Resilience in Complex Networks

Aditya Acharya, Keval Jain, Pranav Agarwal DPCN Spring 2024

1 Introduction

Resilience, a characteristic property of many complex networks, is defined as a system's ability to make adjustments to its network activity so as to retain its basic functionalities when subject to errors, failures or changes in its environment^[1].

1.1 Motivation

Events leading to loss of resilience in many real-world complex networks have catastrophic consequences. Examples include, but are not limited to:

- Cascading failures of technological systems^[1]: Interconnected technological systems such as power grids, telecommunications networks, and transportation systems, if not resilient to cascading failures, can lead to widespread outages or malfunctions.
- Mass extinction in ecological networks^[1]: Ecological networks, including food webs and ecosystems, can experience mass extinctions if not resilient to various external and internal factors such as habitat destruction, pollution, invasive species, and climate change. These extinctions can disrupt the delicate balance of ecosystems, leading to irreversible changes in biodiversity and ecosystem functioning.
- Economic Collapse in Financial Networks: A loss of resilience in large financial networks can lead to widespread economic failures. Small disturbances can cascade into large failures, impacting all economic agents (nodes) involved in the network

Such events are rarely predictable are often irreversible. It thus becomes vital that there exists a framework to understand resilience patterns and predict their occurrence.

2 Objective

In this project, we aim to analyze the resilience of a well-known network, the transcription regulatory networks of *E. Coli* when subjected to node losses. Post this analysis, we aim to extend our assessment to a network previously unexplored in the paper [1].

2.1 Methods

In our methodology, we adopt a systematic approach in understanding the network dynamics and its activities when subject to node loss and analyze how the network resilience evolves in response to these perturbations.

We begin by trimming 2% of the nodes iteration-by-iteration until there are no nodes left in the network. Throughout the node removal process, at every iteration, we calculate the average activity of the network, given by the statistical mean of the activities of all the nodes.

We repeat this process, subject to the original network configuration, for 50 runs. Following the completion of each run, we plot the average activity of the network against the fraction of nodes removed. This graphical representation assists in gaining insights regarding the relationship between the average activity of the network and the extent of node removal.

3 Network 1 - The E. Coli transcription regulatory network

The first network we focus our analysis on is the transcription regulatory network of E. Coli.

3.1 Network Definition

The transcription regulatory network of E. Coli is a gene regulatory network governed by Michaelis-Menten dynamics

$$\frac{dx_i}{dt} = -Bx_i^f + \sum_{j=1}^N A_{ij} \frac{x_j^h}{x_j^h + 1}$$
 (1)

The left-hand side term indicates the time evolution of the ith node of the network. The first term on the right-hand side of the equation describes degradation(f=1) or dimerization(f=2); the second term encapsulates genetic activation, captured by the adjacency matrix A, which captures the network connectivity and the hill coefficient h, which captures the level of cooperation in gene regulation [1].

3.1.1 Large Connected Components

The "large connected components" (LCCs) refers to the large connected subgraphs of a network, whose size crosses a cutoff-value. A connected subgraph is a subset of nodes and edges of a network such that a path can be constructed between any two nodes using the edges in the subset. Large connected component, therefore, represents the most substantial portion of the network where nodes are directly or indirectly connected to each other.

3.2 Simulating the Network Dynamics

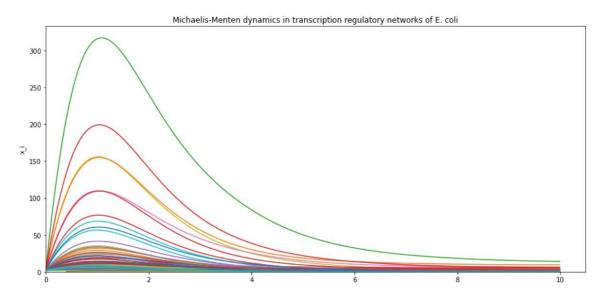


Figure 1: Dynamics of the E. Coli transcription regulatory network

We leverage NetworkX's method to find the largest strongly connected component and pick only those LCCs whose length crosses out the defined cutoff value. We then allow the LCCs network to evolve through time, and capture the dynamics of the network; plotting a graph of the dynamics of all its nodes against time. The graph is depicted in Figure 1.

