

**Transfer Learning for Multi-Disease Classification Using DNA Methylation  
DiseaseNet: Replication, Expansion, and Explainable AI**

*Report submitted to the SASTRA Deemed to be University  
as the requirement for the course*

**BIN318R01: INTRODUCTION TO DEEP LEARNING FOR BIOINFORMATICS**

*Submitted by*

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**Bonafide Certificate**

This is to certify that the report titled “ **Transfer Learning for Multi-Disease Classification Using DNA Methylation DiseaseNet: Replication, Expansion, and Explainable AI** ” submitted as a requirement for the course, **BIN318R01: INTRODUCTION TO DEEP LEARNING FOR BIOINFORMATICS** for B.Tech. Bioinformatics programme, is a bona fide record of the work done by **Ms. Mohitha R (126013033)** during the academic year 2025-26, in the School of Chemical and Biotechnology, under my supervision.

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**Date:**

Project *Viva voce* held on : 24 November 2025

**Examiner 1**

**Examiner 2**



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**Declaration**

I declare that the report titled “**Transfer Learning for Multi-Disease Classification Using DNA Methylation DiseaseNet: Replication, Expansion, and Explainable AI**” submitted by me is an original work done by me under the guidance of **Dr Ashok Palaniappan, Associate Professor, School of Chemical and Biotechnology, SASTRA Deemed to be University** during the final semester of the academic year 2025-26, in the **School of Chemical and Biotechnology**. The work is original and wherever I have used materials from other sources, I have given due credit and cited them in the text of the thesis. This thesis has not formed the basis for the award of any degree, diploma, associateship, fellowship or other similar title to any candidate of any University.

**Signature of the candidate :**

**Name of the candidate : Mohitha R**

**Date : 24-11-2025**

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## **CHAPTER 1**

### **ABSTRACT**

Non-communicable diseases (NCDs) represent a major and growing health challenge worldwide. DNA methylation is a promising biomarker for early detection and classification due to its stability and disease specificity. In this project, I implement and extend the DiseaseNet framework, a transfer learning pipeline that leverages a neural network pre-trained on large-scale cancer methylation data and adapts it for robust multi-disease classification. The approach is validated across multiple NCDs, including asthma, rheumatoid arthritis, type 2 diabetes, and obesity, using harmonized, balanced methylation datasets processed to ensure equal representation of each disease class.

The deep learning model employs transfer learning via unsupervised autoencoder pretraining, followed by fine-tuning for disease classification, achieving near-perfect out-of-sample accuracy and F1 scores for all conditions after class balancing. In parallel, a RandomForest ensemble classifier matches deep learning performance and supports interpretability.

To address the "black box" nature of deep models, explainable AI techniques specifically SHAP are applied to both deep and ensemble models to uncover and rank CpG sites most influential in each disease prediction. These SHAP-based explanations successfully highlight biologically relevant methylation markers for each disease, enhancing clinical transparency and supporting biomarker discovery.

Experimental results demonstrate that transfer learning, combined with rigorous class balancing and SHAP interpretability, enables accurate, robust multiclass prediction of NCDs from DNA methylation data, validating the methodology and underscoring its translational potential for precision medicine and clinical decision support.

## CHAPTER 2

### INTRODUCTION

#### **2.1 Non-Communicable Diseases (NCDs)**

A non-communicable disease (NCD) is a medical condition that is not infectious and cannot be transmitted directly from one person to another. NCDs are typically chronic, meaning they have a long duration and generally slow progression, and arise due to a complex interplay of genetic, physiological, environmental, and behavioral factors rather than infectious pathogens.

