

Modeling progressive neuronal ablation in biomimetic hardware Spiking Neural Networks

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Abstract. Biomimetic Spiking Neural Networks (SNNs) provide a powerful framework to investigate how neuronal loss reshapes population-level dynamics under controlled and reproducible conditions. In this study, we employed a previously optimized biomimetic SNN, implemented on the real-time FPGA-based BioemuS platform, to investigate the effects of progressive neuronal ablation. Selected neurons were functionally removed by suppressing their incoming and outgoing synaptic interactions. Two ablation strategies were compared: random, representing distributed neuronal loss, and fixed-center, representing a focal lesion-like perturbation. Network activity and organization were assessed through firing and bursting measures, together with graph-theoretical descriptors of residual structural synaptic connectivity. The comparison between distributed and spatially structured ablation showed that neuronal loss cannot be interpreted only as a quantitative reduction of active units. Rather, the spatial organization of the perturbation plays a central role in shaping the residual functional state of the network. These findings support the use of real-time hardware biomimetic SNNs as controllable models to study how neural-like systems respond to structural damage. Such a framework is relevant not only for neuroengineering, but also for the design of increasingly biomimetic artificial systems, where real-time, robustness, resilience, and functional reorganization after perturbation are becoming key computational properties.

Keywords: Structural connectivity, Network dynamics, SNN, Structural perturbation

1 Introduction

The human brain remains the most efficient and resilient computational system known, capable of continuously processing information while adapting to an ever-changing structural and functional organization [1]. Unlike conventional computational architectures, whose performance strongly depends on the integrity of their components, biological neural networks preserve their functionality despite continuous

neuronal turnover during development, synaptic remodeling throughout learning, and neuronal loss associated with ageing, injury and disease [2, 3]. This remarkable robustness does not arise simply from the large number of neurons and synapses composing the nervous system, but from the complex interactions among neuronal populations organized across multiple spatial and temporal scales. Indeed, brain networks can be investigated at different topological levels, from individual neurons to large-scale functional networks, where collective dynamics emerge from the interaction of distributed neuronal assemblies rather than from isolated computational units [4].

A growing body of evidence suggests that the computational capabilities of the brain are intrinsically linked to this distributed organization. Since Hebb first introduced the concept of cell assemblies [5], neuronal populations have been recognized as the fundamental substrates of information processing, where individual neurons simultaneously participate in multiple functional assemblies [6]. At the network level, this organization gives rise to modular and small-world architectures, allowing the brain to efficiently balance local specialization and global integration while maintaining a remarkable tolerance to local failures [7-10]. Such distributed representations are widely believed to underlie one of the most distinctive properties of biological intelligence: resilience. Understanding how resilience emerges from network organization is therefore a fundamental challenge for neuroscience [11, 12] and, at the same time, a major source of inspiration for the development of future brain-inspired computational systems. One of the most effective approaches to investigate network resilience consists in observing how neuronal activity reorganizes following structural perturbations, such as progressive neuronal loss. Experimental paradigms based on targeted neuronal ablation have demonstrated that the functional impact of neuronal perturbations depends not necessarily on the number of ablated neurons [13], but especially on their functional role within the network and on the underlying recurrent connectivity [14]. These studies have considerably advanced our understanding of neuronal function. However, systematically exploring different damage scenarios remains experimentally demanding, because of limited controllability, experimental time, and ethical constraints.

Biomimetic computational models offer a complementary strategy for investigating these questions under highly controlled and reproducible conditions. Recent advances in neuromorphic engineering have enabled the development of biologically grounded (i.e. biomimetic) Spiking Neural Networks (SNNs) capable of reproducing key dynamical features of biological neuronal networks in real time [15-18]. As such, biomimetic SNNs represent promising experimental platforms and computational counterparts of biological networks [19], enabling systematic *in silico* investigations of structural perturbations that are difficult to perform experimentally.

Building upon a biomimetic SNN previously shown to recapitulate key dynamical features of neuronal networks *in vivo* implemented in the BioemuS platform [15], in this work we investigated the effects of progressive neuronal ablation on collective network dynamics. Specifically, we compared increasing levels of neuronal loss under both localized and spatially distributed damage paradigms to evaluate how structural perturbations reshape spontaneous network activity. Rather than modelling a specific neurological disorder, our objective was to establish a controlled experimental framework in which neuronal damage can be systematically investigated.

Here, we show that the resilience of biomimetic SNNs is not solely determined by the extent of neuronal loss, but also by the spatial organization of the perturbation and the topology of the residual network. Distributed random ablation led to a progressive impairment of spontaneous activity, whereas focal neuronal loss induced distinct patterns of network reorganization despite comparable levels of damage. Moreover, changes in small-world-related structural properties revealed that network topology contributes to shaping the functional consequences of neuronal loss. These findings highlight how biomimetic SNNs can be used to investigate how structural damage propagates through neuronal architecture and affects emergent network dynamics.

Such a framework has the potential to guide future *in vivo* and *in vitro* studies, contribute to the reduction of animal experimentation, and ultimately provide insights into the computational principles underlying resilient brain-inspired systems.

2 Materials and Methods

2.1 Biomimetic Hardware Spiking Neural Network

BioemuS. The experiments presented in this work were performed using BioemuS, a real-time hardware platform for the emulation of neuronal networks through biologically inspired neuronal and synaptic models, recently presented in the literature [15]. Briefly, BioemuS is implemented on a Kria KR260 development board with Xilinx Zynq UltraScale+ MPSoC System-on-Chip (SoC), integrating CPU cores (software) and programmable logic (FPGA). Network configurations are generated through dedicated scripts, which translate user-defined network specifications into hardware-ready implementations. The resulting SNNs comprise up to 1024 single-compartment Hodgkin–Huxley (HH) neurons [20] interconnected through up to 2^{20} conductance-based synapses. The framework supports the customization of different cortical neuronal types (Regular Spiking – RS and Fast Spiking – FS, Intrinsically Bursting – IB, Low Threshold Spiking – LTS), synaptic models (e.g. AMPA, NMDA, GABA_A, GABA_B) and connectivity rules, allowing the generation of biomimetic SNNs, whose emergent activity reproduces the characteristic dynamics observed in biological neuronal networks while preserving real-time execution. Further details on the platform architecture and implementation are available in [16].

