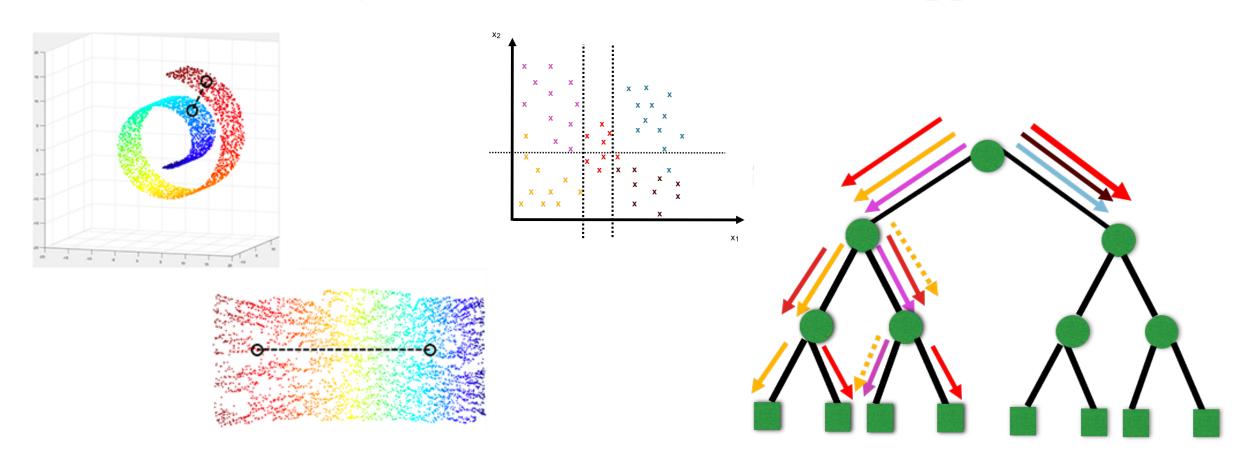
#### Machine Learning for Biomedical/Healthcare Applications



#### **Laplacian Eigenmaps and Decision Trees**

Dr Emma Robinson

### Learning Objectives

- 1. Gain an **intuition for the reasoning behind manifold learning** and define the conditions, under which it is needed, over linear techniques such as PCA
- 2. Learn how to implement **Laplacian Eigenmaps** from scratch and scikit learn
- 3. Be able to define what is meant by a weak learner, a **decision stump** a **decision tree**
- 4. Be able to define and use **weak learning rules: Information Gain and Gini Index**,
  - to split a training set into two groups, on the values of one features
- 5. Learn step by step how to construct a **decision tree classifier from scratch** and using scikit-learn

#### **New teams channel for Level 7!**

### I Laplacian Eigenmaps

#### Open 6.1.Laplacian\_Eigenmaps.ipynb ; To do

- 1. Exercise 2 Create a *symmetric* k-Nearest neighbour graph (30 mins)
- 2. Exercise 3 implement the Laplacian Eigenmaps embedding of the swiss roll data set (10 mins)
- 3. Exercise 4 Implementing Laplacian Eigenmaps with Scikit Learn (10 mins)

### Laplacian Eigenmaps -Summary

- Non-linear manifold learning methods seek a low-dimensional embedding which preserves local manifolds
- The Laplacian embedding can be estimated through the following steps
  - 1. Estimate the squared distances between all points
  - 2. Use this to calculate the k-nearest neighbour adjacency graph A
    - Setting k-nearest neighbours to 1, make all other values o
    - Make this symmetric
  - 3. Calculate the degree matrix **D** a diagonal matrix with entries  $\mathbf{D}_{ii} = \sum_{j} A_{ij}$
  - 4. Estimate graph Laplacian L = D A
  - 5. Estimate the embedding from the eigenvectors of L corresponding to the N smallest eigenvalues (above 0)

