SURYA GROUP OF INSTITUTIONS

VIKRAVANDI-605652

NAAN MUDHALVAN PROJECT

AI BASED DIABETES PREDICTION

PHASE 2:INNOVATION

PRESENTED BY

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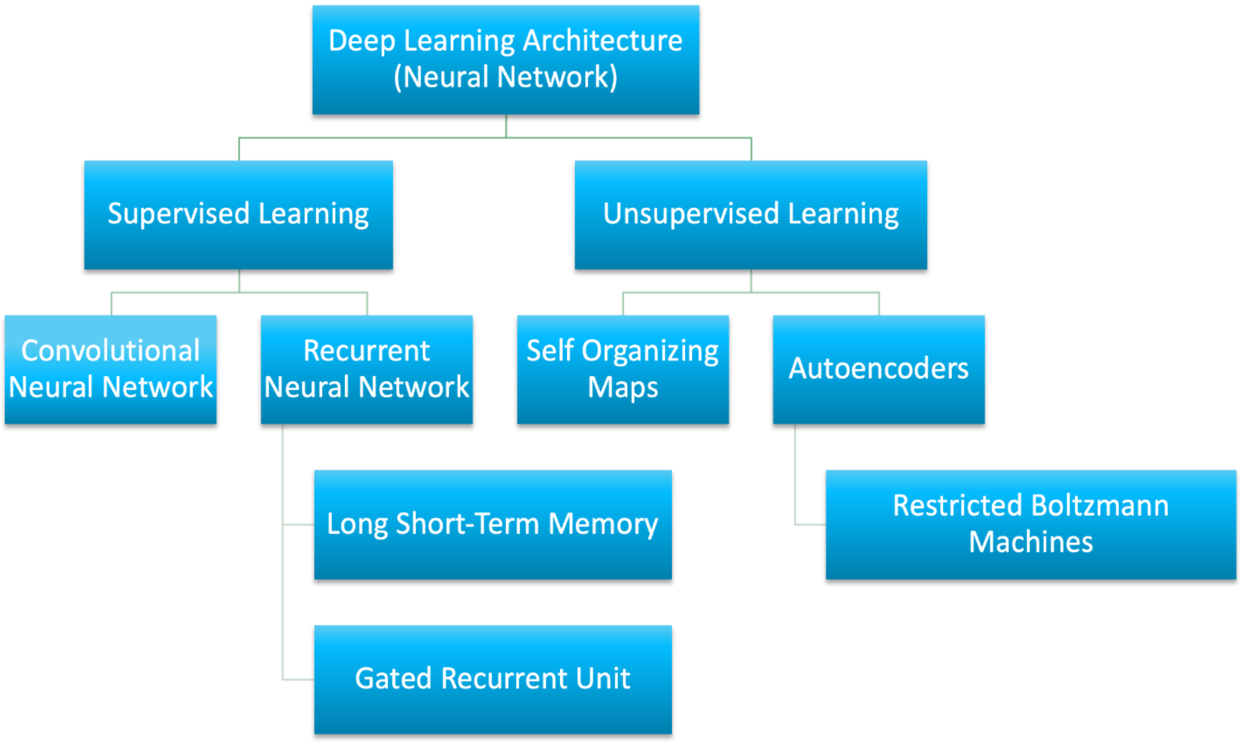
DEPARTMENT:ECE 3rd year

INTRODUCTION:

We have implemented various methods or approaches to use our data systematically and in synchronized way for the purpose of the development of our model. Moreover the test plan is according to our model and can be helpful if we wants to make further improvements and developments to our model.

