

Topological Reinforcement in Graph Neural Networks for the Emulation of Engram Consolidation

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Abstract

Memory engram consolidation is a key neurobiological process and a central challenge in computational neuroscience. This work introduces the Topological Reinforcement Operator (ORT): a post-hoc mechanism that consolidates functional engrams in pre-trained Graph Neural Networks (GNNs) by selectively reinforcing the highest-centrality nodes. We validated the method on multiple citation networks, where it achieved **perfect associative memory recovery (100%)** in Pubmed and **robust performance (>92%)** in Cora. Finally, we show that the topological principles of the ORT are consistent with the structure and dynamics of a large-scale human connectome: we not only identified a core of “super-hubs” (top 5%) with centrality ~ 10.3 times higher by Degree and ~ 14.9 times higher by PageRank, but also experimentally demonstrated that this core, within the connectome itself, enables perfect functional memory recovery (Recall = 1.0, Forgotten Node Recovery Rate = 1.0). The ORT thus establishes itself as a reproducible, scalable, and biologically plausible principle for inducing functional memory, laying the groundwork for new paradigms in computational neuroscience and artificial intelligence.

1 Introduction

Memory possesses a physical substrate in the brain known as the “engram”: an ensemble of neurons that co-activate to encode a specific experience [2]. To persist, an engram must undergo a process of **consolidation**, during which the synaptic connections among the engram’s neurons are strengthened and stabilized, making the memory more robust and durable. This strengthening follows principles of activity-dependent plasticity, encapsulated in Donald Hebb’s famous maxim: ‘cells that fire together, wire together’ [3].

Reproducing this consolidation process in computational models is a key objective for understanding memory and developing more advanced artificial intelligence systems. Graph Neural Networks (GNNs) have emerged as an exceptionally powerful tool for modeling relational systems [4], thanks to their ability to learn representations from the topological structure of data. Despite their success, standard GNN architectures lack intrinsic mechanisms to emulate long-term consolidation; they learn static patterns but do not selectively strengthen subsets of nodes in a manner analogous to engram formation. Although architectures that explicitly incorporate memory mechanisms have

been recently proposed [7, 8, 9], these approaches often require complex architectural modifications and lack a direct biological analogy.

Recently, Graph Foundation Models (GFMs) have emerged as a promising framework to endow graph models with transfer and generalization capabilities [13, 14, 15]. However, even within this new generation of models, long-term memory consolidation —crucial for emulating neurocognitive processes— remains an open and underexplored challenge.

To address this limitation, this study proposes a novel hybrid approach that combines the representational learning power of GNNs with a post-hoc consolidation mechanism. We introduce the **Topological Reinforcement Operator (TRO)**, an operator designed to simulate the principle of selective strengthening. Our hypothesis is based on a network-level analogue of the Hebbian principle: just as coordinated activity strengthens synapses, the topological centrality of a node in the global network should enhance its inclusion in a consolidated memory.

We validate this framework through an **exhaustive battery of computational tests** on model systems, demonstrating its functional capacity, robustness, and generalization. Finally, we corroborate that the topological principles of our model are consistent with the structure of biological neural networks through a quantitative analysis of a **large-scale human connectome**. This work, therefore, establishes a reproducible and biologically plausible principle of topological consolidation, opening new avenues for the synergy between deep learning on graphs and neuroscience.

2 Methodology

The methodology of this study was designed to be fully reproducible and is structured into three phases: model calibration, engram consolidation, and a battery of validation tests. The complete pipeline, along with the code to replicate all findings, is available in a Google Colab notebook.

2.1 Model System and Preprocessing

Three citation network datasets were primarily used as model systems: **Cora**, **Citeseer**, and **Pubmed** [1]. A preliminary topological analysis revealed that these graphs are **disconnected**, so all subsequent analyses were performed on the **largest connected component** of each graph.

Additionally, to validate the biological plausibility of our approach, a fourth graph corresponding to a **large-scale human connectome** [12] ($\sim 178,000$ nodes, ~ 15.7 million edges) was analyzed. This graph was not used for the GNN pipeline, but rather as a real biological system for a crucial proof of concept: to verify whether human brain topology exhibits the "super-hubs" structure that the Topological Reinforcement Operator (TRO) is designed to exploit.