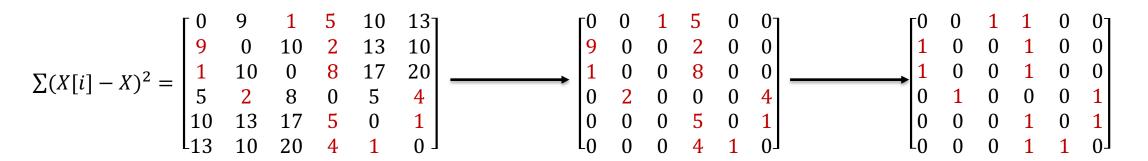
## Tutorial: estimate a K-nearest Neighbour graph

- The first step of many manifold learning techniques is to define the k-nearest neighbour graph
- For some pre-defined k, estimate the Adjacency matrix  $A \in \mathbb{R}^{n \times n}$ 
  - Estimate the *Euclidean* (squared) distances **between all points**  $SSD_i = \sum_j (x_i x_j)^2$  Set **the k-nearest** distances to 1 (evaluating its also)

  - Set all other distances to o
- Typically we want A to be symmetric which means setting  $A_{ij} = A_{ji}$  if either  $A_{ij} = 1$  or  $A_{ii}=1$ 
  - E.g. using np.maximum(A, A.T)
  - np.maximum returns the element-wise maximum of its arguments

## Tutorial: estimate a K-nearest Neighbour graph

To go from distances to k-NN



Make symmetric

$$A = \begin{bmatrix} 0 & 1 & 1 & 1 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 1 & 0 & 0 & 1 & 1 \\ 0 & 0 & 0 & 1 & 0 & 1 \\ 0 & 0 & 0 & 1 & 1 & 0 \end{bmatrix}$$

Diagonals stay o!

#### Tutorial: Implemented in Scikit-Learn

• Scikit learn refers using Laplacian Eigenmaps as Spectral Embedding

```
class sklearn.manifold. SpectralEmbedding(n_components=2, *, affinity='nearest_neighbors', gamma=None, random_state=None, eigen_solver=None, n_neighbors=None, n_jobs=None)
```

[source]

- By default it solves for the normalized graph Laplacian  $L = D^{-1/2}(D A) D^{-1/2}$
- which can lead to more stable solutions is degree is not distributed evenly across all points
- E.g.

```
>>> from sklearn.datasets import load_digits
>>> from sklearn.manifold import SpectralEmbedding
>>> X, _ = load_digits(return_X_y=True)
>>> X.shape
(1797, 64)
>>> embedding = SpectralEmbedding(n_components=2)
>>> X_transformed = embedding.fit_transform(X[:100])
>>> X_transformed.shape
(100, 2)
```

#### Solutions – Ex 2 Laplacian Eigenmaps

- Exercise 2 Create a *symmetric* k-Nearest neighbour graph (30 mins)
  - 1. Estimate squared distances  $(SSD_i = \sum_i (x_i x_i)^2)$  between each point X[i] and all others
    - Distances can be estimated with broadcasting X-X[i]
    - Need square distance so use power operator \*\*2
    - Want sum of squares over features (columns) achieved using np.sum over column axis (1)

```
def my knn(X, k):
        """ Finds k-nearest neighbours in X """
       N, D = X.shape
       A = np.zeros((N, N))
       for i in range(N):
           # 2.1 estimate the squared distances between point i and all neighbours
           i sq distances =np.sum((X - X[i])**2, axis=1)
           # 2.2 find the nearest points
           nearest points = np.argsort(i sq distances)
           # [1:k+1] is because the nearest point to i is i itself - but we don't want it
10
11
           k nearest
                          = nearest points[1:k+1]
           for j in k nearest:
12
13
               A[i,j] = 1
14
       return A
15
   A = my knn(X, 20)
```

### Solutions – Ex 2 Laplacian Eigenmaps

- Exercise 2 Create a *symmetric* k-Nearest neighbour graph (30 mins)
  - 2. Find nearest distances
    - First get indices of nearest points using np.argsort(i\_sq\_distances)
    - Return the k nearest (ignoring the first one as that will be the distance between point and itself)
       nearest points[1:k+1]
    - A is initialised using np.zeros((N,N)) so we just need to add ones for the ids of nearest neighbours

```
def my knn(X, k):
       """ Finds k-nearest neighbours in X """
       N, D = X.shape
       A = np.zeros((N, N))
       for i in range(N):
           # 2.1 estimate the squared distances between point i and all neighbours
           i sq distances =np.sum((X - X[i])**2, axis=1)
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           nearest points = np.argsort(i sq distances)
 9
           # [1:k+1] is because the nearest point to i is i itself - but we don't want it
10
11
           k nearest
                          = nearest points[1:k+1]
           for j in k nearest:
12
13
               A[i,j] = 1
14
       return A
15
   A = my knn(X, 20)
```