Expert-driven optimization. The biomimetic SNN (Fig. 1A) employed in this study corresponds to a previously optimized network configuration presented in [15]. The biological data used for the optimization were collected during *in vivo* experiments, in which electrophysiological recordings were acquired from the Rostral Forelimb Area (RFA) of six adult Long-Evans rats during spontaneous cortical activity. Extracellular signals were recorded using 16-channel Micro-Electrode Arrays (MEAs), providing the Biological Neural Network (BNN) against which the hardware SNN was optimized. All the experimental procedures were approved by the Italian Ministry of Health (authorization n. 509/2020-PR) and conducted at the Animal Facility of the Italian Institute

of Technology (IIT), Genoa, Italy. Details regarding the *in vivo* experimental procedures, surgical protocol, data acquisition, and preprocessing are reported in [15].

An expert-driven iterative optimization procedure was adopted to minimize the discrepancy between the spontaneous dynamics of the BNN and the hardware SNN (Fig. 1A). Starting from the configurable BiømuS architecture, neuronal, synaptic and connectivity parameters were iteratively adjusted until the SNN reproduced a predefined set of standard electrophysiological descriptors extracted from the BNN, including Inter-Spike Interval (ISI, ms), Mean Firing Rate (MFR, spikes/s), Mean Bursting Rate (MBR, bursts/min), Pearson’s Correlation (PC), and Burstiness Index (BI) [21]. This process yielded a biomimetic SNN capable of recapitulating the key dynamical features of the biological recordings. Specifically, the final SNN comprises 1024 HH neurons, including 783 excitatory and 241 inhibitory neurons as per optimization procedure, corresponding to approximately 76.5% excitatory and 23.5% inhibitory units. In this optimized configuration, all electrophysiological descriptors achieved a matching score between 84% and 100% with respect to the corresponding target values extracted from the BNN [16].

2.2 Ablation protocols

To investigate the effect of neuronal loss on network activity, selected units were functionally removed from the SNN through a progressive ablation procedure. Ablation was implemented by suppressing all incoming and outgoing synaptic connections of the selected neurons, thereby completely isolating them from the network while leaving the remaining connectivity unchanged. Two ablation strategies were investigated (Fig. 1B): random and fixed-center. In the random strategy, neurons were randomly selected from the entire network, producing a spatially distributed perturbation. In the fixed-center strategy, neurons were removed according to their spatial proximity to a predefined lesion center, producing a progressively expanding localized lesion.

For both ablation strategies, four ablation levels were considered, corresponding to the removal of 50, 100, 200, and 500 neurons. For each level, 10 repetitions were generated, each lasting 5 min. In the random ablation protocol, the randomization unit was the identity of the ablated neurons. Specifically, for each ablation level, 10 repetitions were generated by independently sampling different neuronal subsets from the whole 1024-unit population, while keeping the number of removed neurons fixed. In the fixed-center protocol, neurons were selected according to their spatial proximity to a predefined lesion center. For each ablation level, the same lesion center and the same ablated-neuron set were preserved across the 10 repetitions. Therefore, fixed-center repetitions did not introduce variability in lesion location or residual structural topology. However, while structural graph metrics were expected to show negligible variability, activity descriptors could still vary across repeated emulations of the same focal structural perturbation.

Overall, the dataset included the intact baseline condition and 80 simulations of the ablation protocols, corresponding to 4 ablation levels $\times$ 10 repetitions $\times$ 2 ablation

configurations. The intact optimized SNN was used as a common baseline reference for all comparisons, to avoid introducing any repetition-dependent baseline variability.

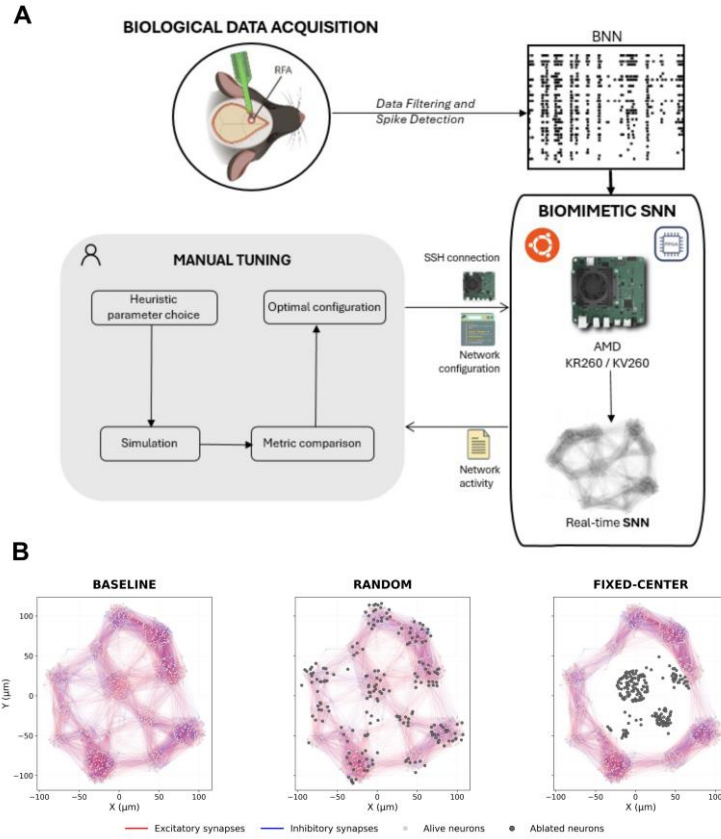


Fig. 1. Overview of the biomimetic SNN and ablation protocols. A) Schematic of the expert-driven optimization procedure. Spontaneous cortical activity recorded from the Rostral Forelimb Area (RFA) of Long-Evans rats using 16-channel MEAs served as the Biological Neural Network (BNN) reference for the SNN optimization. Neurons were modeled in silico as Hodgkin–Huxley (HH) units and classified as excitatory (AMPA/NMDA) or inhibitory (GABAa/GABAb) based on outgoing synaptic profiles. The biomimetic SNN was emulated in the BioMuS hardware platform. The optimization procedure consisted of simulating SNNs with different values of the configuration parameters (see text) and identifying the parameter sets that best matched the BNN. B) Neuronal loss was modeled through random or fixed-center ablation, with increasing damage levels obtained by progressively enlarging the number of silenced neurons. Each structural connectivity graph reports the position of the neurons (red - excitatory and blue-inhibitory dots) and their links within the optimized SNN. Three conditions are considered for the subsequent analysis: baseline (i.e. intact) (*left*), random ablation (*center*) and the fixed-center ablation (*right*). Black dots indicate ablated neurons.

