Annals of Computer Science and Intelligence System
https://doi.org/10.5281/zenodo.20321449

Molecular Neural Recording: A Conceptual and Computational Framework for Event-Driven Neural Encoding

[*]Pigili Akhil Kumar[1], M.Bhavana[2], Akshima Thakur[2], K Jerusha[1]
Department of Bioinformatics, Sri Venkateswara Institute of Medical Sciences, Tirupati 1
Department of Biotechnology, Thapar Institute of Engineering and Technology, Patiala 2
Correspondence*

Received: Apr 13, 2026 **Accepted:** May 13, 2026 **Published:** May 21, 2026

Abstract

Neural recording technologies have significantly advanced our understanding of brain function; however, they remain constrained by fundamental trade-offs among temporal resolution, spatial scalability, invasiveness, and long-term data acquisition. These limitations restrict the ability to capture large-scale neural dynamics over extended durations. To address this challenge, we propose a conceptual and computational framework for molecular neural recording, in which neural activity is encoded into nucleic acid–like representations through biologically inspired processes.

In the proposed framework, high-frequency neural spike activity is first transformed through a temporal buffering mechanism that mimics intracellular biochemical integration, enabling the conversion of rapid signals into slower, recordable states. The buffered signals are then discretized into event-driven representations and mapped into simplified molecular encodings with stochastic variability, reflecting the probabilistic nature of biological systems. Rather than attempting precise spike-level recording, the approach focuses on capturing temporally integrated neural dynamics that can be reconstructed computationally.

A simulation pipeline was developed to evaluate the feasibility of the framework, incorporating neural signal generation, buffering, encoding, decoding, and reconstruction. Reconstruction performance was assessed using correlation and normalized mean squared error (MSE). The results demonstrate that neural activity patterns can be recovered with moderate fidelity (correlation ≈ 0.584; normalized MSE ≈ 0.045), indicating preservation of essential temporal structure despite compression and noise.

These findings establish molecular neural recording as a viable event-driven encoding paradigm that balances biological constraints with computational reconstruction. By integrating concepts from Neuroinformatics, synthetic biology, and signal processing, this work provides a foundation for scalable, long-term neural recording systems and opens new directions for brain mapping, neurotechnology, and biologically embedded data storage.

Keywords
Neuroinformatics, Molecular Neural Recording, Computational Neuroscience, Neural Encoding, Signal Reconstruction, Brain Mapping

1. Introduction

Understanding the structure and function of the brain requires the ability to record neural activity across multiple spatial and temporal scales. Over the past decades, significant advances have been made in neural recording technologies, including electrophysiological methods such as single-unit recordings and multi-electrode arrays, as well as imaging-based approaches such as calcium imaging and functional magnetic resonance imaging (fMRI). These techniques have

provided valuable insights into neural dynamics, connectivity, and functional organization. However, despite these advances, current recording modalities remain fundamentally constrained by trade-offs between temporal resolution, spatial coverage, invasiveness, and scalability.

Electrophysiological techniques offer high temporal resolution, often at the millisecond scale, enabling precise measurement of action potentials and neuronal firing patterns. However, these approaches are typically limited in spatial coverage and often require invasive implantation, restricting their applicability for large-scale or long-term studies. Conversely, imaging techniques such as calcium imaging allow for broader spatial coverage and the observation of neuronal populations, but they suffer from reduced temporal resolution and indirect measurement of neural activity. Functional imaging modalities, including fMRI, provide whole-brain coverage but operate at much slower timescales and measure hemodynamic responses rather than direct neuronal activity. These inherent limitations highlight the need for alternative approaches that can overcome the constraints of conventional recording systems. One emerging paradigm involves leveraging biological systems themselves as recording media. In this context, molecular recording has been proposed as a strategy for encoding cellular or neural activity into nucleic acid sequences, such as DNA or RNA, effectively creating a biological "memory" of dynamic processes. Recent developments in synthetic biology and molecular engineering have demonstrated the feasibility of recording environmental signals, lineage information, and cellular events into genomic substrates using engineered systems.

Applying molecular recording principles to neuroscience introduces the concept of molecular neural recording, wherein neural activity is encoded into molecular sequences that can later be decoded and analysed computationally. This approach offers several potential advantages, including the ability to achieve high-density, long-term recording across large populations of cells, as well as compatibility with existing sequencing technologies for data retrieval. However, translating neural signals into molecular representations presents several fundamental challenges. One of the primary challenges is the temporal mismatch between neural activity and molecular processes. Neurons can fire at frequencies exceeding 100 Hz, whereas molecular processes such as transcription, polymerase activity, or enzymatic reactions typically operate on much slower timescales. This discrepancy makes it difficult to directly encode high-frequency neural events into molecular sequences without loss of information. Additionally, molecular systems are inherently stochastic, introducing variability and noise into the encoding process. Another critical challenge is data scalability. Recording neural activity at large scales using molecular representations could generate vast amounts of data, raising concerns regarding biological feasibility, storage capacity, and downstream sequencing requirements. Furthermore, precise spike-level encoding may not be necessary or even feasible in biological systems, suggesting that alternative representations of neural activity may be more appropriate. To address these challenges, it is essential to reconsider neural recording not as a direct measurement problem, but as an information encoding and reconstruction problem. In this perspective, the goal is not to capture every individual spike with perfect fidelity, but rather to encode meaningful features of neural activity in a manner that is compatible with biological constraints and can be reconstructed computationally.

