





Transforming healthcare with AI-powered disease prediction based on patient data.

Student Name: S.Tamil selvan

Register Number: 412323205047

Institution: Sri Ramanujar Engineering College

Department: B.Tech / IT

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Github Repository Link: [Update the project source code to

your Github Repository]

1.project statement

- **1.Late Diagnosis:** Diseases are often detected too late, limiting treatment effectiveness and increaseing cost.
- **2.Data Underutilization:** patient data is not fully levaraged for early disease prediction, missing crucial insights.
- **3.Resource misallocation:**Healthcare resources are are not optimized due to inability to predict at-risk patients early.
- **4.Generic Care:** lack of personalized predictions leads to one-size-fits- all treatment plans, reducing treatment efficacy.

2.project objectives

1. Develop an Al-based model capable of accurately predicting the onset of specific diseases using historical and real-time patient data.

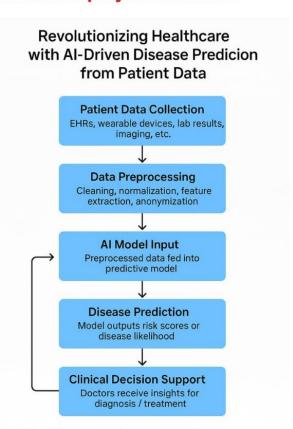






- 2. Integrate diverse data sources, including electronic health records (EHR), lab results, medical imaging, and wearable device data, to enhance prediction accuracy.
- 3. Ensure patient data privacy and security by implementing strong encryption and compliance with healthcare regulations (e.g., HIPAA, GDPR).
- 4. Improve early diagnosis rates for targeted diseases, reducing the time from symptom onset to clinical intervention.
- 5. Deploy a user-friendly interface for healthcare providers to interpret Al predictions and integrate them into clinical workflows.

3.Flowchart of the project work flow









4. Data description

1. Patient Demographics

Attributes: Age, gender, ethnicity, weight, height, BMI, smoking status

Purpose: Establish baseline risk factors and personalize predictions

2. Medical History

Attributes: Chronic conditions (e.g., diabetes, hypertension), previous surgeries, allergies, family history of diseases

Purpose: Identify long-term risk patterns and hereditary influences

3. Clinical Data

Attributes: Lab test results (blood tests, cholesterol levels), imaging results (X-rays, MRIs), vital signs (blood pressure, heart rate, temperature)

Purpose: Provide measurable indicators of current health status

4. Medications

Attributes: Current prescriptions, dosage, frequency, past medications

Purpose: Analyze potential side effects or interactions affecting disease risk

5. Lifestyle Data

Attributes: Physical activity, diet, alcohol consumption, sleep patterns

Source: Self-reported surveys, fitness trackersSure! Here's a single key point:

5.Data preprocessing







1. Data Collection:

Sources: EHRs (Electronic Health Records), lab results, wearable devices, imaging data, etc.

2. Data CleanHandling Missing:

Values: Drop rows/columns with excessive missingness

Impute with mean/median/mode or use model-based imputation

Removing Duplicates

Outlier Detection:

Use Z-score, IQR, or domain-specific rules (e.g., BP > 300 is invalid)

3. Data Transformation:

Encoding Categorical Variables:

One-hot encoding (for nominal data)

Label encoding (for ordinal data)

Feature Scaling:

Standardization (Z-score)

Normalization (Min-Max scaling)

Date and Time Features:

Extract age, day of week, time since diagnosis, etc

4. Feature Engineering:

Combine Features: E.g., BMI = weight / height²

Domain-Specific Ratios: Lab value ratios, risk scores

Interaction Features: Age × chronic condition statement

5. Dimensionality Reduction (if needed):

PCA, t-SNE (for visualization), or domain-driven feature selection







6. Exploratory Data Analysis

1. Understand the Dataset:

Load the data: Use tools like pandas to read CSV, Excel, or database files.

Preview: Use .head(), .info(), .describe() to inspect structure and basic statistics.

Data types: Check for categorical, numerical, boolean, and datetime features.

2. Clean the Data:

Missing values: Use df.isnull().sum() to detect, and impute or drop as needed.

Duplicates: Use df.duplicated().sum() and df.drop_duplicates() if necessary.

