Project 2 on Fuzzy system

Subject: Application in medicine

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In [1]:
```
import numpy as np
from my_io import read_dataset_to_X_and_y
from copy import deepcopy
import matplotlib.pyplot as plt
```

Build Class to easily have all the variables

I like to have my variable all together so I build a class and named it UniSet(short form of universal set)

Read dataset with my function on my_io module that can shuffle sample and correct missing values also normalized the feature.

In here I shuffle data and use class-mean for the missing values then normalized it with the z-score method(zero-mean unit-variance)

I use all the features(12) and change sex from m, f to 0, 1 (actually I map each string to a specific number in my_io module)

In [2]:
```
class UniSet():
    def __init__(self, file, range_feature, range_label,
                 normalization=None, shuffle=False, about_nan='class_mean'):
        np.random.seed(1)
        sample, label = read_dataset_to_X_and_y(
            file, range_feature, range_label, normalization, shuffle=shuffle,
            about_nan=about_nan)
        self.universal = sample.astype(float)
        self.label = label
        self.number_of_feature = sample.shape[1]
        self.size_of_universal = sample.shape[0]
        self.diffrent_label = np.unique(label)
        self.number_of_diffrent_label = self.diffrent_label.shape[0]
        self.relation = None
        self.equivalence_relation = None
        self.predicted_label = None
        self.diffrent_predicted_label = None
        self.number_of_diffrent_predicted_label = None


uni_total = UniSet(
```

```
    'dataset/hcvdat0.csv', (2, 14), (1, 2),
    normalization='z_score', shuffle=True, about_nan='class_mean')


print(f'The whole dataset is {uni_total.universal.shape} matrix')
```

```
The whole dataset is (615, 12) matrix
```

> ### Details
>
> In my_io module I have a function named read_dataset_to_X_and_y that get dataset file, range of attributes that are our features, range of attributes that are our labels, normalization which is our normalization method, shuffle which if be True our samples be shuffled, and about_nan that can be "delete" which delete samples with NA values or "class_mean" which replace NA values with mean of that feature in the sample class
>
> Also as I mentioned above this function can get string attributes too by mapping each string to a specific value so now our labels $\in [0, 4]$
>
> I change NA value with class-mean because It doesn't change the similarity(or distance) of two samples in one class
>
> In my class, I have all things that I'll need such as universal (sample data), their label, number of features, size of universal (dataset), different labels (unique labels), number of different labels, a relation (on our universal set), and an equivalence relation.
>
> Our labels in this dataset is attributed [1, 2) and features are attributed [2, 14) (12 features)

Split the whole dataset to Train and Test

As I shuffle the dataset before, now I just consider the first 80% of the data for the train and the rest for the test case

In [3]:

```
def split_train_test(universe: UniSet, train_size: float) -> list[UniSet]:
    train = deepcopy(universe)
    test = deepcopy(universe)
    train.size_of_universal = \
        int(universe.size_of_universal*train_size)
    train.universal = \
        universe.universal[0:train.size_of_universal]
    train.label = \
        universe.label[0:train.size_of_universal]
    test.size_of_universal = (
        universe.size_of_universal - train.size_of_universal)
    test.universal = \
        universe.universal[train.size_of_universal:]
    test.label = \
        universe.label[train.size_of_universal:]
```

```
    return train, test


uni_train, uni_test = split_train_test(uni_total, 0.8)
print(f'The train dataset is {uni_train.universal.shape} matrix')
print(f'The test dataset is {uni_test.universal.shape} matrix')
```

```
The train dataset is (492, 12) matrix
The test dataset is (123, 12) matrix
```

> ### Details
>
> I create two classes for train and test by copying the total set and just changing universal, level, and size of universal for both train and test