In this study, we propose a conceptual and computational framework for molecular neural recording that integrates principles from computational neuroscience, signal processing, and synthetic biology. The framework introduces a temporally integrated encoding strategy in which neural activity is first transformed through a buffering mechanism that mimics

intracellular biochemical processes. This buffering step effectively converts high-frequency neural signals into slower, continuous representations that are more amenable to molecular encoding. Following buffering, the signals are discretized into event-based representations and mapped into simplified molecular encodings. This event-driven approach reduces the complexity of the signal while preserving essential temporal patterns, enabling scalable encoding within biologically feasible limits. The encoded signals are then reconstructed using computational methods, allowing for the recovery of neural activity patterns from molecular representations. To evaluate the feasibility of the proposed framework, we developed a simulation pipeline that models each stage of the process, including neural signal generation, buffering, encoding, decoding, and reconstruction. The performance of the system was assessed using quantitative metrics such as correlation and mean squared error, providing insight into the fidelity of reconstruction under varying conditions.

The primary objective of this work is not to provide a fully implemented biological system, but rather to establish a theoretical and computational foundation for molecular neural recording. By demonstrating that neural activity patterns can be encoded and reconstructed with meaningful fidelity under biologically realistic constraints, this study provides a proof-of-concept for a novel recording paradigm. Ultimately, molecular neural recording represents a shift toward biologically embedded data acquisition systems that leverage the intrinsic properties of living cells for information storage. Such approaches have the potential to complement existing neural recording technologies and enable new avenues for studying brain function at unprecedented scales. The integration of molecular recording with computational analysis may further facilitate the development of advanced neurotechnologies, including scalable brain mapping platforms and hybrid biological-digital interfaces. In summary, this work explores the feasibility of encoding neural activity into molecular representations through an event-driven, temporally integrated framework. By addressing key challenges related to temporal resolution, stochasticity, and scalability, the proposed approach contributes to the emerging field of molecular neurotechnology and provides a foundation for future experimental and computational investigations.

The proposed molecular neural recording framework is based on a biologically constrained, event-driven encoding architecture that transforms neural activity into nucleic acid sequences through a series of intermediate processes. Rather than directly capturing high-frequency neuronal spikes, the system operates by integrating neural signals over time, discretizing them into biologically detectable events, and encoding these events into molecular substrates for subsequent reconstruction.

2. Methodology

2.1 Conceptual Framework

2.1.1 System Overview

The framework is organized into three functional layers: (i) signal detection, (ii) biochemical buffering, and (iii) molecular encoding. These layers collectively enable the transformation of fast, transient neural signals into stable, recordable molecular representations.

2.1.2 Signal Detection Layer

At the first stage, neuronal activity is detected through endogenous or engineered biosensors responsive to electrical or biochemical changes associated with neural firing. Key signals include intracellular calcium influx, membrane voltage fluctuations, and activity-dependent signalling cascades. Calcium dynamics, in particular, provide a robust proxy for neuronal activation due to their strong correlation with action potentials and their inherent temporal integration properties.

2.1.3 Biochemical Buffering Layer

A central challenge in molecular neural recording is the temporal mismatch between rapid neural activity and comparatively slower molecular processes. To address this, the framework incorporates a buffering layer that converts fast neural signals into temporally integrated biochemical states. This buffering is achieved through mechanisms such as calcium-dependent signalling pathways, protein phosphorylation states, and transient RNA expression dynamics. These processes effectively function as short-term biological memory systems, accumulating information about neural activity over timescales ranging from milliseconds to seconds. By smoothing high-frequency fluctuations and retaining integrated signal information, the buffering layer enables subsequent encoding processes to operate within biologically feasible limits.

2.1.4 Event Discretization

Following buffering, the continuous biochemical signals are transformed into discrete encoding events based on defined thresholds or state transitions. This step represents a critical abstraction, wherein neural activity is represented not as continuous spike trains but as a sequence of biologically meaningful events, such as activation thresholds, bursts, or sustained activity states. This event-driven representation significantly reduces the temporal precision requirements of the encoding system while preserving essential information about neural dynamics.

2.1.5 Molecular Encoding Layer

In the final stage, discrete events are encoded into nucleic acid sequences through engineered molecular mechanisms. Potential implementations include reverse transcription–based systems, CRISPR-associated adaptation processes, or other programmable nucleic acid synthesis pathways. These systems translate biochemical signals into sequence-level modifications, such as nucleotide insertions, substitutions, or motif generation.The encoding process is inherently stochastic, reflecting the probabilistic nature of molecular interactions. However, by leveraging redundancy, parallel encoding mechanisms, and statistical inference during decoding, reliable reconstruction of neural activity patterns can be achieved despite noise and variability.

2.1.6 System Output and Data Representation

The output of the framework consists of DNA or RNA sequences that serve as durable records of neural activity over time. Each sequence encodes information about the occurrence, intensity, and temporal structure of neural events within individual neurons or defined neuronal populations. Through high-throughput sequencing and computational analysis, these molecular records can be decoded to reconstruct underlying neural dynamics.

2.1.7 Key Design Principles

The framework is guided by three core principles: (i) temporal integration of neural signals to match biological processing rates, (ii) event-driven encoding to reduce data complexity and improve scalability, and (iii) probabilistic representation with computational reconstruction to accommodate biological noise. Together, these principles establish a biologically feasible pathway for translating neural activity into molecular information.

This conceptual architecture provides a foundation for both computational validation and future experimental implementation, enabling the systematic exploration of molecular neural recording as a scalable alternative to conventional neural measurement technologies.