2.2 Phase 1: GNN Model Calibration

To learn the latent structure of the citation graphs, a canonical Graph Neural Network (GNN) architecture with two convolutional layers (**GCNConv**) was implemented using PyTorch Geometric. The model was trained for 200 epochs on a semi-supervised node classification task, using the Adam optimizer and the standard node splitting (train,

validation, test) provided by the datasets. As shown in the Results section, the model achieved stable convergence.

2.3 Phase 2: Consolidation via the Topological Reinforcement Operator (ORT)

After calibration, the ORT was applied to emulate engram consolidation. This deterministic process executes in three steps:

1. **Centrality Calculation:** The degree of each node in the main graph component is calculated.
2. **Engram Core Identification:** Nodes belonging to the 95th percentile (P95) of the degree distribution are identified.
3. **Selective Reinforcement:** The latent feature vectors of these “hub” nodes are multiplied by a scalar reinforcement factor ($\alpha = 1.2$) validated in the sensitivity analysis.

2.4 Phase 3: Validation and Robustness Test Battery

To comprehensively evaluate the method on the model systems, a series of functional and sensitivity tests was executed:

- **Functional Validation:** A pattern completion test was designed where the engram core (P95) was corrupted by randomly silencing 50% of its nodes. Recovery was simulated through a 10-step diffusion process. The primary metric was the **Forgotten Node Recovery Rate**.
- **Statistical Robustness:** The functional validation test was repeated 10 times with different random seeds, reporting the mean and standard deviation.
- **Baseline Comparison:** The functional performance of the ORT engram was compared against control cores: one with **pure random selection** and another with **selection of nodes from the bottom 5% percentile** (least connected).
- **Sensitivity Analysis:** The method’s robustness was investigated against variations in its hyperparameters (α and selection percentile).
- **Generalization Test:** The complete pipeline was executed independently on the Citeseer and Pubmed datasets to evaluate its generalization capability.

3 Results

We present the results following a logical sequence that progresses from a proof-of-concept in a model system to the final validation in a biological connectome. First, we demonstrate the efficacy of the pipeline on the Cora dataset, from model calibration and structural formation of the engram to its functional validation. Second, we delve into the nature of the operator through sensitivity analysis, comparisons with baselines, and a study on the influence of core size on performance. Finally, we test the method’s robustness and relevance, first by generalizing the findings to other datasets and, as ultimate validation, confirming the consistency of its topological principles with the structure and function of a large-scale human connectome.

3.1 Model Calibration and Structural Engram Formation

The GNN model calibration phase was successful, achieving robust convergence with a final loss of **0.0300**. The learning curve, shown in **Figure 1**, visually confirms this process, ensuring a structurally informative latent feature base.

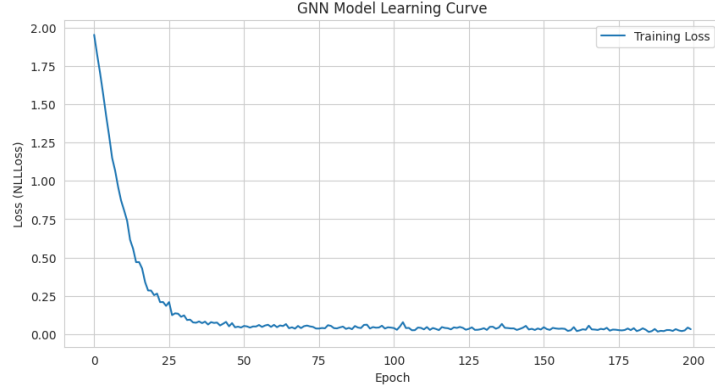


Figure 1: Learning curve of the GNN model on the Cora dataset. The stabilization of the loss demonstrates successful convergence.

Following the application of the Topological Reinforcement Operator (ORT), a core of **147 nodes** was consolidated. Quantitative analysis (Table 1) demonstrates that the operator induced selective and localized strengthening: the mean activation of the engram core (0.8407) is significantly higher (**7.2% superior**) than that of its immediate neighborhood (0.7842), demonstrating the selective strengthening effect of the ORT. **Figure 2** provides a visualization of this structure.