The observed trend in the graph reflects the dynamics described by equation (1). Initially, the activity of the majority of nodes rises, indicating dominance of the 2^{nd} term on the RHS. This increase reaches a peak when the 1^{st} term and 2^{nd} term of the RHS neutralize each other. Subsequently, a gradual decline in activities is observed as the 1st term of the RHS begins to dominate. This dominance persists until eventually, the activities approach stable values significantly less than the peak activity.

3.3 Node Loss Resilience Analysis

To test for the network's resilience to node loss, we subject it's LCCs to the method previously outlined. Figure 2 depicts the graph of average activity against the fraction of nodes for all 50 runs. To understand the nature of the graph observed, the plot for 1 of the runs is highlighted in red.

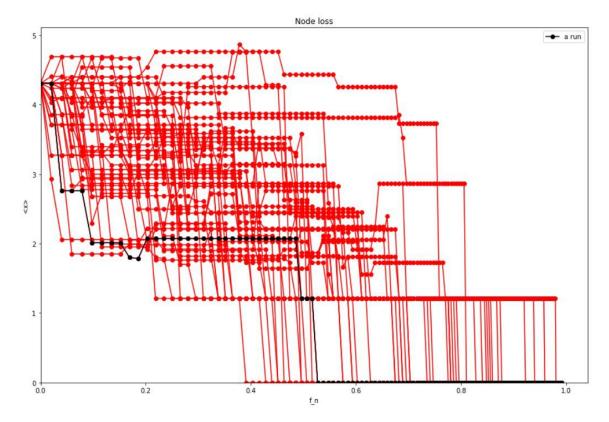


Figure 2: Dynamics of the E. Coli transcription regulatory network

Observing Figure 2 reveals a steady decrease in overall average network activity as the fraction of nodes removed increases. However, this decrease is moderate, indicating the network's ability to retain most of its activity i.e. it exhibits resilience to node removal.

However, at a critical juncture; when a significant fraction of the nodes have been removed, we observe that the activity falls sharply to 0, indicating a loss of the network's resilience, leading to its death, captured by a state in which the activity of the network falls to 0.

4 Network 2 - Random Neural Network

With a better understanding of node loss resilience in networks, we proceed to extend our analysis to a network previously unexplored in [1], a random neural network (rNN), as outlined in [2]

4.1 Network Definition

The random neural network (rNN), that is the focus of our investigation here, is defined as a cluster of N interconnected nodes (called units^[2]); each unit is a cluster of neurons; described by activation variables x_i , obeying the dynamics:

$$\frac{dx_i}{dt} = -x_i + s \cdot \tanh(x_i) + g \cdot \sum_{j=i}^{N} A_{ij} \cdot \tanh(x_j)$$
(2)

The left-hand side term indicates the time evolution of the ith node of the network. The 2^{nd} term on the right-hand side describes the self-coupling dynamics within a node, exhibited by its constituting clusters of neurons. The strength of this self-coupling is abstracted by the strength parameter s.

The 3^{rd} term on the right-hand side reflects the node-to-node interactions, captured by the strength parameter g, also known as network gain and the connectivity matrix (adjacency matrix) J. The elements of the N x N matrix J are drawn independently from a Gaussian distribution with mean 0 and variance 1/N.