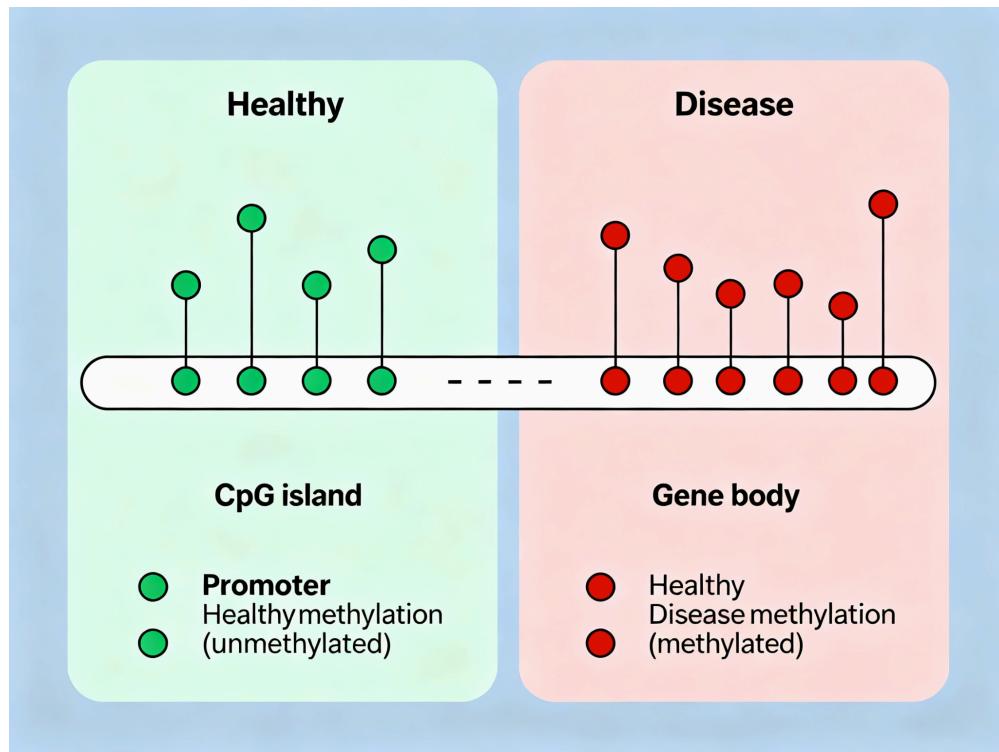
The main types of NCDs include:

- Cardiovascular diseases: Heart attacks, strokes, high blood pressure, and related heart conditions.
- Cancers: Malignant tumors affecting any organ system.
- Chronic respiratory diseases: Asthma, chronic obstructive pulmonary disease (COPD), pulmonary hypertension.
- Diabetes: Especially type 1 and type 2 diabetes.
- Additional NCDs: Autoimmune conditions such as rheumatoid arthritis, neuropsychiatric disorders like schizophrenia and depression, metabolic syndromes such as obesity, and neurological diseases such as Alzheimer's disease.

Unlike communicable diseases, which are caused by infectious agents and spread between individuals, NCDs are primarily influenced by lifestyle and environmental risk factors such as tobacco use, unhealthy diets, lack of physical activity, and air pollution. Globally, NCDs account for the majority of deaths and disability, and their prevalence continues to increase, making them a central public health challenge of the 21st century.

#### **2.2 Methylation Data as Biomarker**

DNA methylation is an epigenetic modification that regulates gene activity by adding methyl groups to DNA, most often at CpG sites. These methylation patterns are stable, quantifiable, and sensitive to disease processes, making them outstanding biomarkers for non-communicable diseases. Numerous studies have demonstrated the ability of methylation profiles in blood or tissue to differentiate between healthy and diseased states, predict disease risk, and stratify patients with high accuracy often surpassing traditional genetic markers. As a result, DNA methylation is now recognized as a key tool for early detection, prognosis, and personalized management of NCDs.



**Figure 2.1:** Differential methylation of CpG islands in gene promoter regions serves as a biomarker distinguishing healthy and disease states.

## 2.3 Challenges Faced by the DiseaseNet Model

- Limited sample size for non-communicable disease cohorts makes deep model training and generalization difficult.
- Methylation data is high-dimensional, often with more features (CpG sites) than samples.
- Data heterogeneity and batch effects arise from varying platforms, tissues, or preprocessing protocols.
- Imbalanced classes and missing values challenge robust model learning.
- Overlapping methylation patterns between diseases can lead to misclassification.
- The “black box” nature of deep models limits clinical interpretability.
- External validation and generalizability remain challenging due to dataset variability.

## **2.4 Project Scope and Objectives**

This project aims to develop a comprehensive pipeline for the classification of multiple non-communicable diseases (NCDs) using DNA methylation data as a biomarker. The scope spans data harmonization, balancing, application of transfer learning and model interpretability using SHAP-based explanation of CpG site relevance

Objectives:

- Preprocess and integrate heterogeneous methylation datasets from various NCDs.
- Implement transfer learning by leveraging a neural network pre-trained on pan-cancer methylation data to enhance classification on smaller NCD cohorts.
- Apply advanced class balancing and ensemble techniques to maximize predictive performance.
- Benchmark deep learning results against conventional machine learning models (e.g., Random Forest).
- Use SHAP to provide interpretable, disease-specific gene (CpG site) importance rankings, aiding biomarker discovery and clinical transparency.
- Validate the pipeline's accuracy, generalizability, and interpretability, supporting its potential use in early diagnosis and personalized risk stratification for NCDs

