PCOS AI: Intelligent risk assessment diagnosis and assistance

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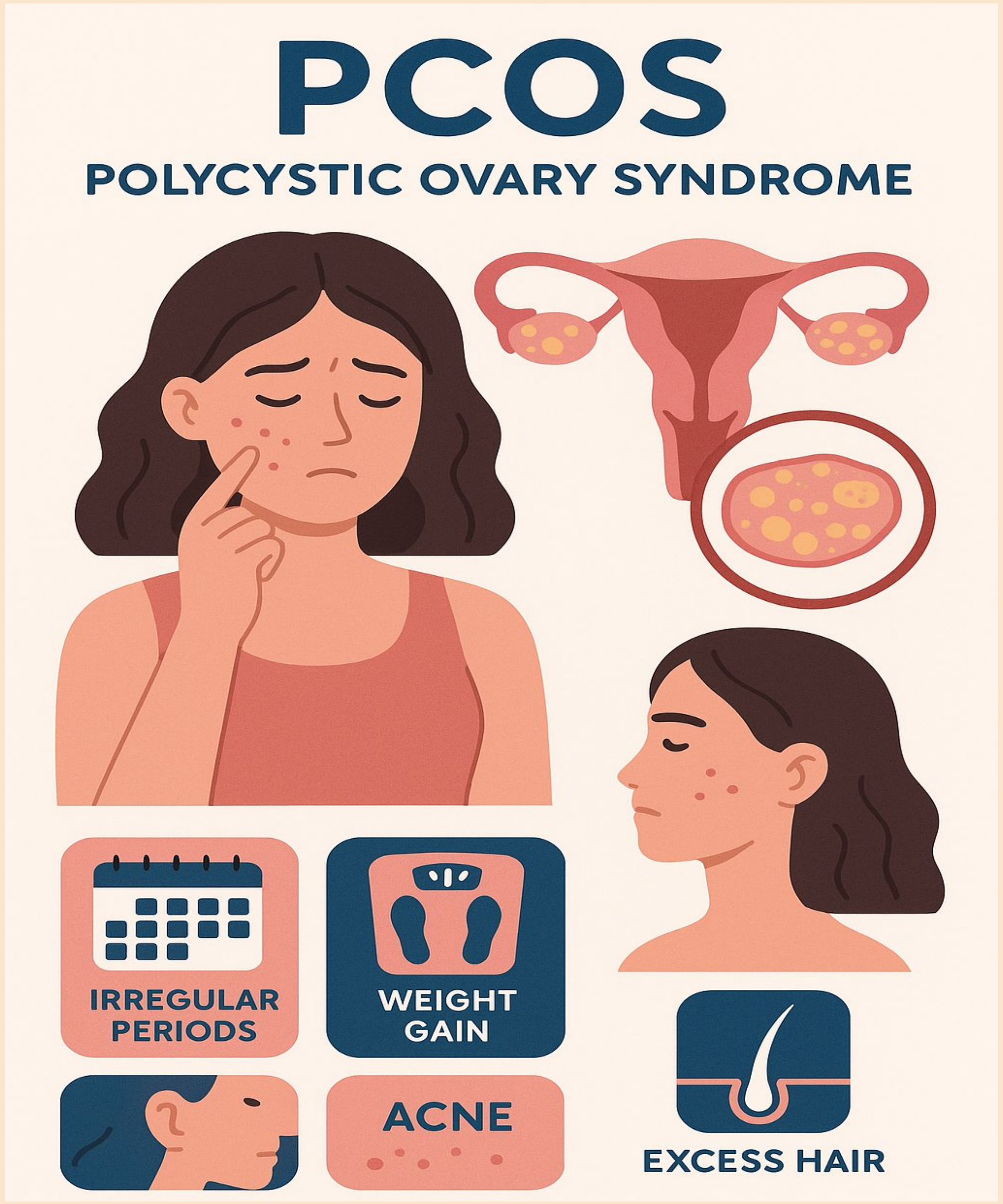
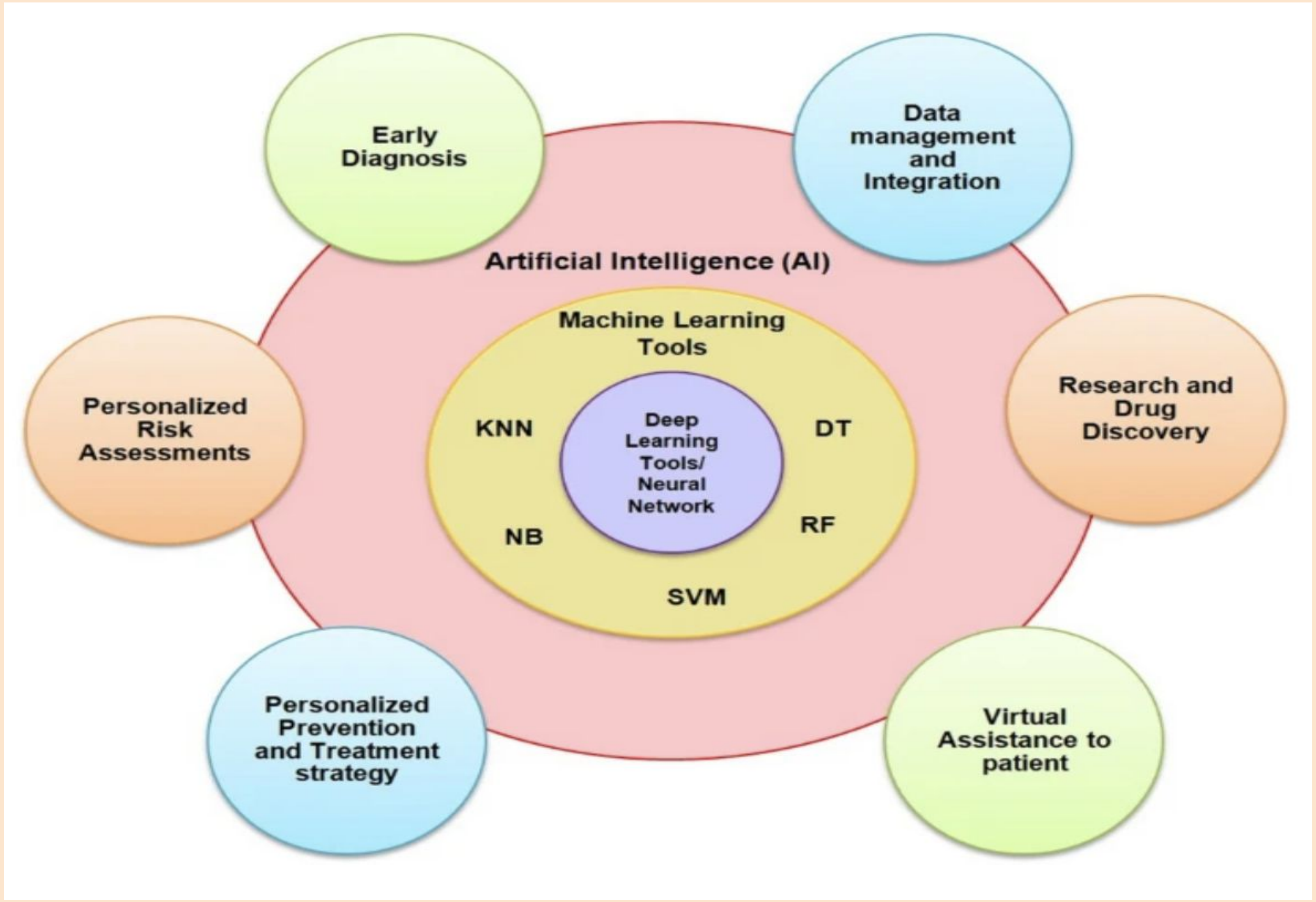
Content