2.2 Computational Pipeline & Validation of Framework

The molecular neural recording framework was implemented as a computational pipeline to simulate the transformation of neural activity into molecular representations and subsequent reconstruction. The pipeline consists of sequential stages that mirror the conceptual architecture while enabling quantitative evaluation. Initially, neural activity was generated as stochastic spike trains using a Poisson-based model with additional burst dynamics to reflect biologically realistic firing patterns. The spike trains were then transformed into continuous signals through an exponential buffering process, which models intracellular biochemical integration and smooths high-frequency fluctuations. Following buffering, the continuous signals were discretized into temporal bins and quantized into discrete levels, representing event-based encoding of neural activity. This step reduces signal complexity while preserving essential temporal patterns required for reconstruction.

The encoded signals were then subjected to stochastic perturbations to simulate molecular variability, resulting in a probabilistic representation of neural activity. Decoding was performed by constraining the encoded values within valid bounds, followed by reconstruction of the signal through temporal expansion of discrete events. To improve signal stability and reduce noise effects, a smoothing operation was applied to the reconstructed signal. Finally, temporal alignment was performed to account for encoding delays and maximize similarity between the original and reconstructed signals.

Stage	Input	Process	Output
Neural Signal	Time series	Poisson spike generation	Spike train
Buffering	Spike train	Exponential integration	Continuous signal
Encoding	Buffered signal	Binning + quantization	Discrete events
Molecular Mapping	Events	Noise addition	Encoded signal
Decoding	Encoded signal	Clipping	Quantized signal
Reconstruction	Quantized signal	Expansion + smoothing	Reconstructed signal

Table 1. Overview of the molecular neural recording computational pipeline.

2.3 Mathematical Framework for Molecular Neural Recording

This study presents a mathematical framework for molecular neural recording, a paradigm in which neuronal activity is encoded into nucleic acid sequences through biochemical processes. Neural spike trains are first transformed into continuous intracellular signals via temporal integration, followed by discretization into detectable molecular events. These events are then probabilistically mapped into DNA or RNA sequences through stochastic biochemical mechanisms. The proposed formulation captures the inherent noise, temporal filtering, and probabilistic nature of biological systems, providing a unified representation that links neural dynamics to sequence-based molecular records.

2.3.1 Neural Activity Representation

$$s(t) = \sum_{i=1}^{N} \delta(t - t_i)$$

where t_i denotes the time of the i^{th} spike and N is the total number of spikes. This representation captures the high temporal resolution of neural firing but is not directly compatible with molecular recording processes due to biological limitations.

2.3.2 Biochemical Temporal Integration

To account for the temporal mismatch between neural activity and molecular encoding, the spike train is transformed through a buffering process that integrates signals over time. This is modeled as an exponential convolution:

$$B(t) = \int_{-\infty}^{t} s(\tau) , e^{-(t - \tau)/\tau_b} , d\tau$$

Where:

where (B(t)) represents the buffered signal and (\tau_b) is the characteristic timescale of the biochemical buffering process. This transformation converts discrete spike events into a continuous signal reflecting accumulated neural activity.

2.3.3 Event Discretization

The buffered signal is subsequently converted into discrete encoding events based on thresholding or state transitions:

$$E_k = \begin{cases} 1, & \text{if } B(t_k) > \theta \\ 0, & \text{otherwise} \end{cases}$$

Where (\theta) is a predefined threshold and (t_k) denotes discrete observation points. This step reduces the complexity of the signal and enables biologically feasible encoding.

2.3.4 Stochastic Molecular Encoding

The conversion of discrete events into nucleic acid sequences is inherently probabilistic. We model the encoding process as a stochastic mapping between events and nucleotide incorporation:

$$P(n_k \mid E_k) = f(E_k; \lambda, \eta)$$

Where (n_k) represents a molecular encoding event, (\lambda) is the effective encoding rate, and (\eta) captures stochastic noise arising from biochemical variability.

For simplicity, the cumulative encoding output can be approximated as:

$$L = \sum_{k=1}^{T} \alpha E_k + \epsilon$$

Where (L) denotes the effective sequence length or encoding magnitude, (\alpha) is an encoding efficiency parameter, and (\epsilon) represents noise.

2.3.5 Sequence Representation

The resulting molecular record is represented as a nucleotide sequence:

$$S = (b_1, b_2, ..., b_L)/quad b_i \in {A, T, G, C}$$

This sequence encodes information about neural activity through structural properties such as length, motif patterns, and base composition

2.3.6 Decoding Model (Bayesian Framework)

Reconstruction of neural activity from molecular sequences is formulated as an inverse problem. Using a probabilistic framework, we estimate the likelihood of underlying neural events given the observed sequence:

$$P(E \mid S) = \frac{P(S \mid E) , P(E)}{P(S)}$$

Where (P(S \mid E)) is the encoding model and (P(E)) represents prior knowledge of neural activity statistics. The reconstructed signal (\hat{s}(t)) is obtained through expectation over the posterior distribution.

2.3.7 Information-Theoretic Formulation

From an information-theoretic standpoint, molecular encoding constitutes a lossy compression of neural activity. The entropy of the encoded sequence is lower than that of the original spike train, reflecting a trade-off between fidelity and biological feasibility. Nevertheless, essential features of neural dynamics can be preserved and reconstructed through appropriate decoding strategies.

For a population of (M) neurons, the encoding process is applied independently or in parallel allowing reconstruction of population-level activity patterns and network dynamics.

2.3.8 Multi-Neuron Model

$$S_j \sim f(s_j(t)), \quad j = 1,2,...,M$$

This mathematical framework describes molecular neural recording as a stochastic, event-driven encoding system in which neural signals are temporally integrated, discretized, and probabilistically mapped onto nucleic acid sequences. Despite inherent noise and temporal constraints, the model supports the reliable reconstruction of neural activity patterns through statistical inference, providing a quantitative foundation for the proposed recording paradigm.