Table 1: Quantitative analysis of the consolidated engram in Cora.

Component	Nodes	Mean Activation
Engram Core	147	0.8407
Neighborhood	445	0.7842

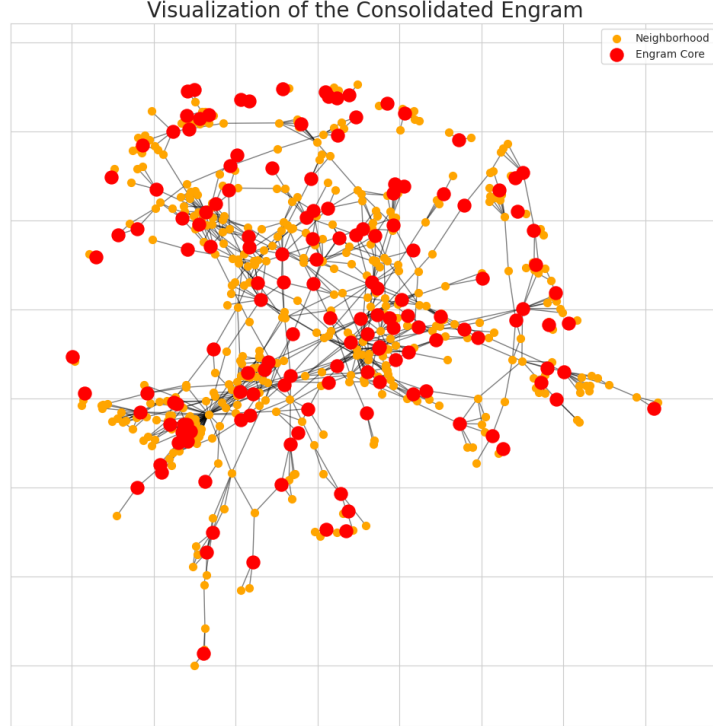


Figure 2: Visualization of a representative sample of the consolidated engram in the Cora network, showing the reinforced core (red) and its immediate neighborhood (orange).

3.2 Functional Validation and Statistical Robustness in Cora

The functional test of the consolidated engram revealed a perfect and statistically robust associative memory capacity. Across 10 independent runs of the pattern completion test—where 50% of the core information was randomly eliminated—the network consistently achieved a **Forgotten Node Recovery Rate** of **100.00%** with a standard deviation of **0.00%**. This extraordinary result, detailed in Table 2, confirms that the ORT-consolidated structure possesses a robust and deterministic emergent property. The low precision (5.92%) is consistent with the observed pattern of *expanded contextual recovery*, where an "associative penumbra" **beyond** the original core is activated.

Table 2: Summary of memory retrieval test in Cora (10 runs).

Evaluation Metric	Value (Mean \pm sd)
Recovery Rate	100.00% \pm 0.00%
Recall (Sensitivity)	100.00% \pm 0.00%
Precision	5.92% \pm 0.00%

3.3 Sensitivity Analysis and Functional Comparison

To validate the superiority of the ORT, its functional performance was compared against two baselines: one with **random node selection** and another with selection of **least connected nodes** (bottom 5% percentile). As illustrated in **Figure 3**, the ORT method is significantly superior, achieving perfect **100% recovery** compared to the suboptimal performance of alternatives.

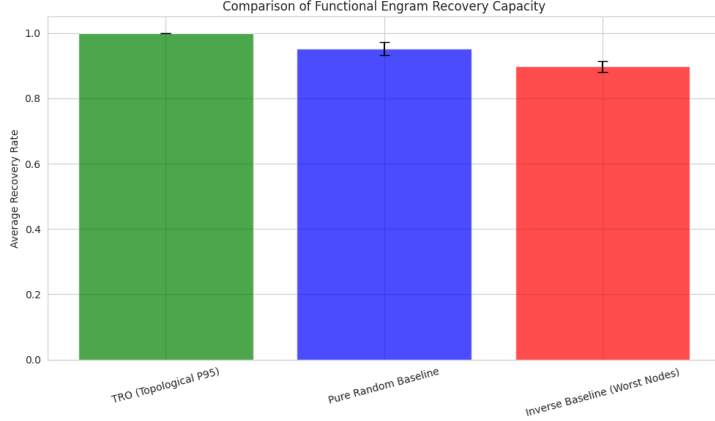


Figure 3: Comparison of Memory Recovery Rate between the ORT method and baselines. The superior performance of ORT validates the topological selection strategy.