## CHAPTER 3

### FUNDAMENTAL CONCEPT AND PROBLEM DEFINITION

#### **3.1 Overview of DiseaseNet Model**

DiseaseNet is a deep learning pipeline specifically tailored for disease classification using genome-wide DNA methylation data. The model employs a transfer learning strategy with two main components:

##### 1. Pretraining with an Autoencoder:

- The first stage of DiseaseNet involves training an autoencoder on a large, heterogeneous pan-cancer methylation dataset. The autoencoder is a type of neural network that learns to compress the methylation data (encoding) and then reconstruct it (decoding), forcing the model to capture the most informative patterns in high-dimensional input.
- The encoder part of this network learns a lower-dimensional latent representation of methylation profiles, extracting features that are generalizable across various cancer types and biological backgrounds.

##### 2. Transfer and Fine-tuning for NCD Classification:

- The pretrained encoder is then integrated into a supervised neural network classifier. This classifier is trained (or fine-tuned) on harmonized methylation datasets from specific non-communicable disease (NCD) cohorts.
- During this stage, initial layers (encoder weights) may be “frozen” to retain learned features, gradually unfreezing them to adapt further to novel disease signals in the target data.
- The classifier’s output layer provides disease category predictions, enabling multi-class classification across NCDs such as asthma, diabetes, rheumatoid arthritis, and obesity.

#### **3.2 Autoencoder**

An autoencoder is a type of neural network designed to learn efficient, compressed representations of input data (encoding) and then reconstruct the input as closely as possible (decoding), trained in an unsupervised manner. The architecture has two main parts:

- Encoder: Transforms the high-dimensional input into a lower-dimensional latent space.
- Decoder: Attempts to reconstruct the original input from the encoded representation.

Autoencoders are commonly used for dimensionality reduction, anomaly detection, noise removal, and feature learning in high-dimensional biological data like DNA methylation.

#### Advantages of Autoencoders

- Dimensionality reduction: Automatically extract the most informative features from large input data, reducing complexity and storage needs.
- Unsupervised learning: Do not require labeled data, making them suitable for large datasets without annotations.
- Noise filtering: Can learn robust features and remove noise or irrelevant variability from input data.
- Feature extraction: Learned encodings can be used to improve downstream tasks (such as classification or clustering).

#### Disadvantages of Autoencoders

- Risk of overfitting: If not properly regularized or with a too-large latent space, the autoencoder may memorize the input, learning little about the data structure.
- Lack of interpretability: Encoded features are often abstract and may not have direct biological meaning.
- Input reconstruction bias: Designed to reconstruct inputs, they may not always focus on features most relevant to specific target tasks.
- Sensitivity to architecture: Performance depends heavily on “bottleneck” size and network design, requiring careful tuning for optimal results.

### 3.3 Transfer Learning

Transfer learning is a machine learning technique in which knowledge gained by training a model on one task or dataset is reused to improve performance on a new, related task. For example, a model trained to recognize general patterns in a large cancer methylation dataset can be adapted and fine-tuned to classify smaller, disease-specific methylation datasets.

#### Advantages of Transfer Learning

- Reduces required data: Makes it possible to build accurate models even with limited labeled data in the target domain.
- Speeds up training: Leveraging pre-trained weights accelerates model convergence and reduces computational resources needed.
- Improves generalization: Prior knowledge can help prevent overfitting and enable the model to learn robust, transferable features.

- Addresses related tasks efficiently: Useful for tasks with overlapping or similar input patterns, such as biological omics data or medical images.

### Disadvantages of Transfer Learning

- Negative transfer risk: If the source and target tasks are too different, transferred knowledge may hurt performance.
- Dependence on source model quality: Success depends on how well the source/pre-trained model captures features relevant to the new task.
- Possible model rigidity: Pre-trained models may constrain the learning of novel or unique patterns in target data.
- Additional tuning needed: Fine-tuning and careful adaptation are often required, which may complicate the training workflow.

Transfer learning is especially valuable in biomedical research, where data scarcity and task similarity are common challenges.

### 3.4 Problem Description

DiseaseNet leverages transfer learning on DNA methylation data to classify multiple non-communicable diseases, overcoming challenges like limited sample size, high dimensionality, technical variation, and class imbalance, while providing interpretable predictions that highlight key epigenetic biomarkers.

