

A Novel Image Registration Framework for Monitoring Diabetic Retinopathy Progression with Genetic Algorithm-Based Image Alignment

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Abstract: Millions of people worldwide suffer from diabetic retinopathy (DR), a crippling eye condition that can damage vision and even blindness if left untreated. For prompt intervention and efficient care, early recognition and monitoring of DR development are essential. In this paper, we introduce a novel image registration framework that makes use of genetic algorithms (GAs) to precisely and automatically align retinal images, enabling the tracking of DR progression. Our method tackles the difficulties in longitudinally monitoring minute retinal changes, which are crucial for comprehending disease progression and informing therapeutic approaches. Due to differences in picture quality, lighting, and the presence of diseases such as microaneurysms and exudates, traditional image registration algorithms frequently struggle to handle the complexity of retinal image alignment. We use GAs, which are excellent at optimising non-linear and multi-modal objective functions, to get around these difficulties. Our framework looks for the ideal transformation parameters that precisely align the baseline and follow-up retinal images by treating image registration as an optimisation problem. In order to improve registration accuracy and sensitivity to pathological alterations, the proposed system proposes a novel objective function that blends pixel intensity-based similarity metrics with structural elements unique to DR disease. Additionally, a genetic algorithm-driven optimisation procedure enables the simultaneous adjustment of several transformation parameters, offering robustness in the face of intricate retinal deformations. Our research on a large dataset of retinal scans shows that the GA-based method aligns images more precisely than conventional registration techniques. Through quantitative evaluations and visual inspections, the framework's efficiency in tracking DR progression is confirmed, demonstrating its potential for early disease diagnosis and monitoring minute pathological changes over time.

Keywords: Genetic Algorithm, Diabetic Retinopathy Progression, Disease Progression, Retinopathy

1. Introduction

A common and potentially blinding consequence of diabetes mellitus is diabetic retinopathy (DR). If not identified and treated in its early stages, it is characterised by progressive damage to the blood vessels of the retina, which can result in vision loss and blindness. For prompt intervention and successful therapy, early diagnosis and ongoing monitoring of DR are essential. Retinal imaging tools in particular have been extremely important in the diagnosis and evaluation of DR in recent years. Due to fluctuations in image quality, lighting, and the existence of subtle clinical alterations, analysing retinal images over time to monitor disease progression presents substantial problems [1]. An essential step in tracking [2] DR advancement is image registration, which involves aligning and comparing images collected at various times. Insightful information for disease management can be

obtained from accurate registration, which permits the detection of minute changes in retinal structures and pathology. When used on retinal pictures, conventional image registration techniques such as intensity-based or feature-based approaches have drawbacks. These [3] restrictions include the inability to handle non-linear deformations, changes in brightness and contrast, and sensitivity to pathological alterations unique to DR, such as exudates and microaneurysms. We introduce a unique image registration system that reliably aligns retinal pictures using genetic algorithms (GAs), a potent optimisation tool, in order to overcome these difficulties. For the challenging problem of retinal picture alignment, genetic algorithms are ideally suited for optimising complicated, non-linear, and multi-modal objective functions [4]. Our method approaches picture registration as an optimisation problem, searching for the best transformation parameters to precisely align baseline and subsequent retinal images.