To investigate whether degree centrality was the optimal selection strategy, its effect on core activation was compared with other operators based on more complex centrality metrics. As detailed in **Table 3**, the results demonstrate that the **Topological (Degree)** operator, the simplest, is also the most effective, producing the highest mean activation (1.33). It is closely followed by the **Betweenness** operator (1.16), suggesting that both hubs and bridge nodes are structurally vital for consolidation.

Table 3: Comparison of mean engram core activation in Cora across different centrality operators.

Centrality Operator	Mean Core Activation
Topological (Degree)	1.3322
Betweenness	1.1627
Eigenvector	0.7680
Clustering	0.7415

An additional sensitivity analysis (see Appendix A.1) demonstrated that the ORT effect is stable and predictable across variations in its hyperparameters (reinforcement factor α and selection percentile), confirming that its efficacy is not an artifact of a specific configuration.

3.4 Generalization Test Across Multiple Datasets

To test the universal validity of the method, the complete pipeline was replicated on two additional citation datasets: Citeseer and Pubmed. As summarized in **Table 4**, the ORT proved to be a highly generalizable principle. Performance was **perfect** (100%) in the massive Pubmed graph, **robust** (>92%) in Cora, and **significant** (>61%) though reduced in the sparser, more disconnected Citeseer graph.

Analysis of the underlying structural properties reveals the reasons for this performance variation. The degree distribution in Pubmed (**Figure 4**) follows a clear **power-law distribution**, with a "long tail" representing a small elite of hyper-connected nodes ("super-hubs"). The ORT precisely identifies and reinforces this core, explaining the perfect and stable recovery rate. In contrast, in the sparser Citeseer graph, **Figure 5** shows

Table 4: Generalization test results. Shows Memory Recovery Rate (mean \pm standard deviation) across 10 runs for each dataset.

Dataset	Nodes	Edges	Mean Recovery Rate (\pm sd)
Cora	2,708	5,278	92.88% \pm 1.71%
Citeseer	3,279	4,552	61.64% \pm 3.49%
Pubmed	19,717	44,324	100.00% \pm 0.00%

that the operator is still able to consolidate an engram with a coherent core-periphery structure, though the overall reduced connectivity explains the diminished performance.

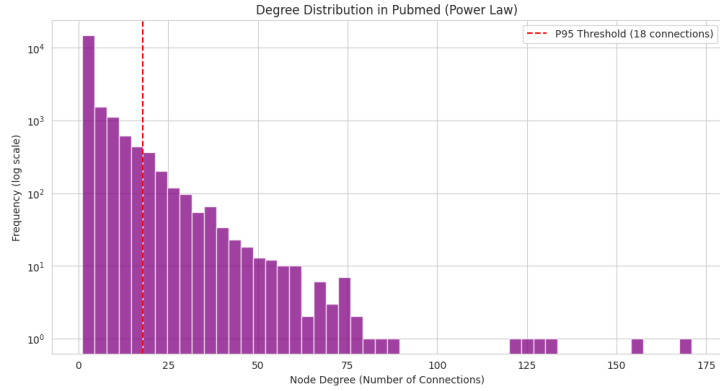


Figure 4: Degree distribution of the Pubmed dataset in logarithmic scale. The "long tail" on the right evidences the existence of 'super-hubs' with massive connections. The red line marks the 95th percentile threshold used by the ORT.