2.3 Data analysis

Network activity was characterized by using both qualitative and quantitative analyses. Raster plots were employed to qualitatively visualize the temporal organization of neuronal spiking activity under baseline and progressive neuronal ablation conditions.

Quantitative analysis was performed by extracting electrophysiological descriptors from the spike trains of the generated SNNs. Specifically, the Mean Firing Rate (MFR, spikes/s) was computed as the average firing activity across the network. The Mean Bursting Rate (MBR, bursts/min) was used to quantify the occurrence of burst events. Burst detection was performed using an inter-spike-interval-based criterion, as reported in [22]: a burst was identified as a sequence of at least five consecutive spikes separated by inter-spike intervals shorter than 100 ms. The number of detected bursts was then normalized by the recording duration to obtain the bursting rate. Noteworthy, firing and bursting rates were computed for all neurons with non-zero MFR and MBR, respectively (i.e., excluding the ablated neurons). This is consistent with standard practice in neuronal electrophysiology studies using Multi-Electrode Arrays to quantify neuronal firing and bursting (see, e.g., [23-25]).

To facilitate comparison across different lesion conditions, both metrics were then normalized with respect to the intact (non-ablated) SNN, whose values were set to 100%. The normalized descriptors are referred to as ΔMFR and ΔMBR . Two complementary normalization strategies were used.

For the full-population analysis, the numerator contained the activity generated by the ablated network, generated by the surviving neurons only, while the denominator was kept equal to the original population size of 1024 units. Thus, full-population ΔMFR and ΔMBR quantify the activity remaining at the level of the original network after ablation. In the surviving-neuron-only normalization, ΔMFR and ΔMBR were recomputed by excluding ablated neurons from the denominator, thus with respect to the corresponding baseline activity of the same surviving neuronal subset. This analysis was used to assess whether the remaining neurons preserved or altered their average firing and bursting activity independently of the direct loss of ablated units.

Statistical comparisons were performed independently at each ablation level and separately for ΔMFR and ΔMBR . Two complementary statistical analyses were conducted. First, to assess the effect of the normalization strategy, full-population and surviving-neuron-only values were compared separately within each ablation protocol. Since the two normalization strategies were applied to the same network repetitions, the resulting values were treated as paired observations and compared using a two-sided Wilcoxon signed-rank test. Second, to assess differences between ablation protocols, random and fixed-center ablations were compared separately for each normalization strategy. For each metric and ablation level, the 10 repetitions obtained with the random protocol were compared with the 10 repetitions obtained with the fixed-center protocol using a two-sided Mann–Whitney U test. Effect sizes were quantified using rank-biserial correlation, reported as random minus fixed-center. Positive rank-biserial values therefore indicate higher values in the random condition, whereas negative values indicate higher values in the fixed-center condition.

For both analyses, p-values were corrected for multiple comparisons using the Benjamini–Hochberg false discovery rate procedure. Statistical significance was assessed after correction using a threshold of $p_{\text{FDR}} < 0.05$. Results are reported as mean $\pm$ standard deviation across the 10 repetitions.

2.4 Connectivity analysis

To evaluate how different ablation protocols affected network organization, residual synaptic (i.e. structural) connectivity was quantified following neuronal removal and compared across the intact baseline, random ablation, and fixed-center ablation conditions at matched ablation sizes. For each condition, the synaptic connectivity encoded in the corresponding hardware configuration was converted into a binary adjacency matrix. Ablated neurons were removed from the graph together with all their incoming and outgoing synaptic connections, so that the analysis was performed only on the surviving network. The directed synaptic matrix was converted into an undirected binary graph, where an edge between two neurons was retained if at least one synaptic connection was present between them. Graph-theoretical analysis was then used for quantitative purposes [26]. Specifically, we used the Clustering Coefficient (CC) to capture changes in local connectivity organization and the average Path Length (PL) to assess alterations in global network integration. These complementary properties were integrated into the structural Small World Index (SWI), which quantifies the balance between local clustering and efficient global communication relative to equivalent random graphs [7, 27]. This framework is widely used in neuroscience to describe the balance between local segregation and global integration in brain networks [8, 9].

To obtain normalized small-world measures, each residual network was compared with degree-preserving null networks. Null networks were generated through random edge rewiring, preserving the number of nodes, number of edges, and degree distribution of each residual graph while disrupting higher-order topological organization. This reference model was selected because it controls for changes in degree distribution induced by neuronal ablation, allowing small-world organization to be assessed beyond what can be explained by node degree alone. The average clustering coefficient and characteristic path length of the degree-preserving null networks were used as reference values for SWI computation. The structural SWI was calculated as follows (eq. 1):

$$SWI = \frac{\frac{CC}{CC_{null}}}{\frac{PL}{PL_{null}}} \quad (1)$$

Where CC_{null} and PL_{null} are the corresponding mean values obtained from the degree-preserving null networks.