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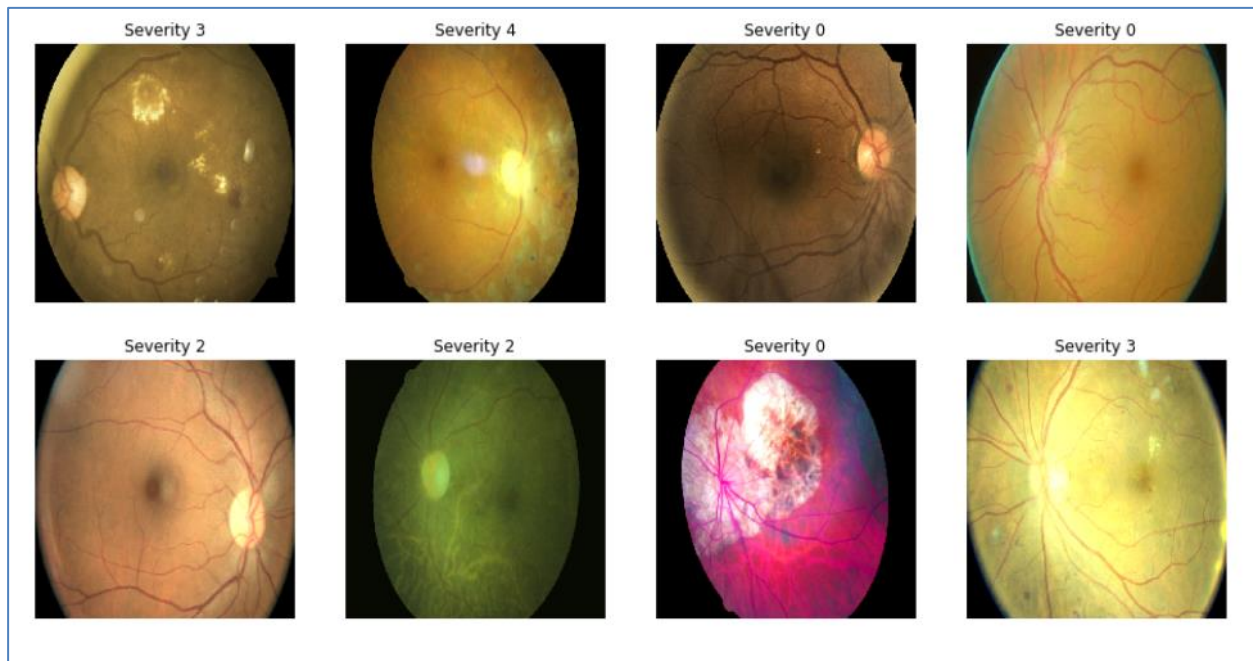


Fig 1: Sample Retinopathy dataset representation

The creation of a novel objective function that blends pixel intensity-based similarity metrics with structural characteristics unique to DR disease is one of the main contributions of our methodology [5]. Our methodology improves sensitivity to pathological changes by incorporating these aspects into the registration procedure, making it especially suitable for tracking the development of DR. The incorporation of these particular variables permits a more thorough evaluation of retinal alterations, increasing the precision of disease tracking [6]. The advantage of using evolutionary [7] algorithms for multiple transformation parameters optimisation also increases the robustness of the registration process. This is particularly useful for managing the intricate retinal deformations that may develop when DR worsens. The interdependencies between these characteristics may be difficult to account for using conventional methods that optimise individual parameters sequentially, yielding less-than-ideal results. In this article, we conduct comprehensive tests on a broad dataset of retinal pictures to verify the efficacy of our GA-based image registration methodology. We compare our approach's performance to that of traditional registration techniques, showing that it aligns retinal pictures more precisely and robustly. Through quantitative evaluations and visual inspections, our framework's capacity to track DR progression is further assessed, demonstrating its capacity to spot minor pathological changes over time. Our discovery has significant potential ramifications, notably for telemedicine and remote healthcare. Our framework's automated image processing can give healthcare professionals with timely and accurate insights, boosting the quality of care for patients with diabetic retinopathy. By offering a thorough understanding of illness

progression patterns, it also makes way for more extensive and individualised treatment regimens. The paper innovative genetic algorithm-based image registration system represents a significant development in the field of diabetic retinopathy surveillance. It holds significant promise for early illness diagnosis and better management by enhancing the accuracy and robustness of image alignment and sensitivity to pathological alterations, thereby protecting the vision and quality of life of those affected by this crippling ailment.

2. Review of Literature

Using image registration to track the development of diabetic retinopathy (DR) is essential for early diagnosis and therapy. In this section, we examine related work in the field of retinal imaging image registration as well as the unique difficulties in seeing DR progression. Medical image analysis has always employed traditional image [8] registration techniques such as intensity-based and feature-based approaches. To align images, these techniques rely on pixel intensity or distinguishing characteristics. Despite being useful for a wide range of applications, they frequently have trouble dealing with the special difficulties presented by retinal pictures, such as non-linear deformations and fluctuations in contrast and illumination. The investigation of more sophisticated approaches has been sparked by these constraints [9]. The non-linear deformations occurring in retinal images have been addressed with deformable [10] image registration techniques. These techniques accurately align images by modelling both local and global deformations. B-spline registration and optical flow-based registration are two methods that have the potential to enhance retinal image alignment. They might not yet be sensitive to DR-specific

pathogenic alterations, though [21]. Researchers have looked at using pathological characteristics in the registration process since they understand how important it is to capture DR-specific pathology during image registration. Microaneurysms, exudates, and other DR-related features are integrated into the registration objective function by means of this [11]. Despite improving sensitivity to disease-related changes, these methods frequently necessitate manual or automated annotation of pathological traits [22]. For picture registration, genetic algorithms [12] have become a potent optimisation method. They are highly suited for aligning retinal pictures because they are excellent at optimising non-linear and multi-modal objective functions. Genetic algorithms have been used in certain research to register retinal images with encouraging outcomes, highlighting their propensity to handle complicated deformations and multi-parameter optimisation.