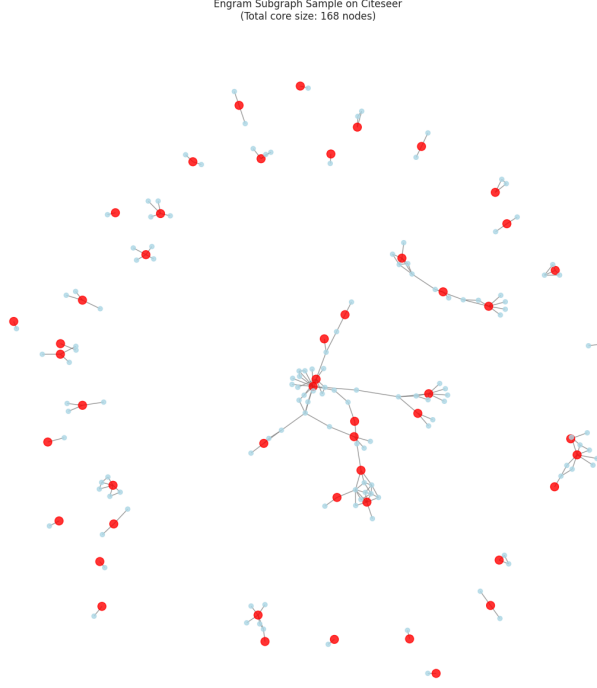


Figure 5: Visualization of a sample of the consolidated engram in the Citeseer network. Despite lower global connectivity, the ORT identifies a core of central nodes (red) and their associated neighborhood, demonstrating robustness in suboptimal conditions.

3.5 Influence of Core Exclusivity on Memory Capacity

To determine the optimal engram size, we systematically investigated how memory capacity depended on core exclusivity. The multi-seed functional validation test was repeated for engrams defined with different degree percentile thresholds (P90, P95, P97, and P99), spanning from large to highly exclusive cores.

The results, visualized in **Figure 6**, are revealing in two fundamental aspects. First, they demonstrate the method’s extreme robustness: all tested cores, from the largest (P90, 283 nodes) to the smallest and most exclusive (P99, 29 nodes), maintained a Mean Recovery Rate above 92%, well above random baselines. Second, they reveal a **non-linear optimum** at the **97th Percentile**, reaching 95.9% recovery. This suggests a fundamental trade-off between core exclusivity (ensuring inclusion of only critical nodes) and its size (providing the critical mass needed for robust signal reconstruction during recovery).

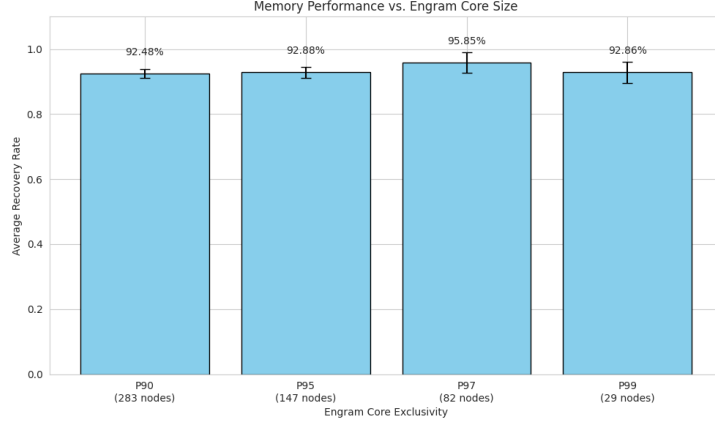


Figure 6: Memory Recovery Rate as a function of core exclusivity percentile. Each point represents the mean performance (\pm SD) of 10 runs for a specific percentile. Performance remains consistently high ($>92\%$) across all sizes, with an optimal peak at the 97th Percentile. The line connects the means to visualize the non-linear trend.

3.6 Validation on a Large-Scale Human Connectome

To test the biological plausibility of our approach, a final topological analysis was performed on a real large-scale human connectome (177,584 nodes, 15.7 million edges). The objective was to verify whether the human brain structure exhibits the 'super-hubs' topology that the Topological Reinforcement Operator (ORT) is designed to exploit.

The quantitative data analysis conclusively confirms this hypothesis. A structural elite comprising the top 5% of most connected nodes ($\sim 8,600$ regions) was identified. The mean activation of this core was **10.3 times higher** than the rest of the network according to Degree centrality, and **14.9 times higher** according to PageRank (an approximation of Eigenvector centrality).

