

Network Science as a Falsifiable Discipline: From Graphs to Testable Laws

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An often-told narrative depicts the rise of network science as a sudden event at the very end of the twentieth century. Yet, its intellectual roots extend much further back in time, beginning in 1735 with Leonhard Euler's Königsberg Bridges¹ problem, which is often cited as an early abstraction anticipating graph theory. It continues through Santiago Ramón y Cajal's 1894 discovery², which established that the brain is composed of discrete cells—neurons—rather than continuous tissues, effectively framing it as a network. In the social sciences, it traces back to Jacob Moreno's sociograms³ of the 1930s and extends to a little-known but foundational manuscript written around 1960 by Ithiel de Sola Pool and Manfred Kochen⁴—unpublished until 1978—that nonetheless inspired Stanley Milgram's 1967 small-world experiment⁵ and led to Mark Granovetter's theories of weak ties⁶ in the 1970s.

Many of these developments were deeply disciplinary, rooted in mathematics, biology and sociology, and were largely unaware of each other. By 2000, this 265-year history of disciplinary focus on networks had yielded less than 20,000 papers according to Microsoft Academic Graph (MAG⁷) (**Figure 1**). Most of these originated in two disjoint communities: graph theory and social network research (**Figure 2a**). According to Figure 1, interest in network research underwent a significant shift in the early 21st century, driven primarily by two publications. One of these built upon sociological foundations initially laid by de Sola Pool and Kochen, revitalizing decades-long discussions in sociology by rigorously examining the small-world property⁸. The other drew from statistical physics and random graph theory, to identify a novel, universal characteristic: the scale-free structure inherent in real-world networks⁹. Together, these studies sparked a rapid, cross-disciplinary surge of interest in network analysis, leading to approximately 192,000 publications by 2023 (Figure 1). Furthermore, they provided a unified theoretical framework that attracted scholars from diverse fields—including physics, computer science, biology, epidemiology, and other disciplines—many of whom had previously shown limited or no interest in connectivity and network theory.

By 2005, when the U.S. National Academies of Science issued the report titled *Network Science*¹⁰, it was already documenting the presence of a robust interdisciplinary field with its own independent intellectual foundation. Twenty years later, network scientists are no longer seeking their place in the scientific canon, but relay on widespread institutional support: multiple international conference series, several specialized journals, PhD programs on several continents, and countless network-focused institutes and centers, along with dedicated support from funding agencies worldwide. This has also fueled a rapidly expanding ecosystem of subfields—ranging from network medicine and network neuroscience to network economics and network epidemiology—each with its own distinct intellectual pursuits and communities.

Most chapters in this volume focus on social networks and their applications in social and economic systems. My goal is to offer a complementary perspective—one rooted in the physics

and the study of complex systems. In response to the request of the 2023 Nobel Symposium organizers, the following is not intended as a review of network science, as thorough overviews already exist in specialized journals^{11 12 13 14} monographs¹⁵ and textbooks^{16 17 18 19}. Rather, I offer an intentionally subjective account of the key conceptual forces that shaped the field, focusing on foundational ideas and illustrating how they connect with the broader effort to understand complex systems.

Early Motivations: Percolation and Underground Water Flows

I can date my interest in networks with unusual precision—it began in December 1994, a few months into my brief postdoctoral appointment in the Physics Division at IBM’s T. J. Watson Research Center. As the winter holidays brought a predictable slowdown to life at Watson, I decided to use the break to learn more about my new environment. At the time, IBM was synonymous with computing, so I visited the Watson library in search of an introduction to computer science. I left with a book that covered a wide range of topics, from algorithms to Boolean logic and NP-completeness.

One chapter focusing on the minimum spanning tree problem caught my attention. I realized that Kruskal’s algorithm, used by both graph theorists and engineers to identify the optimal tree in a network, was equivalent to a well-known model in statistical physics, invasion percolation, which describes flow in porous media. That insight led to my first network paper, submitted on February 24, 1995, to *Physical Review Letters*, where I used a network perspective to demonstrate the equivalence of two much-studied problems in statistical physics and computer science²⁰.

Over the next few months, I worked through Béla Bollobás’ classic text on random graphs²¹, which introduced me to the foundational work of Erdős and Rényi²². I spent the remainder of my time at IBM finishing a second paper, titled *Dynamics of Random Networks: Connectivity and First-Order Phase Transitions*²³, examining how network topology affects system behavior and dynamics. The central observation was simple: if one alters the average degree of a random network, the Boolean system defined on that network undergoes a dynamical phase transition. Its implications were deeper—it pointed toward a question that only became a subject of inquiry a decade later: how the structure of a network defines its dynamics.

I posted the paper on arXiv in November 1995, after it was rejected by four journals—*Nature*, *Science*, *Physical Review Letters*, and *Europhysics Letters*. Despite the many rejections, it marked a turning point in my thinking, showing me that networks are not just an abstraction or a way to document the dependencies within a complex system, but that changes in the network can fundamentally alter a system’s behavior. That realization solidified my interests in the topic, and from that moment on, networks became the primary focus of my research.

Reconciling Network Perspectives: From Infrastructure to Social Systems

What distinguishes physics from mathematics is its empirical foundation—the need to find experimental evidence to support or falsify mathematical theories. So, while I was struggling to publish my second network paper, I became increasingly convinced that the next step had to be empirical. I must collect data on real networks.

This was early 1996—five years after Tim Berners-Lee released the first web protocols, and two years before Google was founded. The Web was just beginning to take shape. An odd assortment of academic search engines—names like JumpStation, RBSE Spider, and WebCrawler—were attempting to map its growing structure. In February 1996, I emailed several researchers engaged in developing these early crawlers, asking for a sample of their data. But no one replied. Progress stalled until 1998, when Hawoong Jeong joined my group as a postdoc. His knowledge of computing was remarkable, so I asked if he could build a crawler—a robot that could map the Web. A few weeks later, Hawoong's crawler was online, and I could return to the problem I was forced to abandon two years earlier: examining the network behind the World Wide Web (WWW).

My goal was to answer a foundational question: Is the WWW a single connected network, or a collection of isolated clusters? A random network undergoes a phase transition when its link density crosses a critical threshold, forming a giant connected component out of many small, disconnected parts. If the WWW were random, its degree distribution should follow a Poisson distribution, meaning that most nodes have comparable degree, in the close vicinity of the average degree, $\langle k \rangle$. Then all we needed was the critical average degree, $\langle k \rangle$, to determine if the Web had crossed the critical threshold.

Yet, once the data arrived, the premise of our approach fell apart: the empirically observed degree distribution did not follow the Poisson distribution predicted by random network theory. Instead, it was well-approximated by a power law, or a fat-tailed distribution (**Figure 2**). This meant that while most webpages had very few links, a few had a vast number—functioning as hubs. Such extreme outliers were mathematically impossible in a random graph.