DEEP LEARNING ARCHITECTURE:



Importing libraries

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
```

Importing dataset

```
dataset = pd.read_csv('../input/diabetes-data-set/diabetes.csv')
```

Viewing the dataset, its dimensions, features and statistical Summary

```
dataset.head()
```

	Pregnancies	Glucose	BP	Skin thickness	Insulin	BMI	Diabetes pedigree function	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1

1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

```
dataset.shape
```

```
(768, 9)
```

```
dataset.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 768 entries, 0 to 767
Data columns (total 9 columns):
 #   Column                  Non-Null Count  Dtype
---  ------                  --------------  -----
 0   Pregnancies             768 non-null    int64
 1   Glucose                 768 non-null    int64
 2   BloodPressure           768 non-null    int64
 3   SkinThickness           768 non-null    int64
 4   Insulin                 768 non-null    int64
 5   BMI                     768 non-null    float64
 6   DiabetesPedigree
     Function                768 non-null    float64
 7   Age                     768 non-null    int64
 8   Outcome                 768 non-null    int64
dtypes: float64(2), int64(7)
memory usage: 54.1 KB
```

```
dataset.describe().T
```

count	mean	std	min	25%	50%	75%	max	
Pregnancies	768.0	3.845052	3.369578	0.000	1.00000	3.0000	6.00000	17.00
Glucose	768.0	120.894531	31.972618	0.000	99.00000	117.0000	140.25000	199.00
BloodPressure	768.0	69.105469	19.355807	0.000	62.00000	72.0000	80.00000	122.00
SkinThickness	768.0	20.536458	15.952218	0.000	0.00000	23.0000	32.00000	99.00
Insulin	768.0	79.799479	115.244002	0.000	0.00000	30.5000	127.25000	846.00
BMI	768.0	31.992578	7.884160	0.000	27.30000	32.0000	36.60000	67.10

count	mean	std	min	25%	50%	75%	max	
DiabetesPedigreeFunction	768.0	0.471876	0.331329	0.078	0.24375	0.3725	0.62625	2.42
Age	768.0	33.240885	11.760232	21.000	24.00000	29.0000	41.00000	81.00
Outcome	768.0	0.348958	0.476951	0.000	0.00000	0.0000	1.00000	1.00

Detecting null values

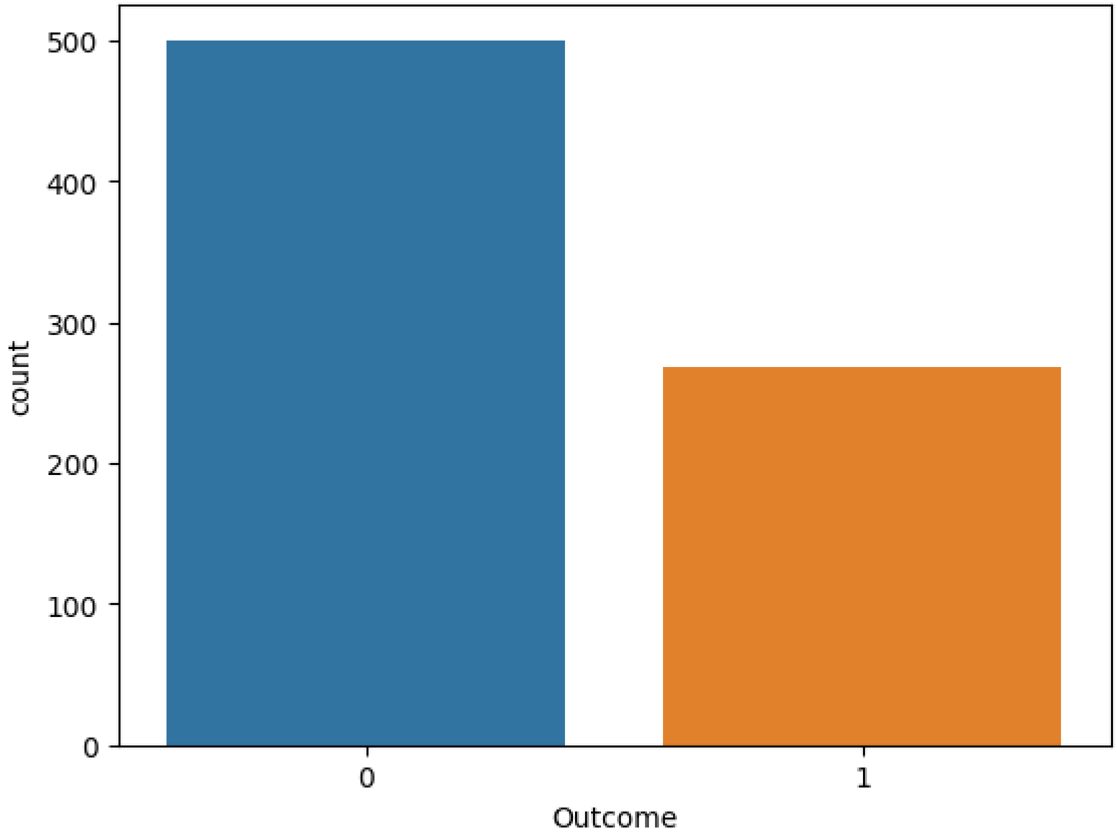
```
dataset.isnull().sum()
```

