

Article

Modeling Innovations: Levels of Complexity in the Discovery of Novel Scientific Methods

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Abstract: Scientists often disagree on the best theory to describe a scientific event. While such debates are a natural part of healthy scientific discourse, the timeframe for scientists to converge on an ideal method may not always align with real-life knowledge dynamics. In this article, I use an event from the history of chemistry as inspiration to develop Agent-Based Models of epistemic networks, exploring method selection within a scientific community. These models reveal several situations where incorrect, simpler methods can persist, even when substantial evidence supports a more complex method. This becomes particularly evident when different evidence-sharing timeframes are analyzed. The network structure connecting the scientists plays a crucial role in determining how and when convergence on the correct method is achieved, guided by real-world evidence. This framework provides a foundation for further exploration of scientists' behavior in past and future discoveries, as well as how agents internalize scientific information.

Keywords: agent-based models; epistemic networks; method selection; scientific consensus; complexity analysis



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1. Introduction

At the end of the 19th century, European wine traders were surprised by the ban on renowned Portuguese Port wines, accused of containing a dangerous poison [1]. The resulting embargo of one of the most influential products of Portugal's economy led to a near collapse of the country's Port wine commerce [2,3]. But years later, it was discovered that the accusations were unfounded: an error in method interpretation led scientists to state incorrect findings as scientific facts. Evidence spread as a false belief, driven by the lack of scientific complexity of the poison detection method [4]. After the error was uncovered, many scientists and politicians still advocated for the veracity of the original analysis, claiming that the Port wine was fraudulent [5]. Whether because of a lack of scientific authority or political pressures, it took years for the retraction to be universally accepted as a fact. Remarkably, the retracted evidence of a flawed analytical method persisted even after being discredited. This case, dubbed the "Salicylation of Port Wines", mirrors other episodes in the history of science, where methods subject to significant scientific complexity continue to be disputed despite the accumulation of clear evidence.

This article addresses how scientific complexity influences the spread of false information. Through an exploratory experiment with Agent-Based Models (ABMs), inspired by a historical case where scientists shared their beliefs on different methodologies, I explore how new knowledge spreads asymmetrically among scientific peers. These dynamics on consensus formation have long been described by philosophers of science, where Lakatos,

Kuhn, and Popper debated the mechanisms through which science resists innovation. This work builds on these foundational ideas, using ABMs to explore epistemic challenges.

One such challenge is when scientists take a long time to reach a consensus based on accurate information, particularly when false beliefs are tied to method complexity. The adoption of a novel method—more consistent but also more complex—often struggles due to its complexity and the composition of the scientific community. This behavior reflects the “resistance to change” observed in contemporary studies of scientific communities. Model simulations suggest that belief in imprecise, low-complexity methods can persist for a long time, even when evidence supports more accurate methodologies. This results from how scientists are organized to receive information, despite updating their beliefs when exposed to better methods.

This study also explores how complex and accurate methods are successfully disseminated within scientific communities. Method complexity and the frequency with which scientists revise them emerge as key factors influencing the outcome of belief adoption. A robust method that takes a long time to develop may be disseminated more successfully if scientists are slower to update their beliefs. These findings were analyzed across different types of scientific network structures, each reflecting various levels of complexity and group organization.

Historical episodes frequently serve as valuable case studies for philosophical inquiry, providing concrete contexts to examine abstract epistemic and methodological issues. The “Salicylation of Port Wines” controversy is not merely a historical event but an example of how scientific progress can be impeded by a confluence of political, social, and methodological factors. It highlights the dynamics of scientific miscommunication, the resistance to complex methodologies, and the interplay between science and its socio-political context. This paper leverages ABMs to unpack these dynamics, using the historical case both as a real-world example of the challenges inherent in disseminating complex methods and as a testing ground to validate the insights generated by the models. By simulating how method complexity and communication networks affect the spread of scientific beliefs, this paper bridges abstract modeling with historical epistemic challenges, demonstrating how ABMs can deepen our understanding of the factors that influence scientific consensus.