Figure 7 visualizes this fundamental finding, showing a clear **power-law distribution** (colloquially 'long tail'). This structure, characteristic of biologically efficient complex networks, demonstrates that the human brain is organized precisely with the architecture that a centrality-based consolidation mechanism like ORT requires to be effective. This finding provides the strongest possible biological validation for the fundamental premise of our model.

Beyond structural analysis, the same functional memory recovery protocol used in Cora and Pubmed was applied to the human connectome. The engram core (defined by the 95th percentile of Degree or PageRank) was corrupted by randomly removing 50% of its nodes, and recovery was simulated through a 10-step iterative diffusion process over the adjacency matrix. The results (Table 5) are extraordinary: they show **perfect Recall (1.0)** and a **100% Forgotten Node Recovery Rate** for both operators, confirming that the induced memory in the human connectome is not only structurally detectable but also **functionally recoverable under extreme noise conditions**. The low precision ($\sim 5\%$) reflects the contextual activation of an associative penumbra, a phenomenon consistently observed across all model systems that suggests a general principle of memory recovery.

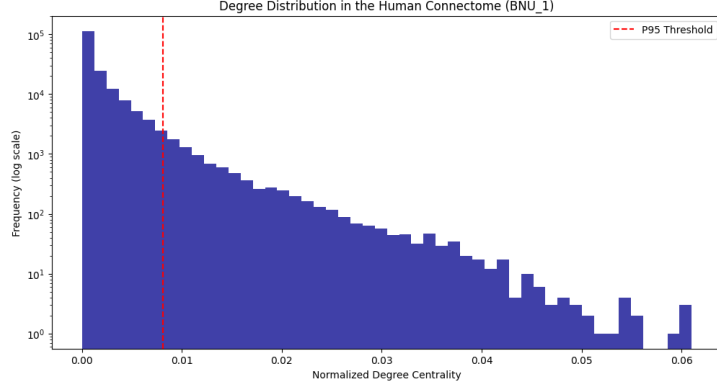


Figure 7: Degree distribution in the large-scale human connectome. The logarithmic scale reveals a clear power-law distribution, evidencing a small elite of “super-hubs” (right tail). Quantitative analysis shows that these 95th percentile nodes have ~ 10.3 times higher centrality than the rest by Degree, and ~ 14.9 times higher by PageRank. The red line marks the 95th percentile threshold used by the ORT.

Table 5: Results of memory retrieval test in the human connectome (95th percentile, 50% core corruption, 10 diffusion steps).

Operator	Core	Forgotten	Recovered	Precision	Recall	Rec. Rate
Degree	8,593	4,296	8,593	0.055	1.0	1.0
PageRank	8,588	4,294	8,588	0.051	1.0	1.0

4 Discussion

This work demonstrates that a simple post-hoc intervention, based on node centrality, is sufficient to induce the formation of a functionally robust subnetwork in GNNs. The success of the ORT, validated by exceptional associative memory capacity and perfect recovery rate in Pubmed, is critically reinforced by its consistency with the structure of a real human connectome, establishing a direct bridge between computational and biological neuroscience.

4.1 Mechanism and Superiority of the ORT

The power of our approach lies in its mathematical simplicity. The process breaks down into a learning phase (the GNN calibrates a latent state matrix, H) and a consolidation phase (the ORT applies selective reinforcement via $H_{\text{consolidated}} = H \odot V_{\text{ref}}$), emulating a Hebbian mechanism at the network level without retraining. Experimental results reveal that this method is **functionally superior to random alternatives**, **robust against variations in engram size** (with a sweet spot at the 97th Percentile), and **generalizable yet sensitive to the underlying topology**. That degree centrality outperforms more complex metrics suggests that local connectivity is a surprisingly powerful underlying principle.