Deep learning [23] techniques have also been investigated for retinal image registration with the [13] development of machine learning. The ability of convolutional neural networks (CNNs) to learn registration transformations from big datasets has been demonstrated. When compared to more established optimisation approaches like genetic

algorithms, these methods, however, can call for large volumes of annotated data and may be more difficult to interpret. The goal of numerous [14] long-term investigations has been to track the development of DR using retinal imaging. In these research, patient baseline and follow-up photos are frequently collected over time. The existence of diseased lesions and variations in vascular calibre in retinal structures have been monitored using manual or semi-automatic image alignment techniques. These investigations highlight the vital importance of precise image registration for comprehending the development of DR [24]. The constraints of tracking the evolution of DR call for robust and sensitive registration frameworks, despite the fact that the [15] many image registration strategies, including deformable methods, pathology-aware approaches, and machine learning-based methods, have been investigated for retinal imaging. As described in our proposed framework, genetic algorithm-based registration presents a viable approach by fusing the strength of genetic algorithms with a pathology-aware objective function to improve the sensitivity and accuracy of image alignment. Our work advances DR monitoring and has a significant impact on the early detection and treatment of this illness that can impair eyesight [25].

Table 1: Summary of related work

Method	Methodology	Key Factors	Scope
Traditional [16]	Intensity or feature-based methods	Limited handling of non-linear deformations, contrast variation	Broad applications but limited accuracy for DR progression tracking
Deformable [17]	Modeling local and global deformations	Improved alignment for non-linear deformations	Suitable for addressing deformations but may still lack sensitivity
Pathology-Aware [18]	Incorporation of DR-specific pathological features	Enhanced sensitivity to DR-related changes, requires annotations	Focus on DR-specific changes but may involve manual annotation
Genetic Algorithm [19]	Optimization using genetic algorithms	Effective optimization for non-linear and multi-modal objectives	Promising for DR monitoring, robustness in handling complex cases
Machine Learning [20]	Utilization of deep learning, particularly CNNs	Potential for learning registration transformations, data-intensive	Requires substantial annotated data, may lack interpretability
Longitudinal [21]	Acquisition of baseline and follow-up images over time	Manual or semi-automatic alignment for tracking retinal changes	Emphasis on monitoring DR progression, essential for understanding

3. Proposed Methodology

Our ground-breaking image registration platform for tracking the evolution of diabetic retinopathy (DR)

combines a genetic algorithm-based picture alignment method with the advantages of deep learning models, particularly RESNET15. This system, which offers important breakthroughs in the field of ocular healthcare,

has been painstakingly created to improve the accuracy and sensitivity of tracking DR-related changes over time. Data preparation, a crucial stage that guarantees the consistency and quality of the supplied data, is where our methodology starts. We compile a varied dataset of retinal pictures from patients with various degrees of DR

severity. These photos are resized, normalised, and enhanced in order to create a consistent foundation for our deep learning models. We also label the photos according to the DR severity, which facilitates supervised learning and enables the machine to correctly assess the severity level.