3 Results

3.1 Progressive random ablation

The intact biomimetic SNN exhibited sustained spontaneous activity, with spiking events broadly distributed across the neuronal population (Fig. 2, top panel). Progressive random ablation disrupted this activity pattern as shown by the raster plots in Fig. 2, from second to fifth panel. At low ablation levels (50 and 100 neurons), spontaneous activity remained broadly distributed, although bursts appeared less synchronized and spike density was moderately reduced. Increasing the number of randomly removed neurons to 200 and 500 resulted in a marked reduction of firing activity, with sparse spiking and a progressive loss of coordinated bursting, indicating a widespread degradation of network dynamics.

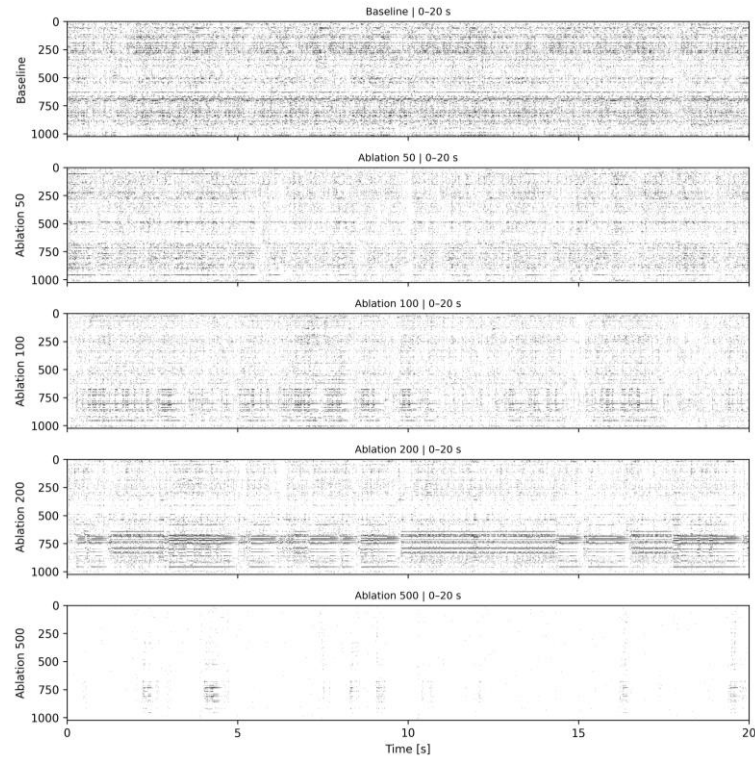


Fig. 2. Progressive random ablation: raster plots. Representative 20 s raster plots showing spontaneous spiking activity in the intact baseline network and after progressive random ablation of 50, 100, 200, and 500 neurons (from top to bottom). In each raster, each row represents one neuron, and each dot indicates a spike event.

Quantitative analysis confirmed this progressive degradation. Adopting the full-population normalization (cf. Section 2.3 ‘Data analysis’), both ΔMFR (Fig. 3A) and

Δ MBR (Fig. 3B) decreased with increasing ablation size, indicating that random neuronal removal affected not only the overall firing output of the network, but also its ability to sustain coordinated burst-like activity. Despite the general trend being consistent across repetitions, variability increased at intermediate and high ablation levels, indicating that different randomly selected neuronal subsets produced distinct residual activity states.

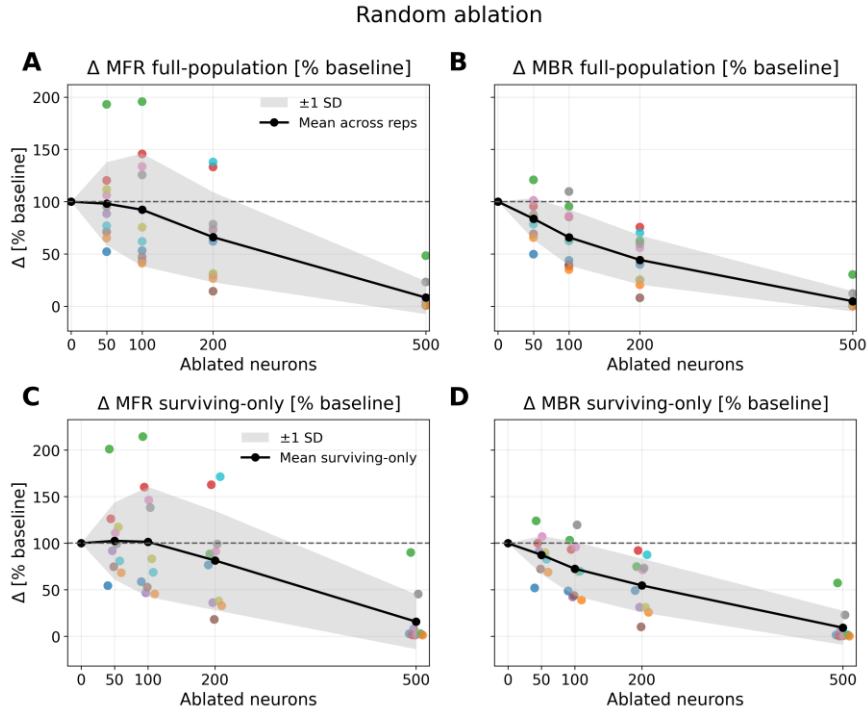


Fig. 3. Progressive random ablation: firing and bursting activity. Full population normalization: (A) Mean firing rate variation, Δ MFR, and (B) mean bursting rate variation, Δ MBR, computed as percentages of the intact baseline network. Surviving-neuron-only normalization: (C) Mean firing rate variation, Δ MFR, and (D) mean bursting rate variation, Δ MBR, computed as the activity of the remaining neurons normalized to the baseline activity of the corresponding surviving neuronal subset. Colored dots show individual repetitions, the black line indicates the mean across repetitions, and the gray shaded area indicates ± 1 standard deviation.

The bottom panels of Fig. 3 report the surviving-neuron-only analysis. In this case, Δ MFR (Fig. 3C) showed a decreasing trend similar to that observed in the full-population analysis, particularly beyond the 100-ablated-neuron condition. This suggests that, up to 100 ablated neurons, the reduction observed at the full-population level is primarily attributable to the loss of neuronal units. Beyond this point, however, the decline in activity exceeds that expected from neuronal loss alone, indicating an additional reduction in the firing activity of the surviving neurons. For Δ MBR (Fig. 3D), in contrast, a decrease was already evident from the first ablation step, with the surviving-neuron-

only analysis showing a trend comparable to that observed in the full-population analysis.

