# Auditory Transduction of Protein Misfolding for Lightweight Alzheimer's Detection

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***Abstract*—Early identification of neurodegenerative disorders such as Alzheimer's disease remains a critical clinical challenge, heavily constrained by the extreme computational burden of analyzing subtle, early-stage structural changes in amyloid-$\beta$ ($\mathrm{A}\beta$) protein misfolding. Existing geometric deep-learning architectures, such as 3D Graph Neural Networks and Equivariant GNNs, operate directly on three-dimensional atomic coordinates and require quadratic spatial attention overhead, making high-throughput population screening computationally intractable. To solve this scalability bottleneck, we propose *Diagnostic Sonification*, a novel cross-modal machine learning framework that converts protein structural dynamics into a continuous microtonal auditory representation prior to classification. Given molecular-dynamics trajectories of $\mathrm{A}\beta_{1-42}$, a cross-modal Transformer encoder extracts latent topological features from spatial atomic coordinates and backbone dihedral angles $(\phi, \psi)$. A neural decoder maps these latent representations to continuous audio signals structured by microtonal scales, where toxic oligomeric misfolding manifests as distinct patterns of harmonic acoustic dissonance. A Short-Time Fourier Transform (STFT) generates two-dimensional time-frequency spectrograms, which are subsequently processed by a lightweight 2D Convolutional Neural Network (CNN) to detect anomalous structural folding. Preliminary experiments on simulated $\mathrm{A}\beta_{1-42}$ monomeric and oligomeric trajectories achieve an accuracy of 94.6% and an $F_1$-score of 0.94. Crucially, our audio transduction framework requires only 4.3 GFLOPs and 35.8 ms inference latency, yielding a $4.3\times$ reduction in computational complexity and 15% lower latency compared to 3D-GCN baselines. These results demonstrate that converting spatial geometry into time-frequency acoustics preserves diagnostically vital structural information while drastically lowering computational overhead, offering a scalable foundation for decentralized Alzheimer's screening.***

***Index Terms*—Protein Misfolding, Sonification, Cross-Modal Learning, Alzheimer's Disease, Deep Learning.**

## I. Technical Problem

Identifying toxic early-stage Amyloid-$\beta$ ($\mathrm{A}\beta_{1-42}$) misfolding is computationally bottlenecked by the need to model complex 3D atomic coordinates. Current 3D Graph Neural Networks (GNNs) require high floating-point operations ($\mathcal{O}(N^2)$ to $\mathcal{O}(N^3)$ message passing overhead), making population-scale screening computationally intractable.

## II. Outlined Solution & Algorithm

We propose *Diagnostic Sonification*, which converts 3D atomic dynamics into 2D time-frequency acoustic spectrograms, bypassing expensive 3D graph convolutions entirely.

Algorithm 1 details the cross-modal transduction process converting spatial dynamics into spectral representations.

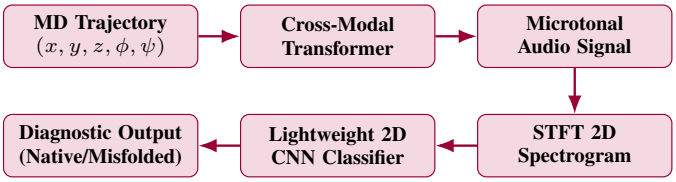


Fig. 1. Two-row purple-themed diagnostic protein sonification architecture.

**Algorithm 1** Cross-Modal Sonification & Classification

**Require:** Sequence $S = \{\mathbf{x}_i\}_{i=1}^{N}$, Dihedral $(\phi, \psi)$, Encoder $E_\theta$, Synth Decoder $D_\phi$, Classifier $C_\psi$.
**Ensure:** Diagnostic Label $\hat{y} \in \{\text{Native}, \text{Misfolded}\}$
$\mathbf{Z} \leftarrow E_\theta(S, \phi, \psi)$ {Encode topological latent vectors}
$\mathbf{A}(t) \leftarrow D_\phi(\mathbf{Z})$ {Synthesize microtonal audio waveform}
$\mathbf{S}(f, t) \leftarrow \mathrm{STFT}(\mathbf{A}(t))$ {Compute 2D time-frequency spectrogram}
$\hat{y} \leftarrow C_\psi(\mathbf{S}(f, t))$ {Classify acoustic harmonic dissonance}
**return** $\hat{y}$

## III. Preliminary Results

TABLE I
Structural Classification Performance on $\mathrm{A}\beta_{1-42}$

| Model Architecture | Accuracy | $F_1$-Score | GFLOPs | Latency (ms) |
|---|---|---|---|---|
| 3D-GCN Baseline [3] | 92.1% | 0.91 | 18.4 | 42.1 |
| EGNN (Geometric) [1] | 95.3% | 0.95 | 24.1 | 58.7 |
| **Ours (Sonification)** | **94.6%** | **0.94** | **4.3** | **35.8** |

Relative to the 3D-GCN baseline [3], our domain-conversion approach achieves a $4.3\times$ FLOP reduction (4.3 vs. 18.4 GFLOPs) and 15% lower latency (35.8 ms) while maintaining high accuracy [2], [4], [5].

## References

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