Find relation matrix

To find the relation between each sample, first, we need metric for similarity

Similarity metric

First I find the distance between each pair of samples and, then normalized it by dividing them to maximum distance, now all the distances are between [0, 1] and now similarity is just equal to 1 - distance

$$R\left(\mathbf{x}_i, \mathbf{x}_k\right) = 1 - \delta\left(\sum_{j=1}^{p} \left|x_{ij} - x_{kj}\right|^q\right)^{\frac{1}{q}}$$

which δ is maximum distance

In [4]:

```
def distance(sample1: np.ndarray, sample2: np.ndarray) -> float:
    return np.linalg.norm(sample1-sample2)


def find_relation(universal: UniSet) -> np.ndarray:
    dis = np.array(
        list(map(lambda x: list(map(
            lambda y: distance(
                universal.universal[x], universal.universal[y]),
            range(universal.size_of_universal))),
            range(universal.size_of_universal))))
    return 1 - dis / np.max(dis)


uni_train.relation = find_relation(uni_train)
print(f'The relation on train dataset is {uni_train.relation.shape} matrix')


uni_test.relation = find_relation(uni_test)
print(f'The relation on test dataset is {uni_test.relation.shape} matrix')
```

```
The relation on train dataset is (492, 492) matrix
```

```
The relation on test dataset is (123, 123) matrix
```

> ### Details
>
> Our Similarity metric has some properties:
>
> Similarity $(x, y) \in [0, 1]$
>
> Similarity $(x, x) = 1$
>
> Similarity $(x, y) =$ Similarity (y, x)

How to make a relation transitive?

I use the following algorithm to find a transitive closure of a relation.

1. $R' = R \cup (R \circ R)$.
2. If $R' \neq R$, make $R = R'$ and go to Step 1 .
3. Stop: $R' = R_T$.

In [5]:

```python
def max_min(sample1: np.ndarray, sample2: np.ndarray) -> float:
    both_sample = np.vstack((sample1, sample2))
    return np.max(np.min(both_sample, axis=0))


def composition_RoR(relation: np.ndarray) -> np.ndarray:
    result = np.array(
        list(map(lambda x: list(map(
            lambda y: max_min(relation[x], relation[y]),
            range(relation.shape[0]))),
            range(relation.shape[0]))))
    return result


def union_two_relation(
        relation1: np.ndarray, relation2: np.ndarray) -> np.ndarray:
    both_relation = np.dstack((relation1, relation2))
    return np.max(both_relation, axis=2)


def make_transitive(relation: np.ndarray) -> np.ndarray:
    R = None
    Rp = np.copy(relation)
    iter = 0
    while((Rp != R).any()):
        R = np.copy(Rp)
        RoR = composition_RoR(R)
        Rp = union_two_relation(R, RoR)
        iter += 1
        print(iter)
    return Rp


print('#Iteration to make train relation transitive')
uni_train.equivalence_relation = make_transitive(uni_train.relation)
```

```
print('The equivalence relation on train dataset is',
        f'{uni_train.equivalence_relation.shape} matrix')

print('\n#Iteration to make test relation transitive')
uni_test.equivalence_relation = make_transitive(uni_test.relation)
print('The equivalence relation on test dataset is',
        f'{uni_test.equivalence_relation.shape} matrix')
```

```
#Iteration to make train relation transitive
1
2
3
4
5
6
The equivalence relation on train dataset is (492, 492) matrix

#Iteration to make test relation transitive
1
2
3
4
5
The equivalence relation on test dataset is (123, 123) matrix
```

> ### Details
>
> Order of max-min is $O\left(n\right)$ and in composition R and R we compose each pair of sample ($O\left(n^2\right)$) with max-min so function composition_RoR has order $O\left(n^3\right)$. To make relation transitive we need to compose our result $\lg\left(\left\lceil\frac{n}{2}\right\rceil\right)$ to find transitive relation along the longest path so out algotrithm is $O\left(n^3\lg n\right)$

Equivalence relation

Before find similar classes, we must find equivalence relation (be reflexive, symmetric, and transetive) to be sure If $R(x,y)\geqslant\alpha$ and $R(y,z)\geqslant\alpha\Rightarrow R(x,z)\geqslant\alpha$ which cause all pairs in similarity class have similarity $\geqslant\alpha$ (transitive) and $R(x,y)=R(y,x)$ to be sure if x and y is in same class y and x can be in same class (symmetric) and $R(x,y)=1$ to be sure x and x can be in a same similarity class (reflexive).

By having all three property we sure that every element in a specific similarity class (cluster) have the same similarity class.

