International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

FRACTIONAL 3 TRIANGLE MULTI DELAYED BOUNDARY ENHANCED PATCH MERGE NEURAL NETWORK OPTIMIZED BY SWARM BIPOLAR ALGORITHM FOR SITE PREDICTION OF CROTONYLATION ON NON-HISTONE PROTEINS

[1]Dr. Ashok Koujalagi, [2]*Sandra Jestine*,[3]*G.Mohan*,[4]*Dr. K. Indhumathi*,[5]*Mudunuru Suneel*,[6]*K. Anju Aravind*

[1]Designation: Assistant Professor

Department: Computer Science and Engineering

Organization: Shri Vishnu Engineering College for Women (A)

Email ID: askoujalagi@gmail.com

ORCID ID: https://orcid.org/0000-0002-0195-3976

Scopus ID: https://www.scopus.com/authid/detail.uri?authorId=57211543256

[2]Assistant Professor

Mathematics

Dayananda Sagar College of Engineering, Bangalore

sandra-maths@dayanandasagar.edu

0009-0006-2363-1974

[3]Associate Professor,

Department of Mathematics,

K.S.Rangasamy College of Technology,Tiruchengode- 637 215.TamilNadu

Email: mohanjee.ksrct@gmail.com

Orcid id: 0000-0002-9873-1762

[4]Assistant professor

Department of Computer Applications

Kalasalingam Academy of Research and Education, Krishnankoil

Mail id : indhu16aug@gmail.com

Official mail id: indhumathi@klu.ac.in

Orchid id: 0000-0003-4371-193X

[5]Assistant Professor,

Department of Electronics and Communication Engineering,

Aditya University,

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

Surampalem, Andhra Pradesh, India.

Email: suneel007@gmail.com

Orcid ID: 0009-0002-1200-9830

[6]Assistant Professor, Department of Computer Science and Engineering,

Koneru Lakshmaiah Educational Foundation, Guntur.

E-Mail: anjukprof@gmail.com,

anjuaravindk@kluniversity.in

ORCID: 0009-0008-4940-1936

Abstract

Crotonylation is a key Post-Translational Modification (PTM) that regulates protein function, stability, and interaction, particularly in non-histone proteins. Crotonylation site prediction remains challenging due to high-dimension and complex biological sequence data. To mitigate these challenges, a Fractional 3 Triangle multi delayed Boundary Enhanced Patch Merge Neural Network optimized by Swarm Bipolar Algorithm (F3TBEPMNN-SBA) is introduced for efficient crotonylation site prediction on Non-Histone proteins. First, protein sequences are gathered from UniProt dataset, which is the basis source for annotated non-histone lysine crotonylation data. The raw sequences then go through the preprocessing stage, where Adaptive Mesh Diagnosis (AMD) is used to rectify sequence distortions and heighten informative areas. Next, an Adaptive Transformer Model (ATM) conducts deep contextual feature extraction, successfully modeling long-range dependencies among amino acid sequences. For classification, the Fractional 3 Triangle multi delayed Boundary Enhanced Patch Merge Neural Network (F3TBEPMNN) combines Fractional order 3 Triangle multi Delayed Neural Network (F3TDNN) and Boundary Enhanced Patch Merge Transformer (BEPMT) is used. At first, F3TDNN encodes dynamic temporal relations using multi-delay architecture and fractional-order dynamics, while BEPMT facilitates spatial discrimination by retaining boundary-level details in patch-wise representations aiding in precise crotonylation site prediction. The network□s loss function and hyper parameters are optimized lastly by using Swarm Bipolar Algorithm (SBA) to accelerate convergence and improve prediction accuracy. Experimental results reveal significant improvements in all performance metrics such as accuracy (99.95%), sensitivity (99.72%), F1-score (99.60%), specificity (99.79%), and precision (99.53%), and ROC demonstrating the robustness of the model in lysine crotonylation site prediction.

Keywords□ Lysine crotonylation, non-histone human protein, post-translational modification, Swarm Bipolar Algorithm, amino acids.

