Validation of a Neural Network Architecture for Approximating an Analytical Model of Eye Condition

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Abstract

This paper presents an intelligent deep learning-based model for comprehensive analysis of the human eye's condition. The developed neural network system integrates key ophthalmological parameters, including intraocular pressure, volumetric blood circulation, visual acuity, visual field index, and perfusion pressure, along with additional factors such as age, vascular health, and genetic predisposition. A synthetic dataset of 250,000 samples was generated based on clinically observed parameter ranges from the Filatov Institute of Eye Diseases and Tissue Therapy. This controlled dataset enabled architectural validation of a neural network model designed to approximate a physiologically meaningful function (Seye). Although real patient data were not used, the study demonstrates the feasibility of building a robust diagnostic framework, laying the groundwork for future application to clinical datasets. The neural network architecture includes three hidden layers with ReLU activation, ensuring high prediction accuracy. Model evaluation demonstrated a high coefficient of determination and low values of root mean squared error and mean absolute percentage error, indicating a strong correlation between predicted and actual values. The obtained results confirm the potential of neural network methods for automated eye condition analysis. The proposed model can be applied for early diagnosis and monitoring of ophthalmological diseases, as well as a decision-support tool in clinical practice. Future work includes integrating real medical data to enhance the model's generalizability and developing hybrid approaches that combine traditional mathematical methods with deep learning.

Keywords
machine learning, neural network, ophthalmology, prediction, eye condition modeling

1. Introduction

Ophthalmological research plays a vital role in preserving vision, as the condition of the eye is influenced by a wide range of interacting physiological and clinical parameters, including intraocular pressure, volumetric blood circulation, visual acuity, visual field index, tear production, and perfusion pressure [1, 2]. Traditional diagnostic methods often rely on simplified models such as regression equations or differential systems. While useful, these approaches may not fully capture the complex, nonlinear relationships between variables and often depend on subjective interpretation [1, 2, 5]. This limits their ability to integrate multiple heterogeneous factors and reduces predictive accuracy in practical settings. In recent years, machine learning and deep learning methods have gained considerable attention in ophthalmology, providing powerful tools for analyzing large volumes of data and identifying hidden patterns in visual and clinical indicators [3, 4, 5, 6]. These models enable more objective and data-driven decision-making. However, most existing studies are focused on the detection of specific diseases or classification tasks, without addressing generalized modeling of the eye's functional state [4, 5]. This paper presents a neural network-based approach to approximating a physiologically informed analytical model of overall eye condition (Seye), constructed from expert knowledge and clinical reasoning [7, 8, 9]. The

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function Seye integrates key ophthalmological parameters using nonlinear transformations that reflect known physiological dependencies. Importantly, the current stage of research focuses on validating the neural network architecture under idealized, controlled conditions using a synthetically generated dataset. The target variable is calculated analytically to ensure that the model structure and training process are reliable and stable. This methodological step lays the groundwork for future application to real clinical data, where variability, noise, and missing values will present greater challenges [7, 8, 9].

2. Literature review and existing methods

2.1. Traditional methods for eye condition modeling

In the early stages of ophthalmic modeling, traditional methods such as regression analysis and differential equations were widely used. These approaches enabled the description of key processes such as intraocular pressure fluctuations, blood flow dynamics, and the relationship between physiological parameters and visual function [10, 11]. For instance, in [10], mathematical models are presented that describe the dynamics of intraocular pressure using fluid balance equations, allowing for the simulation of steady-state and oscillatory pressure regimes under various external influences. In [11], the importance of choosing the correct unit of analysis (e.g., one or both eyes) is emphasized, as it directly impacts the validity of statistical inference. However, these traditional approaches face several significant limitations: subjectivity in interpretation, due to reliance on manual analysis and expert opinion [12]; limited parameter coverage, as most models incorporate only a few variables and ignore other potentially important clinical or biometric indicators [11]; insufficient capacity to capture nonlinear dependencies, which is crucial given the multifactorial and dynamic nature of ocular processes. These limitations have fueled a transition toward more powerful and flexible data-driven methods.

2.2. Modern methods and neural network architectures

CNNs are widely used in ophthalmology for analyzing retinal fundus images, OCT scans, and fundus photography [13, 14, 15]. These models can automatically extract clinically significant features such as microaneurysms, neovascularization, and retinal detachment, often without requiring manual feature engineering. Studies such as [13, 14] have demonstrated CNN-based systems achieving diagnostic performance comparable to human experts. In [13], transfer learning is used to improve model accuracy, especially when training data is limited. RNNs, including LSTM and GRU variants, are applied to analyze temporal dynamics in ophthalmological measurements — such as intraocular pressure trends, blood flow oscillations, and visual field progression [16, 17]. For example, the RNN model in [16] enables real-time prediction of eye condition changes, making it useful for longitudinal disease monitoring (e.g., glaucoma or age-related macular degeneration). Such approaches are particularly valuable for detecting early pathological changes across multiple examination points.

2.3. Hybrid and ensemble models

Many modern studies implement hybrid models that combine classical statistical techniques with machine learning algorithms. These models offer improved robustness, adaptability, and performance in the presence of noisy, incomplete, or multimodal data [18, 19, 20]. In [18], a structure combining SVMs and CNNs is described, while [20] introduces ensemble methods combining gradient boosting and neural networks to reduce overfitting and improve generalizability.

Study [19] also highlights the integration of therapeutic and biometric data for more holistic eye condition modeling.

