National Institute of Technology Raipur

Practical Lab File

Artificial Intelligence and Data Mining and Warehousing

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(6th Semester Computer Science & Engineering)

CONTENTS

Experiment-1

- **Aim:**

  Perform an experiment on data cleaning.

- **Description:**

  Data cleaning is one of the important processes involved in data analysis, with it being the first step after data collection. It is a very important step in ensuring that the dataset is free of inaccurate or corrupt information. Data cleaning is the process of modifying data to ensure that it is free of irrelevances and incorrect information. Also known as data cleansing, it entails identifying incorrect, irrelevant, incomplete, and the "dirty" parts of a dataset and then replacing or cleaning the dirty parts of the data. Data cleansing is very important to companies, as lack of it may reduce marketing effectiveness, thereby reducing sales. Although the issues with the data may not be completely solved, reducing it to a minimum will have a significant effect on efficiency.

  Some methods to clean data –

  1. You can ignore the tuple. This is done when the class label is missing. This method is not very effective unless the tuple contains several attributes with missing values.
  2. You can fill in the missing value manually. This approach is effective on small data sets with some missing values.
  3. You can replace all missing attribute values with global constants, such as a label like "Unknown" or minus infinity.
  4. You can use the attribute mean to fill in the missing value. For example, customer's average income is 25000 then you can use this value to replace the missing value for income.
  5. Use the most probable value to fill in the missing value.

- **Program:** Language - Python

  1)
  ```
  import pandas as pd

  df=pd.read_csv('missing.csv')

  print(df)
  ```
  2)
  ```
  new_df=df.fillna(method='backfill')
  ```

```
print(new_df)
```

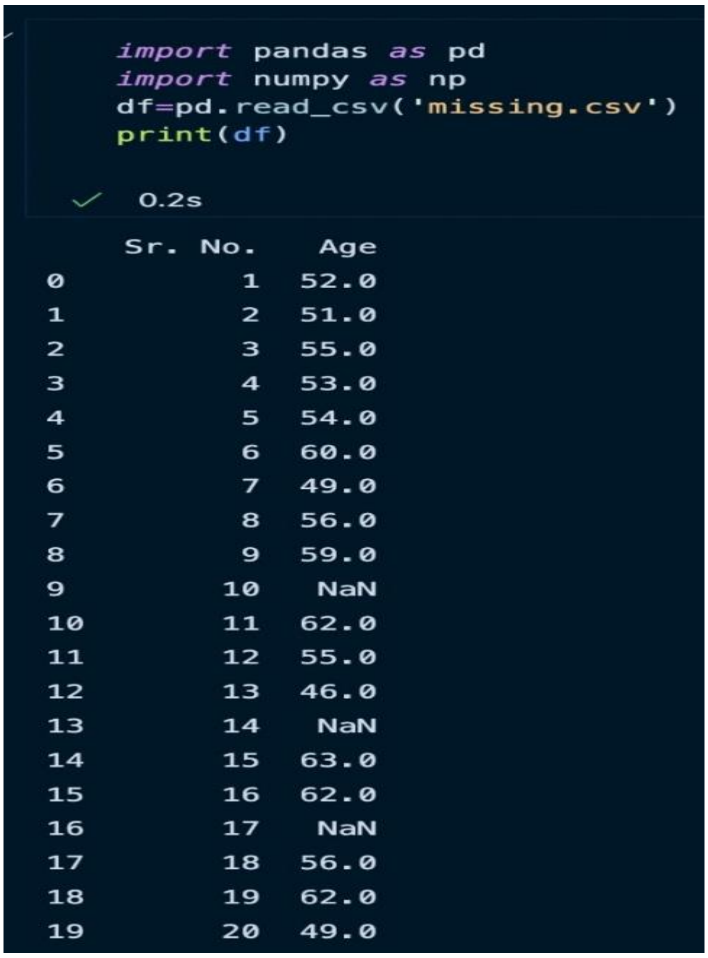
3)
```
df=pd.read_csv('missing.csv')
print(df)
new_df=df.fillna(0)
print(new_df)
```

4)
```
help(df.fillna)
```

5)
```
df=pd.read_csv('missing.csv')
print(df)
new_df=df.fillna(method='backfill')
print(new_df)
```

- **Output:**

1)

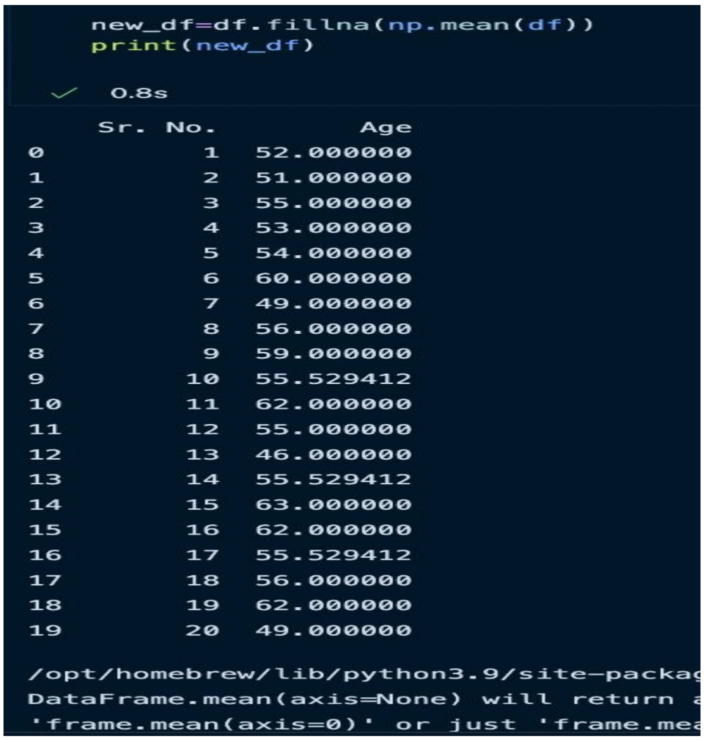


```
import pandas as pd
import numpy as np
df=pd.read_csv('missing.csv')
print(df)
```

```
✓ 0.2s
```

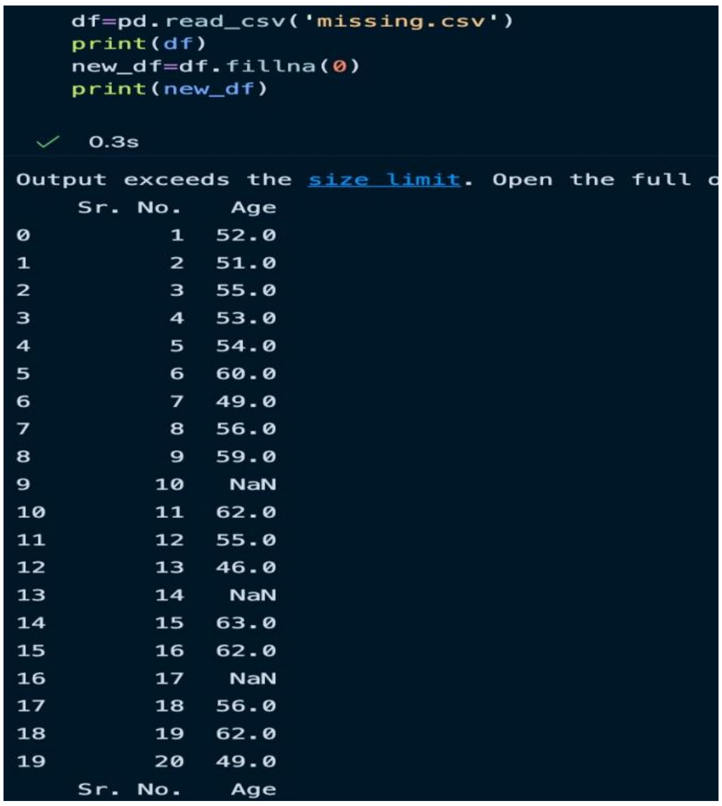
```
    Sr. No.   Age
0         1  52.0
1         2  51.0
2         3  55.0
3         4  53.0
4         5  54.0
5         6  60.0
6         7  49.0
7         8  56.0
8         9  59.0
9        10   NaN
10       11  62.0
11       12  55.0
12       13  46.0
13       14   NaN
14       15  63.0
15       16  62.0
16       17   NaN
17       18  56.0
18       19  62.0
19       20  49.0
```

2)



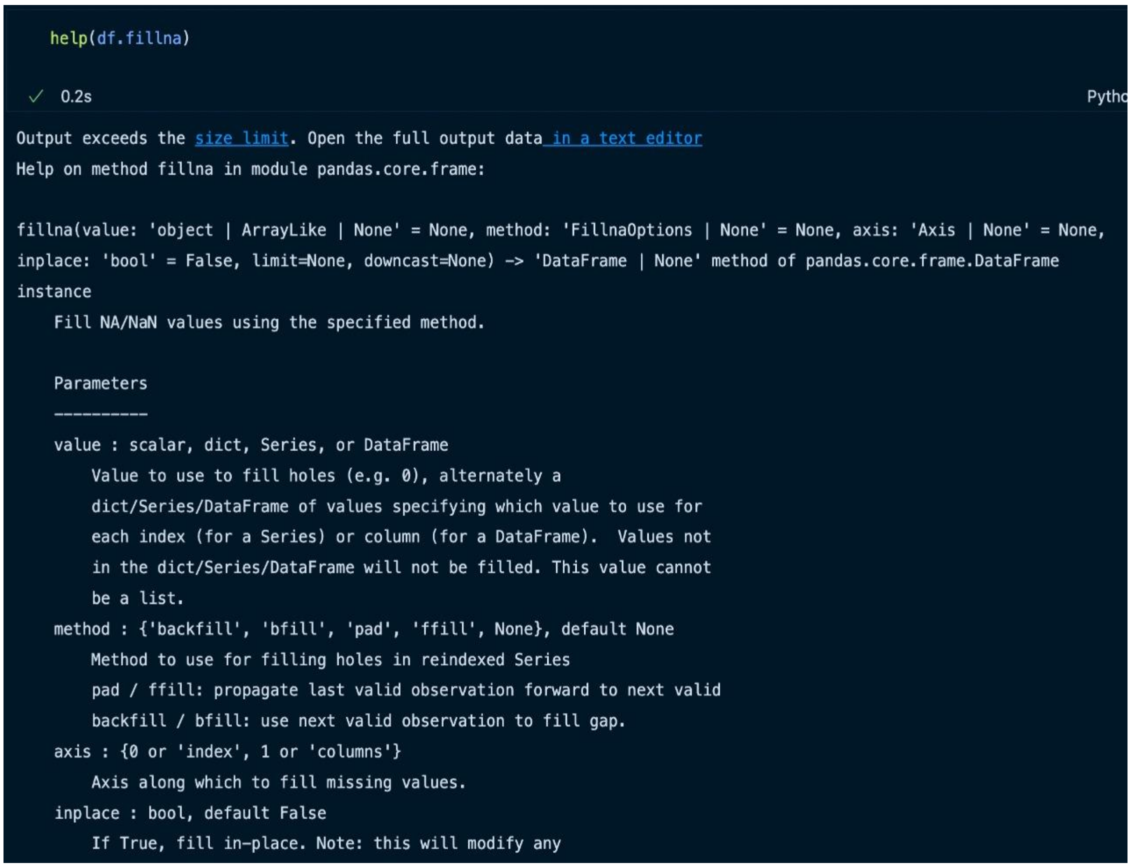
```
    new_df=df.fillna(np.mean(df))
    print(new_df)

  ✓  0.8s

    Sr. No.        Age
0         1  52.000000
1         2  51.000000
2         3  55.000000
3         4  53.000000
4         5  54.000000
5         6  60.000000
6         7  49.000000
7         8  56.000000
8         9  59.000000
9        10  55.529412
10       11  62.000000
11       12  55.000000
12       13  46.000000
13       14  55.529412
14       15  63.000000
15       16  62.000000
16       17  55.529412
17       18  56.000000
18       19  62.000000
19       20  49.000000

/opt/homebrew/lib/python3.9/site-packag
DataFrame.mean(axis=None) will return a
'frame.mean(axis=0)' or just 'frame.mea
```

3)



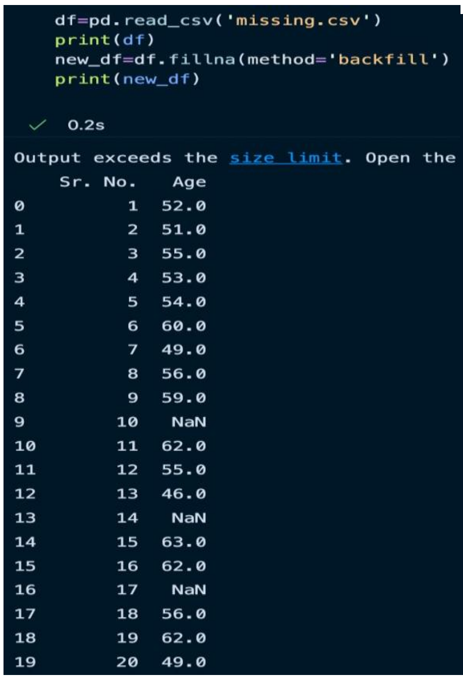
```
    df=pd.read_csv('missing.csv')
    print(df)
    new_df=df.fillna(0)
    print(new_df)

  ✓  0.3s

Output exceeds the size limit. Open the full c
    Sr. No.   Age
0         1  52.0
1         2  51.0
2         3  55.0
3         4  53.0
4         5  54.0
5         6  60.0
6         7  49.0
7         8  56.0
8         9  59.0
9        10   NaN
10       11  62.0
11       12  55.0
12       13  46.0
13       14   NaN
14       15  63.0
15       16  62.0
16       17   NaN
17       18  56.0
18       19  62.0
19       20  49.0
    Sr. No.   Age
```

4)

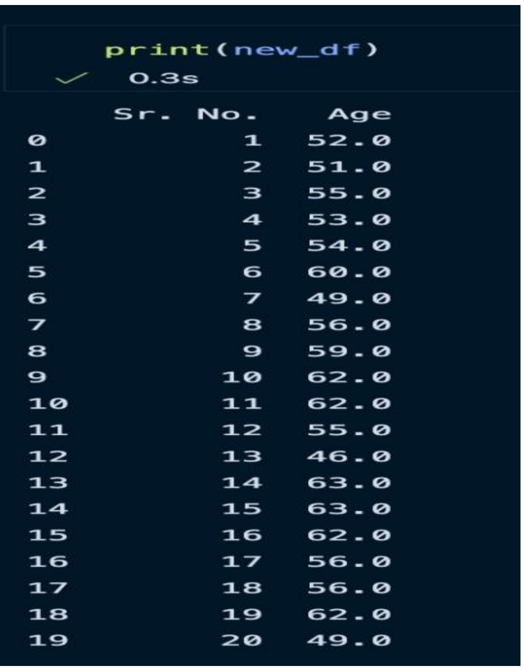


```
help(df.fillna)

✓ 0.2s                                                                              Pytho

Output exceeds the size limit. Open the full output data in a text editor
Help on method fillna in module pandas.core.frame:

fillna(value: 'object | ArrayLike | None' = None, method: 'FillnaOptions | None' = None, axis: 'Axis | None' = None,
inplace: 'bool' = False, limit=None, downcast=None) -> 'DataFrame | None' method of pandas.core.frame.DataFrame
instance
    Fill NA/NaN values using the specified method.

    Parameters
    ----------
    value : scalar, dict, Series, or DataFrame
        Value to use to fill holes (e.g. 0), alternately a
        dict/Series/DataFrame of values specifying which value to use for
        each index (for a Series) or column (for a DataFrame).  Values not
        in the dict/Series/DataFrame will not be filled. This value cannot
        be a list.
    method : {'backfill', 'bfill', 'pad', 'ffill', None}, default None
        Method to use for filling holes in reindexed Series
        pad / ffill: propagate last valid observation forward to next valid
        backfill / bfill: use next valid observation to fill gap.
    axis : {0 or 'index', 1 or 'columns'}
        Axis along which to fill missing values.
    inplace : bool, default False
        If True, fill in-place. Note: this will modify any
```

5)



```
    df=pd.read_csv('missing.csv')
    print(df)
    new_df=df.fillna(method='backfill')
    print(new_df)

✓ 0.2s

Output exceeds the size limit. Open the
    Sr. No.   Age
0         1  52.0
1         2  51.0
2         3  55.0
3         4  53.0
4         5  54.0
5         6  60.0
6         7  49.0
7         8  56.0
8         9  59.0
9        10   NaN
10       11  62.0
11       12  55.0
12       13  46.0
13       14   NaN
14       15  63.0
15       16  62.0
16       17   NaN
17       18  56.0
18       19  62.0
19       20  49.0
```



```
    print(new_df)
✓   0.3s
    Sr. No.   Age
0         1  52.0
1         2  51.0
2         3  55.0
3         4  53.0
4         5  54.0
5         6  60.0
6         7  49.0
7         8  56.0
8         9  59.0
9        10  62.0
10       11  62.0
11       12  55.0
12       13  46.0
13       14  63.0
14       15  63.0
15       16  62.0
16       17  56.0
17       18  56.0
18       19  62.0
19       20  49.0
```

Experiment-2

- **Aim:**

Perform an experiment on binning equal width and binning equal depth.