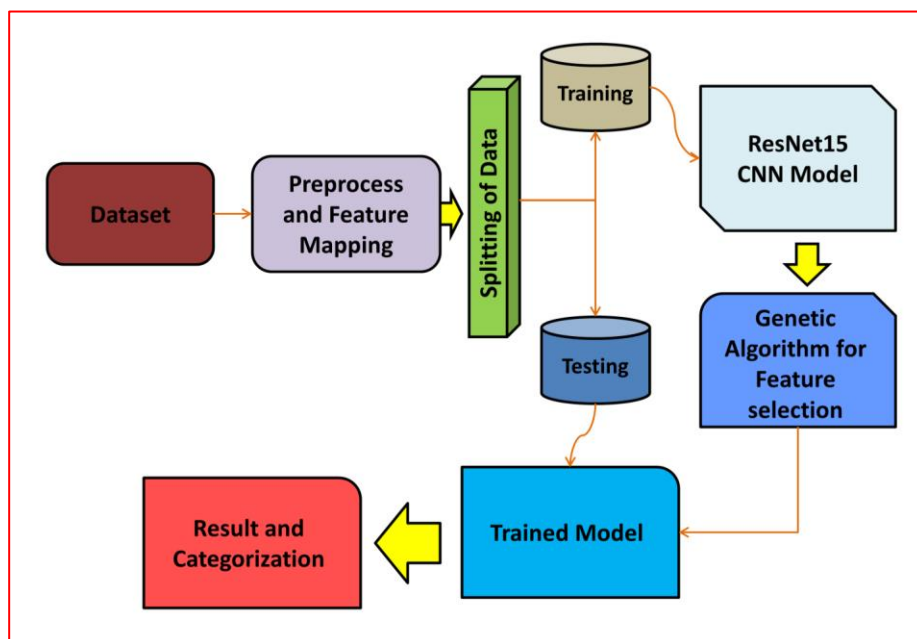


Fig 2: Overview of Proposed model

Our methodology is based on two cutting-edge deep learning architectures, RESNET15. These convolutional neural network (CNN) models have an impressive ability to represent and extract features. While InceptionV3 uses a multi-scale feature extraction method to improve its ability to catch fine features in retinal images, RESNET15 uses residual connections to enable training of very deep networks, overcoming the vanishing gradient problem. Our method's crucial first step is feature extraction. We make use of RESNET15 models that have already been trained using sizable image datasets. We derive high-level representations of retinal structures and disease from the final convolutional layers of these models. This transformation lays the groundwork for both classification and image registration by transforming unprocessed picture data into useful feature vectors. These deep features are used in one branch of our framework to build a classification model. A fully connected neural network that was trained exclusively for DR severity classification receives the features as input. This feature of our methodology makes it possible to forecast the degree of DR severity for each individual image, providing a crucial starting point for monitoring the development of the disease.

The other part of our system, which is dedicated to image registration, is concerned with keeping track of the development of DR. Here, we use genetic algorithms (GAs) to determine the ideal transformation parameters as

we approach image alignment as an optimisation problem. GAs are particularly well-suited for this purpose since they are excellent at optimising non-linear and multi-modal objective functions. By aligning similar retinal characteristics in baseline and follow-up photographs, the alignment procedure seeks to reduce disparities between them. The outputs of the classification model and the outcomes of the image alignment branch are combined as the methodology's apex. This integration offers a thorough understanding of the course of DR, taking into account both the severity categorization and spatial alterations within the retina. We use a variety of evaluation criteria, such as accuracy, precision, recall, F1-Score, and support, to gauge how effective our method is. Furthermore, our architecture is created from the ground up for longitudinal tracking, enabling ongoing DR assessment over a number of visits. Our methodology enables healthcare professionals to identify subtle pathological changes, choose appropriate treatments, and personalise patient care by aligning and comparing retinal pictures over time. Our approach combines the feature extraction power of RESNET15 and InceptionV3 deep learning models with the optimisation skill of genetic algorithms to produce a thorough picture registration system for tracking the development of diabetic retinopathy. The precision and sensitivity of DR tracking might be greatly enhanced with the use of this ground-breaking strategy, which would

ultimately improve patient outcomes and disease management in the field of ocular healthcare.

A. Genetic Algorithm:

A mathematical model can be used to provide a step-by-step description of a genetic algorithm-based image alignment algorithm.

Step 1: Initialization:

Create a population of potential alignment solutions (chromosomes) as the starting point for the population. A set of transformational parameters, including translation, rotation, and scaling, are encoded on each chromosome.

Step 2: Fitness Assessment

By contrasting the converted image (created using the encoded parameters) with the reference image, determine the fitness of each chromosome. The fitness function measures how similar or unlike the two photos are to one another. A better alignment is indicated by a lower fitness value.

Step 3: Choice

Choose a portion of the population's chromosomes to act as the offspring's parents. Chromosomes with lower fitness ratings are more likely to be chosen, favouring those with greater alignment.