For someone trained in statistical physics, the presence of a power law carried deep significance. Indeed, power-law distributions often emerge at the critical point of phase transitions, describing phenomena ranging from magnetization to liquid condensation. Physicists have developed both the theoretical tools and the experimental intuition to study such behavior—backed by decades of evidence and several Nobel Prizes. Thus, the discovery that the Web is characterized by a power-law degree distribution was not only highly unexpected but also placed networks squarely within the realm of statistical physics, offering a rich analytical and numerical tool set to explore this emerging structure.

Excited by this development, we soon submitted the discovery of the power law degree distribution to *Nature*²⁴. We understood, however, that this was merely an empirical observation—an experiment, if you will—that nevertheless revealed something truly unexpected about real networks. We still lacked the crucial next step physicists typically demand: a theoretical framework and a mechanism to explain the origin of the observed power laws.

Universality

Social scientists often focus on the particular. When mapping social ties, they pay close attention to cultural rituals, status hierarchies, and historical legacies—factors that help explain why certain connections form or dissolve. For example, a school's friendship network may cluster around race, gender, or extracurricular interests, while in a neighborhood, class distinctions or shared linguistic practices can create “micro-partitions” that influence patterns of connectivity.

Physicists, too, recognize that such differences lead to varied outcomes. No one expects the friendship network in a low-income urban setting to mirror the networks observed in protein interactions or the arrangement of atoms in amorphous materials. To the contrary, any similarity would be unexpected. Consequently, a central objective in physics is to identify evidence of universality—patterns or laws that hold despite these obvious local and contextual differences. If such universality persists, it indicates deep, unifying principles—potentially even fundamental laws of nature—underlying what might otherwise appear to be unrelated phenomena.

From this perspective, the discovery that the World Wide Web follows a power-law degree distribution was initially regarded as a quirk of the medium—perhaps a unique feature of this new information network. However, that view changed once we and others observed similar patterns across many different real systems. Reports of the scale-free property—a term originating in statistical physics to describe power-law distributions—began to surface elsewhere, suggesting the possibility that it might indeed be universal. Let me list a few examples.

Infrastructural Systems (Internet): Unlike the World Wide Web—an information network where nodes represent documents and links are URLs—the Internet is an infrastructural network composed of routers as nodes, connected by physical links such as copper and optical cables or wireless connections. Despite this distinction, Faloutsos, Faloutsos, and Faloutsos found that the Internet’s degree distribution also follows a power law²⁵.

Large Social Networks: With the rise of online social platforms, researchers have started to gain access to maps of large social networks. Across a wide range of datasets, from follower networks on Twitter and friendship networks on Facebook, a consistent pattern has emerged: the degree distribution is fat-tailed and well-approximated by a power law^{26 27}. Notably, while most users have only a few connections, a few individuals serve as highly connected hubs.

Collaboration and Citation Networks: In science collaboration networks, nodes represent scientists, linked to those they have co-authored papers with. In citation networks, links represent citations from one paper to another. Both types of networks, widely studied in both scientometrics and the science-of-science community, consistently display fat-tailed degree distributions. The presence of such scale-free features indicates that while most scientists have only a few collaborators, a few gather an exceptional number of connections^{28 29}; similarly, while most papers receive few (or no) citations, a few prominent discoveries become hubs of the citation network^{30 31}.

Biological Systems: The networks discussed so far are the product of human action or design, raising the possibility that their observed scale-free architecture stem from intentional choices. To determine whether such features require human intervention, we shifted our attention to biological systems, where networks arise through evolution rather than human design or individual choices. The first discovery came from metabolic networks, where nodes represent metabolites and directed edges represent enzyme-catalyzed reactions. In our analysis of 43 species—spanning eukaryotes, bacteria, and archaea—we found that while most metabolites participate in only one or two reactions, a small subset (such as pyruvate and coenzyme A) act as metabolic hubs³². We observed a similar pattern in protein–protein interaction (PPI) networks, which capture the direct binding

among proteins³³. Across multiple eukaryotic species, including humans, both metabolic and PPI networks exhibit scale-free properties.

The recurring appearance of scale-free networks across a wide range of domains—digital, infrastructural, social, and biological—spanning vastly different length scales and time frames, suggests a striking form of universality. Their emergence in biological systems with a three-billion-year evolutionary history indicates that hubs and power-law topologies predate humans and therefore do not depend on human intervention. This observation raised the possibility of a shared underlying mechanism that drives the formation of hubs and high heterogeneity in networks, regardless of their origin. It also pointed to a deeper question: might there exist mechanisms governing network evolution that transcend specific systems? In other words, these findings suggest that networks may be governed by generic principles—rules independent of any system’s form or function. The challenge was thus to identify the mechanisms responsible for these laws and to develop a suitable mathematical framework to describe them.

The Origins of the Scale-Free Property

From a statistical physics perspective, the observation that the World Wide Web obeys a power-law degree distribution was an experimental discovery: we had empirical evidence of hubs and power law degree distributions, first on the WWW and then in multiple other networks, but we still lacked a theoretical explanation for their origin. This prompted Réka Albert and me to ask the question: what is missing in the Erdős–Rényi model of random networks that prevents the emergence of hubs?

This inquiry led us to identify two assumptions embedded in the random network paradigm that do not hold in real systems. First, the Erdős–Rényi model assumes that links are added between nodes within a system of fixed size—that is, the number of nodes remains constant during the network’s formation. In contrast, real networks—such as the World Wide Web, citation networks, or social systems—exhibit continuous growth, typically through the addition of new nodes. This occurs, for example, when new web pages are created and linked to existing ones, or when newly published scientific papers cite earlier work.

Second, the attachment of new links in real systems is not uniform or random, as assumed by the Erdős–Rényi model. Instead, there is a systematic bias: nodes that already have many links are more likely to acquire additional ones. Indeed, we are more likely to encounter a highly connected webpage or a highly cited paper, and since we tend to link to or cite what we know, the process inherently favors well-connected nodes. We termed this mechanism *preferential attachment*, and formalized it mathematically by assuming that the probability $\Pi(k_i)$ that a new node connects to an existing node i is proportional to its degree k_i ⁹

$$\Pi(k_i) = \frac{k_i}{\sum_j k_j}$$

As we showed in 1999, these two mechanisms—growth combined with preferential attachment—naturally lead to networks that develop hubs and follow a power-law degree distribution^{9 34}. In the model, the more connections a node already has, the faster it accumulates new ones—a “rich-get-

richer” phenomenon that parallels what Robert Merton called³⁵ the “Matthew Effect.” The model offered a testable mechanism to explain the universality of scale-free structures across many real networks. Equally important, it provided an analytical framework—based on standard tools of statistical physics, like continuum theory and rate equations—that enabled us to predict the evolution of multiple network characteristics analytically. Shortly thereafter, mathematicians joined the effort, offering exact proofs for the emergence of power laws in the model³⁶.