- **Description:**

Data binning, bucketing is a data pre-processing method used to minimize the effects of small observation errors. The original data values are divided into small intervals known as bins and then they are replaced by a general value calculated for that bin. This has a smoothing effect on the input data and may also reduce the chances of overfitting in the case of small datasets

There are 2 methods of dividing data into bins:

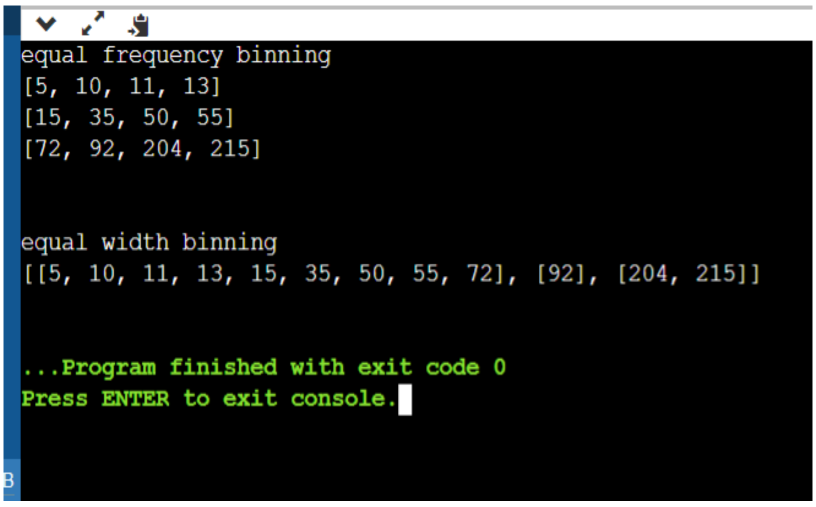
1. Equal Frequency Binning: bins have an equal frequency.
2. Equal Width Binning : bins have equal width with a range of each bin are defined as [min + w], [min + 2w] …. [min + nw] where w = (max – min) / (no of bins).

- **Program:** Language - Python

```
# equal frequency
def equifreq(arr1, m):
        a = len(arr1)
        n = int(a / m)
        for i in range(0, m):
                arr = []
                for j in range(i * n, (i + 1) * n):
                        if j >= a:
                                break
                        arr = arr + [arr1[j]]
                print(arr)
# equal width
def equiwidth(arr1, m):
        a = len(arr1)
        w = int((max(arr1) - min(arr1)) / m)
        min1 = min(arr1)
        arr = []
        for i in range(0, m + 1):
                arr = arr + [min1 + w * i]
```

```
    arri=[]

    for i in range(0, m):
        temp = []
        for j in arr1:
            if j >= arr[i] and j <= arr[i+1]:
                temp += [j]
        arri += [temp]
    print(arri)
# data to be binned
data = [5, 10, 11, 13, 15, 35, 50, 55, 72, 92, 204, 215]
# no of bins
m = 3
print("equal frequency binning")
equifreq(data, m)
print("\n\nequal width binning")
equiwidth(data, 3)
```

- **Output:**



```
equal frequency binning
[5, 10, 11, 13]
[15, 35, 50, 55]
[72, 92, 204, 215]


equal width binning
[[5, 10, 11, 13, 15, 35, 50, 55, 72], [92], [204, 215]]


...Program finished with exit code 0
Press ENTER to exit console.
```

Experiment-3

- **Aim :**

  Perform an experiment on normalization.

- **Description:**

  Normalization is used to scale the data of an attribute so that it falls in a smaller range, such as -1.0 to 1.0 or 0.0 to 1.0. It is generally useful for classification algorithms.

  Following normalization techniques are used:

  1. **Min-Max Normalization** - The min-max approach (often called normalization) rescales the feature to a hard and fast range of [0,1] by subtracting the minimum value of the feature and then dividing by the range. We can apply the min-max scaling in Pandas using the .min() and .max() methods.

  2. **z-Score Normalization.** - The z-score method (often called standardization) transforms the info into distribution with a mean of 0 and a typical deviation of 1. Each standardized value is computed by subtracting the mean of the corresponding feature and then dividing by the quality deviation.

- **Program:**

1)
```
from sklearn import preprocessing

import numpy as np

a = np..random.random((1,4))

a =  a * 20

print(“ Data = ”, a)

normalized = preprocessing.normalize(a)

print(“Normalized Data = ”, normalized)
```

2)
```
df  = pd.DataFrame( [180000, 110, 18.9, 1400],

          [36000, 905, 23.4, 1800],

          [230000,230,14.0,1300],

          [6000,450,135, 1500],
```

Columns = [‘Col A’, ‘Col B’, ‘Col C’, ‘Col D’])

display(df)

df_scale = df.copy

for column in df_scale.columns :

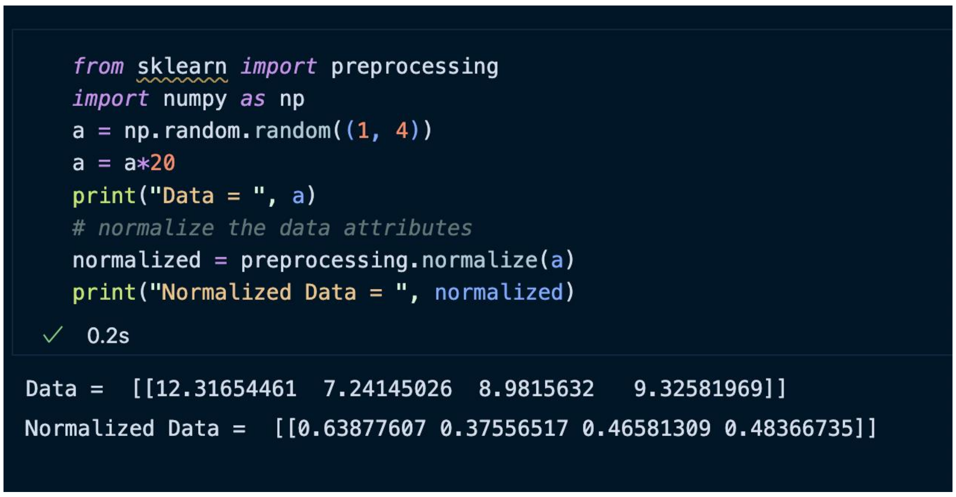
df_scale[column] = (df_scale[column] - df_scale[column].min()) /

df_scale[column]

print(df_scale)

- **Output:**

1)

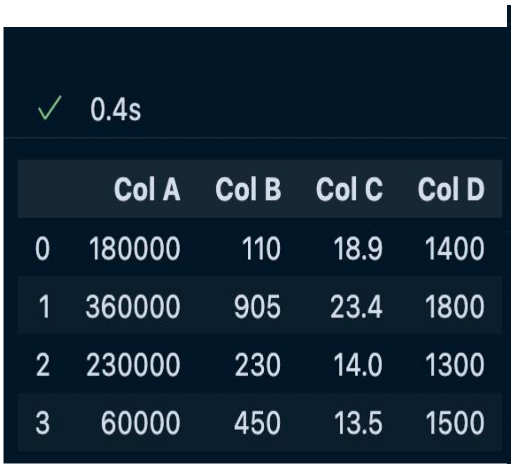


```
from sklearn import preprocessing
import numpy as np
a = np.random.random((1, 4))
a = a*20
print("Data = ", a)
# normalize the data attributes
normalized = preprocessing.normalize(a)
print("Normalized Data = ", normalized)
```

✓ 0.2s

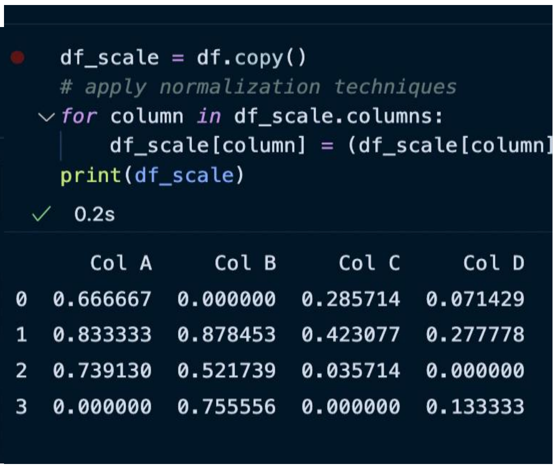
```
Data =  [[12.31654461  7.24145026  8.9815632   9.32581969]]
Normalized Data =  [[0.63877607 0.37556517 0.46581309 0.48366735]]
```

2)



✓ 0.4s

	Col A	Col B	Col C	Col D
0	180000	110	18.9	1400
1	360000	905	23.4	1800
2	230000	230	14.0	1300
3	60000	450	13.5	1500



```
df_scale = df.copy()
# apply normalization techniques
for column in df_scale.columns:
    df_scale[column] = (df_scale[column]
print(df_scale)
```

✓ 0.2s

```
      Col A     Col B     Col C     Col D
0  0.666667  0.000000  0.285714  0.071429
1  0.833333  0.878453  0.423077  0.277778
2  0.739130  0.521739  0.035714  0.000000
3  0.000000  0.755556  0.000000  0.133333
```

Experiment-4

- **Aim:**

Perform an experiment on data pre-processing.

- **Description:**

Pre-processing refers to the transformations applied to our data before feeding it to the algorithm. Data Preprocessing is a technique that is used to convert the raw data into a clean data set. In other words, whenever the data is gathered from different sources it is collected in raw format which is not feasible for the analysis.

Following normalization techniques are used:

1. **Rescale Data** - When our data is comprised of attributes with varying scales, many machine learning algorithms can benefit from rescaling the attributes to all have the same scale.

2. **Binarize Data (Make Binary)** - We can transform our data using a binary threshold. All values above the threshold are marked 1 and all equal to or below are marked as 0.

3. **Standardize Data** - Standardization is a useful technique to transform attributes with a Gaussian distribution and differing means and standard deviations to a standard Gaussian distribution with a mean of 0 and a standard deviation of 1.

- **Program:**

1) **Python code to Rescale data (between 0 and 1)**

```
# importing libraries

import pandas

import scipy

import numpy

from sklearn.preprocessing import MinMaxScaler

# data set link

url =
"https://archive.ics.uci.edu/ml/machine-learning-
databases/pima-indians-diabetes/pima

-indians-diabetes.data"

# data parameters

names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age',
'class']

# preparating of dataframe using the data at given link and
defined columns list

dataframe = pandas.read_csv(url, names = names)

array = dataframe.values

# separate array into input and output components

X = array[:,0:8]

Y = array[:,8]

# initialising the MinMaxScaler

scaler = MinMaxScaler(feature_range=(0, 1))

# learning the statistical parameters for each of the data and
transforming

rescaledX = scaler.fit_transform(X)

# summarize transformed data

numpy.set_printoptions(precision=3)

print(rescaledX[0:5,:])
```

2) **Python code for binarization**

```
# import libraries

from sklearn.preprocessing import Binarizer

import pandas
import numpy

# data set link

url = "https://archive.ics.uci.edu/ml/machine-learning-databases/pima-indians-diabetes/pima-indians-diabetes.data"

# data parameters

names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age', 'class']

# preparating of dataframe using the data at given link and defined columns list

dataframe = pandas.read_csv(url, names = names)

array = dataframe.values

# separate array into input and output components

X = array[:, 0:8]

Y = array[:, 8]

binarizer = Binarizer(threshold = 0.0).fit(X)

binaryX = binarizer.transform(X)

# summarize transformed data

numpy.set_printoptions(precision = 3)

print(binaryX[0:5,:])
```

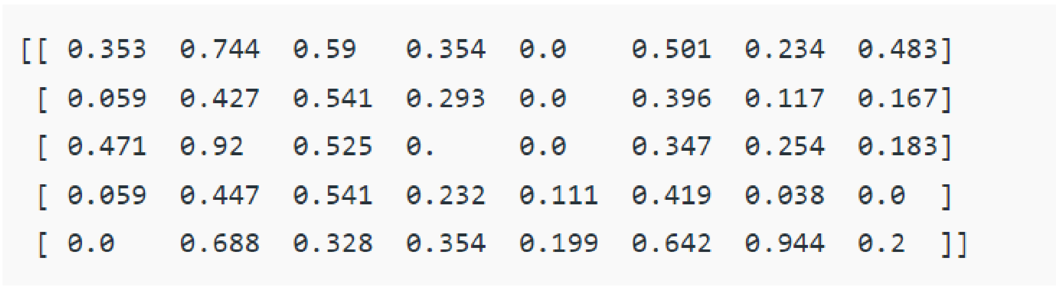
3) **Python code to Standardize data (0 mean, 1 stdev)**

```
# importing libraries

from sklearn.preprocessing import StandardScaler

import pandas

import numpy
```

```
# data set link
Url =
"https://archive.ics.uci.edu/ml/machine-learning-databases/pima-indians-dia
betes/pima-indians-diabetes.data"
# data parameters
names = ['preg', 'plas', 'pres', 'skin', 'test', 'mass', 'pedi', 'age',
'class']
# preparating of dataframe using the data at given link and defined columns list
dataframe = pandas.read_csv(url, names = names)
array = dataframe.values
# separate array into input and output components
X = array[:, 0:8]
Y = array[:, 8]
scaler = StandardScaler().fit(X)
rescaledX = scaler.transform(X)
# summarize transformed data
numpy.set_printoptions(precision = 3)
print(rescaledX[0:5,:])
```

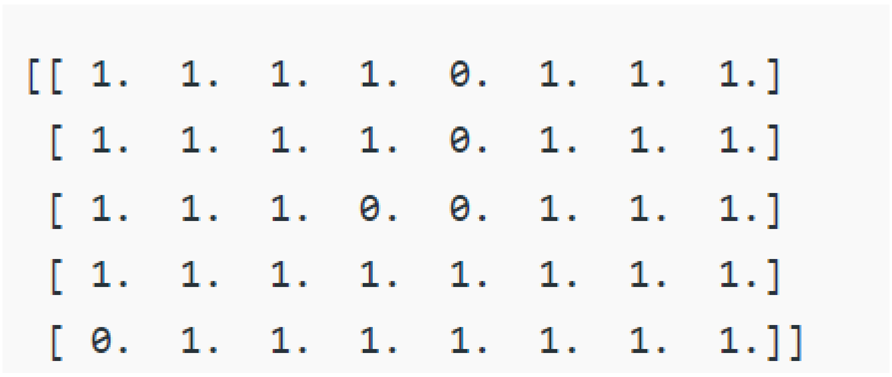
- **Output:**

1)



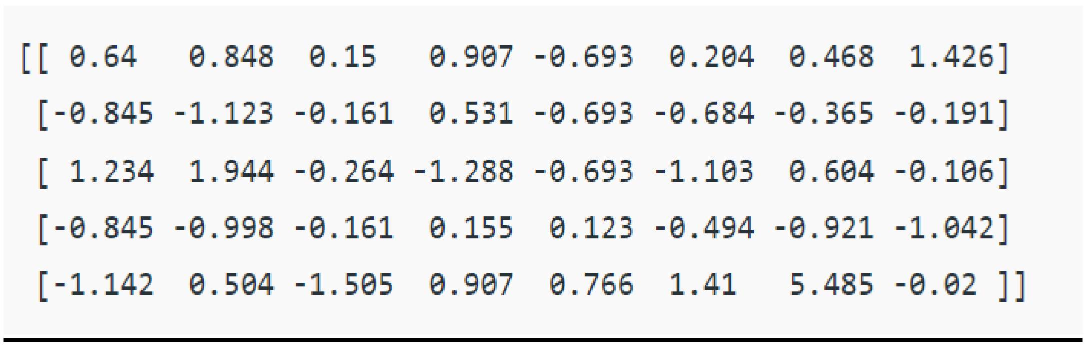
```
[[ 0.353  0.744  0.59   0.354  0.0    0.501  0.234  0.483]
 [ 0.059  0.427  0.541  0.293  0.0    0.396  0.117  0.167]
 [ 0.471  0.92   0.525  0.     0.0    0.347  0.254  0.183]
 [ 0.059  0.447  0.541  0.232  0.111  0.419  0.038  0.0  ]
 [ 0.0    0.688  0.328  0.354  0.199  0.642  0.944  0.2  ]]
```

2)



```
[[ 1.  1.  1.  1.  0.  1.  1.  1.]
 [ 1.  1.  1.  1.  0.  1.  1.  1.]
 [ 1.  1.  1.  0.  0.  1.  1.  1.]
 [ 1.  1.  1.  1.  1.  1.  1.  1.]
 [ 0.  1.  1.  1.  1.  1.  1.  1.]]
```

3)



```
[[ 0.64   0.848  0.15   0.907 -0.693  0.204  0.468  1.426]
 [-0.845 -1.123 -0.161  0.531 -0.693 -0.684 -0.365 -0.191]
 [ 1.234  1.944 -0.264 -1.288 -0.693 -1.103  0.604 -0.106]
 [-0.845 -0.998 -0.161  0.155  0.123 -0.494 -0.921 -1.042]
 [-1.142  0.504 -1.505  0.907  0.766  1.41   5.485 -0.02 ]]
```

Experiment-5

- ## Aim:

  Write a program to perform decision tree classification.

