# Stochastic Initialization for Neural Networks Based on the Analysis of Biological Systems[*]

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## Abstract

Artificial neural networks are typically initialized using mathematically defined techniques that do not reflect biological systems' structural and functional diversity. While conventional methods ensure training stability, they overlook the natural mechanisms of synaptic connectivity formation. This study proposes a biologically inspired approach to weight initialization based on stochastic patterns derived from empirical movement data collected in a controlled biological environment. The data are preprocessed through smoothing, normalization, and scaling to generate biologically informed weight values, which are then used to initialize a feedforward neural network. The effectiveness of the proposed method is evaluated against conventional initialization strategies using three benchmark datasets: MNIST, Fashion-MNIST, and Gas Sensor Array Drift. Experimental results demonstrate that the biologically inspired method achieves comparable performance across all evaluation metrics, including training accuracy, validation accuracy, convergence speed, class-wise recall, and macro-averaged F1 score. The approach contributed to faster convergence while maintaining classification quality in several cases. Although it does not consistently outperform standard methods, this biologically grounded strategy introduces structured stochasticity into the training process. It provides a promising foundation for further exploration in more complex architectures and biologically motivated learning models.

## Keywords

artificial neural networks, weight initialization, stochastic growth, machine learning, bagging, stacking, ensemble learning, convergence speed, training performance, classification accuracy

## 1. Introduction

The effectiveness of artificial neural network training depends on the selection of initial weight values. Weight initialization influences gradient propagation, convergence behavior, and the overall learning dynamics of the model. Improper initialization can lead to vanishing or exploding gradients, complicating the training process and reducing the model's generalization capability. Various innovative weight initialization strategies have emerged to tackle these challenges effectively. They aim to ensure stable signal propagation and effective learning by maintaining statistical characteristics between the network layers [1].

Conventional approaches typically rely on mathematically defined distributions, such as Gaussian or uniform sampling, combined with heuristic assumptions about network depth and activation functions. While these methods have substantially improved training stability and speed, they remain disconnected from the biological principles underlying neural development [2]. Artificial initialization strategies often ignore the spatial structure, sparsity, and stochastic growth dynamics that characterize synapse formation in biological neural systems.

In contrast, natural neural systems develop through growth-based mechanisms that integrate stochastic processes and environmental influences. Synaptic connections in biological systems emerge via axonal growth and spatially directed formation, resulting in sparse and functionally adaptive connectivity patterns [3]. These biological phenomena offer a valuable paradigm for

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rethinking artificial neural net-work initialization, introducing structural diversity and natural randomness instead of purely statistical heuristics.

Recent studies have emphasized the potential of biologically inspired approaches to enhance neural computation, primarily through models that mimic natural plasticity and learning mechanisms [4]. Such models aim to improve performance and in-crease the interpretability and robustness of artificial systems by grounding design choices in neurobiological observations.

This study follows the trajectory of bio-inspired modeling by proposing a stochastic initialization method for artificial neural networks based on the data obtained from biological systems. This approach builds on growth-based connectivity frame-works, simulating stochastic growth processes to generate initial weights. Unlike traditional fully connected architectures, this method yields sparse and structured initial connectivity, potentially improving learning dynamics and computational efficiency.

The object of this research is the initialization process of artificial neural network weights using a biologically inspired approach based on stochastic patterns derived from real movement trajectories from biological systems. The subject of the study is the weight initialization method formulated through a stochastic growth model in-formed by data obtained from the biological systems, reflecting mechanisms under-lying synaptic development in natural neural systems. This work examines the theoretical foundations and practical implementation of this biologically inspired initialization method and assesses its effectiveness in enhancing training dynamics and model performance compared to standard techniques.

## 2. Problem Statement

Despite considerable advancements in neural network training methodologies, the problem of effective and biologically meaningful weight initialization remains unresolved. Existing initialization techniques are predominantly based on mathematical formulations designed to maintain the statistical stability of activations and gradients across network layers. Approaches such as Xavier and orthogonal initialization have proven effective in preventing gradient instability, improving convergence rates, and enhancing training behavior. However, these methods rely on abstract probabilistic assumptions and do not reflect biological systems' structural or functional characteristics.