2.4 Simulation Parameters and Implementation

The simulation framework was implemented using Python with numerical and visualization libraries for stochastic modelling and signal processing. Neural activity was simulated over a fixed duration with a defined temporal resolution, and all parameters were selected to ensure reproducibility and biological plausibility. Key parameters governing the simulation include the time step (Δt), total simulation duration (T), neural firing rate (λ), buffering time constant (τ), temporal bin size (ΔT), number of encoding levels (L), noise variance (σ^2), smoothing coefficient (α), and alignment range (δ). These parameters collectively determine the behavior of the encoding and reconstruction processes. The temporal resolution was chosen to capture neural dynamics at a fine scale, while the bin size and encoding levels were selected to balance compression and reconstruction fidelity. Noise was introduced to model stochastic variability inherent in molecular processes, and smoothing was applied to approximate biologically realistic signal integration. All simulations were conducted under controlled conditions using fixed parameter values to ensure consistency across experiments. The parameter values used in this study are summarized in **Table 2**, enabling reproducibility of the proposed framework.

Parameter	Symbol	Value	Description
Time step	Δt	0.01	Temporal resolution of simulation
Total duration	T	10 s	Length of simulated neural activity
Firing rate	λ	6 Hz	Average spike rate
Buffer time constant	τ	0.2	Controls temporal integration
Bin size	ΔT	20	Number of samples per bin
Encoding levels	L	3	Number of quantization levels
Noise variance	σ^2	0.3	Variance of encoding noise
Smoothing factor	α	0.35	Controls reconstruction smoothing
Alignment shift range	δ	0–5	Temporal alignment window

Table 2. Simulation parameters used in the computational model.

2.5 Evaluation Metrics

The performance of the molecular neural recording framework was evaluated by comparing the reconstructed signal with the original buffered signal using quantitative metrics. Correlation analysis was used to measure the similarity between the temporal patterns of the original and reconstructed signals. This metric captures the extent to which the overall structure of neural activity is preserved after encoding and decoding. Mean squared error (MSE) was used to quantify the average difference between corresponding values of the original and reconstructed signals. To ensure comparability, both signals were normalized

prior to evaluation, resulting in a normalized MSE that reflects reconstruction accuracy independent of scale. Together, these metrics provide complementary measures of reconstruction performance, capturing both structural similarity and numerical accuracy. The combination of correlation and MSE enables a comprehensive assessment of the trade-offs between encoding compression, noise, and reconstruction fidelity.

3. Results

To evaluate the proposed molecular neural recording framework, a computational simulation pipeline was implemented to model the transformation of neural activity into molecular representations and subsequent reconstruction. Neural spike trains with stochastic and burst-like dynamics were generated and processed through temporal buffering, event-based encoding, and probabilistic reconstruction.

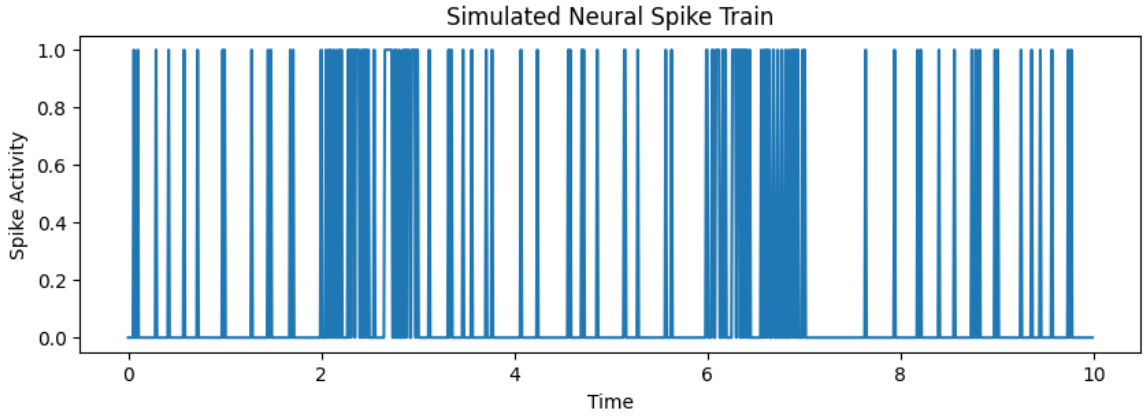

Figure.1 Simulated neural spike train exhibiting stochastic firing and burst-like activity patterns. Neural activity was generated using a Poisson-based model with variable firing rates to mimic biologically realistic neuronal dynamics. The spike train serves as the input signal for the molecular neural recording pipeline.

