🫀 Heart Disease Prediction ML Pipeline

A comprehensive machine learning pipeline for predicting heart disease risk using the UCI Heart Disease dataset. This project implements end-to-end ML workflow including data preprocessing, feature selection, model training, evaluation, and deployment with a Streamlit web interface.

🎯 Project Overview

This project demonstrates a complete machine learning pipeline with the following components:

- **Data Preprocessing & Cleaning**
- **Exploratory Data Analysis (EDA)**
- **Principal Component Analysis (PCA)**
- **Feature Selection** (Random Forest, RFE, Chi-Square)
- **Supervised Learning Models** (Logistic Regression, Decision Tree, Random Forest, SVM)
- **Unsupervised Learning** (K-Means, Hierarchical Clustering)
- **Hyperparameter Tuning** (GridSearchCV, RandomizedSearchCV)
- **Model Deployment** with Streamlit UI
- **Live Deployment** using Ngrok

📊 Dataset

The project uses the **Heart Disease UCI Dataset** containing 303 instances with 14 attributes:

- **age**: Age in years
- **sex**: Gender (1 = male; 0 = female)
- **cp**: Chest pain type (0-3)
- **trestbps**: Resting blood pressure (mm Hg)
- **chol**: Serum cholesterol (mg/dl)
- **fbs**: Fasting blood sugar > 120 mg/dl (1 = true; 0 = false)
- **restecg**: Resting electrocardiographic results (0-2)
- **thalach**: Maximum heart rate achieved
- **exang**: Exercise induced angina (1 = yes; 0 = no)
- **oldpeak**: ST depression induced by exercise
- **slope**: Slope of the peak exercise ST segment (0-2)

- **ca**: Number of major vessels (0-3) colored by fluoroscopy
- **thal**: Thalassemia (1 = normal; 2 = fixed defect; 3 = reversable defect)
- **target**: Heart disease presence (1 = disease; 0 = no disease)

🗂️ Project Structure

```
Heart_Disease_Project/
├── 📁 data/
│   └── heart_disease.csv
├── 📁 notebooks/
│   ├── 01_data_preprocessing.ipynb
│   ├── 02_pca_analysis.ipynb
│   ├── 03_feature_selection.ipynb
│   ├── 04_supervised_learning.ipynb
│   ├── 05_unsupervised_learning.ipynb
│   └── 06_hyperparameter_tuning.ipynb
├── 📁 models/
│   ├── final_model.pkl
│   └── final_model_metadata.pkl
├── 📁 ui/
│   └── app.py
├── 📁 src/
│   └── heart_disease_pipeline.py
├── 📁 deployment/
│   └── ngrok_setup.txt
├── 📁 results/
│   └── evaluation_metrics.txt
├── 📋 README.md
├── 📋 requirements.txt
└── 📋 .gitignore
```

🚀 Quick Start

1. Clone the Repository

bash

```
git clone https://github.com/yourusername/heart-disease-ml-pipeline.git
cd heart-disease-ml-pipeline
```

2. Install Dependencies

```bash
pip install -r requirements.txt
```

3. Run the Complete Pipeline

```python
python src/heart_disease_pipeline.py
```

4. Launch the Streamlit App

```bash
streamlit run ui/app.py
```

5. Deploy with Ngrok (Optional)

```bash
# Install ngrok
pip install pyngrok

# In another terminal, run:
ngrok http 8501
```

🔧 Installation & Setup

Prerequisites

- Python 3.8 or higher
- pip package manager

Environment Setup

```bash
```

```
# Create virtual environment
python -m venv heart_disease_env

# Activate virtual environment
# On Windows:
heart_disease_env\Scripts\activate
# On macOS/Linux:
source heart_disease_env/bin/activate

# Install required packages
pip install -r requirements.txt
```

📈 Model Performance

The pipeline trains and evaluates multiple models:

Model	Accuracy	Precision	Recall	F1-Score	AUC
Random Forest	0.870	0.880	0.850	0.870	0.925
Logistic Regression	0.850	0.840	0.860	0.850	0.910
SVM	0.830	0.820	0.840	0.830	0.895
Decision Tree	0.790	0.770	0.810	0.790	0.850

Note: Actual performance may vary based on data splits and hyperparameter tuning.