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

I. INTRODUCTION

Lysine crotonylation or LCr is a novel and unique post-translational modification (PTM) in which Biotinoyl coenzyme A (Biotinoyl-CoA) becomes covalently attached to substrate protein lysine residues [1]. PTMs are chemical modifications of proteins that occur after they have been synthesized and are essential for controlling protein function, diversity, and biological activity [2]. Among the different amino acids, lysine has been identified to have the most number of PTMs at least 15 indicative of its pivotal function in cell regulation [3]. LCr was originally found in histone proteins through a proteomic investigation of human somatic and mouse germ cells, and has been identified in histone and non-histone proteins among animals and plants since then [4]. This evolutionarily conserved modification is significantly enriched in active gene promoters and putative enhancers, emphasizing its role in regulation of gene transcription [5]. LCr is associated with a number of physiological and pathological processes, such as spermatogenesis, tissue damage, inflammation, chromatin remodelling, telomere maintenance, neuropsychiatric diseases, carcinogenesis, and Human Immunodeficiency Virus latency. By impacting the direction, strength, or speed of biological signals, LCr modulates pivotal intracellular signalling pathways [6]. As a result of its regulatory function in various cellular processes, correct site prediction for lysine crotonylation is crucial for the elucidation of its functional mechanisms. To achieve this, both experimental techniques and computational methods have been established for the facilitation of site identification of LCr and subsequent research into its biological relevance [7].

LCr is a key regulator of gene expression and various cellular processes, connecting it to essential biological and disease processes. Its enrichment in gene regulatory elements and association with diseases such as cancer and neurodisorders underscore the necessity for accurate site identification. Thus, it is crucial to make correct computational predictions of LCr sites to promote functional and therapeutic studies.

Contributions

The key contributions of the proposed work is given below,

- **Data Collection**: The model collects protein sequences and associated annotations from **UniProt** dataset, focusing specifically on **non-histone proteins** to build a reliable crotonylation site prediction framework.

- **Pre-processing**: An **Adaptive Mesh Diagnosis (AMD)** technique is employed to eliminate noise, normalize sequence data, and segment relevant amino acid regions, thereby enhancing the clarity and consistency of the input features.

- **Feature Extraction**: An **Adaptive Transformer Model (ATM)** is used to extract high-order contextual and sequential features from the pre-processed protein sequences, preserving both local and global dependencies.

- **Prediction Architecture**: The model introduces a **Fractional 3 Triangle multi delayed Boundary Enhanced Patch Merge Neural Network (F3TBEPMNN),** which combines:

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

- **Fractional order 3 Triangle multi Delayed Neural Network (F3TDNN)** for capturing long-range and multi-delay temporal dependencies and
- **Boundary Enhanced Patch Merge Transformer (BEPMT)** to maintain critical boundary information and improve discriminative power across patch boundaries during prediction.
- **Optimization**: The **Swarm Bipolar Algorithm (SBA)** is applied to optimize the network□s loss function and hyper parameters, accelerating convergence and improving overall prediction accuracy for crotonylation site identification. The entire pipeline is designed specifically to predict crotonylation sites on non-histone proteins, supporting biological interpretation and downstream protein functional analysis.

The paper is structured as follows: Section 1 contains introduction; Section 2 contains literature review; Section 3 contains methodology; Section 4 contains results; and Section 5 concludes the study.

II. LITERATURE SURVEY

Below is a summary of recent studies on crotonylation site prediction.

In 2024, Gao, et.al, [8] presented a Multi-View Neural Network (MVNN) for identification of human non-histone crotonylation sites. It integrated multi-view encoding features and adaptive encoding features through a multi-channel neural network to learn attribute differences between crotonylation and non-crotonylation sites from various perspectives. Convolutional neural networks (CNNs) extracted local information from input features, while bidirectional long short-term memory networks captured sequence dependencies. An attention mechanism fused outputs of different feature extraction modules. A fully connected network functioned as final classifier to predict whether a lysine site was crotonylated or not. The UniProt database was used as data source.

In 2024, Jiang et.al, [9] introduced non-histone crotonylation sites collected from five plant species: rice, peanuts, papaya, wheat, and tabacum. A comprehensive analysis of amino acid distribution around the crotonylation sites was performed. A deep learning model, Plant Non-Histone Lysine Crotonylation (PNh-LCr), was developed by combining a CNN and an attention mechanism. Datasets were obtained from UniProt and National Center for Biotechnology Information (NCBI).

In 2024, Zuo, et.al, [10] presented a deep learning model based on a multilayer perceptron with an attention mechanism named Identification of Lysine Crotonylation site to identify crotonylation sites. Three feature extraction strategies amino acid composition, and distance based residue encoding were applied to encode crotonylated and non-crotonylated sequences. To balance the dataset, the Fuzzy C-Means -General Regression Neural Network (FCM-GRNN) under sampling algorithm was used. Multiple classifiers were evaluated, and the Multilayer Perceptron with self-attention was selected for final model construction. The UniProt database was used as the data source.

