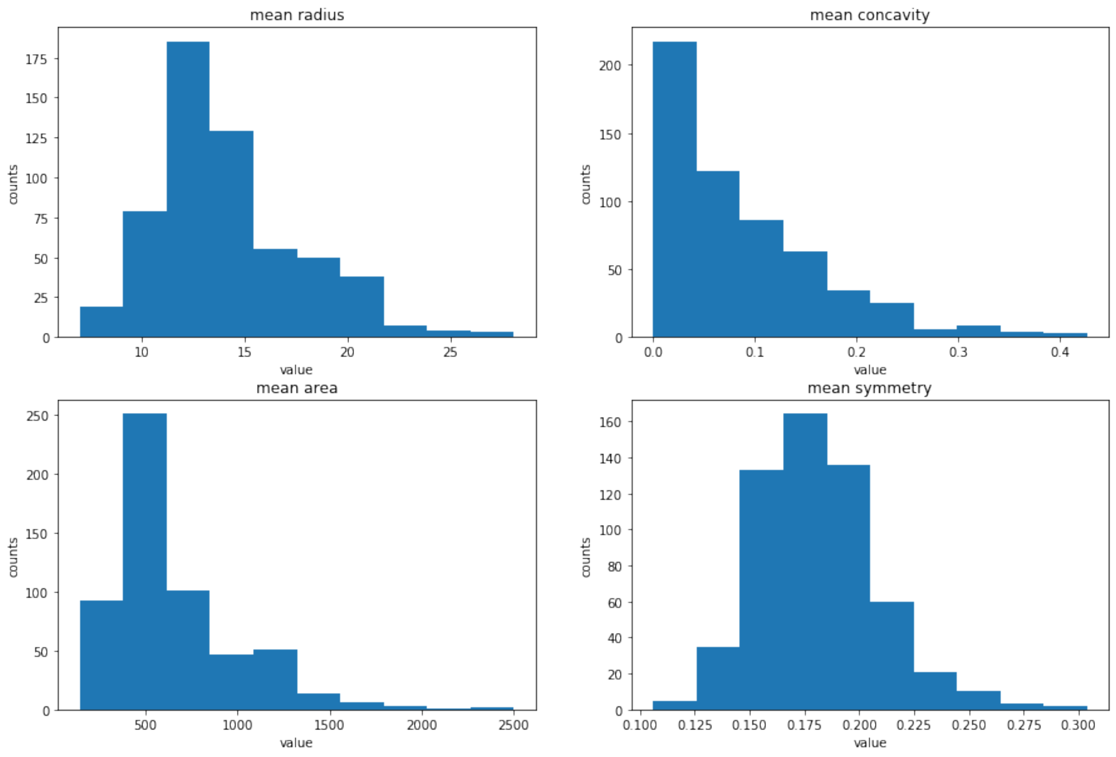
[7]:
```
"""
Feature Column Indices
The values observed for each feature resides within a particular
column of the feature matrix, X. For example, column 0 contains the
values of the mean radius for each observation, the column at index
3 contains the values for the mean area, and so on.
"""
```

```
mean_radius_idx = 0
mean_area_idx = 3
mean_concavity_idx = 6
mean_symmetry_idx = 8

"""
Create a list of the select subset of features
"""
predictors = [mean_radius_idx, mean_area_idx, mean_concavity_idx,␣
 ↪mean_symmetry_idx]

"""
Create a variable, storing the number of predictors
"""
npredictors = len(predictors)# TODO

"""
Create a list of corresponding names for the selected set of features.
This is conveniently done using list comprehension
"""
pred_names = feature_names[predictors]# TODO

"""
Print the list of predictor names
"""
print("Predictor Feature Names:")
print(pred_names)
```