The statistical analysis reported in Table 1 revealed significant differences between the two normalization strategies for both metrics at all ablation levels, with the surviving-neuron-only values higher than the corresponding full-population values. Nevertheless, both normalization strategies followed the same decreasing trend and yielded values well below 100%, indicating a marked reduction relative to baseline, particularly in bursting activity.

Table 1. Progressive random ablation: statistical comparison between the full-population and the surviving-neuron-only analysis for ΔMFR and ΔMBR . Values are reported as mean $\pm$ standard deviation across repetitions. For comparison, the two-sided Wilcoxon signed-rank test was used. P-values were corrected using the Benjamini–Hochberg false discovery rate procedure. Statistical significance was assessed using $\text{pFDR} < 0.05$.

Metric	Ablated neurons	Full-population	Surviving-only	pFDR
ΔMFR	50	98.1 ± 39.7	102.5 ± 41.4	<0.002
ΔMFR	100	92.3 ± 53.9	101.5 ± 59.0	<0.002
ΔMFR	200	66.1 ± 43.1	81.5 ± 53.2	<0.002
ΔMFR	500	8.3 ± 15.7	15.8 ± 29.4	<0.002
ΔMBR	50	83.7 ± 19.9	87.5 ± 20.4	<0.002
ΔMBR	100	65.9 ± 26.9	72.5 ± 29.0	<0.002
ΔMBR	200	44.3 ± 23.5	54.7 ± 28.8	<0.002
ΔMBR	500	4.9 ± 9.7	9.3 ± 18.3	<0.002

3.2 Progressive fixed-center ablation

Fixed-center ablation produced a spatially structured pattern of network degradation. Raster plots showed that the expansion of the ablated region progressively modified spontaneous activity across the whole network (Fig. 4). At lower and intermediate ablation levels, spontaneous firing remained visible outside the lesioned region, indicating that part of the residual network was still able to sustain spiking activity despite the focal perturbation. In contrast, larger ablations produced a marked reduction in spike density and burst events, with the strongest impairment observed after the removal of 500 neurons.

The electrophysiological descriptors reflected the qualitative changes observed in the raster plots. ΔMFR and ΔMBR were computed as percentages of the baseline network (Fig. 5), following two normalization strategies. Overall, fixed-center ablation resulted in a non-linear degradation profile for both metrics.

In the full-population analysis, activity was markedly reduced at 50 ablated neurons, with ΔMFR (Fig. 5A) and ΔMBR (Fig. 5B) indicating an almost 50% reduction relative

to the intact baseline. At 100 ablated neurons, activity was partially preserved. At 200 ablated neurons, ΔMFR increased, whereas ΔMBR remained reduced, suggesting that the residual network was still able to sustain firing activity despite a more pronounced impairment in burst organization. At 500 ablated neurons, both ΔMFR and ΔMBR showed a marked reduction, indicating a substantial loss of residual network activity. These results indicate that fixed-center ablation did not simply induce a monotonic decrease in activity proportional to the number of removed neurons. Rather, the residual activity depended on the spatial extent of the focal perturbation and on the connectivity preserved outside the lesioned region.

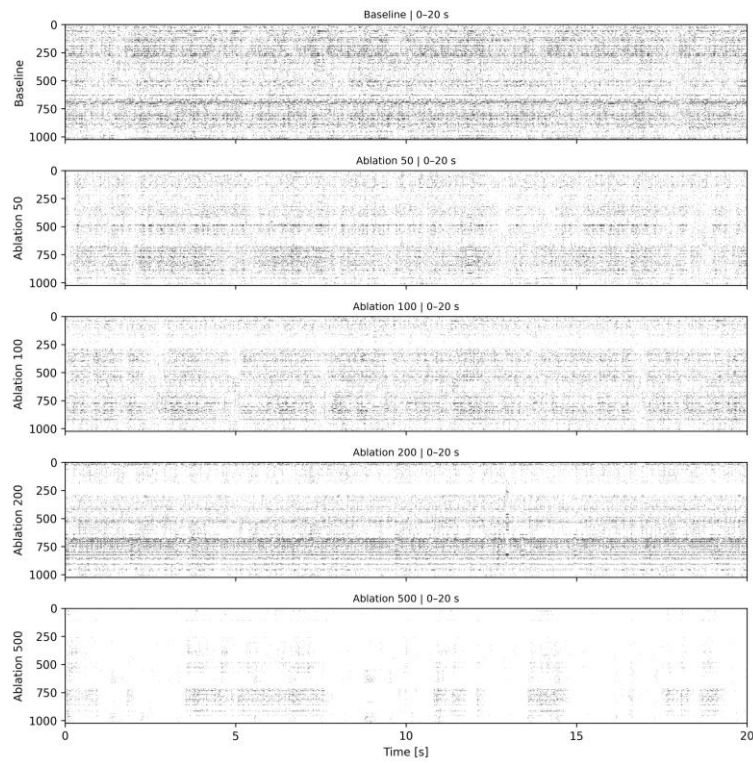


Fig. 4. Progressive fixed-center ablation: raster plots. Representative 20 s raster plots showing spontaneous spiking activity in the intact baseline network and after progressive fixed-center ablation of 50, 100, 200, and 500 neurons (from top to bottom). In each raster, each row represents one neuron, and each dot indicates a spike event.