PCOS
POLYCYSTIC OVARY SYNDROME
IRREGULAR PERIODS
WEIGHT GAIN
ACNE
EXCESS HAIR

Introduction

- Polycystic Ovary Syndrome (PCOS) is the most common endocrinopathy in reproductive aged women, with an estimated prevalence ranging from 4% to 20%.
- PCOS is associated with increased incidence of cardiovascular disease, infertility, and of endometrial cancer.
- Diagnosing PCOS can be complicated due to its diverse symptoms and similarities with other endocrine disorders.
- However, advancements in machine learning are proving beneficial in analyzing complex biomedical data, which can enhance the identification of diagnostic biomarkers.
- Objective: Build a reliable machine learning model that supports early diagnosis and reduces misdiagnosis using patient data.

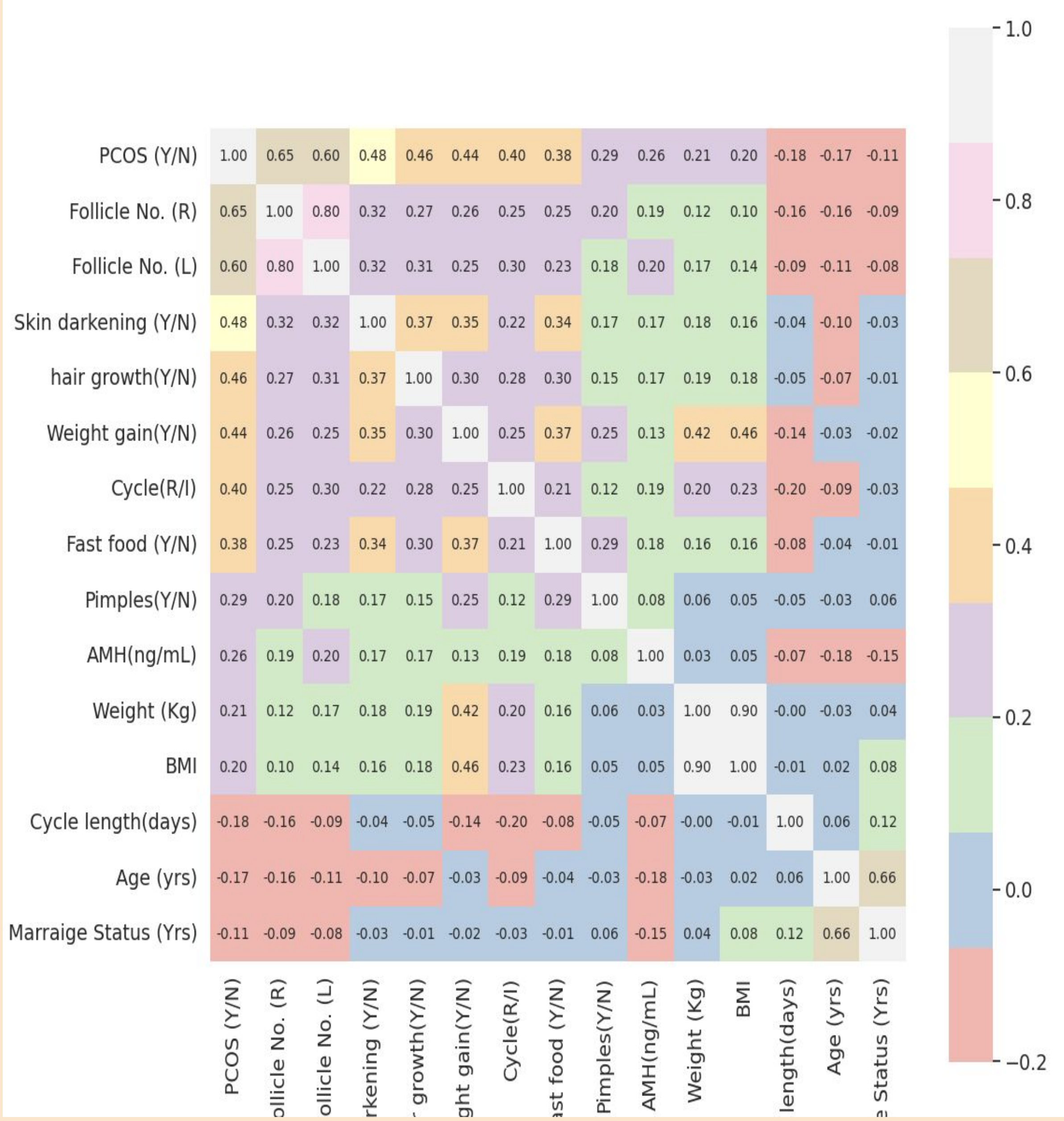

Early Diagnosis
Data management and Integration
Artificial Intelligence (AI)
Machine Learning Tools
Personalized Risk Assessments
KNN
Deep Learning Tools/ Neural Network
DT
Research and Drug Discovery
NB
RF
SVM
Personalized Prevention and Treatment strategy
Virtual Assistance to patient

Data & Preprocessing

- The dataset combines clinical, biochemical, and lifestyle features such as hormone levels, follicle counts, BMI, diet, and menstrual data.
- Data cleaning involved converting incorrectly typed numerical values stored as strings, removing extra spaces in column headers, and renaming for consistency.
- Missing values were addressed using median imputation to maintain robustness against outliers.