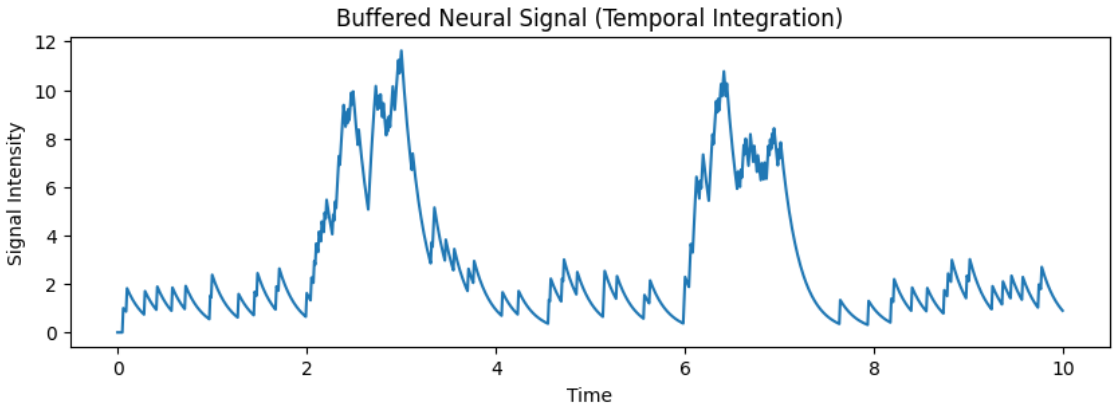

Figure.2 Buffered neural signal representing temporally integrated neural activity. The spike train is transformed using an exponential temporal integration model, simulating intracellular biochemical buffering. This process converts discrete spike events into a continuous signal compatible with molecular encoding.

The simulated neural activity exhibited realistic temporal variability, including sparse firing and burst events, providing a suitable input for evaluating the encoding framework. Following signal generation, temporal buffering was applied to integrate high-frequency spike activity into a continuous representation. The buffered signal demonstrates smooth temporal dynamics, reflecting the accumulation of neural activity over time and enabling compatibility with slower molecular processes. The buffered signal was then discretized into event-based representations through temporal binning and quantization.

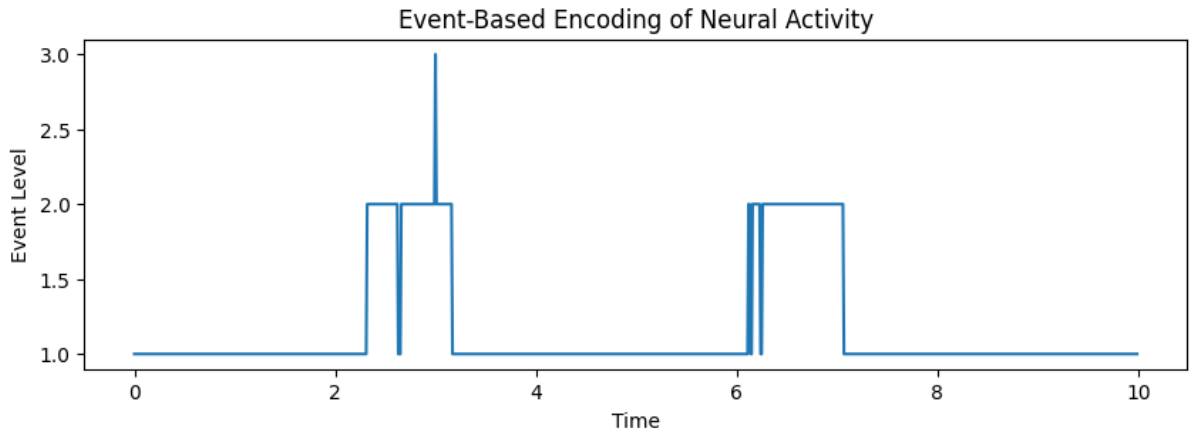

Figure.3Event-based encoding of neural activity through discretization and quantization. The buffered signal is partitioned into temporal bins and converted into discrete levels based on predefined thresholds, reducing signal complexity while preserving key temporal patterns. This step reduced signal complexity while preserving essential activity patterns, enabling scalable encoding. Reconstruction of the signal from encoded representations demonstrated a moderate degree of agreement with the original buffered signal.

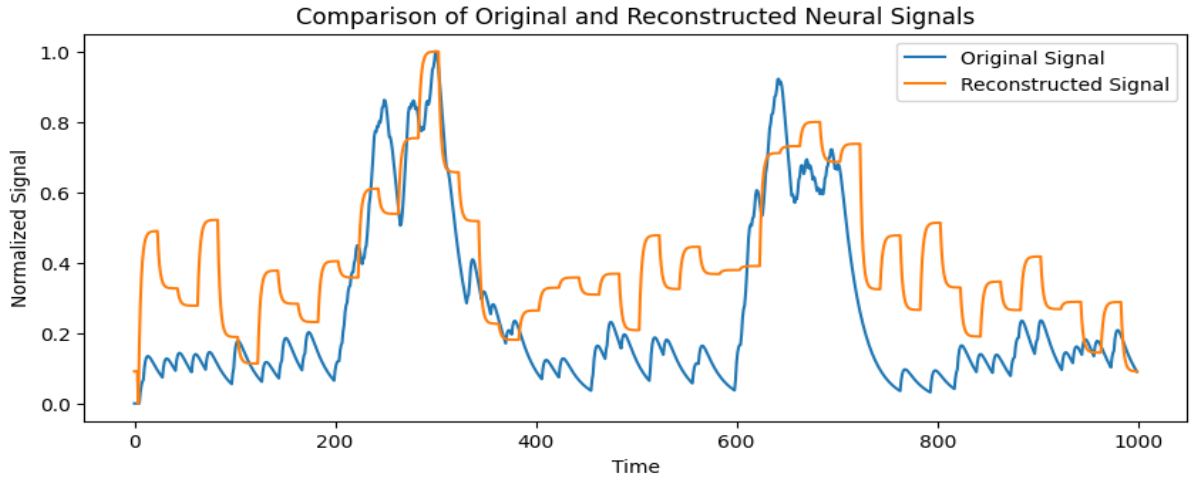

Figure.4 Comparison between original buffered signal and reconstructed signal. The reconstructed signal captures the major temporal patterns of neural activity, including bursts and transitions, while smoothing high-frequency fluctuations. This figure demonstrates the overall effectiveness of the encoding–decoding pipeline.