In the scale-free model the power law emerges from the combined effects of growth and preferential attachment. The fact that real networks are the result of a growth process was self-evident—we can witness networks expanding over time through the addition of new nodes. However, for a while preferential attachment remained only a hypothesis, a mathematical necessity to explain the empirically observed power laws. While physics has a long tradition of developing mathematical formalisms that successfully account for empirical data, even when their underlying mechanisms are not immediately understood, we recognized that preferential attachment could not remain a purely theoretical construct. To complete the scale-free paradigm, preferential attachment must be measurable, testable, and ultimately falsifiable.

Soon we learned that the presence or absence of preferential attachment can indeed be decided in real networks for which we have temporal data. For example, if we have access to two snapshots of a network—taken at times t and $t+\Delta t$, we can measure the probability $\Pi(k)$ that a node with degree k acquires a new link. If preferential attachment is present, $\Pi(k)$ must increase with k ; in contrast, if link formation is purely random, then $\Pi(k)$ should be independent of k .

Such temporal network data started to become available around 2002, allowing us to measure $\Pi(k)$ in multiple real systems³⁷, from collaboration to citation networks, and even in protein interactions³⁸. These measurements indicated that in real networks, the attachment probability $\Pi(k)$ increases with node degree, confirming the presence of preferential attachment. These findings—and many subsequent studies—demonstrated that preferential attachment is not merely a theoretical construct, but a measurable phenomenon supported by empirical data. These results also helped resolve a long-standing question about whether alternative or unknown mechanisms might be needed to explain the scale-free property. On one hand, there now existed a robust analytical framework showing how growth and preferential attachment together give rise to the scale-free state, accurately predicting network structures observed in data. On the other hand, the mechanism of preferential attachment could now be empirically detected and quantified in real systems, leaving little room for alternative explanations.

Evolving Networks

The scale-free model was never intended as a direct representation of any specific real system, such as the World Wide Web or a cellular network. Rather, in the tradition of physics, which often relies on idealized models—such as the Ising model for magnetism, the harmonic oscillator for molecular vibrations, or the hydrogen atom for quantum mechanics—the scale-free model aimed to capture the essential mechanisms responsible for the emergence of hubs and power laws. Real networks are shaped by a broad range of additional processes that were purposefully excluded from the model—for example, competition between nodes (formally captured by node fitness), node and link deletion, and node aging, to name only a few. These and other phenomena that

influence how networks evolve—and ultimately shape their topology—have motivated the development of a general theory of evolving networks, capable of analytically predicting the impact of each elementary process on network structure.

The results revealed that many of these processes can alter the degree exponent, can induce low-degree saturation, and predicted multiple testable deviations from a simple power law. The key insight is that, to understand the topology of a network, one must first map out the local processes that define the placement of nodes and links. In this view, network topology is not the input—it is the consequence.

Degree Heterogeneity and its Consequences

A central question in network science is whether the presence of a certain structural features, like power-law degree distribution, changes a system's behavior. Early insights into this question came from the study of network robustness, asking how many nodes must fail before a network fragment into isolated clusters³⁹. For instance, how many router outages do we need to break the Internet into mutually unreachable subnetworks? The framework for answering this question lies in percolation theory, a branch of statistical physics⁴⁰. Percolation theory predicts that randomly removing nodes or edges can induce a phase transition from a single connected component to a fragmented network of disconnected clusters. However, as we found in 2000, this transition effectively disappears in scale-free networks³⁹. Rather, networks with a power-law degree distribution exhibit extraordinary robustness to random node failure—an attribute not shared by random networks. Mathematically, the critical threshold for network fragmentation depends on the second moment of the degree distribution, $\langle k^2 \rangle$, a measure of degree heterogeneity. Specifically, when a fraction f of nodes is randomly removed from a network, the system undergoes fragmentation at a critical threshold given by⁴¹

$$f_c = 1 - \frac{1}{\frac{\langle k^2 \rangle}{\langle k \rangle} - 1} \quad (1)$$

where $\langle k \rangle$ is the average degree and $\langle k^2 \rangle$ is the second moment of the degree distribution $P(k)$. In scale-free networks, this second moment depends on the size of the network (number of nodes N), as

$$\frac{\langle k^2 \rangle}{\langle k \rangle} \sim N^{\frac{3-\gamma}{\gamma-1}} \quad (2)$$

In other words, for large N , the second moment diverges. Consequently, the ratio $\langle k^2 \rangle / \langle k \rangle$ increases, causing f_c in (1) to approach 1. In practical terms, this means that a network with a large $\langle k^2 \rangle$ remains intact under random failures unless nearly all nodes are removed.

At the same time, this very heterogeneity renders scale-free networks highly vulnerable to targeted attacks^{39 42}. Removing just a few hubs—nodes with an unusually high number of connections—can rapidly dismantle the network, fragmenting it into isolated pieces. This dual behavior became known as the “Achilles’ heel” property³⁹: scale-free networks are highly resilient to random failures but fragile when their hubs are deliberately targeted.

We soon learned that this dependence on network heterogeneity is not limited to network robustness. Indeed, a dependence on $\langle k^2 \rangle$ was shown to emerge in epidemic models capturing the spread of a pathogen on the contact network of individuals. The epidemic threshold, defined as the critical transmission rate λ_c below which an infection cannot persist, is given by⁴³

$$\lambda_c = \frac{\langle k^2 \rangle}{\langle k \rangle} \quad (3)$$

Hence, as the second moment $\langle k^2 \rangle$ increases, λ_c converges to zero. This implies that in heterogeneous networks even a weakly transmissible pathogen can spread, explaining why real contact and sexual networks are particularly susceptible to epidemic outbreaks, from SARS to HIV⁴⁴. An analogous relationship appears in synchronization phenomena, relevant to systems as diverse as magnetic oscillators, power grids, neural circuits, and synchronized fireflies^{45 46 47 48}. In such systems, the threshold coupling strength required to achieve global synchrony scales as^{49 50 51}

$$J_c = 2 \sqrt{\frac{2 \langle k \rangle^2}{\pi \langle k^2 \rangle}} \quad (4)$$

Once again, a large second moment lowers the coupling threshold, promoting more rapid or robust global coordination.

Taken together, these findings underscore the critical role of degree heterogeneity—a hallmark of scale-free networks—in shaping network behavior and dynamics. Notably, they reveal that observing a statistically rigorous power-law distribution is not a prerequisite for detecting the effects of heterogeneity. Analytical results indicate that the magnitude of the second moment, a robust and easily measurable parameter, is sufficient to capture these effects.

This is particularly important because, as discussed above, continuum models predict that in real systems, a pure power-law behavior is inevitably modified by various processes—just as most atoms contain more than a single electron, rendering the simple Bohr model insufficient and requiring more advanced quantum mechanical descriptions to accurately compute orbitals. Consequently, statistical exercises that aim to fit ideal power laws are expected to fail unless they test the precise (and often rather complex) functional form of the degree distribution predicted by theoretical models. However, Eqs. (1), (3), and (4) indicate that such precise fits are not required to capture the true implications of the scale-free state: a high degree of heterogeneity—quantified by the second moment—is sufficient to reproduce the key features associated with scale-free networks.