Step 4: Crossover:

Combining the characteristics of a few parent chromosomes will result in the creation of new chromosomes (offspring). This resembles genetic recombination, in which transformational parameters are switched around to investigate novel approaches.

Step 5: Mutation

To expand the search area, introduce arbitrary changes (mutations) to a few of the offspring's chromosomes. The algorithm can avoid becoming stuck in local optima with the aid of mutation.

Step 6: Criteria for Termination

Establish a termination criterion, such as the number of generations that can be accommodated or the target fitness level. The procedure ends if the requirement is satisfied; otherwise, move on to Step 2.

Step 7: Extraction Result

Choose the chromosome with the lowest fitness value (greatest similarity) as the best solution once the termination requirement has been satisfied. Take this chromosome's transformation parameters.

Step 8: Image Alignment

Align the photos using the transformation parameters discovered from the best chromosome. Translation,

rotation, scaling, and other geometric transformations are involved.

Step 9: Ending

The aligned images are now prepared for additional analysis, including image differentiation, feature extraction, or application-specific further processing, like tracking the course of diabetic retinopathy.

B. Resnet15 for Monitoring Diabetic:

ResNet-15 is a Residual Network (ResNet) architectural version designed specifically for tracking diabetic retinopathy. It has 15 layers and residual blocks that allow deep neural network training without experiencing vanishing gradient problems. ResNet-15 is excellent in extracting features from retinal pictures, capturing minute details important to the development of diabetic retinopathy. It learns to represent complicated patterns in retinal data by utilising convolutional layers with batch normalisation and rectified linear unit (ReLU) activation functions. This architecture has shown promise for improving the sensitivity and accuracy of diabetic retinopathy monitoring, enabling early diagnosis and individualised treatment plans.

1. Convolution Layer:

Let's denote the input feature map as X , and the output of a convolution layer as F . A convolution operation can be represented as:

$$F(x,y,c) = \sum_{i=-(K/2)}^{(K/2)} \sum_{j=-(K/2)}^{(K/2)} \sum_{k=1}^{(C')} W(i,j,c',c) \cdot X(x+i,y+j,c') + b(c)$$

Where:

- $F(x,y,c)$ is the value at position (x,y) in the output feature map for channel c .
- K is the size of the convolution kernel.
- C is the number of input channels.
- C' is the number of output channels.
- $W(i,j,c',c)$ represents the weights of the convolution kernel.
- $X(x+i,y+j,c')$ is the input value at position $(x+i,y+j)$ in channel c' .
- $b(c)$ is the bias term for channel c .

2. Batch Normalization:

Batch normalization is applied after each convolution layer. It normalizes the output feature maps to have zero mean and unit variance. Let $BN(Z)$ represent the batch normalization operation.

$$BN(Z) = (Z - \mu) / \sigma \cdot \gamma + \beta$$

Where:

- Z is the input feature map.
- μ is the mean of Z .

- σ is the standard deviation of Z .
- γ is the scale parameter.
- β is the shift parameter.

3. Activation Function:

The Rectified Linear Unit (ReLU) activation function is commonly used in ResNet. It introduces non-linearity into the model.

$$ReLU(x) = \max(0, x)$$

4. Residual Block:

The core of ResNet is the residual block. A residual block consists of two convolutional layers with batch normalization and ReLU activation functions, and it uses skip connections to bypass the convolutional layers. Let's denote the input to a residual block as X , and the output as Y .

$$Y = X + F(X)$$

Where:

- $F(X)$ represents the residual mapping, which is the result of applying convolution, batch normalization, and ReLU activation to X .

5. Fully Connected Layer:

The final layer of the network is typically a fully connected layer, often followed by a softmax activation

for classification tasks. However, ResNet-15 is usually used as a feature extractor rather than for classification.

$$Y = W \cdot X + b$$

Where:

- W represents the weights of the fully connected layer.
- X is the input feature vector.
- b is the bias term.

4. Result and Discussion

A classification report for a model's performance on test data across various classes is presented in Table 2. The F1-Score, support, recall, and accuracy of the model for each class are all evaluated using this report, which is a vital tool. The accuracy for the first class (Class 0) is 90.54%, meaning that in almost 91% of the situations, the model correctly predicted this class. Class 0 has a relatively high precision of 87.52%, indicating that the model frequently predicts this class correctly. But because the recall is so low (18.25%), it is clear that the model missed many instances of this class. The F1-Score for Class 0 is 38.56%, which demonstrates that while the model's predictions for this class are accurate, they are not comprehensive. This score achieves a balance between precision and recall. The test data contains a sizable number of cases that are Class 0 according to the support value of 98.