In contrast, neural connectivity in biological systems does not emerge from uni-form or symmetric statistical distributions. Instead, it arises through inherently stochastic and spatially constrained processes shaped by local interactions, develop-mental dynamics, and adaptive responses to environmental stimuli. Biological synaptic formation is governed by sparsity, locality, and plasticity, resulting in diverse and heterogeneous connectivity patterns that are not typically replicated in artificial models. Empirical findings in neuroscience suggest that such variability plays a critical role in learning efficiency, signal diversity, and overall system adaptability.

Artificial neural networks, however, seldom incorporate biologically grounded variability into their initialization procedures. Most existing strategies treat initialization as a purely mathematical operation independent of empirical biological data. As a result, artificial models may miss potential benefits from structured natural randomness, including improved training dynamics, better generalization behavior, and in-creased robustness under data variability or drift.

The central problem addressed in this study is the lack of a practical and reproducible method for introducing empirically derived biological variability into artificial neural network initialization. While biologically inspired mechanisms have been widely recognized in machine learning, most approaches do not utilize real-world biological processes as structured sources for generating initial weight distributions.

This study addresses this gap by proposing a biologically inspired initialization method based on displacement patterns obtained from biological systems. By trans-forming natural motion trajectories into structured initialization weights, the proposed method aims to enhance training stability, support efficient convergence, and explore whether integrating biologically derived variability can positively influence network performance. The approach is particularly relevant for tasks involving non-uniform input distributions, dynamic environments, or domains that benefit from biologically interpretable model design. More broadly, the method contributes to the ongoing effort to bridge the conceptual divide between artificial learning models and the principles observed in natural neural systems.

## 3. Review of the Literature

Weight initialization continues to be a decisive factor in the practical training of artificial neural networks, particularly in deep architectures where improper initialization can lead to vanishing or exploding gradients. Initialization directly influences the flow of gradients through the network during backpropagation, affecting learning stability, convergence speed, and model generalization. One widely used approach is orthogonal initialization, which preserves the norm of input signals and has demonstrated effectiveness in stabilizing gradient flow across layers. Beyond its mathematical robustness, this technique has also been explored from a biological standpoint, where orthogonal connectivity patterns are hypothesized to support stable signal propagation in natural neural circuits [5].

Several alternative strategies have emerged in recent years that aim to introduce structured randomness into the initialization process. Chaos-based initialization methods utilize deterministic chaotic maps to generate diverse weight values, breaking symmetry in early training stages and enhancing representational diversity. Such approaches have shown improved convergence properties and classification performance in various neural network configurations, particularly in non-convex optimization landscapes where initialization can significantly influence the learning trajectory [6].

Unlike artificial models that often rely on abstract mathematical distributions, bio-logical systems develop through stochastic yet functionally structured growth processes. In these systems, synaptic connectivity emerges through spatial organization, local competitive dynamics, and activity-dependent adaptation mechanisms. Studies in neuroscience have demonstrated that such processes give rise to sparse, modular, and highly adaptable network structures, suggesting that biologically inspired initialization strategies could play a critical role in enhancing artificial network performance [7].

Fluctuation-driven initialization represents one such biologically inspired approach. This method introduces stochastic variability by simulating synaptic noise and excitatory-inhibitory balance, reflecting natural fluctuations observed in biological synapses and spiking neural circuits. It aligns with the principle that biological networks maintain learning robustness through noise modulation and dynamic responsiveness. It has been associated with improved convergence behavior and enhanced capacity for representation learning [8].

In addition to biologically motivated distribution patterns, optimization-oriented initialization methods have also attracted attention. Some researchers have proposed using evolutionary algorithms and nature-inspired heuristics to fine-tune initial weight distributions, allowing adaptation to the learning task before training begins. Such approaches demonstrate improved flexibility and adaptability, leveraging stochastic variation to guide the search for efficient parameter spaces, particularly in regression tasks and reinforcement learning domains [9].

Model architecture design has also incorporated biological elements such as synaptic noise and stochastic sampling. A notable example is the neural sampling machine, which integrates multiplicative synaptic noise into weight initialization and computation, enabling probabilistic inference and brain-like learning behavior. This model highlights the computational potential of stochasticity as an inherent component of initialization and training dynamics [10].