Correlation and its interpretation

- Correlation matrix helped identify strong predictors of PCOS, with Follicle Count (Left and Right) showing highest correlation (> 0.6).
- Heatmap visualization revealed multicollinearity, especially between Right and Left Follicle Count, and between Weight and BMI.
- As a result, redundant features like Right Follicle Number and BMI were removed to enhance model clarity and performance.



	PCOS (Y/N)	ollicle No. (R)	ollicle No. (L)	rkening (Y/N)	growth(Y/N)	ght gain(Y/N)	Cycle(R/I)	ast food (Y/N)	Pimples(Y/N)	AMH(ng/mL)	Weight (Kg)	BMI	length(days)	Age (yrs)	e Status (Yrs)
PCOS (Y/N)	1.00	0.65	0.60	0.48	0.46	0.44	0.40	0.38	0.29	0.26	0.21	0.20	-0.18	-0.17	-0.11
Follicle No. (R)	0.65	1.00	0.80	0.32	0.27	0.26	0.25	0.25	0.20	0.19	0.12	0.10	-0.16	-0.16	-0.09
Follicle No. (L)	0.60	0.80	1.00	0.32	0.31	0.25	0.30	0.23	0.18	0.20	0.17	0.14	-0.09	-0.11	-0.08
Skin darkening (Y/N)	0.48	0.32	0.32	1.00	0.37	0.35	0.22	0.34	0.17	0.17	0.18	0.16	-0.04	-0.10	-0.03
hair growth(Y/N)	0.46	0.27	0.31	0.37	1.00	0.30	0.28	0.30	0.15	0.17	0.19	0.18	-0.05	-0.07	-0.01
Weight gain(Y/N)	0.44	0.26	0.25	0.35	0.30	1.00	0.25	0.37	0.25	0.13	0.42	0.46	-0.14	-0.03	-0.02
Cycle(R/I)	0.40	0.25	0.30	0.22	0.28	0.25	1.00	0.21	0.12	0.19	0.20	0.23	-0.20	-0.09	-0.03
Fast food (Y/N)	0.38	0.25	0.23	0.34	0.30	0.37	0.21	1.00	0.29	0.18	0.16	0.16	-0.08	-0.04	-0.01
Pimples(Y/N)	0.29	0.20	0.18	0.17	0.15	0.25	0.12	0.29	1.00	0.08	0.06	0.05	-0.05	-0.03	0.06
AMH(ng/mL)	0.26	0.19	0.20	0.17	0.17	0.13	0.19	0.18	0.08	1.00	0.03	0.05	-0.07	-0.18	-0.15
Weight (Kg)	0.21	0.12	0.17	0.18	0.19	0.42	0.20	0.16	0.06	0.03	1.00	0.90	-0.00	-0.03	0.04
BMI	0.20	0.10	0.14	0.16	0.18	0.46	0.23	0.16	0.05	0.05	0.90	1.00	-0.01	0.02	0.08
Cycle length(days)	-0.18	-0.16	-0.09	-0.04	-0.05	-0.14	-0.20	-0.08	-0.05	-0.07	-0.00	-0.01	1.00	0.06	0.12
Age (yrs)	-0.17	-0.16	-0.11	-0.10	-0.07	-0.03	-0.09	-0.04	-0.03	-0.18	-0.03	0.02	0.06	1.00	0.66
Marraige Status (Yrs)	-0.11	-0.09	-0.08	-0.03	-0.01	-0.02	-0.03	-0.01	0.06	-0.15	0.04	0.08	0.12	0.66	1.00