“The Salicylation of Port Wines” is not the central focus of this paper but rather a case study to demonstrate the application of ABMs in exploring the dynamics of scientific information dissemination. Similar patterns of resistance to accurate but complex ideas are evident throughout the history of science. For instance, Semmelweis’ discovery of the importance of handwashing in reducing maternal mortality faced rejection from the entrenched medical establishment. The theory of plate tectonics, initially dismissed despite supporting evidence, required a paradigm shift in geological thought before gaining acceptance. And in the ongoing debate over climate change, notwithstanding overwhelming scientific consensus, socio-political and economic forces continue to fuel skepticism. These cases, like the “Salicylation” episode, underscore the complex factors shaping the trajectory of scientific knowledge. By modeling these dynamics, ABMs offer a singular tool to explore the interplay between information dissemination, resistance, and consensus in scientific communities.

This article is divided as follows: Section 2 provides a review of the relevant literature, including an approach to epistemological model design and a historical contextualization of the case study. Section 3 outlines the development of the model and its applicability to the case study. Section 4 presents model results in various scenarios for the dissemination of scientific methods. Section 5 reflects on the outcomes of this exploratory experiment and includes suggestions for future model adaptations.

2. How to Study the Dynamics of Scientific Discovery?

2.1. Models and Methodologies

The pursuit of scientific methodologies through experimentation has already been explored in several formal learning studies [6–8]. Optimal learning interactions depend on the diverse connections' weights established between scientists and their peers [9–11]. These interactions are key in describing scientists' conduct as an organizational unit¹. For example, if an idea spreads quickly among scientists, they may retain this idea and stop looking for a better solution. On the other hand, if this information transmission is spaced out, only a few scientists may encounter novel ideas, keeping a large part of the community in the blind.

To develop these models, Šešelja outlines several essential conditions for their design [12]. The first step involves representing different scientific theories and their role in knowledge development. Then, by categorizing how scientists gain information about previous theories, the study addresses how they share information among themselves. Finally, the study must describe how scientists update and evaluate theories through information sharing (that is, at least one theory should explain the phenomenon scientists aim to study). By representing the processes of sharing and disseminating evidence, these studies provide significant insights into depicting a scientific community.

ABMs have been considered ideal candidates for these types of models. Important ABMs focus on studying the dissemination of scientific knowledge, particularly the interaction between scientists and other societal members [13–15]. Aligning with philosophical efforts to understand scientific change, particularly Lakatos' view of research programs and Kuhn's theory of paradigm shifts, ABMs provide a formalized way to test hypotheses. Aim to clarify the dynamics of scientific information influenced by social, economic, and political interests, these models describe how they shape knowledge and institutions throughout the process [16]. A highly successful ABM, described through an epistemological network, was first reported by economists Bala and Goyal [17] and later introduced to the philosophy of science by Kevin Zollman [10,18]. Zollman's models use a classic bandit problem, where agents in the community choose between two theories based on the evidence they encounter. This process unfolds in two steps: agents first test theories and then share information with other members. The model continues through successive simulations until all community members converge on a theory based on the accumulated information. In the philosophy of science, Zollman views agents as scientists, shaping the network to test and disseminate information. Each scientist follows one of the two theories as the community converges on one, adopting it as scientific knowledge. Zollman considers that each scientist has a different probability of choosing a particular action based on their beliefs, which represents their scientific background².

Another object of Zollman's study is what type of communication networks favor the choice of the best theory. This is important because as scientists search for the hypothesis that guarantees them the highest probability of success, their own belief is influenced by the information they receive from other colleagues. By studying three trivial social interaction networks with increasing connectivity, Zollman found that a fully linked network is, on average, less successful at reaching the best decision than a less connected one [19]. This finding reveals a type of "buffer effect", as less connected networks prevent emerging misleading information³. This outcome is referred to as the "Zollman Effect", which has been studied and successively confirmed for different research purposes [20]. For example, it has also been confirmed that the effect is likely to occur in cases where finding the optimal hypothesis takes more time to achieve [15].

An interesting adaptation of this model combines ABMs with the network-contagion paradigm. Commonly used in epidemiological studies [21], it assumes that introducing in-

formation into a community works similarly to the spread of an infection: communication, hypothesis confirmation, and dissemination take place through established scientists' connection routes. Such a framework applies best to easily transmitted concepts in one-to-one interactions, as the final decision depends on peer feedback when evaluating hypotheses. Incorporating a contagion framework into an ABM simulation is highly beneficial, particularly for exploring the dynamics of information dissemination in complex systems [22]. It allows for flexibility in simulating various network structures and interaction patterns, making it a valuable tool for studying a wide range of scenarios, from tightly knit groups with frequent interactions to more loosely connected networks with sporadic exchanges.