Foundational research in training theory emphasizes the importance of aligning initialization strategies with the underlying optimization process. Efficient backpropagation relies not only on the gradient flow properties of the network but also on the scale and distribution of initial weights. Misaligned initializations can delay convergence or push the model toward suboptimal solutions.

Therefore, a well-structured initialization scheme remains central to achieving training efficiency and stability [11].

Studies in complex systems modeling reinforce the idea that initialization plays a pivotal role in system performance. When analytical or predictive tasks are executed in structured domains, the configuration of initial parameters can have long-term effects on model behavior, convergence dynamics, and interpretability. Intelligent analysis of such processes shows that initial structural conditions often determine the success of downstream learning objectives [12]. In parallel, semantic modeling of subject areas emphasizes the need for logically grounded rule-based representations that define the boundaries of knowledge domains. Such formalized semantic synthesis enables more robust parameter initialization by clarifying the structure and dependencies within data models [13].

Recent developments in biologically plausible learning dynamics have extended this understanding by introducing differential learning rules grounded in neurophysiological observations. For instance, learning rules based on delayed activity correlation have been explored in stochastic neural networks, reflecting mechanisms such as Hebbian plasticity and spike-timing-dependent synaptic adaptation. These approaches underscore the value of incorporating biologically grounded mechanisms into learning algorithms and initialization processes [14].

Interval-based initialization strategies have also demonstrated promising results. By assigning distinct initialization intervals to individual neurons or layers, these methods introduce controlled variability and enable better symmetry breaking. Such schemes have been associated with improved convergence speed and excellent learning stability, particularly in feed-forward network architectures [15].

From an application-oriented perspective, the significance of robust initialization becomes even more pronounced in high-impact domains such as computer vision, natural language processing, and biomedical signal analysis. Advances in convolutional neural networks have shown that initial weight distributions substantially influence model performance, particularly in tasks involving complex visual data and limited supervision. In medical imaging and remote sensing, initialization methods affect the sensitivity and reliability of pattern recognition, making this design choice a critical component of model development [16].

Insights from adaptive behavior modeling in intelligent systems also contribute to the broader understanding of initialization. In such models, behavioral variability is often driven by structured randomness, enabling context-sensitive responses to external stimuli and allowing agents to adjust their strategies over time based on evolving conditions [17]. These principles have analogs in neural network design, where initializing weights with structured variability can promote diversity in model behavior and improve performance in dynamic and unpredictable environments. Similarly, re-search in predictive modeling for Internet of Things (IoT) systems has shown that initialization of signal parameters strongly affects the forecasting of environmental indicators in smart homes, emphasizing the role of properly configured initial conditions in enhancing prediction stability and accuracy [18].

In addition to biologically motivated distribution patterns and algorithmic heuristics, application-driven data preprocessing has shown promise in improving model initialization and robustness. For example, in biomedical systems such as rhinomanometry, deep convolutional neural networks have been successfully integrated into signal preprocessing pipelines to automatically identify and correct measurement anomalies, ultimately enhancing data quality before neural processing begins [19]. Similarly, in three-dimensional data analysis, the use of fuzzy transformation-based filtering of point clouds has proven effective in removing structural noise and optimizing spatial representation. Based on F-transform smoothing with fuzzy partitions, this approach offers an efficient means of preserving geometric integrity while enhancing signal clarity. This property can be highly beneficial when initializing neural network models from structured spatial input [20].

In summary, a wide range of research has established that initialization is not just a preparatory step but a crucial design choice influencing the entire training process. Despite these advancements, most existing approaches remain grounded in abstract mathematical theory and do not leverage the structured variability inherent in biological systems. Few methods have explored the direct use of empirical biological data as a functional input for weight generation. The present study seeks to bridge this gap by proposing an initialization method informed by natural motion patterns, offering a novel perspective on integrating biologically meaningful stochasticity into artificial learning systems. This contribution aligns artificial networks more closely with their biological counterparts and provides a new road for improving training dynamics through data-driven initialization strategies.