The bottom panels of Fig. 5 show the surviving-neuron-only analysis for ΔMFR (Fig. 5C) and ΔMBR (Fig. 5D). This analysis revealed that focal perturbation affected not only the overall output of the network, but also the activity of the surviving neuronal population, following a strong non-linear pattern. At 50 ablated neurons, both descriptors showed a marked reduction, indicating a substantial decrease in the activity of the surviving neurons. At 100 ablated neurons, both ΔMFR and ΔMBR partially recovered, and this recovery became more pronounced at 200 ablated neurons. Notably, at

200 ablated neurons, ΔMFR returned to approximately 100% of baseline, indicating an almost complete recovery of firing activity among the surviving neurons. In contrast, although ΔMBR increased compared with the corresponding full-population analysis, it remained well below baseline, at approximately 70%. This dissociation suggests that, at that level of ablation, the surviving neuronal population was able to restore its overall firing activity, but not its baseline bursting activity. Finally, at 500 ablated neurons, both ΔMFR and ΔMBR were strongly reduced, indicating that, under more extensive perturbation, the surviving neurons were no longer able to preserve their baseline activity.

Fixed-center ablation

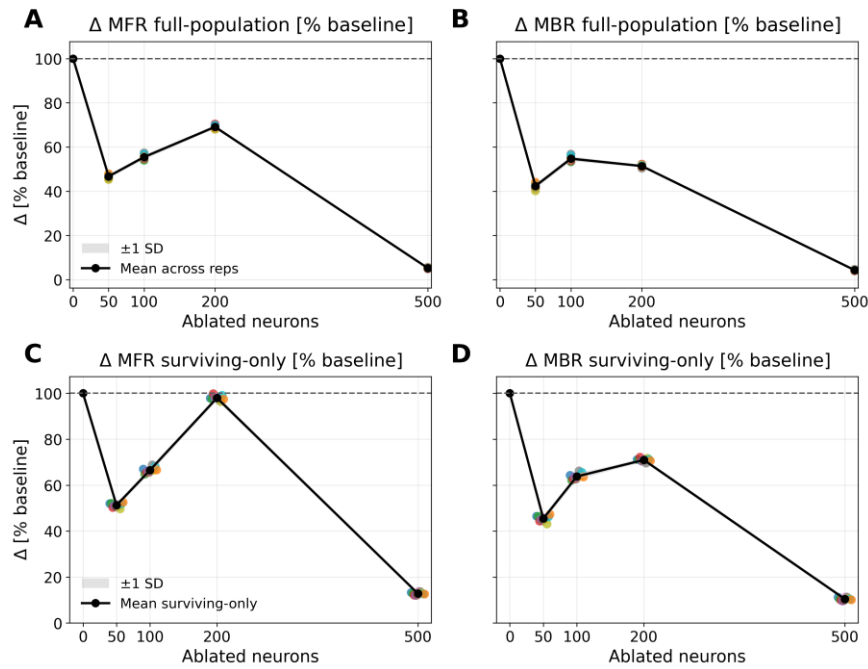


Fig. 5. Progressive fixed-center ablation: firing and bursting activity. Full population normalization: (A) Mean firing rate variation, ΔMFR , and (B) mean bursting rate variation, ΔMBR , computed as percentages of the intact baseline network. Surviving-neuron-only normalization: (C) Mean firing rate variation, ΔMFR , and (D) mean bursting rate variation, ΔMBR , computed as the activity of the remaining neurons normalized to the baseline activity of the corresponding surviving neuronal subset. Colored dots show individual repetitions, the black line indicates the mean across repetitions, and the gray shaded area indicates ± 1 standard deviation.

The statistical analysis reported in Table 2 confirmed the significant differences between the full-population and surviving-neuron-only analyses for both metrics at all ablation levels. Despite these differences, the two normalization strategies showed broadly similar trends, with both indicating a marked reduction relative to baseline. The main exception was the previously identified recovery in the surviving-neuron-only condition, particularly evident for firing activity at intermediate ablation levels.

Table 2. Progressive fixed-center ablation: statistical comparison between the full-population and the surviving-neuron-only analysis for ΔMFR and ΔMBR . Values are reported as mean $\pm$ standard deviation across repetitions. For comparison, the two-sided Wilcoxon signed-rank test was used. P-values were corrected using the Benjamini–Hochberg false discovery rate procedure. Statistical significance was assessed using $\text{pFDR} < 0.05$.

Metric	Ablated neurons	Full-population	Surviving-only	pFDR
ΔMFR	50	46.7 ± 0.8	51.2 ± 0.9	<0.002
ΔMFR	100	55.5 ± 1.0	66.5 ± 1.2	<0.002
ΔMFR	200	69.1 ± 0.7	98.0 ± 1.0	<0.002
ΔMFR	500	5.2 ± 0.3	12.8 ± 0.6	<0.002
ΔMBR	50	42.4 ± 1.2	45.4 ± 1.2	<0.002
ΔMBR	100	54.7 ± 1.1	63.8 ± 1.3	<0.002
ΔMBR	200	51.4 ± 0.5	71.0 ± 0.7	<0.002
ΔMBR	500	4.3 ± 0.3	10.4 ± 0.6	<0.002

3.3 Statistical comparison between random and fixed-center ablation

After separately characterizing random and fixed-center ablation, statistical comparisons were performed between the two protocols at each matched damage level. For the main full-population descriptors, at 50 ablated neurons, fixed-center produced significantly lower activity in terms of both ΔMFR and ΔMBR than random ablation. At 100 and 200 ablated neurons, differences between random and fixed-center protocols were not significant after correction. At 500 ablated neurons, the comparison was borderline but did not pass the corrected significance threshold. These results indicate that ablation geometry strongly affected residual network output at low damage levels, whereas extensive ablation drove both protocols toward a severely impaired activity state. The full-population statistical comparison is reported in Table 3.

Table 3. Statistical comparison of full-population activity descriptors between random and fixed-center ablation. Values are reported as mean $\pm$ standard deviation across repetitions. Random and fixed-center ablation were compared independently at each ablation level using two-sided Mann–Whitney U tests. P-values were corrected using the Benjamini–Hochberg false discovery rate procedure. Statistical significance was assessed using $\text{pFDR} < 0.05$.