- ## Description:

  A **decision tree** is one of the most powerful and popular algorithms. Decision-tree algorithm falls under the category of supervised learning algorithms. It works for both continuous as well as categorical output variables.

  Data-set Description :

  Title : Balance Scale Weight & Distance Database

  Number of Instances : 625 (49 balanced, 288 left, 288 right)

  Number of Attributes : 4 (numeric) + class name = 5

  Attribute Information:

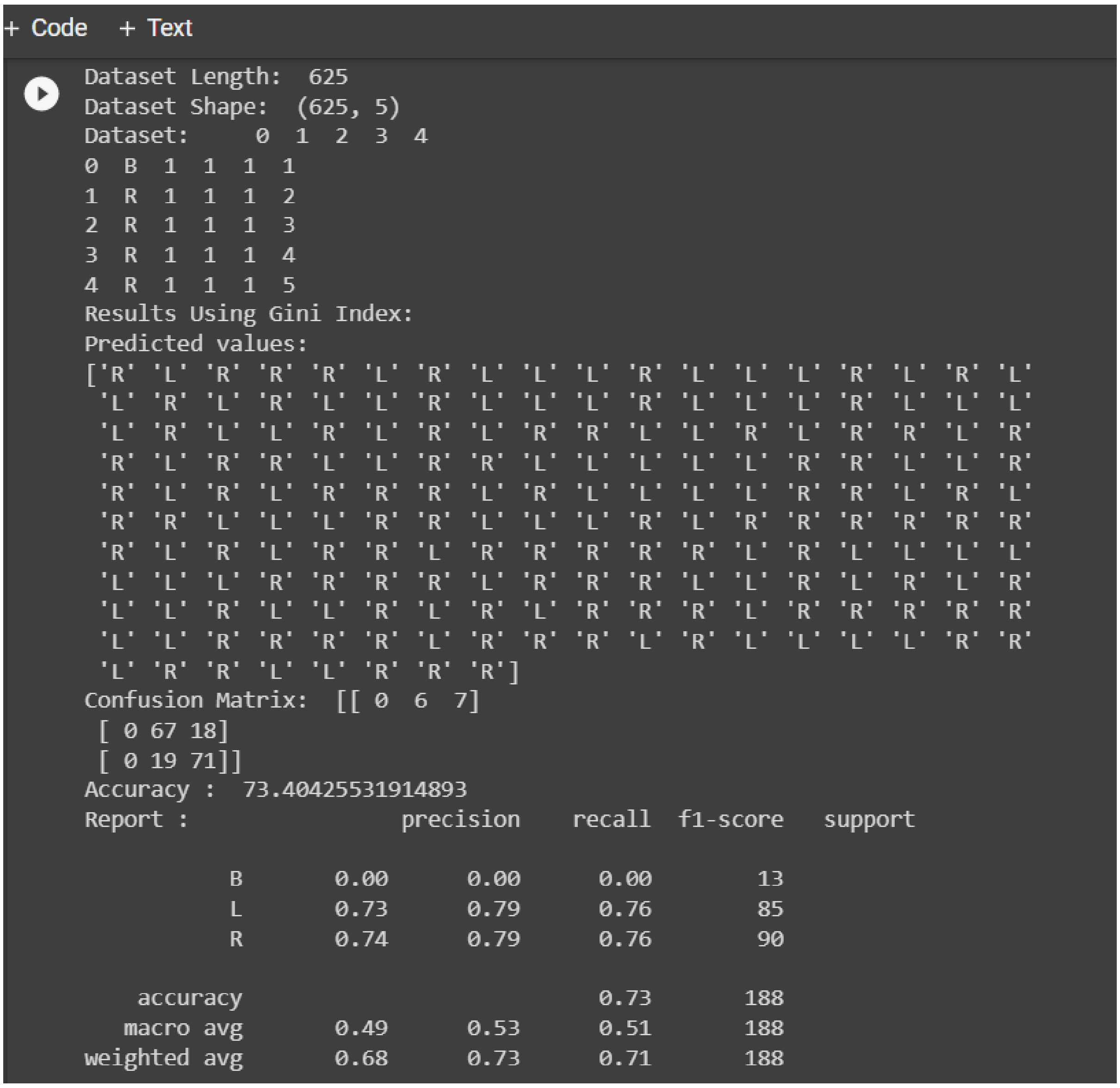
  1. **Class Name (Target variable)**:
     - L [balance scale tip to the left]
     - B [balance scale be balanced]
     - R [balance scale tip to the right]
  2. **Left-Weight**: 5 (1, 2, 3, 4, 5)
  3. **Left-Distance**: 5 (1, 2, 3, 4, 5)
  4. **Right-Weight**: 5 (1, 2, 3, 4, 5)
  5. **Right-Distance**: 5 (1, 2, 3, 4, 5)
  6. **Missing Attribute Values**: None
  7. **Class Distribution:**
     - 46.08 percent are L
     - 07.84 percent are B
     - 46.08 percent are R

- **Program:**

```
!python get.pip.py

!pip install -U scikit-learn

import numpy as np

import pandas as pd

from sklearn.metrics import confusion_matrix

from sklearn.model_selection import train_test_split

from sklearn.tree import DecisionTreeClassifier

from sklearn.metrics import accuracy_score

from sklearn.metrics import classification_report



def importdata():

        balance_data = pd.read_csv(

'https://archive.ics.uci.edu/ml/machine-learning-'+

'databases/balance-scale/balance-scale.data',

        sep= ',', header = None)

        print ("Dataset Length: ", len(balance_data))

        print ("Dataset Shape: ", balance_data.shape)

        print ("Dataset: ",balance_data.head())

        return balance_data



def splitdataset(balance_data):

        X = balance_data.values[:, 1:5]

        Y = balance_data.values[:, 0]
```

```
    X_train, X_test, y_train, y_test = train_test_split(
    X, Y, test_size = 0.3, random_state = 100)
    return X, Y, X_train, X_test, y_train, y_test

def train_using_gini(X_train, X_test, y_train):
    clf_gini = DecisionTreeClassifier(criterion = "gini",
            random_state = 100,max_depth=3, min_samples_leaf=5)
    clf_gini.fit(X_train, y_train)
    return clf_gini

def tarin_using_entropy(X_train, X_test, y_train):
    clf_entropy = DecisionTreeClassifier(
            criterion = "entropy", random_state = 100,
            max_depth = 3, min_samples_leaf = 5)
    clf_entropy.fit(X_train, y_train)
    return clf_entropy



def prediction(X_test, clf_object):
    y_pred = clf_object.predict(X_test)
    print("Predicted values:")
    print(y_pred)
    return y_pred

def cal_accuracy(y_test, y_pred):
    print("Confusion Matrix: ",
            confusion_matrix(y_test, y_pred))
    print ("Accuracy : ",
    accuracy_score(y_test,y_pred)*100)
    print("Report : ",
    classification_report(y_test, y_pred))



def main():
    data = importdata()
    X, Y, X_train, X_test, y_train, y_test = splitdataset(data)
    clf_gini = train_using_gini(X_train, X_test, y_train)
    clf_entropy = tarin_using_entropy(X_train, X_test, y_train)

    print("Results Using Gini Index:")
    y_pred_gini = prediction(X_test, clf_gini)
    cal_accuracy(y_test, y_pred_gini)

    print("Results Using Entropy:")
    y_pred_entropy = prediction(X_test, clf_entropy)
    cal_accuracy(y_test, y_pred_entropy)

if __name__=="__main__":
    main()
```

- **Output:**



```
Dataset Length:  625
Dataset Shape:  (625, 5)
Dataset:     0  1  2  3  4
0  B  1  1  1  1
1  R  1  1  1  2
2  R  1  1  1  3
3  R  1  1  1  4
4  R  1  1  1  5
Results Using Gini Index:
Predicted values:
['R' 'L' 'R' 'R' 'R' 'L' 'R' 'L' 'L' 'L' 'R' 'L' 'L' 'L' 'R' 'L' 'R' 'L'
 'L' 'R' 'L' 'R' 'L' 'L' 'R' 'L' 'L' 'L' 'R' 'L' 'L' 'L' 'R' 'L' 'L' 'L'
 'L' 'R' 'L' 'L' 'R' 'L' 'R' 'L' 'R' 'R' 'L' 'L' 'R' 'L' 'R' 'R' 'L' 'R'
 'R' 'L' 'R' 'R' 'L' 'L' 'R' 'R' 'L' 'L' 'L' 'L' 'L' 'R' 'R' 'L' 'L' 'R'
 'R' 'L' 'R' 'L' 'R' 'R' 'R' 'L' 'R' 'L' 'L' 'L' 'L' 'R' 'R' 'L' 'R' 'L'
 'R' 'R' 'L' 'L' 'L' 'R' 'R' 'L' 'L' 'L' 'R' 'L' 'R' 'R' 'R' 'R' 'R' 'R'
 'R' 'L' 'R' 'L' 'R' 'R' 'L' 'R' 'R' 'R' 'R' 'R' 'L' 'R' 'L' 'L' 'L' 'L'
 'L' 'L' 'L' 'R' 'R' 'R' 'R' 'L' 'R' 'R' 'R' 'L' 'L' 'R' 'L' 'R' 'L' 'R'
 'L' 'L' 'R' 'L' 'L' 'R' 'L' 'R' 'L' 'R' 'R' 'R' 'L' 'R' 'R' 'R' 'R' 'R'
 'L' 'L' 'R' 'R' 'R' 'R' 'L' 'R' 'R' 'R' 'L' 'R' 'L' 'L' 'L' 'L' 'R' 'R'
 'L' 'R' 'R' 'L' 'L' 'R' 'R' 'R']
Confusion Matrix:  [[ 0  6  7]
 [ 0 67 18]
 [ 0 19 71]]
Accuracy :  73.40425531914893
Report :                precision    recall  f1-score   support

           B       0.00      0.00      0.00        13
           L       0.73      0.79      0.76        85
           R       0.74      0.79      0.76        90

    accuracy                           0.73       188
   macro avg       0.49      0.53      0.51       188
weighted avg       0.68      0.73      0.71       188
```

Experiment-6

- ## Aim:

  Write a program to perform Support Vector Machine Classification.

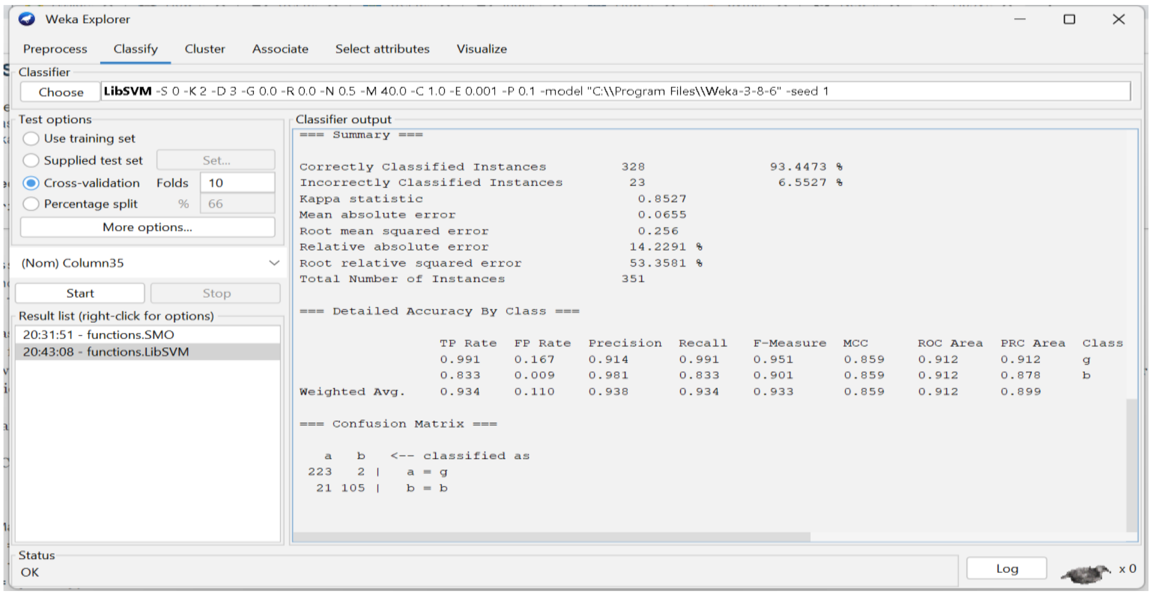
- ## Description:

  The goal of the SVM algorithm is to create the best line or decision boundary that can segregate n-dimensional space into classes so that we can easily put the new data point in the correct category in the future. This best decision boundary is called a hyperplane. SVM chooses the extreme points/vectors that help in creating the hyperplane. These extreme cases are called support vectors, and hence algorithm is termed as Support Vector Machine.

- ## Program:

  1. Open the Weka GUI Chooser.
  2. Click the “Explorer” button to open the Weka Explorer.
  3. Load the dataset from the downloads/ionosphere.csv file.
  4. Click “Classify” to open the Classify tab.
  5. Select functions and select the LibSVM classifier for implementing SVM.

- ## Output:



Classifier: **LibSVM** -S 0 -K 2 -D 3 -G 0.0 -R 0.0 -N 0.5 -M 40.0 -C 1.0 -E 0.001 -P 0.1 -model "C:\\Program Files\\Weka-3-8-6" -seed 1

Test options: Use training set; Supplied test set; [✓ Cross-validation] Folds 10; Percentage split % 66

(Nom) Column35

Result list (right-click for options):
20:31:51 - functions.SMO
20:43:08 - functions.LibSVM

Status: OK

Classifier output

```
=== Summary ===

Correctly Classified Instances         328               93.4473 %
Incorrectly Classified Instances        23                6.5527 %
Kappa statistic                          0.8527
Mean absolute error                      0.0655
Root mean squared error                  0.256
Relative absolute error                 14.2291 %
Root relative squared error             53.3581 %
Total Number of Instances              351

=== Detailed Accuracy By Class ===

                 TP Rate  FP Rate  Precision  Recall   F-Measure  MCC      ROC Area  PRC Area  Class
                 0.991    0.167    0.914      0.991    0.951      0.859    0.912     0.912     g
                 0.833    0.009    0.981      0.833    0.901      0.859    0.912     0.878     b
Weighted Avg.    0.934    0.110    0.938      0.934    0.933      0.859    0.912     0.899

=== Confusion Matrix ===

   a   b   <-- classified as
 223   2 |   a = g
  21 105 |   b = b
```

Experiment-7

- **Aim:**

  Write a program to perform K-means Clustering.

- **Description:**

  This experiment illustrates the use of simple k-mean clustering with Jupyter Notebook. The sample data set used for this example is based on the iris data available in ARFF format. This document assumes that appropriate pre-processing has been performed. This iris dataset includes 150 instances.