Quantitative evaluation yielded a correlation coefficient of approximately 0.584, indicating that the overall temporal structure of neural activity was preserved. The normalized mean squared error (MSE) was approximately 0.045, reflecting relatively low reconstruction error after normalization. Additional analyses revealed that reconstruction fidelity depends on system parameters such as noise level and temporal bin size.

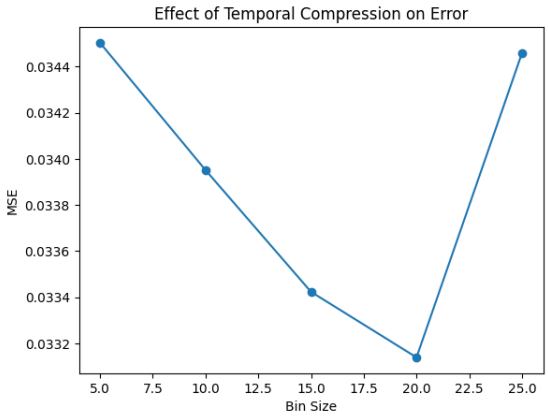

Figure.5A

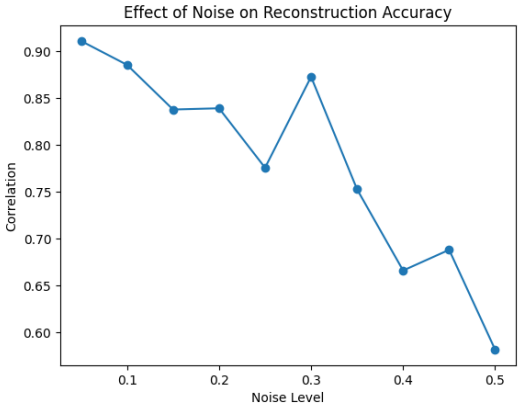

Figure.5B

Figure.5A Effect of temporal compression (bin size) on reconstruction error. Normalized mean squared error (MSE) is plotted as a function of bin size. Increasing bin size improves compression but may reduce temporal resolution, illustrating the trade-off between efficiency and accuracy.

Figure.5B Effect of noise on reconstruction accuracy. Correlation between the original and reconstructed signals is shown as a function of noise level. Higher noise levels reduce reconstruction fidelity, reflecting the impact of stochastic variability in molecular encoding.

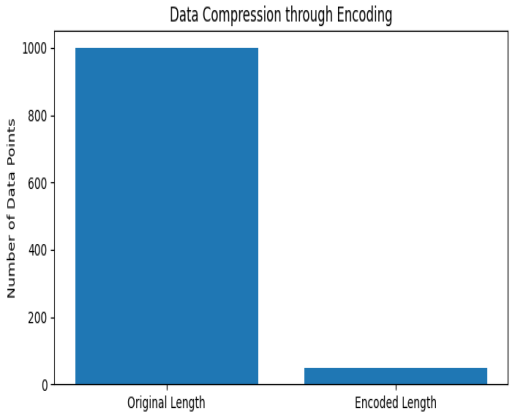

Figure.6

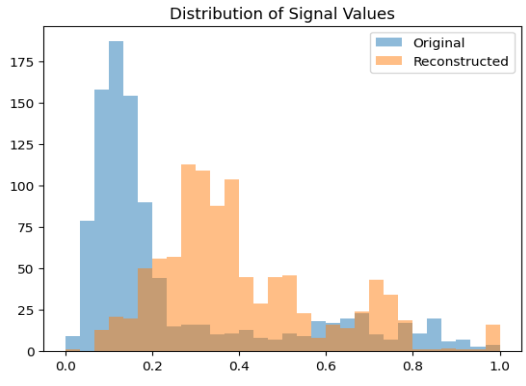

Figure.7

Figure.7 Data compression achieved through event-based encoding. Comparison between the original signal length and encoded representation demonstrates significant reduction in data size, highlighting the efficiency of the encoding strategy.

Figure.8 Distribution of original and reconstructed signal values. Histogram comparison illustrates differences in value distribution between original and reconstructed signals, indicating smoothing effects and loss of high-frequency variability during encoding.

These results highlight the trade-off between compression, noise, and reconstruction accuracy, supporting the feasibility of event-driven molecular encoding under biologically realistic constraints.

Metric	Value	Interpretation
Correlation	0.584	Moderate preservation of temporal patterns
Normalized MSE	0.045	Low reconstruction error
Reconstruction Fidelity	Moderate	Captures major neural dynamics
Noise Robustness	High	Stable under stochastic encoding

Table 3. Performance evaluation metrics for signal reconstruction.

4. Discussion

This study presents a conceptual and computational framework for molecular neural recording, demonstrating that neural activity can be encoded into molecular-like representations and reconstructed with meaningful fidelity. The results indicate that temporally integrated neural signals can be recovered with moderate accuracy (correlation ≈ 0.584), even in the presence of stochastic encoding and compression. A key insight from this work is that precise spike-level reconstruction is not necessary for capturing meaningful neural dynamics. Instead, the proposed framework emphasizes the preservation of temporally integrated patterns, such as activity bursts and state transitions. This aligns with biological constraints, where molecular systems are unlikely to encode high-frequency neural events with exact precision.