2.2. A Case Study—Historical Complexity of Chemistry Methods

When a scientific methodology is first introduced to describe a phenomenon, any explanation can be volatile. Result interpretation may change quickly as scientists test alternative hypotheses, as this is a pivotal part of the scientific process. Although individual endeavors may fail, science moves forward by subjecting findings to scrutiny, refining the conclusions shared with the scientific community. It is just as important to know why a process “does not work” as it is to know “how to get it working”.

In chemistry, scientists often debate the best mathematical model to represent a chemical property. Even with access to many samples, chemical behavior does not always conform to a straightforward mathematical rule [23]. The success of a chemical method depends on its ability to explain a phenomenon, but also on how well it can be tested, replicated, and communicated. By analyzing the strengths and weaknesses of previous methods, it is possible to develop a process that produces a “clear conclusion”, which is crucial for the broad understanding of a scientific explanation.

One significant episode where discussions of chemical methods played a vital role in public policy design was the emergence of the concept of “food safety”. Its popularization gained prominence in Europe in the second half of the 19th century [24], while global consensus on chemistry methods for food safety tests was still developing. Although the production mechanisms of foodstuffs were generally understood, the methods for analyzing and quantifying chemical properties for safety varied across different regions.

Reports on the introduction of this new “chemical language” revealed a lack of strong pedagogical policy, leading to serious misinterpretation issues [25]. Suddenly, all food-trade stakeholders were required to understand the language of food chemistry—its methods, substances, detection limits, etc. If keeping up with emerging practices was difficult for scientists, it was even more challenging for ordinary traders and legislators, who had to base legal decisions on chemical grounds. This explains why some policymakers misinterpreted analytical values and why a minor variation in a reference value was often wrongly seen as a sign of counterfeiting⁴. This learning curve, which was perhaps not fully addressed in the introduction of these methodologies, contributed to the vagueness surrounding the establishment of food inspection services.

Recently, historians of science have argued that the spread of misleading methodological conclusions played a pivotal role in the popularization of food safety [26]. This had a significant impact on the trade dispute between Portugal and Brazil, known as the “*Salicylation Quarrel of Port Wines (1885–1905)*”, which became a paradigmatic case in which scientific knowledge eventually debunked false evidence [1]. Brazilian authorities claimed that Port wines contained salicylic acid⁵, a substance deemed a poisonous adulterant, in a ruling that damaged traders' reputations and halted major Portuguese exports⁶. Confident in their products' quality, the Portuguese sponsored scientists to challenge the Brazilians' faulty claims. In a battle of technological prowess, both sides published articles on the accuracy of their opponents' tests. Interestingly, although the Brazilians and the Portuguese

tested different methods, they used the same chemical principle: if salicylic acid was present, the wine in contact with iron (III) chloride would turn violet. Portuguese scientists discovered that the violet reaction was caused by a natural substance in Port wines, not salicylic acid. It was another natural molecule, found in certain grape berry varieties, that was mistaken for salicylic acid.

As the dispute unfolded, scientist Henri Pellet, who developed the technique used in Brazil, acknowledged that his method could indeed produce false positives for salicylic acid in wines containing this natural, harmless substance [4]. However, Pellet did not argue that the Brazilian scientists had misused his method. Rather, he stated that his method was not complex enough to distinguish salicylic acid from other similar compounds, proposing modifications to enhance specificity.

After the dispute, Pellet updated his methodology and eventually wrote articles accepting the Portuguese scientists' arguments, particularly those of António Ferreira da Silva, the eminent chemist who led the Portuguese effort. While this clarification enriched the scientific debate on the authority of food safety laboratories, the same could not be said for the legislative aspect. The Brazilian government insisted on the original results for several years, delaying the update to the analytical method. Historical sources suggest possible political interference in updating these regulations, with reports of Brazilian scientists supporting the legislators' doubts, even after the method's clarification⁷. It was only after a long diplomatic quarrel that Brazil lifted the trade ban on Portuguese wines. This case became a significant example of scientific misinformation, as the controversy rose from incorrect conclusions drawn from faulty data.

