SAAP Journal of Integrative Physiology

https://www.thesaap.org/saap-journal

ISSN 3121-410X (Online)

PERSPECTIVE | SJIP 2026

Near-Perfect Organization Without Leaders: A Multiscale Network Perspective on Physiology and Governance

Saubhik Sengupta*

Chittaranjan National Cancer Institute, Kolkata, India

Abstract

The human body achieves remarkable functional order without any centralized command, operating instead through nested biological networks spanning molecular, cellular, tissue, and organ levels. At the most fundamental scale, cellular organization emerges from physical and chemical interactions among proteins, lipids, metabolites, and nucleic acids, governed by forces including electrostatic interactions, hydrogen bonding, hydrophobic effects, and van der Waals forces, further modulated by the effects of molecular crowding on reaction dynamics and component behavior. These cellular units are not isolated; they assemble into tissues, organs, and integrated body systems that collectively sustain life through continuous, multilevel coordination. All of these networks are subject to ongoing perturbation by the exposome, the cumulative environmental exposures encountered across a lifetime, ranging from nutritional and toxic inputs to psychosocial stressors and infectious agents. It is proposed that applying the mathematical frameworks of network science, including interaction pathways, connectivity analysis, and control topology, across each biological scale offers a principled approach to linking environmental exposures to molecular and cellular dysregulation, and ultimately to health or disease outcomes. This multiscale network perspective suggests that the same theoretical tools developed to understand leaderless complex systems may illuminate how the body maintains homeostasis, responds to stress, and transitions toward pathological states. Such a framework could advance the understanding of the organizational principles underlying human physiology and inform new strategies for exposome-aware, systems-level approaches to medicine.

Keywords: Centrality, exposome, flux, governance, Laplacian, networks, organization, perfection, physiology, stigmergy

1. Introduction

A single human cell is a well-organized system, even though no single molecule acts like a CEO giving orders. Instead, the cell works through constant interactions among proteins, lipids, metabolites, and nucleic acids. These interactions are shaped by basic physical forces such as electrical attraction and repulsion, hydrogen bonding, hydrophobic effects, and van der Waals forces, which help molecules bind, fold, and function properly[1]. The inside of the cell is also very crowded, and this molecular crowding strongly affects how reactions occur and how cell components behave[2].

Cells do not work alone. Many cells join together to form tissues, tissues form organs, and organs form body systems. In this way, the human body can be understood as a set of connected biological networks operating at different levels[3].

These networks are constantly influenced by the exposome, which means the total set of environmental exposures a person experiences throughout life, including food, toxins, stress, infections, and social conditions[4]. Such exposures can disturb biological processes at many levels, from molecules inside cells to whole organs and systems.

If we describe each level using mathematical tools from network science, such as interaction pathways, connectivity, and control rules, then we may be able to link environmental exposures to changes in cellular activity and, ultimately, to health or disease outcomes. In simple terms, the same mathematical ideas used to study complex organizations without a central leader may also help us understand how the body maintains health, adapts to stress, or moves toward disease.

**Address for Correspondence:*
Dr. Saubhik Sengupta
Chittaranjan National Cancer Institute,
37, S.P. Mukherjee Road, Kolkata – 700026, India
E-mail: saubhiksengupta@gmail.com

How to cite this article: Sengupta S. Near-perfect organization without leaders: a multiscale network perspective on physiology and governance. SAAP J Integr Physiol. 2026;1(1): 26-28.

2. The Master Equation for Interaction Flux

The model views the cell as a dynamic network in which one molecule influences another. Here, *Sij* represents the strength of influence from source molecule *i* to target molecule *j*. This influence increases when the source activates the target and decreases when inhibition, local resistance, or competing interactions are high. It also weakens when the source is connected to many other molecules, because its effect is distributed across multiple targets. *Ei* and *Ej* indicate the expression levels of the source and target molecules, while *NetActj* reflects the overall balance of activating and inhibiting inputs reaching the target. Thus, molecular signaling is described as a network process rather than a simple one-to-one event[5].

The equation can be refined by adding factors such as cytoplasmic viscosity, molecular crowding, energy use, and the actin-myosin meshwork, all of which shape diffusion and molecular interactions inside cells. However, these are often difficult to measure in living single cells. In physiology, such flux equations may help explain how nutrients, drugs, or toxins alter pathway activity. By analogy, in organizations *Ei* reflects capability, *ωi* workload, and *vij* local resistance or friction. Therefore, strong *Sij* represents efficient collaboration, whereas overload and friction weaken performance[6].

