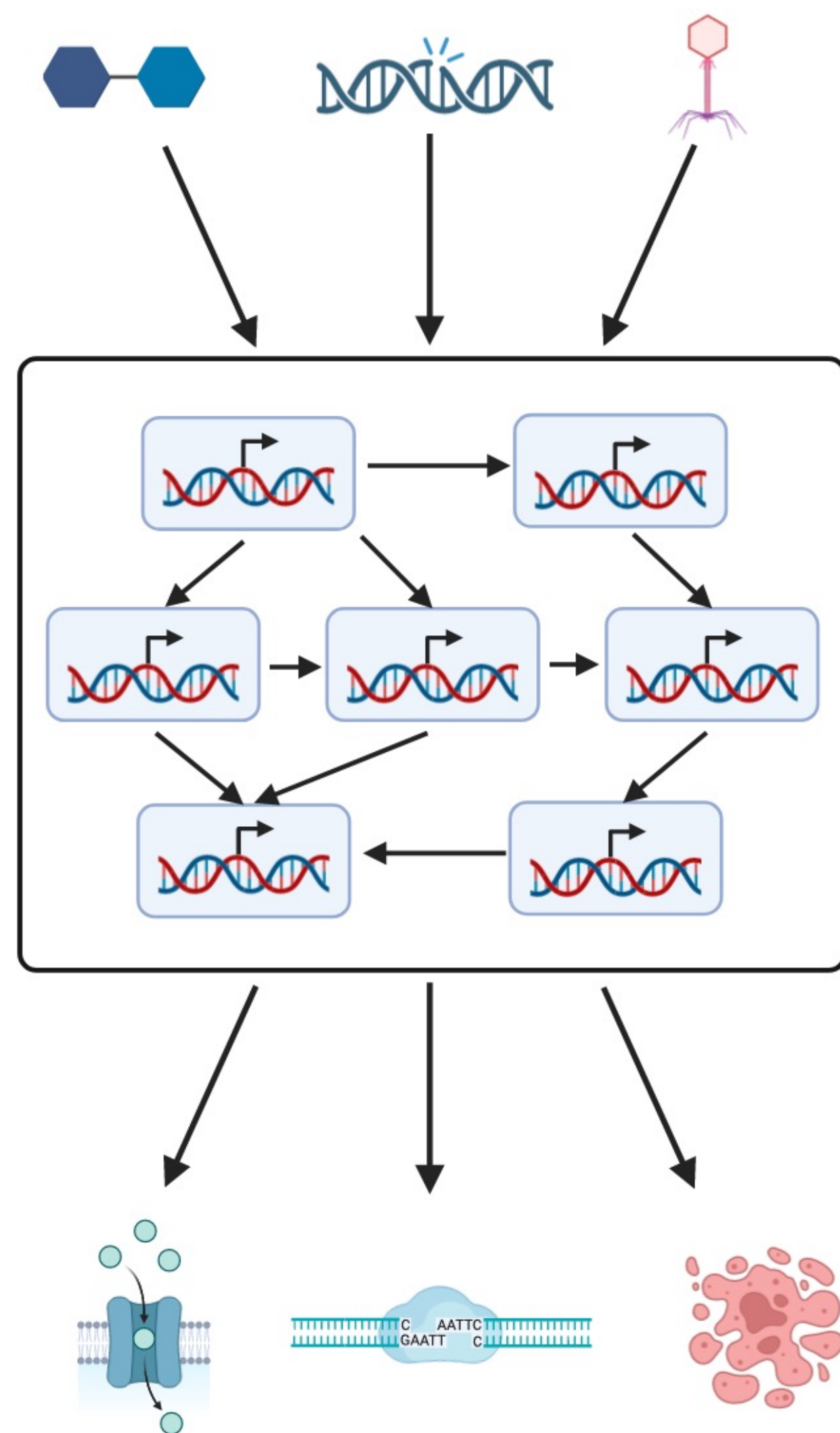


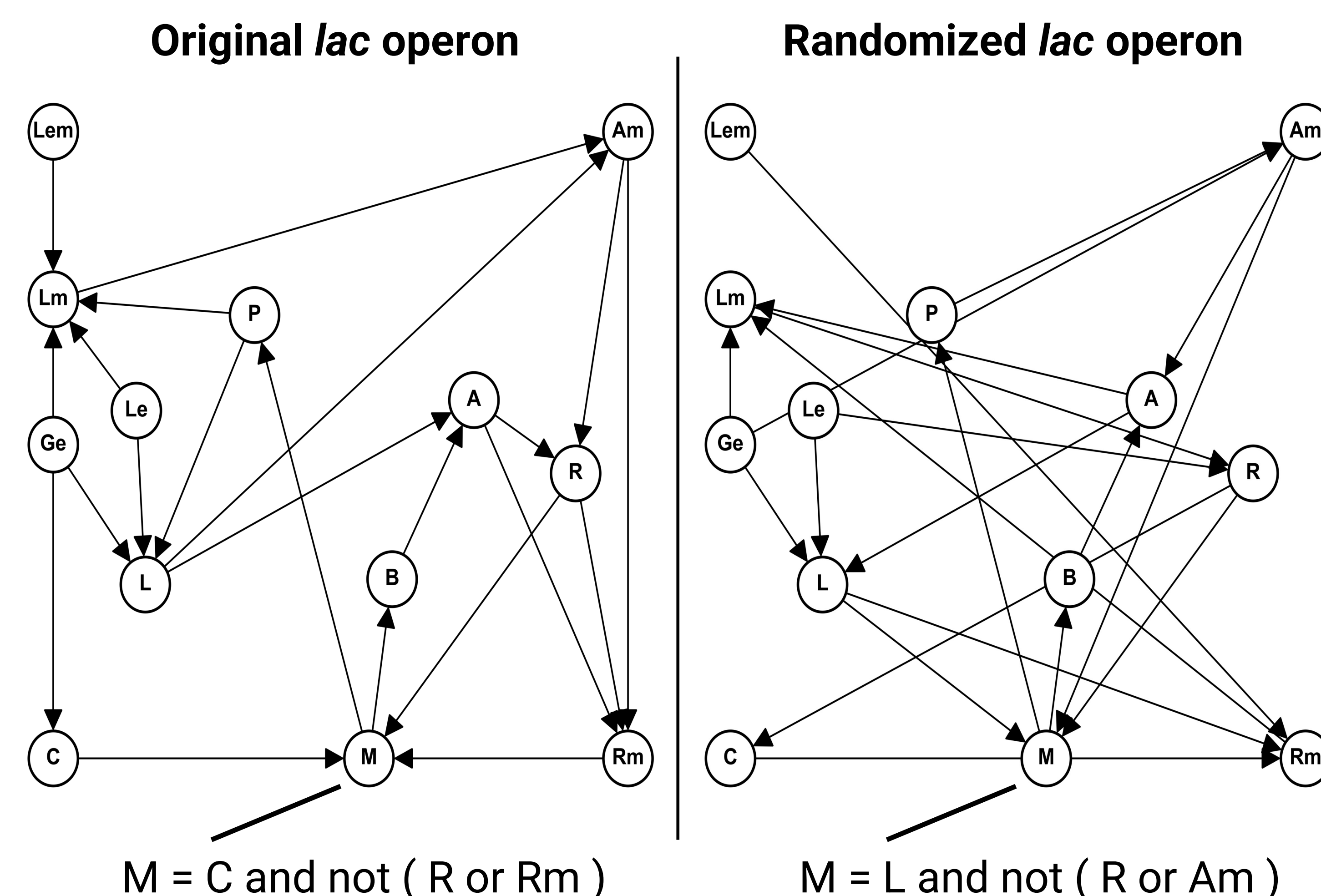
Motivation and Questions

- Gene regulatory networks (GRNs) allow cells to respond to environmental signals.
 - GRNs can be modeled as Boolean networks with a logic function governing each node.
 - Simplistic model makes complex systems computationally tractable.
 - Objective: compare Boolean GRN models to null models with equivalent properties.
- To what extent does topology contribute to network stability?
 - Which topological features best account for network stability?

