```
import pandas as pd
df=pd.read_csv("/kaggle/input/heart-disease-prediction/Heart_Disease_P
rediction.csv")
df.head()
```

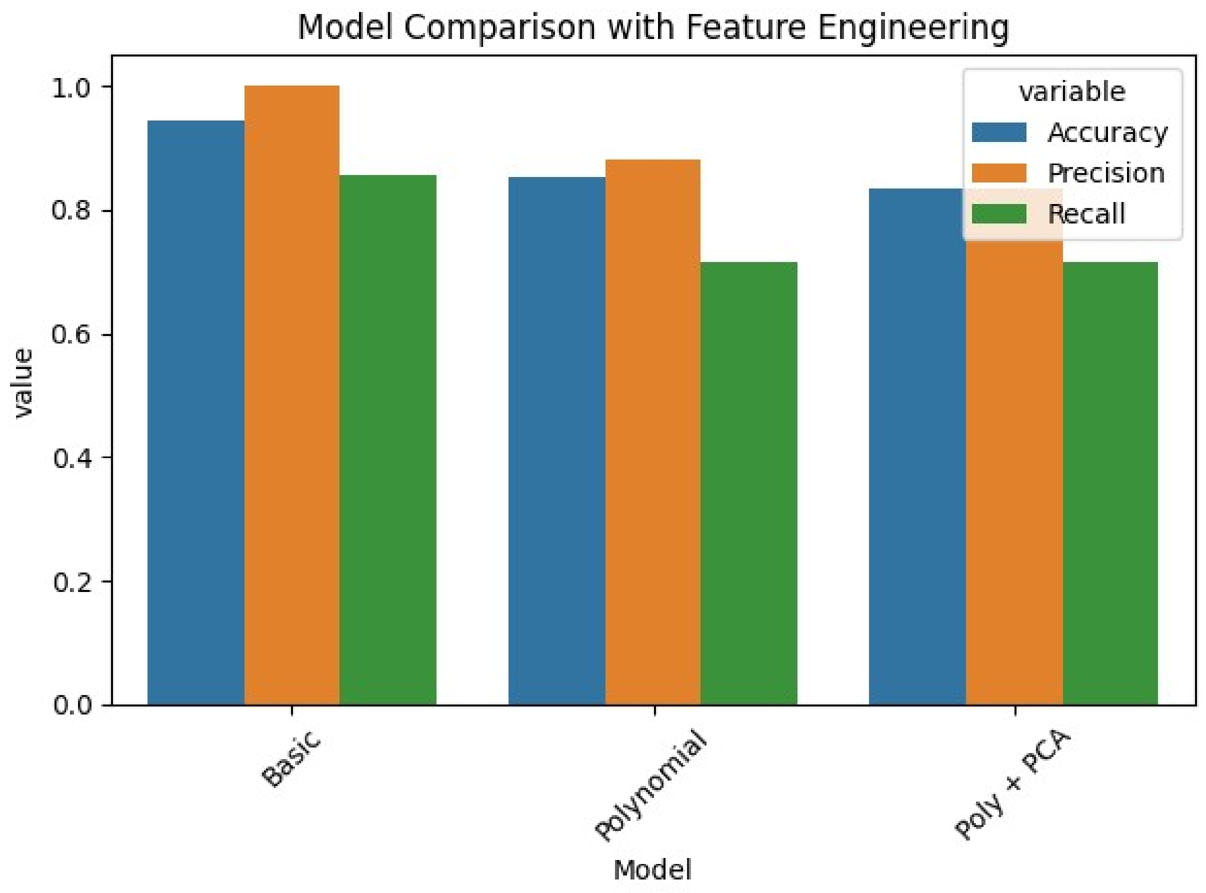
```
   Age  Sex  Chest pain type   BP  Cholesterol  FBS over 120  EKG
results  \
0   70    1                4  130          322             0
2
1   67    0                3  115          564             0
2
2   57    1                2  124          261             0
0
3   64    1                4  128          263             0
0
4   74    0                2  120          269             0
2

   Max HR  Exercise angina  ST depression  Slope of ST  \
0     109                0            2.4            2
1     160                0            1.6            2
2     141                0            0.3            1
3     105                1            0.2            2
4     121                1            0.2            1

   Number of vessels fluro  Thallium Heart Disease
0                        3         3      Presence
1                        0         7       Absence
2                        0         7      Presence
3                        1         7       Absence
4                        1         3       Absence
```

```
# 🫀 Heart Disease Prediction with Feature Engineering (Your Dataset
Version)

import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, OneHotEncoder,
PolynomialFeatures
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, precision_score,
recall_score
from sklearn.decomposition import PCA
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
import matplotlib.pyplot as plt
import seaborn as sns
```

```python