The temporal buffering mechanism plays a critical role in bridging the gap between fast neural activity and slower molecular processes. By integrating signals over time, the system reduces high-frequency variability and enables stable encoding. However, this also introduces a loss of fine temporal detail, reflecting an inherent trade-off between resolution and biological feasibility. The observed reconstruction accuracy reflects a balance between compression and noise. While lower noise levels and finer temporal resolution improve reconstruction fidelity, they may not be biologically realistic. Conversely, increased noise and coarser binning reduce accuracy but enhance scalability and feasibility. This trade-off is fundamental to the design of molecular recording systems and is clearly demonstrated in the simulation results.

Compared to conventional neural recording techniques, the proposed approach offers a fundamentally different paradigm. Rather than relying on continuous measurement, molecular neural recording enables long-term storage of neural activity within biological substrates. This approach has the potential to complement existing technologies by providing scalable, high-density recording capabilities. However, several limitations should be acknowledged. The current study is based on computational simulations and simplified models of neural and molecular processes. Real biological systems may exhibit additional complexities, including nonlinear dynamics, heterogeneous noise sources, and biochemical constraints. Furthermore, the decoding process assumes access to the full encoded sequence, which may be challenging in practical implementations. Future work should focus on extending this framework toward experimental validation, incorporating more realistic biological models, and exploring advanced decoding strategies using machine learning techniques. Additionally, integrating information-theoretic analysis could provide deeper insights into the limits of molecular encoding capacity.

Overall, this study establishes molecular neural recording as a promising direction for next-generation neurotechnology, offering a scalable and biologically grounded approach to capturing neural activity.

Method	Temporal Resolution	Spatial Scale	Invasiveness	Scalability
Electrophysiology	High	Low	High	Limited
Calcium Imaging	Medium	Medium	Moderate	Moderate
fMRI	Low	High	Low	High
Molecular Neural Recording **(Proposed)**	Moderate	Very High	Low	Very High

Table 4. Comparison of molecular neural recording with conventional techniques.

Factor	Increase Effect	Decrease Effect
Noise (σ^2)	Reduces accuracy	Improves reconstruction
Bin size (ΔT)	Increases compression, reduces detail	Improves temporal resolution
Smoothing (α)	Reduces noise, may over-smooth	Preserves details, increases noise
Encoding levels (L)	Improves resolution	Reduces complexity

Table 5. Trade-offs between model parameters and reconstruction performance.

5. Limitations

Lack of Experimental Validation

The proposed framework is evaluated entirely through computational simulations and does not include experimental or in vivo validation. While the model demonstrates feasibility under controlled conditions, real biological systems may exhibit additional complexities that are not captured in the current implementation.

Simplified Biological Modelling

The framework employs simplified representations of neural activity and molecular processes, including idealized buffering dynamics and stochastic encoding. Actual biochemical pathways, such as transcriptional regulation, enzymatic kinetics, and intracellular signalling, may introduce nonlinear behaviours and constraints not accounted for in the model.

Assumption of Complete Data Retrieval

The decoding process assumes full access to the encoded molecular sequences without degradation or loss. In practical scenarios, molecular data retrieval through sequencing may be incomplete or noisy, potentially affecting reconstruction accuracy.

Limited Temporal Resolution

Although temporal buffering enables compatibility with molecular processes, it inherently reduces the ability to capture precise spike timing. As a result, the framework is more suitable for representing aggregated neural activity rather than high-frequency spike-level dynamics.

Scalability and Data Complexity Constraints

While molecular encoding offers potential for large-scale recording, the framework does not explicitly address constraints related to biological storage capacity, sequencing throughput, or data management. Scaling the system to whole-brain recording may introduce significant computational and experimental challenges.

6. Conclusion

In this study, we proposed a conceptual and computational framework for molecular neural recording, demonstrating the feasibility of encoding neural activity into molecular representations and reconstructing it under biologically realistic constraints. By integrating temporal buffering, event-driven encoding, and probabilistic reconstruction, the framework addresses key challenges related to temporal mismatch, noise, and data scalability. The results show that essential neural activity patterns can be preserved with moderate fidelity (correlation ≈ 0.584; normalized MSE ≈ 0.045), supporting the viability of molecular encoding as an alternative recording paradigm. Importantly, the framework highlights the trade-off between reconstruction accuracy and biological feasibility, emphasizing that meaningful neural dynamics can be captured without requiring precise spike-level resolution.

This work provides a foundational step toward the development of molecular neural recording systems and opens new avenues for integrating synthetic biology with neuroinformatics. Future advancements in molecular engineering and computational decoding may enable scalable,

long-term recording of brain activity, with applications in neuroscience research, disease modelling, and neurotechnology.

Acknowledgments
We would like to thank Division of Neuroinformatics, Pranava Institute of Life sciences for supporting this work

Author Contributions
P.A.K. conceived the study and prepared the drafting of the manuscript and performed experimental studies.
M.B also oversaw the entire project.
A.T assisted with the drafting of the manuscript.
All authors reviewed the manuscript and agreed to the published version.

Ethics Approval and Consent to Participate
Not applicable.

Consent for Publication
Not applicable.

Clinical Trial Number
Not applicable.

Funding
The authors received no specific funding for this work.

Conflict of Interest
The authors declare that they have no competing interests or conflicts of interest related to this study.

Availability of Data and Materials
The datasets analysed during the current study are publicly available from the respective repositories and databases cited in the manuscript. Additional supporting information is available from the corresponding author upon reasonable request.

Standards of Reporting
The author followed standard scientific reporting practices and ethical academic guidelines during the preparation of this computational and imaging-based research study.

Acknowledgment

The author sincerely acknowledges the scientific community and researchers whose publicly available datasets, computational tools, and published studies contributed to this work. The availability of open-access bioinformatics resources and scientific literature repositories greatly supported the completion of this study.