Reflexive

Base on our similatiry metric, $similarity(x,x)=1$ because distance x and x is zero and zero devided by any number is still zero and finally $1-0=1$ and for checking that our relation is reflexive we only need to check if $diag(R)=\vec{1}$

Symmetric

Base on our similatiry metric, $similarity(x, y) = similarity(y, x)$ because only variable in our metric is distance and by using lebesgue norm, distance x from y is equal to distance y from x $\Rightarrow similarity(x, y) = similarity(y, x)$ and for checking that our relation is symmetric we only need to check if $R = R^\intercal$

Transitive

With the above algorithm (in the previous cell) we make our relation transitive and for checking that our relation is transitive we only need to check if $R = R \cup (R \circ R)$.

In [6]:
```
def is_reflexive(relation: np.ndarray) -> bool:
    return (relation.diagonal() == 1).all()


def is_symmetric(relation: np.ndarray) -> bool:
    return (relation == relation.T).all()


def is_transitive(relation: np.ndarray) -> bool:
    RoR = composition_RoR(relation)
    Rp = union_two_relation(relation, RoR)
    return (Rp == relation).all()


def is_equivalece(relation: np.ndarray) -> bool:
    return is_reflexive(relation) & is_symmetric(relation) & \
        is_transitive(relation)


print('Is our train equivalence relation, equivalence?',
    f'{is_equivalece(uni_train.equivalence_relation)}')

print('Is our test equivalence relation, equivalence?',
    f'{is_equivalece(uni_test.equivalence_relation)}')
```

```
Is our train equivalence relation, equivalence? True
Is our test equivalence relation, equivalence? True
```

> #### Details
>
> For checking if our relation is equivalence we should check to be reflexive, symmetric, and transitive

Clustering

With our equivalence similarity relation, we can cluster our data by finding similarity classes and as our relation is equivalent if we find similarity class for sample x, we don't need to find the equivalent class for the other members of equivalence class x because as I proof before all of them has the same equivalence class as x so we'll cluster the equivalence class for x and then cluster rest of the data