```
Pregnancies                 0
Glucose                     0
BloodPressure               0
SkinThickness               0
Insulin                     0
BMI                         0
DiabetesPedigreeFunction    0
Age                         0
Outcome                     0
dtype: int64
```

Data Visualization

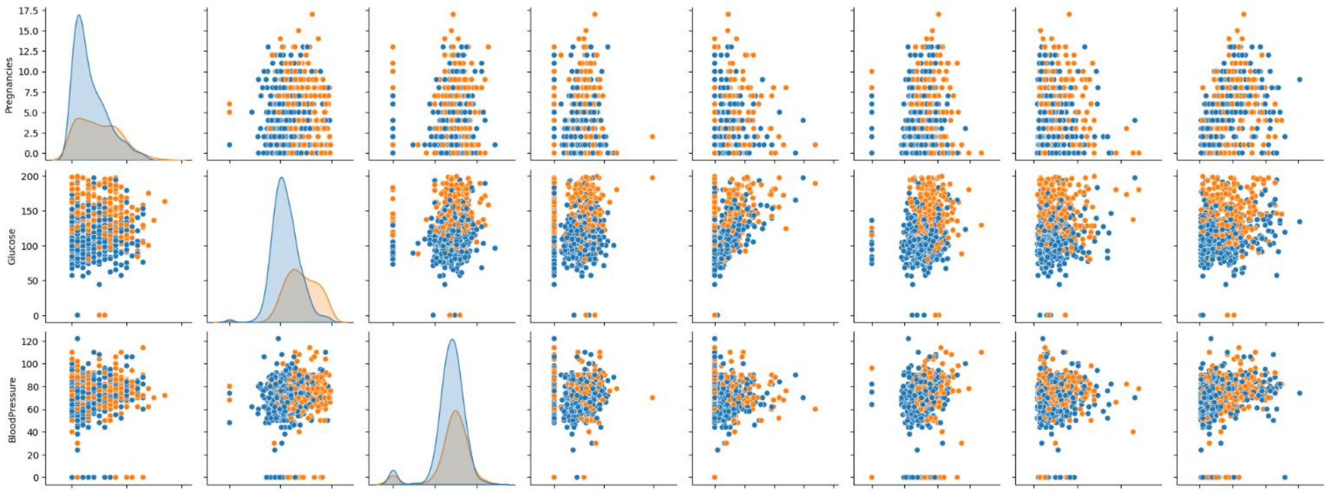
```
sns.countplot(x = 'Outcome',data = dataset)
```

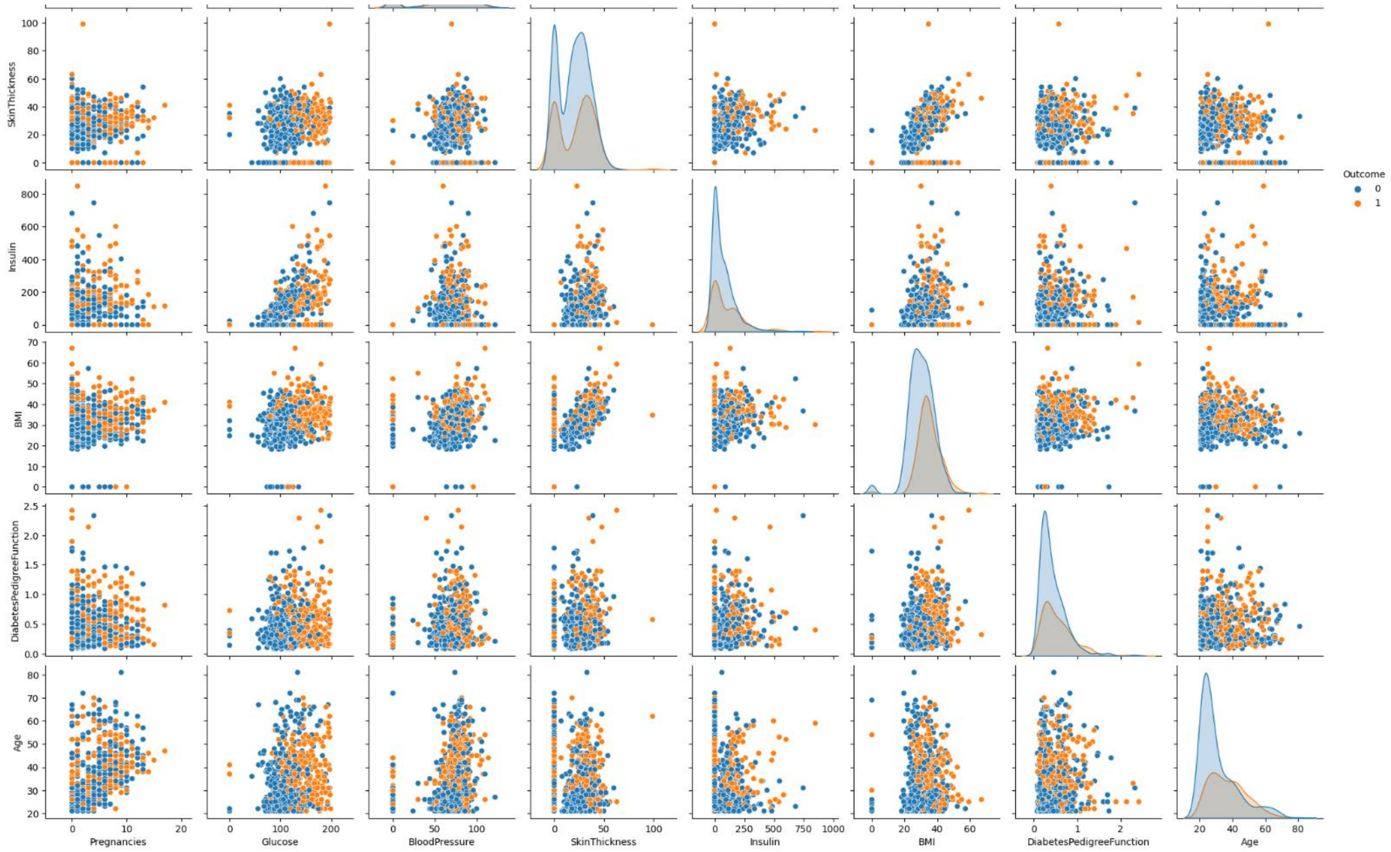
```
<Axes: xlabel='Outcome', ylabel='count'>
```



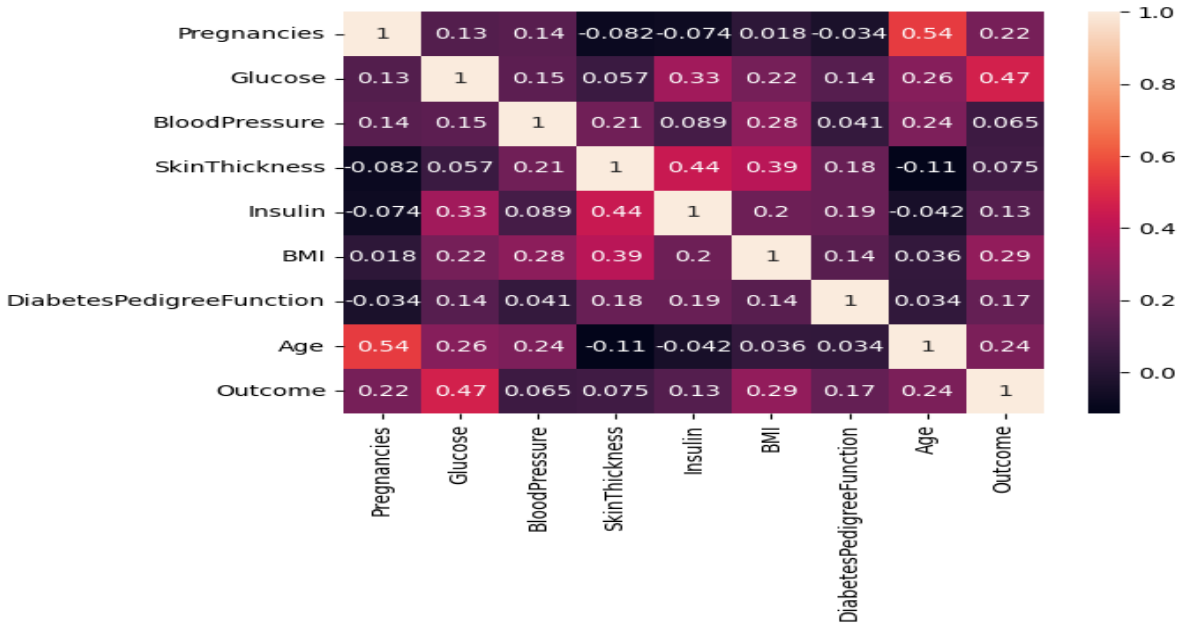
```
# Pairplot
sns.pairplot(data = dataset, hue = 'Outcome')
plt.show()
```