### Solutions – Ex 2 Laplacian Eigenmaps

- Exercise 2 Create a *symmetric* k-Nearest neighbour graph (30 mins)
  - 3. Make symmetric by running

To do Run the cell below to return a symmetric your k-nearest neighbour adjacency matrix A

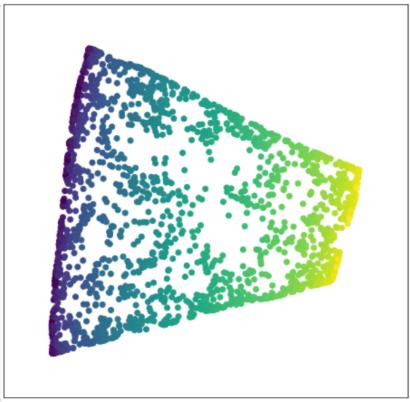
```
def symmetrise(X):
    """ Symmetrises the matrix X.

Notes
    ----
    np.maximum returns the element-wise maximum of its arguments."""
    return np.maximum(X, X.T)
    A = symmetrise(A)
```

### Solutions – Ex 3 Laplacian Eigenmaps

• Exercise 3 - implement the Laplacian Eigenmaps embedding of the swiss roll data set

```
def my laplacian eigenmap(X, k=20, d=2):
       # 3.1 a use function my knn to return A
       A = my knn(X, k)
       # 3.1 b use function symmetrise to make A symmetric
       A = symmetrise(A)
       # 3.2 create diagonal matrix D from A
       # the degree of each number is the sum the Adjacency for that row/column
       #(remember symmetric so these are the same)
       # to make a vector into a diagonal matrix using np.dig
       D = np.diag(np.sum(A, axis=0))
11
       # 3.3 create L
12
       L = D - A
       # 3.4 return eigenvectors of L using np.eigh
       # eigvals=(1,d) returns the d smallest (above 0 - in this case corresponding to indices 1 and 2)
15
       v, X = eigh(L, eigvals=(1,d))
16
       return X
17
   Z = my laplacian eigenmap(X)
19
20 fig = plt.figure(figsize=(8,8))
21 ax = fig.add subplot(111)
22 ax.set xticks([])
23 ax.set yticks([])
   = ax.scatter(Z[:,0], Z[:,1], c=X m[:,1], marker='o')
```



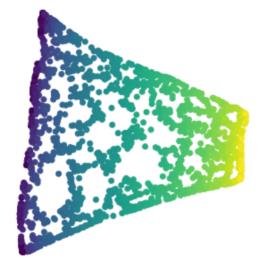
#### Solutions – Ex 4 Laplacian Eigenmaps

• Exercise 4 - Implementing Laplacian Eigenmaps with Scikit Learn

```
from sklearn.manifold import SpectralEmbedding
model=SpectralEmbedding(n_components=2,n_neighbors=10)

Z_2 = model.fit_transform(X)

fig = plt.figure(figsize=(8,8))
ax = fig.add_subplot(111)
ax.set_xticks([])
ax.set_yticks([])
10 ax.set_yticks([])
11 _ = ax.scatter(Z_2[:,0], Z_2[:,1], c=X_m[:,1], marker='o')
```



May need to re-download – very slight typo wrt line numbers reported in Exercise 1.4

#### II Decision stumps and Trees

Open **6.2.Decision\_Trees.ipynb** ; To do

- 1. Exercise 1 building a decision stump classifier from scratch (30-45 mins)
- 2. (optional) Exercise 2: building and testing a complete decision tree (15 mins)
- 3. Exercise 3 Running Decision Trees with Scikit-Learn (15 mins)
  - 1. (optional) Compare against the decision tree built in Exercise 2