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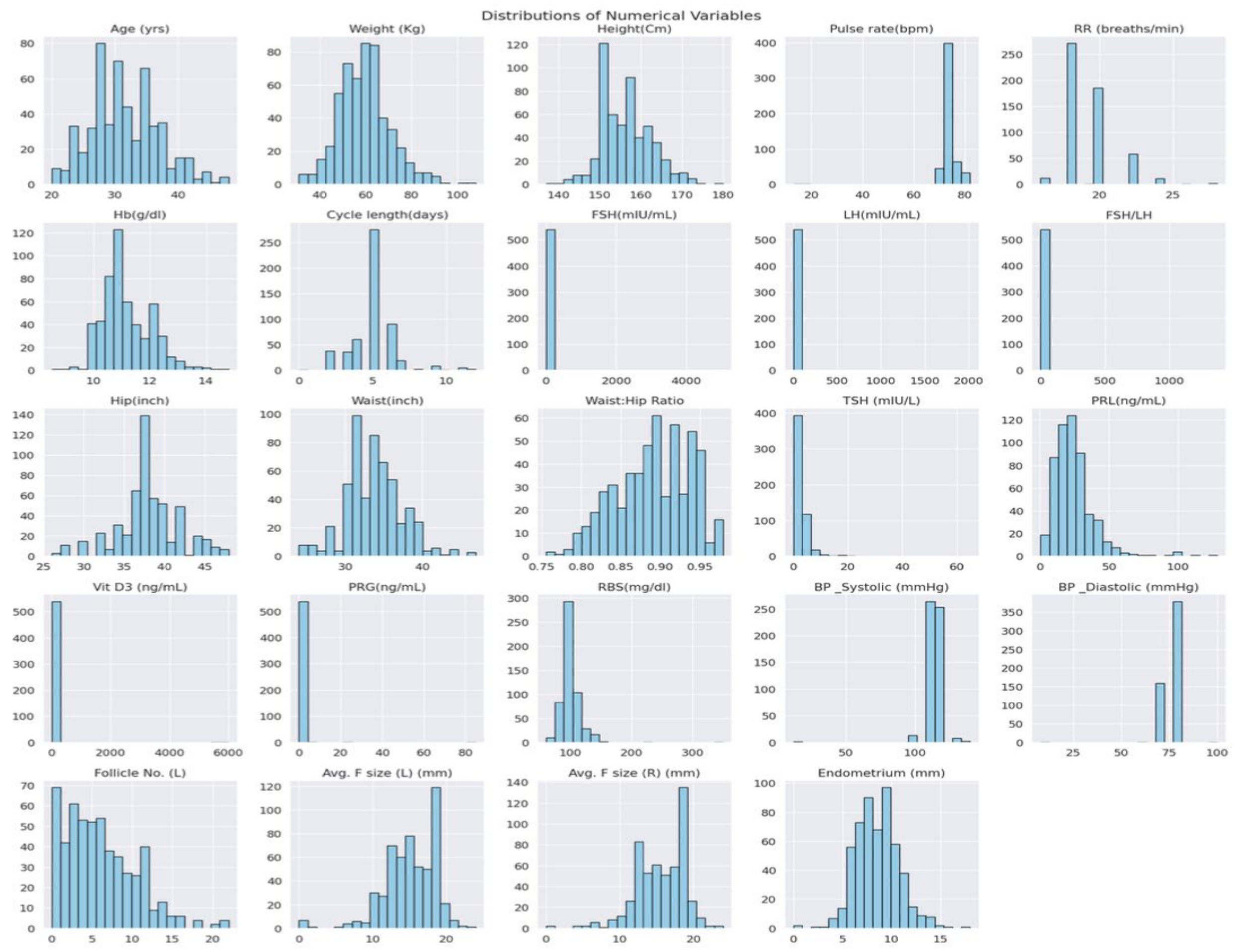
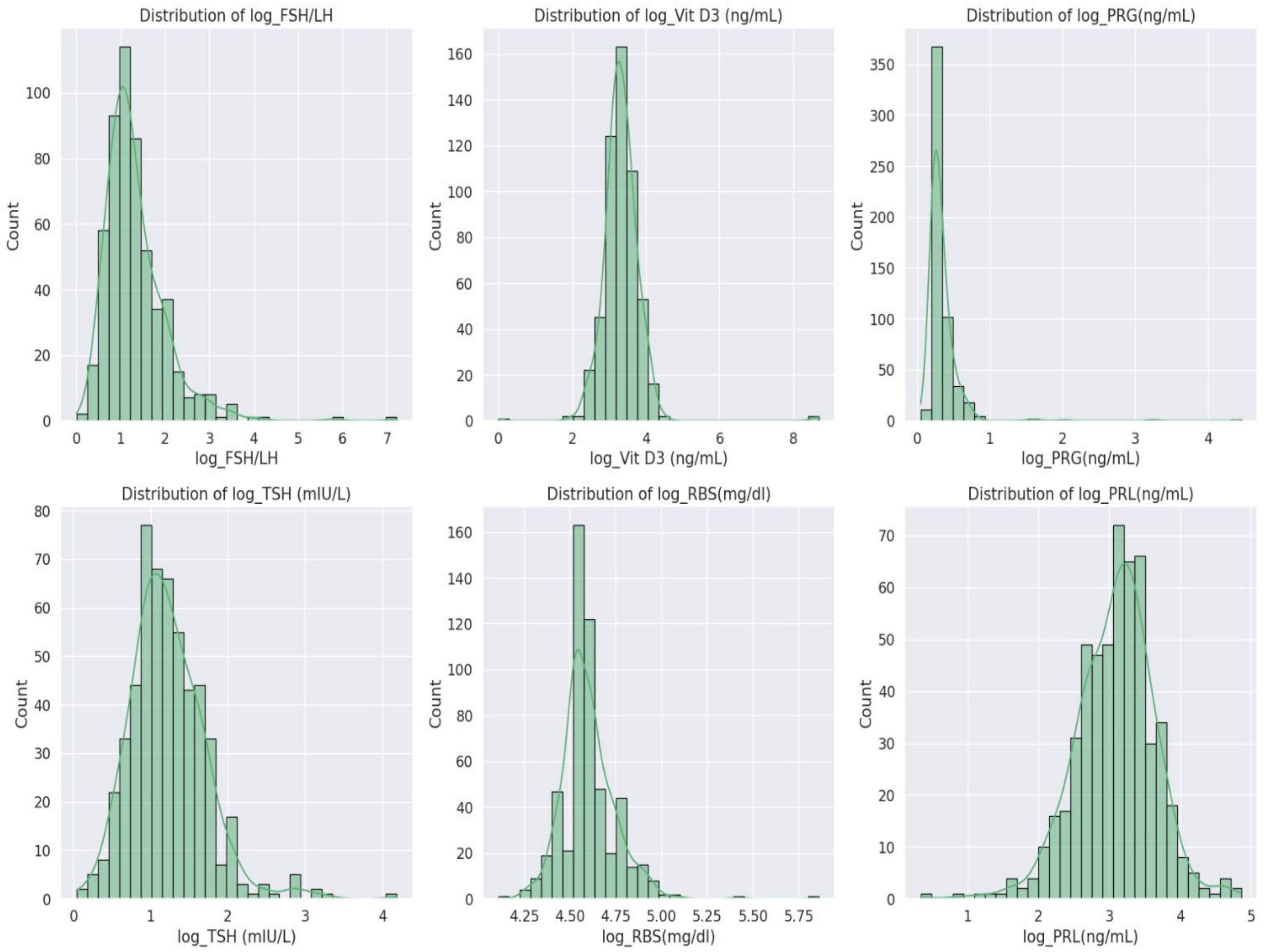
Exploratory data analysis

EDA revealed skewed clinical features that were log-transformed, and highlighted patterns such as higher weight and longer cycle lengths in PCOS-positive women, while lifestyle habits showed minimal distinction between groups.