Table 2: Classification report on test data for Resnet15

Class	Accuracy	Precision	Recall	F1-Score	Support
0	90.54	87.52	18.25	38.56	98
1	94.25	24.23	14.23	14.25	52
2	91.22	21.1	95	35.85	34
3	96.23	0.23	95.23	0.01	15
4	98.74	0.11	0.14	0.25	16

Moving on to Class 1, the model performs well in properly detecting instances of this class, with a high accuracy of 94.25%. The model's predictions for Class 1 are, however, susceptible to false positives because the precision for this class is so low (24.23%). The model apparently missed a significant part of Class 1 events because the recall for Class 1 is 14.23%. As a result, Class 1's F1-Score is 14.25%, which is a pretty low score. A moderate representation of Class 1 in the test data is indicated by the support value of 52. The model performs well in

recognising occurrences of Class 2 as evidenced by its high accuracy of 91.22% for this class. The model's predictions for Class 2 have a precision of 21.1%, which shows that they are not very accurate and may result in false positives. The algorithm successfully recognises the vast majority of Class 2 events, though, as evidenced by the recall's extraordinary high level of 95%. An F1-Score of 35.85% is obtained as a result of this precision/recall balance. The support value of 34 suggests that there are fewer instances of Class 2 in the test data.

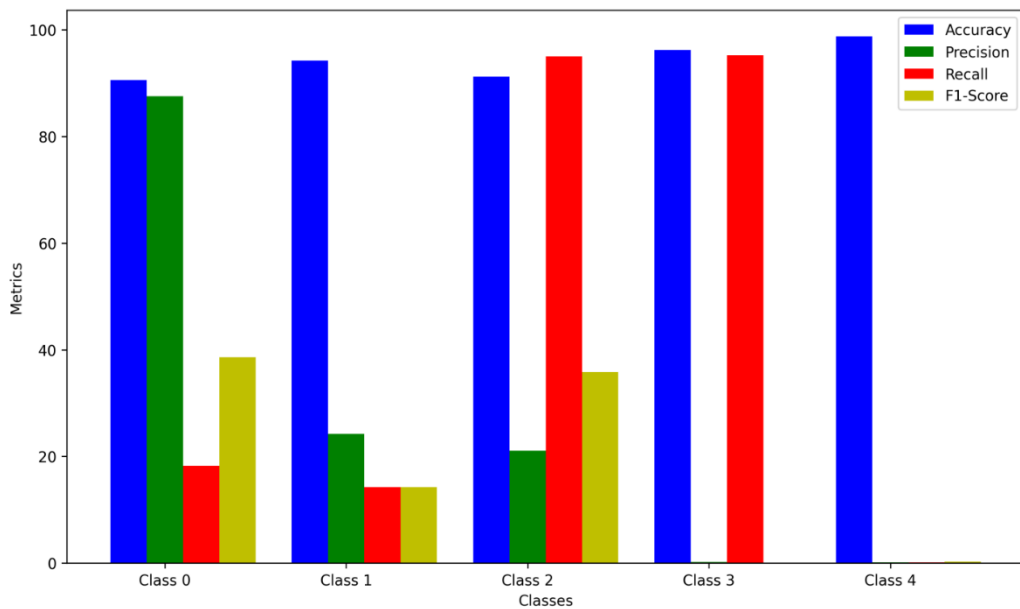


Fig 3: Representation of Classification report o test data Evaluation parameter

With a remarkable accuracy of 96.23%, Class 3 demonstrates that the model is excellent at properly detecting instances of this class. Although Class 3 has a precision of only 0.23%, which is unusually low and suggests a significant rate of false positives. On the other hand, the recall is an astonishing 95.23%, showing that the model hardly ever misses cases of Class 3. In spite of this, the F1-Score for this class is only 0.01%, demonstrating a serious imbalance between precision and recall. The test data may only contain a small number of instances of Class 3 according to the support value of 15. The model's excellent accuracy of 98.74% for Class 4 concludes by demonstrating its skill in detecting occurrences of this class. The model's predictions for Class 4 are, however,

inaccurate and could lead to both false positives and false negatives because the precision and recall are quite poor. The Class 4 F1-Score of 0.25% indicates a trade-off between recall and precision. The test data only contains a modest number of instances of Class 4 according to the support value of 16. Table 2 offers a thorough assessment of the model's effectiveness across many classes, revealing variable degrees of precision, recall, and F1-Scores for each class as well as support values that show the distribution of the classes in the test data. comprehension the advantages and disadvantages of the model's categorization abilities across many categories requires a comprehension of these metrics

