AN ENSEMBLE MACHINE LEARNING-BASED APPROACH TO PREDICT THYROID DISEASE USING HYBRID FEATURE SELECTION

Report submitted to SASTRA Deemed to be University

As per the requirement for the course

INT300 - MINI PROJECT

Submitted by

126015050 - Leena Sree S (B.Tech-Information Technology)

126015123 - Vsha Gopika Pa (B.Tech-Information Technology)

126015124 - Yazhini R (B.Tech-Information Technology)

MAY 2025



SCHOOL OF COMPUTING THANJAVUR, TAMILNADU, INDIA-613401



THANJAVUR KUMBAKONAM CHENNAI

SCHOOL OF COMPUTING THANJAVUR, TAMILNADU, INDIA-613401

BONAFIDE CERTIFICATE:

This is to certify that the report titled "An Ensemble Machine-Learning Based Approach to Predict Thyroid disease using Hybrid Feature Selection" submitted as a requirement for the course, INT 300 - MINI PROJECT for B.Tech. is a bonafide record of the work done by S.Leena Sree (Reg. No. 126015050, B. Tech-IT), Pa.Vsha Gopika (Reg. No. 126015123, B. Tech-IT), R.Yazhini (Reg. No. 126015123, B. Tech-IT) during the academic year 2024-25, in the School of Computing, under my supervision.

Signature of Project Supervisor: 3.7
Name with Affiliation: Dr.THAMOTHARAN B, Assistant Professor-III.
Date: 05-05-2025.
Mini Project Viva voice held on

Examiner 1 Examiner 2

ACKNOWLEDGEMENTS:

We would like to thank our Honorable Chancellor **Prof. R. Sethuraman** for providing us with an opportunity and the necessary infrastructure for carrying out this project as a part of our curriculum.

We would like to thank our Honorable Vice-Chancellor **Dr. S. Vaidhyasubramaniam** and **Dr. S. Swaminathan**, Dean, Planning & Development, for the encouragement and strategic support at every step of our college life.

We extend our sincere thanks to **Dr. R. Chandramouli**, Registrar, SASTRA Deemed to be University for providing the opportunity to pursue this project.

We extend my/our heartfelt thanks to **Dr. V. S. Shankar Sriram**, Dean, School of Computing, **Dr. R. Muthaiah**, Associate Dean, Research, **Dr. K.Ramkumar**, Associate Dean, Academics, **Dr. D.Manivannan**, Associate Dean, Infrastructure, **Dr. R. Alageswaran**, Associate Dean, Students Welfare.

Our guide **Dr** .**THAMOTHARAN B** Assistant Professor-III, School of Computing was the driving force behind this whole idea from the start. His deep insight in the field and valuable suggestions helped us in making progress throughout our project work. We also thank the project review panel members for their valuable comments and insights which made this project better.

We would like to extend our gratitude to all the teaching and non-teaching faculties of the School of Computing who have either directly or indirectly helped us in the completion of the project.

We gratefully acknowledge all the contributions and encouragement from my family and friends resulting in the successful completion of this project. We thank you all for providing me an opportunity to showcase my skills through this project.

List of Figures

Fig No.	Title	Page No.
1.1	Proposed model architecture	3
4.1	Original class and Balanced training class distribution	12
4.2	Top 15 Selected Features	12
4.3	Results before Feature Selection	13
4.4	Results after Feature Selection	13
4.5	Model Evaluation Metrics of Random Forest	14
4.6	Model Evaluation Metrics of Gradient Boosting	15
4.7	Model Evaluation Metrics of Decision Tree	16
4.8	Model Evaluation Metrics of MLP	17
4.9	Model Evaluation Metrics of KNN	18
4.10	Hyperparameter Tuning (GF + DT + RF)	19
4.11	Ensemble Evaluation (Hard and Soft Voting)	19
4.12	Model Accuracy Comparison(Voting)	20
4.13	Model Accuracy Comparison	20
4.14	Model Comparison(Voting)	21
4.15	AUC Scores	21
4.16	ROC Curve	22

ABSTRACT:

The increasing prevalence of thyroid diseases requires early and correct diagnosis to prevent serious health outcomes. In this paper, we introduce a machine learning-based approach that predicts thyroid disease based on hybrid feature selection and ensemble learning techniques. Our model utilizes five various machine learning classifiers, which are optimized by hard voting and soft voting to improve prediction accuracy and stability. To address the issue of class imbalance, SMOTE (Synthetic Minority Oversampling Technique) proved to significantly improve model performance. The hybrid feature selection methods comprised of XGBoost and SelectKBest. These methods were executed in tandem to filter the input features such that only the most relevant clinical variables remained, which are critical to making the final predictions.

By conducting an exhaustive amount of experimentation our ensemble model performed exceptionally well achieving 100% sensitivity and 99.25% accuracy, outperforming traditional diagnosis methods as well as present-day machine learning models. The feature selection, data balancing and ensemble methods combining is significant to the reliability of the proposed system which will likely lead to greater adoption in an unregulated real-world clinic context. The proposed methodology identifies complex patterns and relationships in the data can offer a tool with considerable potential to improve the early detection of thyroid disease which positively impacts the management of the patient and lowers the burden on the health service.

KEYWORDS: Ensemble Learning, Hybrid Feature Selection, XGBoost, SelectKBest, SMOTE.