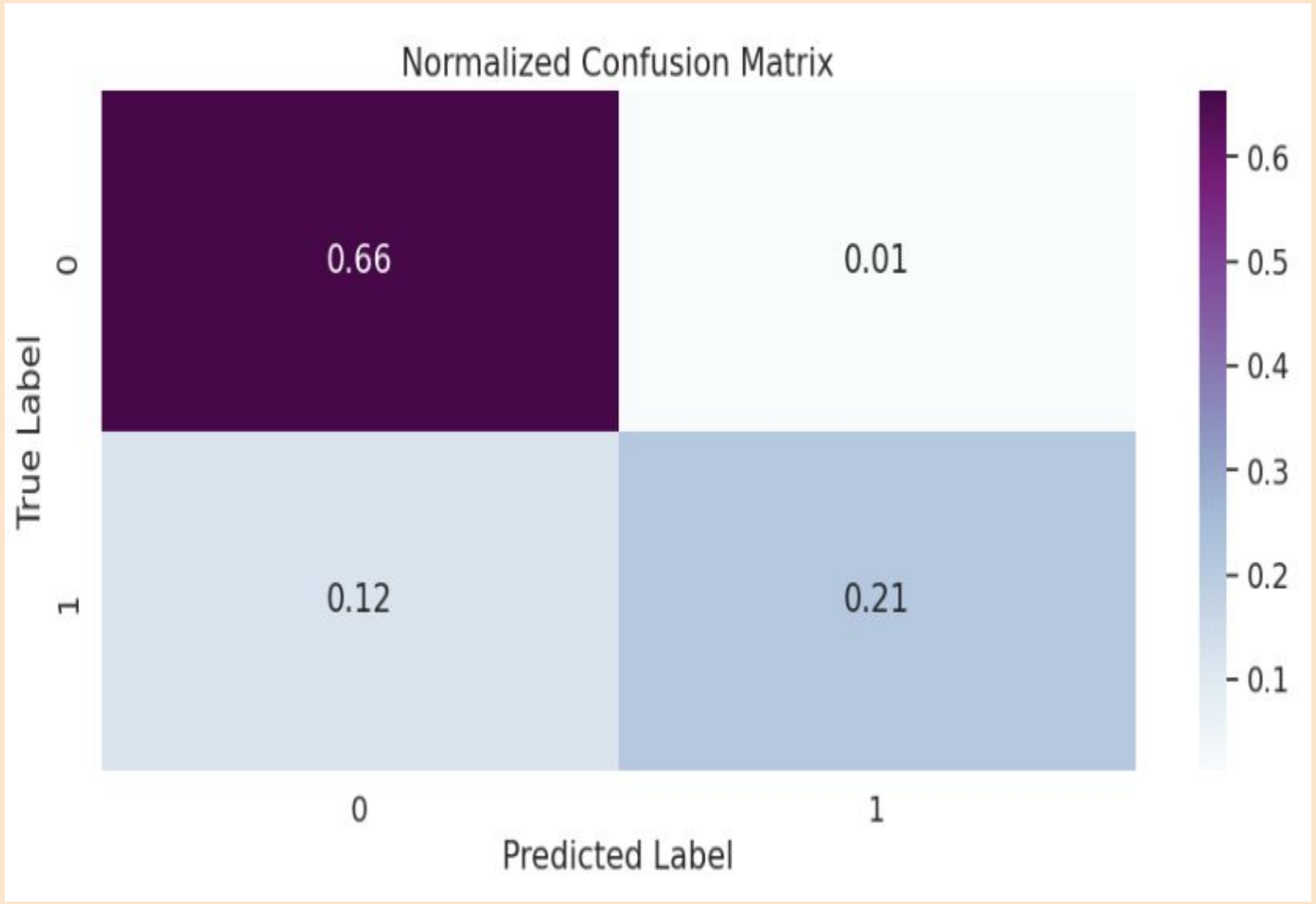




Model building:

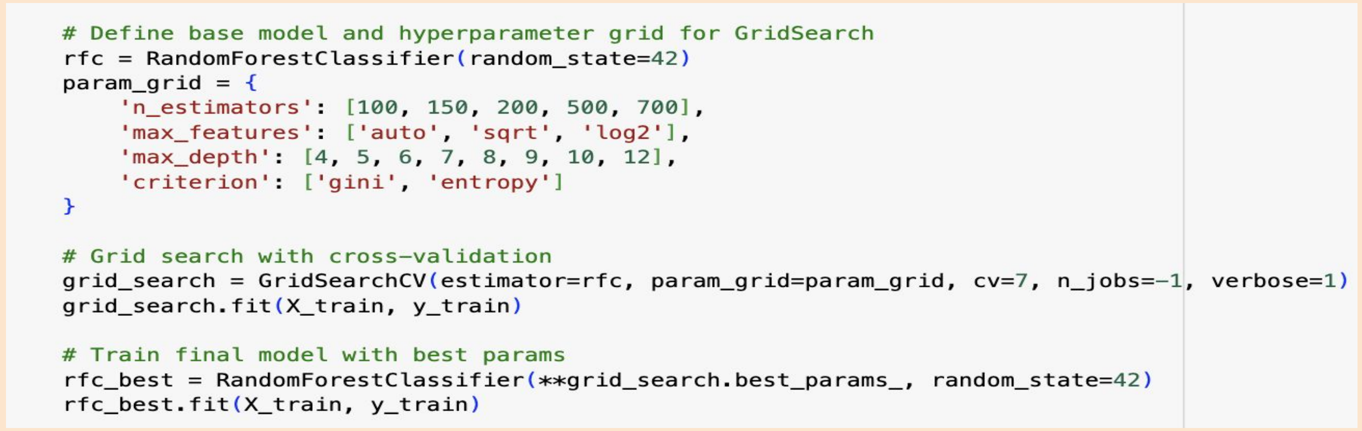
1. Random Forest classifier:

- Random Forest was selected for its ability to handle complex, non-linear data and provide feature importance insights.
- It gave 87% accuracy but missed many PCOS cases (64% recall).
- Good start, but not enough for medical use.



Random Forest - Hyperparameter tuning

- We used GridSearchCV to fine-tune the Random Forest model. Key parameters included max_depth, n_estimators, and the splitting criterion.
- The best results were achieved with a max_depth of 8 and 150 estimators. A lower depth helped reduce overfitting while maintaining accuracy.
- This tuning improved the model's ability to generalize, but recall was still limited, suggesting the need for further balancing or alternative models.
- GridSearchCV tuned parameters: max_depth=8, n_estimators=150.