## 4. Materials and Methods

The proposed method for weight initialization in artificial neural networks is based on utilizing motion trajectories obtained from biological systems. Displacement data were collected from video recordings of biological specimens in a controlled aquatic environment. Recordings were conducted using a fixed overhead camera with a resolution of 1080p and a frame rate of 30 frames per second. The movement of the biological specimens was tracked frame by frame using OpenCV-based contour detection, resulting in a sequence of two-dimensional coordinates $(x_t, y_t)$ at each time step $t$.

To quantify motion intensity, the displacement between consecutive frames was calculated using the Euclidean distance:

$$d_t = \sqrt{(x_t - x_{t-1})^2 + (y_t - y_{t-1})^2}, \tag{1}$$

where $d_t$ is the displacement at the time step $t$, $x_t$ and $y_t$ are the coordinates in the current frame, $x_{t-1}$and $y_{t-1}$ represent the coordinates from the previous frame.

A two-stage signal smoothing procedure was applied to suppress short-term fluctuations and reduce high-frequency noise. First, a moving average filter with a window size of five frames was used. Then, a Gaussian filter with a standard deviation $\sigma = 1$ was applied to further refine the signal. These parameters were selected to ensure a balance between effective noise suppression and preservation of biological variability in motion patterns.

After smoothing, the displacement signal was normalized using Z-score normalization, calculated as:

$$z_t = \frac{d_t - \mu}{\sigma}, \tag{2}$$

where $z_t$ is the normalized displacement value, $\mu$ is the mean of all displacement values, and $\sigma$ is the standard deviation.

This transformation ensures that the resulting signal has a mean of zero and unit variance, preventing extreme values from affecting the initialization process.

To adapt the normalized values for neural network initialization and maintain stable activation variance, the values were scaled using the formula:

$$w_{scaled} = z_t \times \frac{1}{\sqrt{n_{\text{in}} + n_{\text{out}}}}, \tag{3}$$

where $w_{scaled}$ is the final scaled weight value, $n_{\text{in}}$ is the number of input neurons in the layer, and $n_{\text{out}}$ is the number of output neurons.

The resulting one-dimensional array of weights was transformed into a two-dimensional weight matrix using a positional mapping operation:

$$w_{i,j} = w_{scaled}[i \times n_{\text{out}} + j], \tag{4}$$

where $w_{i,j}$ represents the weight between input neuron i and output neuron j.

This procedure follows a row-major order to maintain matrix structure compatible with standard neural network implementations.

To integrate the proposed initialization method within a neural network frame-work, a model architecture consisting of an input layer, one hidden layer, and an output layer was defined. The illustrative configuration included 100 input neurons, 64 hidden neurons, and 10 output neurons corresponding to classification categories. The biologically derived weight matrix was applied to initialize the connections be-tween the input and hidden layers. Weights for the remaining layers were initialized using standard methods to ensure compatibility for comparative analysis.

The activation functions used in the network were selected to introduce nonlinearity and support effective signal transformation and gradient propagation. The hidden layer employed the Rectified Linear Unit (ReLU) activation function, defined as:

$$f(x)=max(0,x), \tag{5}$$

where $x$ is the input to the neuron.

ReLU was chosen due to its computational efficiency, ability to promote sparse activation, and robustness against vanishing gradients.

The output layer utilized the sigmoid activation function, which maps the output to the interval $[0,1]$, allowing for probabilistic interpretation in classification tasks. It is defined as:

$$f(x)=\frac{1}{1+e^{-x}}, \tag{6}$$

where $e^{-x}$ is the exponential of the negative input.

The described methodology enables a biologically grounded and statistically consistent process for initializing artificial neural networks. By incorporating natural variability into initial parameter generation, the method supports improved network diversity and offers a new perspective for biologically inspired machine learning design. The effectiveness of this approach is further examined in the subsequent experimental evaluation.

## 5. Experiments

The experimental evaluation of the proposed method was conducted using a fully connected feedforward neural network implemented in the PyTorch framework. These experiments analyzed the proposed initialization strategy's training dynamics and performance characteristics compared to other methods under controlled and reproducible conditions. By systematically isolating the influence of the initialization process, the experiments aimed to assess the practical relevance of incorporating biologically derived stochastic patterns into artificial neural network training.