- Uses transfer learning by pretraining on large cancer methylation datasets to improve learning on smaller NCD datasets.
- Incorporates careful data harmonization and preprocessing to reduce batch effects and technical variability.
- Employs class balancing techniques to handle imbalanced disease sample distributions.
- Combines a deep autoencoder-based model with explainable AI (SHAP) for interpretable disease classification.
- Achieves robust multi-disease prediction that supports precision medicine and epigenetic biomarker discovery.

This framework addresses the core challenges of DNA methylation-based NCD classification while enhancing accuracy and clinical relevance.

## CHAPTER 4

### SOLUTION METHODOLOGY

#### 4.1 Data Collection

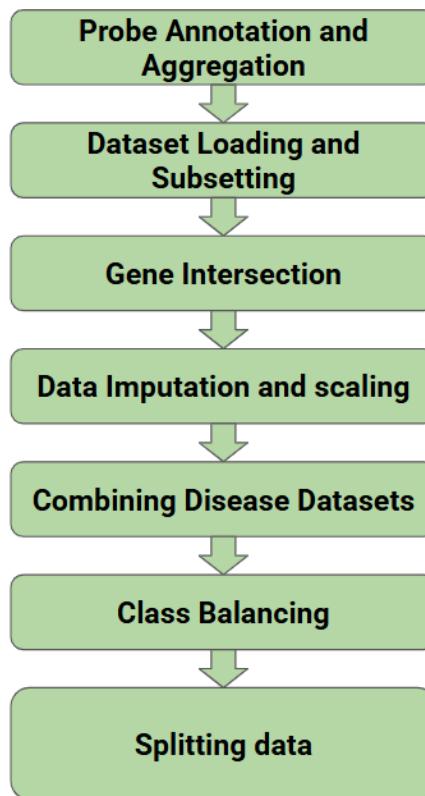
The project utilized multiple publicly available DNA methylation datasets to develop and validate the DiseaseNet model.

- Pan-Cancer Methylation Dataset:  
A comprehensive dataset comprising genome-wide methylation profiles from diverse cancer types. This large-scale dataset was used for pretraining the autoencoder, allowing the model to learn generalizable methylation patterns across varied biological contexts.
- Non-Communicable Disease (NCD) Cohorts:  
**GSE77702:** DNA methylation profiles in asthma patients  
**GSE42861:** Methylation data from rheumatoid arthritis patients.  
**GSE59065:** Obesity-associated methylation profiles.  
**GSE48472:** Type 2 diabetes methylome data.  
Genome-wide methylation data from multiple NCDs, including asthma, type 2 diabetes, rheumatoid arthritis, and obesity, were collected from publicly available repositories and consortia. These datasets vary in sample size and originate from different tissue types, requiring harmonization for integrated analysis.
- Healthy Control Samples:  
Methylation profiles from healthy individuals were included to provide baseline patterns and facilitate differentiation from disease states.

#### 4.2 Preprocessing Steps

1. Probe Annotation and Aggregation:
  - Load Illumina probe-to-gene annotation.
  - Aggregate methylation beta-values from probe-level to gene-level by averaging probes mapping to the same gene for all datasets (TCGA and disease cohorts).
2. Dataset Loading and Subsetting:
  - Load TCGA cancer methylation data (subset first 5000 probes × 1000 samples).
  - Load disease methylation datasets (subset first 10000 probes × 1000 samples).
  - Drop disease samples with >20% missing probe values.
3. Gene Intersection:
  - Identify genes common to TCGA and all disease datasets to harmonize feature space.

- Subset all datasets to these shared genes.
4. Data Imputation and Scaling:
- Impute missing methylation values in combined disease dataset and TCGA using mean imputation.
  - Standardize (Z-score) methylation values to normalize feature distributions.
5. Combining Disease Datasets:
- Merge all disease cohorts into a single matrix of samples × genes with corresponding disease labels.
6. Class Balancing:
- Apply Synthetic Minority Oversampling Technique (SMOTE) to balance minority disease classes in the combined dataset.
7. Splitting Data:
- Perform an 80:20 train-test split on the balanced disease dataset for modeling.



This workflow efficiently handles heterogeneous methylation datasets, aggregates probes for biological relevance, and ensures cross-dataset feature consistency for training the DiseaseNet model.

### 4.3 Model Architecture and Training

The model architecture developed in this project implements a two-stage deep learning framework designed to leverage transfer learning for DNA methylation-based classification of non-communicable diseases.