Metric	Ablated neurons	Random ablation	Fixed-center ablation	pFDR	Effect size
ΔMFR	50	98.1 ± 39.7	46.7 ± 0.8	<0.001	1.0
ΔMFR	100	92.3 ± 53.9	55.5 ± 1.0	0.630	1.0
ΔMFR	200	66.1 ± 43.1	69.1 ± 0.7	1.000	1.0
ΔMFR	500	8.3 ± 15.7	5.2 ± 0.3	0.051	1.0

ΔMBR	50	83.7 ± 19.9	42.4 ± 1.2	<0.001	1.0
ΔMBR	100	65.9 ± 26.9	54.7 ± 1.1	0.630	1.0
ΔMBR	200	44.3 ± 23.5	51.4 ± 0.5	1.000	1.0
ΔMBR	500	4.9 ± 9.7	4.3 ± 0.3	0.051	1.0

The surviving-neuron-only analysis revealed distinct responses to random and fixed-center ablation, particularly at the lowest ablation level, as reported in Table 4. At 50 ablated neurons, random ablation largely preserved the activity of the surviving population, with ΔMFR remaining close to baseline and only a moderate reduction in ΔMBR . In contrast, fixed-center ablation resulted in an immediate reduction of approximately 50% in both firing and bursting activity. Accordingly, the difference between the two ablation protocols was statistically significant at this ablation level for both ΔMFR and ΔMBR ($\text{pFDR} < 0.001$). At higher ablation levels, no significant differences were detected between the two protocols. Nevertheless, their response profiles remained qualitatively different: random ablation showed a progressive decline in both descriptors with increasing ablation size, whereas fixed-center ablation followed a non-linear pattern, characterized by a recovery of activity at intermediate ablation levels followed by a marked decrease at 500 ablated neurons. At this highest ablation level, the difference in ΔMBR approached, but did not reach, statistical significance ($\text{pFDR} = 0.051$), with random ablation showing lower bursting activity than fixed-center ablation, thus reversing the direction observed at lower ablation levels.

Table 4. Statistical comparison of surviving-neuron-only activity descriptors between random and fixed-center ablation. Values are reported as mean $\pm$ standard deviation across repetitions. Random and fixed-center ablation were compared independently at each ablation level using two-sided Mann–Whitney U tests. P-values were corrected using the Benjamini–Hochberg false discovery rate procedure. Statistical significance was assessed using $\text{pFDR} < 0.05$. Rows highlighted in gray indicate significant comparisons after FDR correction.

Metric	Ablated neurons	Random ablation	Fixed-center ablation	p	Effect size
ΔMFR	50	102.5 ± 41.4	51.2 ± 0.9	<0.001	1.0
ΔMFR	100	101.5 ± 59.0	66.5 ± 1.2	0.658	1.0
ΔMFR	200	81.5 ± 53.2	98.0 ± 1.0	0.224	1.0
ΔMFR	500	15.8 ± 29.4	12.8 ± 0.6	0.251	1.0
ΔMBR	50	87.5 ± 20.4	45.4 ± 1.2	<0.001	1.0
ΔMBR	100	72.5 ± 29.0	63.8 ± 1.3	0.630	1.0
ΔMBR	200	54.7 ± 28.8	71.0 ± 0.7	1.000	1.0
ΔMBR	500	9.3 ± 18.3	10.4 ± 0.6	0.051	1.0

3.4 Small worldness of the ablated SNNs

To evaluate whether neuronal ablation altered the structural organization of the residual network, we analyzed the clustering coefficient (CC), path length, (PL) and small-world index (SWI) from the surviving structural connectivity (Fig. 6). SWI was computed using degree-preserving null networks, as described in Section 2.4.

Random and fixed-center ablation produced clearly distinct trajectories as the number of ablated neurons increased. Under random ablation, CC remained close to the baseline value across all ablation levels, indicating that distributed neuronal removal did not substantially alter the local clustering structure of the surviving network. PL showed only a moderate increase, suggesting that global paths between surviving nodes became slightly longer but remained largely preserved. As a consequence, SWI decreased only mildly, indicating that the small-world organization of the residual network was mostly maintained despite progressive random neuronal loss. In contrast, fixed-center ablation produced a markedly different topological response. As the focal perturbation expanded, CC progressively increased, indicating that the surviving nodes became relatively more clustered within the remaining local neighborhoods. At the same time, PL increased more strongly than in the random condition, showing that communication across distant portions of the residual network became less efficient. This divergence between increased local clustering and impaired global integration led to a progressive reduction in SWI. Thus, fixed-center ablation did not simply reduce network size but reorganized the residual structural topology by making it more locally segregated and less globally integrated. Overall, these results show that the structural impact of neuronal loss depends not only on the number of ablated neurons, but also on their spatial arrangement. Compared with distributed random ablation, focal lesion-like ablation produced a stronger disruption of the small-world balance of the SNN.

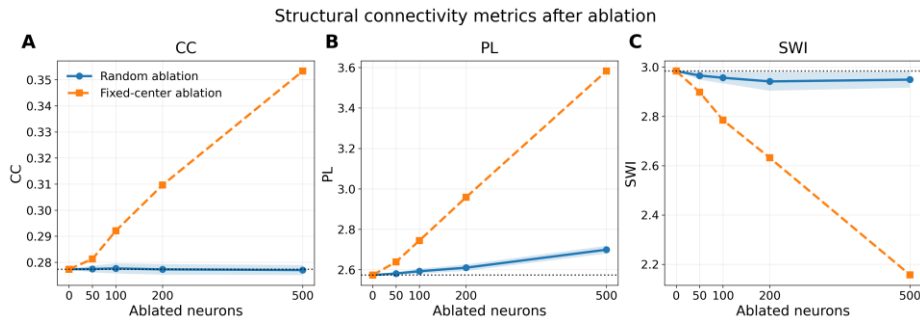


Fig. 6. Structural connectivity metrics after progressive neuronal ablation. (A) Clustering coefficient, CC, quantifying local connectivity organization. (B) Characteristic path length, PL, measuring global integration through the average shortest-path distance between surviving nodes. (C) Small-World Index, SWI, summarizing the balance between local clustering and global communication efficiency. Metrics are reported as raw values computed from the residual structural networks. The baseline network is shown at 0 ablated neurons, while ablated conditions

correspond to the removal of 50, 100, 200, and 500 neurons. Lines represent the mean across 10 repetitions, and shaded areas indicate ± 1 standard deviation. Random ablation is shown with solid lines, and fixed-center ablation is shown with dashed lines. SWI was computed using degree-preserving null networks generated by random edge rewiring.