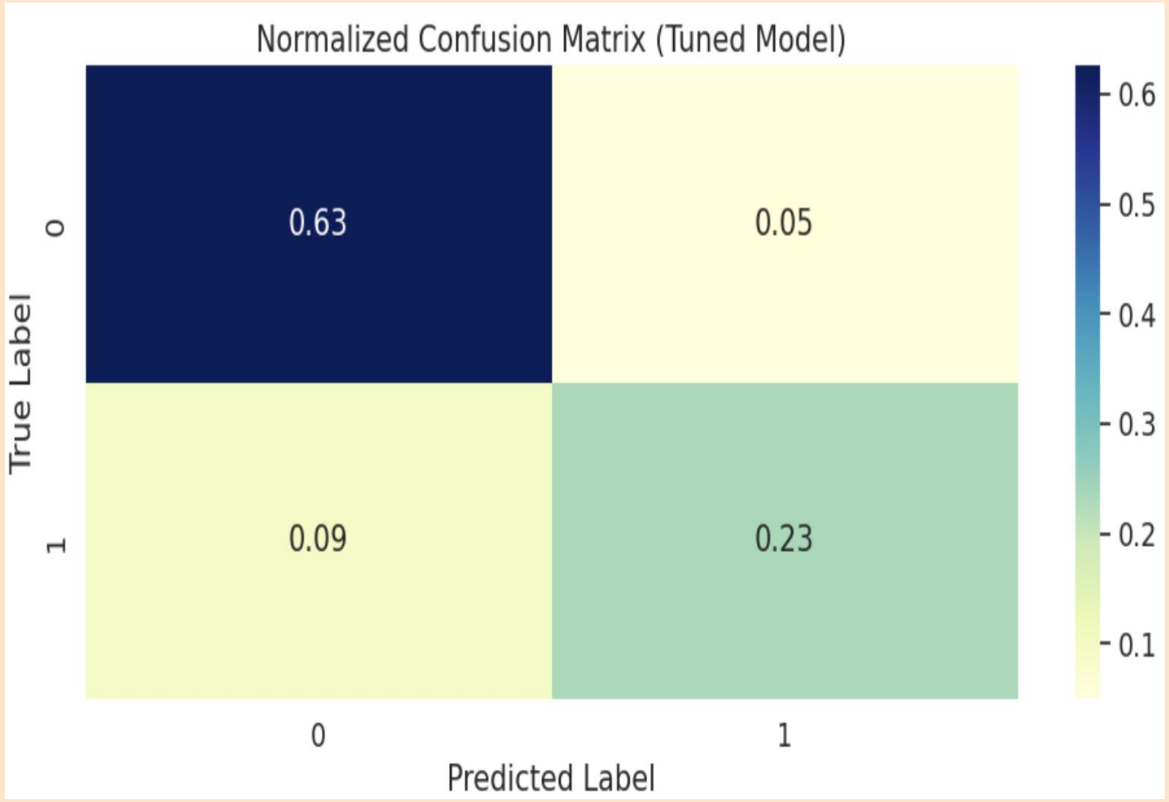


```
# Define base model and hyperparameter grid for GridSearch
rfc = RandomForestClassifier(random_state=42)
param_grid = {
    'n_estimators': [100, 150, 200, 500, 700],
    'max_features': ['auto', 'sqrt', 'log2'],
    'max_depth': [4, 5, 6, 7, 8, 9, 10, 12],
    'criterion': ['gini', 'entropy']
}

# Grid search with cross-validation
grid_search = GridSearchCV(estimator=rfc, param_grid=param_grid, cv=7, n_jobs=-1, verbose=1)
grid_search.fit(X_train, y_train)

# Train final model with best params
rfc_best = RandomForestClassifier(**grid_search.best_params_, random_state=42)
rfc_best.fit(X_train, y_train)
```

Model Building

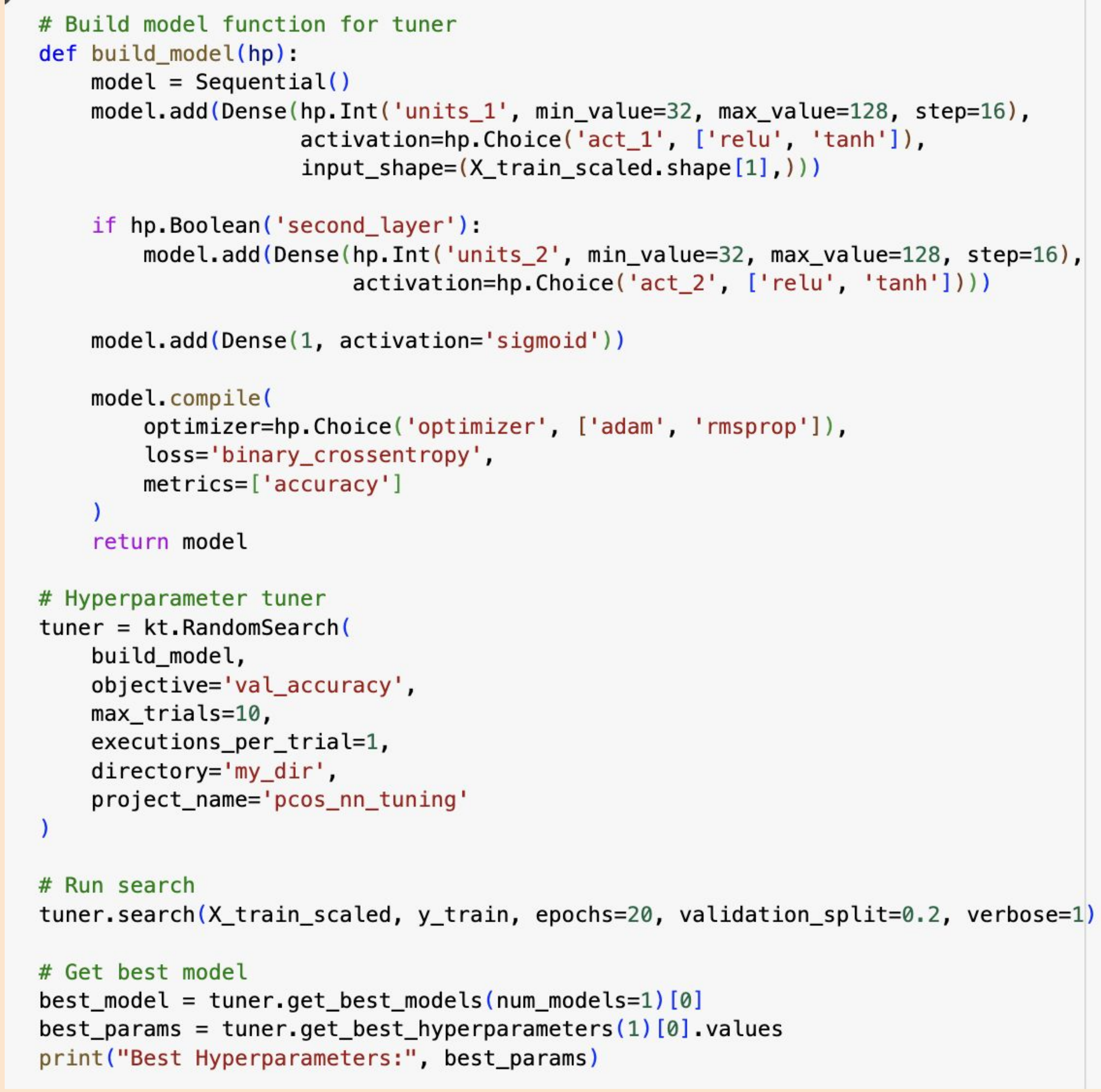
2. Neural network:

- A feedforward neural network was trained using KerasTuner with hyperparameter optimization and a standard scaling and one-hot encoding were applied.
- Final model achieved 86% accuracy and 72% recall which is better than random forest, reducing false negatives.