2.4. Interpretability and generalization

Despite the complexity of neural architectures, increasing attention is being paid to interpretability, which is crucial in clinical applications. Works such as [23, 24] focus on creating interpretable AI systems capable of explaining the contribution of each parameter to the final prediction. Furthermore, [22] demonstrates the potential of hybrid modeling-merging simulation-based and machine learning-based approaches—which is especially effective when dealing with limited data or highly complex physiological systems.

2.5. Comparative analysis of methods

Modern neural network methods demonstrate high accuracy in classification and prediction tasks in ophthalmology, significantly outperforming classical algorithms in identifying complex patterns within high-dimensional data. For example, Moradi et al. [20] showed that deep ensemble learning achieves superior performance in the automated classification of early-stage age-related macular degeneration (AMD), offering better generalization than individual models. Meanwhile, Archana et al. [21] reviewed the application of traditional machine learning algorithms for glaucoma detection, highlighting that, despite their simplicity and interpretability, classical models lag behind deep learning methods when processing nonlinear and heterogeneous ophthalmic data. A prominent trend in current research is the development of hybrid models and stacked generalization techniques, which combine the strengths of various deep architectures. Kaushik et al. [25], for instance, proposed a stacked ensemble of convolutional neural networks for diabetic retinopathy diagnosis, achieving both high accuracy and robustness across diverse datasets.

Similarly, Kansal et al. [26] introduced a visual feature embedding and selection method that significantly enhances model performance for ocular disease classification. Vidivelli et al. [27] focused on strategies for optimizing deep learning architectures tailored to ophthalmological diagnostics.

Their work emphasizes domain-specific attention mechanisms, advanced regularization techniques, and model calibration to improve interpretability and reliability in clinical decision-making. In summary, contemporary research underscores the promise of hybrid and explainable AI systems that combine the strong feature extraction capabilities of deep learning with the transparency and robustness of classical approaches. This integration is pivotal for the advancement of intelligent decision support systems in ophthalmology and for increasing trust among clinical practitioners.

2.6. Research objectives and tasks

Objective: develop a neural network model for accurately predicting the overall condition of the eye. Tasks:

- Collect and preprocess data (clinical), including normalization and outlier removal;
- Develop a mathematical model that reflects nonlinear dependencies;
- Design an optimal neural network architecture (potentially incorporating CNN and RNN elements) and ensemble models;
- Train and validate the model using RMSE, MAPE, and R^2 metrics;
- Analyze the contribution of individual parameters to enhance model interpretability;.
- Compare the model's performance with traditional methods to assess its advantages and future potential.

Modern neural network methods offer automatic feature extraction, high prediction accuracy, and the ability to integrate heterogeneous data. However, challenges such as the need for large datasets and limited interpretability remain. Addressing these issues is key to developing a universal model capable of effectively assessing eye health.

3. Research methodology

3.1. Model parameters

Key ophthalmological parameters were selected for developing the eye condition model [28]: IOP (Intraocular Pressure) – a primary indicator of ocular tone and a crucial diagnostic criterion for glaucoma and other eye diseases; RQ (Volumetric Intraocular Circulation) – reflects ocular blood supply, with impairments indicating potential vascular pathologies; BCVA (Best Corrected Visual Acuity) – a standard measure of visual function used for diagnosing and monitoring treatment effectiveness; Tr (Tear Production) – an indicator of the tear film's condition, essential for diagnosing dry eye syndrome; VFI (Visual Field Index) – assesses the extent of visual field preservation, particularly relevant for monitoring glaucoma progression; Pperf (Perfusion Pressure) – reflects the efficiency of blood flow in ocular tissues, with impairments potentially leading to vision disorders; Additional Parameters (Age, Vascular Condition, Genetic Predisposition) – considered as significant risk factors for ophthalmological diseases. The interdependencies of the parameters characterizing eye condition are presented in Table 1.

Table 1
Interdependencies of parameters characterizing eye condition

Parameters	Interaction	Effect description
IOR Pperf	$\mathrm{IOP} \uparrow - \mathrm{Pperf} \downarrow$	Increased IOP reduces perfusion pressure, impairing ocular blood supply and increasing ischemic risk (glaucoma).
IOR RQ	$\mathrm{IOP} \uparrow - \mathrm{RQ} \downarrow$	High IOP disrupts retinal blood flow, causing ischemia and optic nerve damage, lowering RQ (e.g.. glaucoma).
Pperf. RQ	$\mathrm{Pperf} \downarrow — \mathrm{RQ} \downarrow$	Reduced Pperf (due to high IOP or low systemic pressure) worsens retinal ischemia and decreases RQ (e.g.. glaucoma, diabetes, retinal vein thrombosis).
BCVA. VFI	$\mathrm{BCVA} \downarrow — \mathrm{VFI} \downarrow$	Loss of visual fields (VFI) is linked to progressive decline in visual acuity (BCVA) (e.g.. glaucoma, high myopia).
Age. Ra VFI	$\mathrm{Age} \uparrow - \mathrm{RQ} \downarrow . \mathrm{VFI} \downarrow$	Aging leads to reduced intraocular blood flow and narrowing of visual fields due to vascular degeneration.
Tr. IOP	$\mathrm{Age} \uparrow — \mathrm{Tr} \downarrow$	Tear production declines with age. leading to dry eye syndrome, negatively affecting quality of life.
a/t1. Pperf. RQ	$\mathrm{cr/t1} \uparrow - \mathrm{Pperf} \downarrow . \mathrm{RQ} \downarrow$	Vascular tone changes affect retinal blood flow, contributing to degenerative retinal diseases (e.g.. glaucoma, diabetic retinopathy).
Additional factors. IOP. RQ	Stress, lifestyle, and external factors influence IOP and RQ	Alters overall eye condition and affects patients' quality of life.