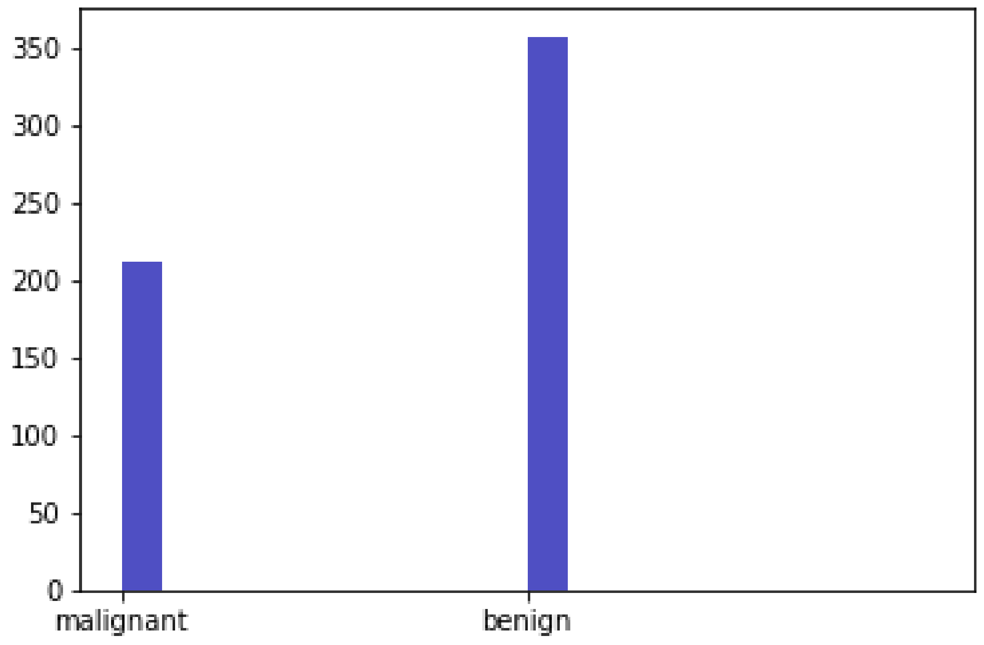
```
Predictor Feature Names:
['mean radius' 'mean area' 'mean concavity' 'mean symmetry']
```

2.3 BASIC HISTOGRAMS OF FEATURES

[8]:
```
""" TODO
HISTOGRAMS OF THE CHOSEN PREDICTOR FEATURES
You may plot the histrograms within their
own figure or within their own subplot of
the same figure
"""


fig, ax= plt.subplots(2,2, figsize=(15,10))
for n, feature in enumerate(predictors):
    j=0 if n<2 else 1
    i=n if n<2 else n-2
    ax[i,j].hist(X[:,feature])
    ax[i,j].set_title(pred_names[n])
    ax[i,j].set_xlabel('value')
    ax[i,j].set_ylabel('counts')
```



[9]:
```
""" TODO
Create a histogram or barplot for the counts
for each target class
"""

plt.figure()
plt.hist(target_names, width = 0.1, align='mid', color='#0504aa',alpha=0.7,␣
 ↪range=(0,2))
plt.xticks(np.arange(0,2,1), ['malignant','benign'])
plt.show()
```