Neural Network - Hyperparameter Tuning

- We used KerasTuner's RandomSearch to explore combinations of layers, units, activation functions, and optimizers.
- The tuning process helped find an architecture that balanced depth and complexity, resulting in improved recall while maintaining good overall accuracy.
- Parameters like dropout and learning rate were also adjusted to prevent overfitting and ensure model stability.
- Standard scaling and one-hot encoding were applied.



```python
# Build model function for tuner
def build_model(hp):
    model = Sequential()
    model.add(Dense(hp.Int('units_1', min_value=32, max_value=128, step=16),
                    activation=hp.Choice('act_1', ['relu', 'tanh']),
                    input_shape=(X_train_scaled.shape[1],)))

    if hp.Boolean('second_layer'):
        model.add(Dense(hp.Int('units_2', min_value=32, max_value=128, step=16),
                        activation=hp.Choice('act_2', ['relu', 'tanh'])))

    model.add(Dense(1, activation='sigmoid'))

    model.compile(
        optimizer=hp.Choice('optimizer', ['adam', 'rmsprop']),
        loss='binary_crossentropy',
        metrics=['accuracy']
    )
    return model

# Hyperparameter tuner
tuner = kt.RandomSearch(
    build_model,
    objective='val_accuracy',
    max_trials=10,
    executions_per_trial=1,
    directory='my_dir',
    project_name='pcos_nn_tuning'
)

# Run search
tuner.search(X_train_scaled, y_train, epochs=20, validation_split=0.2, verbose=1)

# Get best model
best_model = tuner.get_best_models(num_models=1)[0]
best_params = tuner.get_best_hyperparameters(1)[0].values
print("Best Hyperparameters:", best_params)
```

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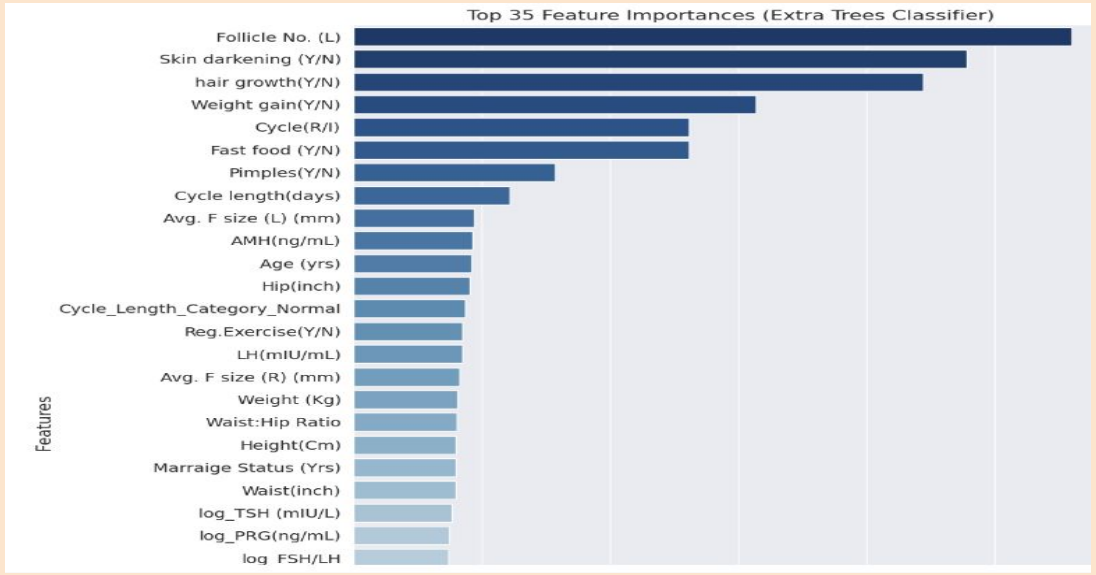
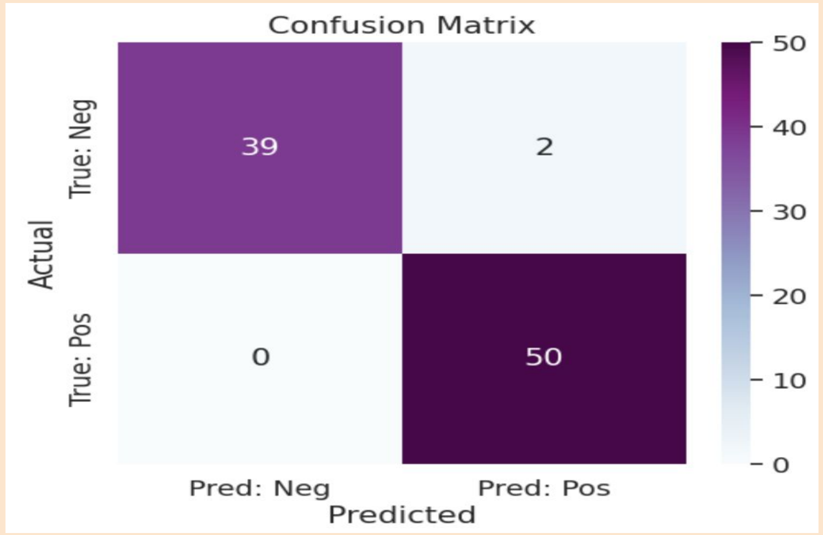
Model building