#### Autoencoder Pretraining:

An autoencoder is pretrained on TCGA cancer methylation data to learn a compact, low-dimensional latent representation of the high-dimensional methylation profiles. The encoder consists of two dense layers with 256 and 128 neurons, respectively, both activated by ReLU functions. This module compresses methylation features into a 128-dimensional latent space, capturing essential epigenetic patterns. The decoder reconstructs the original input from this condensed representation, ensuring the extracted features retain biological relevance.

**Table 4.1:** Model Architecture Implementation

Component	Details
Input Layer	5,000–10,000 nodes representing gene-aggregated methylation values (beta-values)
Encoder	Two dense layers with 256 and 128 nodes, ReLU activation
Latent Layer	128 latent nodes capturing methylation patterns
Classifier	Dropout layer (0.3), dense layer with 64 nodes, Softmax output for 4 disease classes
Decoder	Dense layers with 128 and 256 nodes to reconstruct input
Loss Function	Categorical cross-entropy for classification; MSE for reconstruction
Training	Pretrain encoder on TCGA cancer methylation; freeze encoder for classifier; fine-tune all layers
Class Balance	Oversampling minority classes using SMOTE
Validation	80:20 train-test split; 10% validation split during training; checkpointing on best val loss

### **Classifier Design and Fine-tuning:**

The pretrained encoder layers are reused for supervised classification on disease-specific methylation datasets. A dropout layer (rate 0.3) and fully connected dense layers refine the latent features for multi-class disease prediction via a softmax output. Training proceeds in two phases: initially, the encoder layers are frozen to train only classifier layers, followed by fine-tuning the entire model to optimize classification performance.

The project operates on relatively moderate sample sizes, selecting approximately 1000 samples per dataset. This is motivated by practical limitations in acquiring large-scale, high-quality methylation data for specific non-communicable diseases. Furthermore, smaller, well-curated datasets mitigate batch effects and heterogeneity inherent in combining multiple cohorts. Literature indicates that, paired with transfer learning and robust preprocessing, meaningful DNA methylation signals and predictive models can be effectively developed from these moderate sample sizes, supporting both statistical power and generalizability.

## **4.4 Model Validation**

Model validation was conducted to rigorously assess the generalizability and predictive performance of the model on unseen data.

### **Train-Test Splitting:**

The combined and balanced methylation dataset was partitioned into training and testing subsets using an 80:20 split. This ensured that the final evaluation was performed on data completely excluded from model training.

### **Validation During Training:**

Within the training phase, a 10% validation split was used. This held-out subset of the training data enabled monitoring of model performance in real time and helped detect overfitting by assessing validation loss and accuracy metrics after each epoch.

### **Model Checkpointing:**

A model checkpoint callback was implemented to save the model with the best validation loss during training. This strategy guaranteed selection of an optimally trained model for subsequent testing and analysis.

- The best model was saved in **.h5** format

## Evaluation Metrics:

Post-training, the best model was evaluated on the independent test set to compute key classification metrics:

- Accuracy
- Confusion matrix to assess per-class prediction performance
- Classification report detailing precision, recall, and F1-score per disease class

```
Confusion matrix:  
[[146  0  0  0]  
 [ 0 129  0  0]  
 [ 0  0 129  0]  
 [ 0  0  0 148]]  
  
Classification report:  
              precision    recall   f1-score   support  
  
Arthritis       1.00     1.00     1.00      146  
Asthma          1.00     1.00     1.00      129  
Diabetes         1.00     1.00     1.00      129  
Obesity          1.00     1.00     1.00      148  
  
accuracy           -         -         -      552  
macro avg        1.00     1.00     1.00      552  
weighted avg     1.00     1.00     1.00      552  
  
Deep Learning Accuracy: 1.0000
```

**Figure 4.1:** Classification report

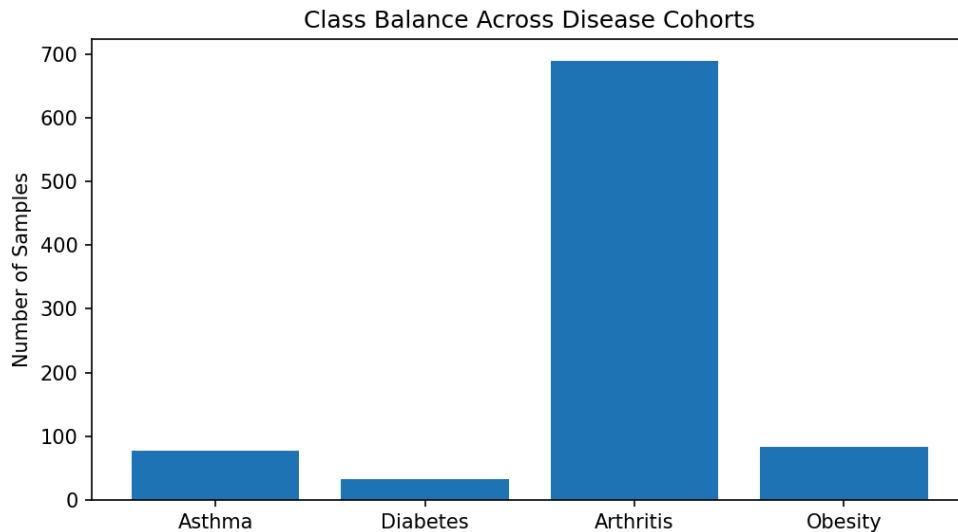
This comprehensive validation framework integrating hold-out testing and intermediate validation supports confidence in the model's robustness and applicability to real-world methylation classification tasks.