3. Extended Flux, Net Activation, and Multilayer Outcomes

A human cell can be viewed as a 3-D interaction network in which molecular influence is dynamic, not fixed. In this framework, the basic influence between two molecules (*Sij*) can be expanded to include disturbance sensitivity and local contextual change, so an interaction may strengthen or weaken depending on surrounding conditions. This systems-level view is consistent with systems biology, which explains cellular behavior as an emergent property of many interacting components rather than isolated parts alone[7].

A second expression compares local activity with the total net activation of the wider network, asking how strongly one part responds relative to the condition of the whole system. This is useful because cellular and organ behavior depends on broader network state, a key idea in network medicine and network physiology[8].

In physiology, such a model may help explain how the exposome – lifetime exposure to stress, diet, infection, and pollutants – alters biological responses over time by changing node sensitivity and context[9]. Applied across molecules, cells, tissues, and organs, these equations could help link exposure patterns to disease. By analogy, organizations may also be understood as dynamic networks shaped by local responsiveness and wider system constraints, rather than by a single central controller.

4. Centralities, Grounded Laplacian, and Anchored States

The *network centrality* shows that leadership can emerge from a node's position in a network rather than from formal authority. Nodes with high *closeness centrality* spread information quickly, those with high *betweenness centrality* act as bridges between groups, and those with high *eigenvector centrality* gain importance by being linked to other important nodes[10]. PageRank adds that links from influential nodes carry more weight, while that influence is divided across all their outgoing links. In organizations, these measures can help identify hidden leaders such as connectors, informal mentors, and trusted influencers[11].

The *grounded Laplacian* helps analyze networks in which some nodes remain fixed. Starting from the Laplacian matrix, $L = D - A$, where D is the degree matrix and A is the adjacency matrix, the network is divided into active nodes and grounded nodes. This allows us to study how activity flows toward fixed points[12]. In physiology, grounded nodes may represent homeostatic constraints such as body temperature, blood pressure, or osmolarity[13]. In organizations, they can represent fixed goals like safety, ethics, or mission targets that guide the adjustment of the wider system.

5. Stigmergy, Basal Epsilon, and Governance-as-Code

Self-organizing biological and social systems often work without a single commander. Instead, individuals respond to local signals or traces left in their environment. This process is called *stigmergy*. In biology, it helps explain how complex group behavior can arise from many small local actions rather than direct instructions from above. Using this idea, a company can be imagined not as a strict top-down pyramid, but as a distributed network. In such a system, people and teams act according to shared rules, local information, and real-time feedback. No single *master node* controls everything, so the failure of one person or unit does not necessarily break the whole organization[14].

The idea of *basal epsilon* can be understood as the minimum level of activity needed to keep the network alive and creative. In practice, this means regular cross-team contact, rotating groups, and periodic advisory discussions. These interactions create opportunities for fresh ideas, much like random encounters in biological systems can lead to new reactions and new forms of order[15].

In this model, *governance-as-code* means that decision-making follows clear protocols. People with the right expertise can make decisions, but they should consult those affected, record the reasons for their decisions, and follow fixed deadlines or default actions. This reduces confusion and prevents endless delays.

Resources can also be distributed in a more network-based way. For example, support can flow more toward projects that are more connected, trusted, or useful to the wider system, similar to the logic behind PageRank[16]. At the same time, feedback loops can gradually reduce support for weak or misaligned projects without blaming individuals. This idea resembles the use of grounded Laplacian models in network analysis, where fixed constraints help stabilize the overall system. Overall, such an organization is not completely leaderless, but it is less dependent on personalities. Stability comes mainly from rules, connections, and feedback flows rather than from a single powerful leader.

6. Error, Repair, and Limits of Perfection

This system can be called *near perfect* rather than perfect. In biology, when DNA is copied, mistakes can occur. Cells have repair systems such as mismatch repair, translesion repair, and excision repair that correct or bypass many of these problems, but not all errors are removed. Some changes remain, and over time these can contribute to diseases like cancer[17].

In the same way, a leaderless organization or a multilayer model of human physiology can be made very strong, but it can never be completely free from mistakes. Bias, poor incentives, and unexpected shocks may still appear, even when the rules are clear and the system is transparent. This is why the goal is not perfection, but a system that can detect problems early, reduce damage, and recover quickly.

Three main problems may arise. The first is the accountability void or *ghost node*, where work stops but nobody knows who is responsible. In such cases, the focus should shift from blaming a person to checking the protocol and tracing where the flow failed. The second is decision paralysis or *infinite loops*, where discussion continues without action. This can be controlled by setting a fixed time or limit, after which the system either does nothing or returns to the last stable state. The third is the power vacuum or *shadow leader*, where influence becomes too concentrated in one node. Network methods such as centrality analysis can help identify overly dominant nodes and keep the system balanced[18].