```
/opt/conda/lib/python3.10/site-packages/seaborn/axisgrid.py:118: UserWarning: The figure layout has changed to tight
  self._figure.tight_layout(*args, **kwargs)
```





```
# Heatmap
sns.heatmap(dataset.corr(), annot = True)
plt.show()
```



Processing the Data

```
# Replacing zero values with NaN
dataset_new = dataset
dataset_new[["Glucose", "BloodPressure", "SkinThickness", "Insulin", "BMI"]] = dataset_new[["Glucose",
"BloodPressure", "SkinThickness", "Insulin", "BMI"]].replace(0, np.NaN)
```

linkcode

```
# Count of NaN
dataset_new.isnull().sum()
```

```
Pregnancies             0
Glucose                 5
BloodPressure           35
SkinThickness          227
Insulin                374
BMI                    11
DiabetesPedigree
Function               0
Age                    0
Outcome                0
dtype: int64
```

```
# Replacing NaN with mean values
dataset_new["Glucose"].fillna(dataset_new["Glucose"].mean(), inplace = True)
dataset_new["BloodPressure"].fillna(dataset_new["BloodPressure"].mean(), inplace = True)
dataset_new["SkinThickness"].fillna(dataset_new["SkinThickness"].mean(), inplace = True)
dataset_new["Insulin"].fillna(dataset_new["Insulin"].mean(), inplace = True)
dataset_new["BMI"].fillna(dataset_new["BMI"].mean(), inplace = True)
```

```
dataset_new.isnull().sum()
```

```
Pregnancies             0
Glucose                 0
BloodPressure           0
SkinThickness           0
Insulin                 0
BMI                     0
DiabetesPedigree
Function                0
Age                     0
Outcome                 0
dtype: int64
```

Logistic Regression

```
y = dataset_new['Outcome']
X = dataset_new.drop('Outcome', axis=1)
```

```
# Splitting X and Y
from sklearn.model_selection import train_test_split
X_train, X_test, Y_train, Y_test = train_test_split(X, y, test_size = 0.20, random_state = 42, stratify = datase
t_new['Outcome'] )
```