- **Program:**

1)
```
from sklearn.cluster import KMeans

import pandas as pd

from sklearn.preprocessing import MinMaxScaler

from matplotlib import pyplot as plt

from sklearn.datasets import load_iris

%matplotlib inline

iris = load_iris()

df = pd.DataFrame(iris.data, columns = iris.feature_names)

df.head()
```

2)
```
df['flower'] = iris.target

df.head()
```

3)
```
df.drop(['sepal length (cm)', 'sepal width (cm)','flower'],axis = 'columns' , inplace = True)

df.head(3)
```

4)
```
km = KMeans(n_clusters=3)

yp = km.fit_predict(df)

yp
```

5)
```
df['cluster'] = yp
```

df.head(2)

6) df['cluster'].unique()
7) df1 = df[df.cluster==0]

   df2 = df[df.cluster==1]

   df3 = df[df.cluster==2]

   plt.scatter(df1['petal length (cm).],df1['petal width (cm)],color= 'blue')

   plt.scatter(df1['petal length (cm).],df2['petal width (cm)],color= 'green')

   plt.scatter(df1['petal length (cm).],df3['petal width (cm)],color= 'yellow')

8) sse = []

   K_rng = range(1,10)

   for k in k_rng :

   km = KMeans(n_clusters = k)

   km.fit(df)

   sse.append(km.inertia_)

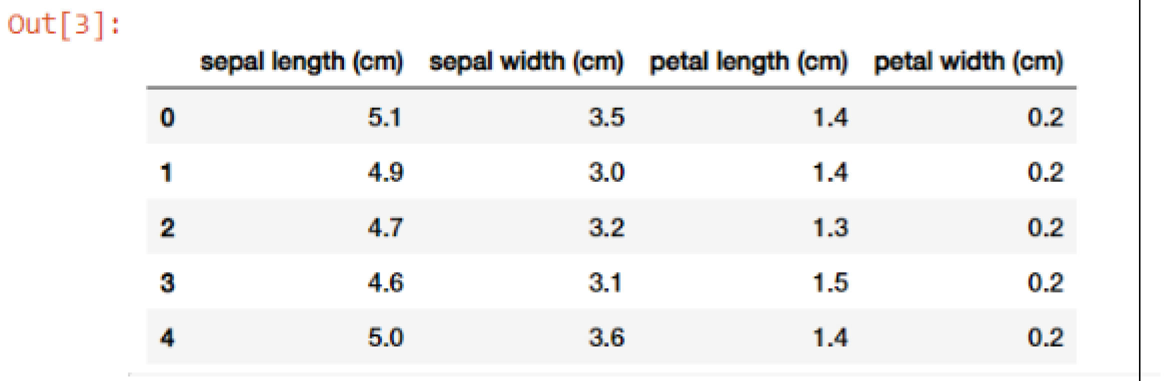
   plt.xlabel('K')

   plt.ylabel('Sum of squared error')

   plt.plot(k_rng,sse)

- **Output:**

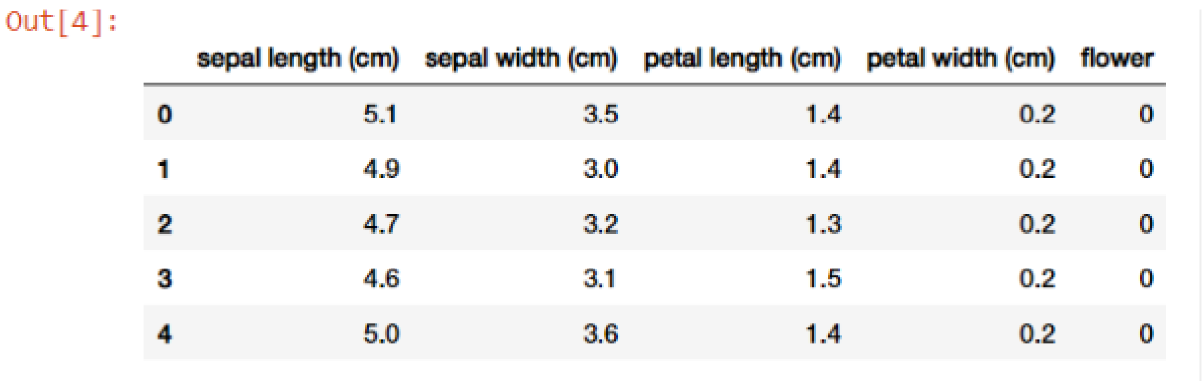
1)



Out[3]:

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)
0	5.1	3.5	1.4	0.2
1	4.9	3.0	1.4	0.2
2	4.7	3.2	1.3	0.2
3	4.6	3.1	1.5	0.2
4	5.0	3.6	1.4	0.2

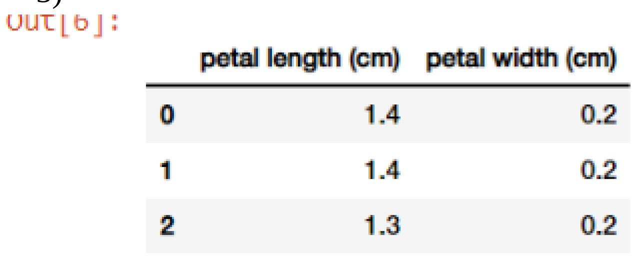
2)



Out[4]:

	sepal length (cm)	sepal width (cm)	petal length (cm)	petal width (cm)	flower
0	5.1	3.5	1.4	0.2	0
1	4.9	3.0	1.4	0.2	0
2	4.7	3.2	1.3	0.2	0
3	4.6	3.1	1.5	0.2	0
4	5.0	3.6	1.4	0.2	0

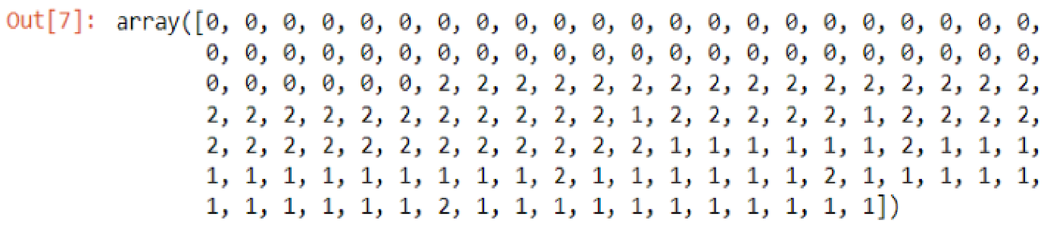
3)



Out[6]:

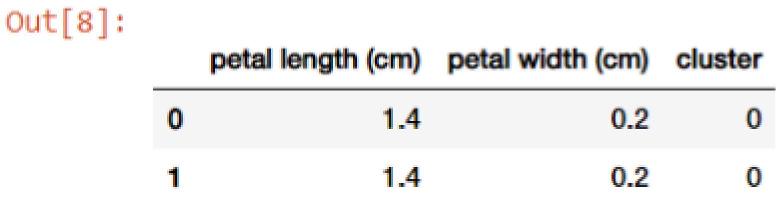
	petal length (cm)	petal width (cm)
0	1.4	0.2
1	1.4	0.2
2	1.3	0.2

4)



```
Out[7]: array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
               0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
               0, 0, 0, 0, 0, 0, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,
               2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2,
               2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1,
               1, 1, 1, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1,
               1, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1])
```

5)



Out[8]:

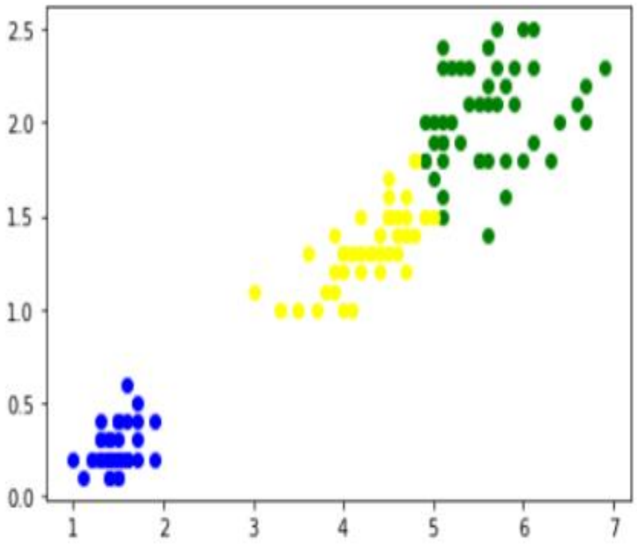
	petal length (cm)	petal width (cm)	cluster
0	1.4	0.2	0
1	1.4	0.2	0

6)

```
Out[9]: array([0, 2, 1])
```

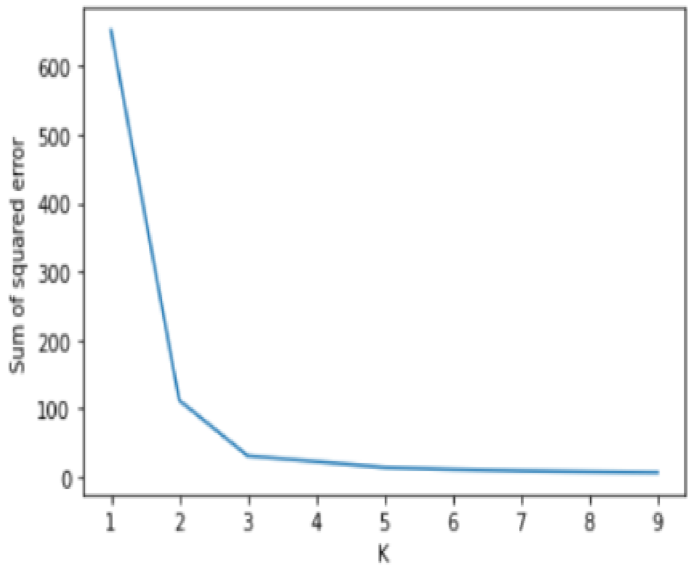
7)

```
Out[11]: <matplotlib.collections.PathCollection at 0x23b7bd5ef10>
```



8)

```
Out[13]: [<matplotlib.lines.Line2D at 0x23b7c2f8d00>]
```



Experiment-8

- **Aim :**

  Write a program to perform Fuzzy c-means Clustering.

- **Description :**

  Fuzzy C-Means clustering is a soft clustering approach, where each data point is assigned a likelihood or probability score to belong to that cluster. The step-wise approach of the Fuzzy c-means clustering algorithm is:

  - Fix the value of c (number of clusters), and select a value of m (generally 1.25<m<2), and initialize partition matrix U.

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

  - Calculate cluster centers (centroid).
    Here,

$$V_{ij} = (\sum_{1}^{n}(\gamma_{ik}^{m} * x_k) / \sum_{1}^{n} \gamma_{ik}^{m}$$

    μ: Fuzzy membership value

    m: fuzziness parameter

  - Update Partition Matrix
  - Repeat the above steps until convergence.

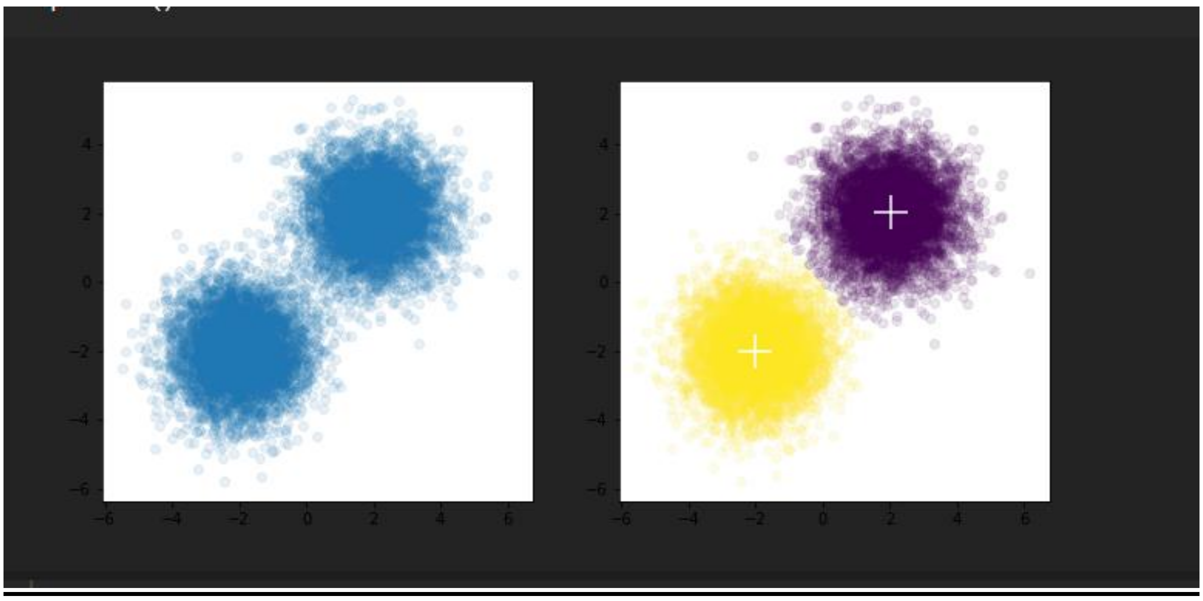
$$\gamma = \sum_{1}^{n} (d_{ki}^{2}/d_{kj}^{2})^{1/m-1}]^{-1}$$

- **Program :**

```
pip install fuzzy-c-means
```

```
import numpy as np

from fcmeans import FCM

from matplotlib import pyplot as plt

n_samples = 5000

X = np.concatenate((

np.random.normal((-2, -2), size=(n_samples, 2)),

np.random.normal((2, 2), size=(n_samples, 2))

))

fcm = FCM(n_clusters=2)

fcm.fit(X)

# outputs

fcm_centers = fcm.centers

fcm_labels = fcm.predict(X)

# plot result

f, axes = plt.subplots(1, 2, figsize=(11,5))

axes[0].scatter(X[:,0], X[:,1], alpha=.1)

axes[1].scatter(X[:,0], X[:,1], c=fcm_labels, alpha=.1)

axes[1].scatter(fcm_centers[:,0], fcm_centers[:,1], marker="+", s=500, c='w')

plt.show()
```

- **Output :**



Experiment-9

- **Aim :**

  Write a program to perform DBSCAN clustering.

- **Description :**

  Density Based Spatial Clustering of Applications with Noise(DBCSAN) is a clustering algorithm which was proposed in 1996. In 2014, the algorithm was awarded the ‘Test of Time’ award at the leading Data Mining conference, KDD.

  DBSCAN algorithm can be abstracted in the following steps :

  Find all the neighbor points within eps and identify the core points or visited with more than MinPts neighbors.

  - For each core point if it is not already assigned to a cluster, create a new cluster.
  - Find recursively all its density connected points and assign them to the same cluster as the core point.
  - A point a and b are said to be density connected if there exist a point c which has a sufficient number of points in its neighbors and both the points a and b are within the eps distance. This is a chaining process. So, if b is neighbor of c, c is neighbor of d, d is neighbor of e, which in turn is neighbor of a implies that b is neighbor of a.
  - Iterate through the remaining unvisited points in the dataset. Those points that do not belong to any cluster are noise.

  Link to Dataset Used: Credit Card Dataset

- **Program :**

```
# Step 1: Importing the required libraries

import numpy as np

import pandas as pd

import matplotlib.pyplot as plt
```

```
from sklearn.cluster import DBSCAN
from sklearn.preprocessing import StandardScaler
from sklearn.preprocessing import normalize
from sklearn.decomposition import PCA

# Step 2: Loading the data
# modify the input path as per your system path
X = pd.read_csv('..input_path/CC_GENERAL.csv')
# Dropping the CUST_ID column from the data
X = X.drop('CUST_ID', axis = 1)
# Handling the missing values
X.fillna(method ='ffill', inplace = True)

#Step 3: Preprocessing the data
# Scaling the data to bring all the attributes to a comparable level
scaler = StandardScaler()
X_scaled = scaler.fit_transform(X)
# Normalizing the data so that
# the data approximately follows a Gaussian distribution
X_normalized = normalize(X_scaled)
# Converting the numpy array into a pandas DataFrame
X_normalized = pd.DataFrame(X_normalized)

#Step 4: Reducing the dimensionality of the data to make it visualizable
pca = PCA(n_components = 2)
X_principal = pca.fit_transform(X_normalized)
X_principal = pd.DataFrame(X_principal)

X_principal.columns = ['P1', 'P2']


#Step 5: Building the clustering model

# Numpy array of all the cluster labels assigned to each data point

db_default = DBSCAN(eps = 0.0375, min_samples = 3).fit(X_principal)

labels = db_default.labels_


# Step 6: Visualizing the clustering

# Building the label to colour mapping

colours = {}

colours[0] = 'r'

colours[1] = 'g'

colours[2] = 'b'

colours[-1] = 'k'

# Building the colour vector for each data point

cvec = [colours[label] for label in labels]

# For the construction of the legend of the plot

r = plt.scatter(X_principal['P1'], X_principal['P2'], color ='r');

g = plt.scatter(X_principal['P1'], X_principal['P2'], color ='g');

b = plt.scatter(X_principal['P1'], X_principal['P2'], color ='b');

k = plt.scatter(X_principal['P1'], X_principal['P2'], color ='k');

# Plotting P1 on the X-Axis and P2 on the Y-Axis

# according to the colour vector defined

plt.figure(figsize =(9, 9))

plt.scatter(X_principal['P1'], X_principal['P2'], c = cvec)
```