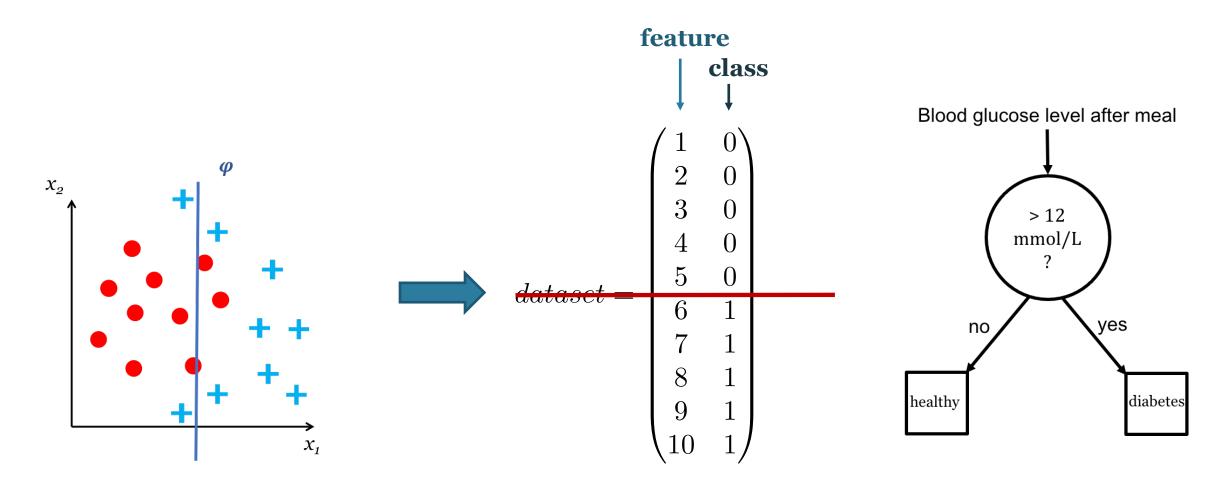
#### Summary

- Decision Trees are hierarchies of decision stumps; they are powerful because
  - Easy to interpret
  - Can be **used for classification or regression**
  - Don't require normalization of features
- Each decision stump must be fit by
  - Iterating over all features

- **Todays Tutorial**
- Finding optimal threshold for each features
- Choosing the feature which performs best (has optimal cost) relative to all others
- Labels must be assigned to each leaf from distribution of the labels of the training examples which reach that node
- The robustness of decision trees can be increased through combining them in ensembles (next week)

#### Weak Learners/Decision stump

A **weak learner** is defined to be a classifier that is only slightly correlated with the true classification (it can label examples slightly better than random guessing) e.g **axis-aligned** 



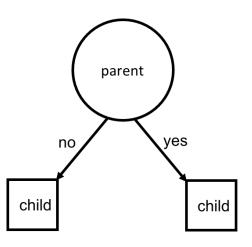
## Decision Stump: Learning Rules

Two choices for deciding on threshold **for a classification problem**:

1. Information gain: Decrease in entropy after a dataset is split on an attribute.

$$I(S_j) = H(S_j) - \sum_i \frac{|S_j^i|}{|S_j|} H(S_j^i)$$

- Here  $H(S_j)$  is entropy of root node and  $H(S_j^i)$  is entropy of leaf node
- $|S_j|$  = total number of data points reaching parent node j;
- $|S_i^i|$  = total number of data points reaching child *i* from parent *j*;



2. Gini index: Indicates how mixed the classes are following the split.

$$I(S_j) = \sum_i \frac{\left|S_j^i\right|}{\left|S_j\right|} Gini_i$$
 where  $Gini = 1 - \sum_{y_k \in Y} p(y_k)^2$ 

•  $p(y_k)$  is proportion at given node that are of class k;

## Tutorial: Decision tree/stump - Optimisation:

At each tree node *j*:

For each possible feature k:

I.e. try thresholding on each feature value

 $set = \begin{bmatrix} 3 & 0 \\ 4 & 0 \\ 5 & 0 \\ 6 & 1 \\ 7 & 1 \\ 8 & 1 \\ 9 & 1 \\ 10 & 1 \end{bmatrix}$ 

For each possible threshold  $\tau$  on this feature:

Evaluate function  $I(S_i, k)$ 



This estimates the cost of splitting training data into left/right\* components  $(S_j^1, S_j^1)$ \*: leaf 1, leaf 2

Chose the best feature  $(k_{opt})$  corresponding to optimum cost  $(I_{opt})$  and threshold  $\tau_{ont}$ 





until termination criterion is met

**REPEAT\*** 



### Important points to remember! (see Tuesdays tutorial)

1. When using each splitting criteria:

**Gini** index must be **MINIMISED Information Gain** must be **MAXIMISED** 

- 2. Try  $I(S_i, k)$  on each value of the column X[:,k] to find your optimum  $\tau$
- 3. The **amount of training examples will decrease** as you move down the tree
  - And different examples pass down different branches
- 4. When looping through features and threshold you must retain variables memorising the current best feature/threshold/data split
  - In **Tuesday's Tutorial** we will go through these steps for **creating a** single decision stump in Python from scratch
  - With option to extend to building a whole decision tree

## Tutorial: Decision Trees in Python (optional)

- The decision tree can therefore be defined by a nested dictionary which defines, **for each tree node** *j* keys:
  - Index: The feature  $k_{opt}^{j}$  that's split on
  - Value: The threshold  $\tau_{opt}^{j}$  needed for an optimal split on that feature (for the training data that reaches it)
  - **Branches: the split of the data** (i.e. tuple of 2 data arrays) indicating the data rows (examples) sent down each branch
- Note that for each subsequent node of the tree a new dictionary is created for each split
- Thus the **branches** key gets replaced each time with new dictionaries representing the {'index':  $k_{opt}^{j+1}$ , 'value':  $\tau_{opt}^{j+1}$ , 'branch':  $(X_{left}, X_{right})$ }
- Leaf nodes are assigned a class label or a predicted fit  $\hat{y}$

#### 1.1 estimate gini index for a given split

- 1. Estimate the total number of samples by summing over the list branch
- 2. Proportion in each branch equals (total number of samples in branch)/(total number of samples)
  - Total number of samples in branch is given by variable class\_total (each item in list branch)
  - Total overall is given by output of step 1 variable split\_size
- 3. Gini=  $1 \sum_{y_k \in Y} p(y_k)^2$

```
def gini coefficient(branch):
           Estimates Gini Coefficient for a given class split
            input:
                split: list of length k (where k= number of classes).
                       The values at each index reflect the toal number of instances
                      of each class, for this proposed branch split
 9
10
            output:
11
                gini: gini coefficient for this split
12
13
       # 1.1.1 estimating total number of samples in branch split (by summing contents of split list)
14
       split size=np.sum(branch)
       gini=1
15
16
       # iterating over all items in the array
17
       for class total in branch:
18
            # 1.1.2. estimating p*p for this class label; subtracting from current gini total
19
           proportion class k=(class total/split size)
           # 1.1.3. subract the squaree of the propoertion per class from current estimate of the gininindex
20
21
            gini--proportion class k*proportion class k
22
23
       return gini
```

#### 1.2 Propose splits

- 1. check all the values of the features at that indexed position
  - Given by row[index] for each row (here index is the feature/attribute index)
- 2. split the data into a left branch (if that data example's feature is below the threshold) and into a right branch (if that data example's feature is below the threshold).

```
def test split(index, value, dataset):
           Split a dataset based on an attribute and an attribute value
           input:
               index = feature/attribute index (i.e. data column index) on which to split on
               value = threshold value (everything below this goes to left split,
                        everything above goes to right)
                dataset = array (n samples, n features+1)
                        rows are examples
10
                        last column indicates class membership
11
                        remaining columns reflect features/attributes of data
12
13
           output:
14
               left, right: data arrays reflecting data split into left and right branches, respectively
15
16
17
       # create empty list that you will populate with rows of dataset
       left=[]
19
       right = []
       # the loop below will slice rows from data set
21
       for row in dataset:
           # if the value of this feature for this row is less than
23
           # the (threshold) value split into left branch, else split into right
24
           if row[index] < value:</pre>
25
               left.append(row)
26
           else:
27
                right.append(row)
28
29
       return np.asarray(left), np.asarray(right)
```