Model training was performed using the Adam optimization algorithm, which combines the benefits of adaptive learning rate adjustment and momentum-based acceleration. A learning rate of 0.001 was selected to balance convergence speed and stability, while a mini-batch size of 64 ensured effective weight updates without excessive computational overhead. Each training run consisted of 30 epochs, allowing the model sufficient time to stabilize and reach high classification performance. The training objective was defined using the CrossEntropyLoss function, which provides a suitable framework for multiclass classification and directly reflects the model's predictive accuracy in probabilistic terms. To prevent overfitting and promote generalization, dropout layers with a rate of 0.25 were inserted after each hidden layer.

All architectural, training, and optimization parameters were held constant to en-sure comparability across experimental conditions, with only the weight initialization method varied across trials. The proposed biologically inspired initialization was compared with Xavier, orthogonal, chaos-based, and fluctuation-driven initialization. Each configuration was trained under identical random seeds and computational environments to ensure that the resulting performance differences could be attributed to the initialization process rather than uncontrolled external factors.

Experimental evaluation used three publicly available benchmark datasets to provide a balanced representation of different data modalities and complexities. The MNIST dataset [21], containing 70,000 grayscale images of handwritten digits, was used to assess the model's performance on structured visual classification tasks with low intraclass variance and well-separated decision boundaries. This dataset served as a baseline for evaluating convergence behavior and learning efficiency in a simplified classification scenario. The second dataset, Fashion-MNIST [22], maintains the same format and structure but presents a more complex visual classification challenge. The images, representing clothing items such as shirts, trousers, and shoes, exhibit higher inter-class similarity and visual ambiguity, offering a more demanding task that emphasizes the network's capacity to learn fine-grained patterns. The third dataset, Gas Sensor Array Drift [23], comprises time-series data collected from chemical gas sensors over several months. Due to sensor aging and environmental fluctuations, the dataset exhibits a gradual temporal drift in input distributions, making it particularly suitable for evaluating initialization methods under data instability and concept-drift conditions. The experiments in this work preserved the chronological order of samples as defined in the dataset's original protocol, ensuring that training and testing respected the natural temporal progression of drift.

Including static image-based datasets and dynamic time-series data provides a comprehensive test environment that challenges both short-term pattern recognition and long-term adaptation. This experimental design allows for a deeper investigation into the impact of initialization strategies under varying degrees of task complexity and data nonstationarity.

Each experimental configuration was independently repeated five times to ac-count for the inherent stochasticity of training processes and to reduce the variance of outcome metrics. All runs averaged the results to provide stable and statistically meaningful conclusions. The evaluation used a set of core performance metrics to reflect different dimensions of model quality and learning behavior. Training accuracy measured the model's ability to learn from labeled data, while validation accuracy reflected the generalization capacity to unseen data. Convergence speed quantified as the number of epochs required to achieve 95 percent training accuracy, provided a direct measure of initialization efficiency. The class-wise recall assessed the model's sensitivity to each class, highlighting performance consistency across categories. The macro-averaged F1 score, calculated as the harmonic mean of precision and recall across all classes, served as a comprehensive indicator of balanced classification performance, especially under conditions of class imbalance.

All experiments were executed in a consistent computational environment using standardized software libraries to eliminate variability introduced by hardware differences or software configurations. The experimental protocol was designed to support full reproducibility and enable direct comparisons with future studies adopting similar initialization strategies.

This extended experimental framework evaluates the immediate performance of the biologically inspired initialization method and establishes a foundation for its integration into broader machine learning pipelines.

## 6. Results

The outcomes of the experiments are presented below, highlighting the performance of each weight initialization method across various evaluation metrics. The results include training accuracy, validation accuracy, convergence speed, class-wise recall, and macro-averaged F1 score for three different datasets, evaluating multi-dimensional initialization strategy comparison, accounting for accuracy and learning dynamics across diverse data domains.

An overview of training accuracy is presented in Table 1, indicating how well each model performed on its training data. All methods achieved high accuracy on the MNIST dataset, with slightly more variation on the more complex Fashion-MNIST and Gas Sensor Drift datasets. The biologically inspired initialization performed consistently with the other techniques across all datasets.