This historical case demonstrates how scientific methods, particularly more complex ones, can face resistance within scientific communities. Like Kuhn's concept of paradigm resistance, which helps explain why complex yet accurate methods often face challenges in gaining acceptance, this case sheds light on the interplay between consensus, dissent, and socio-political dynamics. While consensus can serve as a marker of stability, it is not infallible. History has shown that dissenting perspectives have often catalyzed scientific discoveries. The controversy surrounding salicylic acid in Port wines is a prime example of how scientific disputes often extend beyond methodological disagreements, being deeply embedded in the socio-political context. By applying ABMs, the case underscores the importance of simulating these challenges, as it highlights how method complexity interacts with the social structures of communication and belief adoption.

While the historical case of salicylic acid in Port wines inevitably involves industrial and technological aspects, the primary focus remains on the epistemic challenges and methodological evolution. Any references to these practices or advancements are intended to contextualize the dynamics influencing scientific debates. This paper carefully distinguishes between the domains of chemical science, industry, and technological innovation but recognizes their interconnected roles in shaping scientific progress.

This case of misinformation raises important questions about the role of false interpretations in science, their dissemination, and the development of science-based regulations [27]. It also raises issues regarding the duration of such misinterpretations. What impact did these erroneous decisions have on foodstuff evaluations while the analytical methods were still being perfected? How many products and merchants were discriminated against, and who might have profited from this? There are two lines of inquiry to address: first, to verify the extent of decisions based on false interpretations in public debates, tackling conflicts between scientists and policymakers; and second, to understand how scientists interpret experimental results based on cutting-edge, complex scientific methods. This paper focuses on the second issue. Given that scientific communities are known to polarize [28] and even conform in the presence of fundamental actor-based

theories [29], what happens when scientists deal with methods prone to misinterpretation due to a lack of complexity? Are scientists more likely to disseminate incorrect methods, even when evidence suggests better alternatives are available? If so, does this explain why scientists are often reluctant to change their views?

This article's case study aims to show how a group of scientists sharing evidence on recent scientific methods with the same values can diverge and settle on beliefs based on scientific misinterpretation. The initial premise follows the logic of discovering an ideal method to describe reality. In this approach, reality is represented as a curve, and scientists sample it through various methods of differing mathematical complexity. The curve's behavior reflects a particular chemical property, with more complex methods involving additional variables or intricate relationships. Scientists gather samples, testing whether their models successfully predict outcomes. They share their results with peers, gradually accumulating data until the community converges on the model that most accurately represents the real curve.

This historical case of the "Salicylation of Port Wines" sheds light on the often-opaque nature of the selective dissemination of evidence. Political and social factors, alongside scientific ones, contributed to the persistence of flawed methods despite contradictory evidence. This case underscores how difficult it can be to trace the full mechanics of information dissemination through historical documentation, raising important questions about how evidence is spread. The ABMs here developed are specifically designed to simulate the complex dynamics of method dissemination, belief adoption, and the communication structures that played a critical role in the "Salicylation" case. These models explore how flawed methods can persist in scientific communities even when superior methods are available, as seen in the historical case. By connecting the model to this real-world example, we can test hypotheses about the conditions under which correct methods eventually gain acceptance and what network structures affect epistemic progress.

2.3. *The Role of Complexity in Misinformation and ABM Simulations*

One of the central research questions of this paper focuses on how complexity affects the spread of misinformation and method adoption in scientific communities. This relationship between complexity and belief dissemination has not been extensively studied, particularly in the context of ABMs, which have typically focused more on network structures or the speed of information dissemination. The introduction of complexity as a key variable in these models adds a new dimension to the understanding of how scientific communities navigate competing methods. The motivation behind investigating complexity comes from historical cases like the "Salicylation of Port Wines", where a relatively simple but incorrect scientific method gained widespread acceptance, while a more complex but accurate method struggled to disseminate. This suggests that method complexity may serve as an obstacle to the adoption of accurate information, even in well-connected communities. This paper proposes that ABMs, which simulate belief dissemination across networks, are well suited to model these dynamics, allowing us to explore how method complexity interacts with network structure, communication frequency, and belief updating processes. However, it is important to recognize that ABMs are not without limitations. The perception of computational tools as infallible, often perpetuated by journalistic narratives, risks diminishing the indispensable role of human interpretation and critical reasoning. To mitigate this tendency, ABMs should be positioned not as substitutes but as complementary tools that enhance and support traditional analytical methodologies.