# Rename target column if necessary
df['Heart Disease'] = df['Heart Disease'].map({'Presence': 1,
'Absence': 0})

# Separate features and target
X = df.drop('Heart Disease', axis=1)
y = df['Heart Disease']

# Identify categorical and numerical columns
cat_cols = ['Sex', 'Chest pain type', 'FBS over 120', 'EKG results',
'Exercise angina', 'Slope of ST', 'Number of vessels fluro',
'Thallium']
num_cols = [col for col in X.columns if col not in cat_cols]

# Column transformer: scale numeric + one-hot encode categorical
preprocessor = ColumnTransformer([
    ('num', StandardScaler(), num_cols),
    ('cat', OneHotEncoder(handle_unknown='ignore'), cat_cols)
])

# Evaluation function
def evaluate(pipe, label):
    X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)
    pipe.fit(X_train, y_train)
    y_pred = pipe.predict(X_test)
    return {
        'Model': label,
        'Accuracy': accuracy_score(y_test, y_pred),
        'Precision': precision_score(y_test, y_pred),
        'Recall': recall_score(y_test, y_pred)
    }

results = []

# 1 Basic pipeline
pipe_basic = Pipeline([
    ('prep', preprocessor),
    ('clf', LogisticRegression(max_iter=1000))
])
results.append(evaluate(pipe_basic, 'Basic'))

# 2 Polynomial features
pipe_poly = Pipeline([
    ('prep', preprocessor),
    ('poly', PolynomialFeatures(degree=2, include_bias=False)),
    ('clf', LogisticRegression(max_iter=1000))
])
results.append(evaluate(pipe_poly, 'Polynomial'))
```

```
# 3 Polynomial + PCA
pipe_pca = Pipeline([
    ('prep', preprocessor),
    ('poly', PolynomialFeatures(degree=2, include_bias=False)),
    ('pca', PCA(n_components=0.95)),
    ('clf', LogisticRegression(max_iter=1000))