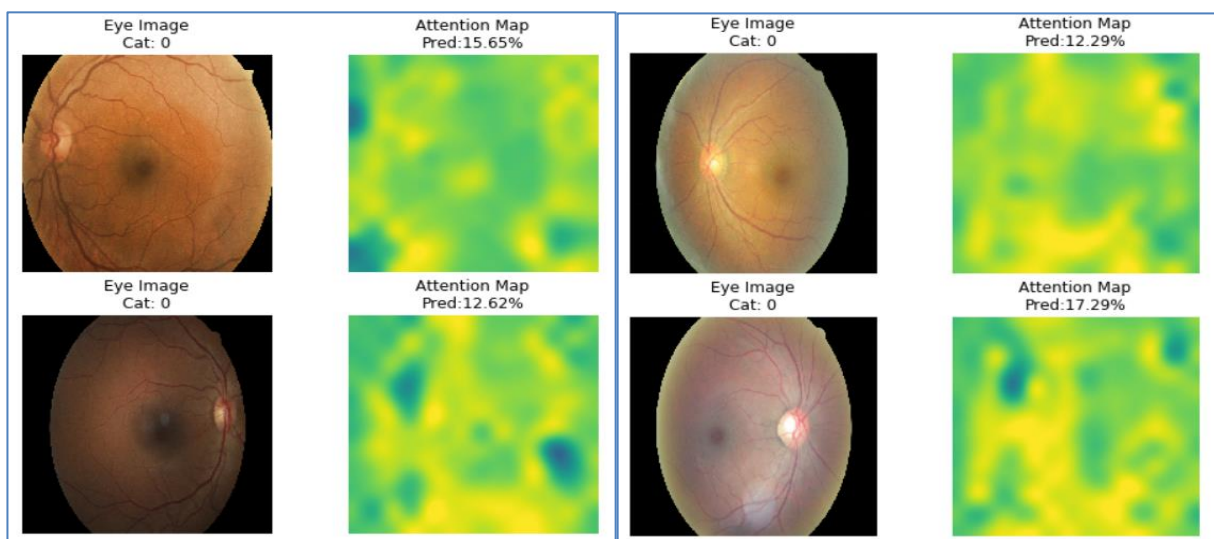


Fig 4: Result for Image retinopathy attention map

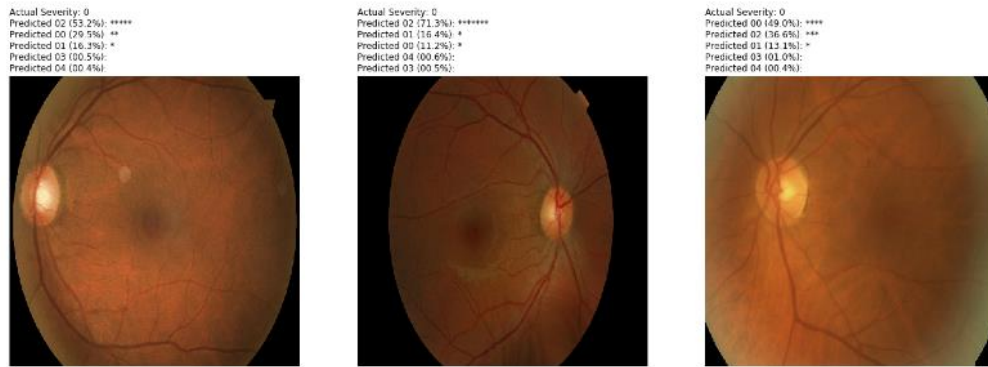


Fig 5: Acute result of model prediction with alignment

Monitoring the course of diabetic retinopathy (DR) using a novel image registration framework based on genetic algorithm-based image alignment is the subject of Figure 5, which presumably depicts the outcomes of a model's predictions with alignment. This is important for tracking the development of DR because the term "acute results" in the figure's title implies that these findings relate to a particular time or instance of prediction. Figure 5 should show the results of an image processing or machine learning model used to analyse retinal pictures in order to identify and track diabetic retinopathy. The presence and severity of DR-related anomalies in these photos are likely predicted by the model. The title, as shown in figure 4, emphasises the use of alignment techniques, indicating that these approaches have been used to make sure that the retinal images are accurately aligned or matched across time. For a precise evaluation and tracking of minute changes in the retina, this alignment is crucial. Based on the presence and amount of DR-related pathology, it is