Outliers: Use box plots or IQR method.

3. Univariate Analysis:

Numerical features: Histograms, box plots. Categorical features: Bar plots, value counts.

import matplotlib.pyplot as plt
 import seaborn as sns
sns.histplot(df['age'], kde=True)
sns.countplot(x='gender', data=df)

4. Bivariate/Multivariate Analysis:

Correlations: Heatmap for numeric features.

Target relationship: Analyze how each feature relates to disease presence or severity.

Correlation heatmap

plt.figure(figsize=(12, 8))

sns.heatmap(df.corr(), annot=True, cmap='coolwarm')

Boxplot of age by disease outcome

sns.boxplot(x='disease', y='age', data=df)







5.Summary Insights

Highlight patterns, such as risk factors.

Identify which features are most associated with disease.

7. Feature Engineering

1. Handling Categorical Variables:

Convert non-numeric features into numbers so machine learning models can use them.

One-Hot Encoding: For unordered categories (e.g., gender).

Creates binary columns like gender_male = 1/0.

Label Encoding: For ordered categories (e.g., disease stage).

Assigns numbers based on rank (e.g., mild = 0, severe = 2)

2. Creating New Features:

Derive meaningful new variables from existing data to improve prediction.

BMI:

BMI = weight_kg / (height_m)^2 — useful for identifying obesity-related risks.

Age Groups:

Group ages into categories like young, middle-aged, senior.

Risk Flags:

Create binary indicators like:

high_bp = 1 if systolic BP > 130 or diastolic BP > 80

high_glucose = 1 if glucose > 126







8. Model Building

1. Data Preprocessing

Clean Data: Handle missing values, remove outliers, and encode categorical variables (e.g., One-Hot or Label Encoding).

Feature Scaling: Normalize or standardize numerical features if using algorithms like SVM or KNN.

Split Data: Divide into training and test sets (e.g., 80/20 split).

2. Model Selection

Algorithm Choice: Start with simpler models like Logistic Regression or Decision Trees, then move to more complex ones like Random Forest or XGBoost.

Cross-validation: Use k-fold cross-validation to evaluate model stability.

Hyperparameter Tuning: Tune models using grid search or random search.

3. Model Evaluation

Metrics: Use appropriate evaluation metrics like accuracy, precision, recall, F1-score, ROC-AUC (especially for imbalanced datasets).

Confusion Matrix: Helps visualize true positives, false positives, true negatives, and false negatives.

9.visualization Of Results ව model insight







1. Confusion Matrix

Shows how well the model classifies:

True Positives (TP), False Positives (FP), etc.

from sklearn.metrics import confusion_matrix, ConfusionMatrixDisplay

ConfusionMatrixDisplay.from_estimator(model, X_test, y_test)

2. ROC Curve & AUC Score

Visualizes the trade-off between true positive rate and false positive rate.

from sklearn.metrics import roc_curve, auc

fpr, tpr, _ = roc_curve(y_test_rmodelppredict_proba(X_test)[:,1])

plt.plot(fpr, tpr, label=f"AUC = {auc(fpr, tpr):.2f}"

3. Feature Importance

Shows which features contributed most to predictions (for tree-based models).

import seaborn as sns

importances = model.feature_importances_

sns.barplot(x=importances, y=feature_names)

10.Tools and technologies used







1. Programming Language

Python – Widely used for data science and machine learning.

2. Data Handling & Analysis

Pandas – For data manipulation and analysis.

NumPy – For numerical operations.

3. Visualization

Matplotlib & Seaborn – For data and result visualization.

Plotly – For interactive visualizations.

4. Machine Learning

Scikit-learn – For model building, evaluation, and preprocessing.

XGBoost / LightGBM – For high-performance gradient boosting models.

5. Model Tuning & Evaluation

GridSearchCV / RandomizedSearchCV – For hyperparameter tuning.

SHAP / LIME – For model explainability and insights.

6. Environment & Tools

Jupyter Notebook / Google Colab – For interactive coding and experiments.

Anaconda – For managing packages and environments.







11.Team members and contribution

- S.Tamilselvan (Data cleaning, EDA)
- J.Jabanesh (Feature engineering, Model development)
- **L.Vijay Documention and reporting**