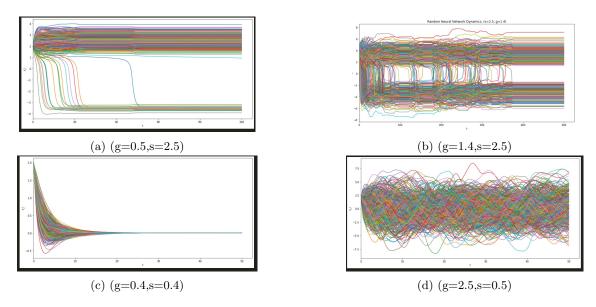


Figure 3: Plots of $x_i(t)$ against time for different values of (g,s)

4.2 Simulating the Network Dynamics

To simulate the network's dynamics, we construct networks consisting of 400 units and sample the edges from the Gaussian distribution with parameters mentioned in Section 4.1. The network dynamics are then simulated, allowing its activation variables to evolve through time governed by equation (2).

The self-coupling strength parameter s and the network gain g together determine the nature of network dynamics. We undertake multiple network realizations for different values of s and g.

In the case where s = 0, For g < 1, all network activity decays to 0 while for g > 1, the network exhibits chaotic behaviour (A state where the evolution of network dynamics becomes highly sensitive to the initial conditions and exhibits unpredictable behaviour)[3].

In the case where g = 0, s < 1, the only solutions possible are $x_i=0$, which is stable i.e. activities of all units decay to 0 irrespective of their initial state. For s > 1, there exists 1 unstable state ($x_i=0$ for all units) and two stable states that are negatives of each other.

Between s and g, the parameter that asserts its dominance on the network is determined by how significant the difference in values of both the parameters. To illustrate, in Figure 3(a), the bi-stable behaviour due to s dominates over the chaotic behaviour due to g since the value of s is much more pronounced over g. A similar effect is observed in Figure 3(d), where the chaotic behaviour (at x_i) due to g is dominated by the behaviour due to s, since here the value of g is much more pronounced over s.

The observations in Figure (3) reaffirm the dependence of network dynamics on values of s and g.

4.3 Node Loss Resilience Analysis

We now focus our analysis on the network's resilience when subject to node loss. We subject the network to the method previously outlined in Section 2.1 and plot the graph of its average activity against the fraction of nodes removed. We do so for each of the aforementioned network realizations.

To accommodate for activities whose values fall below 0, we calculate the statistical average activity separately for values that were positive and those that were negative.

We observe that the patterns of resilience in the graphs in Figure 4 are different, from each other and the one in Figure 2. Only figure 4 (c) and (d) show some similarity with the pattern in figure 2, average activity becomes zero after a certain value of fn.

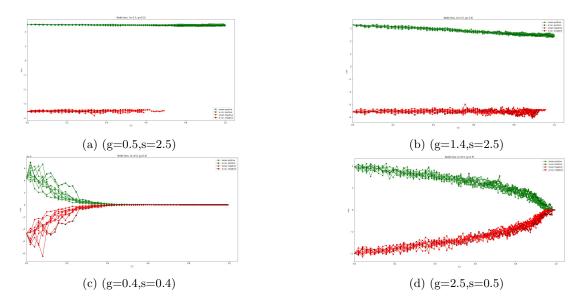


Figure 4: Plots of average activities against fraction of nodes removed for different values of (g,s)

For Figures 4 (a) and (b), strong resilience to node removal is observed. This can be explained by the high value of the self-coupling parameter 's', which ensures a non-zero fixed point for the network.

5 Network 3 - *E. Coli* Transcription Regulatory Network Governed by rNN Dynamics

We aim to go one step further by analysing the node loss resilience of a network whose structure is identical to the *E. Coli* Transcription Regulatory Network (defined in Section 3.1) but is governed by the dynamics of the random neural network (defined in Section 4.1)

5.1 Network Definition and Dynamics

The network is defined by the adjacency matrix of the $E.\ Coli$ Transcription Regulatory Network and its dynamics are driven by equation (2). To simulate, we allow the activities of all the nodes to evolve through time.