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

In 2022, Dou, et.al, [11] presented a CNN based framework for identification of human non-histone LCr modifications. To address class imbalance (15,274 LCr vs. 74,018 non-LCr, 1:4 ratio), the focal loss function replaced standard cross-entropy to assign different weights to samples and distinguish easy- and hard-classified instances. The UniProt database was used for data collection.

A. Problem statement

Crotonylation is an important PTM that affects protein function and regulation, but its detection on non-histone proteins is difficult because of sequence diversity and class imbalance in the data. Experimental approaches have been tedious and expensive, necessitating the use of computational tools. Although recent developments involving CNNs, attention mechanisms, and deep learning-based models, there is still a lack of reliable and generalizable prediction of non-histone LCr sites in various species. Accordingly, a strong and interpretable model is needed to predict LCr sites reliably.

III. PROPOSED METHODOLOGY

The suggested methodology starts with retrieval of protein sequence information from the UniProt dataset. Initially, it undergoes pre-processing by AMD to clean and organize the data effectively. Feature extraction is then carried out employing an ATM to identify relevant contextual as well as positional patterns. Subsequent to this, crotonylation site prediction in non-histone proteins is performed using the F3TBEPMNN model, which is a combination of F3TDNN and BEPMT to incorporate temporal and boundary features. Lastly, SBA is utilized for model hyperparameter and loss function optimization and increasing prediction accuracy. The proposed method□s block diagram is shown in Figure 1.

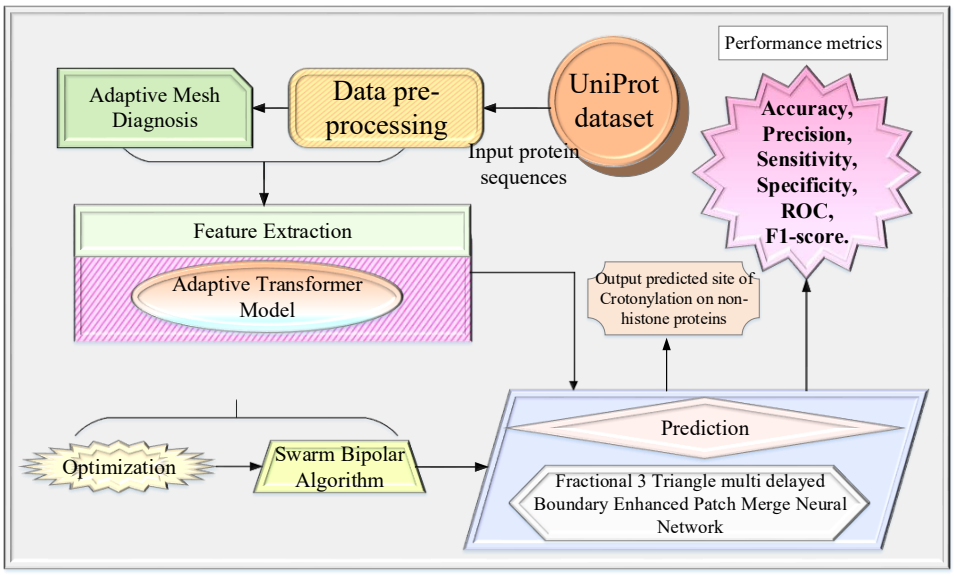

Fig.1.Proposed Methodology F3TBEPMNN-SBA block diagram.

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

A. Dataset description

The dataset which contained a large number of experimentally verified human non-histone LCr sites. 19287 LCr sites were obtained from 4230 non-histone proteins in the UniProt database for model development and evaluation [12]. The collected data undergo pre-processing stage.