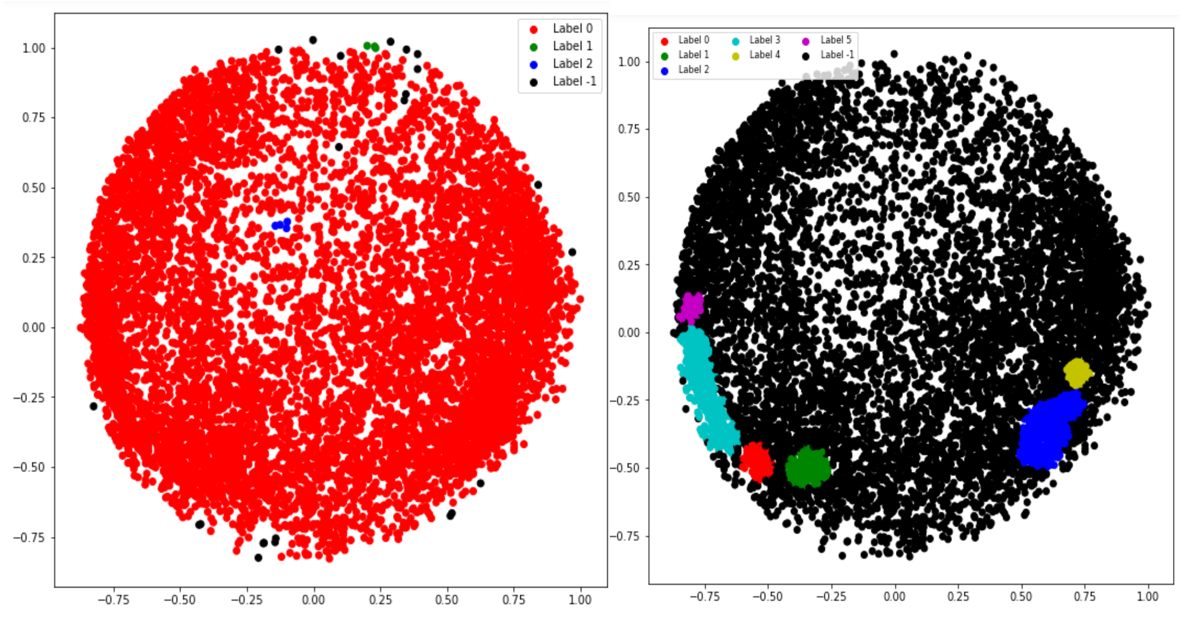
```
# Building the legend
plt.legend((r, g, b, k), ('Label 0', 'Label 1', 'Label 2', 'Label -1'))
plt.show()
```

Step 7: Tuning the parameters of the model

```
db = DBSCAN(eps = 0.0375, min_samples = 50).fit(X_principal)
labels1 = db.labels_
#Step 8: Visualizing the changes
colours1 = {}
colours1[0] = 'r'
colours1[1] = 'g'
colours1[2] = 'b'
colours1[3] = 'c'
colours1[4] = 'y'
colours1[5] = 'm'
colours1[-1] = 'k'
cvec = [colours1[label] for label in labels]
colors = ['r', 'g', 'b', 'c', 'y', 'm', 'k' ]
r = plt.scatter(
X_principal['P1'], X_principal['P2'], marker ='o', color = colors[0])
g = plt.scatter(
X_principal['P1'], X_principal['P2'], marker ='o', color = colors[1])
b = plt.scatter(
X_principal['P1'], X_principal['P2'], marker ='o', color = colors[2])
c = plt.scatter(
X_principal['P1'], X_principal['P2'], marker ='o', color = colors[3])
```

```
y = plt.scatter(
X_principal['P1'], X_principal['P2'], marker ='o', color = colors[4])
m = plt.scatter(
X_principal['P1'], X_principal['P2'], marker ='o', color = colors[5])
k = plt.scatter(
X_principal['P1'], X_principal['P2'], marker ='o', color = colors[6])
plt.figure(figsize =(9, 9))
plt.scatter(X_principal['P1'], X_principal['P2'], c = cvec)
plt.legend((r, g, b, c, y, m, k),
('Label 0', 'Label 1', 'Label 2', 'Label 3 'Label 4',
'Label 5', 'Label -1'),
scatterpoints = 1,
loc ='upper left',
ncol = 3,
fontsize = 8)
plt.show()
```

- **Output :**


Label 0
Label 1
Label 2
Label -1
Label 0
Label 1
Label 2
Label 3
Label 4
Label 5
Label -1

Experiment-10

- **Aim :**

Write a program for performing Linear Regression.

- **Description :**

Linear Regression is a machine learning algorithm based

on supervised learning. It performs a regression task. Regression models a

target prediction value based on independent variables.

Linear regression is one of the easiest and most popular Machine Learning algorithms. It is a statistical method that is used for predictive analysis. Linear regression makes predictions for continuous/real or numeric variables such as sales, salary, age, product price, etc.

Linear regression algorithm shows a linear relationship between a dependent (y) and one or more independent (y) variables, hence called linear regression. Since linear regression shows the linear relationship, which means it finds how the value of the dependent variable is changing according to the value of the independent variable.

Mathematically, we can represent a linear regression as:

$y= a_0+a_1x+ \varepsilon$

Here,

Y= Dependent Variable (Target Variable)

X= Independent Variable (predictor Variable)

a_0= intercept of the line (Gives an additional degree of freedom)

a_1 = Linear regression coefficient (scale factor to each input value).

ε = random error

The values for x and y variables are training datasets for Linear Regression model representation.

Types of Linear Regression

Linear regression can be further divided into two types of the algorithm:

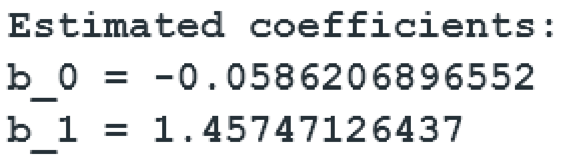
- **Simple Linear Regression**: If a single independent variable is used to predict the value of a numerical dependent variable, then such a Linear Regression algorithm is called Simple Linear Regression.
- **Multiple Linear regression**:If more than one independent variable is used to predict the value of a numerical dependent variable, then such a Linear Regression algorithm is called Multiple Linear Regression.

- ## Program :

```
import numpy as np
import matplotlib.pyplot as plt
def estimate_coef(x, y):
# number of observations/points
n = np.size(x)
# mean of x and y vector
m_x = np.mean(x)
m_y = np.mean(y)
# calculating cross-deviation and deviation about x
SS_xy = np.sum(y*x) - n*m_y*m_x
SS_xx = np.sum(x*x) - n*m_x*m_x
# calculating regression coefficients
b_1 = SS_xy / SS_xx
b_0 = m_y - b_1*m_x
return (b_0, b_1)
def plot_regression_line(x, y, b):
# plotting the actual points as scatter plot
plt.scatter(x, y, color = "m",
marker = "o", s = 30)
# predicted response vector
y_pred = b[0] + b[1]*x
# plotting the regression line
plt.plot(x, y_pred, color = "g")
# putting labels
plt.xlabel('x')
plt.ylabel('y')
# function to show plot
plt.show()
def main():
# observations / data
x = np.array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
y = np.array([1, 3, 2, 5, 7, 8, 8, 9, 10, 12])
# estimating coefficients
b = estimate_coef(x, y)
```

```
print("Estimated coefficients:\nb_0 = {} \
\nb_1 = {}".format(b[0], b[1]))
# plotting regression line
plot_regression_line(x, y, b)
if __name__ == "__main__":
main()
```

- **Output :**



```
Estimated coefficients:
b_0 = -0.0586206896552
b_1 = 1.45747126437
```

Experiment-11

- **Aim :**

Perform an experiment for finding frequent item sets, confidence, and support using association rules of mining.

- **Description :**

Apriori algorithm was given by R. Agrawal and R. Srikant in 1994 for finding frequent itemsets in a dataset for boolean association rule. Name of the algorithm is Apriori because it uses prior knowledge of frequent itemset properties. We apply an iterative approach or level-wise search where k-frequent itemsets are used to find k+1 itemsets.

To improve the efficiency of level-wise generation of frequent itemsets, an important property is used called Apriori property which helps by reducing the search space.

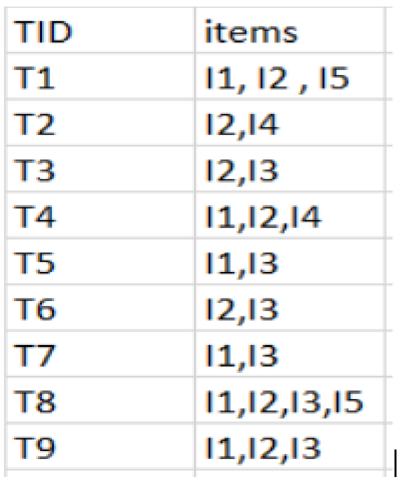
Apriori Property –

All non-empty subsets of frequent itemset must be frequent. The key concept of Apriori algorithm is its anti-monotonicity of support measure. Apriori assumes that

All subsets of a frequent itemset must be frequent(Apriori property).
If an itemset is infrequent, all its supersets will be infrequent.

- **Steps :**

Consider the following dataset and we will find frequent itemsets and generate association rules for them.

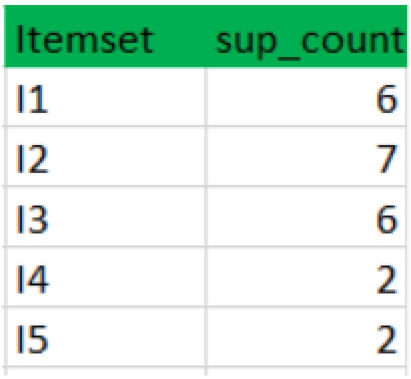


TID	items
T1	I1, I2 , I5
T2	I2,I4
T3	I2,I3
T4	I1,I2,I4
T5	I1,I3
T6	I2,I3
T7	I1,I3
T8	I1,I2,I3,I5
T9	I1,I2,I3

minimum support count is 2
minimum confidence is 60%

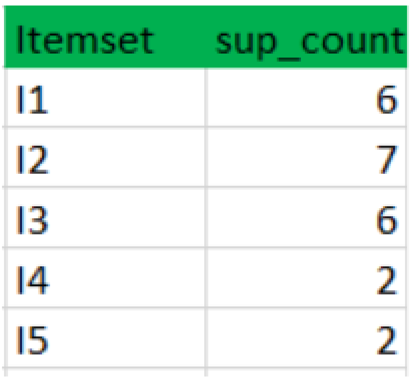
Step-1: K=1

(I) Create a table containing support count of each item present in dataset – Called C1(candidate set)



Itemset	sup_count
I1	6
I2	7
I3	6
I4	2
I5	2

(II) compare candidate set item's support count with minimum support count(here min_support=2 if support_count of candidate set items is less than min_support then remove those items). This gives us itemset L1.



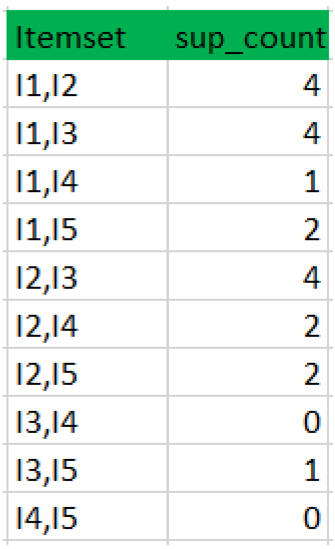
Itemset	sup_count
I1	6
I2	7
I3	6
I4	2
I5	2

Step-2: K=2

Generate candidate set C2 using L1 (this is called join step). Condition of joining Lk-1 and Lk-1 is that it should have (K-2) elements in common.

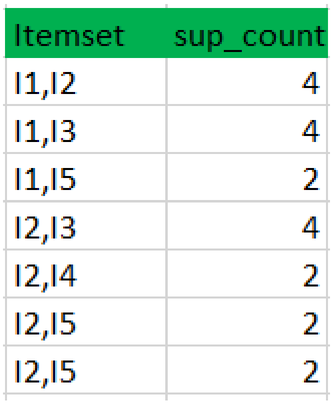
Check all subsets of an itemset are frequent or not and if not frequent remove that itemset.(Example subset of{I1, I2} are {I1}, {I2} they are frequent.Check for each itemset)

Now find the support count of these itemsets by searching in the dataset.



Itemset	sup_count
I1,I2	4
I1,I3	4
I1,I4	1
I1,I5	2
I2,I3	4
I2,I4	2
I2,I5	2
I3,I4	0
I3,I5	1
I4,I5	0

(II) compare candidate (C2) support count with minimum support count(here min_support=2 if support_count of candidate set item is less than min_support then remove those items) this gives us itemset L2.



Itemset	sup_count
I1,I2	4
I1,I3	4
I1,I5	2
I2,I3	4
I2,I4	2
I2,I5	2
I2,I5	2

Step-3:

- Generate candidate set C3 using L2 (join step). Condition of joining Lk-1 and Lk-1 is that it should have (K-2) elements in common. So here, for L2, first element should match.So itemset generated by joining L2 is {I1, I2, I3}{I1, I2, I5}{I1, I3, i5}{I2, I3, I4}{I2, I4, I5}{I2, I3, I5}

- Check if all subsets of these itemsets are frequent or not and if not, then remove that itemset.(Here subset of {I1, I2, I3} are {I1, I2},{I2, I3},{I1, I3} which are frequent. For {I2, I3, I4}, the subset {I3, I4} is not frequent so remove it. Similarly check for every itemset)

- Find the support count of these remaining itemset by searching in the dataset.

Itemset	sup_count
I1,I2,I3	2
I1,I2,I5	2

(II) Compare candidate (C3) support count with minimum support count(here min_support=2 if support_count of candidate set item is less than min_support then remove those items) this gives us itemset L3.

Itemset	sup_count
I1,I2,I3	2
I1,I2,I5	2

Step-4:

- Generate candidate set C4 using L3 (join step). Condition of joining Lk-1 and Lk-1 (K=4) is that they should have (K-2) elements in common. So here, for L3, first 2 elements (items) should match.
- Check if all subsets of these itemsets are frequent or not (Here the itemset formed by joining L3 is {I1, I2, I3, I5} so its subset contains {I1, I3, I5}, which is not frequent). So no itemset in C4
- We stop here because no frequent itemsets are found further

Thus, we have discovered all the frequent item-sets.

Now generation of strong association rule comes into picture. For that we need to calculate the confidence of each rule.

Confidence –

A confidence of 60% means that 60% of the customers, who purchased milk and bread also bought butter.

$$\text{Confidence}(A \longrightarrow B) = \frac{\text{Support}_{\text{Count}}(A \cup B)}{\text{Support}_{\text{Count}}(A)}$$

So here, by taking an example of any frequent itemset, we will show the rule generation.

Itemset {I1, I2, I3} //from L3

SO rules can be

- [I1^I2]=>[I3] //confidence = sup(I1^I2^I3)/sup(I1^I2) = =50%
- [I1^I3]=>[I2] //confidence = sup(I1^I2^I3)/sup(I1^I3) ==50%
- [I2^I3]=>[I1] //confidence = sup(I1^I2^I3)/sup(I2^I3) ==50%
- [I1]=>[I2^I3] //confidence = sup(I1^I2^I3)/sup(I1) ==33%
- [I2]=>[I1^I3] //confidence = sup(I1^I2^I3)/sup(I2) = =28%
- [I3]=>[I1^I2] //confidence = sup(I1^I2^I3)/sup(I3) ==33%

So if minimum confidence is 50%, then the first 3 rules can be considered as strong association rules.

● Conclusion :

Apriori Algorithms can be slow. The main limitation is time required to hold a vast number of candidate sets with frequent itemsets, low minimum support or large itemsets i.e. it is not an efficient approach for a large number of datasets. For example, if there are from frequent 1- itemsets, it needs to generate more than candidates into 2-lengths which in turn they will be tested and accumulate. Furthermore, to detect frequent patterns in size 100 i.e. , it has to generate candidate itemsets that yield on costly and wasting of time of candidate generation. So, it will check for many sets from candidate itemsets, also it will scan the database many times repeatedly for finding candidate itemsets. Apriori will be very low and inefficiency when memory capacity is limited with large number of transactions

Experiment-12

- **Aim :**

Implement Apriori algorithm for association rules of mining.

- **Description :**

The steps for Apriori algorithm are:

• In the first iteration of the algorithm, each item is a member of the set of candidate1-itemsets, *C*1. The algorithm simply scans all the transactions to count the number of occurrences of each item. Suppose that the minimum support count required is k, that is, *min sup* = k.

• The set of frequent 1-itemsets, *L*1, can then be determined. It consists of the candidate 1-itemsets satisfying minimum support. Here, *Li* shows the database with *i* elements in each set.

• To discover the set of frequent 2-itemsets, *L*2, the algorithm uses the join *L*1 * *L*1 to generate a candidate set of 2-itemsets.

• The set of frequent 2-itemsets, *L*2, is then determined, consisting of those candidate2-itemsets in *C*2 having minimum support.

• The generation of the set of the candidate3-itemsets, *C*3, is then calculated. It is based on the Apriori property that all subsets of a frequent itemset must also be frequent.