2.4 BASIC BOXPLOTS OF FEATURES

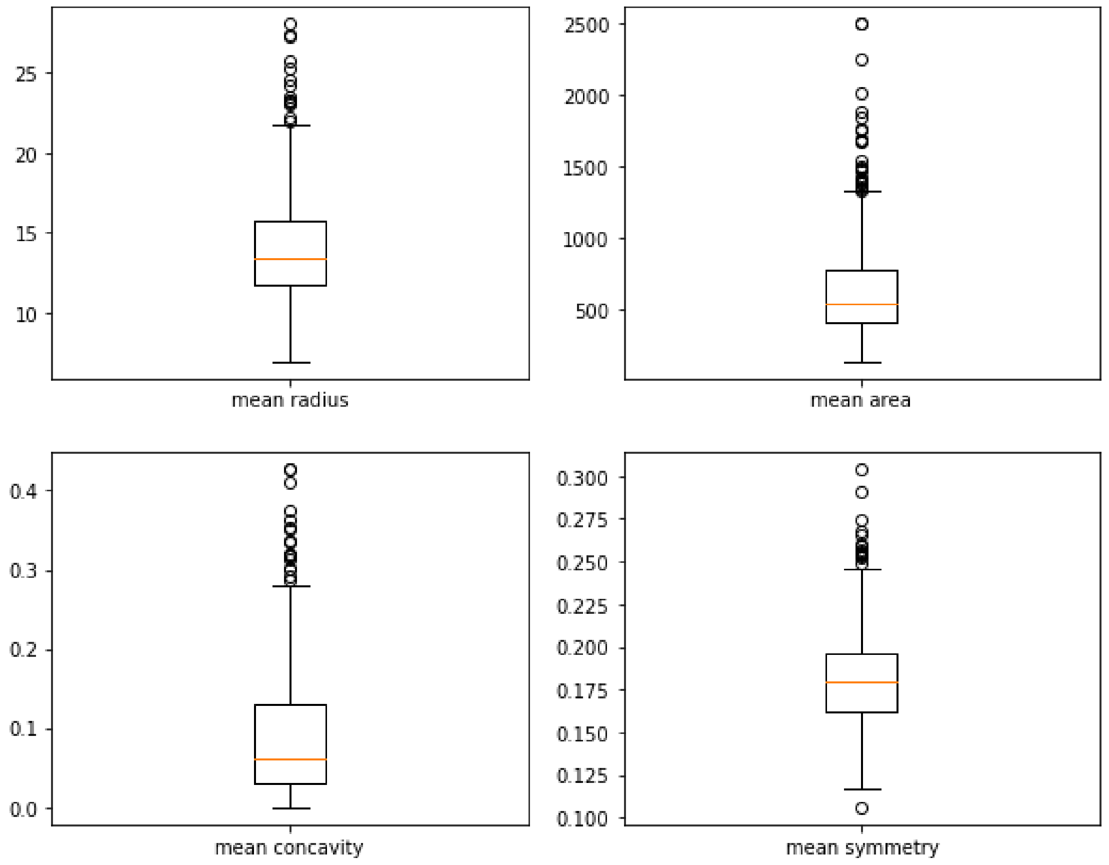
Boxplots or box-and-whisker plots are used to obtain a perspective of the distribution of the data. The box within the figure displays the 25th percentile (Q1), the median, and the 75th percentile (Q3) of the data. The range between the 75th percentile value and the 25th percentile value is the interquartile range (IQR = Q3 - Q1). The end of bottom line is Q1 - 1.5 * IQR. The end of top line is Q3 + 1.5 * IQR. Anything beyond the lines, the circles, are suggested outliers.

<

>

One can use the `boxplot(data_values, labels=[name])` to generate a boxplot. `data_values` would be the set of observed values for a paritucular feature and `labels` should be provided as a list, with the name of the feature, in place of `name`.

[10]:
```
""" TODO
BOXPLOTS OF THE CHOSEN PREDICTOR FEATURES
You may place the boxplots within their
own figure or within their own subplot of
the same figure
"""

fig, ax= plt.subplots(2,2,figsize=(10,8))
ind=0
for i in range(2):
    for j in range(2):
        ax[i,j].boxplot(X[:, predictors[ind]], labels=[pred_names[ind]]);
        ind+=1
```



2.5 DESCRIPTIVE STATISTICS

[11]:
```
# Simply run this cell
"""
Create a separate variable of the data from the
predictors
"""
Xpreds = X[:, predictors]

"""
Check if any values are NaN (not a number)
"""
np.any(np.isnan(X[:, predictors]))
```