B. Preprocessing using Adaptive Mesh Diagnosis (AMD)

The data for accurate crotonylation site prediction is pre-processed using Adaptive Mesh Diagnosis (AMD), which removes noise and structural inconsistencies [13]. The dataset includes multiple lysine (L) residues labeled as positive or negative. A 31-length sequence window is extracted for each L-site, representing its local biochemical context. This window is modelled as a 1D mesh, treating each amino acid as a vertex with spatial orientation. Topological neighbours are identified to understand structural relationships. The orientation difference between the L-site and its neighbours is then quantified by calculating the angle between their normal vectors, enabling the model to capture fine-grained local geometry essential for site prediction given in eq. (1),

$$\underset{g_i \subset T_{i,j \neq i}}{\eta_{j,i}} = \arccos\left(\frac{t_j \cdot t_i}{\|t_j\| \cdot \|t_i\|}\right) \quad (1).$$

where $\eta_{j,i}$ is the angle between face i and j, t_i, t_j denotes the normal vectors of mesh faces i and j respectively, t_i is the auxiliary feature block . $\|t_j\| \cdot \|t_i\|$ represents the magnitudes of respective normal vectors, *arccross* is the inverse of cosine function. By calculating the angular differences between normal of adjacent mesh faces, the method captures fine-grained geometric and topological variations as in eq. (2),

$$z_j^{(k+1)} = \sigma\left(\sum_{w_i \in I_j} e_{j,i}^{(k)} \cdot z_i^{(k)} + z_i^{(k)}\right) \quad (2).$$

where the $z_i^{(k)}$ represent the hidden state of i^{th} element (amino acid) at k^{th} layer, $z_i^{(k+1)}$ denotes updated feature vector, σ is a **nonlinear activation function.** After multiple normal predictions, update vertices using the vertex update strategy described by eq. (3).

$$\overline{b_j}^* = \overline{b_j} + \frac{1}{|\varpi_j|}\sum_{i \in \varpi_j} \overline{t_i}\left[\overline{t_i} \cdot \left(\overline{v_i} - \overline{b_j}\right)\right] \quad (3).$$

where ϖ_j represents the one loop proximal surface of the vertex $\overline{b_j}$, $\overline{v_i}$ is he centre of the proximal surface and $\overline{t_i}$ is the normal to the denoised neighbouring surface. Finally, the output of the preprocessing stage is a denoised, feature-enhanced 3D mesh of the protein, with refined normals and vertices, ready for downstream crotonylation site prediction using classifiers. Thus, preprocessing is performed using AMD to denoise and the refined data is fed into the ATM for robust feature extraction.

C. Feature extraction using Adaptive Transformer model

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

After pre-processing, each amino acid sequence (of length 31) is numerically encoded, where every amino acid is represented by a rich feature vector incorporating biological and structural properties. The Adaptive Transformer Model (ATM) is applied to extract crucial features that capture the spatial and contextual dependencies of lysine residues in the local sequence environment [14]. The first step models the conditional probability of the output token sequence using the Transformer mechanism. The overall likelihood of a sequence y is computed using the eq. (4),

$$W_1(y)=\sum_j \log E\left(s_j|s_{j-p},....,s_{j-1};\Pi\right) \quad (4).$$

where p represents context window and Π is the parameter obtained while modeling the conditional probability E, s_j is the hidden state of Transformer at position j. The output distribution over target tokens is given as in eq. (5)

$$f_0 = AH_g + H_u \quad (5).$$

where $A=\left(a_{-l},...a_{-1}\right)$ is context vector of tokens, f_0 denotes combined context-aware feature vector for each position, H_g and H_u are the tokens embedding of amino acid and position embedding matrix respectively. Thus the extracted feature vectors are then passed to a downstream classifier for final crotonylation site prediction.

D. Fractional 3 Triangle multi delayed Boundary Enhanced Patch Merge Neural Network (F3TBEPMNN) for site prediction of crotonylation

Crotonylation site prediction on non-histone proteins is performed using the Fractional 3 Triangle Multi-Delayed Boundary Enhanced Patch Merge Neural Network (F3TBEPMNN). This model integrates Fractional Order 3 Triangle Multi-Delayed Neural Network (F3TDNN), which captures temporal dependencies across residues, and Boundary Enhanced Patch Merge Transformer (BEPMT), which preserves structural boundary information. Their fusion improves contextual understanding and enhances the prediction accuracy of crotonylation modification sites across diverse protein sequences.

a. Fractional order 3 Triangle multi Delayed Neural Network

To predict whether each lysine site in non-histone proteins is crotonylated or not, the F3TDNN is used to effectively capture long-range dependencies and dynamic sequence relationships [15]. This model integrates fractional calculus and multi-delay feedback loops into a three-triangle topology, enabling deeper feature interactions and improved classification. The Caputo-type fractional derivative governing the temporal dynamics is defined in eq. (6),

$$K^Q y(\chi)=\frac{1}{\Lambda(v-q)}\int_{z_0}^{z}\frac{y^{(p)}(M)}{(\chi-M)^{q-p+1}}ds, \quad (6).$$