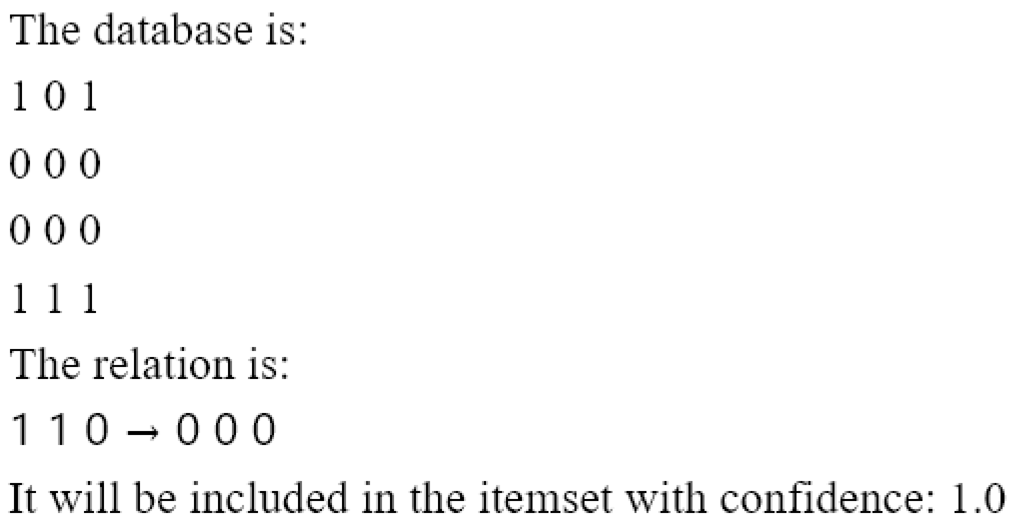
• Further, higher order candidate sets are generated and finally determine the maximum of such set that also satisfies the minimum support.

- **Program :**

```
package lab14;
public class AssociationRule {
public static void main(String[] args) {
int totalAttrs = 3, numberTransac = 4, c1 = 0, c2 = 0;
double minsup = 0.5, sup = 0.0;
// a → b Shows the association rule between two sets.
int a[] = {1, 1, 0};
int b[] = {0, 0, 0};
int aorb[] = new int[totalAttrs];
49
int aInt = 0;
int aorbInt = 0;
int dbInt[] = new int[numberTransac];
int db[][] = {{1, 0, 1},
{0, 0, 0},
{0, 0, 0},
{1, 1, 1}};
// show data set
System.out.println("The database is: ");
for(int i = 0; i < numberTransac; i++) {
for(int j = 0; j < totalAttrs; j++) {
System.out.print(db[i][j] + " ");
}
System.out.println();
}
// show item set.
System.out.println("The relation is: ");
for(int i = 0; i < totalAttrs; i++)
System.out.print(a[i] + " ");
System.out.print("-> ");
for(int i = 0; i < totalAttrs; i++)
System.out.print(b[i] + " ");
for(int i = 0; i < totalAttrs; i++) {
aorb[i] = a[i] | b[i];
}
// convert the values to integers.
for(int i = totalAttrs - 1; i >= 0; i--)
aInt = aInt + a[i] * (int) Math.pow(2, totalAttrs - 1 - i);
for(int i = totalAttrs - 1; i >= 0; i--)
aorbInt = aorbInt + aorb[i] * (int) Math.pow(2, totalAttrs - 1
- i);
for(int i = 0; i < numberTransac; i++)
for(int j = totalAttrs - 1; j >= 0; j--)
dbInt[i] = dbInt[i] + db[i][j] * (int) Math.pow(2,
50
totalAttrs - 1 - j);
// 101 & 111 => 101 i.e a.b = a means the attributes of first are
present in second.
for(int i = 0; i < numberTransac; i++)
if((aInt & dbInt[i]) == aInt)
c1 = c1 + 1;
```

```
// calculate confidence.
for(int i = 0; i < numberTransac; i++)
if((aorbInt & dbInt[i]) == aorbInt)
c2 = c2 + 1;
sup = c2 / c1;
System.out.println();
// print output.
if(sup > minsup)
System.out.println("It will be included in the itemset with
confidence: " + sup);
else
System.out.println("It won't be included in itemset with
confidence: " + sup);
}
}
```

- **Output :**



```
The database is:
1 0 1
0 0 0
0 0 0
1 1 1
The relation is:
1 1 0 → 0 0 0
It will be included in the itemset with confidence: 1.0
```

Experiment-13

- **Aim :**

  Implement Snow-flake schema in Data warehousing

- **Description :**

  The snowflake schema is a variant of the star schema. In this, the centralized fact table is connected to multiple dimensions, presented in a normalized form in multiple related tables. The snowflake structure is formed when the dimensions of a star schema are detailed and densely structured, having several levels of relationship, and the child tables have multiple parent tables. The snowflake effect influences only the dimension tables and not the fact tables.

  Characteristics of Snowflake Schema:

  - The major benefit is that it employs smaller disk space.
  - It is easier to implement the addition of a dimension into the Schema.
  - Presence of multiple tables reduces query performance.
  - The primary challenge is to bear the maintenance efforts because of the larger number of lookup tables.

- **Program :**

  The following DMQL program code can be used to define Snowflake schema -

  DEFINE CUBE Sales [Timestamp, Product, Branch, Location]:

  Dollars_sold = sum(sales in dollars), Units_sold = count(*), Avg_sales = avg(sales in dollars)

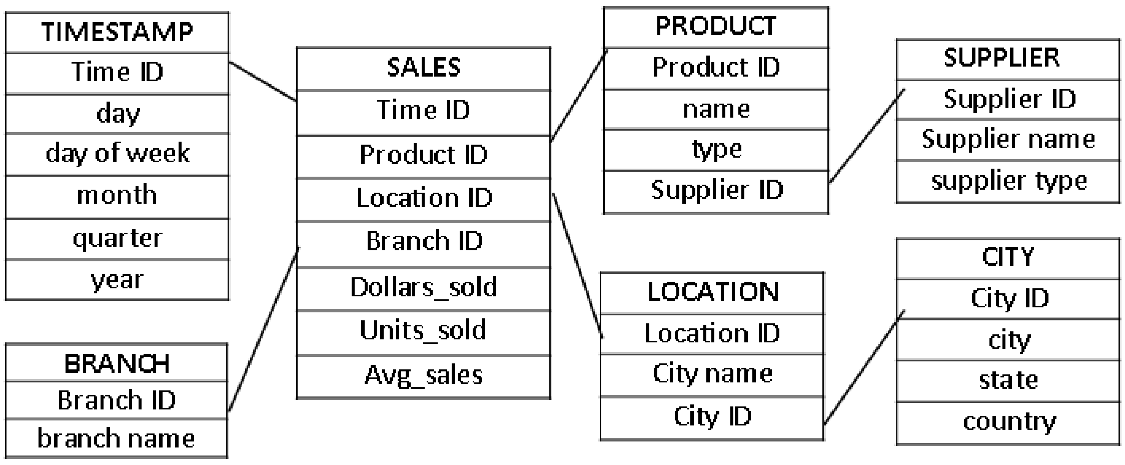
  DEFINE DIMENSION Timestamp as (Time ID, day, day of week, month, quarter, year)

  DEFINE DIMENSION Product as (Product ID, name, type, Supplier (Supplier ID, supplier type))

  DEFINE DIMENSION Branch as (Branch ID, branch name)

  DEFINE DIMENSION Location as (Location ID, City (City ID, city, state, country))

- **Output :**



TIMESTAMP
Time ID
day
day of week
month
quarter
year
BRANCH
Branch ID
branch name
SALES
Time ID
Product ID
Location ID
Branch ID
Dollars_sold
Units_sold
Avg_sales
PRODUCT
Product ID
name
type
Supplier ID
SUPPLIER
Supplier ID
Supplier name
supplier type
LOCATION
Location ID
City name
City ID
CITY
City ID
city
state
country

Experiment-14

- **Aim :**

  Implement Star schema in Data warehousing

- **Description :**

  A star schema is the elementary form of a dimensional model, in which data are organized into facts and dimensions. A fact is an event that is counted or measured, such as a sale or log in. A dimension includes reference data about the fact, such as date, item, or customer.A star schema is a relational schema where a relational schema whose design represents a multidimensional data model. The star schema is the explicit data warehouse schema. It is known as star schema because the entity-relationship diagram of this schema simulates a star, with points, diverge from a central table. The center of the schema consists of a large fact table, and the points of the star are the dimension tables.

  A table in a star schema which contains facts and connected to dimensions. A fact table has two types of columns: those that include fact and those that are foreign keys to the dimension table. The primary key of the fact tables is generally a composite key that is made up of all of its foreign keys.

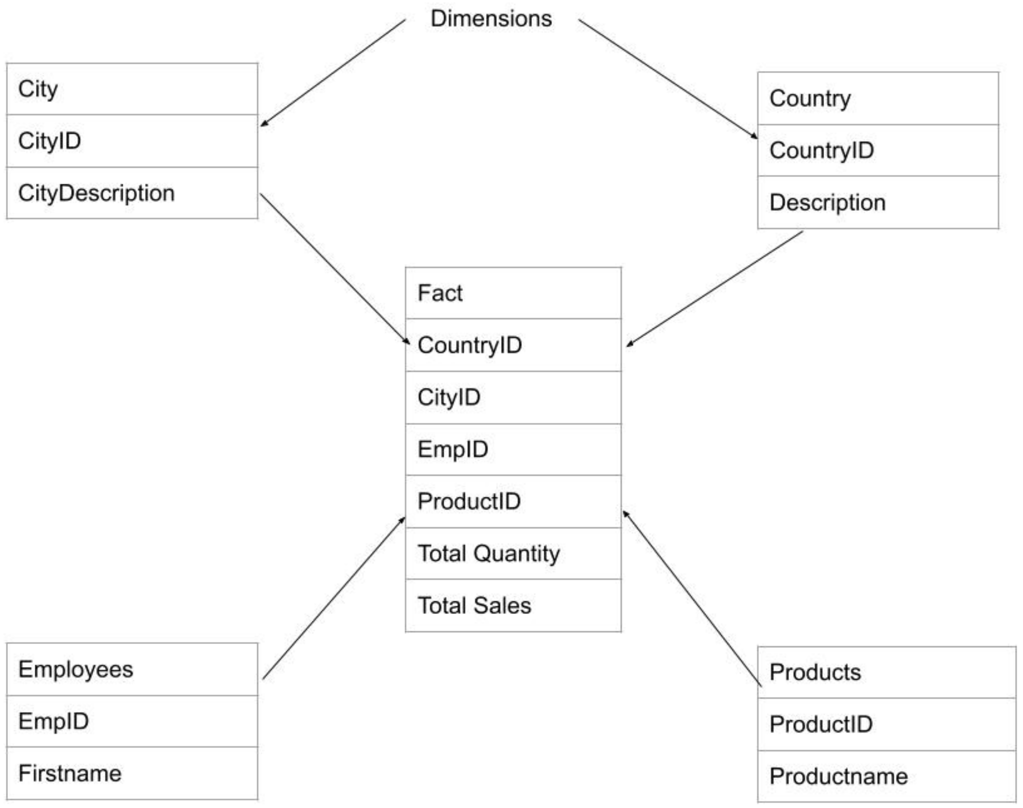
  A dimension is an architecture usually composed of one or more hierarchies that categorize data. If a dimension has not got hierarchies and levels, it is called a flat dimension or list. The primary keys of each of the dimensions table are part of the composite primary keys of the fact table. Dimensional attributes help to define the dimensional value. They are generally descriptive, textual values. Dimensional tables are usually smaller in size than the fact table.

  Fact tables store data about sales while dimension tables data about the geographic region (markets, cities), clients, products, times, channels.

- **Program :**

```
DEFINE CUBE Fact [CityID, CountryID, EmpID, ProductID]:
TotalQuantity = count(UnitSold), TotalSales = sum(ProductSold).
DEFINE DIMENSION City AS (CityID, CityDescription).
DEFINE DIMENSION Country AS (CountryID, Description).
DEFINE DIMENSION Employees AS (EmpID, Firstname).
DEFINE DIMENSION Products AS (ProductID, Productname).
```

- **Output :**



Dimensions
City
CityID
CityDescription
Country
CountryID
Description
Fact
CountryID
CityID
EmpID
ProductID
Total Quantity
Total Sales
Employees
EmpID
Firstname
Products
ProductID
Productname

Experiment-15

- **Aim :** Write a prolog program to find the rules for the parent, child, male, female, son, daughter, brother, sister, uncle, aunt, ancestor given the facts about father and wife only.
- **Description :**

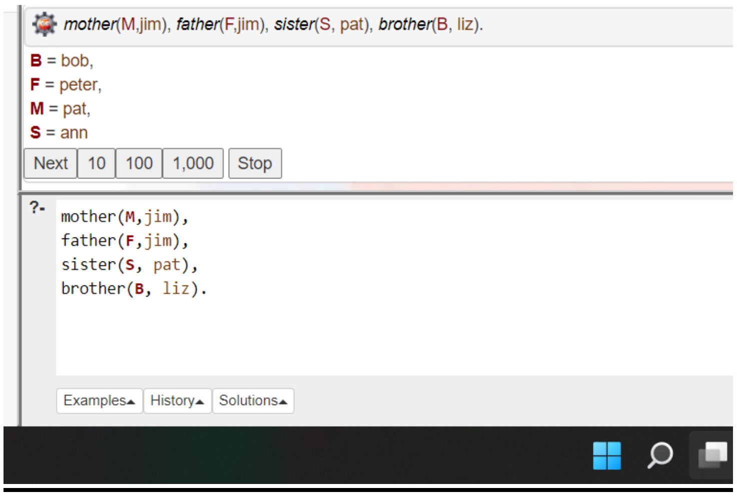
PROLOG stands for PROgramming in LOGic and has a very important role in artificial intelligence. It expresses any objects in the form of relations which are described using facts and rules. In this program we derive the different blood relations among the family members, and some logics like male, female and parent are given as facts while the relations between these like mother, father, brother, sister are described using the rules.

- **Program :**

```
female(pam).
female(liz).
female(pat).
female(ann).
male(jim).
male(bob).
male(tom).
male(peter).
parent(pam,bob).
parent(tom,bob).
parent(tom,liz).
parent(bob,ann).
parent(bob,pat).
parent(pat,jim).
parent(bob,peter).
parent(peter,jim).
mother(X,Y):- parent(X,Y),female(X).
father(X,Y):- parent(X,Y),male(X).
```

```
haschild(X):- parent(X,_).

sister(X,Y):- parent(Z,X),parent(Z,Y),female(X),X\==Y.

brother(X,Y):-parent(Z,X),parent(Z,Y),male(X),X\==Y.
```

- **Output :**



```
mother(M,jim), father(F,jim), sister(S, pat), brother(B, liz).
B = bob,
F = peter,
M = pat,
S = ann
```

```
?- mother(M,jim),
   father(F,jim),
   sister(S, pat),
   brother(B, liz).
```

Experiment-16

- **Aim :**

  Write a prolog program to find the length of a given list.

- **Description :**

  Length calculation is used to determine the length of list L. Suppose the noun name is list_length (L, N). This takes L and N as the input counter. This will list the elements in list L and put N in their number. As was the case with our previous relationships which included lists, it is helpful to consider two situations -

  - If the list is empty, the length is 0.
  - If the list is empty, it means L = [Head | Tail], then its length is 1+ tail length.

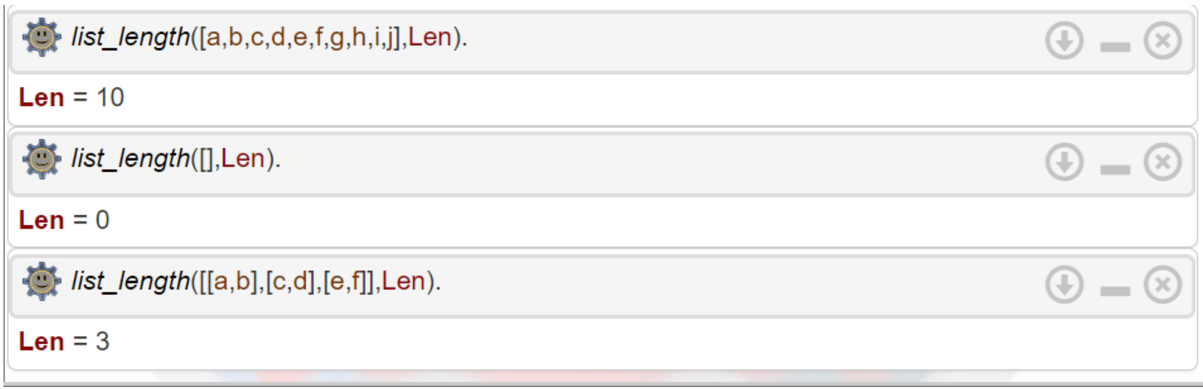
- **Program :**

```
list_length([],0).
list_length([_|TAIL],N) :- list_length(TAIL,N1), N is N1 + 1.
```

Query -

```
list_length([a,b,c,d,e,f,g,h,i,j],Len).
list_length([],Len).
list_length([[a,b],[c,d],[e,f]],Len).
```

- **Output :**



```
list_length([a,b,c,d,e,f,g,h,i,j],Len).
Len = 10
list_length([],Len).
Len = 0
list_length([[a,b],[c,d],[e,f]],Len).
Len = 3
```

Experiment-17

- **Aim :**

Write a prolog program to find the last element of a given list.