🎛️ Features & Capabilities

🔍 Data Analysis

- **Comprehensive EDA** with visualizations
- **Missing value handling** and data cleaning
- **Statistical analysis** and correlation studies
- **Feature distribution** analysis

🧠 Machine Learning Models

- **Supervised Learning**: Logistic Regression, Decision Tree, Random Forest, SVM
- **Unsupervised Learning**: K-Means, Hierarchical Clustering
- **Dimensionality Reduction**: Principal Component Analysis (PCA)
- **Feature Selection**: Random Forest importance, RFE, Chi-Square test

⚙️ Model Optimization

- **Hyperparameter Tuning** with GridSearchCV and RandomizedSearchCV
- **Cross-validation** for robust model evaluation
- **Performance metrics** including ROC curves, confusion matrices
- **Model comparison** and selection

🌐 Web Application

- **Interactive UI** built with Streamlit
- **Real-time predictions** with user input
- **Risk visualization** with gauges and charts
- **Data exploration** tools and insights
- **Model performance** dashboards

📊 Usage Examples

Making Predictions Programmatically

```python
import joblib
import numpy as np

# Load the trained model
model = joblib.load('models/final_model.pkl')

# Example patient data
patient_data = np.array([[63, 1, 3, 145, 233, 1, 0, 150, 0, 2.3, 0, 0, 1]])

# Make prediction
prediction = model.predict(patient_data)
probability = model.predict_proba(patient_data)

print(f"Heart Disease Risk: {'High' if prediction[0] else 'Low'}")
print(f"Risk Probability: {probability[0][1]:.2%}")
```

Using the Streamlit App

1. **Navigate** to the prediction page
2. **Input** patient information using the form

3. **Click** "Predict Heart Disease Risk"
4. **View** results with risk level and confidence
5. **Explore** data visualizations and model insights

🔧 Advanced Configuration

Custom Feature Selection

```python
# Modify feature selection parameters
feature_selector = RFE(RandomForestClassifier(), n_features_to_select=8)
selected_features = feature_selector.fit_transform(X, y)
```

Hyperparameter Tuning

```python
# Custom parameter grid for Random Forest
param_grid = {
    'n_estimators': [100, 200, 300],
    'max_depth': [10, 20, None],
    'min_samples_split': [2, 5, 10],
    'min_samples_leaf': [1, 2, 4]
}
```

🚀 Deployment Options

Local Deployment

```bash
# Run Streamlit locally
streamlit run ui/app.py --server.port 8501
```

Ngrok Deployment

```bash
```

```
# Terminal 1: Start Streamlit
streamlit run ui/app.py

# Terminal 2: Create public tunnel
ngrok http 8501
```

Cloud Deployment

The application can be deployed on:

- **Streamlit Cloud**
- **Heroku**
- **AWS EC2**
- **Google Cloud Platform**
- **Azure**

📝 API Documentation

Model Prediction Endpoint

```python
def predict_heart_disease(age, sex, cp, trestbps, chol, fbs,
                          restecg, thalach, exang, oldpeak,
                          slope, ca, thal):
    """
    Predict heart disease risk based on patient features.

    Args:
        age (int): Patient age
        sex (int): Gender (0=female, 1=male)
        cp (int): Chest pain type (0-3)
        ... (other parameters)

    Returns:
        dict: Prediction result with risk level and probability
    """
```

🧪 Testing

Run Unit Tests

```bash
python -m pytest tests/
```

Validate Model Performance

```python
from src.validation import validate_model
results = validate_model('models/final_model.pkl')
```

🤝 Contributing

1. **Fork** the repository
2. **Create** a feature branch (`git checkout -b feature/AmazingFeature`)
3. **Commit** your changes (`git commit -m 'Add some AmazingFeature'`)
4. **Push** to the branch (`git push origin feature/AmazingFeature`)
5. **Open** a Pull Request

Development Guidelines

- Follow **PEP 8** style guidelines
- Write **comprehensive tests** for new features
- Update **documentation** for any changes
- Use **meaningful commit messages**

📚 Resources & References

- UCI Heart Disease Dataset
- Scikit-learn Documentation
- Streamlit Documentation
- Plotly Documentation
- Heart Disease Research Papers

🔍 Troubleshooting

Common Issues

1. Model Loading Error

```python
# Error: FileNotFoundError: [Errno 2] No such file or directory: 'final_model.pkl'
# Solution: Run the main pipeline first to generate model files
python src/heart_disease_pipeline.py
```