The results discussed so far do not give justice to the breath of theoretical developments that network science has offered in the past decades. The field has seen remarkable advances across many directions, from the characterization and detection of network communities^{52 53 54 55}, the identification of network motifs⁵⁶, modeling degree assortativity⁵⁷, the development of multiplex and multilayer systems^{58,59 60 59}, temporal and dynamic networks^{61 62}, higher-order interactions and hypergraphs^{63 64 65}, controllability and observability of networked systems^{66 67 68 69 70 67}, network inference and reconstruction methods^{58 71}, network embeddings and graph neural

networks⁷², resilience⁷³ and percolation in interdependent networks, resulting in a family of network growth models that offer accurate predictions for the structure and the dynamics of a wide range of real-world systems.

Applications across disciplines have been equally striking. The emergence of network neuroscience has enabled the mapping of functional and structural brain networks, providing insights into cognition, disease and brain control^{74 75 76}. Network medicine has developed new tools to understand the molecular underpinnings of complex diseases⁷⁷, and to repurpose drugs based on network proximity in protein interaction maps^{78 79}. Network science has helped transform our understanding of ecosystems⁸⁰, economic and social development^{81 82 83}, and the dynamics of scientific innovation⁸⁴, illustrating its remarkable capacity to unify insights across diverse systems.

Unable to do justice to all these developments, I will next focus on a defining feature of network science: its *falsifiability*. This principle, central to the physical sciences, demands that theoretical claims yield testable predictions—subject to empirical or experimental validation or refutation. In network science, models are not merely descriptive; they are predictive, offering quantitative forecasts of system behavior. Over the past decade, many of these predictions have been experimentally tested—and in several cases, have given rise to practical applications and technologies now in routine use.

Network Epidemiology: From Theory to Practice

Traditional epidemic models assumed homogeneous mixing—treating all individuals as having equal chances of encountering a pathogen. In reality, however, disease spreads across heterogeneous contact networks, where a small number of highly connected individuals—hubs or superspreaders—play a disproportionate role in transmission dynamics. For decades, epidemiology lacked the tools to systematically account for such structural complexity.

A conceptual breakthrough came with the work of Pastor-Satorras and Vespignani⁴³, who reformulated the classical epidemic models to incorporate network topology. Over the next two decades, Vespignani transformed these theoretical advances into predictive frameworks that integrate real-time transportation and mobility data to forecast the spread of emerging pathogens. The major test came during the 2009 H1N1 pandemic⁸⁵, marking the first instance in which global disease spread was predicted months in advance using network-based simulations.

By the time COVID-19 emerged, these tools were fully operational, allowing network scientists and physicists, such as Alessandro Vespignani (US, Italy), Vittoria Colizza (France), and Dirk Brockmann (Germany) to take leading roles in advising their respective governments. They employed network-based models to forecast infection trajectories and evaluate the effectiveness of intervention strategies. Their predictions shaped policies on travel restrictions, vaccine prioritization, and public health interventions⁸⁶.

Importantly, these were not retrospective fits, but forward-looking forecasts grounded in the real-time evolution of the pandemic—predictions that were successfully validated as events unfolded. And the utility of network epidemiology has not ended with COVID-19. The same models are now used to track and anticipate the spread of Zika, Ebola, Mpox, Marburg, and other emerging threats.

In doing so, they demonstrate that network epidemiology is not a one-time success, but a generalizable and testable framework—one that builds on network science, to integrate data and public health practice in real time. It has become an indispensable, routinely used tool in guiding health interventions when confronting emerging pathogens.

Network Control: Predicting and Experimentally Falsifying Neuronal Roles

One of the clearest experimental demonstrations of the falsifiability of network theory comes from its application to biological systems via network control. Network control poses a fundamental question: given the architecture of a network and the dynamics it supports, can we predict where—and how—to intervene to steer the system toward a desired state? Introduced in 2011⁶⁶, the framework of network control has since spurred broad developments across both network science and control theory^{68 69 70 87}. Its experimental validation arrived in 2017 through a precise inquiry: given a fully mapped neural system, can network control predict which neurons are required for a specific behavior, such as locomotion?

The test case was *Caenorhabditis elegans*, at that time the only organism with a complete connectome. Over decades, ablation studies had identified approximately twelve neuronal classes as essential for movement. Remarkably, network control theory—starting only from the network structure—predicted precisely the same set of twelve neuronal classes, recovering 30 years of experimental work. More significantly, the theory identified the neuron PDB, previously uncharacterized in this context, as critical for locomotion. This was a falsifiable, forward-looking prediction. When PDB was experimentally ablated to test the network control predictions, the worm exhibited a collapse in dorsoventral coordination, confirming the neuron’s essential role⁸⁸.

The model also made finer predictions. Within known neuronal classes, like the GABAergic motor neurons DD, it predicted that specific members—such as DD04 and DD05—would impair posterior body movement if individually ablated, but other members of the same family, like DD02 and DD03—should not have an effect, serving as controls. These predictions, too, were confirmed experimentally. These experiments demonstrated that network science can produce accurate, experimentally falsifiable predictions not only about the global state of a system, but also about the functional and mechanistic roles of individual neurons.

Interdependent Networks: Falsifying Theory through Experiment

A major theoretical advance in network science concerns interdependent networks—systems in which the functionality of one network depends on another^{58 59}. A 2010 study demonstrated that even small failures in one layer of such systems can cascade catastrophically through others, prompting a wave of research into the dynamics of interdependence⁵⁸. In contrast to isolated networks, which often become more robust as their degree distribution becomes broader, interdependent networks exhibit the opposite trend: increasing heterogeneity leads to greater fragility, as tightly coupled dependencies create vulnerability to cascading failures.

For years, these predictions remained purely theoretical, supported only by numerical simulations, as no experimental platform could replicate the necessary bidirectional dependencies. This is not to say that we lack systems that behave like interconnected networks—many from technological

to environmental systems do. We just lacked the possibility to do controlled experiments on these. Recently, however, Bonamassa et al.⁸⁹ built a system composed of two disordered superconducting films separated by an insulating layer. Large electrical currents introduced Joule heating, which coupled the layers via electrothermal feedback—creating a real-world mechanism for link interdependency.

The experimental results aligned strikingly with theory: cascading failures, mutual phase transitions, and critical phenomena emerged exactly as predicted. More importantly, the study showed that failures propagate not only through structural dependencies, but also through adaptive, feedback-driven dynamics—expanding the theoretical framework to include more realistic modes of interdependence. With that, for the first time, cascading interdependent collapse was observed in a material system, offering experimental validation of more than a decade of work needed to develop the underlying theoretical framework.

Symmetry Breaking in Network Dynamics: Theory Meets Experiment

A surprising theoretical prediction in network dynamics emerged from the study of oscillator networks: symmetry in structure does not guarantee symmetry in behavior, and conversely, asymmetric networks can sometimes exhibit perfectly symmetric dynamics. This phenomenon, known as *converse symmetry breaking* (CSB), was first predicted by Nishikawa and Motter⁴⁶. Their work demonstrated that network topology alone does not dictate synchronization patterns, challenging long-standing assumptions about structural determinism in complex systems.