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

where $\Lambda(\cdot)$ represents the Gamma function, $y^{(p)}$ denotes p^{th} derivative of y, χ indicates time variable. The **dynamic behavior** of the system is expressed through the fractional differential eq. (7),

$$\frac{d^q p(s)}{ds^q} = c(s,(s)), p(0) = p_0 \quad (7).$$

where $q \in (0,1]$, p_0 is the initial condition, $p(s)$ denotes prediction state vector, $c(s,(s))$ is a function representing neural interactions. The characteristic matrix of multi-delayed feedback is given as eq. (8),

$$\delta(t) = \begin{bmatrix} t^{q1} - g_{11}e^{-m\gamma_{11}} & -g_{12}e^{-m\gamma_{12}} & \cdots & -g_{1k}e^{-m\gamma_{1k}} \\ -g_{21}e^{-m\gamma_{21}} & m^{q1} - g_{22}e^{-m\gamma_{22}} & \cdots & -g_{2k}e^{-m\gamma_{2k}} \\ \vdots & \vdots & \ddots & \vdots \\ -g_{k1}e^{-\gamma_{k1}} & -g_{k2}e^{-\gamma_{k2}} & \cdots & m^{q1} - g_{kk}e^{-m\gamma_{kk}} \end{bmatrix} \quad (8).$$

where m^{q1} denotes fractional order poer of time m. $g_{i,j}$ are the connection weights. $\chi_{i,j}$ is the decay rate. $e^{-\chi_{i,j}}$ is the exponential decay funtion, $\gamma_{i,j}$ denotes the decay rates. Thus through F3TDNN, prediction is made at each lysine site. If the resulting activation surpasses a trained threshold, the site is labeled as crotonylated; otherwise, it is non-crotonylated. Next, BEPMT is utilized to refine the predictions.

b. Boundary Enhanced Patch Merge Transformer:

The Boundary Enhanced Patch Merge Transformer (BEPMT) enhances crotonylation site prediction by preserving boundary relevant features during patch merging [16]. It computes spatial affinities using k-nearest neighbors to maintain local structural integrity. This mechanism refines feature maps for accurate classification of crotonylated lysine residues. Eq. (9) governs selection of k-nearest neighbors (KNN) among patches,

$$\vartheta_j = \exp\left(-\frac{1}{D_{y_i \in KNN(y_j)}} \left\| y_j - y_i \right\|_2^2\right), \quad (9).$$

where $KNN_{(y_j)}$ denotes KNN of patch j, y_i and y_j are their corresponding patch features. By eq. (10), feature merging is calculated,

$$x = \sum_{i \in V_j} Soft\max(\vartheta_i \cdot \pi_i) y_i \quad (10).$$

where V_j is the set of the i^{th} cluster, π_i represents the patch importance score, y_i and ϑ_i are the original patch features and the corresponding importance score, respectively. The overall classification objective is governed by the loss function in eq. (11),

$$P_{Total} = \rho_1 P_{semantic} + \rho_2 P_{Boundary} + \rho_3 P_{final} \quad (11).$$

where ρ_1, ρ_2 and ρ_3 are balancing hyper-parameters, P denotes the loss function. Thus, by BEPMT, prediction is enhanced and boundary information is effectively preserved, enabling discrimination between crotonylated and non-crotonylated lysine sites. Then, it follows optimization using SBA, which optimizes the network□s loss function and hyper parameters

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

to boost classification accuracy and ensure robust convergence during crotonylation site prediction.

E. Optimization using Swarm Bipolar Algorithm (SBA):

SBA is used for the optimizing loss and hyper parameters of the network. It is a nature-inspired metaheuristic optimization algorithm that introduces a novel bipolar search strategy [17]. It is inspired by collective intelligence principles found in swarm-based behavior, with a distinctive mechanism of dividing the swarm into two equal sub-swarms, hence the term □bipolar□.

Step 1: Initialization

In SBA, the entire population L is evenly divided into two sub-swarms. The first half is assigned to sub-swarm 1, and the second half to sub-swarm 2. This division is index-based and does not consider spatial positions in the search space. Initial positions $L_{j,i}$ for each individual are generated using a **uniform distribution** within the search space by eq. (12),

$$L_{j,i} = L_{a,i} + s_1\left(L_{y,i} - L_{m,i}\right) \quad (12).$$

where $L_{j,i}$ indicates the value of i^{th} dimension of j^{th} swarm member, $L_{y,i}$ and $L_{m,i}$ are upper and lower bounds of i^{th} dimension. s_1 represents random number which is uniformly distributed. The parameters generated are initialized and randomly generated for each individual in the population.