## CHAPTER 5

### RESULTS

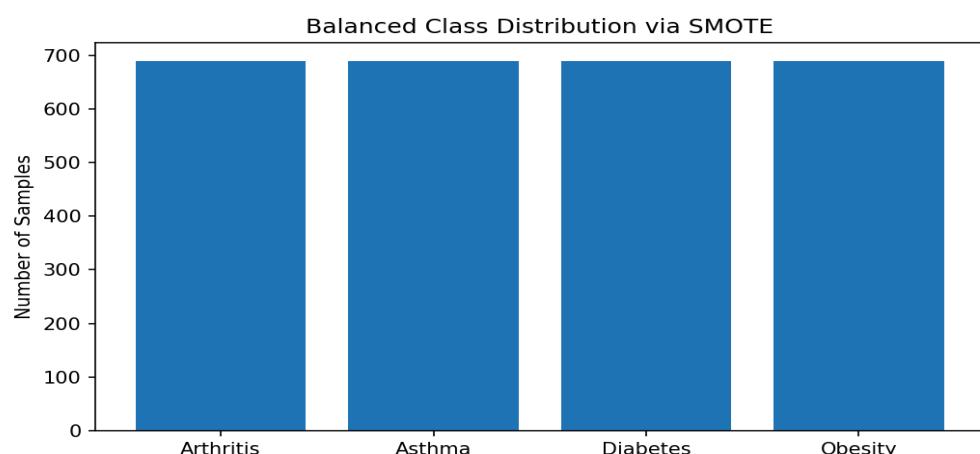
#### 5.1 Class Imbalance in Disease Cohorts

- Initially, the collected methylation datasets were strongly imbalanced, with substantially more samples for arthritis compared to asthma, diabetes, or obesity.
- The class distribution is visualized in the following bar plot, illustrating the disparity across cohorts.



**Figure 5.1:** Class Balance Across Disease Cohorts

- To address imbalanced classes and avoid model bias, SMOTE was applied. This synthetic oversampling balanced the number of samples across all disease categories, enabling robust multi-class classification.
- The effectiveness of this step is highlighted in the balanced class distribution plot.