#### 1.2 Propose splits

- Then test for outcome of splitting on first feature (column index=6)
- With threshold equal to 7<sup>th</sup> value (or row)

```
1 index=0
 2 rowindex=6
 3 threshold=X[rowindex,index]
   print('the value of the feature {} at row {} of the data set is {}'.format(index,rowindex,threshold))
the value of the feature 0 at row 6 of the data set is 9.00220326
    branches=test split(index, X[rowindex,index], X)
   print('Our left branch is \n {}'.format(branches[0]))
   print('Our right branch is \n {}'.format(branches[1]))
Our left branch is
[[2.77124472 1.78478393 0.
[1.72857131 1.16976141 0.
[3.67831985 2.81281357 0.
[3.96104336 2.61995032 0.
[2.99920892 2.20901421 0.
[7.49754587 3.16295355 1.
[7.44454233 0.47668338 1.
 [6.64228735 3.31998376 1.
Our right branch is
[[ 9.00220326 3.33904719 1.
[10.12493903 3.23455098 1.
                                     11
```

#### 1.3: Estimate total cost of split

- 1. Iterate over class IDs (line 26)
- 2. Slices rows corresponding to that class (line 34)
- 3. Count number of rows for that slice (line 36)
- 4. Add these to list: class\_counts\_for\_branch
  - input to gini\_coefficient function
- 5. Estimate gini\_coefficient for that branch
- 6. Weight by proportion of samples in branch
  - branch.shape[0]/total samples

```
Estimates the cost for a proposed split
                splits: tuple or form (L,R) where L reflects the data for the left split and
                        R reflects data for left split
                classes: list of class values i.e. [0,1]
10
11
                cost: sum of gini coefficient for left and right sides of the split
12
13
        cost=0
14
        total samples=0
15
16
        # estimate the relative size of each branch
17
        for branch in split:
18
            total samples+=branch.shape[0]
19
20
        # for each (left/right) split on the proposed tree
21
        for br index, branch in enumerate(split):
            # initialise list of class counts for this branch
23
            class counts for branch=[]
24
            # for each class value, count total of data examples (rows)
25
            # that have for this class, in this branch
26
            for class val in classes:
27
28
                if branch.shape[0] == 0: # don't continue if size of split is 0
29
                    continue
30
31
                # 1.3.1 slice data to return only rows from branch which have this specific class value
32
                # here branch[:,-1] returns the column containing the labels and we want to slice all rows
33
                # for class=class val
                branch per class=branch[branch[:,-1]==class_val]
35
                # 1.3.2 count the number of rows with this class in this branch and append
36
                total rows=branch per class.shape[0]
37
                # this is generating list of class counts per branch which get fed to
38
                # the gini coefficient function
39
                class counts for branch.append(total rows)
40
41
            # 1.3.3. estimate the gini coefficient for this split (or branch)
42
            gini split=gini coefficient(class counts for branch)
43
            # 1.3.4. estimated the weighted contribution for this split
44
            weighted by sample size=gini split*(branch.shape[0]/total samples)
45
            # total cost is a weighted average of gini coefficients for both splits
46
            cost+=weighted by sample size
47
48
49
        return cost
          class values=[0,1]
          splitcost=split_cost(branches,class_values)
          print('The cost of the proposed split is: ', splitcost)
```

The cost of the proposed split is: 0.375

def split cost(split, classes):