])
results.append(evaluate(pipe_pca, 'Poly + PCA'))

# □ Results summary
results_df = pd.DataFrame(results)
print(results_df)

# □ Visual comparison
sns.barplot(data=results_df.melt(id_vars='Model'), x='Model',
y='value', hue='variable')
plt.title("Model Comparison with Feature Engineering")
plt.xticks(rotation=45)
plt.tight_layout()
plt.show()
```

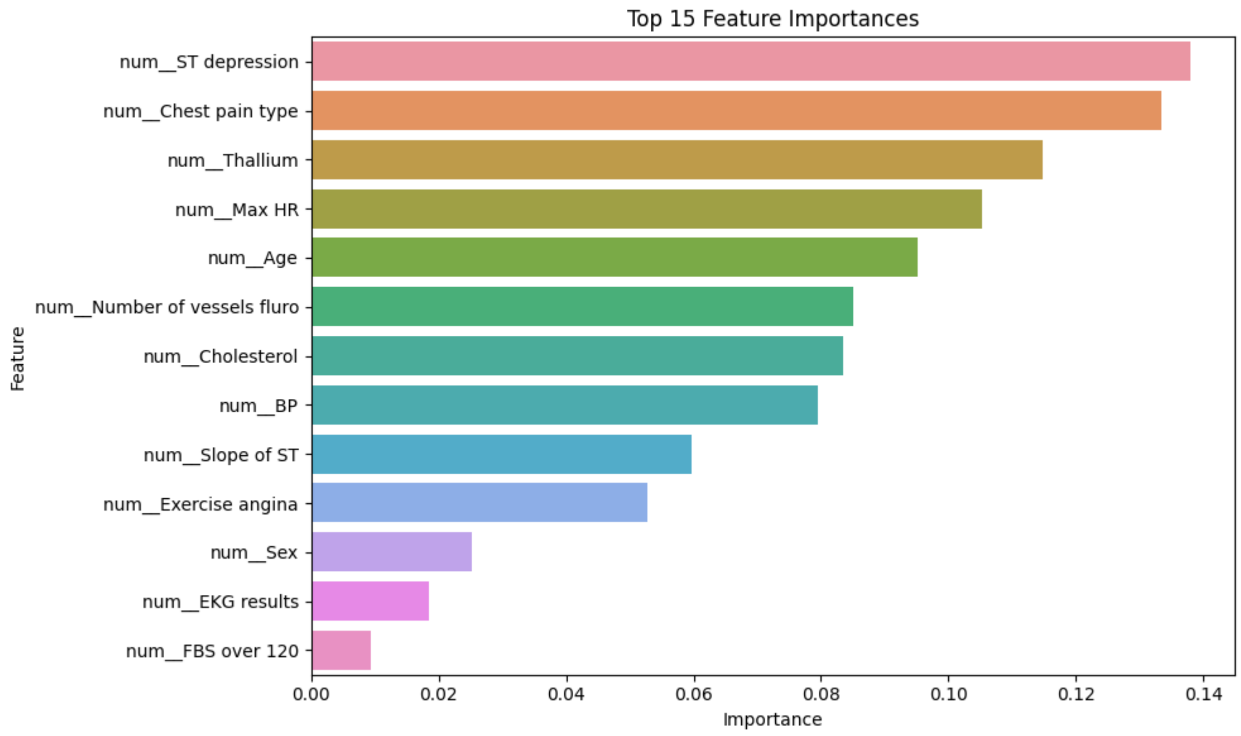
```
        Model  Accuracy  Precision    Recall
0       Basic  0.944444   1.000000  0.857143
1  Polynomial  0.851852   0.882353  0.714286
2  Poly + PCA  0.833333   0.833333  0.714286
```

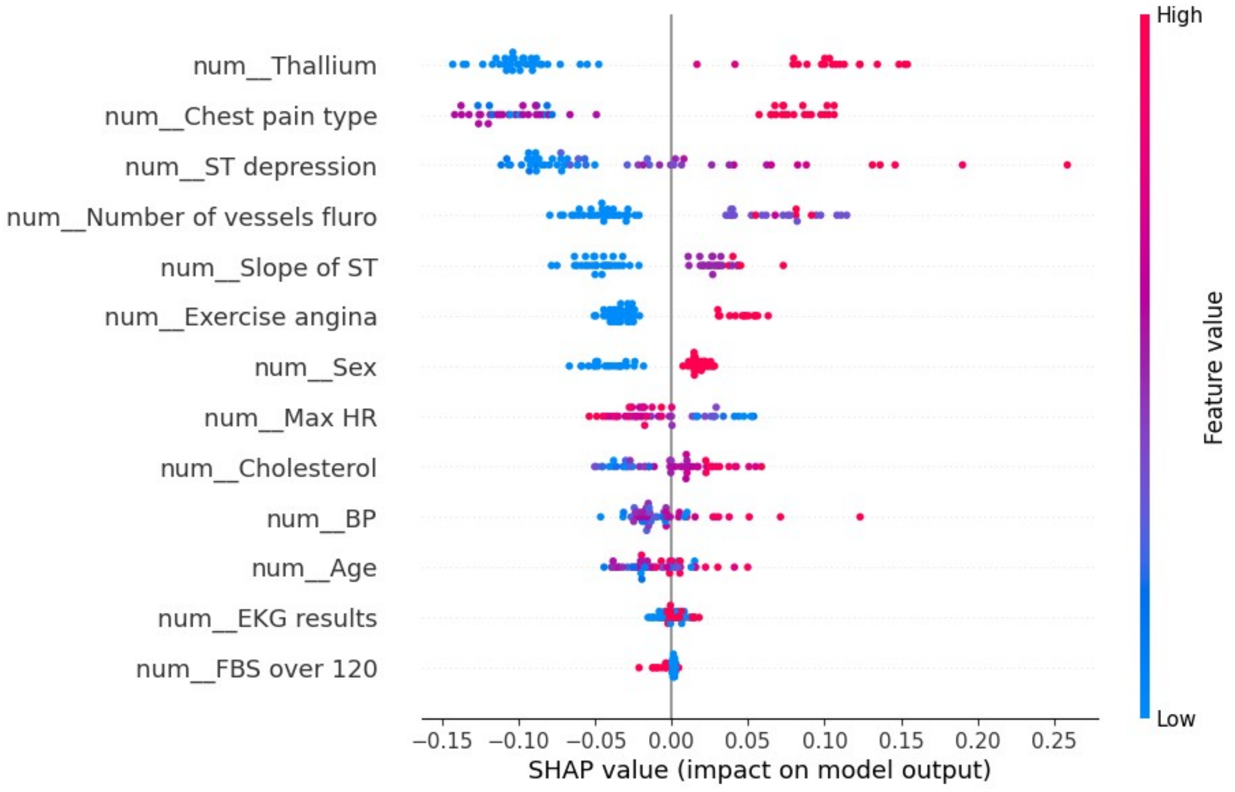


```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import shap

from sklearn.ensemble import RandomForestClassifier
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline

# Load your dataset
df =
pd.read_csv("/kaggle/input/heart-disease-prediction/Heart_Disease_Pred
iction.csv")  # Replace with actual path or URL

# Target encoding (ensure binary: 0 = Absence, 1 = Presence)
df['Heart Disease'] = df['Heart Disease'].map({'Presence': 1,
'Absence': 0})

# Separate features and target
```

```python
X = df.drop('Heart Disease', axis=1)
y = df['Heart Disease']

# Detect categorical columns (dtype = object or string)
cat_cols = X.select_dtypes(include='object').columns.tolist()
num_cols = X.select_dtypes(exclude='object').columns.tolist()

# Preprocessing pipeline
preprocessor = ColumnTransformer([
    ('num', StandardScaler(), num_cols),
    ('cat', OneHotEncoder(handle_unknown='ignore'), cat_cols)
])

# Full pipeline
pipe = Pipeline([
    ('prep', preprocessor),
    ('clf', RandomForestClassifier(n_estimators=100, random_state=42))