To develop the eye condition model, a set of key ophthalmological parameters proposed in [28] was used, including IOP, RQ, BCVA, Tr, VFI, and Pperf. These parameters are recognized as clinically significant and cover the main aspects of the eye's functional state. The combination of physiological and individual factors provides a comprehensive representation of eye health, enabling the construction of an accurate predictive model. The primary variables used in the model,

along with their normal values and variation ranges, are as follows: IOP - normal: 10–21 mmHg, Range - 5–60 mmHg; RQ - normal: 3.2–3.5%; Range - 0.5–9.0%; BCVA - normal: 1.0, Range - 0–2.0; Tr - normal: 10–30 mm, Range: 1–40 mm; VFI - normal: 100%; Pperf - normal: 55–80 mmHg; Range - 20–100 mmHg%; additional parameters: age, vascular condition, genetic factors, etc.

3.2. Model parameters

The target function Seye was constructed based on expert knowledge and a combination of clinical reasoning and mathematical modeling. The selection of specific nonlinear transformations (e.g., logarithmic, exponential, and quadratic terms) reflects the known physiological relationships between ophthalmic parameters and functional eye condition. For instance, intraocular pressure and perfusion pressure are known to affect ocular health nonlinearly, which justifies the use of logarithmic terms. Coefficients k1 through k9, as well as modifying terms A, B, and functions such as henv, hstress, i(lifestyle), and j(genetic factors) were introduced to account for interaction effects and individual variability. Their form was selected based on preliminary simulations, clinical interpretability, and their effectiveness in model calibration. While these coefficients were initially set heuristically, they were subsequently optimized using the training dataset during the neural network fitting process, allowing the network to approximate the nonlinear dependencies encoded in the original equation. The formula for calculating the target variable Seye is presented, incorporating nonlinear dependencies (logarithmic, exponential, and quadratic) on each parameter. The formulas are structured into separate blocks for better readability. The Seye model describes eye health as a function of key ophthalmological parameters, ensuring accurate diagnosis and prediction

$$S_{eye} = k1 \cdot \log(IOP + 1) + A + k2 \cdot \log(RQ + 1) + B + k3 \cdot (BCVA - f_{offcet})^2 \cdot A + k4 \cdot \cdot \log(Tr + 1) \cdot h_{env}(environmental_{factor}) + k5 \cdot e^{-VF1} \cdot A + k6 \cdot \log(1 + Pperf) \cdot B + k7 \cdot \cdot \log\left(1 + \frac{\alpha}{t1}\right) + h_{stress}(stress_{level}, activity_{level}) + k8 \cdot \log(age + 1) \cdot i(life_{style}) + k9 \cdot \cdot e^{eadditional_{factor}} \cdot j(genetic_{factors}), \quad (1)$$

where $A = f(age, disease_{status})$;

$B = blood_{pressure}, vascular_{health}$

$f(age, disease_{status}) = 1 + 0.1 \cdot age - 0.05 \cdot disease_{status}$

$g(blood_{pressure}, vascular_{health}) = 1 + 0.2 \cdot \log(blood_{pressure} + 1) - 0.1 \cdot vascular_{health}$

$h_{env}(environmental_{factor}) = 1 + 0.3 \cdot \exp(-0.01 \cdot environmental_{factor})$

$h_{stress}(stress\_level, activity\_level) = 1 + 0.05 \cdot stress\_level - 0.02 \cdot activity\_level$

$i(life\_style) = 1 + 0.15 \cdot life\_style$

$j(genetic\_factors) = 1 + 0.1 \cdot genetic\_factors$

It is important to note that equation (1) was not derived through formal mathematical derivation but was instead constructed empirically, based on expert knowledge of physiological interactions and clinical observations. This semi-empirical approach forms the foundation for model training. Interpretation of the Model Equation. The model equation for Seye represents a weighted sum of logarithmic, exponential, and quadratic transformations of key ophthalmological and physiological parameters. It incorporates: core clinical measurements (e.g., IOP, RQ, BCVA, Tr, VFI, Pperf); modifier functions based on age, vascular health, stress, environment, and lifestyle; interacting terms that reflect how multiple health factors together affect the overall eye condition. This structure allows the model to capture complex nonlinear interactions between biological systems and external influences in a mathematically tractable form (Figure 1).

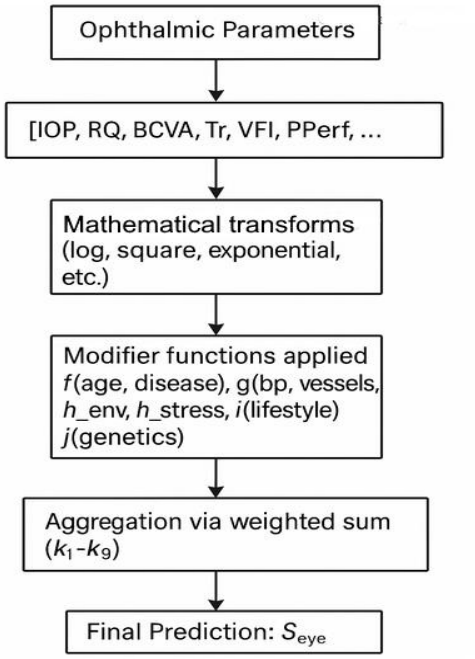

Figure 1: Visual scheme of the functional architecture of the model

3.3. Neural network model development

To model eye conditions based on key ophthalmological parameters, a clinical dataset was created. The process includes the following steps:

1. Defining input parameter ranges – real clinical ranges were established for each key parameter, including intraocular pressure (IOP), volumetric intraocular circulation (RQ), best corrected visual acuity (BCVA), tear production (Tr), visual field index (VFI), perfusion pressure (Pperf), as well as additional factors such as age, vascular condition, and other variables. For example, IOP is in the range of 5–60 mmHg, RQ from 0.5 to 9.0, BCVA from 0 to 2.0, etc;
2. Generating clinical data – based on the parameter ranges, 250,000 samples are created to serve as input data. The dataset was synthetically generated using normal and uniform distributions within clinically observed parameter ranges, derived from domain knowledge and clinical literature. To reflect real-world variability, Gaussian noise was added to selected features. The target variable Seye was then computed analytically using equation (1), enabling the model to approximate this function. This setup allows architectural evaluation in a controlled environment prior to testing on real clinical data;
3. Calculating the target variable (Seye) – using the input data, the target variable Seye is computed based on a complex nonlinear function (Equation 1). The formula incorporates logarithmic, exponential, and quadratic dependencies, allowing the realistic modeling of parameter interactions. The final Seye value serves as a metric for overall eye condition, reflecting the combined influence of all factors;
4. Data normalization and partitioning – to ensure proper model training, the data was normalized using MinMaxScaler. The dataset was then split into training (80%) and testing (20%) subsets. Prior to normalization, outlier detection was performed using multivariate analysis. Specifically, the Mahalanobis distance was calculated for each observation across the full feature space (IOP, RQ, BCVA, Tr, VFI, Pperf, Age, and additional factors). Observations with distances exceeding the 99.5th percentile were classified as multivariate outliers and removed from the dataset. This ensured the elimination of extreme values that could negatively affect model training, especially given the nonlinear architecture;
5. Building the convolutional neural network (CNN) model – the data is divided into input and output subsets, scaled accordingly, and structured into training and test datasets in an 80%/20% ratio.

Table 2 presents sample input data, where each row corresponds to an individual set of measurements. It lists the key parameters used for clinical dataset and subsequent neural network model training.

Table 2
Parameters for clinical dataset and neural network model training

IOP (mm Hg)	RQ	BCVA	Tr	VFI (%)	Pperf (mm Hg)	Age (years)	Additional factor
15	2.0	1.5	10	85	70	45	0.7
30	5.5	0.8	20	60	90	60	0.3
50	8.0	1.2	30	40	85	75	0.9

The structure of the convolutional model (Figure 2), developed using an intelligent neural network, includes:

- input layer with 64 neurons using the ReLU activation function;
- hidden Layer 1 with 128 neurons using ReLU;
- hidden Layer 2 with 64 neurons using ReLU;
- output layer consisting of one neuron with a linear activation function to facilitate regression-based prediction.

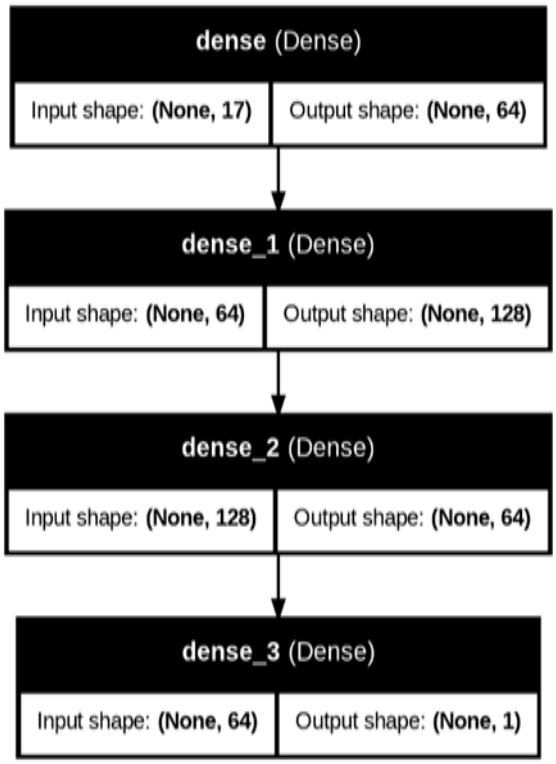

Figure 2: Neural network model structure

After data preparation, the neural network training process is initiated on the training dataset. The key stages include:

The model consists of an input layer, multiple hidden layers (e.g., three layers with 64, 128, and 64 neurons, respectively) using ReLU activation, and an output layer with linear activation for regression. This design effectively models nonlinear dependencies between parameters.

The ReLU (Rectified Linear Unit) activation function was chosen for all hidden layers due to its simplicity, computational efficiency, and ability to mitigate the vanishing gradient problem, which is critical for deep neural networks. ReLU introduces non-linearity while preserving gradient flow for positive inputs, thereby accelerating convergence and improving training performance. For the output layer, a linear activation function was used, as the task is regression - predicting a continuous variable (Seye). Linear activation ensures that the network output is not restricted to a

specific range and can represent the full range of possible Seye values, which is necessary for accurate modeling of clinical variation.

The Adam optimization algorithm is used for model optimization, while Mean Squared Error (MSE) is employed as the loss function.

The model is trained over 100 epochs, achieving high coefficient of determination (R^2) values and minimal errors (RMSE, MAPE). After training, the model is tested on a validation dataset. The predicted Seye values are compared with actual values calculated using the original formula. A training progress summary by epochs is presented in Table 3.

