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FINGERPRINT BASED DISEASE RISK PREDICTION SYSTEM

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Abstract: Dermatoglyphics, the study of ridge patterns on the fingers, palms, and soles, is increasingly recognized as a window into the genetic foundations of various physiological disorders [1, 3]. This study introduces a non-invasive, AI-driven decision-support tool designed to automate biometric analysis for early risk screening. Specifically, the system evaluates markers for type 2 diabetes, essential hypertension, cardiovascular disease (CAD), and perceived stress. The framework utilizes a multi-stage architecture. We first deployed a lightweight Convolutional Neural Network (CNN) to classify primary fingerprint patterns; this model was trained on a dataset of 6,000 scans, bolstered by standard data augmentation. To extract finer details, we developed a computer vision pipeline using OpenCV that applies adaptive binarization and morphological skeletonization. This allowed us to mathematically isolate specific biometric features, such as ridge density and minutiae layouts [5, 7]. For the final risk prediction, we utilized an Extreme Gradient Boosting (XGBoost) algorithm [8].When benchmarked against Support Vector Machine (SVM) and Random Forest baselines, the XGBoost model achieved an accuracy of 80.33%. Our results suggest that this system offers a fast, low-cost, and entirely non-invasive alternative for preliminary health screenings in clinical settings.

Index Terms - Dermatoglyphics, Machine Learning, Computer Vision, OpenCV, Convolutional Neural Networks (CNN), XGBoost, Predictive Healthcare, Non-Invasive Diagnostics.

I. INTRODUCTION

Dermatoglyphics,the study of epidermal ridge formations—is rooted in the fact that these patterns are fixed during the second trimester of fetal development [2]. Because ridge patterns share an embryological origin with the central nervous and vascular systems, they serve as a permanent biometric record of genetic predispositions toward certain systemic health conditions [1, 4]. While the global burden of chronic illnesses like Cardiovascular Disease (CAD), hypertension, and Type 2 Diabetes continues to climb, early detection is often stalled by the need for invasive bloodwork or high-cost imaging.

Despite the scientific backing for dermatoglyphic analysis, it hasn't gained much traction in clinical settings. Traditional manual analysis is simply too slow, inconsistent, and difficult to scale [6]. Furthermore, real-world fingerprint scans are rarely perfect; noise, smudging, and inconsistent lighting often make accurate feature extraction nearly impossible without sophisticated digital processing [7].

In this paper, we present an automated, AI-driven decision-support system designed to move dermatoglyphics into practical clinical use. The architecture combines a custom Convolutional Neural Network (CNN) for initial pattern sorting with an OpenCV-based pipeline for morphological skeletonization and preprocessing [5]. By stripping the raw scans down to their mathematical "skeletons," we can extract structured features that are then processed by an Extreme Gradient Boosting (XGBoost) model for risk assessment [8].

The goal was to turn complex biological patterns into a reliable data stream for early screening. By replacing manual interpretation with this ensemble machine learning approach, we've created a scalable, non-invasive tool that identifies high-risk individuals before more serious symptoms manifest. This integration of deep learning and computer vision offers a fast, cost-effective alternative to traditional preliminary diagnostics.

It is important to emphasize that this system isn't a replacement for a formal clinical diagnosis; it is a first line of defense. Because the framework is designed to run on standard hardware, it can be deployed in rural or under-resourced clinics where high-end lab equipment is often out of reach. By providing an immediate, data-backed risk snapshot, we can help healthcare providers prioritize their time and resources where they are needed most.

II. Literature Survey

Dermatoglyphic analysis is gaining traction as a non-invasive window into various physiological and psychological states. For instance, Abdul et al. [3] utilized Henry's classification system to explore the link between fingerprint patterns, specifically loops, whorls, and arches and Type 2 Diabetes. While they identified a notable prevalence of loop patterns in diabetic patients, the research was constrained by its reliance on manual observation and lacked a dedicated predictive mechanism.

Similar patterns emerge in cardiovascular and hypertensive research. Wijerathne et al. [2] noted that hypertensive individuals often exhibit higher ridge density and a frequency of whorl patterns, yet their work stopped short of proposing a standardized computational framework. This gap is also evident in the study of coronary artery disease (CAD), where Lu et al. [1] observed increased structural complexity and whorl frequency in affected individuals. While these findings validate dermatoglyphics as a biomarker, the lack of advanced predictive modeling limits their clinical utility.

Beyond physical health, the field has touched on psychological markers. Shakir et al. [4] investigated stress levels via the Perceived Stress Scale (PSS), finding that radial loops were common across stress categories, whereas arches were less frequent in high-stress individuals. Like the clinical studies mentioned above, this research leaned heavily on traditional statistical analysis rather than leveraging the predictive power of modern machine learning.