```
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()
model.fit(X_train, Y_train)
y_predict = model.predict(X_test)
```

```
from sklearn.linear_model import LogisticRegression
model = LogisticRegression()
model.fit(X_train, Y_train)
```

```
y_predict = model.predict(X_test)
```

```
/opt/conda/lib/python3.10/site-packages/sklearn/linear_model/_logistic.py:458: ConvergenceWarning: lbfgs
failed to converge (status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
    https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
    https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
  n_iter_i = _check_optimize_result(
```

```
y_predict
```

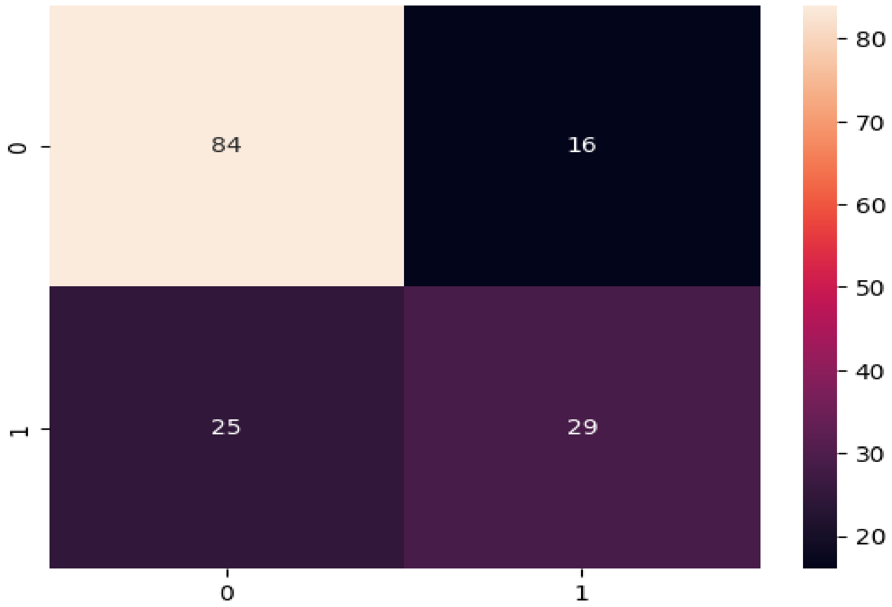
```
array([1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1,
       0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0,
       0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 0,
       1, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
       0, 0, 1, 1, 0, 0, 0, 1, 1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 1,
       0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 1, 0, 1, 1, 1, 0, 0, 0, 1,
       0, 1, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0])
```

```
# Confusion matrix
from sklearn.metrics import confusion_matrix
cm = confusion_matrix(Y_test, y_predict)
cm
```

```
array([[84, 16],
       [25, 29]])
```

```
# Heatmap of Confusion matrix
sns.heatmap(pd.DataFrame(cm), annot=True)
```

```
<Axes: >
```



```
from sklearn.metrics import accuracy_score
accuracy =accuracy_score(Y_test, y_predict)
accuracy

0.7337662337662337
y_predict = model.predict([[1,148,72,35,79.799,33.6,0.627,50]])
print(y_predict)
if y_predict==1:
    print("Diabetic")
else:
    print("Non Diabetic")
[1]
Diabetic
/opt/conda/lib/python3.10/site-packages/sklearn/base.py:439: UserWarning: X does not have valid feature n
ames, but LogisticRegression was fitted with feature names
  warnings.warn(
```

CONCLUSION:

In conclusion ,implementing innovative techniques such as machine learning algorithms ,big data analytics, and continuous model refinement are pivotal in enhancing prediction system accuracy. Embracing advancements in artificial intelligence, leveraging diverse data sources and fostering a culture of ongoing research and development can significantly contribute to the precision and realiability of prediction systems, ensuring their effectiveness in various domains and industries.