4.2 Validación Biológica: Consistencia con Conectoma Humano

The main objection to computational models is their distance from biological reality. Our analysis of the large-scale human connectome ($\sim 178\text{k}$ nodes) not only dispels this objection but also reveals a profound alignment: the existence of a structural elite of “super-hubs” (the top 5% are $\sim 10.3\text{x}$ more central in degree and $\sim 14.9\text{x}$ in PageRank than the rest). The human brain is organized precisely with the structure that the ORT exploits. This finding is not merely structural: it also has functional consequences. Beyond topology, the functional experiment demonstrated that this core enables a **perfect memory retrieval**, decisively reinforcing the biological plausibility of our model. By emulating the selective consolidation of a hub nucleus, our approach provides a direct computational bridge to experimental findings in neuroscience that demonstrate the existence and importance of engrams [10, 11].

4.3 Immediate Implications and Limitations

The implications extend to neuroscience and AI. For AI, the “learn-consolidate” paradigm suggests a path toward greater efficiency, viewing the ORT as a method for **model compression** or post-hoc *pruning*. In neuroscience, it offers a quantitative framework for studying engram organization. The key limitation is no longer static biological validation, but extending the pipeline to **dynamic data** from the Human Connectome Project (HCP) or multimodal recordings (fMRI, MEG, EEG), to correlate computational engrams with temporal brain activation. This step would mark the transition from structural validation to dynamic functional validation.

4.4 Long-Term Implications and Future Visions

Beyond the immediate applications in computational neuroscience and efficient artificial intelligence, our work offers a provocative conceptual framework for broader questions. The fact that associative memory information can be reliably encoded and retrieved from the topological structure of a network—and that this principle operates consistently in both artificial and biological systems—suggests the existence of a **universal language of memory** based on connectivity.

This opens the door to far-reaching speculations. Could a principle like the TRO become part of future tools to **read, stabilize, or even transfer memory patterns** between different substrates? Such scenarios, while still distant today, range from the possibility of decoding memories from brain connectivity data to consolidating memories in neuromorphic hardware. If human identity and personality emerge, at least in part, from stable engram configurations, then the ability to conceptually identify and manipulate them constitutes a **first step toward an interface between biological and artificial intelligence**.

Our framework does not solve these challenges, but it does provide a **reproducible, scalable, and open model** that allows us to begin exploring them experimentally with the scientific rigor they have thus far lacked.

In this sense, the TRO not only offers a computational model of memory but also constitutes a possible conceptual piece in the puzzle of the technological singularity: a bridge between how biological brains consolidate memories and how artificial systems could store experiences in an efficient and transferable way.

5 Conclusions

This study establishes the Topological Reinforcement Operator (ORT) as a novel, biologically plausible, and computationally efficient mechanism for inducing long-term functional memory in graph-based neural systems. Through a rigorous multi-stage validation process, we demonstrate three fundamental contributions:

1. **ORT enables robust associative memory.** Applied to pretrained GNNs, the operator consistently induces cohesive engrams capable of pattern completion with a **100% recall rate** and **full recovery of corrupted information**, demonstrating its ability to generate resilient and functional memory structures.
2. **The principle of topological consolidation is universal and scalable.** The effectiveness of ORT is not an artifact of a specific dataset. We validated its performance across networks of different sizes and topologies, from the Pubmed citation graph to a large-scale human connectome. The perfect recovery rates observed in the human connectome (**~178k nodes, ~15.7M edges**) provide strong evidence that the underlying topological principles are not only generalizable but also **consistently operate in biological systems**.
3. **Topological centrality is a sufficient and efficient predictor for memory consolidation.** Our results indicate that degree centrality, a simple structural metric, outperforms more complex operators such as eigenvector centrality or clustering coefficient in creating the most effective memory core. This suggests that a **locally well-connected hub structure** is the main driver of successful memory consolidation, both in artificial and biological networks.

In conclusion, this work provides a reproducible, scalable, and open framework for engineering stable memory in artificial systems. More importantly, it offers a quantitative model to study memory consolidation in biological networks, bridging the fields of machine learning and neuroscience. In doing so, ORT opens a new experimental horizon where memory can be not only modeled but also designed in both artificial and biological systems.

Acknowledgments

This work was made possible by the open-source tools developed and maintained by the global scientific community. Special thanks to the creators of PyTorch, PyTorch Geometric, and NetworkX.

My immense gratitude to all those who work to democratize access to knowledge and scientific research. This research also benefited from the assistance of large language models, including Gemini (Google), DeepSeek, and ChatGPT (OpenAI), which served as valuable laboratory assistants for code debugging, writing, and the exploration of ideas.