From a technical standpoint, the field of computer vision has recently offered tools to overcome these manual limitations. Morphological skeletonization, for example, allows ridge structures to be reduced to a single-pixel width, which drastically improves the accuracy of minutiae extraction [5]. Furthermore, adaptive thresholding has proven effective in cleaning up noise and lighting issues in low-quality scans [7]. When it comes to the actual prediction, ensemble models like Extreme Gradient Boosting (XGBoost) have consistently outperformed traditional Support Vector Machines (SVM) or Random Forests, particularly when dealing with the non-linear complexities of biomedical data [6, 8].

The Gap and Proposed Solution The current literature clearly establishes a statistical link between finger ridges and disease, but there is a distinct lack of scalable, real-time automation. Most existing studies are diagnostic post-mortems rather than proactive screening tools. To address this, our work introduces a hybrid framework. By combining Convolutional Neural Networks (CNN) for automated feature extraction with the predictive efficiency of XGBoost, we aim to move dermatoglyphics from a manual statistical exercise into a robust, AI-driven clinical tool.

III. System Design

The system's architecture is structured into two distinct stages: the initial training phase and the live prediction phase.

System Architecture:

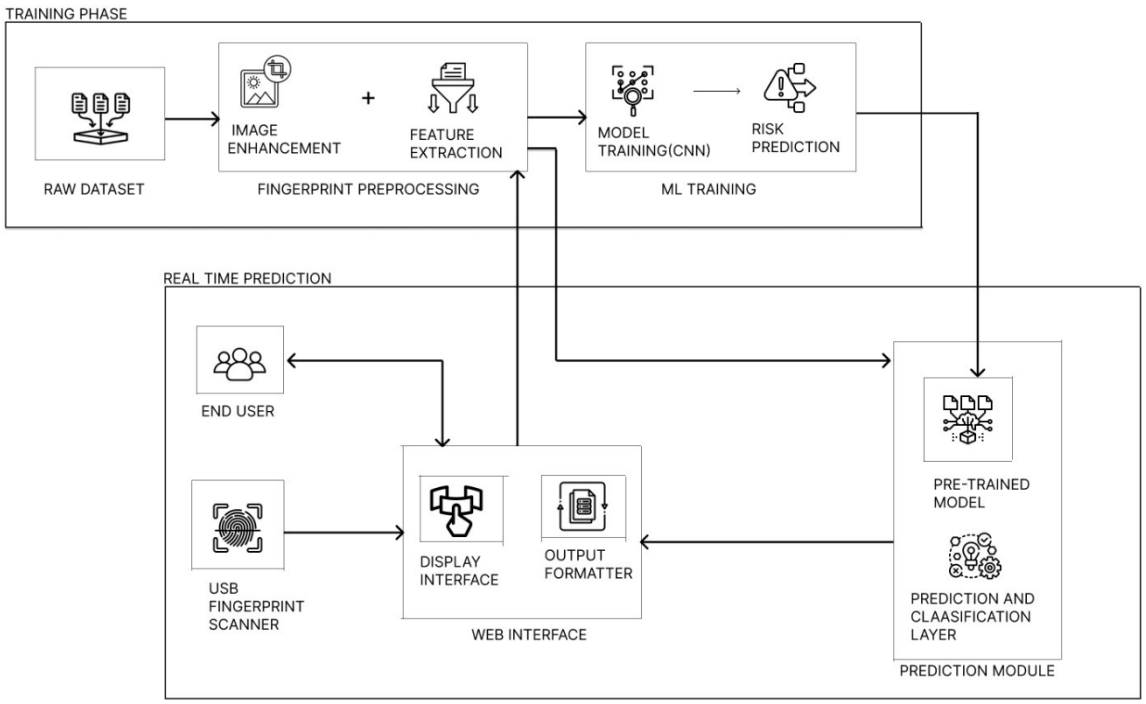

Fig 1. Fingerprint-based disease risk prediction system

A. Training Phase

The training phase begins with a curated dataset of dermatoglyphic images that serve as the ground truth for our architecture. Before any training occurs, the raw scans pass through a specialized preprocessing sequence in OpenCV. This sequence involves image enhancement and adaptive binarization followed by morphological thinning. These steps are vital for stripping away noise and isolating the core ridge density and minutiae structures that the models depend on.

Once the data is refined, it is fed into our learning modules. We trained a custom Convolutional Neural Network (CNN) on an augmented set of roughly 6,000 images to ensure the system can handle varied pattern categories reliably. These extracted features then power an Extreme Gradient Boosting (XGBoost) model that maps the biometric data to specific disease risk probabilities.