# 1.4 Choose optimal feature/threshold split

- 1. Line 28 Iterate over all but last column:
  np.arange(dataset.shape[1]-1)
- 2. Iterate over all rows to propose threshold value (line 31)
- 3. Line 33 Create split accordingly:
  - Function test split
  - Arguments: index (feature)
     row[index] (threshold) dataset
- 4. Estimate cost using split\_cost (line 35)
- 5. If improved (cost < best\_cost) as Gini must be minimized (l. 36)
- 6. If cost<best\_cost then save current set of parameters as 'best'

```
def get best split(dataset):
            Search through all attributes and all possible thresholds to find the best split for the data
            input:
                dataset = array (n samples, n features+1)
                        rows are examples
                        last column indicates class membership
                        remaining columns reflect features/attributes of data
10
11
            output:
                dict containing: 1) 'index' : index of feature used for splittling on
12
13
                                 2) 'value': value of threshold split on
14
                                 3) 'branches': tuple of data arrays reflecting the optimal split into left and right
15
16
17
18
        # estimating the total number of classes by looking for the total number of different unique values
        # in the final column of the data set (which represents class labels)
19
20
        class values=np.unique(dataset[:,-1])
21
22
        # initalising optimal values prior to refinment
23
       best cost=sys.float info.max # initialise to max float
24
       best value=sys.float info.max # initialise to max float
25
        best index=dataset.shape[1]+1 # initialise as greater than total number of features
                              # the best split variable should contain the output of test split that corresponds to
26
27
        #1.4.1 iterating over all features/attributes (columns of dataset)
28
        for index in np.arange(dataset.shape[1]-1):
29
30
            #Trialling splits defined by each row value for this attribute
31
            for r index,row in enumerate(dataset):
32
               # 1.4.2. return branches corresponding to thresholding on feaure (index) and threshold value (for row.
33
                branches=test split(index, row[index], dataset)
34
35
                cost=split cost(branches, class values) # 1.4.3 estimate cost for this split
36
                if cost < best_cost: # 1.4.4. if this cost is an improvement on previous costs then save the
37
                    best cost=cost # cost
38
                    best split=branches #branches
39
                    best index=index # feature index
40
                    best value=row[index] # threshold value
41
                    print('Best cost={}; Best feature={}; Best row={}'.format(best cost,index,r index)
42
43
        return { 'index':best index, 'value':best value, 'branches':best split}
44
```

# 1.4 Choose optimal feature/threshold split

- 1. Line 28 Iterate over all but last column:
  np.arange(dataset.shape[1]-1)
- 2. Iterate over all rows to propose threshold value (line 31)
- 3. Line 33 Create split accordingly:
  - Function test split
  - Arguments: index (feature)
     row[index] (threshold) dataset
- 4. Estimate cost using split\_cost (line 35)
- 5. If improved (cost < best\_cost) as Gini must be minimized (l. 36)
- 6. If cost<best\_cost then save current set of parameters as 'best'

```
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            Search through all attributes and all possible thresholds to find the best split for the data
            input:
                dataset = array (n samples, n features+1)
                        rows are examples
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            output:
                dict containing: 1) 'index' : index of feature used for splittling on
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                                 2) 'value': value of threshold split on
14
                                 3) 'branches': tuple of data arrays reflecting the optimal split into left and right
15
16
17
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        # estimating the total number of classes by looking for the total number of different unique values
        # in the final column of the data set (which represents class labels)
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20
        class values=np.unique(dataset[:,-1])
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        # initalising optimal values prior to refinment
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       best cost=sys.float info.max # initialise to max float
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        best index=dataset.shape[1]+1 # initialise as greater than total number of features
                              # the best split variable should contain the output of test split that corresponds to
26
27
        #1.4.1 iterating over all features/attributes (columns of dataset)
28
        for index in np.arange(dataset.shape[1]-1):
29
30
            #Trialling splits defined by each row value for this attribute
31
            for r index,row in enumerate(dataset):
32
               # 1.4.2. return branches corresponding to thresholding on feaure (index) and threshold value (for row.
33
                branches=test split(index, row[index], dataset)
34
35
                cost=split cost(branches, class values) # 1.4.3 estimate cost for this split
36
                if cost < best_cost: # 1.4.4. if this cost is an improvement on previous costs then save the
37
                    best cost=cost # cost
38
                    best split=branches #branches
39
                    best index=index # feature index
40
                    best value=row[index] # threshold value
41
                    print('Best cost={}; Best feature={}; Best row={}'.format(best cost,index,r index)
42
43
        return { 'index':best index, 'value':best value, 'branches':best split}
44
```