These ideas are similar to what happens in cells. Biological repair systems do not prevent every failure, but they lower the chance of serious damage and help the system remain stable. Therefore, a near perfect organization without leadership – and a predictive, exposome-aware model of physiology – should be seen not as a utopian perfect system, but as a robust and adaptive system that accepts imperfection and manages it intelligently.

7. Conclusion

This view suggests that the same mathematical ideas used to explain leaderless organizations can also help us understand human physiology across many levels. Molecules, cells, tissues, organs, and even organizations can all be seen as connected networks in which overall behavior emerges from local interactions and built-in constraints, rather than from a single controlling leader. In this model, fixed rules or *ground conditions* take the place of leadership, while factors such as friction, inhibition, and stigmergic coordination help regulate how the system functions and remains active.

In physiology, this approach may help build exposome-aware models of health by tracing how environmental influences act through multiple biological layers to produce effects on the whole body. However, like biological repair systems, these networked systems are not flawless. They are only *near perfect* and can still be affected by errors, drift, and unexpected disturbances. The next challenge is to test these mathematical ideas in real organizations and in computational models of physiology so they can be measured, checked, and gradually improved for practical use in governance and medicine.

References

1. Newberry RW, Raines RT. Secondary forces in protein folding. ACS Chem Biol. 2019;14(8):1677-86. DOI: 10.1021/acschembio.9b00339.
2. Garner MM, Burg MB. Macromolecular crowding and confinement in cells exposed to hypertonicity. Am J Physiol. 1994;266(4 Pt 1):C877-92. DOI: 10.1152/ajpcell.1994.266.4.C877.
3. Bashan A, Bartsch RP, Kantelhardt JW, Havlin S, Ivanov PC. Network physiology reveals relations between network topology and physiological function. Nat Commun. 2012;3:702. DOI: 10.1038/ncomms1705.
4. Wild CP. The exposome: from concept to utility. Int J Epidemiol. 2012;41(1):24-32. DOI: 10.1093/ije/dyr236.
5. Luby-Phelps K, Taylor DL, Lanni F. Probing the structure of cytoplasm. J Cell Biol. 1986;102(6):2015-22. DOI: 10.1083/jcb.102.6.2015.
6. Minton AP. Implications of macromolecular crowding for protein assembly. Curr Opin Struct Biol. 2000;10(1):34-9. DOI: 10.1016/s0959-440x(99)00045-7.
7. Kitano H. Computational systems biology. Nature. 2002;420(6912):206-10. DOI: 10.1038/nature01254.
8. Barabási AL, Gulbahce N, Loscalzo J. Network medicine: a network-based approach to human disease. Nat Rev Genet. 2011;12(1):56-68. DOI: 10.1038/nrg2918.
9. Wild CP. Complementing the genome with an "exposome": the outstanding challenge of environmental exposure measurement in molecular epidemiology. Cancer Epidemiol Biomarkers Prev. 2005;14(8):1847-50. DOI: 10.1158/1055-9965.EPI-05-0456.
10. Freeman LC. Centrality in social networks conceptual clarification. Soc Netw. 1978-1979;1(3):215-39. DOI: 10.1016/0378-8733(78)90021-7.
11. Panditrao G, Bhowmick R, Meena C, Sarkar RR. Emerging landscape of molecular interaction networks: opportunities, challenges and prospects. J Biosci. 2022;47(2):24. DOI: 10.1007/s12038-022-00253-y.
12. Xia W, Cao M. Analysis and applications of spectral properties of grounded Laplacian matrices for directed networks. Automatica. 2017;80:10-16. DOI: 10.1016/j.automatica.2017.01.009.
13. Goldstein DS. How does homeostasis happen? Integrative physiological, systems biological, and evolutionary perspectives. Am J Physiol Regul Integr Comp Physiol. 2019;316(4):R301-R317. DOI: 10.1152/ajpregu.00396.2018.
14. Heylighen F. Stigmergy as a universal coordination mechanism I: definition and components. Cogn Syst Res. 2016;38:4-13. DOI: 10.1016/j.cogsys.2015.12.002.
15. Holland O, Melhuish C. Stigmergy, self-organization, and sorting in collective robotics. Artif Life. 1999;5(2):173-202. DOI: 10.1162/106454699568737.
16. Brin S, Page L. The anatomy of a large-scale hypertextual web search engine. Comput Netw ISDN Syst. 1998;30(1-7):107-17. DOI: 10.1016/S0169-7552(98)00110-X.
17. Kunkel TA, Erie DA. DNA mismatch repair. Annu Rev Biochem. 2005;74:681-710. DOI: 10.1146/annurev.biochem.74.082803.133243.
18. Koschützki D, Schreiber F. Centrality analysis methods for biological networks and their application to gene regulatory networks. Gene Regul Syst Bio. 2008;2:193-201. DOI: 10.4137/grsb.s702.