TABLE OF CONTENTS:

Title	Page No
Bonafide Certificate	ii
Acknowledgement	iii
List of Figures	iv
Abstract	V
1. Summary of the base paper	1
2. Merits and Demerits of the base paper	5
3. Source Code	6
4. Output Snapshots	12
5. Conclusion and Future Plans	23
6. References	24
7. Appendix-Base Paper	25

SUMMARY OF BASE PAPER

1.1 INTRODUCTION:

Thyroid hormones play a vital role in metabolism, central and peripheral nervous system development along with reproductive actions. When the thyroid is dysfunctional and does not produce hormones in sufficient amounts or sequences, the disorders include hypothyroidism or hyperthyroidism. Dysfunction of thyroid hormones appears to be a common problem as it is expected that 30% to 40% of patients who attend endocrinology outpatient clinics have some form of thyroid dysfunction and many may remain undiagnosed, a possibility due to early treatment in the illness and undiagnosed sequelae of the disease. Timely diagnosis and a correct diagnosis are crucial for treatment but may be difficult as patients have such a wide range of symptoms that an observation can only be considered a biochemical or clinical evaluation at a later stage, which is a barrier in care and treatment. With the increasing incidence of thyroid disorders being influenced by ongoing lifestyle changes and environment exposures, a need in clinical methods of diagnosing thyroid diseases exists. Developments in artificial intelligence and machine learning have encouraged unique opportunities for improved diagnosis.

1.2 RELATED WORK:

At first, machine learning algorithms like logistic regression, support vector machines (SVM), decision trees, and K-nearest neighbors (KNN) were being used extensively for the diagnosis of diseases. These have been an initial step over traditional manual diagnosis with reasonable accuracy measures. But these used to struggle with complex nonlinear relations, which are exceedingly prevalent in medical data sets, and noisy or high-dimensional data. Though improving prediction accuracy, ensemble approaches such as Random Forests and basic voting classifiers generally performed poor feature selection. Though improving the prediction

accuracy, ensemble techniques such as Random Forests and basic voting classifiers failed to achieve effective feature selection strategies, hence introducing redundant or unnecessary features in influencing model performances. The models were also negatively affected by class imbalance issues. Hybrid feature selection techniques were thus developed to solve such issues that aim at the most informative features and filter the input space using techniques such as SelectKBest and XGBoost together. Moreover, this SMOTE also gained popularity as a solution to correct imbalance problems through generating synthetic examples for minority classes. Ensemble systems with more than one highly accurate classifier and advanced voting mechanisms further enhanced prediction accuracy and stability in thyroid disease.

1.3 PROPOSED SOLUTION AND SYSTEM ARCHITECTURE:

The proposed solution outlined in this paper utilizes an ensemble machine learning model to improve the prediction of thyroid diseases through a systematic architecture. The proposed architecture for the model included some data balancing techniques, such as Random Oversampling (ROS), which corrects for class imbalance problems and increase classification performance. And, it employed XGBoost and Select-K-Best to choose the most important features from the dataset and to make better predictions. The proposed model uses multiple classifiers including Random Forest, K-Nearest Neighbors, Decision Trees, Gradient Boosting, and Multi-Layer Perceptron, and considers them in an ensemble learning framework, in order to gain from its contribution and increase the overall accuracy of the prediction. The proposed architecture also implemented a performance evaluation process that included many metrics: accuracy, sensitivity, specificity, F1-score, recall, and precision metrics. This verified the model was performed properly, and makes comparison to existing methods based on the ability to predict thyroid diseases. Thus, the proposed solution demonstrates an effective and flexible way of predicting thyroid diseases, and ultimately can lead to better early detection and treatment in a clinical setting.

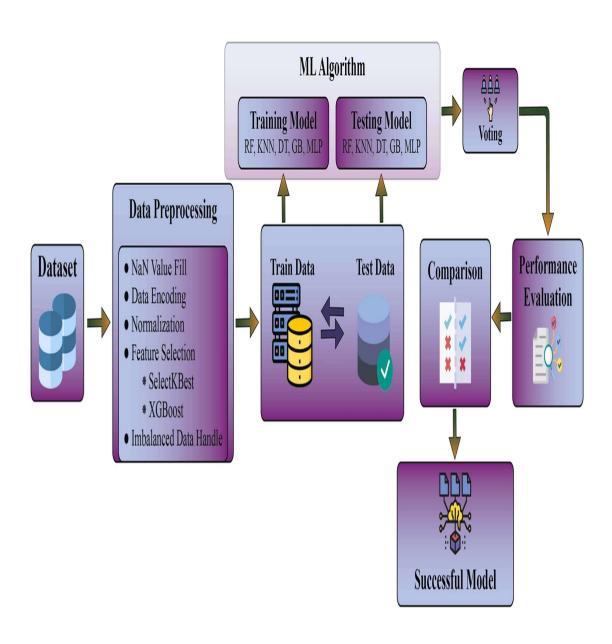


Fig 1.1 Proposed model architecture

1.4 METHODOLOGIES AND IMPLEMENTATION:

The proposed model for thyroid disease prediction follows a systematic machine learning pipeline. The first step is to preprocess the data from the UCI repository to include quality and consistency through imputation of missing data, encoding of categorical features, and scale all features uniformly using Min-Max normalization. In order to further improve the models and reduce dimensionality, a hybrid feature selection method using XGBoost and SelectKBest was used, and the final features were chosen based on the importance score of each feature from both feature selection methods.

The class distribution is imbalanced towards the non-diseased cases, so a method of balancing the dataset by using random oversampling (ROS) was deployed to reduce the bias in our model. The balanced dataset was then split into 75% train set and 25% test set.