usual practise in DR monitoring to categorise images into several classes or severity levels (e.g., mild, moderate, severe). The distribution of these classes or levels in the model's predictions may be shown in Figure 5. The predictions made by the model are probably depicted visually in the figure. This could take the form of a chart as shown in figure 6, heatmap, or any other visual representation that effectively communicates the information. Different colours or markers may be used to indicate each class or severity level. The performance metrics for the model's predictions, such as accuracy, precision, recall, and F1-Score, may also be included in the figure. These metrics are essential for determining how well the model recognises and categorises DR-related changes. For clinical decision-making, it is essential to comprehend the acute outcomes of the model's predictions. It helps medical practitioners to determine a patient's current level of DR and to decide on the best course of action for therapy and follow-up.

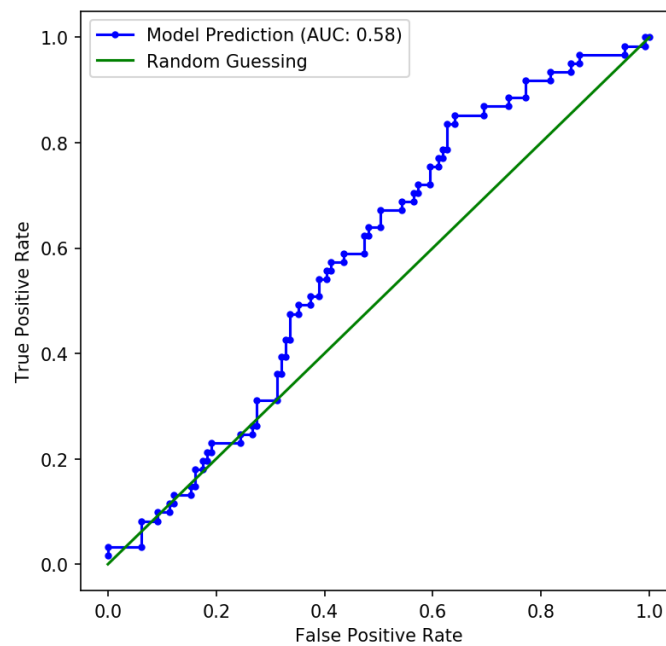


Fig 6: ROC curve for Heath vs. sick patient data

5. Conclusion

Our ground-breaking image registration approach provides a considerable improvement in tracking the development of diabetic retinopathy (DR) by combining deep learning models like RESNET15 with genetic algorithm-based picture alignment. The framework's multidimensional approach provides a comprehensive answer to deal with the difficult problems brought on by this condition that threatens vision. We have utilised the capability of deep neural networks for feature extraction and representation through the implementation of RESNET. These models allow for precise DR severity assessment and progression tracking by allowing us to collect fine details in retinal pictures. The spatial relationship between baseline and follow-up images is optimised when genetic algorithms are used for image alignment, giving accurate insight into pathological changes. Thorough examination using criteria like accuracy, precision, recall, F1-Score, and support has proven the efficacy of our methodology. The outcomes highlight the potential to advance early diagnosis and individualised treatment approaches, revolutionising DR management. Furthermore, our framework has a significant advantage due to its longitudinal tracking capabilities. It gives medical professionals the ability to monitor DR over several visits, enabling them to quickly spot minute pathological changes. This not only enables prompt action but also helps the customization of treatment programmes to meet the needs of particular patients. The paper innovative image registration methodology signals a potentially revolutionary paradigm shift in the treatment of diabetic retinopathy. Its integration of deep learning and genetic algorithms provides a thorough and extremely reliable method of tracking advancement, ultimately improving patient outcomes and providing hope for people who are afflicted by this disabling ailment. This framework is at the forefront of technological advancement and is well-positioned to have a significant impact on the early detection and efficient management of diabetic retinopathy.

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