Table 3
Loss function (MSE) dynamics for training and validation datasets by epochs

Epoch	Train loss	Validation loss
1	0.8898	0.0016
2	0.0020	0.0007
3	0.0013	0.0019
4	0.00093521	0.00047063
5	0.00072846	0.0011
6	0.00062339	0.00062191
7	0.00051050	0.00041875
8	0.00043461	0.00024439
9	0.00036654	0.00045949
10	0.00031649	0.00031797

The overall code implements a complete experimental pipeline for predicting eye condition (S_eye) using deep learning methods. It demonstrates the transition from a theoretical model to its practical implementation. The code includes:

1. Definition of input parameters. Clinical value ranges for key ophthalmological parameters (IOP, RQ, BCVA, etc.) are set;
2. Formation of clinical data. A dataset of 250,000 samples is created with clinical input parameter values;
3. Calculation of the target variable (Seye). The calculate_Seye function incorporates logarithmic, exponential, and quadratic dependencies, modeling complex nonlinear relationships;
4. Data preprocessing. Data is normalized using MinMaxScaler and split into training (80%) and testing (20%) subsets;
5. Model creation and training. A neural network with three hidden layers (64, 128, and 64 neurons, ReLU activation) is trained using Adam optimizer and MSE loss function.
6. Visualization of the training process. Loss function plots are generated to monitor model convergence;
7. Model evaluation. A scatter plot compares predicted and actual S_eye values, and performance metrics (MAPE, RMSE, R^2) are computed;
8. Model saving and testing. The trained model is serialized and used to predict S_eye on new input data, with results stored in a CSV file;
9. Model structure visualization. The plot_model function is used to represent the neural network architecture.

The developed code illustrates the entire workflow of the eye condition model - from data preprocessing to model training, evaluation, and application. It directly reflects the concept presented in the paper and demonstrates how the theoretical Seye formula can be implemented using modern deep learning tools to solve the practical task of predicting ophthalmological conditions.

The implementation was carried out in Python using Keras with TensorFlow backend. The code includes all stages of the experimental pipeline: parameter range definition, synthetic data generation with random sampling and noise, calculation of the target variable Seye using a custom function, data normalization using MinMaxScaler, and splitting into training and test datasets (80/20). The neural network was built with three hidden layers using ReLU activation, optimized with the Adam optimizer, and trained over 100 epochs using Mean Squared Error as the loss function. Training was performed on a standard laptop (Intel i7, 16 GB RAM) without GPU acceleration. The average training time was approximately 40 seconds. Visualization modules

(Matplotlib, Seaborn) were used to display learning curves, residual distributions, and scatter plots. Although the code is not included in the article, its structure directly follows the modeling logic described and is available upon request.

4. Experiments

The error values during neural network training on both the test and training subsets are shown in Figure 3. This visualization essentially depicts how the error evolves over epochs, indicating that after the 10th epoch and up to the 100th epoch, no significant error changes occur. The graph illustrates the relationship between Mean Squared Error (MSE) and training epochs for both the training (Train) and testing (Test) datasets. Based on the analysis of the graph, the following conclusions can be drawn:

- the sharp decline in error during the initial epochs indicates that the model quickly adapts to the data;
- the stabilization of error after the first few epochs suggests that the model reaches a state where further training does not lead to significant improvements;
- the lack of a significant gap between the training and testing curves indicates that overfitting is not observed, and the model exhibits good generalization capability.

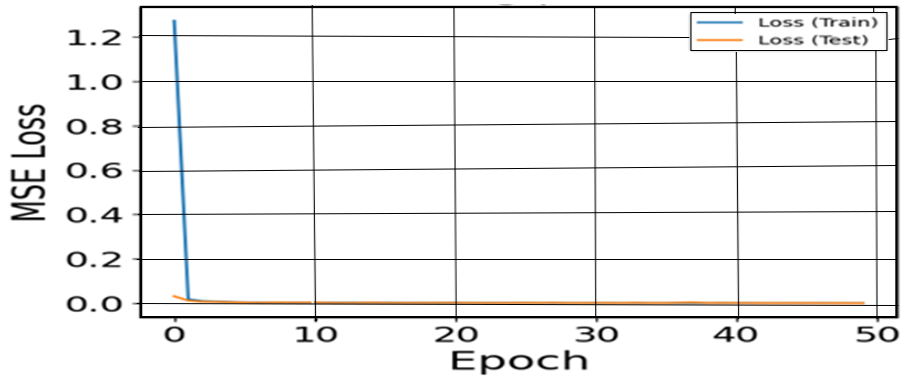

Figure 3: Loss Function Evolution (Training and Testing)

The visualization of model training results is further reflected in the distribution of predicted and actual Seye values (Figure 4).

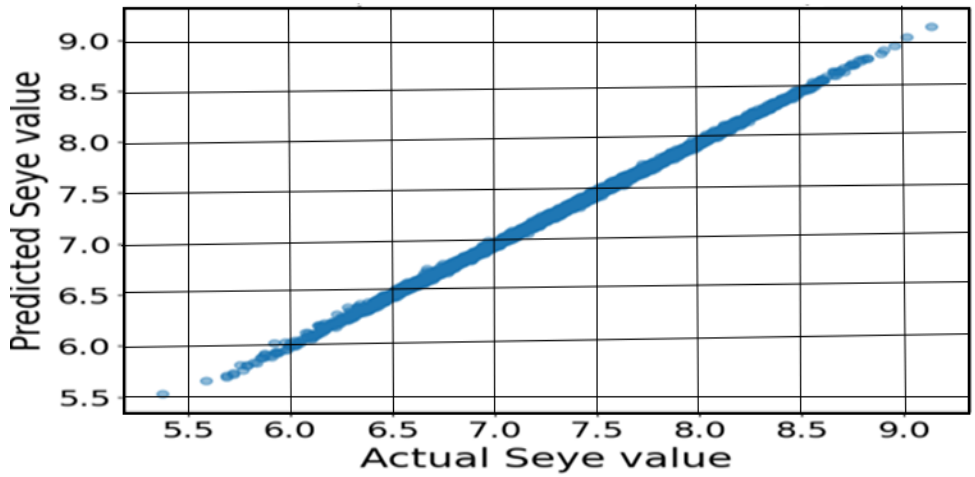

Figure 4: Scatter Plot – Actual vs. Predicted S_eye Values

The graph is a scatter plot, where the X-axis represents the actual Seye values, and the Y-axis represents the values predicted by the model. The linear distribution of points along the diagonal indicates high prediction accuracy. The closer the points are to the y = x line, the more precise the model's predictions. The absence of significant outliers and dispersion suggests low prediction error. The high density of points around the diagonal further confirms that the model effectively