B. Real Time Prediction Phase

In the live prediction environment, the user provides a fingerprint via a USB biometric scanner or a high-resolution digital upload. This input is sent through a web interface directly to the preprocessing module where it undergoes the same feature extraction used during the training phase.

The resulting data is then handed off to the prediction engine. Here, the pre-trained models classify the patterns and evaluate the health markers in tandem. A final classification layer translates these mathematical outputs into a clear risk assessment. The results are categorized as high, moderate, or low risk and then visualized on a structured dashboard. This provides the user or healthcare provider with an immediate diagnostic snapshot for faster clinical decision making

IV. METHODOLOGY

4.1. Initial Pattern Classification via CNN

The pipeline begins by feeding the raw fingerprint scan into a custom Convolutional Neural Network. We pre-trained this CNN on an augmented dataset of roughly 6,000 images, which allows it to handle various image distortions. The goal here is high-level categorical recognition, specifically sorting the fingerprints into Plain Whorls, Ulnar Loops, or Arch types [1, 3]. By processing the raw images first, the CNN functions as a robust feature engine that helps the system maintain accuracy even when dealing with noisy or degraded scans.

4.2. Image Preprocessing and Feature Extraction

Once the CNN has identified the primary fingerprint pattern, the system utilizes an OpenCV pipeline to extract specific numerical data through a series of morphological operations. This stage is critical for converting raw visual patterns into structured biometric features.

- **Adaptive Binarization:** The initial step involves converting the grayscale scan into a binary image to effectively isolate ridge structures from the background. We utilize adaptive thresholding to account for variations in lighting and skin tone across different scans. The mathematical transformation is defined as in Eq.1.

$$dst(x,y) = \{255, if\ src(x,y)\ >\ T(x,y)\ 0, otherwise\ .\#(1)$$

- **Morphological Skeletonization:** To ensure we don't miss fine details, we apply thinning operations, erosion and dilation, to reduce the ridges to a single-pixel width. This "skeleton" makes it much easier to detect minutiae points accurately [5].
- **Feature Calculation:** Finally, we calculate the ridge density (*D*) by counting the number of ridges (*N*) within a standardized 25 mm² area (*A*) as in Eq. 2.

$$D = \frac{N}{A}\ .\#(2)$$

4.3. Predictive Modeling with XGBoost

At this stage, we merge the categorical data from the CNN and the numerical metrics from the OpenCV pipeline into a single feature vector. This unified set is fed into an Extreme Gradient Boosting (XGBoost) model [8]. The strength of XGBoost here is its ability to weigh the importance of different features and find the complex, non-linear links between these physical ridge patterns and underlying health risks [6].

4.4. Final Clinical Risk Assessment

In the final step, the XGBoost engine generates prediction scores which the system maps to clear, clinically relevant categories. Rather than outputting confusing raw probabilities, the tool classifies the results into High, Moderate, or Low Risk levels. This assessment covers four specific conditions: cardiovascular disease, essential hypertension, type 2 diabetes, and perceived stress. The final report is presented in a structured layout, designed to give healthcare providers a clear and immediate diagnostic starting point.

Implementation Details:

We implemented the proposed engine using Python, leveraging the TensorFlow and Keras libraries to develop the Convolutional Neural Network (CNN) for pattern recognition. The backbone of our system is a dataset of approximately 6,000 fingerprint scans. To ensure data consistency, every image undergoes a preprocessing sequence that includes resizing to a standard resolution, normalization of pixel values, and Gaussian noise reduction. This allows the CNN to focus exclusively on extracting core dermatoglyphic features such as loops, whorls, arches, and ridge densities.

Our architecture follows a hybrid approach. While the CNN handles high-level feature extraction, the final disease risk classification is performed by a suite of machine learning classifiers, including Support Vector Machine (SVM), Random Forest, and XGBoost. This layered strategy ensures that we benefit from both deep learning's spatial recognition and the ensemble learning's predictive accuracy.

For accessibility, the system is deployed as a web-based application using the Flask framework. The frontend, built with HTML and CSS, is designed to be lightweight and intuitive for clinical use. The application supports two input methods: real-time acquisition via a USB biometric scanner or the manual upload of digitized fingerprint images. Once an image is received, it is processed through the trained model pipeline.

The resulting output provides a percentage-based score for perceived stress levels and binary risk assessments (High/Low) for diabetes, hypertension, and cardiovascular diseases, with results displayed instantly on the dashboard.

V. Result Analysis

5.1. System Results Overview

The core objective of our experimental evaluation was to test how well different machine learning models could classify disease risk using our extracted dermatoglyphic features. Ultimately, the system is designed to output a percentage-based perceived stress level alongside categorical risk predictions (High, Moderate, or Low) for Type 2 diabetes, hypertension, and cardiovascular disease. All of this data is rendered instantly via the web dashboard.