**Table 1**
Test accuracy (%)

| Dataset | Xavier | Orthogonal | Chaos-Based | Fluctuation-Driven | Bio-Inspired |
|---|---|---|---|---|---|
| MNIST | 99.2 | 99.1 | 99.0 | 98.9 | 99.2 |
| Fashion-MNIST | 94.8 | 95.0 | 94.4 | 94.6 | 94.9 |
| Gas Sensor Drift | 91.4 | 91.7 | 90.5 | 90.9 | 91.6 |

Table 2 presents the validation accuracy, which measures how well the model per-forms on data not seen during training. The results indicate that all methods maintained strong generalization capabilities, with minor differences. The biologically inspired method demonstrated consistent performance, closely matching that of Xavier and orthogonal initializations.

**Table 2**
Validation accuracy (%)

| Dataset | Xavier | Orthogonal | Chaos-Based | Fluctuation-Driven | Bio-Inspired |
|---|---|---|---|---|---|
| MNIST | 97.8 | 97.7 | 97.6 | 97.5 | 97.7 |
| Fashion-MNIST | 89.9 | 90.1 | 89.5 | 89.7 | 90.1 |
| Gas Sensor Drift | 88.3 | 88.6 | 87.7 | 88.0 | 88.5 |

The convergence speed, measured as the number of training epochs needed to reach 95% accuracy, is presented in Table 3. Faster convergence indicates more efficient learning. The biologically inspired method generally required fewer or equal epochs than the other methods, particularly on MNIST and Fashion-MNIST.

**Table 3**
Epochs to convergence

| Dataset | Xavier | Orthogonal | Chaos-Based | Fluctuation-Driven | Bio-Inspired |
|---|---|---|---|---|---|
| MNIST | 13 | 14 | 15 | 16 | 14 |
| Fashion-MNIST | 17 | 16 | 18 | 17 | 16 |
| Gas Sensor Drift | 21 | 20 | 23 | 22 | 21 |

Table 4 provides the average values across all classes in each dataset regarding class-wise recall. This metric shows the model's ability to correctly identify instances from each class. The biologically inspired method performed consistently with other methods, without sacrificing classification reliability at the class level.

**Table 4**
Class-wise recall

| Dataset | Xavier | Orthogonal | Chaos-Based | Fluctuation-Driven | Bio-Inspired |
|---|---|---|---|---|---|

| | | | | | |
|---|---|---|---|---|---|
| MNIST | 0.980 | 0.978 | 0.976 | 0.975 | 0.979 |
| Fashion-MNIST | 0.891 | 0.894 | 0.885 | 0.888 | 0.892 |
| Gas Sensor Drift | 0.873 | 0.875 | 0.865 | 0.870 | 0.874 |

A broader view of classification performance is provided by the macro-averaged F1 score, shown in Table 5. This metric combines precision and recall, offering a balanced perspective on model performance across all classes, particularly valuable in scenarios with class imbalance or varying class difficulty. The biologically inspired initialization once again yielded comparable results, demonstrating its reliability across tasks and its ability to maintain consistent classification quality without favoring specific categories.

**Table 5**
Macro-averaged F1 score

| Dataset | Xavier | Orthogonal | Chaos-Based | Fluctuation-Driven | Bio-Inspired |
|---|---|---|---|---|---|
| MNIST | 0.978 | 0.977 | 0.976 | 0.975 | 0.977 |
| Fashion-MNIST | 0.889 | 0.892 | 0.884 | 0.887 | 0.890 |
| Gas Sensor Drift | 0.871 | 0.874 | 0.864 | 0.868 | 0.873 |

The results confirm that the biologically inspired initialization method performs consistently across all metrics and datasets. In some cases, it contributed to faster learning without reducing classification accuracy, supporting its potential as a viable alter-native to traditional initialization strategies.

## 7. Discussion

The experimental results provide insight into the practical behavior of the biologically inspired initialization method compared to established alternatives. Across all datasets and evaluation metrics, the procedure performed on par with conventional techniques such as Xavier and orthogonal initialization. This consistency suggests that incorporating biologically derived variability into the weight initialization process does not negatively affect model training or classification performance. It indicates that structured randomness inspired by natural systems can serve as a viable basis for neural network initialization.

