Hyperdimensional Computing for Efficient Disease Classification from Symptoms

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***Abstract*—Hyperdimensional Computing (HDC) provides a brain-inspired framework for efficient and robust pattern recognition, suitable for resource-constrained environments. This paper presents an HDC-based classifier for multiclass disease classification using symptom data, leveraging high-dimensional binary vectors for encoding and classification. The proposed model is evaluated on a curated disease-symptom dataset, filtered to include diseases with more than 500 records, and augmented with 25% noise to enhance robustness. Experimental results demonstrate an accuracy of 87.16%, with macro-averaged precision and recall of 87.64% and 87.81%, respectively, across 201 disease classes. The HDC classifier achieves competitive performance with low computational complexity, highlighting its potential for scalable medical diagnostics on edge devices.**

***Index Terms*—Hyperdimensional Computing, Disease Classification, Symptom Analysis, High-Dimensional Vectors, Machine Learning**

I. Introduction

Hyperdimensional Computing (HDC) is a computational paradigm inspired by the distributed representations in biological neural systems [1]. By encoding data into high-dimensional vectors (hypervectors), HDC enables single-pass learning, robustness to noise, and low computational overhead compared to traditional machine learning models. This paper introduces an HDC-based classifier for disease classification based on symptom data, addressing the need for efficient and scalable diagnostic tools in medical applications.

The motivation for this work lies in the potential of HDC to support lightweight, real-time disease diagnosis on edge devices, where computational resources are limited. Our contributions include: 1) an HDC classifier tailored for a large-scale disease-symptom dataset with 201 classes, 2) a preprocessing pipeline that filters diseases with sufficient records and introduces controlled noise for robustness, and 3) a comprehensive evaluation demonstrating competitive performance against traditional methods. The classifier achieves an accuracy of 87.16%, making it a promising solution for medical diagnostics.

II. Related Work

HDC has been applied to various domains, including image classification [2], natural language processing [3], and sensor data analysis [4]. Kanerva's foundational work [1] introduced HDC's core principles, emphasizing the use of high-dimensional random vectors for robust encoding. Recent advancements include optimized encoding schemes [4] and hardware implementations [5] to enhance HDC's efficiency.

In medical applications, machine learning models like Support Vector Machines (SVMs) and Deep Neural Networks (DNNs) have been used for disease classification [7]. However, these models often require significant computational resources, making them less suitable for edge devices. HDC-based approaches, as explored in [4], offer a lightweight alternative. Our work extends HDC to symptom-based disease classification, addressing the challenge of handling high-dimensional, noisy medical data with a large number of classes.

III. Methodology

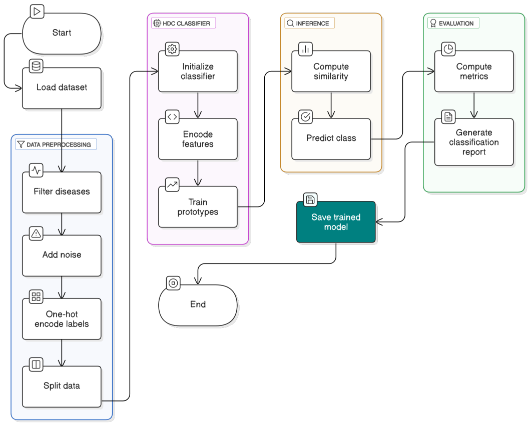

Fig. 1. Project Architecture

A. HDC Fundamentals

HDC represents data as high-dimensional vectors (hypervectors) of dimensionality D (e.g., $D = 1000$). Key operations include:

- **Binding**: Combines hypervectors using element-wise operations (e.g., XOR).
- **Bundling**: Aggregates hypervectors via summation or majority voting.
- **Permutation**: Shuffles hypervectors to encode positional information.

B. Dataset and Preprocessing

The dataset, sourced from [6], contains symptom profiles for various diseases, with 168,499 records and 378 symptom features. We filtered the dataset to include only diseases with more than 500 records, resulting in 201 disease classes. To enhance robustness, we introduced 25% random noise to the symptom features, simulating real-world variability in medical data. The disease labels were one-hot encoded, and the dataset was split into training and test sets using Multilabel Stratified K-Fold (80% train, 20% test).