Under the hood, the architecture runs on a hybrid model. The Convolutional Neural Network (CNN) takes the lead on pattern recognition, generating 128-dimensional feature embeddings. From there, we tested several backend classifiers, namely Random Forest (RF), a Support Vector Machine (SVM with an RBF kernel), and Extreme Gradient Boosting (XGBoost), to determine which algorithm provided the most reliable final predictions.

5.2. Baseline Model Comparison

To establish a baseline, we initially ran the data through standard Random Forest and Support Vector Machine classifiers. The comparative results across the four health categories are outlined in Table 1 below.

Table 1: Performance Comparison of Classification Models

Disease	RF Accuracy (%	SVM Accuracy (%)	XGB Precision	XGB Recall	XGB F1 Score
Stress	48.97	50.87	0.79	0.82	0.80
Type 2 Diabetes	54.98	65.43	0.83	0.81	0.82
Hypertension	50.32	53.88	0.78	0.77	0.77
Cardiovascular	53.48	70.17	0.81	0.78	0.79

Looking at the data, the SVM classifier consistently beat out the Random Forest model across the board. The most striking jump in performance occurred in the cardiovascular disease category, where the SVM achieved a 70.17% accuracy rate compared to a fairly weak 53.48% from the Random Forest. However, it's worth noting that both baseline models struggled when it came to predicting stress and hypertension. This performance drop strongly suggests that traditional classifiers simply can't capture the complex, non-linear relationships hidden within fingerprint features, pointing to the need for a more sophisticated engine.

5.3. XGBoost Model Optimization

To bridge the gap left by the baseline models, we swapped out the traditional classifiers for Extreme Gradient Boosting (XGBoost). We needed an algorithm capable of untangling complex feature interactions without losing computational speed.

Table 2: Performance Metrics for XGBoost Model

Disease	Precision	Recall	F1 Score
Stress	0.79	0.82	0.80
Type 2 Diabetes	0.83	0.81	0.82
Hypertension	0.78	0.77	0.77
Cardiovascular	0.81	0.78	0.79

As shown in Table 2, integrating XGBoost yielded a substantial improvement in overall accuracy. The model proved highly effective at navigating high-dimensional data and mapping the non-linear links between physical ridge patterns and underlying physiological risks.

5.4. Feature Importance Analysis

Beyond just raw accuracy, we wanted to ensure the model's decision-making was actually rooted in clinical logic. By analysing the XGBoost feature importance scores, we identified the specific biometric markers driving the predictions:

- **Ridge Density (0.34 weight):** Proved to be the dominant factor when predicting hypertension.
- **Pattern Type (0.27 weight):** Served as a significant indicator for both diabetes and perceived stress.
- **Minutiae Count (0.22 weight):** Was the major contributor to assessing cardiovascular risk.

5.5. System Output and Clinical Interpretation

From a usability standpoint, the framework generates a highly structured, immediately readable output on the web dashboard. A complete diagnostic snapshot includes the primary pattern classification

(Loop, Whorl, or Arch), a percentage-based stress level, categorical disease risk levels, and a probability-based confidence score.

A sample output looks like this:

- Stress: Low Risk (55% Confidence)
- Type 2 Diabetes: High Risk (68% Confidence)
- Hypertension: Low Risk (53% Confidence)
- Cardiovascular Disease: High Risk (71% Confidence)

By combining straightforward risk categories with transparent confidence scores, the system avoids overwhelming the user with raw data. Ultimately, our results prove that marrying CNN-based feature extraction with XGBoost isn't just a statistical exercise.

It significantly outperforms traditional methods, resulting in a fast, reliable, and highly usable tool for preliminary clinical screening.

VI. Conclusion

This research establishes an automated, non-invasive diagnostic framework that leverages the genetic consistency of dermatoglyphic patterns. By combining CNN-based feature extraction with an XGBoost classifier, the system achieved a 80.33% accuracy rate in identifying risks for diabetes, hypertension, and cardiovascular disease. This hybrid architecture effectively overcomes the limitations of manual analysis, offering a scalable and low-cost alternative for preliminary clinical screenings. Our results demonstrate that this AI-driven approach can serve as a vital first line of defense in early disease detection, particularly in resource-constrained environments where invasive diagnostics are not readily available.

VII. Future Scope

Future enhancements will focus on expanding the dataset to improve cross-demographic reliability and utilizing transfer learning for more nuanced feature extraction. The clinical reach of the system can be scaled by broadening the scope of detectable pathologies and integrating the engine into mobile ecosystems for remote monitoring. Furthermore, merging dermatoglyphic markers with traditional clinical data and implementing explainable AI (XAI) frameworks will be essential to provide the transparency and multi-modal precision required for seamless integration into medical workflows.

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