This research seeks to expand the application of ABMs by introducing complexity as a variable that can influence epistemic outcomes. Complexity is treated here not simply as an inherent characteristic of scientific methods but as a potential lever that impacts the

spread of information (like network topology or communication rate). By investigating complexity through ABMs, it introduces a new theoretical framework for understanding how scientific communities can become entrenched in flawed methods and why they may resist adopting more complex, yet accurate, ones.

Readers might wonder why complexity is expected to make a significant difference in these simulations. This expectation arises from the intersection of learning theory and network epistemology, which suggests that individuals (in this case, scientists) often rely on less complex models to form beliefs when information is difficult to interpret. Complexity increases the cognitive and epistemic load, which can slow down the dissemination of accurate information and lead to persistence in incorrect models. Previous studies have hinted at similar dynamics in other contexts, but this paper extends these findings to show that the complexity of the methods themselves is a crucial factor in whether accurate information is adopted or dismissed. Thus, this study contributes both to the literature on ABMs and to broader discussions in philosophy of science and learning theory by positioning complexity as a key determinant in scientific misinformation. By introducing complexity as a novel lever for ABMs, this research opens the door for future studies to explore how the intricacy of information impacts belief formation and revision in a variety of epistemic settings.

3. Epistemic Model Framework

3.1. Model Network Outline

I present a model based on the ABM network epistemology framework developed by Bala and Goyal [17] and modified by Kevin Zollman [18]. In the original model, agents gather and share evidence on two choices of an action that will produce a better payoff. In this article's model, agents are scientists who choose between two or three methods that reduce the prevalence of flawed methods, maximizing the adoption of accurate, complex ones. This new iteration accounts for how scientists can sometimes analyze novel methods with some doubt due to uncertainty-bound innovation, which is still not clear to experts. The model also intends to simulate experimental sampling and method testing in the scientific process. It explores the dynamics of method discovery, assessing the impact of mathematical complexity. The goal is to see how scientists spread their results until they maximize method adoption, assessing the influence of model complexity on perpetuating their scientific endeavor. It also measures how belief spreads in the community, as method complexity and evidence accumulation drive its evolution.

This model was also inspired by Kevin Zollman's work on scientists' behavior in different epistemological networks, describing how their structure influences information sharing, particularly in two relevant situations. First, a more closely spaced structure between actors may be beneficial to reaching consensus in the community. And second, while an increase in connections among scientists accelerates the consensus process, it also reduces the likelihood that the community will adopt the most effective methodology. In this exercise, four types of structures of epistemological networks with different levels of interaction were studied: cycle, wheel, complete, and small-world (Figure 1). These structures emulate hypothetical situations where scientists communicate through different networks. Increasingly complex structures were used, for example, in the complete structure, all scientists can randomly interact with each other, while this is not as straightforward in other networks.

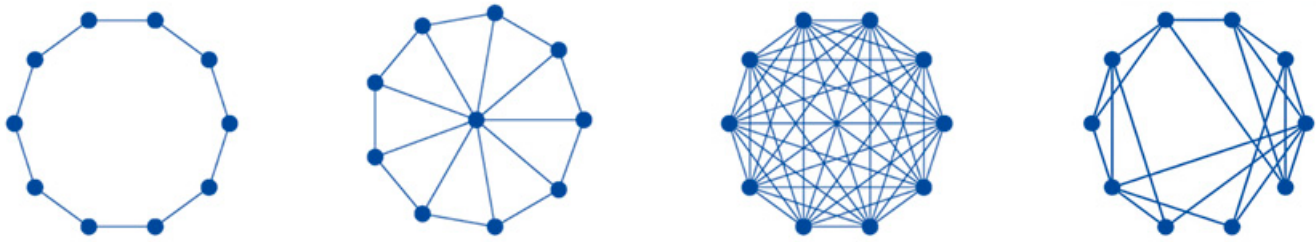


Figure 1. Graphical representation of the studied network structures (left to right): cycle, wheel, complete, and small-world.