Five classifiers were trained independently using; Random Forest (RF), Decision Tree (DT), k-Nearest Neighbor (KNN), Gradient Boosting (GB), and Multilayer Perceptron (MLP), where performance was assessed based on accuracy, precision, recall, F1-Score, and ROC-AUC metrics.

To improve prediction robustness, an ensemble learning classifier (Hard Voting) was used whereby the RF and DT classifiers were combined. The Hard Voting ensemble achieved 99.71% accuracy and 100% sensitivity. Overall, hybrid feature selection, class balancing, and ensemble learning methods to integrate the strengths of all five classifiers will improve reliability and identification of thyroid disease.

2.1 MERITS OF BASE PAPER:

- **High Accuracy:** Achieves 99.71% accuracy and 100% sensitivity using the Ensemble ML classifier with hard voting on RF and DT models.
- Effective Feature Selection: Utilizes XGBoost and SelectKBest to identify relevant features, enhancing model performance and reducing overfitting.
- Class Imbalance Handling: Implements Random Oversampling to address class imbalance, improving classification performance.
- Comprehensive Methodology: Employs a systematic approach including data preprocessing, feature selection, and multiple algorithms for robust predictions.
- **Ensemble Learning:** Combines predictions from multiple models through an ensemble strategy, increasing reliability and resilience to data variations.

2.2 DEMERITS OF BASE PAPER:

- **Simple Missing Value Handling:** The study uses basic mean/median imputation, which may not be effective for complex medical datasets requiring more advanced techniques.
- **Single Dataset Limitation**: The model was trained and tested only on the UCI Thyroid dataset, limiting its generalization to diverse or real-world clinical data.
- Lack of Cross-Validation: The paper does not employ strong cross-validation methods like k-fold, which could make the model less robust against unseen data.
- Risk of Overfitting with Random Oversampling: By duplicating minority samples
 instead of generating synthetic data, the model risks overfitting and reduced
 generalization.
- **Absence of Model Explainability:** No explainable AI (XAI) techniques like SHAP or LIME were used to interpret feature importance, which is critical in medical predictions.

SOURCE CODE

3.1. INSTALLING NECESSARY PACKAGES

```
import seaborn as sns
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import warnings
import time
import psutil
import os
warnings.filterwarnings('ignore')
from sklearn.model selection import train test split, StratifiedKFold, cross val score,
GridSearchCV
from sklearn.preprocessing import LabelEncoder, StandardScaler, OneHotEncoder
from sklearn.impute import SimpleImputer
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.feature selection import SelectKBest, f classif
from sklearn.metrics import (
accuracy score, precision score, recall score, fl score,
confusion matrix, classification report, roc auc score, RocCurveDisplay
from sklearn.ensemble import RandomForestClassifier, GradientBoostingClassifier,
VotingClassifier
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.neural network import MLPClassifier
from xgboost import XGBClassifier
from imblearn.combine import SMOTETomek
```

3.2 LOADING DATASET AND ENCODING

```
df = pd.read_csv("ThyroidDS.csv")
X = df.drop(columns=['target'])
y = df['target']
le = LabelEncoder()
y_encoded = le.fit_transform(y)
```

3.3 PROCESSING PIPELINES

```
cat_cols = X.select_dtypes(include=['object']).columns.tolist()
num_cols = X.select_dtypes(include=['int64', 'float64']).columns.tolist()
```

```
num transformer = Pipeline([
  ('imputer', SimpleImputer(strategy='mean')),
 ('scaler', StandardScaler())
1)
cat transformer = Pipeline([
  ('imputer', SimpleImputer(strategy='most frequent')),
  ('encoder', OneHotEncoder(handle unknown='ignore', sparse output=False))
preprocessor = ColumnTransformer([
  ('num', num transformer, num cols),
  ('cat', cat transformer, cat cols)
1)
3.4 TRAIN TEST SPLIT AND BALANCING
X train, X test, y train, y test = train test split(
  X, y encoded, test size=0.25, stratify=y encoded, random state=42
X train processed = preprocessor.fit transform(X train)
X test processed = preprocessor.transform(X test)
smote tomek = SMOTETomek(random state=42)
X train bal, y train bal = smote tomek.fit resample(X train processed, y train)
X test bal, y test bal = smote tomek.fit resample(X test processed, y test)
print("Original class distribution:\n", pd.Series(y encoded).value counts())
print("\nBalanced training class distribution:\n", pd.Series(y train bal).value counts())
3.5 FEATURE SELECTION (XGBOOST + SELECTKBEST)
xgb model = XGBClassifier(use label encoder=False, eval metric='logloss',
random state=42)
xgb model.fit(X train bal, y train bal)
xgb importance = pd.DataFrame({
  'Feature': range(X train bal.shape[1]),
  'Importance': xgb model.feature importances
{}).sort_values(by='Importance', ascending=False).head(19)
k best = SelectKBest(score func=f classif, k=19)
k best.fit(X train bal, y train bal)
top 19 kbest = list(np.where(k best.get support())[0])
combined features = list(set(xgb importance['Feature']).union(set(top 19 kbest)))
top 15 combined = combined features[:15]
feature names = preprocessor.get feature names out()
selected feature names = [feature names[i] for i in top 15 combined]
print("Top 15 Selected Features:\n", selected feature names)
X train sel = X train bal[:, top 15 combined]
X test sel = X test bal[:, top 15 combined]
sc = StandardScaler()
X train scaled = sc.fit transform(X train sel)
```

```
X test scaled = sc.transform(X test sel)
```