[11]:
```
False
```

[17]:
```
""" TODO
Compute the following descriptive statistics of the
```

```
features ignoring NaN values, using numpy:
mean, median, standard deviation, min, and max

Make sure to compute the statistics of the columns
of X (i.e. of each feature). You can specify this
by setting axis=0 for each of the functions

Compute and print the results
"""
for i in range(len(feature_names)):
    print('mean of feature "%s": %.4f'%(feature_names[i], np.nanmean(X[:, i],␣
 ↪axis=0)))
    print('median of feature "%s": %.2f'%(feature_names[i], np.nanmedian(X[:,␣
 ↪i],axis=0)))
    print('stand deviation of feature "%s": %.4f'%(feature_names[i], np.
 ↪nanstd(X[:, i],axis=0)))
    print('min of feature "%s": %.2f'%(feature_names[i], X[:, i].min(axis=0)))
    print('max of feature "%s": %.2f'%(feature_names[i], X[:, i].max(axis=0)))
```

```
mean of feature "mean radius": 14.1273
median of feature "mean radius": 13.37
stand deviation of feature "mean radius": 3.5210
min of feature "mean radius": 6.98
max of feature "mean radius": 28.11
mean of feature "mean texture": 19.2896
median of feature "mean texture": 18.84
stand deviation of feature "mean texture": 4.2973
min of feature "mean texture": 9.71
max of feature "mean texture": 39.28
mean of feature "mean perimeter": 91.9690
median of feature "mean perimeter": 86.24
stand deviation of feature "mean perimeter": 24.2776
min of feature "mean perimeter": 43.79
max of feature "mean perimeter": 188.50
mean of feature "mean area": 654.8891
median of feature "mean area": 551.10
stand deviation of feature "mean area": 351.6048
min of feature "mean area": 143.50
max of feature "mean area": 2501.00
mean of feature "mean smoothness": 0.0964
median of feature "mean smoothness": 0.10
stand deviation of feature "mean smoothness": 0.0141
min of feature "mean smoothness": 0.05
max of feature "mean smoothness": 0.16
mean of feature "mean compactness": 0.1043
median of feature "mean compactness": 0.09
stand deviation of feature "mean compactness": 0.0528
```

```
min of feature "mean compactness": 0.02
max of feature "mean compactness": 0.35
mean of feature "mean concavity": 0.0888
median of feature "mean concavity": 0.06
stand deviation of feature "mean concavity": 0.0796
min of feature "mean concavity": 0.00
max of feature "mean concavity": 0.43
mean of feature "mean concave points": 0.0489
median of feature "mean concave points": 0.03
stand deviation of feature "mean concave points": 0.0388
min of feature "mean concave points": 0.00
max of feature "mean concave points": 0.20
mean of feature "mean symmetry": 0.1812
median of feature "mean symmetry": 0.18
stand deviation of feature "mean symmetry": 0.0274
min of feature "mean symmetry": 0.11
max of feature "mean symmetry": 0.30
mean of feature "mean fractal dimension": 0.0628
median of feature "mean fractal dimension": 0.06
stand deviation of feature "mean fractal dimension": 0.0071
min of feature "mean fractal dimension": 0.05
max of feature "mean fractal dimension": 0.10
mean of feature "radius error": 0.4052
median of feature "radius error": 0.32
stand deviation of feature "radius error": 0.2771
min of feature "radius error": 0.11
max of feature "radius error": 2.87
mean of feature "texture error": 1.2169
median of feature "texture error": 1.11
stand deviation of feature "texture error": 0.5512
min of feature "texture error": 0.36
max of feature "texture error": 4.88
mean of feature "perimeter error": 2.8661
median of feature "perimeter error": 2.29
stand deviation of feature "perimeter error": 2.0201
min of feature "perimeter error": 0.76
max of feature "perimeter error": 21.98
mean of feature "area error": 40.3371
median of feature "area error": 24.53
stand deviation of feature "area error": 45.4510
min of feature "area error": 6.80
max of feature "area error": 542.20
mean of feature "smoothness error": 0.0070
median of feature "smoothness error": 0.01
stand deviation of feature "smoothness error": 0.0030
min of feature "smoothness error": 0.00
max of feature "smoothness error": 0.03
mean of feature "compactness error": 0.0255
```

```
median of feature "compactness error": 0.02
stand deviation of feature "compactness error": 0.0179
min of feature "compactness error": 0.00
max of feature "compactness error": 0.14
mean of feature "concavity error": 0.0319
median of feature "concavity error": 0.03
stand deviation of feature "concavity error": 0.0302
min of feature "concavity error": 0.00
max of feature "concavity error": 0.40
mean of feature "concave points error": 0.0118
median of feature "concave points error": 0.01
stand deviation of feature "concave points error": 0.0062
min of feature "concave points error": 0.00
max of feature "concave points error": 0.05
mean of feature "symmetry error": 0.0205
median of feature "symmetry error": 0.02
stand deviation of feature "symmetry error": 0.0083
min of feature "symmetry error": 0.01
max of feature "symmetry error": 0.08
mean of feature "fractal dimension error": 0.0038
median of feature "fractal dimension error": 0.00
stand deviation of feature "fractal dimension error": 0.0026
min of feature "fractal dimension error": 0.00
max of feature "fractal dimension error": 0.03
mean of feature "worst radius": 16.2692
median of feature "worst radius": 14.97
stand deviation of feature "worst radius": 4.8290
min of feature "worst radius": 7.93
max of feature "worst radius": 36.04
mean of feature "worst texture": 25.6772
median of feature "worst texture": 25.41
stand deviation of feature "worst texture": 6.1409
min of feature "worst texture": 12.02
max of feature "worst texture": 49.54
mean of feature "worst perimeter": 107.2612
median of feature "worst perimeter": 97.66
stand deviation of feature "worst perimeter": 33.5730
min of feature "worst perimeter": 50.41
max of feature "worst perimeter": 251.20
mean of feature "worst area": 880.5831
median of feature "worst area": 686.50
stand deviation of feature "worst area": 568.8565
min of feature "worst area": 185.20
max of feature "worst area": 4254.00
mean of feature "worst smoothness": 0.1324
median of feature "worst smoothness": 0.13
stand deviation of feature "worst smoothness": 0.0228
min of feature "worst smoothness": 0.07
```

```
max of feature "worst smoothness": 0.22
mean of feature "worst compactness": 0.2543
median of feature "worst compactness": 0.21
stand deviation of feature "worst compactness": 0.1572
min of feature "worst compactness": 0.03
max of feature "worst compactness": 1.06
mean of feature "worst concavity": 0.2722
median of feature "worst concavity": 0.23
stand deviation of feature "worst concavity": 0.2084
min of feature "worst concavity": 0.00
max of feature "worst concavity": 1.25
mean of feature "worst concave points": 0.1146
median of feature "worst concave points": 0.10
stand deviation of feature "worst concave points": 0.0657
min of feature "worst concave points": 0.00
max of feature "worst concave points": 0.29
mean of feature "worst symmetry": 0.2901
median of feature "worst symmetry": 0.28
stand deviation of feature "worst symmetry": 0.0618
min of feature "worst symmetry": 0.16
max of feature "worst symmetry": 0.66
mean of feature "worst fractal dimension": 0.0839
median of feature "worst fractal dimension": 0.08
stand deviation of feature "worst fractal dimension": 0.0180
min of feature "worst fractal dimension": 0.06
max of feature "worst fractal dimension": 0.21
```