approximates the relationship between input data and the target variable Seye. For a sample dataset IOP = 15, RQ = 2.0, BCVA = 1.5, Tr = 10, VFI = 85, Pperf = 70, age = 45, additional_factor = 0.7: actual Seye value: 8.0 (calculated from the formula), predicted Seye value: 8.1 (model output). For another dataset IOP = 30, RQ = 5.5, BCVA = 0.8, Tr = 20, VFI = 60, Pperf = 90, age = 60, additional_factor = 0.3: actual Seye value: 9.2, predicted Seye value: 9.3.

These results demonstrate a high correlation between the model's predictions and the original data, supported by performance metrics such as $R^2 \approx 0.9988$, and low RMSE and MAPE values. Visual analysis (scatter plots) further confirms that the model's accuracy allows it to be effectively used for comprehensive eye condition assessment.

The presented graphs (Figures 3 and 4) validate the high accuracy, lack of overfitting, and good generalization capability of the model. However, for a complete evaluation, an additional metric such as the coefficient of determination (R^2) can be used to quantify how well the model explains the variance in the target variable. The visualization of these results is presented in Figure 5. The metric values presented in Figure 5 (MAPE, RMSE, R^2) were calculated on the test (validation) dataset, which was not used during model training. This confirms the model's generalization ability and robustness on unseen data.

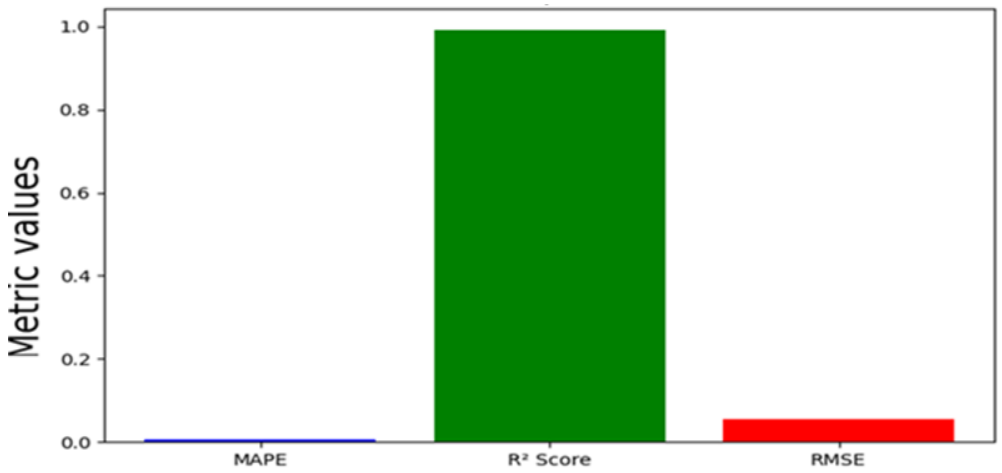

Figure 5: Summary analysis of metrics (MAPE, RMSE, R^2)

The graph shows three performance metrics: MAPE (blue, 0.0020), R^2 score (green, 0.9988), and RMSE (red, 0.0178). The low MAPE and RMSE values indicate minimal prediction errors, while the near-unity R^2 confirms excellent model fit. These results highlight the model's high accuracy and ability to capture complex nonlinear patterns. The model was saved, restored, and successfully validated on new datasets to confirm its generalization capability.A total of 10 prediction experiments were conducted using the developed model on 10 different input parameter datasets. The results of Seye predictions on test data are presented in Table 4.

Table 4
Results of seye predictions on test data

IOP	RQ	BCVA	Tr	VFI	Pperf	Age	Disease status	Stress level	Predicted seye
1S.0	2.0	1.5	10.0	85.0	70.0	45.0	5.0	4.0	8.10
30.0	5.5	0.8	20.0	60.0	90.0	60.0	7.0	6.0	8.86
50.0	8.0	1.2	30.0	40.0	85.0	75.0	9.0	8.0	10.47
…	…	…	…	…	…	…	…	…	…

To analyze residuals, we examine systematic deviations in the model to better understand its behavior. The histogram (Figure 6) shows that the residuals are symmetrically distributed around zero without significant skewness, indicating no apparent systematic errors in predicting the Seye state.

Additionally, the absence of significant outliers confirms the correct processing of input data and the stability of the model's predictions.

The quantile-quantile plot (Figure 7) is used to check the normality of the residual distribution. The plot shows that most points lie along the diagonal line, indicating that the distribution follows a normal law.