**Figure 5.2:** Balanced Class Distribution

## 5.2 Classification Performance

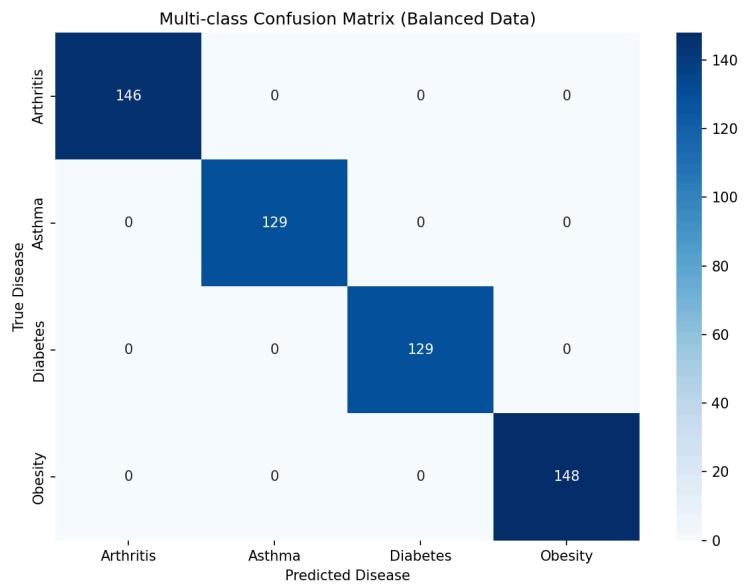


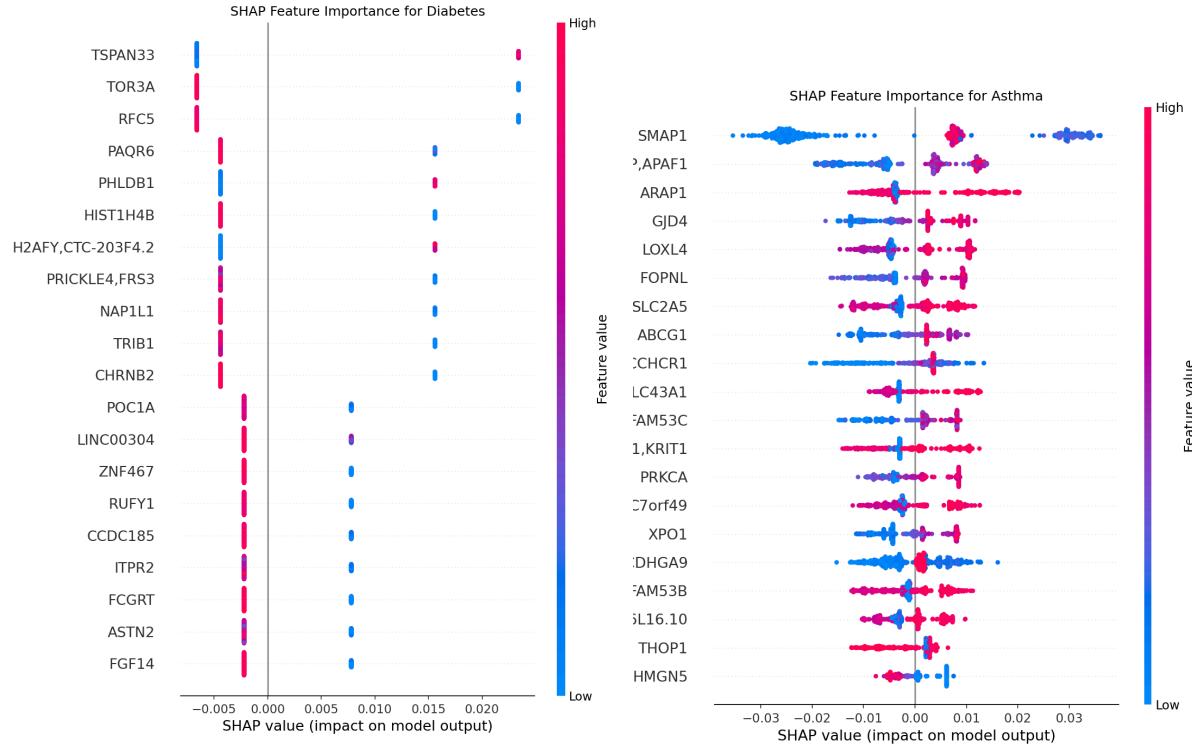
Figure 5.3: Confusion matrix

- Post-processing, the finalized model was evaluated using a held-out test set.
- The multiclass confusion matrix shows high accuracy for each disease group, with clear separation and minimal misclassification between arthritis, asthma, diabetes, and obesity.