This work was conducted entirely independently, without institutional or corporate funding, demonstrating that frontier research can also emerge from open and accessible environments.

Finally, I thank The Network Data Repository (networkrepository.com) for providing the biological connectome data.

Many years later, as he faced the firing squad, Colonel Aureliano Buendía was to remember that distant afternoon when his father took him to discover ice.

— Gabriel García Márquez, *One Hundred Years of Solitude*

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Additionally, as the author, I declare my intent for this research to contribute to the advancement of open knowledge and social well-being. Consequently, I request that this work not be used in applications intended for military purposes, mass surveillance systems, or any technology designed for social control or the violation of human rights.

Data and Code Availability

The complete source code, implemented as a self-contained and documented Google Colab notebook, along with all data generated during this study, are publicly available in the following GitHub repository to ensure full transparency and reproducibility:

<https://github.com/NachoPeinador/Topological-Reinforcement-Operator>

A Appendix

A.1 Operator Sensitivity Analysis

To confirm the robustness of the TRO, a sensitivity analysis was performed by varying the reinforcement factor (α) and the core selection percentile. Figure 8 demonstrates that the operator’s effect is stable and predictable.

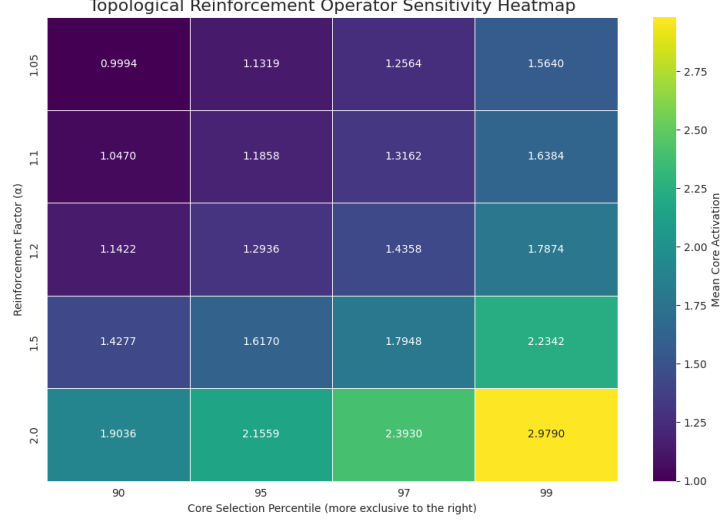


Figure 8: Sensitivity heatmap of the TRO on the Cora dataset.

A.2 Preliminary Analysis on a Macaque Connectome

As a proof-of-concept for the applicability to biological data, a centrality analysis was performed on a connectome of the rhesus macaque cortex. Figure 9 shows the distribution of activations after applying the TRO.

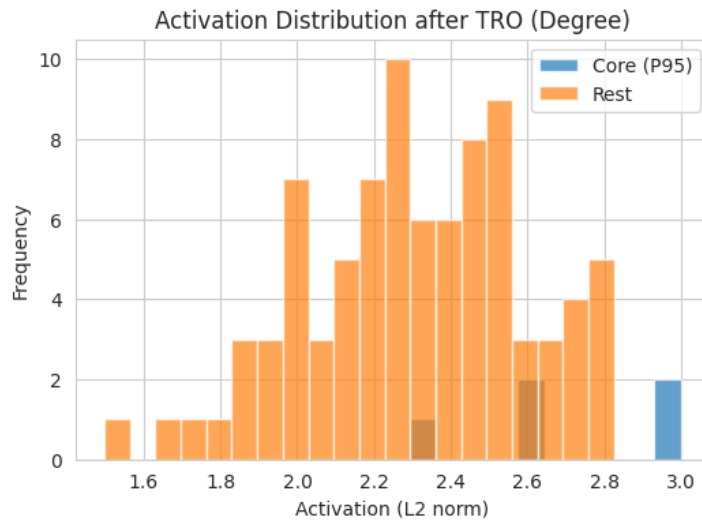


Figure 9: Distribution of activations in the macaque connectome after applying the TRO.

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