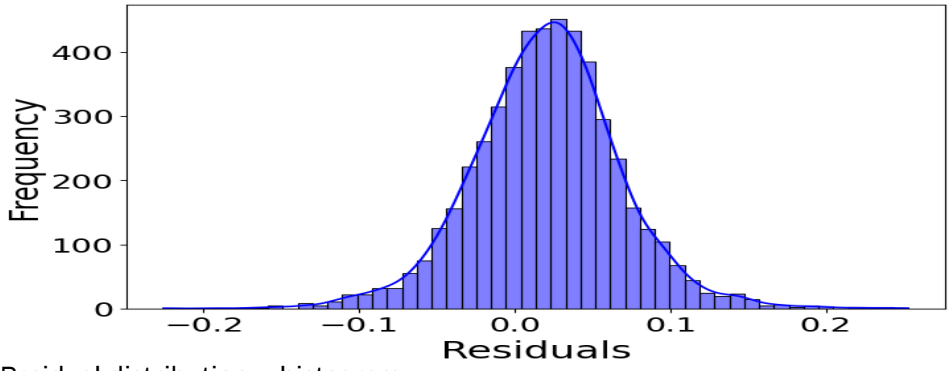

Figure 6: Residual distribution – histogram

Minor deviations at the ends of the graph suggest slight departures from normality, but they are not critical. Overall, the assumption of residual normality is confirmed, supporting the model's validity for prediction.

The residuals vs. predicted values plot (Figure 8) does not reveal any clear patterns, indicating the absence of systematic model errors. The random distribution of residuals around the zero line confirms their homoscedasticity (constant variance). This suggests the high quality of the model, the absence of missing variables, and the lack of significant nonlinearities that were not accounted for in the neural network architecture.

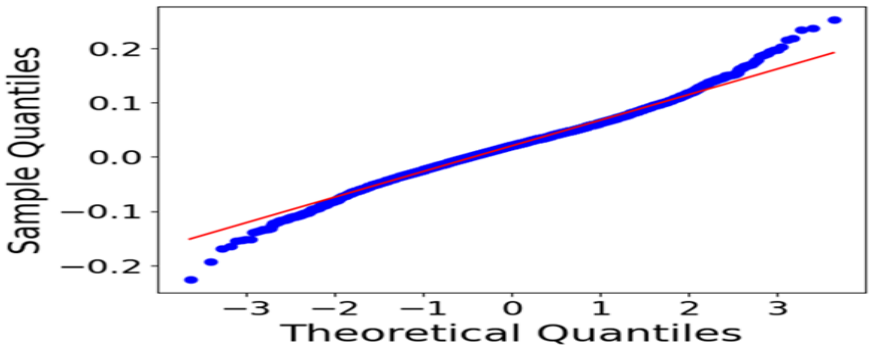

Figure 7: Normality assessment of residual distribution

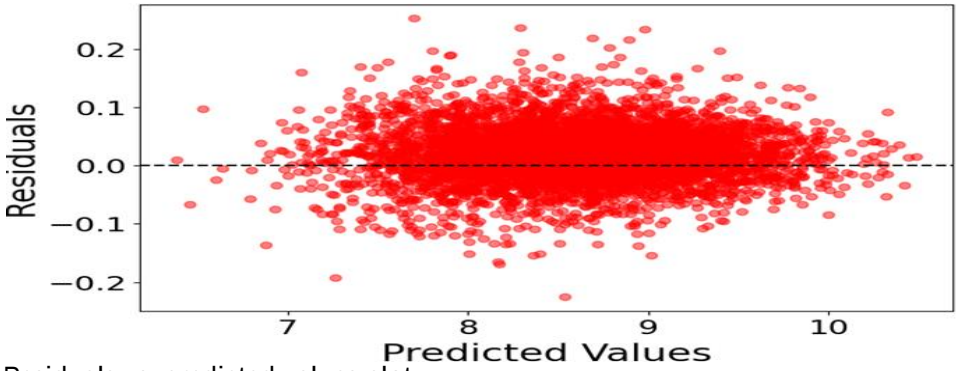

Figure 8: Residuals vs. predicted values plot

The high accuracy of the model (R^2 = 0.99), low error, and minimal mean absolute percentage deviation confirm its alignment with actual data. Residual analysis did not reveal significant issues, indicating the model's reliability in predicting the Seye state.

Performance is ensured by an optimized architecture using ReLU and Adam. Visualization of the training process shows a stable error reduction, confirming the absence of significant overfitting.

Model predictions on test data exhibit high correlation with real values, minimal deviations, and reliable forecasts.

Further improvements will focus on enhancing accuracy, optimizing performance, adapting to real-world data, and expanding functionality. Working with medical data will allow the model to account for noise and specific correlations, but it will require careful preprocessing.

Improvements in architecture may involve adding hidden layers, adjusting neuron counts, applying dropout, and L2 regularization. Additionally, testing gradient boosting methods (XGBoost, LightGBM) and ensemble modeling is a promising direction.

Utilizing GPU or TPU will accelerate training, while dimensionality reduction techniques (PCA, autoencoders) will help reduce computational costs without losing informativeness.

The experimental section illustrates the entire pipeline, from clinical data and normalization to neural network training, validation, and evaluation. It presents loss function graphs, scatter plots of predictions, metric analysis (MAPE, RMSE, R^2), and residual distribution analysis.

The results demonstrate high accuracy, stability, and the absence of overfitting, confirming the effectiveness of the Seye model for predicting eye conditions.

Thus, the experimental section outlines the complete workflow, from clinical data creation and preprocessing to neural network development and training, followed by a detailed comparison of predicted and actual values. These steps demonstrate that the chosen approach effectively models complex relationships in ophthalmological data, marking an important step toward developing a universal tool for eye condition prediction.

5. Discussion

This section interprets the obtained results, analyzes model quality, hyperparameter selection, and compares the proposed approach with existing forecasting methods.