3. SVM with ADASYN

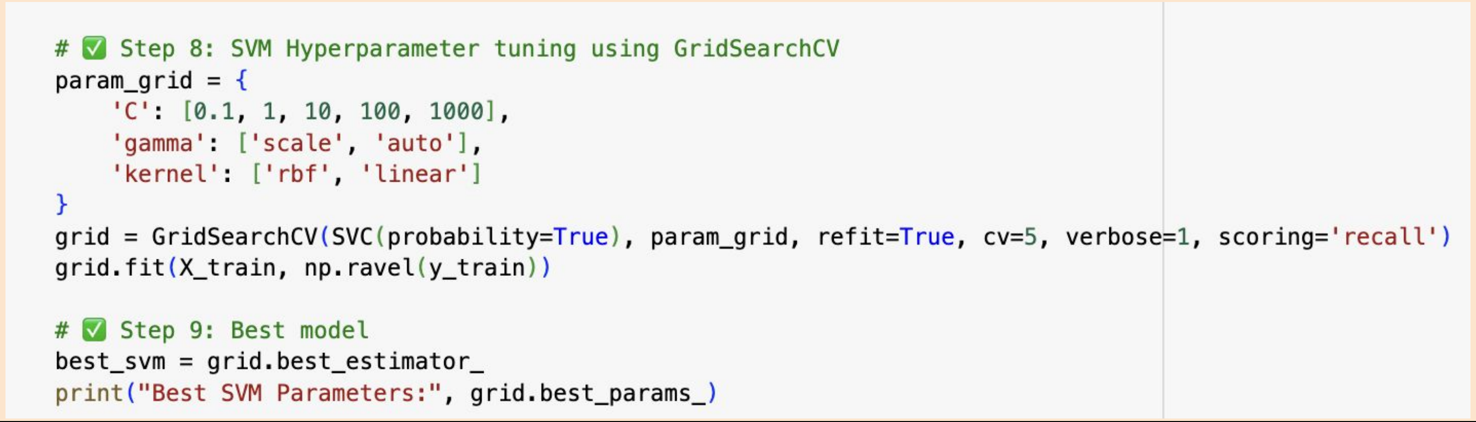
- We used the Extra Trees Classifier to select the top 9 most relevant features for the model.
- To address class imbalance, ADASYN (adaptive-synthetic sampling) was used to generate synthetic PCOS-positive samples, while ENN helped remove noisy examples from the majority class.
- A SVM with an RBF kernel was trained and fine-tuned, achieving 97.8% accuracy, 100% recall making it the best-performing model with no missed PCOS cases.





SVM - Hyperparameter Tuning

- We used GridSearchCV to fine-tune the SVM's kernel, C (regularization strength), and gamma (kernel coefficient).
- The best configuration was found with an RBF kernel, moderate C, and tuned gamma, which allowed the model to create flexible decision boundaries.
- These adjustments, combined with ADASYN for class balancing, significantly enhanced the model's recall and precision.
- To address class imbalance, ADASYN was used to generate synthetic PCOS-positive samples, while ENN helped remove noisy examples from the majority class.



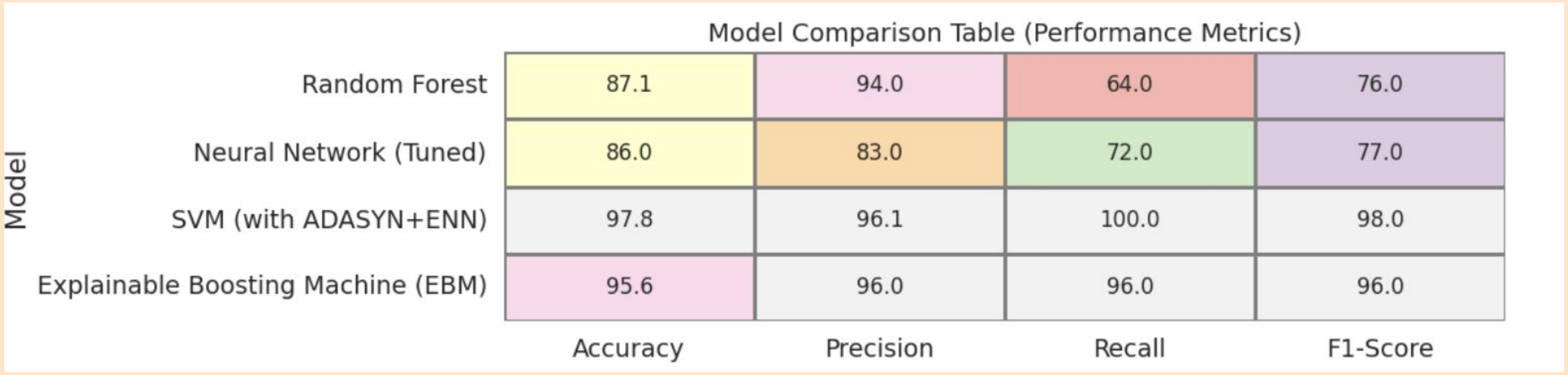
```
# ✅ Step 8: SVM Hyperparameter tuning using GridSearchCV
param_grid = {
    'C': [0.1, 1, 10, 100, 1000],
    'gamma': ['scale', 'auto'],
    'kernel': ['rbf', 'linear']
}
grid = GridSearchCV(SVC(probability=True), param_grid, refit=True, cv=5, verbose=1, scoring='recall')
grid.fit(X_train, np.ravel(y_train))

# ✅ Step 9: Best model
best_svm = grid.best_estimator_
print("Best SVM Parameters:", grid.best_params_)
```

Explainable boosting machine (EBM)

- The Explainable Boosting Machine (EBM) is a model designed to be interpretable, using additive models with interaction terms, making it suitable for clinical applications.
- This model achieved strong results with 95.6% accuracy, and both precision and recall at 96%, producing a balanced and reliable performance.
- This model is Good for real-world clinics where doctors need to understand the model.

Conclusion

- Among the models tested, the Support Vector Machine (SVM) with ADASYN achieved the highest accuracy and recall, while the Explainable Boosting Machine (EBM) also performed well with excellent interpretability; in comparison, Random Forest and Neural Network produced decent results but were weaker in sensitivity and transparency.
- In summary, we recommend using SVM for automated detection and EBM for applications requiring clinician trust. Future work could involve testing on larger datasets, deployment in real-world settings, and gathering feedback from healthcare professionals.


Model Comparison Table (Performance Metrics)

Model	Accuracy	Precision	Recall	F1-Score
Random Forest	87.1	94.0	64.0	76.0
Neural Network (Tuned)	86.0	83.0	72.0	77.0
SVM (with ADASYN+ENN)	97.8	96.1	100.0	98.0
Explainable Boosting Machine (EBM)	95.6	96.0	96.0	96.0

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References

DATASET:

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3. Chen, W., Miao, J., Chen, J., & Chen, J. (2025). Development of machine learning models for diagnostic biomarker identification and immune cell infiltration analysis in PCOS. *Journal of Ovarian Research*, *18*(1), 1.
4. Palomba, S., Seminara, G., Costanzi, F., Caserta, D., & Aversa, A. (2024). Chemerin and Polycystic Ovary Syndrome: A Comprehensive Review of Its Role as a Biomarker and Therapeutic Target. *Biomedicines*, *12*(12), 2859. (DOI)
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