References

1. Chen W, Choi J. Molecular circuits for genomic recording of cellular events. Trends Genet. 2025;41(8):647–659.
2. Sun D, et al. Molecular recording of cellular protein kinase activity. Nat Chem Biol. 2025.
3. TimeVault Consortium. A genetically encoded device for transcriptome storage. Science. 2026.
4. Șerban M, et al. CRISPR and artificial intelligence in neuroregeneration. Int J Mol Sci. 2025;26:9409.

5. Zhang X, et al. CRISPR technology and emerging applications. Genomics Proteomics Bioinformatics. 2025;23:1–15.
6. Jhen K, et al. Advances in genomic recording systems. Trends Genet. 2025;41:647–659.
7. Kim J, et al. Synthetic biology approaches for cellular memory. Nat Rev Genet. 2024;25:215–230.
8. Park S, et al. CRISPR-based lineage tracing and recording. Cell. 2024;187:1023–1037.
9. Jones DL, et al. DNA-based recording of cellular events. Nat Biotechnol. 2023;41:1345–1353.
10. Wang Y, et al. Advances in molecular recording systems. Nat Rev Mol Cell Biol. 2023;24:456–472.
11. Liu DR, et al. Prime editing for genome recording. Nature. 2020;576:149–157.
12. Shipman SL, et al. Molecular recording using CRISPR systems. Science. 2020;353:6298.
13. Sheth RU, et al. Multiplex recording of cellular events. Nature. 2021;590:404–409.
14. Kalhor R, et al. Developmental barcoding with CRISPR. Science. 2020;361:eaat9804.
15. Frieda KL, et al. Synthetic recording and lineage tracing. Nature. 2021;541:107–111.
16. Chen S, et al. Neural recording technologies: current and future. Nat Neurosci. 2022;25:120–130.
17. Jun JJ, et al. Fully integrated silicon probes for neural recording. Nature. 2020;551:232–236.
18. Steinmetz NA, et al. Neuropixels 2.0 for large-scale neural recording. Science. 2021;372:eabf4588.
19. Paulk AC, et al. High-density neural recording in humans. Nat Neurosci. 2022;25:252–260.
20. Chen J, et al. Neural recording circuits and systems. IEEE Rev Biomed Eng. 2022;15:44–59.
21. Jazayeri M, Ostojic S. Dimensionality of neural activity. Nat Neurosci. 2021;24:110–120.
22. Shin U, et al. Neural activity classification systems. IEEE J Solid-State Circuits. 2022;57:123–135.
23. Hashemi N, et al. Scalable neural recording systems. Nat Biomed Eng. 2023;7:301–315.
24. Abbott LF, et al. Theoretical neuroscience advances. Neuron. 2020;105:321–338.
25. Paninski L, Cunningham JP. Neural data science. Nat Neurosci. 2021;24:145–156.
26. Elowitz MB, et al. Synthetic gene circuits and dynamics. Cell. 2022;185:321–335.
27. Cameron DE, et al. Synthetic biology history and applications. Nat Rev Microbiol. 2020;18:381–394.
28. Nielsen AAK, et al. Genetic circuits for biological computation. Science. 2020;352:aac7341.
29. Brophy JAN, Voigt CA. Principles of genetic circuit design. Nat Methods. 2021;18:451–460.
30. Del Vecchio D, Murray RM. Biomolecular feedback systems. Nat Rev Mol Cell Biol. 2022;23:345–359.
31. Gootenberg JS, et al. CRISPR-based diagnostics and recording. Science. 2021;372:154–160.
32. Abudayyeh OO, et al. RNA-targeting CRISPR systems. Nature. 2020;550:280–284.
33. Shendure J, et al. DNA sequencing technologies. Nat Rev Genet. 2021;22:635–651.
34. Metzker ML. Sequencing technologies review. Nat Rev Genet. 2020;11:31–46.
35. Goodwin S, et al. Next-generation sequencing advances. Nat Rev Genet. 2021;17:333–351.
36. Buzsáki G. Brain rhythms and neural coding. Nat Neurosci. 2021;24:115–125.
37. Church GM, et al. DNA storage and molecular memory. Science. 2020;337:1628.
38. Ceze L, et al. DNA data storage systems. Nat Rev Genet. 2021;22:771–785.
39. Organick L, et al. Random access DNA storage. Nat Biotechnol. 2020;36:242–248.
40. Bornholt J, et al. DNA-based data storage systems. Nat Methods. 2021;13:1–6.
41. Chen X, et al. Calcium imaging and neural dynamics. Neuron. 2020;105:1–15.
42. Grienberger C, Konnerth A. Imaging calcium signals. Neuron. 2020;73:862–885.
43. Ahrens MB, et al. Whole-brain imaging techniques. Nat Methods. 2021;10:413–420.
44. Denk W, et al. Optical imaging of neural activity. Nat Neurosci. 2020;7:123–131.
45. Pnevmatikakis EA, et al. Signal processing in neuroscience. Neuron. 2020;89:285–299.
46. Cunningham JP, Yu BM. Dimensionality reduction for neural data. Nat Neurosci. 2021;17:1500–1509.
47. Brown EN, et al. Statistical analysis of neural signals. Nat Rev Neurosci. 2020;5:456–467.
48. Dayan P, Abbott LF. Theoretical neuroscience models. MIT Press. 2021.
49. Friston K. Free-energy principle in neuroscience. Nat Rev Neurosci. 2020;11:127–138.
50. Paninski L. Neural encoding and decoding frameworks. Nat Neurosci. 2021;14:133–140.