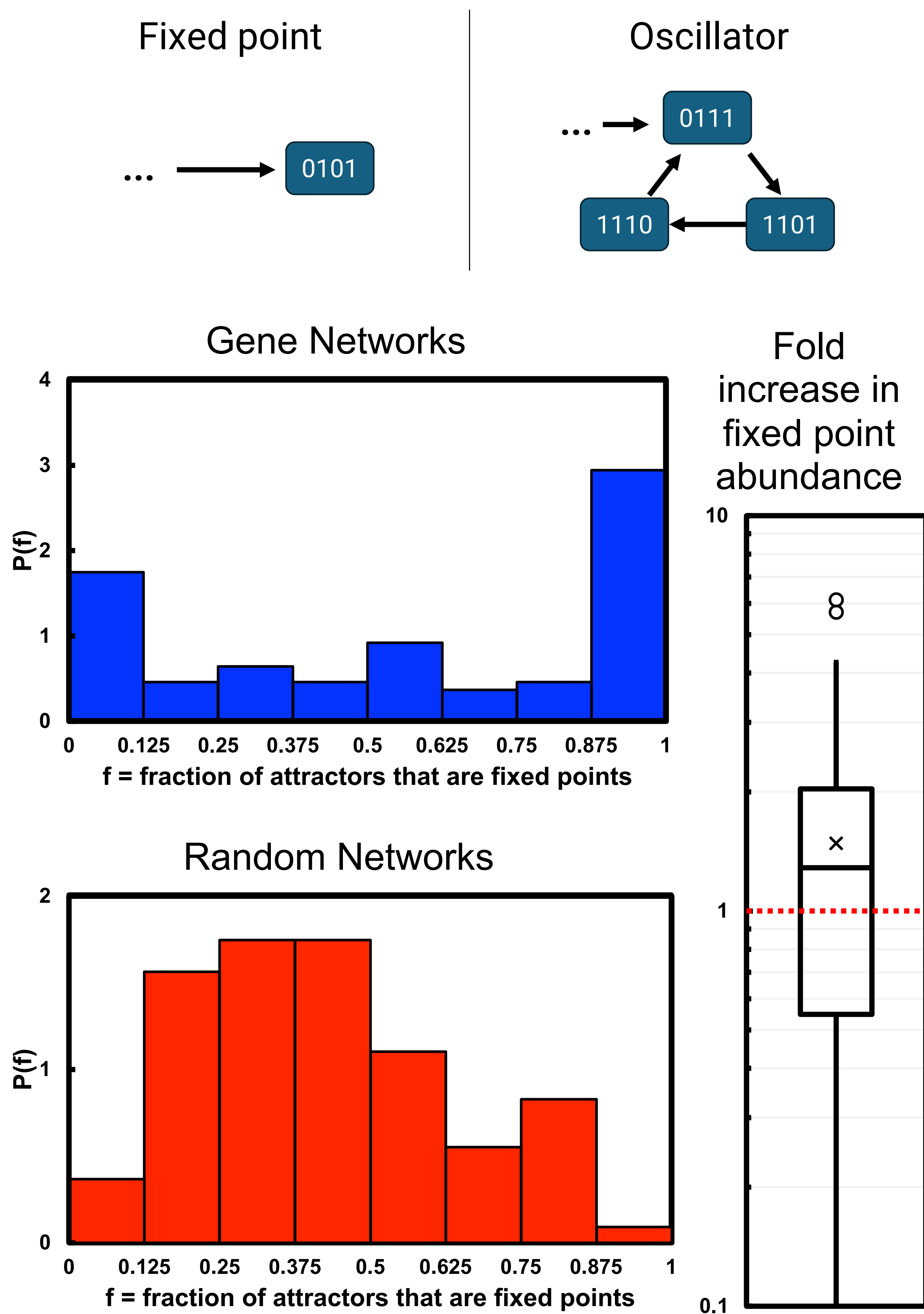


Methods

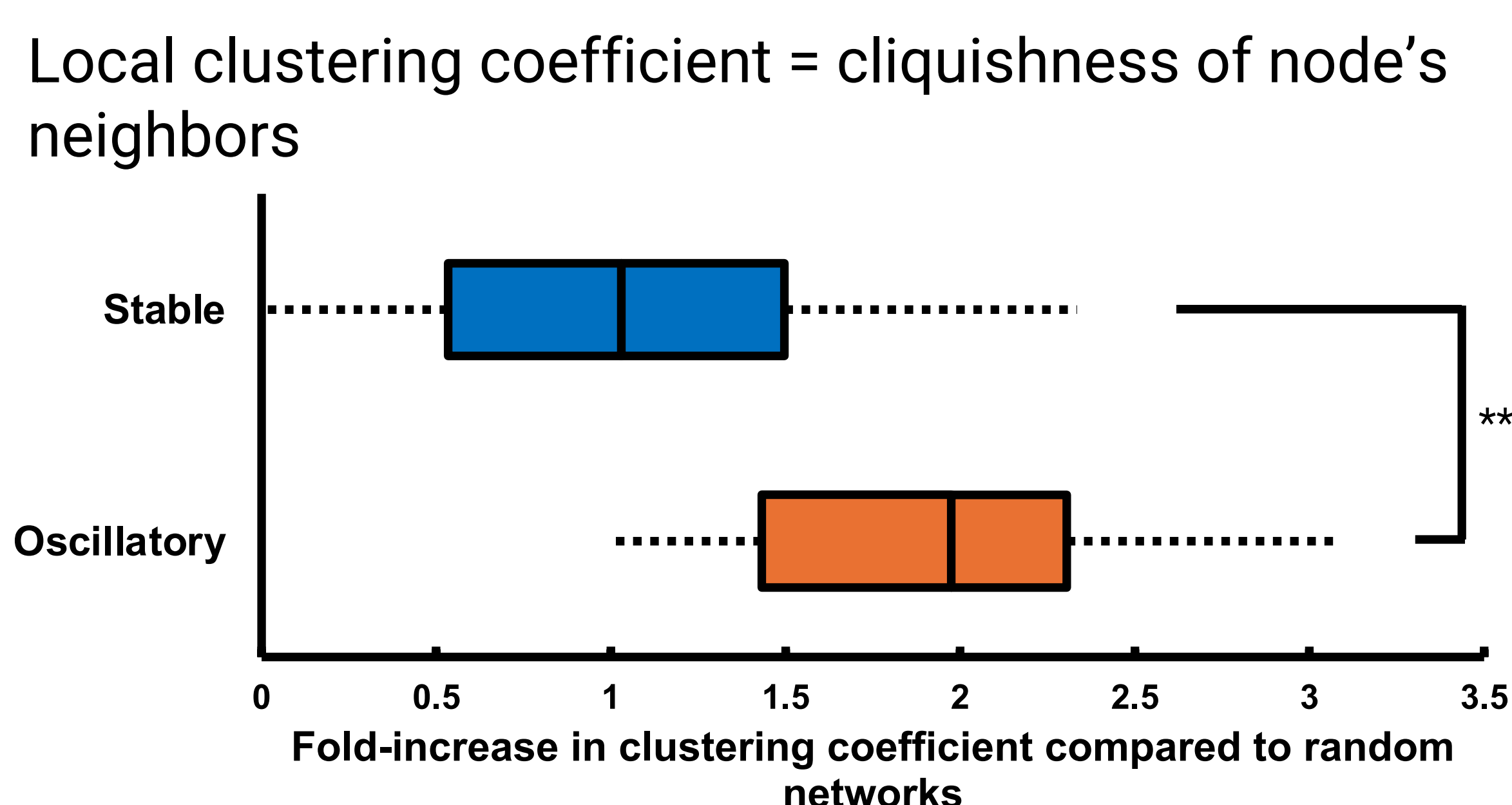
- 87 GRN models were obtained from CellCollective database [1].
- Random networks were generated such that in-degrees, out-degrees, and logic functions were preserved at each node.
- Stability analysis averaged results from 100 random networks with 1000 initial conditions on each. Cluster and loop analyses averaged results over 1000 random networks.