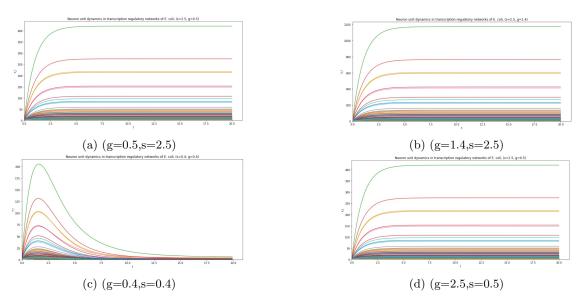


Figure 5: Plots of $x_i(t)$ against time for different values of (g,s)

We simulate the network dynamics with parameter values of s and g identical to the ones chosen for the random neural network. Our observations aligned with our expectations and understanding from the previous

simulations involving rNNs; the dependence of network dynamics on the values of s and g showed similar characteristics.

For g < 1 and s < 1, all activities, irrespective of the initial conditions, eventually decay into the only stable state $x_i=0$ for all nodes in the graph (Shown in Figure 5(c)). For s > 1, the network activities settle into the only non-zero stable states. We omit the negative activity values as they hold no relevance in a transcription regulatory network.

The only observation that stood out differently was for the case g > 1 and s < 1. The network neither decayed towards activity 0 nor towards chaotic behaviour.

5.2 Node Loss Resilience Analysis

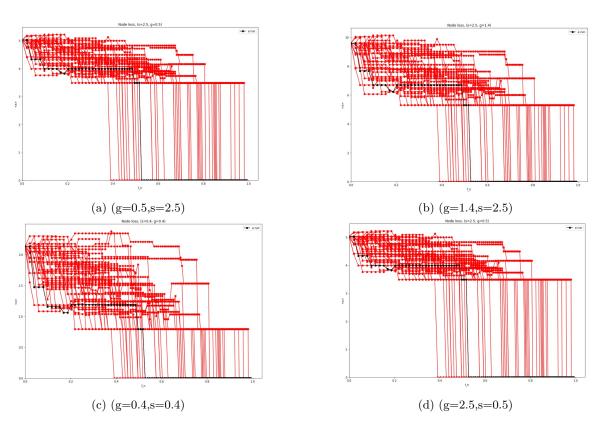


Figure 6: Plots of average network activity against the fraction of nodes removed

All four network realizations are subject to the method outlined in Section 2.1 to test for node loss resilience.

The results observed match our expectations. For all 4 realizations, as the fraction of nodes removed increases, the network manages to retain a very significant portion of its activity, keeping its decrease moderate, therefore exhibiting resilience.

We again observe the presence of a critical juncture at a point where a significant fraction of nodes have been removed when the network loses its resilience ability and dies.

6 Conclusion

After a successful analysis of networks of varying structures and dynamics, we proceed to conclude our findings about the nature of resilience in complex networks. Most networks exhibit resilience, a property wherein it maintains most of its basic functionality, captured by its average activity, when subject to perturbations; in this case, node removal.

The network holds its ability to exhibit resilience only until a certain juncture, after which the perturbations it is subject to become excessive for it to endure. This is the point where it loses its ability to stay resilient, and experiences death, a state in which the activity of the network falls to 0. However, this pattern depends on the network topology, while the value for the juncture depends on the values of the parameters of the dynamics.

7 References

- [1] Gao, J., Barzel, B. & Barabási, AL. Universal resilience patterns in complex networks. Nature 530, 307–312 (2016). https://doi.org/10.1038/nature16948
- [2] Stern, M., Sompolinsky, H., Abbott, L. F. (2014). Dynamics of random neural networks with bistable units. Physical Review E, 90(6), 062710. https://doi.org/10.1103/PhysRevE.90.062710
- [3] Sompolinsky, H., Crisanti, A., Sommers, H. J. (1988). Chaos in Random Neural Networks. Phys. Rev. Lett., 61(3), 259–262. DOI: 10.1103/PhysRevLett.61.259