2.6 FEATURE CORRELATIONS

It’s useful to know the correlation between various features, as well as each feature and the predicted label. Feature correlation is useful for feature selection and understanding the relationship between multiple variables within a dataset. Correlation is either positive, negative, or zero. When two features increase simultaneously, they are positively correlated. When one feature increases while the other decreases, the features are negatively correlated. Zero correlation is when there is no relationship between the features. Correlation is on the range -1 (perfect negative correlation) and 1 (pefect positive correlation).

We can construct scatter plots of one feature versuses another to observe linear or nonlinear relationships.

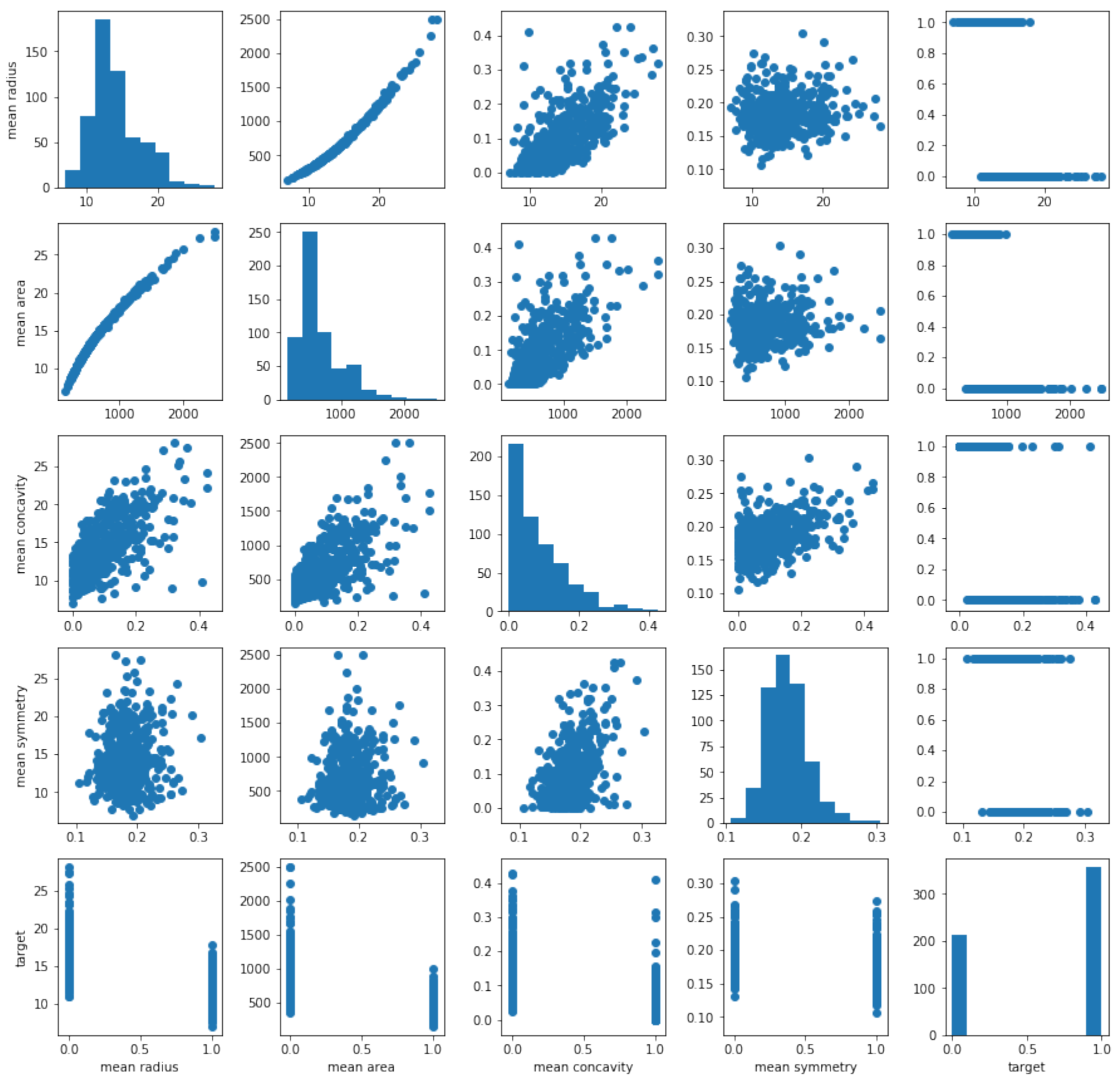
Complete the following set of scatter plots:

<

>

[18]:
```
"""
Using the scatter plot function, construct plots depicting the
correlation between all pairings of the selected predictor features
and between all predictors and the determined target.
The figure will contain r by r subplots, where r = npredictors + 1.
Where subplot(i,j) is a scatter plot of the feature i versus feature j.
```

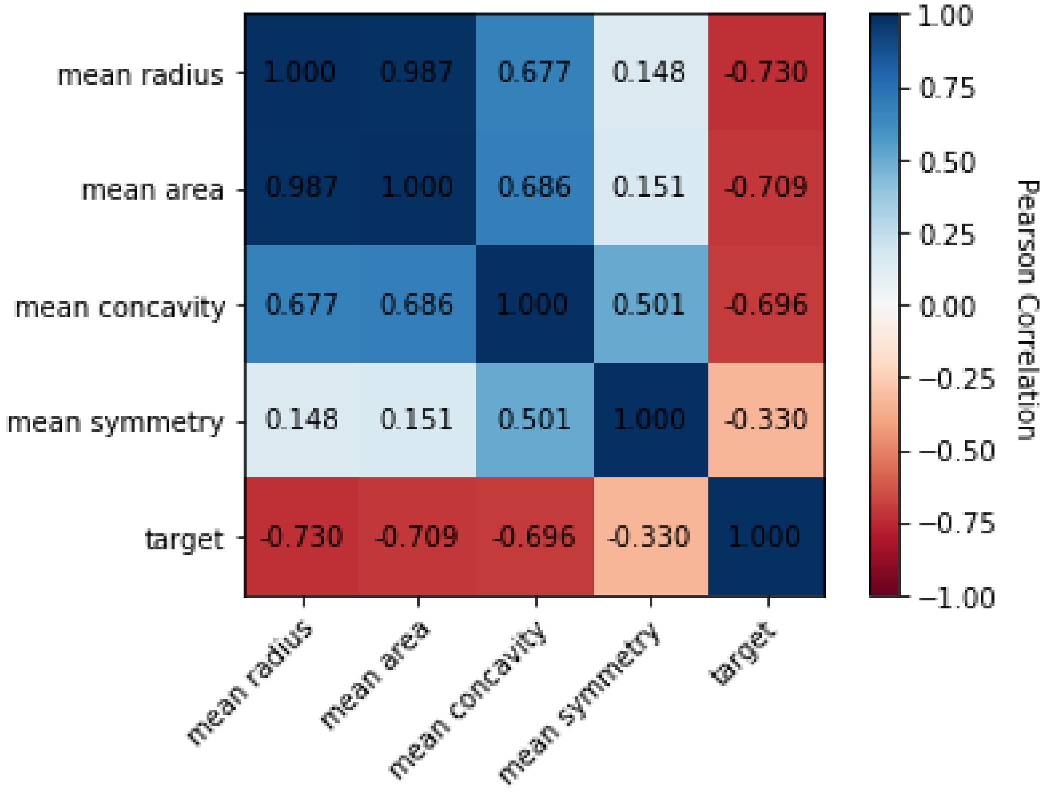
```python
When i == j, plot the histogram of feature i instead of a scatter plot.
We are also interested in the correlation between each of the features
and the target classification, thus we will combine the predictors matrix
and the target vector into one large matrix for convenience.
"""
# Append the y to the end of the matrix of predictors
Xycombo = np.append(Xpreds, y.reshape(-1, 1), axis=1)
# Append the name 'target' to the end of the list of predictor names
Xycolnames = list(pred_names) + ['target']

# Create the scatter plots
fig, axs = plt.subplots(npredictors+1, npredictors+1, figsize=(15, 15))
fig.subplots_adjust(wspace=.35)
for f1 in range(npredictors+1):
    for f2 in range(npredictors+1):
        # v TODO ------------------------------------------------------------

        # INSERT CODE HERE
        if f1==f2:
            axs[f1,f2].hist(Xycombo[:,f1])
        else:
            axs[f1,f2].scatter(Xycombo[:,f1], Xycombo[:,f2])

        # ^ TODO ------------------------------------------------------------

        # include labels only when necessary
        if f1 == npredictors:
            axs[f1, f2].set_xlabel(Xycolnames[f2])
        if f2 == 0:
            axs[f1, f2].set_ylabel(Xycolnames[f1])
```