2. Streamlit Port Already in Use

```bash
# Error: Port 8501 is already in use
# Solution: Use a different port
streamlit run ui/app.py --server.port 8502
```

3. Package Import Errors

```bash
# Error: ModuleNotFoundError: No module named 'sklearn'
# Solution: Install required packages
pip install -r requirements.txt
```

4. Ngrok Authentication

```bash
# Error: ngrok authtoken required
# Solution: Sign up for ngrok and add your authtoken
ngrok authtoken YOUR_AUTH_TOKEN
```

Performance Optimization

Memory Usage

```python
```

```python
# For large datasets, use chunking
chunk_size = 1000
for chunk in pd.read_csv('data.csv', chunksize=chunk_size):
    process_chunk(chunk)
```

Speed Optimization

```python
# Use joblib for parallel processing
from joblib import Parallel, delayed
results = Parallel(n_jobs=-1)(delayed(train_model)(params) for params in param_list)
```

📊 Model Interpretability

Feature Importance Analysis

```python
import shap
import lime

# SHAP values for model interpretation
explainer = shap.TreeExplainer(model)
shap_values = explainer.shap_values(X_test)
shap.summary_plot(shap_values, X_test)
```

LIME Explanations

```python
# Local interpretable explanations
explainer = lime.tabular.LimeTabularExplainer(
    X_train.values,
    feature_names=feature_names,
    class_names=['No Disease', 'Disease'],
    mode='classification'
)
```

🔐 Security & Privacy

Data Protection

- **No sensitive data** is stored permanently
- **Input validation** prevents injection attacks
- **Session management** ensures data privacy
- **HTTPS** recommended for production deployment

Model Security

```python
# Input validation example
def validate_input(age, sex, cp, trestbps, chol):
    if not (1 <= age <= 120):
        raise ValueError("Age must be between 1 and 120")
    if sex not in [0, 1]:
        raise ValueError("Sex must be 0 or 1")
    # Additional validations...
```

📈 Performance Monitoring

Model Drift Detection

```python
def detect_drift(reference_data, current_data, threshold=0.05):
    """Detect data drift using statistical tests"""
    from scipy.stats import ks_2samp

    for column in reference_data.columns:
        statistic, p_value = ks_2samp(
            reference_data[column],
            current_data[column]
        )
        if p_value < threshold:
            print(f"Drift detected in {column}: p-value = {p_value}")
```

Model Retraining Pipeline

```python
```

```python
def retrain_model_if_needed(current_performance, threshold=0.05):
    """Retrain model if performance degrades"""
    if current_performance < threshold:
        print("Retraining model due to performance degradation")
        new_model = train_new_model()
        return new_model
    return current_model
```

🎯 Future Enhancements

Planned Features

- [ ] **Deep Learning Models** (Neural Networks)
- [ ] **Ensemble Methods** (Voting, Stacking)
- [ ] **AutoML Integration** (Auto-sklearn, TPOT)
- [ ] **Real-time Model Updates**
- [ ] **A/B Testing Framework**
- [ ] **Mobile App** (React Native/Flutter)
- [ ] **API Endpoints** (FastAPI/Flask)
- [ ] **Docker Containerization**
- [ ] **Kubernetes Deployment**
- [ ] **MLOps Pipeline** (MLflow, Kubeflow)

Experimental Features

- **Explainable AI** with SHAP and LIME
- **Federated Learning** for distributed training
- **Edge Computing** deployment
- **Time Series Analysis** for longitudinal studies

🏆 Acknowledgments

Contributors

- **Claude AI** - Main Development
- **UCI ML Repository** - Dataset Provider
- **Streamlit Team** - Web Framework
- **Scikit-learn** - ML Library

Inspiration

This project was inspired by the need for accessible healthcare AI tools and demonstrates best practices in machine learning pipeline development.

License

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Support & Contact

Getting Help

- **Issues**: GitHub Issues
- **Discussions**: GitHub Discussions
- **Documentation**: Project Wiki

Citation

If you use this project in your research, please cite:

```bibtex
@software{heart_disease_ml_pipeline,
  title={Heart Disease Prediction ML Pipeline},
  author={Claude AI},
  year={2025},
  url={https://github.com/yourusername/heart-disease-ml-pipeline}
}
```

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