The prediction remained theoretical until it was experimentally tested in 2020. Molnar et al.⁹⁰ engineered networks of coupled optoelectronic oscillators, allowing precise manipulation of both topology and coupling. They confirmed that structurally asymmetric networks could sustain symmetric synchronous states—validating the central claim of CSB. The results offered rare experimental evidence for a deep theoretical principle, also revealing new pathways to design and control symmetry in real-world networks.

Experimental Validation of Network-Based Drug Repurposing

The COVID-19 pandemic provided another unprecedented opportunity to experimentally falsify a central claim of network science—its ability to predict drug repurposing opportunities. With no time for de novo drug development in 2020, the medical community urgently needed to identify existing drugs that might disrupt host–virus interactions. The first network-based drug repurposing methodology had emerged several years prior to the pandemic⁹¹, built on the insight that only drugs targeting the immediate network vicinity of a disease module are likely to exert therapeutic effects. Initial validation drew on a healthcare database covering over 220 million patients, where pharmacoepidemiologic analyses showed that the use of hydroxychloroquine, predicted to target the coronary artery disease (CAD) module, was indeed associated with decreased CAD risk⁷⁸.

COVID-19 introduced a compelling testbed for direct, falsifiable predictions. Faced with the urgent need to evaluate thousands of existing compounds, in March 2020, we applied a network-based drug repurposing approach to predict the efficacy of all approved drugs against COVID-

19⁷⁹. The study integrated network diffusion, network proximity, and AI-based modeling to computationally screen 6,340 compounds, ranking them based on their predicted ability to disrupt the host–virus interaction network.

Following these predictions, 918 drugs were experimentally tested on SARS-CoV-2–infected cell lines (a number later extended to over 6,000 drugs⁹²). The outcome was striking: 62% of the top-ranked compounds inhibited viral infection, compared to a mere 0.8% hit rate observed in unguided high-throughput screens. The study did more than offer a promising shortlist during a global emergency—it provided direct, falsifiable, and experimentally confirmed validation of a network-based prediction. It also underscored where networks models excel --- not by identifying compounds that bind directly to viral proteins, which are always potential drug target candidates—yet only one of the 78 drugs that worked were in this category. Rather, network-based predictions were able to identify the 77 so-called *network drugs*, that successfully modulated the subcellular networks to reach the desired infection outcomes.

Network Science in the Clinic: PrismRA and Personalized Medicine

Network science has also entered clinical practice. A notable example is PrismRA, a blood-based diagnostic test rooted in network-based analysis of the immune system. Developed using the network medicine toolset created in our lab⁹³, PrismRA is designed to guide treatment decisions for rheumatoid arthritis (RA), a chronic autoimmune disorder affecting more than 18 million people worldwide. While TNF-inhibitor therapies remain the most prescribed biologics for RA, only about 30% of patients respond, and it typically takes six months or more to assess their efficacy.

PrismRA addresses this challenge by predicting, prior to treatment, whether a patient is unlikely to benefit from TNF inhibitors. It does so through a blood test that captures the activity of key proteins within the disease-relevant subnetworks known as the disease module⁷⁷ and infer the drug’s ability to perturb the state of the module in a patient. The diagnostic allows physicians to bypass ineffective therapies and consider alternative treatments earlier, resulting in reduced time to care, lower healthcare costs, and decreased patient burden⁹⁴. To date, more than thirty thousand patients have benefited from this network-informed diagnostic tool. What began as an attempt to apply network science to medicine has now become part of routine clinical decision-making, demonstrating how abstract network science models can yield tangible improvements in patient outcomes.

Economic Network Analysis: Mapping the Path to Development

Network science has also proven valuable in shaping economic strategy and development policy, offering a data-driven, falsifiable framework for understanding how countries diversify and grow. There are numerous examples of such applications, several of which are detailed in this book. Here, I will focus on one that I was personally involved in: in collaboration with Ricardo Hausmann and César Hidalgo, we applied network methods to analyze the bipartite network linking countries to the products they export competitively⁹⁵. The central insight from this

analysis—the foundation of the "Product Space"—is path dependency: nations are more likely to succeed in industries that are closely related to their current capabilities. For example, a transition from growing apples to cultivating pears is far more feasible than a leap to semiconductor fabrication.

Today, network-inspired approaches to economic development, such as economic complexity and the product space, are increasingly informing industrial development strategies adopted by governments worldwide. Malaysia's New Industrial Master Plan¹, for instance, explicitly defines economic complexity as the core objective of the country's industrial strategy, while Mexico's Ministry of Economy has integrated economic complexity principles as a foundational element in the creation of its national data dissemination platform, DataMexico.org. In Europe, the report on competitiveness led by Mario Draghi employs economic complexity metrics to compare the technological positioning of Europe, the United States, and China, underscoring the strategic value of these tools in guiding policy⁹⁷. Collectively, such developments reflect the incorporation of network-based tools into the standard analytical and decision-making toolkit used by policymakers confronting the challenges of industrial development in an increasingly complex and interconnected global economy.

Conclusions

Across diverse fields—epidemics, brain science, materials science, clinical diagnostics, and antiviral discovery—network science has passed a critical test: its predictions are falsifiable and withstand experimental scrutiny. What began for me three decades ago as a curiosity-driven framework, inspired by statistical physics and graph theory, has matured into a robust scientific discipline with profound impact across the physical sciences, biology, medicine, and public health.

This trajectory echoes some of the most transformative advances in physics, whose true power was realized far beyond their original domain. Electron microscopy revolutionized cell biology and virology. Magnetic resonance became the foundation of MRI and reshaped diagnostic medicine. Statistical mechanics laid the foundations for modern machine learning and Artificial Intelligence. These examples underscore a fundamental truth: physics is not defined by what it studies, but by the universality of the frameworks it offers. In this spirit, network science has emerged as a highly interdisciplinary heir of both physical sciences and mathematics, with applications spanning a wide range of inquiry and technologies.

What still puzzles me is how completely disjoint the communities thinking about networks were before 1999. As **Figure 2a** shows, in 1997 the landscape was dominated by two isolated communities. One was a small social network community, with intellectual roots stretching back to the 1940s. The other was a graph-theoretic community, focused on random graphs. Before 2000, sociology papers rarely engaged with the growing body of mathematical advances on graph theory. Likewise, graph theorists made no reference to the social network literature—not even passing acknowledgments of small-world ideas. These disciplines existed in parallel, non-communicating intellectual islands.

¹ Malaysian Government, "The New Industrial Master Plan (NIMP 2030)."

The emergence of network science around 2000 dramatically reshaped the intellectual landscape. By 2007 the scientific community had attracted a highly interdisciplinary cohort—physicists, computer scientists, applied mathematicians, and biologists—who bridged the longstanding divide between formal graph theory and social network research (**Figure 2b**). This convergence established a shared intellectual foundation and a common canon. Network science served as a unifying framework—one that not only integrated the tools and insights of both graph theory and social networks, but also introduced new concepts grounded in statistical physics and computer science.