In [7]:
```
```

```python
def find_similarity_class(
        universal: UniSet, target_sample: int, alpha: float) -> np.ndarray:
    size_of_universal = universal.shape[0]
    similarity_class = []
    for sample in range(size_of_universal):
        if(universal[sample, target_sample] >= alpha):
            similarity_class.append(sample)
    return np.array(similarity_class)


def find_cluster(relation: np.ndarray, alpha: float, label=False):
    size_of_universal = relation.shape[0]
    classes = []
    predicted_label = np.full((size_of_universal, 1), -1.0)
    number_of_class = 0.0
    for sample in range(size_of_universal):
        if(predicted_label[sample] == -1):
            new_class = find_similarity_class(relation, sample, alpha)
            predicted_label[new_class] = number_of_class
            number_of_class += 1
            classes.append(new_class)
    number_of_class = int(number_of_class)
    if(label is True):
        return predicted_label, number_of_class
    return classes, number_of_class


cluster_alpha_cut_93 = find_cluster(uni_train.equivalence_relation, 0.93)
print('\nCluster with alpha-cut 0.93 on train equivalence relation is')
print(cluster_alpha_cut_93)
```

```
Cluster with alpha-cut 0.93 on train equivalence relation is
([array([  0,   1,   3,   6,   8,  12,  13,  14,  15,  16,  17,  20,  22,
        31,  41,  44,  45,  46,  47,  49,  52,  57,  58,  59,  60,  66,
        67,  76,  78,  79,  80,  82,  85,  89,  98, 101, 105, 107, 112,
       128, 142, 144, 146, 153, 154, 161, 164, 168, 171, 172, 173, 175,
       176, 178, 180, 185, 186, 190, 195, 197, 200, 203, 210, 214, 222,
       223, 224, 226, 227, 228, 229, 231, 232, 234, 236, 238, 242, 243,
       244, 245, 250, 253, 255, 258, 263, 264, 265, 266, 267, 272, 275,
       276, 279, 284, 285, 288, 290, 291, 293, 295, 297, 299, 302, 305,
       312, 313, 314, 316, 317, 322, 324, 326, 327, 328, 330, 332, 333,
       337, 340, 347, 349, 355, 359, 360, 361, 364, 367, 370, 371, 376,
       381, 382, 383, 388, 395, 398, 413, 423, 427, 437, 439, 441, 442,
       444, 445, 446, 448, 450, 452, 462, 463, 466, 469, 470, 480, 481,
       489, 490]), array([  2,   4,   7,   9,  10,  11,  18,  19,  23,  25,  28,
29,  30,
        32,  33,  34,  35,  39,  40,  43,  48,  50,  51,  53,  55,  56,
        62,  63,  64,  65,  68,  73,  74,  75,  77,  81,  83,  84,  86,
        87,  88,  90,  92,  93,  95,  99, 102, 104, 108, 109, 110, 113,
       114, 115, 116, 118, 119, 120, 123, 124, 126, 127, 129, 130, 131,
       132, 134, 135, 136, 138, 139, 140, 141, 143, 149, 150, 151, 155,
       156, 157, 159, 162, 166, 167, 169, 170, 174, 177, 179, 181, 182,
       187, 188, 189, 191, 193, 194, 198, 199, 201, 202, 204, 205, 206,
       207, 211, 212, 213, 215, 216, 217, 220, 221, 225, 233, 235, 237,
       240, 246, 248, 251, 252, 256, 257, 259, 260, 261, 262, 268, 269,
       270, 271, 273, 274, 277, 278, 280, 281, 282, 283, 286, 287, 289,
       292, 296, 298, 301, 303, 304, 308, 309, 310, 311, 315, 321, 325,
       329, 331, 334, 335, 336, 338, 339, 342, 343, 344, 345, 346, 348,
       350, 351, 352, 353, 356, 357, 358, 362, 363, 365, 366, 368, 369,
       372, 374, 377, 378, 379, 384, 385, 387, 389, 391, 392, 393, 401,
```

```
       402, 403, 405, 406, 407, 409, 411, 414, 415, 416, 418, 419, 420,
       421, 422, 424, 425, 426, 428, 429, 430, 431, 432, 433, 434, 436,
       438, 440, 447, 451, 453, 455, 456, 458, 459, 464, 465, 467, 468,
       471, 473, 474, 475, 476, 484, 485, 491]), array([  5, 443]), array([21]),
array([24, 36]), array([26]), array([27]), array([37]), array([38]), array([4
2]), array([54]), array([61]), array([69]), array([70]), array([71]), array([7
2]), array([91]), array([94]), array([96]), array([97]), array([100]), array([10
3]), array([106]), array([111]), array([117]), array([121]), array([122]), array
([125]), array([133]), array([137]), array([145]), array([147]), array([148]), a
rray([152]), array([158]), array([160]), array([163]), array([165]), array([18
3]), array([184]), array([192]), array([196]), array([208]), array([209]), array
([218]), array([219]), array([230]), array([239]), array([241]), array([247]), a
rray([249]), array([254]), array([294]), array([300]), array([306]), array([307,
318]), array([319]), array([320]), array([323]), array([341]), array([354]), arr
ay([373, 488]), array([375]), array([380]), array([386]), array([390]), array([3
94]), array([396]), array([397]), array([399]), array([400]), array([404]), arra
y([408]), array([410]), array([412]), array([417]), array([435]), array([449]),
array([454]), array([457]), array([460]), array([461]), array([472]), array([47
7]), array([478]), array([479]), array([482]), array([483]), array([486]), array
([487])], 90)
```

> ### Details
>
> #### Function find_similarity_class
>
> Get a relation, sample, and α then find similarity class for that sample by selecting all samples that have similarity $\geqslant \alpha$ with our sample and return a crisp set ([x])
>
> #### Function find_cluster
>
> Get relation, α, and label then find clusters which in each cluster all pair of members have similarity $\geqslant \alpha$. first, all the elements are in cluster -1 (not clustered yet) and every time we select a member of cluster -1 and find its similarity class and create a new cluster with all elements of similarity class and remove them from cluster -1. cluster are labeled from 0 and if label=True our funcion retun vector predicted-label which is predicted label for all samples and if label=False return set of clusters