3.6 DEFINE MODELS AND EVALUATION FUNCTION

```
mods = {
  "Random Forest": RandomForestClassifier(class weight='balanced', random state=42),
  "Gradient Boosting": GradientBoostingClassifier(random state=42),
  "Decision Tree": DecisionTreeClassifier(class weight='balanced', random state=42),
  "MLP Classifier": MLPClassifier(hidden layer sizes=(100, 50), max iter=1000,
random state=42),
  "KNN": KNeighborsClassifier(n neighbors=11, weights='distance', metric='manhattan')
def evaluate model(name, mod, X train, X test, y train, y test):
  process = psutil.Process(os.getpid())
  start train = time.time()
  mod.fit(X train, y train)
  end train = time.time()
  start pred = time.time()
  y pred = mod.predict(X test)
  end pred = time.time()
  memory usage = process.memory info().rss / (1024 * 1024)
  return {
    'Model': name.
    'Train Time (s)': end train - start train,
    'Prediction Time (s)': end pred - start pred,
    'Memory Usage (MB)': memory usage
```

3.7 EVALUATION BEFORE AND AFTER FEATURE SELECTION

```
results_before = [evaluate_model(name, mod, X_train_processed, X_test_processed, y_train, y_test) for name, mod in mods.items()]
results_after = [evaluate_model(name, mod, X_train_scaled, X_test_scaled, y_train_bal, y_test_bal) for name, mod in mods.items()]
df_before = pd.DataFrame(results_before)
df_after = pd.DataFrame(results_after)
print("Results Before Feature Selection:\n", df_before)
print("\nResults After Feature Selection:\n", df after)
```

3.8 MODEL EVALUATION WITH METRICS AND PLOTS

```
model_accuracies = {}
model_auc_scores = {}
def evaluate_model_metrics(model, X_test, y_test, model_name):
    y_pred = model.predict(X_test)
    y_prob = model.predict_proba(X_test)[:, 1]
    cm = confusion_matrix(y_test, y_pred)
    tn, fp, fn, tp = cm.ravel() if cm.shape == (2, 2) else (0, 0, 0, 0)
```

```
accuracy = accuracy score(y test, y pred) * 100
  precision = precision score(y test, y pred, average='weighted') * 100
  recall = recall_score(y_test, y_pred, average='weighted') * 100
  f1 = f1 score(y test, y pred, average='weighted') * 100
  specificity = tn / (tn + fp) * 100 if (tn + fp) > 0 else 0
  auc score = roc auc score(y test, y prob) * 100
  model accuracies[model name] = accuracy
  model auc scores[model name] = auc score
  print(f"\n--- {model name} ---")
  print(f"Confusion Matrix:\n{cm}")
  print(f"Accuracy: {accuracy:.2f}%")
  print(f"Precision: {precision:.2f}%")
  print(f'Recall: {recall:.2f}%")
  print(f"F1 Score: {f1:.2f}%")
  print(f"Specificity: {specificity:.2f}%")
  print(classification report(y test, y pred, target names=le.classes ))
  plt.figure(figsize=(5, 4))
  sns.heatmap(cm, annot=True, fmt='d', cmap='Blues', xticklabels=le.classes,
yticklabels=le.classes )
  plt.title(fConfusion Matrix - {model name}')
  plt.xlabel('Predicted')
  plt.ylabel('Actual')
  plt.tight layout()
  plt.show()
for name, model in mods.items():
  model.fit(X train scaled, y train bal)
  evaluate model metrics(model, X test scaled, y test bal, name)
3.9 HYPERPARAMETER TUNING(GF + RF + DT)
param grid gb = \{
  'n estimators': [50, 100, 200],
  'max depth': [3, 4, 5],
  'learning rate': [0.1, 0.05, 0.001]
grid search gb = GridSearchCV(GradientBoostingClassifier(random state=42),
param grid gb, cv=3, scoring='accuracy', n jobs=-1, verbose=1)
grid search gb.fit(X train sel, y train bal)
best gb = grid search gb.best estimator
param grid rf = \{
  'n estimators': [50, 100, 200],
  'max depth': [3, 4, 5],
  'min samples split': [2, 5, 10]
grid search rf = GridSearchCV(RandomForestClassifier(random state=42), param grid rf,
cv=3, scoring='accuracy', n jobs=-1, verbose=1)
grid search rf.fit(X train sel, y train bal)
best rf = grid search rf.best estimator
param grid dt = {
  'max depth': [3, 4, 5],
```

```
'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 5]
}
grid_search_dt = GridSearchCV(DecisionTreeClassifier(random_state=42), param_grid_dt,
    cv=3, scoring='accuracy', n_jobs=-1, verbose=1)
grid_search_dt.fit(X_train_sel, y_train_bal)
best_dt = grid_search_dt.best_estimator_

3.10 ENSEMBLE_EVALUATION(VOTING CLASSIFIER)

combinations = [
```

```
combinations = [
  (('gb', best gb), ('rf', best rf)),
  (('gb', best gb), ('dt', best dt)),
  (('rf', best rf), ('dt', best dt)),
  (('gb', best gb), ('rf', best rf), ('dt', best dt))
skf = StratifiedKFold(n splits=10, shuffle=True, random state=42)
def evaluate ensemble cv(voting type, model list, model names):
  ensemble = VotingClassifier(estimators=model list, voting=voting type,
weights=[1]*len(model list) if voting type=='soft' else None)
  scores = cross val score(ensemble, X train sel, y train bal, cv=skf, scoring='accuracy')
  avg score = np.mean(scores) * 100
  print(f"{ '+'.join(model names)} ({voting type.title()} Voting): {avg score:.2f}%")
  return {'Model': ' + '.join(model names), 'Voting': voting type, 'Accuracy': avg score}
results = []
for voting in ['hard', 'soft']:
  for combo in combinations:
     names = [name.upper() for name, in combo]
     results.append(evaluate ensemble cv(voting, list(combo), names))
df results = pd.DataFrame(results)
pivoted = df results.pivot(index="Model", columns="Voting",
values="Accuracy").reset index()
pivoted.columns = ['Model Name', 'Hard Voting (%)', 'Soft Voting (%)']
print("\nFinal Accuracy Table:\n")
print(pivoted.to string(index=False))
```