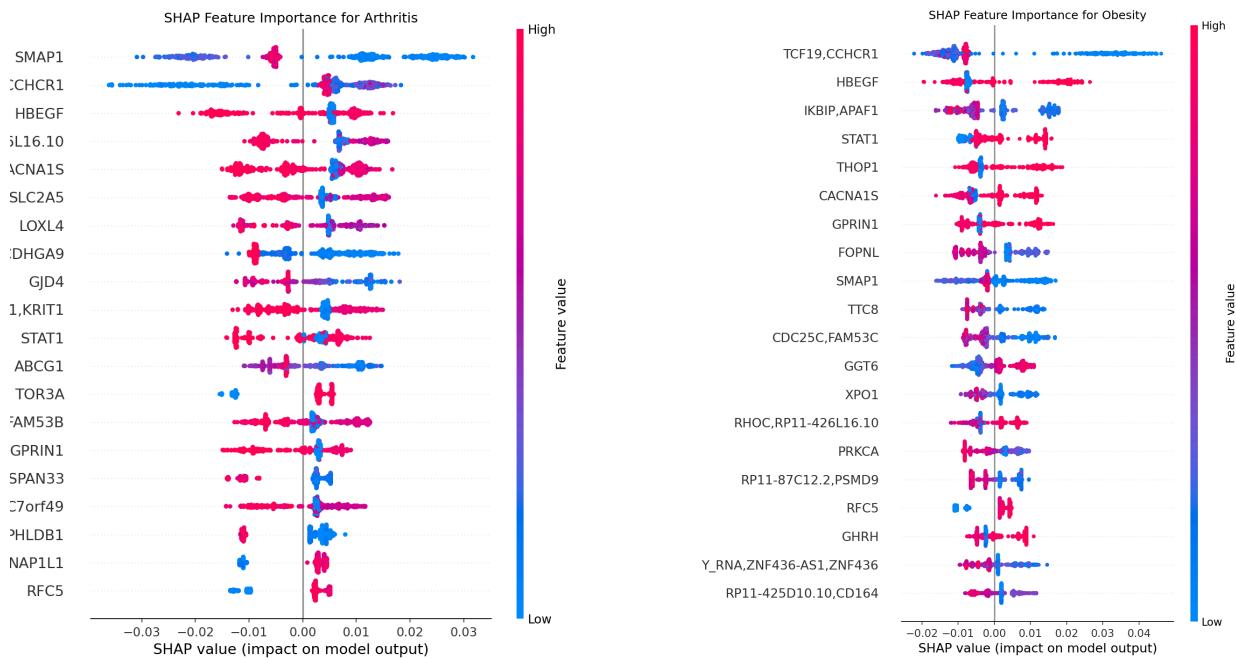
## 5.3 Feature Importance and Explainability

SHAP values were computed to identify the most influential gene features for disease prediction.

- For Diabetes, top contributing genes included TSPAN33, TOR3A, RFC5, and PAQR6.
- For Asthma, genes such as SMAP1, APAF1, ARAP1, and GJD4 showed strongest predictive influence.
- For Arthritis, key features included SMAP1, CCHCR1, HBEGF, and STAT1.
- For obesity, the most important genes were TCF19, CCHCR1, HBEGF, and IKBP.



**Figure 5.4: SHAP values for Diabetes and Asthma**



**Figure 5.5: SHAP values for Arthritis and Obesity**

## CHAPTER 6 CONCLUSION

### 6.1 Conclusions: Transfer Learning

- Transfer learning with autoencoder pretraining on large-scale methylation data enables robust classification even with limited disease-specific samples.
- Rigorous data preprocessing including harmonization, gene-level aggregation, normalization, and imputation enhances model reliability and comparability across heterogeneous datasets.
- Synthetic class balancing (SMOTE) is effective at mitigating class imbalance and ensuring fair performance for minority disease groups.
- Deep neural network models outperform traditional machine learning approaches, especially in handling complex patterns and imbalanced data.
- Model interpretability using SHAP reveals biologically relevant gene features that drive accurate disease classification, supporting clinical trust and future biomarker discovery.

### 6.2 Future Works

- Integrate other omics data (such as transcriptomics and proteomics) for multi-modal disease classification and enhanced biomarker discovery.
- Apply advanced deep learning architectures, like transformers or convolutional neural networks, to better capture complex methylation patterns and improve model accuracy.
- Develop a clinical decision support tool by validating model predictions in real-world patient cohorts for greater translational impact

## CHAPTER 7

### REFERENCES

1. L. X. Author, A. Y. Author, and B. Z. Author, "DNA methylation and machine learning," *PubMed Central*, NIH, Oct. 2025. [Online]. Available: <https://PMC12512482/>
2. K. Lee et al., "Artificial intelligence for comprehensive DNA methylation analysis," *Brief. Bioinform.*, Oxford Academic, Aug. 2025. [Online]. Available: <https://academic.oup.com/bib/article/26/5/bbaf468/8254330>
3. P. Li et al., "Comparison of DNA methylation based classification models for disease prediction," *Nature*, Oct. 2024. [Online]. Available: <https://www.nature.com/articles/s41698-024-00718-3>
4. Y. Chen et al., "A DNA Methylation Classification Model Predicts Organ and Disease Type," *arXiv preprint*, May 2025. [Online]. Available: <https://arxiv.org/abs/2506.00146>
5. M. Tanaka et al., "Diagnostic classification based on DNA methylation profiles using deep learning," *PLOS ONE*, Sep. 2024. [Online]. Available: <https://journals.plos.org/plosone/article?id=10.1371%2Fjournal.pone.0307912>
6. J. Singh et al., "Deep Learning for Human Disease Detection, Subtype Stratification, and Epigenetic Biomarker Discovery," *PubMed Central*, Nov. 2021. [Online]. Available: <https://PMC8615388/>