- **Description :**

Prolog is a logic programming language. It has important role in artificial intelligence. Unlike many other programming languages, Prolog is intended primarily as a declarative programming language. In prolog, logic is expressed as relations (called as Facts and Rules). Core heart of prolog lies at the logic being applied. Formulation or Computation is carried out by running a query over these relations.

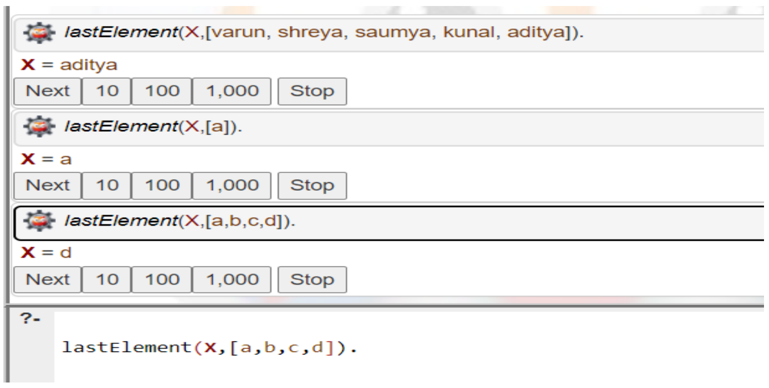
X is a member of list X.
Removes the first element of the list recursively.
Returns the last element of the list.

- **Program :**

Prolog is a logic programming language. It has important role in artificial intelligence. Unlike many other programming languages, Prolog is intended primarily as a declarative programming language. In prolog, logic is expressed as relations (called as Facts and Rules). Core heart of prolog lies at the logic being applied. Formulation or Computation is carried out by running a query over these relations.

X is a member of list X.
Removes the first element of the list recursively.
Returns the last element of the list.

- **Output :**



```
lastElement(X,[varun, shreya, saumya, kunal, aditya]).
X = aditya
lastElement(X,[a]).
X = a
lastElement(X,[a,b,c,d]).
X = d
?-
lastElement(X,[a,b,c,d]).
```

Experiment-18

- **Aim :**

  Write a prolog program to delete the first occurrence and also all occurrences of a particular element in a given list.

- **Description :**

  For deleting single occurrence:

  Suppose we have a list L and an element X, we have to delete X from L. So there are three cases −

  - If X is the only element, then after deleting it, it will return empty list.
  - If X is head of L, the resultant list will be the Tail part.
  - If X is present in the Tail part, then delete from there recursively.

  For deleting all occurrences:

  When the “input” list is empty, then the output list is “empty”.

  delete_all(_Head, [], []).

  When the heads of the “input” and “output” lists don’t match

  the element being deleted:

  delete_all(Item, [Head|Tail], [Head|New_Tail]) :-

  Item \= Head, delete_all(Item, Tail, New_Tail).

  When the heads of the “input” list matches the element being

  deleted:

  delete_all(Item, [Item|Tail], New_Tail) :-

  delete_all(Item, Tail, New_Tail).

- **Program-1 :**

1) (Program to delete first occurrence of an element)

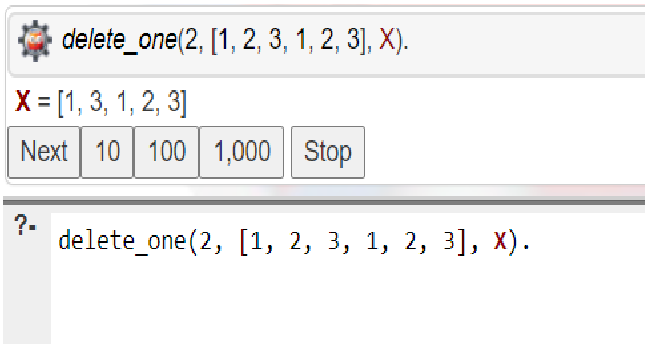
```
delete_one(_, [], []).
delete_one(Term, [Term|Tail], Tail).
delete_one(Term, [Head|Tail], [Head|Result]) :-
delete_one(Term, Tail, Result).
```

2) (Program to delete all occurrences of an element)

```
delete_all(_Head, [], []).
delete_all(Item, [Head|Tail], [Head|New_Tail]) :-
Item \= Head, delete_all(Item, Tail, New_Tail).
delete_all(Item, [Item|Tail], New_Tail) :-
delete_all(Item, Tail, New_Tail).
```

- **Output :**

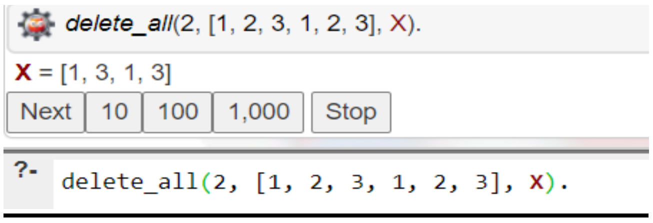
1)



```
delete_one(2, [1, 2, 3, 1, 2, 3], X).
X = [1, 3, 1, 2, 3]
```

```
?- delete_one(2, [1, 2, 3, 1, 2, 3], X).
```

2)



```
delete_all(2, [1, 2, 3, 1, 2, 3], X).
X = [1, 3, 1, 3]
```

```
?- delete_all(2, [1, 2, 3, 1, 2, 3], X).
```

Experiment-19

- **Aim :**

Write a prolog program to find the union of two given sets represented as lists.

- **Description :**

(Y is list1, Z is list2 and W is new list)

• For each element of list1 which is already present in list2 :

```
union([X|Y],Z,W) :- member(X,Z), union(Y,Z,W).
```

• For each element of list1 which is not present in list2:

```
union([X|Y],Z,[X|W]) :- \+ member(X,Z), union(Y,Z,W).
```

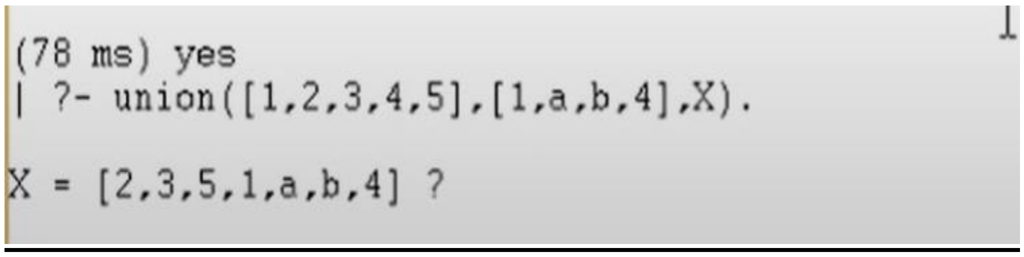
• Copy all the values of list2 into the new list.

```
union([],Z,Z).
```

- **Program :**

```
union([X|Y],Z,W) :-
        list_member(X,Z), union(Y,Z,W).
union([X|Y],Z,[X|W]) :-
        \+ list_member(X,Z), union(Y,Z,W).
union([],Z,Z).  list_member(X,[X|_]).
list_member(X,[_|TAIL])
list_member(X,TAIL).
```

- **Output :**



```
(78 ms) yes
| ?- union([1,2,3,4,5],[1,a,b,4],X).

X = [2,3,5,1,a,b,4] ?
```

<u>**Experiment-20**</u>

- **Aim :**

  Write a prolog program to reverse a given list of values.

- **Description :**

  The first parameter in the reverse/3 predicate is the list. The second parameter is an empty list. The third parameter is the reverse list.

  The reverse/3 recursively pushes the elements from the beginning of the first list to the front of the second list. This reverses the order of the elements.

  Our base condition is reverse([], Y, R). At this point, we have pushed all elements from the input list to Y. We set R to Y and backtrack.

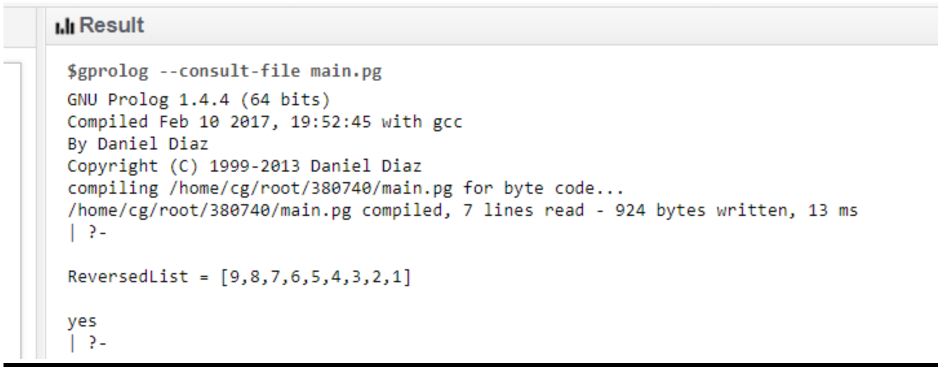
- **Program :**

```
reverse([], Y, R) :-

R = Y.

reverse([H|T] , Y, R) :-

reverse(T, [H|Y], R).
```

STDIN:

```
reverse([1,2,3,4,5,6,7,8,9],[],ReversedList).
```

- **Output :**



Result

```
$gprolog --consult-file main.pg
GNU Prolog 1.4.4 (64 bits)
Compiled Feb 10 2017, 19:52:45 with gcc
By Daniel Diaz
Copyright (C) 1999-2013 Daniel Diaz
compiling /home/cg/root/380740/main.pg for byte code...
/home/cg/root/380740/main.pg compiled, 7 lines read - 924 bytes written, 13 ms
| ?-

ReversedList = [9,8,7,6,5,4,3,2,1]

yes
| ?-
```

Experiment-21

- **Aim:**

Write a prolog program given the knowledge base, If x is on the top of y, y supports x. If x is above y and they are touching each other, x is on top of y. A cup is above a book. The cup is touching that book. Convert the following into wffs, clausal form; Is it possible to deduce that 'The book supports the cup'.

- **Description:**

In this prolog program, we have to find whether it is possible or not to deduce that 'The book supports the cup' with the help of the given knowledge base.

A cup is above a book.

above(cup,book).

The cup is touching that book.

touch(cup,book).

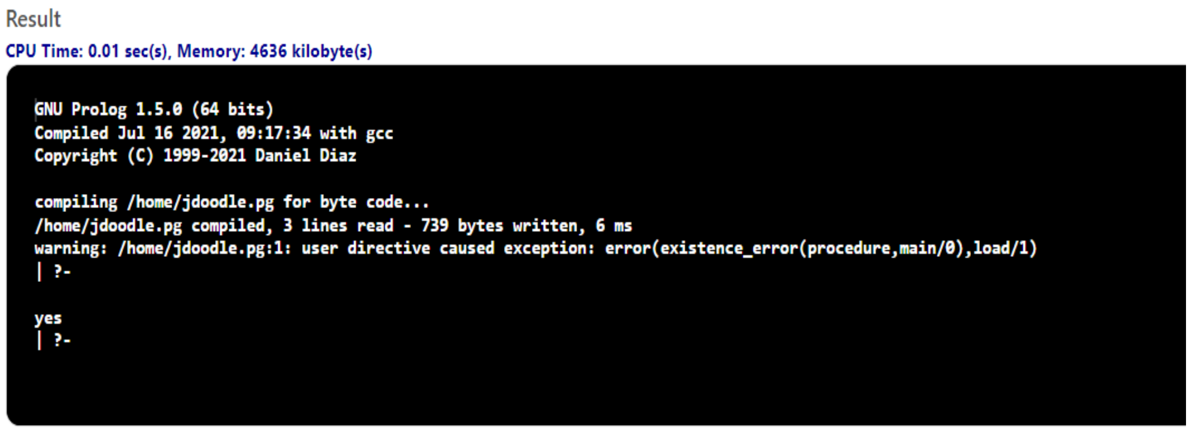
If x is on the top of y, y supports x. If x is above y and they are touching each other, x is on top of y.

support(X,Y) :-above(X,Y), touch(X,Y).

- **Program:**

```
 :- initialization(main).

above(cup,book).

touch(cup,book).

support(Y,X) :- above(X,Y), touch(X,Y).

------------------------------------------------------------------

Input – support(book, cup).
```

- **Output:**



Result

CPU Time: 0.01 sec(s), Memory: 4636 kilobyte(s)

```
GNU Prolog 1.5.0 (64 bits)
Compiled Jul 16 2021, 09:17:34 with gcc
Copyright (C) 1999-2021 Daniel Diaz

compiling /home/jdoodle.pg for byte code...
/home/jdoodle.pg compiled, 3 lines read - 739 bytes written, 6 ms
warning: /home/jdoodle.pg:1: user directive caused exception: error(existence_error(procedure,main/0),load/1)
| ?-

yes
| ?-
```

Experiment-22

- **Aim :**

Write a prolog program given the knowledge base, If Town x is connected to Town y by highway z and bikes are allowed on z, you can get to y from x by bike. If Town x is connected to y by z then y is also connected to x by z. If you can get to town q from p and also to town r from town q, you can get to town r from town p.

a. Town A is connected to Town B by Road1.

b. Town B is connected to Town C by Road2.

c. Town A is connected to Town C by Road3.

d. Town D is connected to Town E by Road4.

e. Town D is connected to Town B by Road5.

f. Bikes are allowed on roads 3, 4, 5.

Bikes are only either allowed on Road1 or on Road2 every day. Convert the following into WFF's, clausal form and deduce that 'One can get to town B from town D'.

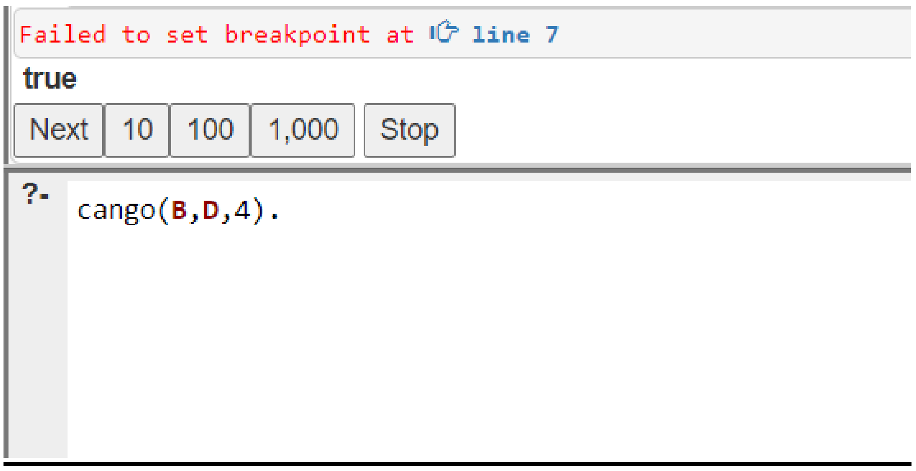
- **Description :**

In this program, we express the given information as facts and then derive rules for conditions of connection, reachability and roads as given in the aim. After deriving the facts and the rules we check whether or not town B can be reached through town D; if the result comes out to be true, then it is reachable, else it is not.

- **Program :**

```
connect(A,B,1).

connect(B,C,2).

connect(A,C,3).

connect(D,E,4).

connect(D,B,5).

connect(P,R,_):- connect(P,Q,_), connect(Q,R,_).

bikeallowed(3).

bikeallowed(4).

bikeallowed(5).
bikeallowed(1) :- not(bikeallowed(2)).

bikeallowed(2) :- not(bikeallowed(1)).

cango(X,Y,Z) :- (connect(X,Y,Z) ; connect(Y,X,Z)), bikeallowed(Z).
```

- **Output :**



```
Failed to set breakpoint at line 7
true
```

```
?- cango(B,D,4).
```

Experiment-23

- **Aim :**

Solve the classical Monkey Banana problem of AI using prolog.

- **Description :**

The monkey can climb up on the block if both the monkey and the block are on the floor and the block is in the centre. As a result, the monkey's vertical position will be altered. The monkey can get the bananas while he is on the block and the block is in the centre.

We have some predicates that will move from one state to another state, by performing action :

● When the block is in the middle, and the monkey is on top of the block, and the monkey does not have the banana (i.e. has no state), then using the grasp action, it will change from has not state to state.

● From the floor, it can move to the top of the block (i.e. on top state), by performing the action climb.

● The push or drag operation moves the block from one place to another.

● Monkey can move from one place to another using walk or move clauses.