This revolution has profoundly changed social network analysis (SNA) as well. The field has its roots in sociology and anthropology—where it served as a methodological tool for mapping and interpreting social structures—and it remained, for decades, largely confined within the realm of these disciplines. The same is true for graph theory: it was, for much of its history, a deeply disciplinary subject practiced and followed primarily by mathematicians.

The reach and influence of both social network analysis and graph theory expanded dramatically with the emergence of network science. Physicists and computer scientists—often ignorant of the traditions and the internal motivations of social science and graph theory—pragmatically integrated the tools of both disciplines and shaped network science into a field with its own intellectual identity, focused research questions, robust theoretical and computational foundations and empirical framework. Armed with this portable toolkit, disciplines that had previously shown limited interest in networks—including economics, neuroscience, political science, epidemiology, and biology—suddenly acquired the means to pursue a network-based inquiry, reframing foundational questions through the lens of connectivity and structure.

This transition is well documented through bibliometric analyses. As shown in **Figure 1**, the number of publications related to network science have surged dramatically around 2000—far outpacing the growth trajectories of both social network analysis (SNA) and graph theory. Yet the rise of network science also reshaped the trajectories of its intellectual predecessors, catalyzing their renewed growth. This is most clearly reflected in the citation patterns of two foundational works: Erdős and Rényi’s seminal paper on random graphs, central to graph theory, and Granovetter’s classic study on the strength of weak ties, foundational to SNA (**Figure 5**). For decades, each received steady but discipline-specific attention—Erdős and Rényi’s work averaged about ten citations per year, primarily from mathematics, while Granovetter’s paper drew around one hundred citations annually before 2000, mainly from sociology and economics. Following the emergence of network science, however, both papers experienced a dramatic rise in citations. This surge reflects the dynamic feedback loop emerged between the traditions of SNA and the expanding domain of network science. Classical SNA constructs—including centrality, homophily, and structural holes—were extended and formalized through the tools of graph theory and statistical mechanics. The theoretical agenda of network science increasingly incorporated sociological concerns such as diffusion, community structure, and collective behavior. This mutual enrichment spurred methodological innovations, including community detection algorithms, models of multiplex and temporal networks, and computational approaches to social contagion.

By 2023, the transformation was both profound and expansive (**Figure 4**). MAG records over 192,000 papers labeled as network-related—reflecting not just steady growth, but remarkable

diversification. Increasing specialization has also led to the emergence of new subfields, appearing as distinct professional modules on the co-citation graphs of **Figure 4**—network neuroscience, network medicine, network epidemiology, machine learning, economics, and engineering—each contributing to and drawing from a shared network vocabulary.

Today the study of social networks is no longer a standalone field—it is now deeply integrated, methodologically, conceptually, and empirically, with work on infrastructure systems, biological processes, and information networks (**Figure 4**). In other words, understanding the current trends in social network analysis requires viewing them not as isolated subjects of the social sciences, but as part of a broader intellectual shift: a science of connectivity grounded in shared principles of network growth, structure, dynamics, and function across both natural and engineered systems.

Ultimately, the story of network science is the story of how seemingly disparate systems—from the human brain and the Internet to ecosystems and protein–protein interaction networks—exhibit deep structural commonalities, governed by common laws and mechanisms. By identifying these universal features, researchers across disciplines can better understand, analyze, predict, and optimize the networks that shape our world. By contrast, the social sciences often thrive by focusing on the specific—the unique circumstances that shape social phenomena. Network science is indispensable for this agenda as well: we must first uncover and understand the generic principles and underlying mechanisms that govern these features, because only then can we meaningfully identify the specific.

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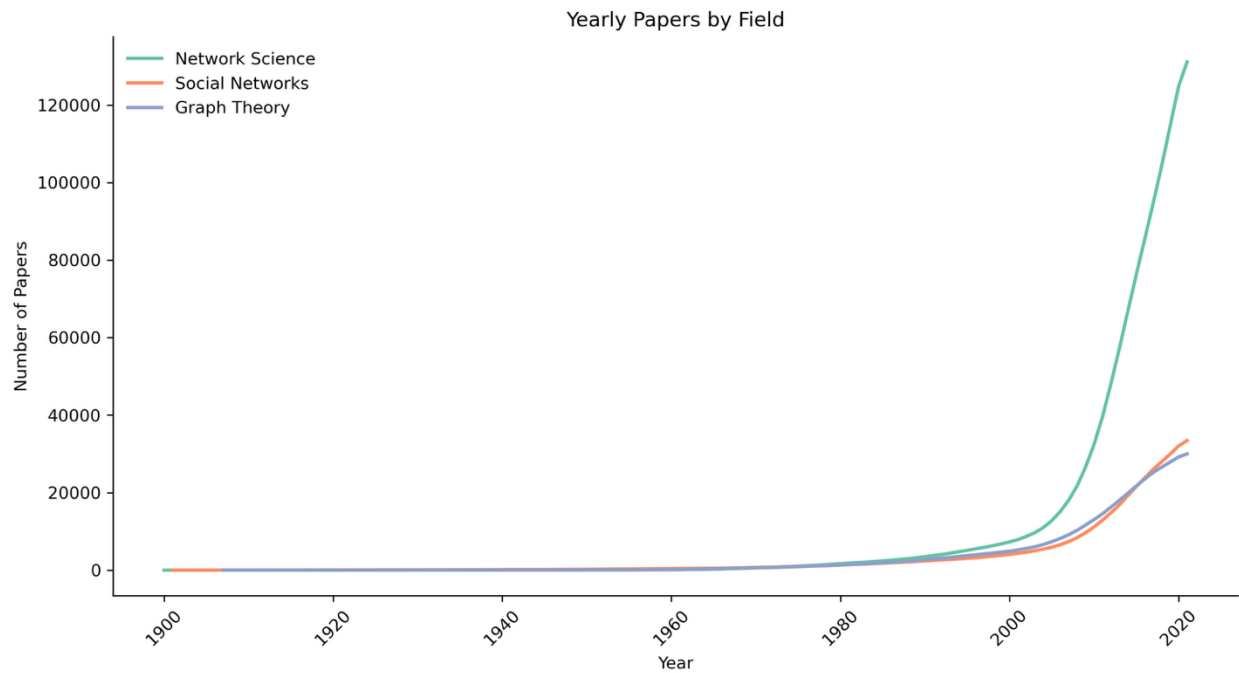


Figure 1. According to the Microsoft Academic Graph (MAG), a database of scholarly data (discontinued at the end of 2021), between 1900 and 2021 there were 192,000 papers classified as related to network science, across all disciplines. The plot splits this corpus of 192,000 papers into three groups, showing the temporal evolution of the number of papers classified as Social Networks (orange) and Graph Theory (blue), and Network Science (green), which encompasses all papers focusing on networks, that are classified neither social networks nor graph theory.