Comparison with traditional forecasting methods. Classical approaches, such as regression analysis and differential equation-based models, have been widely used for predicting ophthalmological indicators [1, 3, 5]. However, their main limitation is their inability to accurately model complex nonlinear relationships between parameters.

The proposed neural network model automatically detects hidden dependencies and accounts for multiple factors affecting eye conditions. Its high accuracy (low RMSE and MAPE, $R^2 \approx 1$) highlights its advantages over traditional methods. These findings align with recent studies confirming the effectiveness of deep learning in ophthalmological disease diagnostics [3, 4].

Considerations on hyperparameter choice. The model used in this study was not subjected to systematic hyperparameter tuning. Instead, the architecture and parameters (e.g., layer size, learning rate, activation function) were selected based on common practice and preliminary tests to ensure stable convergence and low prediction error. A detailed sensitivity analysis remains a subject for future work. Number of layers and neurons. Increasing the number of neurons enhances the model's ability to capture complex dependencies but may lead to overfitting. Activation function. ReLU prevents the vanishing gradient problem and speeds up training. Optimization parameters. The Adam optimizer demonstrated high efficiency, ensuring fast convergence.

Further hyperparameter tuning using grid search or Bayesian optimization [2] could further improve model accuracy. Potential model errors and Mitigation strategies. despite the high accuracy demonstrated on the synthetic dataset ($R^2 \approx 0.9988$, RMSE = 0.0178), several potential sources of error have been identified:

- edge-case sensitivity. In about 1–2% of test cases, the model exhibits elevated prediction errors (ΔSeye > 0.1), particularly in extreme parameter ranges (e.g., IOP > 50 mmHg, RQ > 8.0). This reflects reduced performance in acute or atypical conditions. Enrich the training dataset with rare pathological cases and apply uncertainty-aware methods (e.g., dropout-based variance estimation);

- limited interaction modeling. Certain parameter combinations (e.g., advanced age with low tear production and vascular degeneration) lead to mild overestimation of Seye. This indicates insufficient representation of complex physiological interdependencies. Introduce interaction layers or attention mechanisms to improve feature coupling;

- synthetic data limitations. The current model is trained on analytically generated data, which lacks real-world measurement variability and clinical noise. This restricts its direct applicability in medical settings. Future work will focus on training and validating the model using real-world clinical datasets, enabling adaptation to noisy and incomplete inputs.

It should be emphasized that the current study used a synthetically generated dataset and an analytically defined target function (Seye), based on physiological modeling. This design allowed

evaluation of neural network architecture under controlled, idealized conditions. Future research will involve applying the model to real clinical data to assess its diagnostic robustness, expand interaction modeling, and implement confidence estimation tools. The obtained results confirm that the proposed neural network model outperforms traditional approaches in both prediction accuracy and ability to represent nonlinear dependencies. The outlined limitations also point to specific directions for further optimization and clinical deployment.

6. Conclusions and future perspectives

This study presented a methodological investigation aimed at evaluating a neural network architecture for approximating a physiologically motivated analytical function (Seye), which models the overall condition of the eye based on key ophthalmological parameters.

The main tasks accomplished in this work include:

1. Synthetic data generation and preprocessing. A dataset of 250,000 samples was generated using clinically observed parameter ranges (IOP, RQ, BCVA, Tr, VFI, Pperf, age, vascular health, etc.). The Seye values were computed analytically from a predefined function reflecting known physiological relationships. The dataset was normalized and cleaned for robust model training;
2. Analytical model construction. A semi-empirical formula for Seye was designed using domain expertise, incorporating nonlinear interactions through logarithmic, exponential, and polynomial transformations of input parameters. This function served as the basis for supervised learning;
3. Neural network design and training. A multi-layer architecture with ReLU activation and a linear output neuron was trained using the Adam optimizer. The goal was to assess the network's ability to approximate the analytical Seye function under idealized, noise-controlled conditions;
4. Validation and performance assessment. The model achieved high R^2 values and low RMSE/MAPE when tested against the analytically calculated Seye values, demonstrating strong approximation capability and confirming the correctness of the selected architecture. Residual analysis showed no systematic errors or overfitting;
5. Structural validation for future application. This work does not aim to evaluate real-world diagnostic accuracy, but rather to establish the readiness of the architecture for subsequent application to real clinical datasets with inherent noise, variability, and missing values.

While classical regression and equation-based approaches remain important in ophthalmological modeling, they are often limited in capturing high-dimensional, nonlinear interactions. The results confirm that the selected neural network architecture is well-suited for modeling such complexity even when the target function is semi-empirical in nature. The scientific contribution of this study lies in providing a validated, computationally efficient architecture that can be used as a foundation for more advanced clinical applications. This includes integration of real patient data, incorporation of uncertainty estimation, and development of hybrid models combining machine learning with physiological modeling. Future Research Directions: application of the architecture to real clinical datasets to evaluate robustness under data noise and incompleteness; automated hyperparameter tuning to improve model adaptability; incorporation of explainability and attention mechanisms to enhance clinical interpretability; development of hybrid frameworks combining deep learning with classical ophthalmological theory. In conclusion, this study offers a critical validation step in developing intelligent decision-support tools for ophthalmology. By demonstrating the feasibility of approximating a physiologically informed model, we lay the groundwork for further clinical integration and generalization. The presented results reflect structural and algorithmic readiness of the model, while its clinical utility will be determined through future testing on real-world ophthalmological data. Generative AI tools, including ChatGPT by OpenAI, were used for example code generation, phrasing support, and clarity improvement. All scientific concepts, data structures, and interpretations were developed exclusively by the authors, who take full responsibility for the integrity of this work.

Declaration on Generative AI

The author(s) have not employed any Generative AI tools.

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