Which α-cut clustering our data better

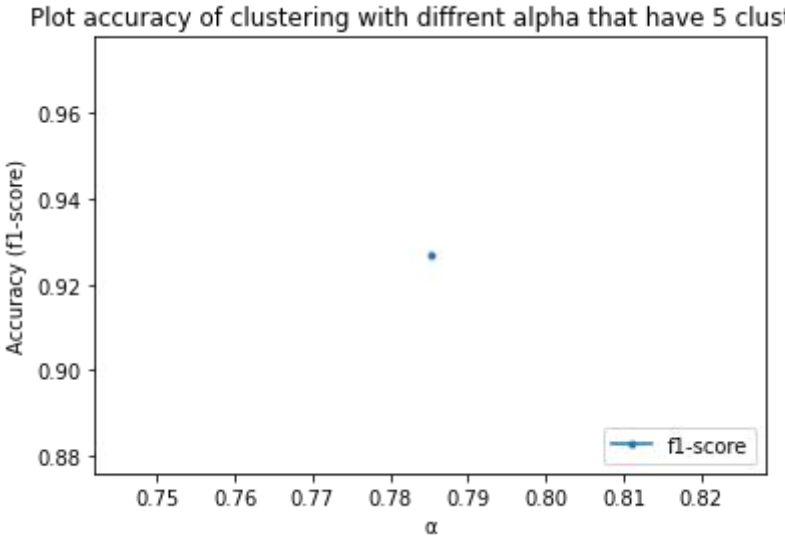
I find all unique membership degrees in our equivalent relation then start from smallest to the biggest and check my accuracy of clustering with that membership degree if ∇ degree $\geqslant \varepsilon$ (with the last degree that I checked) and select the α which split our data into the number of different labels (i.e. 5 in our dataset) as the best α-cut

Accuracy

I use **Confusion matrix** to find the label of clusters (argmax in each row) and then choose f1-score as accuracy metric because as α increase precision increase and recall decrease and I want to find α that satisfy both

In [8]:
```
def evaluate(gold_label: np.ndarray, predict_label: np.ndarray,
```

```
              method: str = 'f1-score') -> float:
    diffrent_label_in_gold_label = np.unique(gold_label)
    diffrent_label_in_predict_label = np.unique(predict_label)
    confusion_matrix = np.array(
        list(map(lambda k: list(map(
            lambda s: sum((predict_label == k)*(gold_label == s))[0],
            diffrent_label_in_gold_label)),
            diffrent_label_in_predict_label)))
    precision = np.sum(
        np.max(confusion_matrix, axis=1)) / np.sum(confusion_matrix)
    recall = np.sum(
        np.max(confusion_matrix, axis=0)) / np.sum(confusion_matrix)
    if(method == 'precision'):
        return precision
    if(method == 'recall'):
        return recall
    if(method == 'f1-score'):
        return 2 * ((precision*recall)/(precision+recall))


def find_best_alpha_cut(universal: UniSet, plotter: bool = False) -> float:
    alpha_cut = []
    accuracy = []
    last_point = -1.0
    for alpha in np.unique(universal.equivalence_relation):
        if(alpha - last_point >= 0.0001):
            alpha_clustered_label, alpha_number_of_class = find_cluster(
                universal.equivalence_relation, alpha, True)
            if(alpha_number_of_class == universal.number_of_diffrent_label):
                alpha_cut.append(alpha)
                accuracy.append(evaluate(universal.label, alpha_clustered_label))
            elif(alpha_number_of_class > universal.number_of_diffrent_label):
                break
            last_point = alpha

    if(plotter is True):
        plt.plot(alpha_cut, accuracy, '.-', label="f1-score")
        plt.legend(loc="lower right")
        plt.xlabel('α')
        plt.ylabel('Accuracy (f1-score)')
        plt.title((
            f'Plot accuracy of clustering with diffrent alpha that have '
            f'{universal.number_of_diffrent_label} clusters'))
        plt.show()

    return alpha_cut[np.argmax(accuracy)], np.max(accuracy)


best_alpha_cut, best_alpha_cut_accuracy = find_best_alpha_cut(uni_train, True)
print(f'Best alpha-cut is {round(best_alpha_cut, 4)} on train-dataset',
        f'with f1-score {round(best_alpha_cut_accuracy*100, 2)}%')

uni_train.predicted_label = find_cluster(
    uni_train.equivalence_relation, best_alpha_cut, True)[0]
uni_train.diffrent_predicted_label = np.unique(uni_train.predicted_label)
uni_train.number_of_diffrent_predicted_label = \
    uni_train.diffrent_predicted_label.shape[0]
```




```
Best alpha-cut is 0.7852 on train-dataset with f1-score 92.69%
```