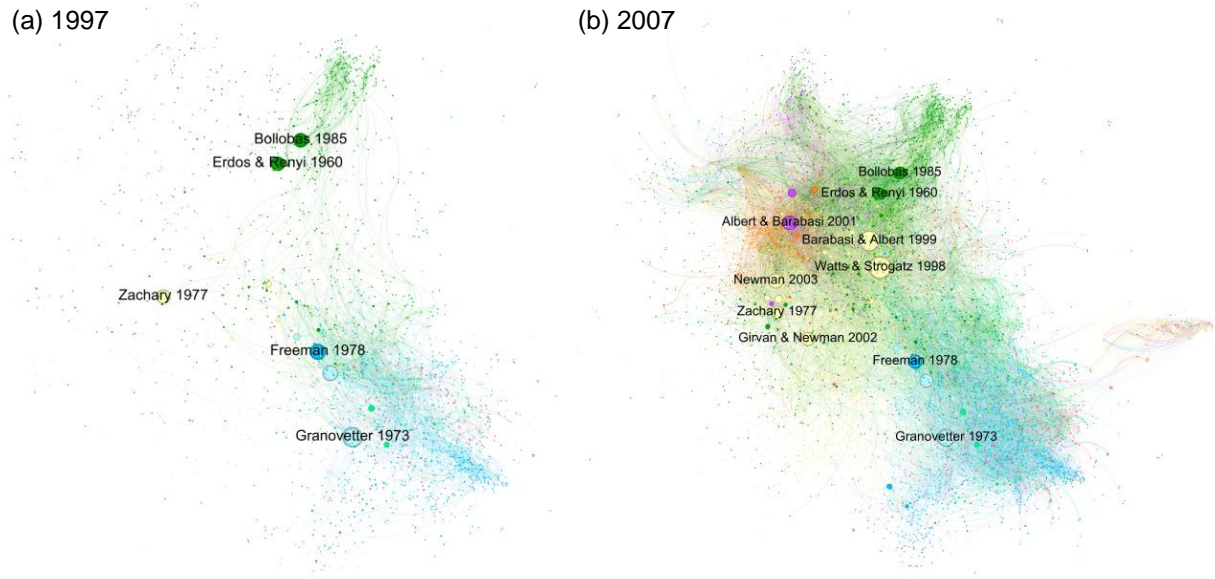


Figure 2. The Emergence of Network Science.

(a) The co-citation network of papers classified as network related by MAG, and published before 1997, i.e. before the emergence of networks science. The graph reveals two largely disconnected subfields: one focused on graph theory and random graphs (top), and the other on social networks (bottom).

(b) The same network ten years later, in 2007, after the emergence of network science. The new network science papers, published in physics, computer science as well as numerous cross-disciplinary venues, have bridged the gap between the graph theory and the social network communities through publications that draw from both traditions while establishing a distinct intellectual agenda.

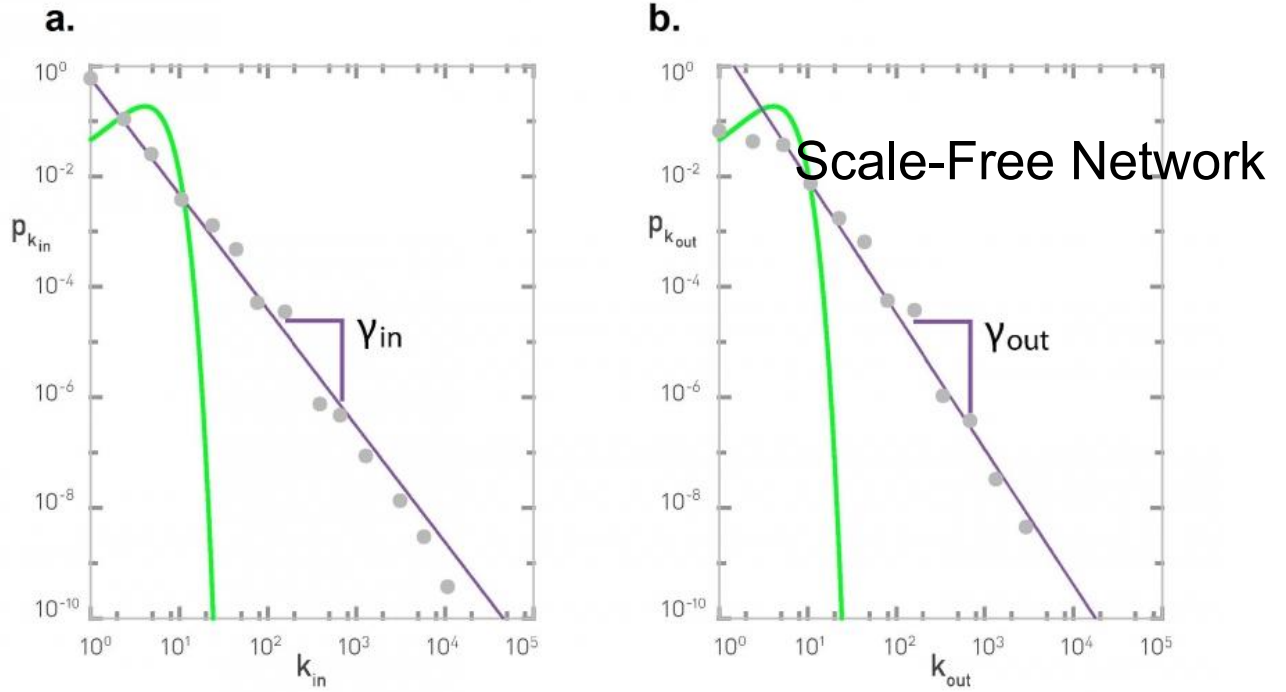


Figure 3: The Discovery of Scale-Free Networks

The incoming (a) and outgoing (b) degree distribution of the WWW sample mapped in the 1999 study of Albert *et al.*²⁴, that lead to the discovery of scale-free networks. The degree distribution is shown on double logarithmic axis (log-log plot), in which a power law follows a straight line. The symbols correspond to the empirical data, and the line corresponds to the power-law fit, with degree exponents $\gamma_{in} = 2.1$ and $\gamma_{out} = 2.45$. We also show as a green line the degree distribution predicted by a Poisson function with the average degree $\langle k_{in} \rangle = \langle k_{out} \rangle = 4.60$ of the WWW sample. After¹⁷