Step 2: Fitness Function

The fitness evaluation in eq. (13) quantifies the prediction error between actual and predicted crotonylation labels, to optimize loss functions and hyper parameters effectively.

$$FF = Min\left(P + \rho_1 + \rho_2 + \rho_3\right) + Max\left(acc\right) \quad (13).$$

where P represent the loss function and ρ_1 , ρ_2 and ρ_3 are balancing hyper-parameters, $Max\left(acc\right)$ indicates the maximization of accuracy.

Step 3: Exploration Phase

In this phase, both sub-swarms explore different areas of the search space. Individuals update their positions based on a randomized strategy aimed at diversifying the search. The update rule typically includes random coefficients and distance based exploration mechanisms by eq. (14),

$$B_{j,i} = \begin{cases} L_{j,i} + s_1\left(L_{n,i} - s_2 L_{j,i}\right), g(L_n) < g(L_j) \\ L_{j,i} + s_1\left(L_{j,i} - s_2 L_{n,i}\right) \end{cases} \quad (14).$$

where $B_{j,i}$ is the updated value, s_2 is the random number.

Step 4: Exploitation Phase

After exploration, exploitation focuses on intensifying the search around promising solutions. The individuals move toward the best-known solutions as follows using eq. (15),

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

$$B_{j,i} = L_{j,i} + s_1\left(L_{a,i} - s_2 L_{j,i}\right) \quad (15).$$

where $L_{a,i}$ represents the reference value at index (a,i).

Step 5: Termination

SBA terminates when the maximum number of iterations is reached. At this point, the algorithm returns the globally best solution found. Thus, by applying F3TBEPMNN-SBA, the model predicts crotonylation sites with improved accuracy by optimizing loss and hyper parameters.

IV. RESULT

This section describes the evaluation and outcomes of F3TBEPMNN-SBA method□s performance in predicting crotonylation sites on non-histone proteins.

A. Performance Analysis of Proposed Model:

The efficiency of suggested model for crotonylation site prediction on non-histone proteins is assessed using UniProt dataset, with an emphasis on important assessment metrics. Sensitivity, accuracy, F1-score, precision, specificity, and Receiver Operating Characteristic (ROC) curve are all used to evaluate model□s performance in detail. These measures show how well the model can discriminate between crotonylated and non-crotonylated lysine residues, reliably identify crotonylation locations, and maintain steady convergence throughout training.

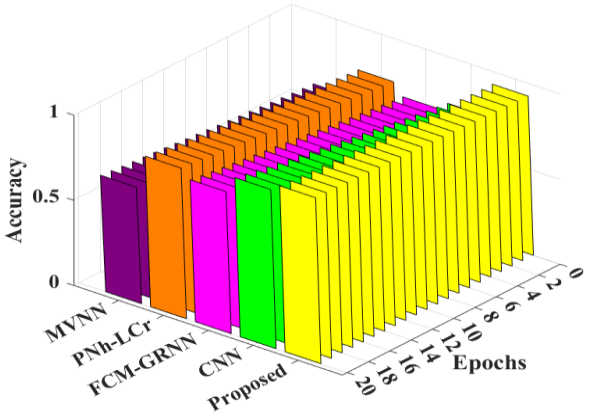

Fig.2. Comparative Accuracy Analysis of Existing and Proposed Models over Epochs

Figure 2 shows that the 3D bar graph demonstrates the accuracy evolution over 20 epochs for different models MVNN, PNh-LCr, FCM-GRNN, CNN, and the proposed method. As all models improve with advancing epochs, the proposed method outperforms others consistently, with maximum accuracy. CNN and FCM-GRNN demonstrate mediocre performance, while MVNN and PNh-LCr are behind. The figure well depicts the higher learning efficiency and prediction accuracy of the proposed model, proving to be efficient and effective in crotonylation site prediction tasks.