In real-life scenarios, not all scientists have social or institutional access to all their peers, affecting both learning and scientific dissemination. To describe such situations, I use the example of small-world networks [30]. A small-world network is characterized by a unique combination of properties and is particularly relevant in the study of social interaction networks. One key condition is a high clustering coefficient, meaning nodes in the network form tightly knit groups. If a node is connected to two other nodes, there is a high likelihood that those two nodes are also connected, creating dense local clusters. Despite this local interconnectedness, the network exhibits a short average path length, meaning any two nodes can be connected through relatively few steps, exemplifying the “six degrees of separation” phenomenon. This structure allows for efficient navigation and rapid dissemination of information across the network. Additionally, small-world networks often include certain “hubs”—agents with a significantly higher number of connections than average, such as well-connected scientists with privileged access to communication channels—further facilitating the flow of information. These networks are typically sparse, with fewer overall connections compared to a fully connected network, yet they maintain the critical properties of high clustering and short path lengths. The dynamics of small-world networks make them especially relevant for understanding the spread of information (and misinformation) within scientific communities, both historically and in contemporary settings.

In the “Salicylation of Port Wines” case, a small-world network model emerges as a fitting representation due to its structural properties, which closely resemble historical scientific networks. This conclusion is supported by previous studies that found small-world networks to be a grounded approach for representing scientific communities [31]. Additionally, historical sources support the three main characteristics of small-world networks: a high clustering coefficient, a short average path length, and network sparseness. In the 19th and early 20th centuries, scientific communities often exhibited high clustering [32]⁸. Scientists typically worked in close-knit groups, sharing methods, data, and critiques. This reflects the structure of small-world networks, where nodes form densely interconnected groups. In the historical case, Portuguese and Brazilian scientists operated within their local clusters but were connected through international academic discourse, allowing for the exchange of information and critique.

Evidence of a high-clustering network is shown by the dense interconnections among the scientific communities involved in the *Salicylation* case. For instance, the close collaboration and communication between key figures such as Ferreira da Silva and international counterparts like Henri Pellet⁹ exemplify this. Sources note how Ferreira da Silva’s findings were “widely disseminated in Brazil by the merchants”, leading to “a long scientific discussion” involving multiple scientists and institutions across different countries [33]. This shows a network where information and influence circulated intensively within a closely knit group, indicative of high clustering. The debates within local communities—such as Portuguese versus Brazilian scientists—further underscore this, as scientists frequently interacted within their regional groups before dissemination.

Although the spread of international information was much slower in the past compared to today's scientific communications, the historical case still demonstrates the small-world network model's suitability. International scientific discourse, though less frequent and slower, acted as long-range connections in the small-world network, allowing for critical information to eventually reach broader audiences. This sporadic yet impactful spread of information enabled scientific communities to challenge initial misinterpretations and move toward scientific consensus.

Despite the high clustering, information could still disseminate relatively quickly across various scientific communities, facilitated by conferences, journals, and correspondence. This rapid dissemination is analogous to the short path lengths in small-world networks, where a few long-range connections reduce the average distance between nodes¹⁰. This is why the "Salicylation" case provides historical evidence of a network characterized by short average path lengths. One indication of this short average path length is the rapid dissemination and response to scientific findings across continents [33]¹¹. The text mentions that "Ferreira da Silva's findings were widely disseminated in Brazil by the merchants", leading to immediate challenges by Brazilian scientists and Henri Pellet [1,33]. This swift exchange signifies that, despite geographical distances, the number of intermediaries between nodes was minimal. This efficient spread of information is a hallmark of small-world networks. The robust network structure, with its combination of local and global connections, reflects how scientific communities could withstand initial misinterpretations and eventually converge on accurate methods through scrutiny.

Regarding sparseness, the network primarily involved a select group of specialized individuals and institutions. Key figures such as Ferreira da Silva, Henri Pellet, and laboratories like the *Laboratório Químico Municipal do Porto* and the *Laboratório Nacional in Rio de Janeiro* were central to the discourse¹². Sources reveal this by noting how Ferreira da Silva's work was "widely disseminated in Brazil by the merchants", leading to a "long scientific discussion" primarily involving these scientists [33,34]. This concentration of interactions among a limited number of nodes highlights the network's sparseness, where only pivotal agents were actively involved in resolving the issue.

3.2. Model Belief Dynamics

The model diverges from the traditional Zollman approach by introducing a contagion dissemination strategy. This simulates the organic spread of beliefs within scientific communities, resembling peer-to-peer interactions and social network structures in the proliferation of scientific information. At the start of the simulation, each scientist holds a "neutral" belief (i.e., no opinion). Then, each model ("Method X") is introduced to an individual within the network. Belief spreads as follows: if a scientist with a "neutral" belief is connected to a neighboring scientist who holds a belief about "Method X," it is assumed that the belief in the method always spreads. This dynamic is depicted in Figure 2. When scientists evaluate and determine that their neighbor's method is superior, they copy and update to that method.