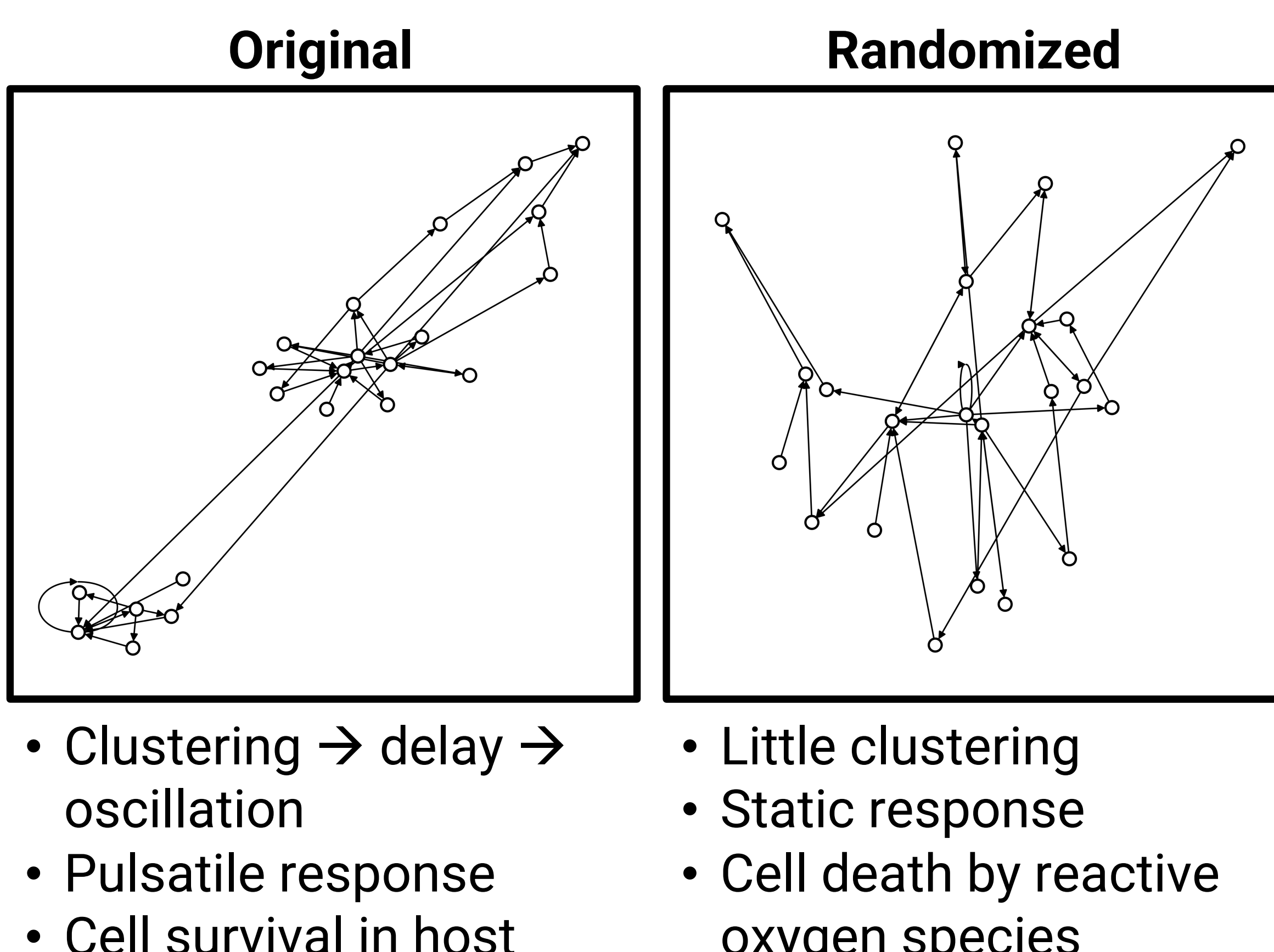
Fixed points are abundant in GRNs



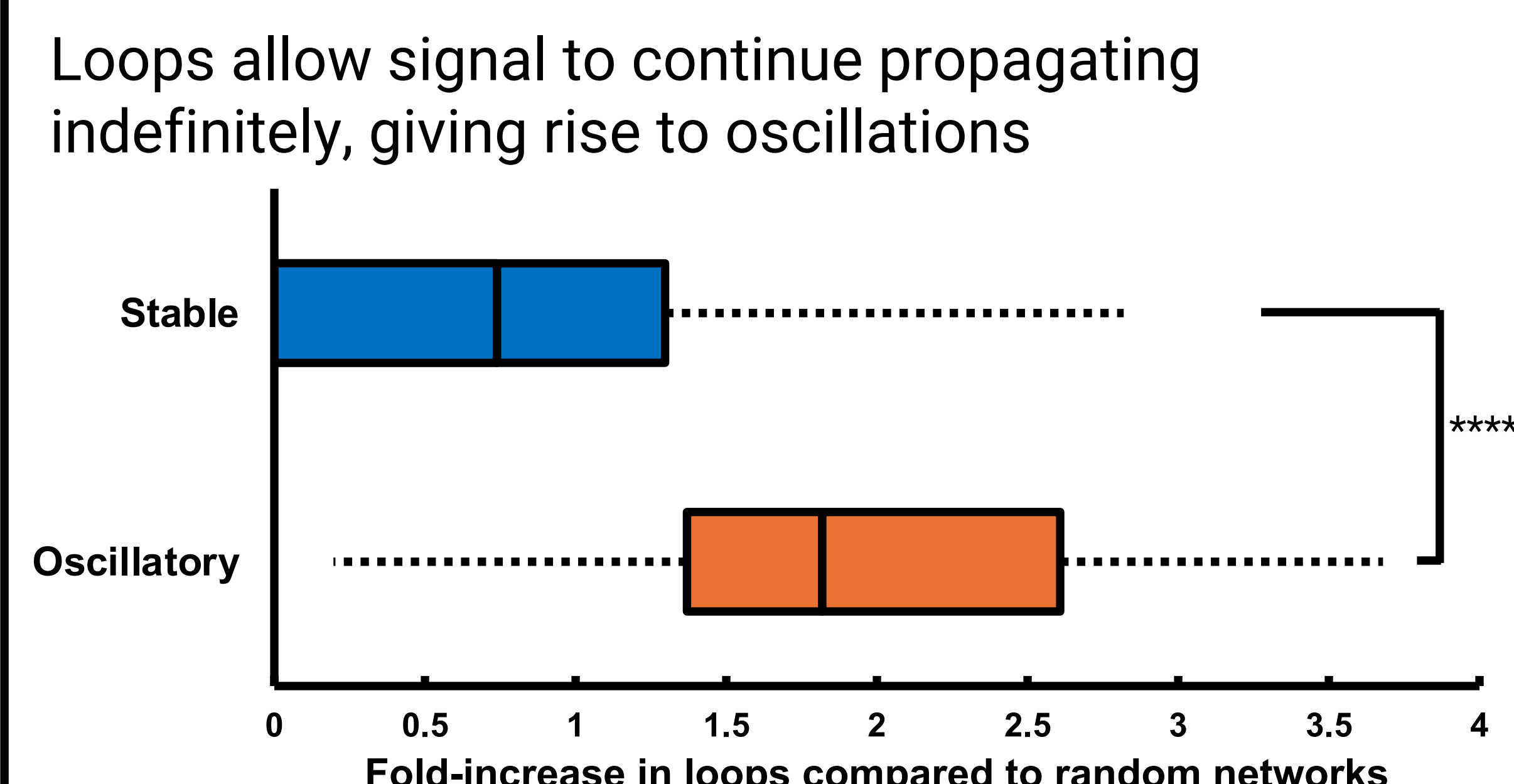
Clusters are overrepresented in oscillatory GRNs



Example: fungus iron acquisition GRN uses clustering to maintain cell survival



Loop frequency decreases in stable GRNs



Potential Applications

- Systems Biology:** Predict cell behaviors from GRNs without needing to know the nature of any gene-gene interactions.
- Synthetic biology:** Use network topology to design cell circuits with pulsatile or static responses.
- Biomedicine:** GRN topologies reveal potential genetic targets for effective disease therapies.

[1] Helikar, T., Kowal, B., McClenathan, S. *et al.* The Cell Collective: Toward an open and collaborative approach to systems biology. *BMC Syst Biol* 6, 96 (2012).