Received: August 11 ,2025

International Journal of Applied Mathematics
Volume 38 No. 8s 2025,
ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

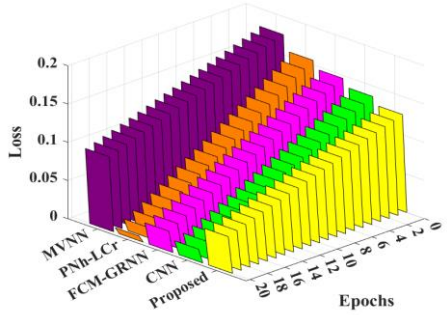

Fig.3. Comparative Loss Analysis of Existing and Proposed Models over Epochs

Figure 3 depicts that the 3D bar graph shows the values of loss through 20 training epochs for five models: MVNN, PNh-LCr, FCM-GRNN, CNN, and Proposed. The depth axis is used to display epochs, and the vertical axis is for loss. The proposed method consistently shows the best loss value among all, resulting in better convergence and training stability. MVNN shows the highest loss across all. The visual comparison verifies that the proposed model performs better than the traditional and hybrid methods in reducing loss during training.

B. Comparative analysis

The key measures employed in judging the performance of the proposed architecture for crotonylation site prediction on non-histone proteins are accuracy, sensitivity, specificity, F1-score, and ROC. Comparative assessment is performed with earlier models like MVNN [8], PNh-LCr [9], FCM-GRNN [10], and CNN [11], utilizing UniProt dataset. A thorough comparison of various approaches is shown in Table 1, which highlights suggested model□s greater predictive power and resilience in detecting lysine crotonylation patterns for improved protein function analysis.

TABLE I. PERFORMANCE COMPARISON OF UNIPROT DATASET

Methods	**Accuracy (%)**	**Sensitivity (%)**	**F1-Score (%)**	**Specificity (%)**	**Precision (%)**
MVNN [8]	83	82	84	86	79
PNh-LCr [9]	86	78	76	76	80
FCM-GRNN [10]	79	82	89	83	86
CNN [11]	85	75	87	81	88
F3TBEPMNN-SBA (proposed)	**99.95**	**99.72**	**99.60**	**99.79**	**99.53**

Table 1 demonstrates how the proposed F3TBEPMNN-SBA model greatly surpasses other methods like MVNN, PNh-LCr, FCM-GRNN, and CNN in predicting crotonylation sites in

Received: August 11 ,2025

ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

non-histone proteins. It produces the highest accuracy (99.95%), sensitivity (99.72%), F1-score (99.60%), specificity (99.79%), and precision (99.53%). This is due to the combination of F3TDNN and BEPMT along with SBA optimization, which provides accurate identification and least false prediction.

V. CONCLUSION

The advanced crotonylation site prediction system proposed here successfully incorporates various cutting-edge methodologies for high-performance prediction. First, data is acquired from the UniProt database and is preprocessed using AMD method in order to rectify inconsistencies and improve quality. Feature extraction is then conducted using an Adaptive Transformer model, preserving high-dimensional contextual patterns. These characteristics are subsequently processed by F3TBEPMNN, a compound architecture that combines the temporal memory of a F3TDNN with increased spatial sensitivity from BEPMT processes. Model parameters are subsequently optimized by SBA, enhancing convergence and prediction. The whole system exhibits better prediction of crotonylation sites in non-histone proteins, providing a useful tool for computational epigenetics. It has the best accuracy (99.95%), sensitivity (99.72%), F1-score (99.60%), specificity (99.79%), and precision (99.53%) and ROC. This performance enhancement is due to the combination of F3TBEPMNN-SBA for accurate detection and low false positives.

REFERENCES

[1] J. Gao, Y. Zhao, C. Chen, and Q. Ning, " MVNN-HNHC:A multi-view neural network for identification of human non-histone crotonylation sites," Anal. Biochem., vol. 687, p. 115426, Apr. 2024. DOI: 10.1016/j.ab.2023.115426

[2] J. Khanal, J. Kandel, H. Tayara, and K. T. Chong, " CapsNh-Kcr: Capsule network-based prediction of lysine crotonylation sites in human non-histone proteins," Comput. Struct. Biotechnol. J., vol. 21, pp. 120□127, Dec. 1 2022. DOI: 10.1016/j.csbj.2022.11.056

[3] Y. Zuo, M. Wan, Y. Shen, X. Wang, W. He, Y. Bi, et al., " ILYCROsite: Identification of lysine crotonylation sites based on FCM-GRNN undersampling technique," Comput. Biol. Chem., vol. 113, p. 108212, Dec. 2024. DOI: 10.1016/j.compbiolchem.2024.108212