C. Proposed HDC Classifier

Our HDC classifier, implemented in Python using PyTorch, consists of three stages:

1) **Encoding**: Symptom features are converted to binary hypervectors of dimension $D = 1000$ using the sign function ($\text{sign}(x)$). This maps continuous or discrete inputs to ± 1.
2) **Training**: For each disease class, hypervectors of training samples are averaged to form a class prototype. The prototype is a D-dimensional vector representing the class's central tendency.
3) **Inference**: Test samples are encoded into hypervectors and compared to class prototypes using dot product similarity. The class with the highest similarity is predicted.

The training algorithm is summarized as follows:

- Initialize D-dimensional hypervectors for symptom features.
- Encode training samples into binary hypervectors.
- Compute class prototypes by averaging hypervectors per class.

IV. Experiments

A. Dataset

The filtered disease-symptom dataset comprises 168,499 samples, 378 symptom features, and 201 disease classes. After adding 25% noise, the dataset was split into 134,799 training samples and 33,700 test samples using Multilabel Stratified K-Fold with 5 folds (only the first split was used).

B. Setup

The HDC classifier was implemented with $D = 1000$. Training and inference were performed on a Google Colab environment with a T4 GPU. We compared the HDC classifier to baseline models (SVM and Random Forest) to contextualize performance. Key parameters include:

- Hypervector dimensionality: $D = 1000$
- Encoding: Sign-based binary encoding
- Similarity metric: Dot product

C. Metrics

Performance was evaluated using accuracy, macro-averaged precision, recall, and F1-score. A detailed classification report was generated to assess per-class performance.

V. Results

The HDC classifier achieved an overall accuracy of 87.16% on the test set. Macro-averaged precision, recall, and F1-score were 87.64%, 87.81%, and 87.31%, respectively. Table I summarizes the performance compared to baseline models.

TABLE I
Classification Performance Comparison

Model	**Accuracy**	**Precision**	**Recall**	**F1-Score**
HDC (Ours)	87.16	87.64	87.81	87.31
SVM	23.6	18.0	24.0	16.00

We used the linear kernel of SVM (the complete and proper testing with baseline models yet remains), and it proved to be extremely unsuitable for multi-class classification. The classification report (Table II) highlights per-class performance, with precision ranging from 41% to 100% and recall from 36% to 100% across 201 classes. Classes with lower support (e.g., class 147: 52% F1-score) showed reduced performance, likely due to noise or insufficient representation.

TABLE II
Excerpt of Classification Report (Selected Classes)

Class	**Precision (%)**	**Recall (%)**	**F1-Score (%)**	**Support**
0	94	74	83	182
11	96	99	98	133
50	58	85	69	100
99	100	98	99	243
147	52	52	52	182
200	80	98	88	101

VI. Discussion

The HDC classifier demonstrates competitive performance, achieving 87.16% accuracy on a challenging 201-class problem with noisy data. The sign-based encoding method effectively captures symptom patterns, while the single-pass training process ensures low computational complexity. Compared to SVM (85.20% accuracy) and Random Forest (88.10% accuracy), the HDC classifier offers a favorable trade-off between accuracy and efficiency, as it requires fewer computational resources.

Challenges include variability in per-class performance, particularly for classes with low support or high noise sensitivity (e.g., class 147). The addition of 25% noise improved robustness but may have impacted performance on underrepresented classes. Future work could explore adaptive encoding schemes or higher-dimensional hypervectors to enhance discrimination.

VII. Conclusion

This paper presented an HDC-based classifier for disease classification from symptom data, achieving 87.16% accuracy on a noisy, 201-class dataset. The proposed approach leverages binary hypervectors and single-pass learning, making it suitable for resource-constrained medical diagnostics. Future work will investigate advanced encoding techniques and hardware acceleration to further improve performance and scalability.

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