4 Discussion

In this study, progressive neuronal ablation was used as a controlled perturbation to probe the vulnerability of a real-time biomimetic hardware SNN. By comparing spatially distributed random ablation with focal fixed-center ablation, we show that the consequences of neuronal loss are not determined only by the number of removed units. Rather, they emerge from the interaction between ablation extent, lesion geometry, and the residual connectivity scaffold. This result is consistent with a central principle of network neuroscience: the impact of a perturbation depends on where it occurs within the network architecture, not only on its size [7, 8]. Random ablation produced a distributed weakening of spontaneous activity, suggesting a progressive reduction of the functional resources available to the network. However, the variability across repetitions indicates that even random neuronal loss is not a purely uniform process. The specific neurons removed, and their embedding within the network, can influence the residual dynamical state. Fixed-center ablation revealed a more structured form of vulnerability. By concentrating neuronal removal within a spatially defined region, this protocol generated a lesion-like perturbation whose effects differed from those produced by random ablation at comparable ablation sizes. Importantly, this difference was not limited to the expected reduction in overall network output but also emerged in the functional response of the surviving neuronal population. This indicates that the spatial organization of neuronal loss plays a relevant role in determining how the residual network responds to damage. At intermediate levels of focal ablation, the surviving network retained, and in some cases partially recovered, its activity, suggesting a certain capacity to compensate for localized damage. However, this capacity was lost at larger ablation sizes, where both firing and bursting activity markedly deteriorated. Taken together, these findings suggest that the network can tolerate focal damage as long as the residual connectivity remains sufficient to support population-wide communication; once this structural support is critically compromised, the ability of the surviving network to sustain collective dynamics rapidly deteriorates. This agrees with experimental evidence showing that neuronal networks can display non-trivial responses to focal damage, where the functional outcome depends on the organization of the remaining circuit rather than on cell loss alone [9, 13, 14].

The graph-theoretical analysis provides a structural interpretation of these effects. Small-world organization is widely considered a key property of neural systems, supporting both local specialization and global integration [27]. In our model, random and fixed-center ablation produced distinct trajectories in clustering coefficient, path length, and small-world index, indicating that lesion geometry reshapes how surviving neurons remain locally clustered and globally connected. Thus, the different

electrophysiological profiles observed after ablation are not only changes in activity level, but reflect distinct reorganizations of the residual network topology.

A central strength of this approach is the use of an FPGA-based real-time biomimetic SNN as a controllable and reproducible experimental substrate. Although simplified with respect to biological lesions, the model allows ablation size, spatial distribution, and network configuration to be manipulated independently and repeatedly under identical conditions. This makes it possible to isolate specific mechanisms of structural perturbation that are difficult to disentangle in biological preparations, where neuronal damage is accompanied by degeneration, inflammation, plasticity, and compensatory remodeling. In this sense, the platform does not replace biological models, but provides a complementary experimental space in which lesion-like perturbations can be tested with high control, reproducibility, and flexibility. This opens relevant perspectives for future work. First, the fixed-center protocol could be extended by systematically changing the position of the ablation center, allowing the identification of network regions whose removal produces stronger alterations in firing, bursting, or small-world organization. Second, the framework is not limited to neuronal ablation. Since the hardware configuration also defines cellular and synaptic parameters, and neurons are implemented through Hodgkin–Huxley-based dynamics, specific biophysical properties such as ionic conductances, membrane excitability, and synaptic parameters could be selectively modified. This would make it possible to move from purely structural perturbations toward disease-inspired functional perturbations, such as pathological conditions affecting ion-channel dynamics, and to evaluate how altered single-neuron properties propagate to population activity and network topology. Future work could extend this framework using multicompartment Hodgkin–Huxley neuron models [17]. Their explicit representation of dendrites and axons would enable the simulation of more realistic neuronal impairments, such as dendritic degeneration or altered axonal conduction, beyond simple neuronal ablation. In addition, the Hodgkin–Huxley formalism offers substantially greater biological realism than simplified neuron models such as Leaky Integrate-and-Fire or Izhikevich neurons. Its explicit representation of ionic currents enables the investigation of disease-related alterations affecting specific ion channels or membrane conductances, providing a much richer framework for modeling neuronal dysfunction than spike-based phenomenological models.

A limitation of the present study is that all analyses were performed on a single previously optimized biomimetic SNN configuration. This choice allowed us to isolate the effects of ablation extent and lesion geometry under controlled conditions, but it does not fully address the sensitivity of the observed responses to the specific optimized topology, connectivity seed, or parameter configuration. Future work should therefore assess the robustness of our results across multiple independently optimized SNN configurations.

Overall, our findings show that lesion-like ablation can reshape both spontaneous activity and structural small-world organization in a biomimetic hardware SNN. The main contribution of this work is to show that ablation outcome depends not only on

the amount of neuronal loss, but also on its spatial arrangement within the connectivity scaffold. More broadly, real-time FPGA-based biomimetic SNNs provide a flexible framework to investigate how structural and biophysical perturbations influence network activity, connectivity, and reorganization in neural-like systems.

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Code and Data Availability. The codebase used for the analyses presented in this work is publicly available at: <https://github.com/samzahe/PAPER-AII-2026/tree/main>. The repository contains the scripts used to process the simulated spiking activity, perform progressive neuronal ablation analyses, compute the reported descriptors, run the statistical comparisons, and generate the figures included in the manuscript. Data and configuration files required to reproduce the reported results are provided in the repository where possible. Any additional material that cannot be openly distributed due to storage, licensing, or other practical constraints is available from the corresponding author upon reasonable request, where legally and ethically permissible.

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