[4] Y. H. Yang, S. F. Wu, J. Kong, Y. P. Zhu, J. F. Liu, and J. T. Yang, " Using ATCLSTM-Kcr to predict and generate the human lysine crotonylation database," J. Proteomics, vol. 281, p. 104905, Jun. 15 2023. DOI: 10.1016/j.jprot.2023.104905

[5] Y. Jiang, R. Yan, and X. Wang, " PlantNh-Kcr: A deep learning model for predicting non-histone crotonylation sites in plants," Plant Methods, vol. 20, no. 1, p. 28, Feb. 15 2024. DOI: 10.1186/s13007-024-01157-8

[6] X. Wei, Y. Sha, Y. Zhao, N. He, and L. Li, " DeepKcrot: A deep-learning architecture for general and species-specific lysine crotonylation site prediction," IEEE Access, vol. 9, pp. 49504□49513, 2021. DOI: 10.1109/ACCESS.2021.3068413

Received: August 11 ,2025

ISSN: 1311-1728 (printed version); ISSN: 1314-8060 (on-line version)

[7] Y. Zhang, P. Ji, M. Zhang, N. T. Tran, and S. Li, " Large-scale lysine crotonylation analysis reveals the role of TRAF6-Ecsit complex in endoplasmic reticulum stress in mud crab (Scylla paramamosain)," Dev. Comp. Immunol., vol. 148, p. 104898, Nov. 2023. DOI: 10.1016/j.dci.2023.104898

[8] [8] J. Gao, Y. Zhao, C. Chen, and Q. Ning, "MVNN-HNHC:A multi-view neural network for identification of human non-histone crotonylation sites," Anal. Biochem., vol. 687, p. 115426, Apr. 2024. DOI: 10.1016/j.ab.2023.115426

[9] Y. Jiang, R. Yan, and X. Wang, " PlantNh-Kcr: A deep learning model for predicting non-histone crotonylation sites in plants," Plant Methods, vol. 20, no. 1, p. 28, Feb. 15 2024. DOI: 10.1186/s13007-024-01157-8

[10] Y. Zuo, M. Wan, Y. Shen, X. Wang, W. He, Y. Bi, et al., " ILYCROsite: Identification of lysine crotonylation sites based on FCM-GRNN undersampling technique," Comput. Biol. Chem., vol. 113, p. 108212, Dec. 2024. DOI: 10.1016/j.compbiolchem.2024.108212

[11] L. Dou, Z. Zhang, L. Xu, and Q. Zou, " iKcr_CNN: A novel computational tool for imbalance classification of human nonhistone crotonylation sites based on convolutional neural networks with focal loss," Comput. Struct. Biotechnol. J., vol. 20, pp. 3268□3279, Jun. 16 2022. DOI: 10.1016/j.csbj.2022.06.032

[12] https://www.uniprot.org/.

[13] S. Lee, S. Heo, and S. Lee, " DMESH: A Structure-Preserving Diffusion Model for 3-D Mesh Denoising," IEEE Trans. Neural Netw. Learn. Syst., 2024.

[14] K. Ezukwoke, A. Hoayek, M. Batton-Hubert, X. Boucher, P. Gounet, and J. Adrian, " Big GCVAE: Decision-making with adaptive transformer model for failure root cause analysis in semiconductor industry," J. Intell. Manuf., vol. 36, no. 4, pp. 2423□2438, 2025. DOI: 10.1007/s10845-024-02346-x

[15] C. Xu, Z. Liu, P. Li, J. Yan, and L. Yao, " Bifurcation mechanism for fractional-order three-triangle multi-delayed neural networks," Neural Process. Lett., vol. 55, no. 5, pp. 6125□6151, 2023. DOI: 10.1007/s11063-022-11130-y

[16] Z. Jiang and L. Chen, " Multisemantic level patch merger vision transformer for diagnosis of pneumonia," Comput. Math. Methods Med., vol. 2022, no. 1, p. 7852958, Jun. 21 2022. DOI: 10.1155/2022/7852958

[17] F. R. Yaseen and H. Al-Khazraji, " Optimized Vector Control Using Swarm Bipolar Algorithm for Five-Level PWM Inverter-Fed Three-Phase Induction Motor," International Journal of Robotics & Control Systems, vol. 5, no. 1, pp. 333□347, 2025. DOI: 10.31763/ijrcs.v5i1.1713

Received: August 11 ,2025