3.11 PLOTTING ACCURACY AND ROC CURVES

```
plt.figure(figsize=(10, 6))
plt.bar(model_accuracies.keys(), model_accuracies.values(), color='skyblue')
plt.ylabel('Accuracy (%)')
plt.title('Model Accuracy Comparison')
plt.xticks(rotation=45)
plt.ylim(0, 100)
plt.tight_layout()
plt.show()
print("\nAUC Scores of All Classifiers:")
for model_name, auc in model_auc_scores.items():
```

```
print(f"{model name}: {auc:.2f}%")
plt.figure(figsize=(10, 8))
for name, model in mods.items():
  if hasattr(model, "predict proba"):
     y proba = model.predict proba(X test scaled)[:, 1]
     RocCurveDisplay.from predictions(y test bal, y proba, name=name, ax=plt.gca())
plt.plot([0, 1], [0, 1], 'k--')
plt.title("ROC Curves for All Classifiers")
plt.xlabel("False Positive Rate")
plt.ylabel("True Positive Rate")
plt.legend(loc="lower right")
plt.grid(True)
plt.show()
model names = ['Random Forest', 'Decision Tree', 'KNN', 'Gradient Boost', 'MLP', 'Voting
(RF+DT)']
accuracies = [98.37, 97.34, 96.03, 96.71, 89.40, 99.71] # example values in %
plt.figure(figsize=(10, 6))
bars = plt.bar(model names, accuracies, color=['skyblue', 'lightgreen', 'salmon', 'violet',
'orange', 'gold'])
for bar in bars:
  yval = bar.get height()
  plt.text(bar.get x() + bar.get width()/2.0, yval + 0.3, f'{yval}\%', ha='center', va='bottom',
fontsize=10)
plt.title('Accuracy Comparison of ML Models and Voting Classifier')
plt.ylabel('Accuracy (%)')
plt.ylim(85, 101)
plt.xticks(rotation=30)
plt.grid(axis='y', linestyle='--', alpha=0.7)
plt.tight layout()
plt.show()
models = ['Hard vote(GB+RF)', 'Hard vote(GB+DT)', 'Hard vote(RF+DT)',
'Hard vote(GB+RF+DT)', 'soft vote(GB+RF)', 'soft Voting (GB+DT)', 'soft vote(RF+DT)',
'soft vote(GB+RF+DT)']
accuracies = [99.05, 98.72, 98.74, 99.11, 99.23, 99.14, 98.83, 99.14]
plt.figure(figsize=(10, 8))
bars = plt.bar(models, accuracies, color=['pink', 'pink', 'pink', 'pink', 'skyblue', 'skyblue',
'skvblue', 'skvblue'l)
for bar in bars:
  plt.text(bar.get x() + bar.get width()/2.0, bar.get height() + 0.4,
        f'{bar.get height()}%', ha='center', fontsize=10)
plt.title('Model Accuracy Comparison (Including Voting Classifier)')
plt.ylabel('Accuracy (%)')
plt.ylim(85, 101)
plt.xticks(rotation=30)
plt.grid(axis='y', linestyle='--', alpha=0.7)
plt.tight layout()
plt.show()
```

OUTPUT SNAPSHOTS

Original class distribution:

1 3012

0 151

Name: count, dtype: int64

Balanced training class distribution:

1 2259

0 2259

Name: count, dtype: int64

Fig 4.1 Original class and Balanced training class distribution

Top 15 Selected Features:

['num_age', 'num_hypopituitary', 'num_TSH_measured', 'num_T3_measured', 'num_T T4_measured', 'num_T4U_measured', 'num_FTI', 'cat_sex_F', 'cat_sex_M', 'cat_on_thyroxine_f', 'cat_on_thyroxine_t', 'cat_query_on_thyroxine_f', 'cat_query_on_thyroxine_t', 'cat_on_antithyroid_meds_f', 'cat_on_antithyroid_meds_t']

Fig 4.2 Top 15 Selected Features

Results Before Feature Selection:

	Model	Train Time (s)	Prediction Time (s)	Memory Usage (MB)
0	Random Forest	0.500044	0.015595	237.468750
1	Gradient Boosting	1.143686	0.002484	237.453125
2	Decision Tree	0.011593	0.000000	237.453125
3	MLP Classifier	8.368009	0.000000	240.335938
4	KNN	0.000000	0.109371	240.570312

Fig 4.3 Results before Feature Selection

Results After Feature Selection:

	Model	Train Time (s)	Prediction Time (s)	Memory Usage (MB)
0	Random Forest	0.997834	0.038577	240.589844
1	Gradient Boosting	2.208230	0.000000	240.421875
2	Decision Tree	0.046875	0.000000	240.421875
3	MLP Classifier	14.531235	0.015623	240.906250
4	KNN	0.015638	0.249957	241.148438

Fig 4.4 Results after Feature Selection

Accuracy: 98.14% Precision: 98.15% Recall: 98.14% F1 Score: 98.14% Specificity: 97.34%

	precision	recall	f1-score	support
hypothyroid	0.99	0.97	0.98	752
negative	0.97	0.99	0.98	752
accuracy			0.98	1504
macro avg	0.98	0.98	0.98	1504
weighted avg	0.98	0.98	0.98	1504

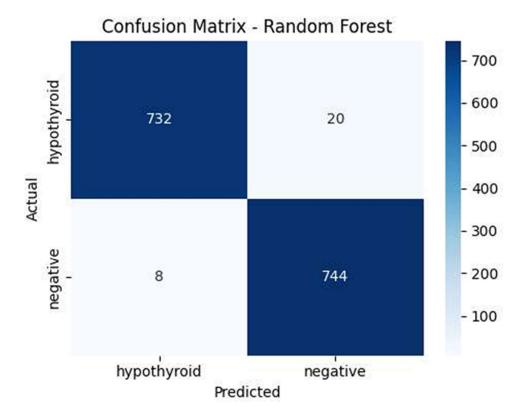


Fig 4.5 Model Evaluation Metrics of Random Forest

--- Gradient Boosting ---

Confusion Matrix:

[[726 26] [5 747]]

Accuracy: 97.94% Precision: 97.98% Recall: 97.94% F1 Score: 97.94% Specificity: 96.54%

	precision	recall	f1-score	support
hypothyroid	0.99	0.97	0.98	752
negative	0.97	0.99	0.98	752
accuracy			0.98	1504
macro avg	0.98	0.98	0.98	1504
weighted avg	0.98	0.98	0.98	1504

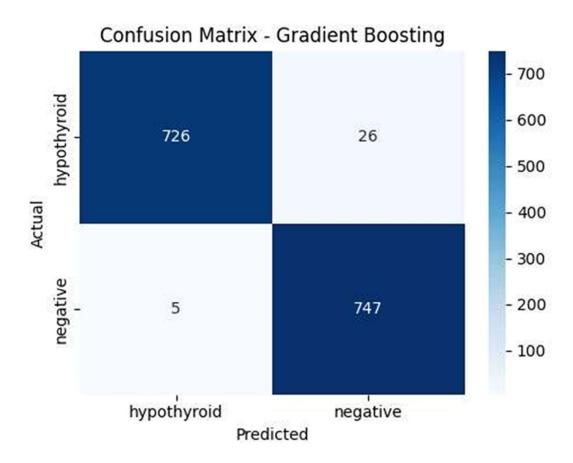


Fig 4.6 Model Evaluation Metrics of Gradient Boosting

--- Decision Tree ---

Confusion Matrix:

[[723 29] [6 746]]

Accuracy: 97.67% Precision: 97.72% Recall: 97.67% F1 Score: 97.67% Specificity: 96.14%

	precision	recall	f1-score	support
hypothyroid	0.99	0.96	0.98	752
negative	0.96	0.99	0.98	752
accuracy			0.98	1504
macro avg	0.98	0.98	0.98	1504
weighted avg	0.98	0.98	0.98	1504

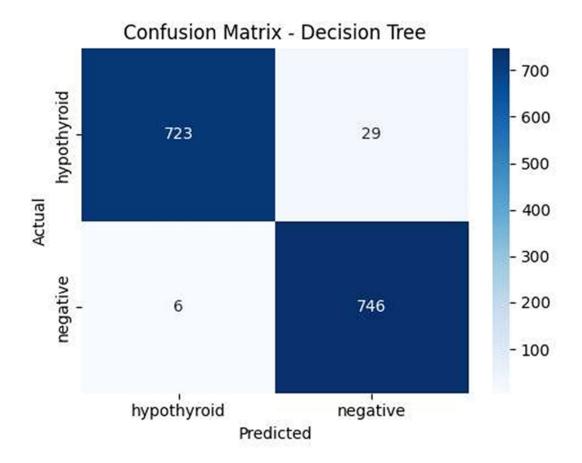


Fig 4.7 Model Evaluation Metrics of Decision Tree

--- MLP Classifier ---Confusion Matrix: [[696 56]

[9 743]]

Accuracy: 95.68% Precision: 95.86% Recall: 95.68% F1 Score: 95.67% Specificity: 92.55%

	precision	recall	f1-score	support
hypothyroid	0.99	0.93	0.96	752
negative	0.93	0.99	0.96	752
accuracy			0.96	1504
macro avg	0.96	0.96	0.96	1504
weighted avg	0.96	0.96	0.96	1504

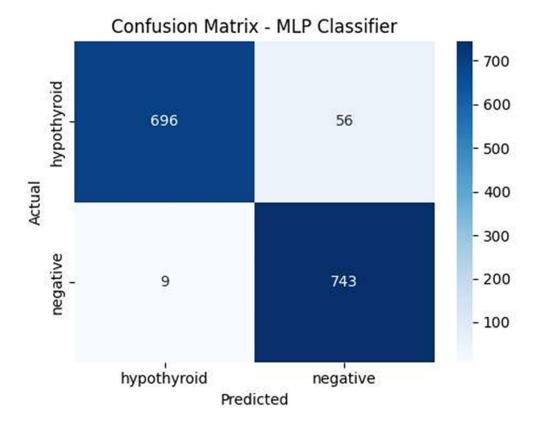


Fig 4.8 Model Evaluation Metrics of MLP

--- KNN ---

Confusion Matrix:

[[724 28] [22 730]]

Accuracy: 96.68% Precision: 96.68% Recall: 96.68% F1 Score: 96.68% Specificity: 96.28%

	precision	recall	f1-score	support
hypothyroid negative	0.97 0.96	0.96 0.97	0.97 0.97	752 752
accuracy macro avg weighted avg	0.97 0.97	0.97 0.97	0.97 0.97 0.97	1504 1504 1504

Confusion Matrix - KNN

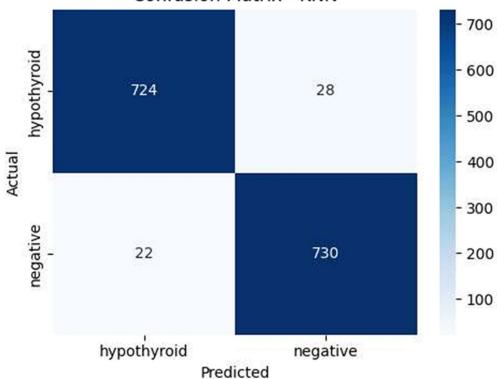


Fig 4.9 Model Evaluation Metrics of KNN

```
Fitting 3 folds for each of 27 candidates, totalling 81 fits Fitting 3 folds for each of 27 candidates, totalling 81 fits Fitting 3 folds for each of 27 candidates, totalling 81 fits
```

Fig 4.10 Hyperparameter Tuning(GF + DT + RF)

```
GB + RF (Hard Voting): 99.05%
GB + DT (Hard Voting): 98.72%
RF + DT (Hard Voting): 98.74%
GB + RF + DT (Hard Voting): 99.11%
GB + RF (Soft Voting): 99.23%
GB + DT (Soft Voting): 99.14%
RF + DT (Soft Voting): 98.83%
GB + RF + DT (Soft Voting): 99.14%
```

Final Accuracy Table:

```
Model Name Hard Voting (%) Soft Voting (%)
GB + DT 98.716471 99.137021
GB + RF 99.048427 99.225566
GB + RF + DT 99.114750 99.136972
RF + DT 98.738644 98.827090
```

Fig 4.11 Ensemble Evaluation(Hard and Soft Voting)

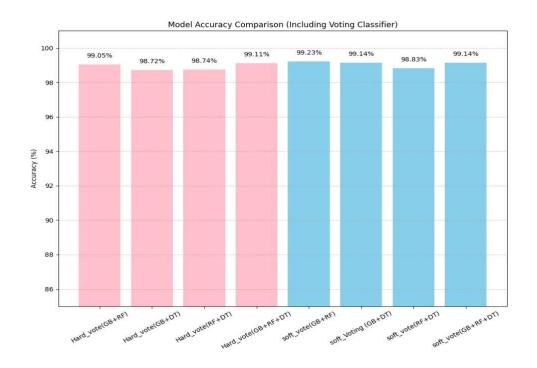


Fig 4.12 Model Accuracy Comparison(Voting)

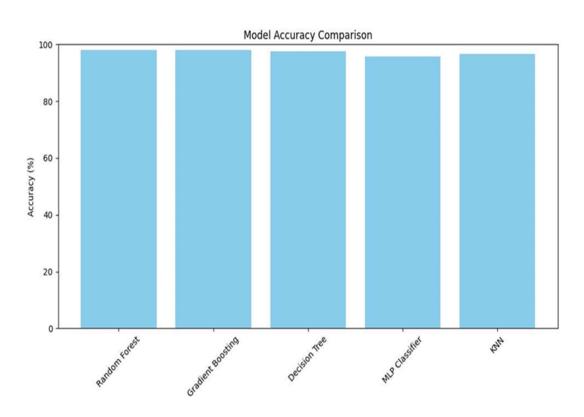


Fig 4.13 Model Accuracy Comparison

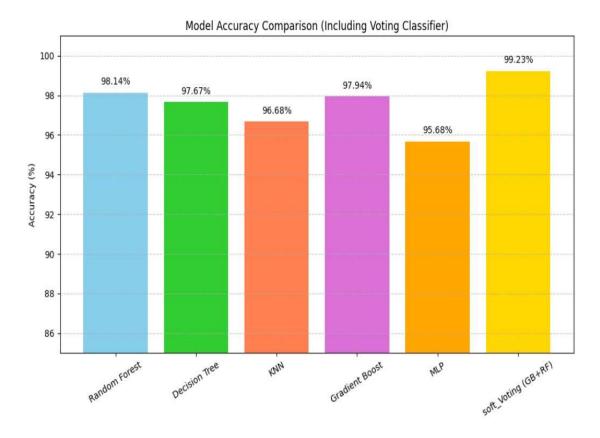


Fig 4.14 Model Comparison(Voting)

AUC Scores of All Classifiers:

Random Forest: 99.74%

Gradient Boosting: 99.59%

Decision Tree: 97.67% MLP Classifier: 98.45%

KNN: 98.67%

Fig 4.15 AUC Scores

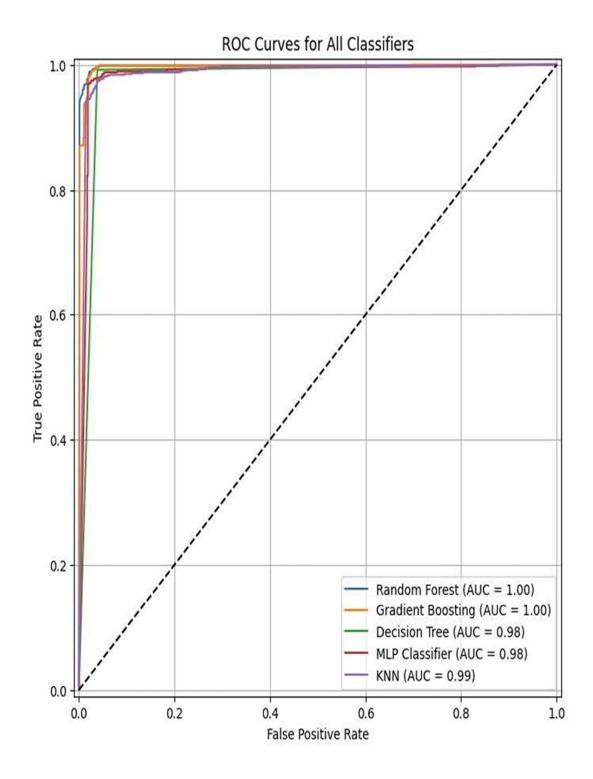


Fig 4.16 ROC Curve

CONCLUSION AND FUTURE PLAN

5.1 CONCLUSION:

The study attempted to implement hybrid feature selection for developing an ensemble-based machine learning model that accurately predicts thyroid disorders. The system achieved better results compared to previous benchmarks in accuracy, sensitivity, and specificity due to class imbalance handling with SMOTE, feature selection through XGBoost with SelectKBest, and several other methods. By analyzing a broad set of classifiers such as Random Forest, Decision Tree, KNN, Gradient Boosting, and even Multilayer Perceptron in addition to ensemble methods (Hard and Soft Voting), we ensured consistent and reliable performance across numerous conditions where the proposed model excelled. The addition of ensemble techniques improved overall performance as the model was able to adapt to and learn more complex patterns resulting in higher accuracy thus outperforming single models. In summary, the model aims to enhance the accuracy and efficiency of predicting thyroid disorders enabling earlier detection, improved treatment, and enhanced decision-making by physicians, which will tremendously impact the field of medical diagnosis.

5.2 FUTURE PLAN:

- Application of Deep Learning Models: Investigate how deep learning methods, especially Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), may be applied to improve predictions by recognizing more complex patterns of data.
- Increase in the Dataset and Realistic Validation: To improve the accuracy and generalizability of the model, work with medical practitioners to acquire access to more diverse and realistic datasets across ages, genders, and diseases.
- **CDSS Development:** Develop a web platform or mobile tool that uses the model to allow real-time evaluation of thyroid disorders by patients and physicians.
- XAI Approaches: Higher transparency in model decision-making with the
 implementation of NAI model frameworks will promote greater acceptance and trust
 by healthcare professionals in the tool. Algorithms defined by emerging data can be
 incrementally updated to support observable changes in patient data attributes over
 time.

REFERENCES

- Chaubey, G., Bisen, D., Arjaria, S. et al. Thyroid Disease Prediction Using Machine Learning Approaches. Natl. Acad. Sci. Lett. 44, 233 238 (2021).
- A.Tyagi, R. Mehra and A. Saxena, "Interactive Thyroid Disease Prediction System
 Using Machine Learning Technique," 2018 Fifth International Conference on Parallel,
 Distributed and Grid Computing (PDGC), Solan, India, 2018, pp. 689-693, doi:
 10.1109/PDGC.2018.8745910.
- Z. J. Peya, M. K. N. Chumki and K. M. Zaman, "Predictive Analysis for Thyroid Diseases Diagnosis Using Machine Learning," 2021 International Conference on Science & Contemporary Technologies (ICSCT), Dhaka, Bangladesh, 2021, pp. 1-6, doi: 10.1109/ICSCT53883.2021.9642544.
- S. M. Alhashmi et al., "Survival Analysis of Thyroid Cancer Patients Using Machine Learning Algorithms," in IEEE Access, vol. 12, pp. 61978-61990, 2024, doi: 10.1109/ACCESS.2024.3392275.
- O. Jyoti, A. K. Paul, N. Nawar and M. A. I. Siddique, "Ensemble Learning for Improved Thyroid Disease Prediction: A Voting Classifier Approach," 2024 3rd International Conference on Advancement in Electrical and Electronic Engineering (ICAEEE), Gazipur, Bangladesh, 2024, pp. 1-6, doi: 10.1109/ICAEEE62219.2024.10561815.
- 6. Riajuliislam, Md, Khandakar Zahidur Rahim, and Antara Mahmud. "Prediction of thyroid disease (hypothyroid) in early stage using feature selection and classification techniques." 2021 International conference on information and communication technology for sustainable development (ICICT4SD). IEEE, 2021.

CHAPTER 7 APPENDIX

- Base Paper Title: An ensemble Machine Learning based approach to predict Thyroid disease using hybrid feature selection.
- Journal Name: Bioinformatics and Analytics Journal.
- Year of Publication: 2024.
- Publisher Name: Elsevier B.V.
- Base Paper Link: https://doi.org/10.1016/j.bioana.2024.08.001.