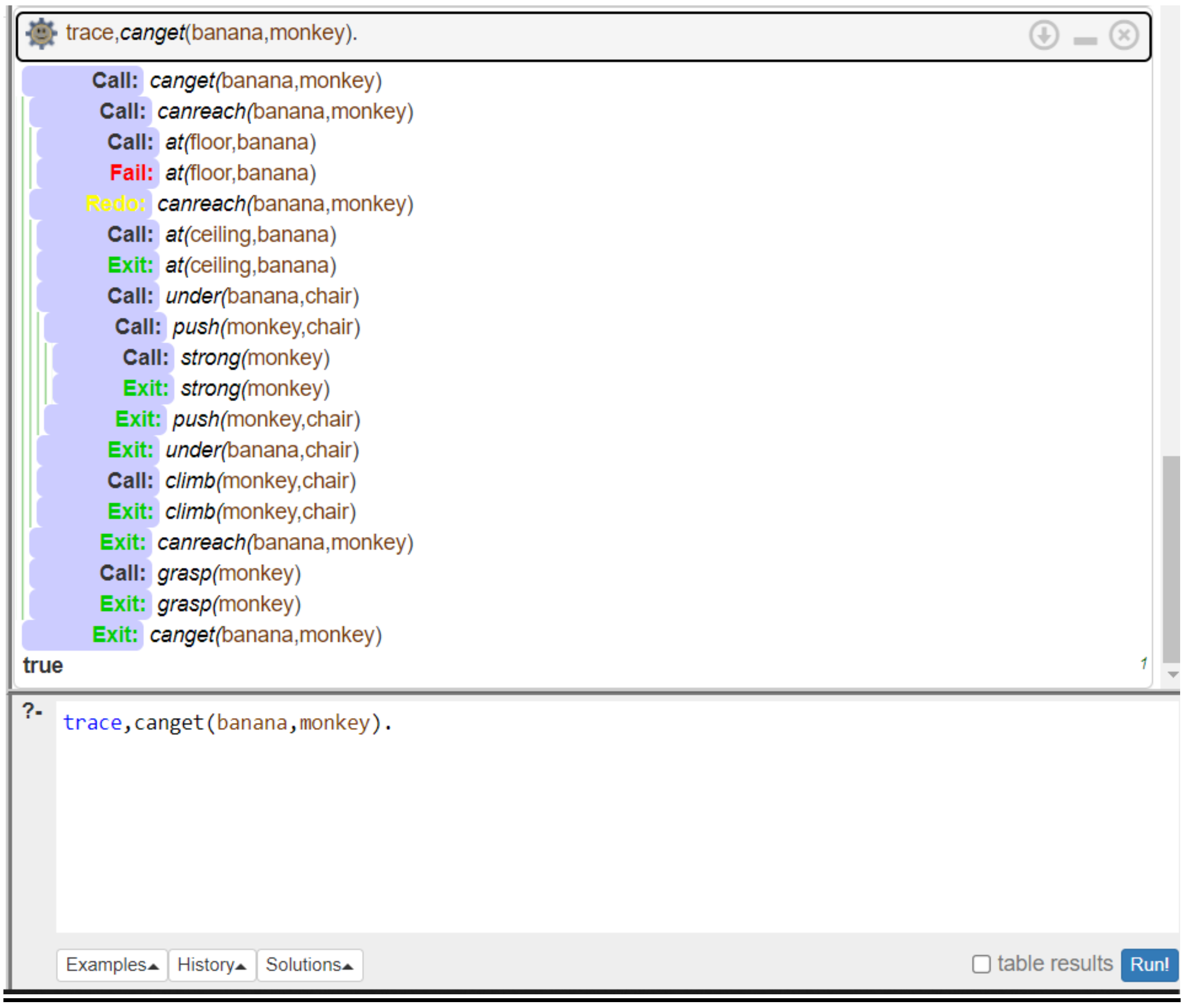
Another predicate will be canget(). Here we pass a state, so this will perform a move predicate from one state to another using different actions, then perform canget() on state 2. When we have reached the state ‘has>’, this indicates ‘has banana’. We will stop the execution.

- **Program :**

```
on(floor,monkey).
on(floor,chair).
in(room,monkey).
in(room,chair).
in(room,banana).
at(ceiling,banana).
strong(monkey).
grasp(monkey).
climb(monkey,chair).
push(monkey,chair):-
strong(monkey).
under(banana,chair):-
```

```
push(monkey,chair).
canreach(banana,monkey):-
at(floor,banana);
at(ceiling,banana),
under(banana,chair),
climb(monkey,chair).
canget(banana,monkey):-
canreach(banana,monkey),grasp(monkey).
```

- **Output :**



```
trace,canget(banana,monkey).
   Call: canget(banana,monkey)
    Call: canreach(banana,monkey)
     Call: at(floor,banana)
     Fail: at(floor,banana)
    Redo: canreach(banana,monkey)
     Call: at(ceiling,banana)
     Exit: at(ceiling,banana)
     Call: under(banana,chair)
      Call: push(monkey,chair)
       Call: strong(monkey)
       Exit: strong(monkey)
      Exit: push(monkey,chair)
     Exit: under(banana,chair)
     Call: climb(monkey,chair)
     Exit: climb(monkey,chair)
    Exit: canreach(banana,monkey)
    Call: grasp(monkey)
    Exit: grasp(monkey)
   Exit: canget(banana,monkey)
true

?- trace,canget(banana,monkey).
```

Experiment-24

- **Aim :**

  Define a LISP function to compute sum of squares.

- **Description :**

  SUM OF SQUARE

  Sum of square means by adding the squares of two numbers.

  Example:

  Sum of Square of x ,y= (x * x) + (y * y)

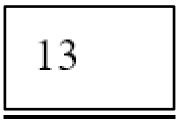
  Now in prefix expression it should be written as,

  (+ (* x x) (* y y))

- **Program :**

```
>>(defun sumsqr(x y)

(+(* x x)(* y y)))

SUMSQR
>>(sumsqr 2 3);
```

- **Output :**



```
13
```

Experiment-25

- **Aim :**

Define a LISP function to compute the difference of squares. (if x > y return $x^2 – y^2$, otherwise return $y^2 – x^2$).

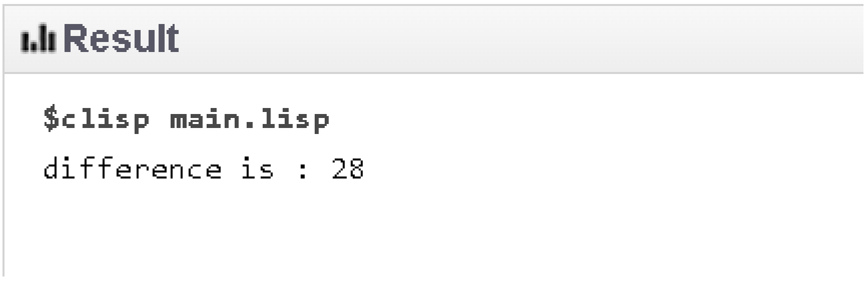
- **Description :**

If: The if construct has various forms. In the simplest form, it is followed by a test clause, a test action, and some other consequent action(s). If the test clause evaluates to true, then the test action is executed otherwise, the consequent clause is evaluated.

- **Program :**

```
(defun diff(x y)
(if (> x y)
(setq result (- (* x x) (* y y)))
(setq result (- (* y y) (* x x)))
)
(format t "difference is : ~d" result)
)
(diff 8 6)
```

- **Output :**



Result

```
$clisp main.lisp
difference is : 28
```

Experiment-26

- **Aim :** Define a LISP function to compute the factorial of a given number.
- **Description :**

  The factorial of any non-negative number n, denoted by n!, is the product of all positive integers less than or equal to n.

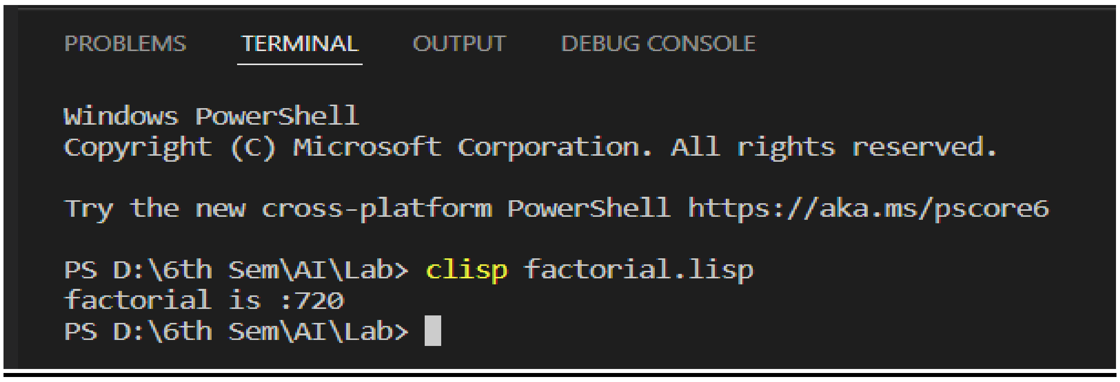
  For example 3! = 3*2*1.

  The value of 0! is 1, according to the conversion for an empty product.

- **Program :**

```
(defun fact(x)
        (setq result 1)
        (loop
                (setq result (* result x))
                (setq x (- x 1))
                (when (= x 1)(eturn))
        )
        (format t “factorial is  :~d “ result)
)
(fact 6)
```

- **Output :**



```
Windows PowerShell
Copyright (C) Microsoft Corporation. All rights reserved.

Try the new cross-platform PowerShell https://aka.ms/pscore6

PS D:\6th Sem\AI\Lab> clisp factorial.lisp
factorial is :720
PS D:\6th Sem\AI\Lab>
```

Experiment-27

- **Aim :**

  Define a LISP function to reverse the number entered as parameter in function call.

- **Description :**

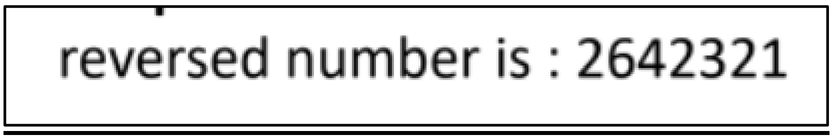
  defun : The defun construct is used for defining a function, we will look into it in the Functions chapter.

  loop: The loop construct is the simplest form of iteration provided by LISP. In its simplest form, it allows you to execute some statement(s) repeatedly until it finds a return statement.

- **Program :**

```
(defun rev(x)
(setq result 0)
(loop
(setq rem (mod x 10))
(setq result (+ (* result 10) rem))
(setq x (floor x 10))
(when (= x 0)(return))
)
(format t "reversed number is : ~d" result)
)
(rev 1232462)
```

- **Output :**



```
reversed number is : 2642321
```

Experiment-28

- **Aim:**

Write a LISP program containing two functions: one to read input values and one to display them.

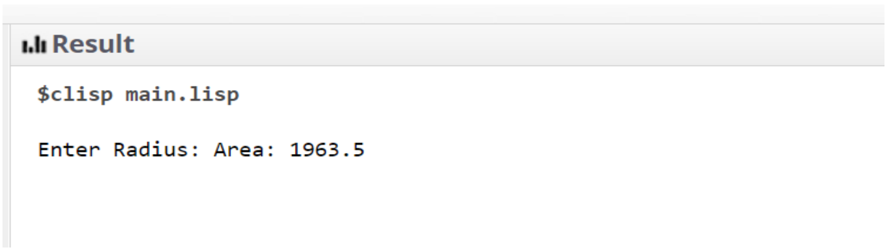
- **Description:**

In LISP, we can read input from STDIN using ‘read’ and output values into STDOUT using ‘write’. This has been demonstrated in the following program which calculates the area of a circle by taking the radius value from STDIN.

- **Program:**

```
; the function AreaOfCircle

; calculates area of a circle

; when the radius is input from keyboard


(defun AreaOfCircle()

(terpri)

(princ "Enter Radius: ")

(setq radius (read))

(setq area (* 3.1416 radius radius))

(princ "Area: ")

(write area))

(AreaOfCircle)
```

- **Output:**



```
$clisp main.lisp

Enter Radius: Area: 1963.5
```

Experiment-29

- **Aim :**

Write a LISP program to compute factorial of a given number using recursion.

- **Description :**

The factorial of a non-negative integer n (denoted by n!), is the product of all positive integers less than or equal to n.

Given by: n! =

$$\begin{cases} 1 \, if \, n = 0, \\ n * (n-1)! \, if \, n > 0 \end{cases}$$

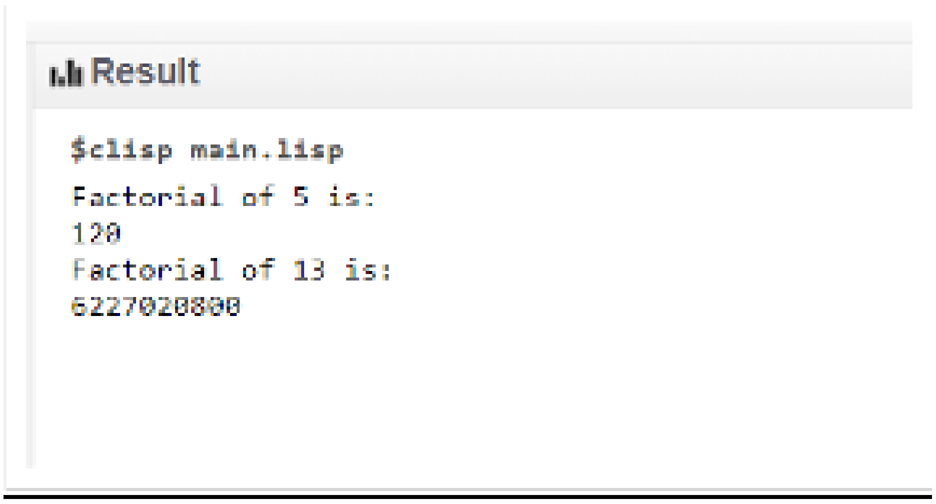
The program code employs recursion to calculate the factorial, by using conditional statements to check the value of n. The function is recalled when n is greater than 0.

- **Program :**

The LISP Code will be as follows-

```
(defun factorial(n)

(if (= n 0) 1

(* n (factorial(- n 1)))

)

)

(write-line "Factorial of 5 is: ")

(write (factorial 5))

(terpri)

(write-line "Factorial of 13 is: ")

(write (factorial 13))
```

- **Output :**


Result

```
$clisp main.lisp
Factorial of 5 is:
120
Factorial of 13 is:
6227020800
```

Experiment-30

- **Aim :**

Write a LISP Program using recursion to perform GCD of two numbers entered by user.

- **Description :**

Euclidean algorithm for computing the greatest common divisor.

Originally, the Euclidean algorithm was formulated as follows: subtract number fro the larger one until one of the numbers is zero. Indeed, if g divides a and b, it also divides a - b. On the other hand, if g divides a - b, it also divides a - b. On the other hand, if g divides a - b and b, then it also divides a = b + (a - b), which means that the sets on the common divisors of {a,b} and {b,a - b} coincide.

Note that a remains the larger number until b is subtracted from it at least ⌊a/b⌋ times. Therefore, to speed things up, a- b is substituted with a - ⌊a/b⌋ b = a mod b. Then the algorithm is formulated in an extremely simple way :

$$\gcd(a,b) = \begin{cases} a, & \text{if } b = 0 \\ \gcd(b, a \bmod b), & \text{otherwise.} \end{cases}$$

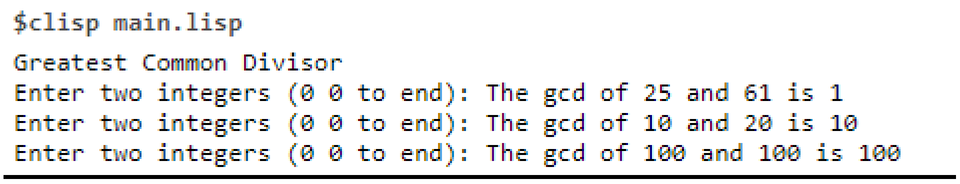
- **Program :**

```
(defun gcd (a b)

(if (= b 0)

a

(gcd b (mod a b))))

;;; -------------------------------------------- Calling gcd

(defun gcdprint(a b)

(let (

        (f (list "The gcd of " a " and " b " is " (gcd a b)))

        )

        (mapcar 'princ f)

        (terpri)

)
)
;;; ------------------------------------------ Top-level
(defun run()
(princ "Greatest Common Divisor")
(terpri)
(loop
(princ "Enter two integers (0 0 to end): " )
        (setq n1 (read)) ; A global. This is non-functional usage.
        (setq n2 (read))        ; There is no need to use assignment in Lisp.
        (cond ((= n1 0)         (return))
                (T              (gcdprint n1 n2))
        )
)
)
(run )
```

Input-

```
25
61
10
20
100
100
0
```

- **Output :**



```
$clisp main.lisp
Greatest Common Divisor
Enter two integers (0 0 to end): The gcd of 25 and 61 is 1
Enter two integers (0 0 to end): The gcd of 10 and 20 is 10
Enter two integers (0 0 to end): The gcd of 100 and 100 is 100
```