- 3 Running Decision Trees with Scikit-Learn
- 1. instantiate a decision tree classifier model (line 29)
- 2. fit the model to training data (line 30)
- 3. Predict test labels (line 31)
- 4. Return performance score on test examples (line 32)

```
from sklearn.tree import DecisionTreeClassifier # import the scikit-Learn Decision Tree module
   from sklearn.model selection import train test split
   from sklearn.preprocessing import StandardScaler
   from sklearn.datasets import make moons
    # CREATE a Random Data set using the sklearn Make Moons dataset
   DATA, LABELS =make_moons(noise=0.3, random_state=0)
10
   # Plot the data
11
   figure = plt.figure(figsize=(5, 5))
13 cm = plt.cm.RdBu
   cm bright = ListedColormap(['#FF0000', '#0000FF'])
   ax = plt.subplot(1,1, 1)
16
   ax.set_title("Input data")
   ax.scatter(DATA[:, 0], DATA[:, 1], c=LABELS, cmap=cm bright,
19
              edgecolors='k')
20
21 # randomly split the data
   X train, X test, y train, y test = train test split(DATA, LABELS, test size=.4, random state=42)
23
   # **to DO** implement scikit learn decision tree classifier on this data
   #**** complete the above steps for the scikit learn classifier *****
   model = DecisionTreeClassifier(random state=0)
   model.fit(X train,y train)
28 pred=model.predict(X test)
   score = model.score(X test, y test)
30
31
   print("Scikit-learn's decision tree Score", score)
32
33 # OPTIONALLY plot your results
34 # suggest plotting with with different colours for each class
   #and different markers for test and train data in order to aid visualisation
36
   # just plot the dataset first
38 f, (ax1, ax2) = plt.subplots(2, 1, sharey=True, figsize=(5,10))
39 cm = plt.cm.RdBu
40 cm bright = ListedColormap(['#FF0000', '#0000FF'])
42 ax1.set title("True labels")
   ax1.scatter(X test[:, 0], X test[:, 1], c=y test, cmap=cm bright,
44
              edgecolors='k')
45
   ax2.set title("Predicted labels")
   ax2.scatter(X_test[:, 0], X_test[:, 1], c=pred, cmap=cm_bright,
              edgecolors='k')
```

Scikit-learn's decision tree Score 0.95

• 3.2 – optional compare own tree against Scikit-Learn

```
# first combine X_train and y_train togeher (and X_test, y_test) to put data into form expected by our tree
dataset=np.concatenate((X_train,y_train.reshape((y_train.shape[0],1))),axis=1)

test_dataset=np.concatenate((X_test,y_test.reshape((y_test.shape[0],1))),axis=1)

# #3.2.1 train your tree - set max depth to 5 and min size to 1

tree = build_tree(dataset, 5,1)

# #3.2.2 Get a prediction from your test data
prediction_DT1=predict(tree, test_dataset)

# #3.2.3 Score the accuracy of your decision tree classifier
score_DT1=tree_score(y_test,prediction_DT1)
print('Our Decision Tree Score', score_DT1)
```

Our Decision Tree Score 0.875

Scikit learn applied pruning (see notebook)

#### Additional exercises

- Try constructing a regression tree from scratch; using the above classification tree as the basis but:
  - creating a new MSE cost, and
  - editing the prediction function accordingly (to fit constant function to mean);
- Try it out the following toy dataset (Taken from: <a href="http://scikit-learn.org/stable/auto\_examples/tree/plot\_tree\_regression.html#sphx-glr-auto-examples-tree-plot-tree-regression-py">http://scikit-learn.org/stable/auto\_examples/tree/plot\_tree\_regression.html#sphx-glr-auto-examples-tree-plot-tree-regression-py</a>)

```
# Create a random dataset
rng = np.random.RandomState(1)
X = np.sort(5 * rng.rand(80, 1), axis=0)
y = np.sin(X).ravel()
y[::5] += 3 * (0.5 - rng.rand(16))
```

Compare your result