2.7 IMAGES AND COLORMAPS

Create a colormap plot of the correlations between the all the predictors and the target

[19]:
```
"""
Generate a figure that plots the a correlation matrix
as a colormap.
PARAMS:
    corrs: matrix of correlations between the features
    varnames: list of the names of each of the features
              (e.g. the column names)
"""
def correlationmap(corrs, varnames):
    nvars = corrs.shape[0]
    # create the figure and plot the correlation matrix
    fig, ax = plt.subplots()
    im = ax.imshow(corrs, cmap='RdBu', vmin=-1, vmax=1)
    cbar = ax.figure.colorbar(im, ax=ax)
    cbar.ax.set_ylabel("Pearson Correlation", rotation=-90, va="bottom")

    # Specify the row and column ticks and labels for the figure
    ax.set_xticks(range(nvars))
    ax.set_yticks(range(nvars))
    ax.set_xticklabels(varnames)
    ax.set_yticklabels(varnames)

    # Rotate the tick labels and set their alignment.
    plt.setp(ax.get_xticklabels(), rotation=45, ha="right",␣
 ↪rotation_mode="anchor")

    # Loop over data dimensions and create text annotations.
    for i in range(nvars):
        for j in range(nvars):
            text = ax.text(j, i, "%.3f" % corrs[i, j],
                           ha="center", va="center", color="k")
# END DEF correlationmap ----------------------------------------------


"""
Compute the Pearson correlation between the columns of Xycombo using
the numpy function corrcoef(). The corrcoef() function performs the
the pairwise correlation on the rows of a matrix, thus you will need to
transpose the input.
"""
Xycorrs = np.corrcoef(Xycombo.transpose())

""" TODO
Call the function defined above, correlationmap(), to generate a
colormap plot of the correlations between columns of the Xycombo matrix.
Mke sure to read any provided code
"""

correlationmap(Xycorrs, Xycolnames)
```


mean radius
mean area
mean concavity
mean symmetry
target
1.000 0.987 0.677 0.148 -0.730
0.987 1.000 0.686 0.151 -0.709
0.677 0.686 1.000 0.501 -0.696
0.148 0.151 0.501 1.000 -0.330
-0.730 -0.709 -0.696 -0.330 1.000
Pearson Correlation
1.00
0.75
0.50
0.25
0.00
−0.25
−0.50
−0.75
−1.00