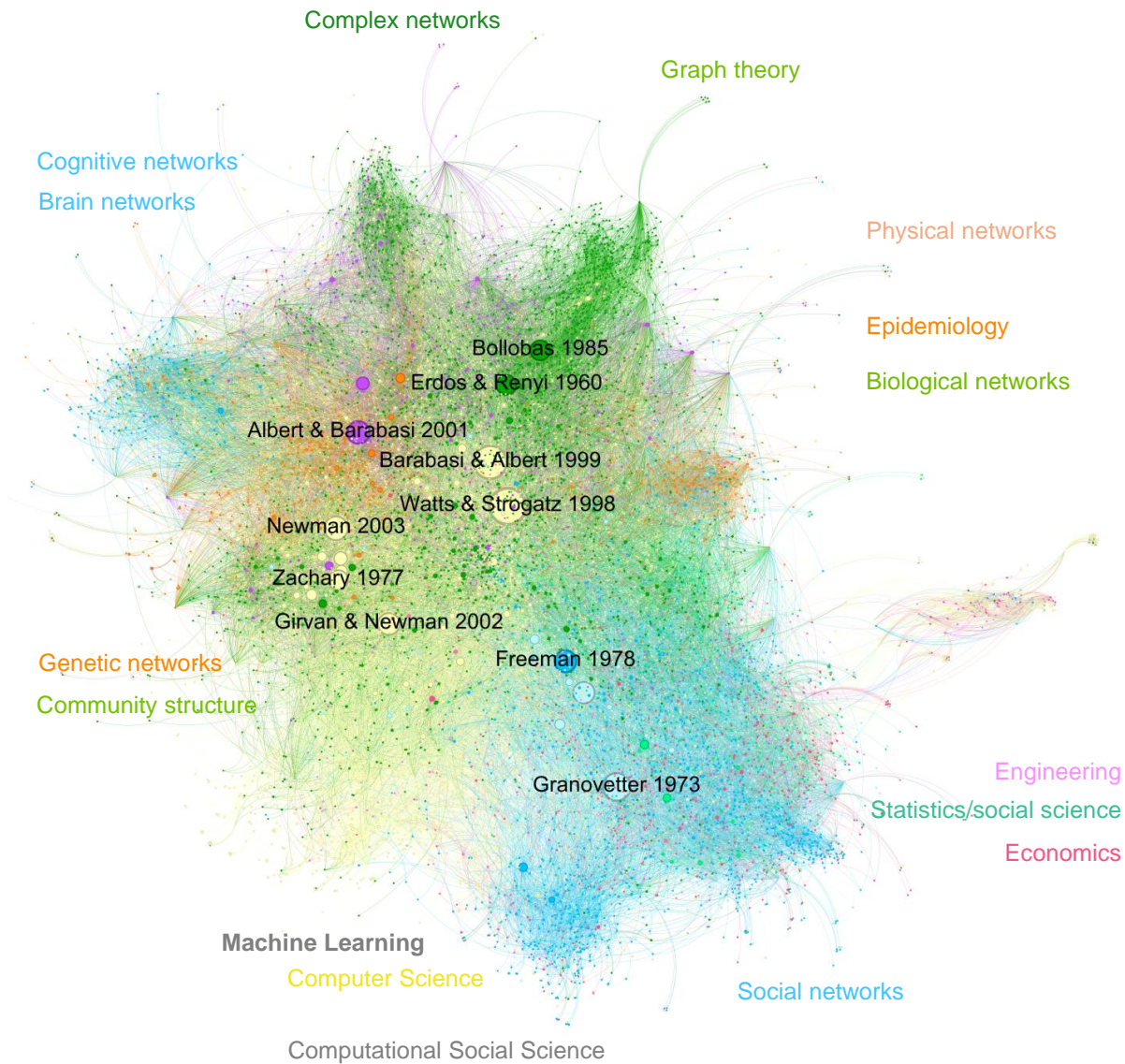


Figure 4: The Cross-Disciplinary Impact of Network Science.

By 2022, over 192,000 papers are labeled as network science in the Microsoft Academic Graph (MAG). For clarity, the figure displays only the top 1% most cited subset of these publications and their co-citation network. Colors correspond to the different subfields and are defined by MAG, illustrating the range of disciplines that actively contribute to and use network science.

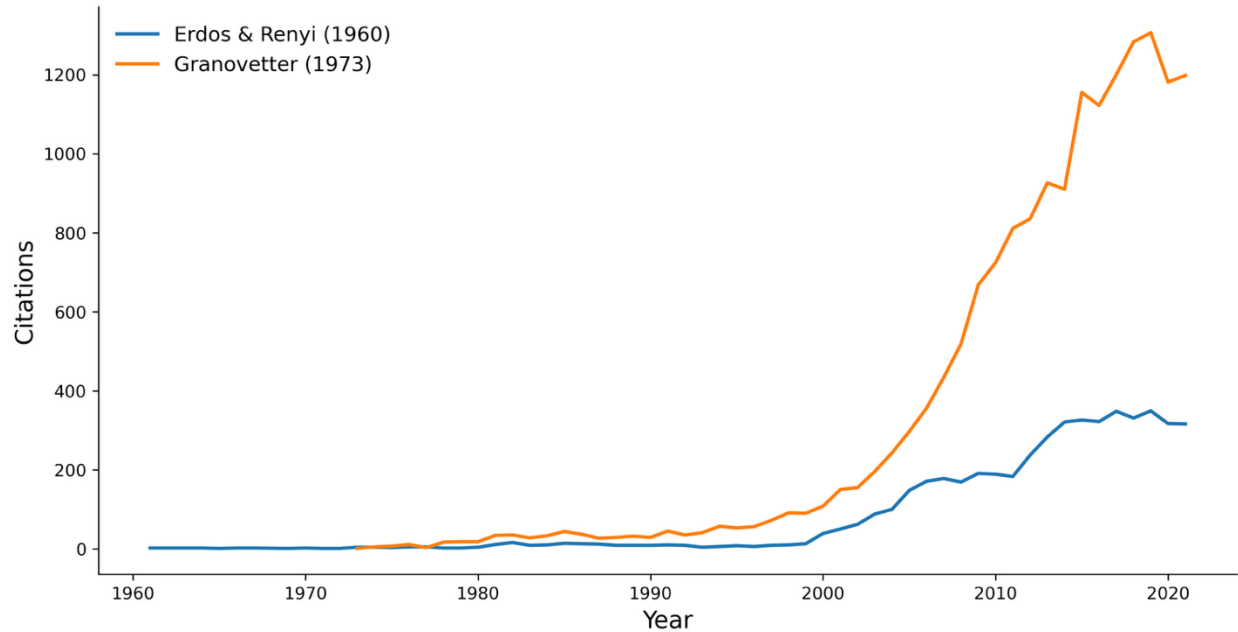


Figure 5. The Emergence of Network Science

While the study of networks has a long history, with roots in graph theory and sociology, the modern chapter of network science emerged only during the first decade of the 21st century. The explosive interest in networks is well documented by the citation pattern of two classic papers, the 1959 paper by Paul Erdős and Alfréd Rényi that marks the beginning of the study of random networks in graph theory [2] and the 1973 paper by Mark Granovetter, the most cited social network paper [3]. The figure shows the yearly citations each paper acquired since their publication. Both papers were highly regarded within their discipline but had only limited impact outside their field. The explosive growth of citations to these papers in the 21st century is a consequence of the emergence of network science, drawing a new, interdisciplinary attention to these classic publications.

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