> ### Details
>
> Set $\varepsilon = 0.0001$ and when the number of clusters with our α-cut cause more than different labels that we have, I stop because after that by increasing α value we get more number of clusters and we want to find the most accurate α that create clusters with number of our different labels
>
> Confusion matrix

Clusters \ Classes	S_1	S_2	S_3	...	S_S
K_1	a_{11}	a_{12}	a_{13}	...	a_{1S}
K_2	a_{21}	a_{22}	a_{23}	...	a_{2S}
K_3	a_{31}	a_{32}	a_{33}	...	a_{3S}
...					
K_K	a_{K1}	a_{K2}	a_{K3}	...	a_{KS}

> Its $(K * S)$ matrix that $a_{k,s}$ = total number of samples clustered to the k[th] cluster and belongs to the s[th] class.

$$\text{Precision } = \frac{\sum_k \max_s \{a_{ks}\}}{\sum_k \sum_s a_{ks}}$$

$$\text{Recall} = \frac{\sum_s \max_k \{a_{ks}\}}{\left(\sum_k \sum_s a_{ks} + U\right)}$$

$$F1 - score = 2 \times \frac{\text{Precision } \times \text{ Recall}}{\text{Precision } + \text{ Recall}}$$

Let's test our α

To do that we use our test set, find relation on the test set and make it transitive to be equivalence relation and then find our clusters with α-cut than we find in the training phase the compute test accuracy to see how well our α-cut works on the test set

In [9]:
```
predicted_label_test = find_cluster(
    uni_test.equivalence_relation, best_alpha_cut, True)[1]
test_accuracy = evaluate(uni_test.label, predicted_label_test)
print('Our f1-score on test-dataset with best alpha-cut on train-set is ',
        f'{round(test_accuracy*100, 2)}%')
```

```
Our f1-score on test-dataset with best alpha-cut on train-set is  93.97%
```

R_o

Occurrence relation: knowledge about the tendency or frequency of appearance of a symptom when the specific disense is present - "How often does symptoms occur with disease d?"

Its a matrix (symptom, disease) and I use the average of each symptom for each disease

In [10]:
```
def find_Ro(universal: UniSet):
    ro = []
    for a_disease in universal.diffrent_predicted_label:
        class_label = universal.universal[(universal.predicted_label == a_diseas
        mean_symptom_a_disease = np.mean(class_label, axis=0)
        ro.append(mean_symptom_a_disease)
    ro = np.array(ro).T

    return ro


R_o = find_Ro(uni_train)
print(f'The R0 is {R_o.shape} matrix')
```

```
The R0 is (12, 5) matrix
```

> ## Details
>
> Here I use predicted label from clustering with our best α-cut on equivalence relation

R_1

$R_1 = R_s \circ R_o$ and Its a matrix (patient, disease)

Then I select the most value as a disease for each patient which is a matrix (patient, 1)

In [11]:
```
def composition_RoS(relation_r: np.ndarray, relation_s: np.ndarray) -> np.ndarra
    result = np.array(
        list(map(lambda x: list(map(
            lambda y: max_min(relation_r[x], relation_s.T[y]),
            range(relation_s.shape[1]))),
            range(relation_r.shape[0]))))
```

```
    return result

R_1 = composition_RoS(uni_test.universal, R_o)
print(f'The R1 is {R_1.shape} matrix')

disease_test = np.argmax(R_1, axis=1).reshape((-1, 1))
print(f'The disease_test is {disease_test.shape} matrix')

disease_test_accuracy = evaluate(uni_test.label, disease_test, 'precision')
print('Our precision on disease_test from R1 is ',
        f'{round(disease_test_accuracy*100, 2)}%')
```

```
The R1 is (123, 5) matrix
The disease_test is (123, 1) matrix
Our precision on disease_test from R1 is  89.43%
```

R_c

Confirmability relation: the discriminating power of the symptom to confirm the presence of the disease - "How strongly does symptoms confirm disease d?"

Thanks for your time