])

# Train-test split
X_train, X_test, y_train, y_test = train_test_split(X, y,
test_size=0.2, random_state=42)

# Fit model
pipe.fit(X_train, y_train)

# Feature names after encoding
feature_names = pipe.named_steps['prep'].get_feature_names_out()

# Feature importances
importances = pipe.named_steps['clf'].feature_importances_
feat_imp = pd.DataFrame({'Feature': feature_names, 'Importance':
importances}).sort_values(by='Importance', ascending=False)

# Plot feature importance
plt.figure(figsize=(10, 6))
sns.barplot(data=feat_imp.head(15), x='Importance', y='Feature')
plt.title('Top 15 Feature Importances')
plt.tight_layout()
plt.show()

# SHAP explainer and beeswarm plot (fixing dimensionality issue)
explainer = shap.Explainer(
    pipe.named_steps['clf'],
    pipe.named_steps['prep'].transform(X_train),
    feature_names=feature_names,
    model_output="probability"
)

# SHAP values for test set
```

```
shap_values = explainer(pipe.named_steps['prep'].transform(X_test),
check_additivity=False)

# If it's multi-class, select SHAP values for class 1
if isinstance(shap_values.values, list) or shap_values.values.ndim ==
3:
    class1_shap = shap_values[:, :, 1]  # Class 1 (positive class)
else:
    class1_shap = shap_values

# Beeswarm plot
shap.plots.beeswarm(class1_shap, max_display=15)
```




num__Thallium
num__Chest pain type
num__ST depression
num__Number of vessels fluro
num__Slope of ST
num__Exercise angina
num__Sex
num__Max HR
num__Cholesterol
num__BP
num__Age
num__EKG results
num__FBS over 120
−0.15
−0.10
−0.05
0.00
0.05
0.10
0.15
0.20
0.25
SHAP value (impact on model output)
High
Low
Feature value