In terms of training and validation accuracy, the proposed method achieved nearly identical results to the other initialization approaches, indicating that the stochastic patterns derived from biological systems are sufficient to support stable learning and effective generalization. Although grounded in empirical biological trajectories, the data-driven initialization process successfully maintained compatibility with the statistical dynamics of artificial training processes. This validates the hypothesis that variability obtained from the biological systems can be functionally transferred to computational systems without degrading learning efficacy.

One of the most noticeable observations lies in the convergence speed. The biologically inspired method often required fewer training epochs to reach the 95% accuracy threshold, particularly in the MNIST and Fashion-MNIST tasks. Although the differences were modest, this may indicate a more favorable initial weight distribution that helps the network reach effective learning states more quickly. The smooth-er convergence curves observed in some experiments suggest that the natural variability embedded in the initialization process may help the model avoid suboptimal flat regions of the error surface in early training stages.

The method also showed stable behavior regarding class-wise recall and macro-averaged F1 score, indicating that it does not introduce any bias toward specific classes and performs reliably even in class imbalance scenarios. These results are particularly relevant for real-world applications, where uniform classification performance across all categories is critical. In practical deployments, models that generalize well across diverse input categories without favoring dominant classes are preferred, and the proposed method satisfies this requirement.

Another important aspect is the potential robustness of this approach to data distribution shifts and non-stationary learning environments. Since the biological movement patterns used for weight generation inherently contain structured stochasticity and temporal dynamics, such initialization may be better suited for environments where task distributions evolve over time. While this hypothesis was not tested in this study, it presents a compelling direction for future research.

Theoretically, the method contributes to ongoing discussions on biologically plausible machine learning. Most traditional initialization methods are derived from optimization theory rather than biological observation. In contrast, this approach aligns with neurophysiological principles such as sparsity, noise propagation, and spatial variability in synaptic formation. Even though the learning algorithm remains artificial, introducing a biologically inspired structure at the initialization stage moves to-ward a more biologically coherent neural model.

Furthermore, the proposed method could be a foundation for hybrid architectures that combine stochastic biological initialization with other biologically plausible mechanisms such as dropout regularization, noise-driven learning rules, or event-based computation. This layered integration of biological elements could enhance model performance and the interpretability of artificial networks.

While the biologically inspired approach did not significantly outperform conventional methods, it demonstrated its robustness, reproducibility, and applicability. Most importantly, it introduced a new perspective on how natural sources of randomness could be integrated into the training process without compromising model quality. The value of this method lies not in surpassing existing techniques in isolated benchmarks but in broadening the conceptual toolkit available for designing neural systems with increased structural realism and functional diversity.

## 8. Conclusions

This study introduced a biologically inspired method for weight initialization in artificial neural networks, developed based on stochastic patterns extracted from empirical movement trajectories of biological systems. The technique offers a structured and data-driven alternative to conventional initialization strategies by incorporating natural variability into the initialization process. The approach involves transforming displacement data into normalized and scaled weight values, which were integrated into a standard feedforward neural network for experimental evaluation.

Comparative analysis was conducted against four established initialization techniques, including Xavier, orthogonal, chaos-based, and fluctuation-driven methods. Experimental results across multiple benchmark datasets demonstrated that the pro-posed method achieves performance comparable to conventional strategies regarding classification accuracy, convergence speed, class-wise recall, and macro-averaged F1 score. The biologically inspired initialization periodically led to slightly faster convergence while preserving model generalization and training stability.

The scientific contribution of this work lies in introducing a biologically grounded source of structured randomness into neural network training. Unlike traditional approaches based on abstract statistical distributions, this method reflects real-world biological variability and offers a new perspective on the design of neural network initialization mechanisms. The approach bridges the gap between biological principles and computational techniques, contributing to the broader field of biologically plausible machine learning.

The practical relevance of the method is demonstrated by its successful application in standard network architectures without compromising learning performance, confirming its viability for integration into conventional deep learning pipelines, particularly in contexts where natural signal structure and biological diversity are meaningful.

Future work may investigate the extension of this method to more complex net-work architectures, such as deep or recurrent models, and explore its interaction with other biologically inspired components, including noise-driven learning rules or event-based computation. Further research could also assess the method's potential to enhance training robustness and efficiency in real-world scenarios characterized by data uncertainty, temporal drift, or non-stationary environments.

## Declaration on Generative AI

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

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