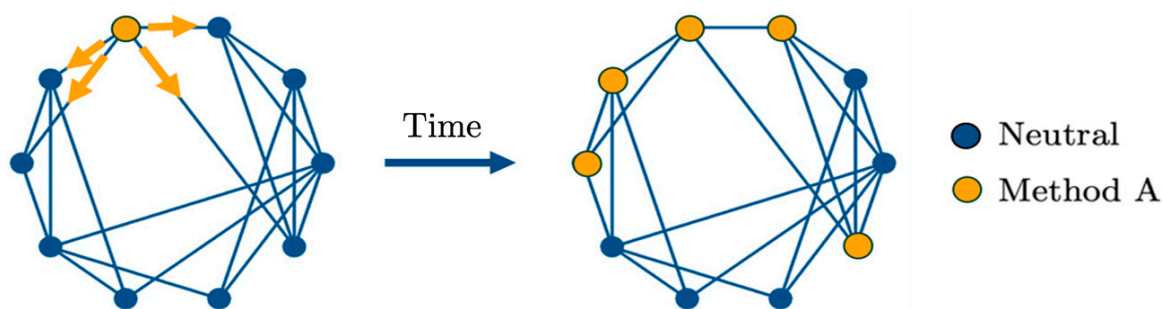


Figure 2. Belief spreading in an organized community of scientists (each node represents an individual).

The simulation stops when the network reaches an equilibrium called a stable state, where no further significant changes in method preference are observed. In this state, scientists cease changing their beliefs, resulting in either the dominance of a single method or the coexistence of multiple methodologies (even if one is theoretically superior). Since belief updates are not immediate and occur at different intervals, there is a possibility that scientists may not encounter the “ideal” method. While the long-term outcome of adopting the correct method, based on years of experimental evidence, is reasonable to expect, the simulations focus on short- and medium-term effects.

Network connectivity plays a significant role, as distinct clusters or limited connectivity can cause groups to converge on different methods based on localized interactions. This relates to the concept of *local optima*, where scientists often settle on methods that are locally optimal within their specific context, even if they are not ideal. Limited cross-group communication can prevent a single method from becoming dominant, allowing multiple methods to persist. Method complexity further influences this equilibrium. The initial effort invested in understanding a method can contribute to the stability of multiple methods. This prevents the widespread adoption of a single method and enables the coexistence of different methodologies in the stable state.

The contagion framework is also relevant to the “Salicylation” affair in several ways. In the historical case, scientists communicated their findings through personal interactions, scientific publications, conferences, and correspondence. The contagion model simulates this natural spread of information, where scientists influence each other’s beliefs based on their interactions. At the start of the dispute, various stakeholders may have held neutral beliefs regarding salicylic acid in Port wines. As evidence was presented by both Portuguese and Brazilian scientists, these neutral groups began forming opinions based on the information they received.

In the contagion model, a new method is introduced to an individual in the network, like how the Brazilian scientists introduced their method for detecting salicylic acid. Reflecting the real-world scenario, Portuguese scientists challenged the Brazilian approach, prompting scientists to evaluate and compare various methods. Those who found their neighbors’ methods superior adopted them, mirroring the model’s assumption that scientists update their beliefs after evaluating methods. As Portuguese scientists demonstrated that the Brazilian method produced false positives, this evidence was evaluated by more scientists, and belief in the Portuguese method gained traction. It also shows how some Brazilian academics and policymakers resisted changing their beliefs despite new evidence, as the contagion model may depict scenarios where belief updating is slow or resisted¹³.

3.3. Model Complexity

The model simulates a population of N scientists, each holding a belief about the best model to represent a chemical property¹⁴. This chemical property is depicted by a curve. As in typical two-dimensional representations of pH, entropy, or phase transitions,

scientists believe that a mathematical method can describe these properties. To illustrate this, each method generates its own rendering of an experimental titration curve. Figure 3 represents this with a simplistic 2D correlation between a solution's pH and the volume of a base (sodium hydroxide—NaOH) added. “Reality” is depicted as a curve representing the variation in a chemical property (pH) in response to changes in another variable (NaOH volume). To mathematically describe this, scientists use a method, conduct experiments, and measure the solution's pH, accumulating enough data points to approximate the curve.

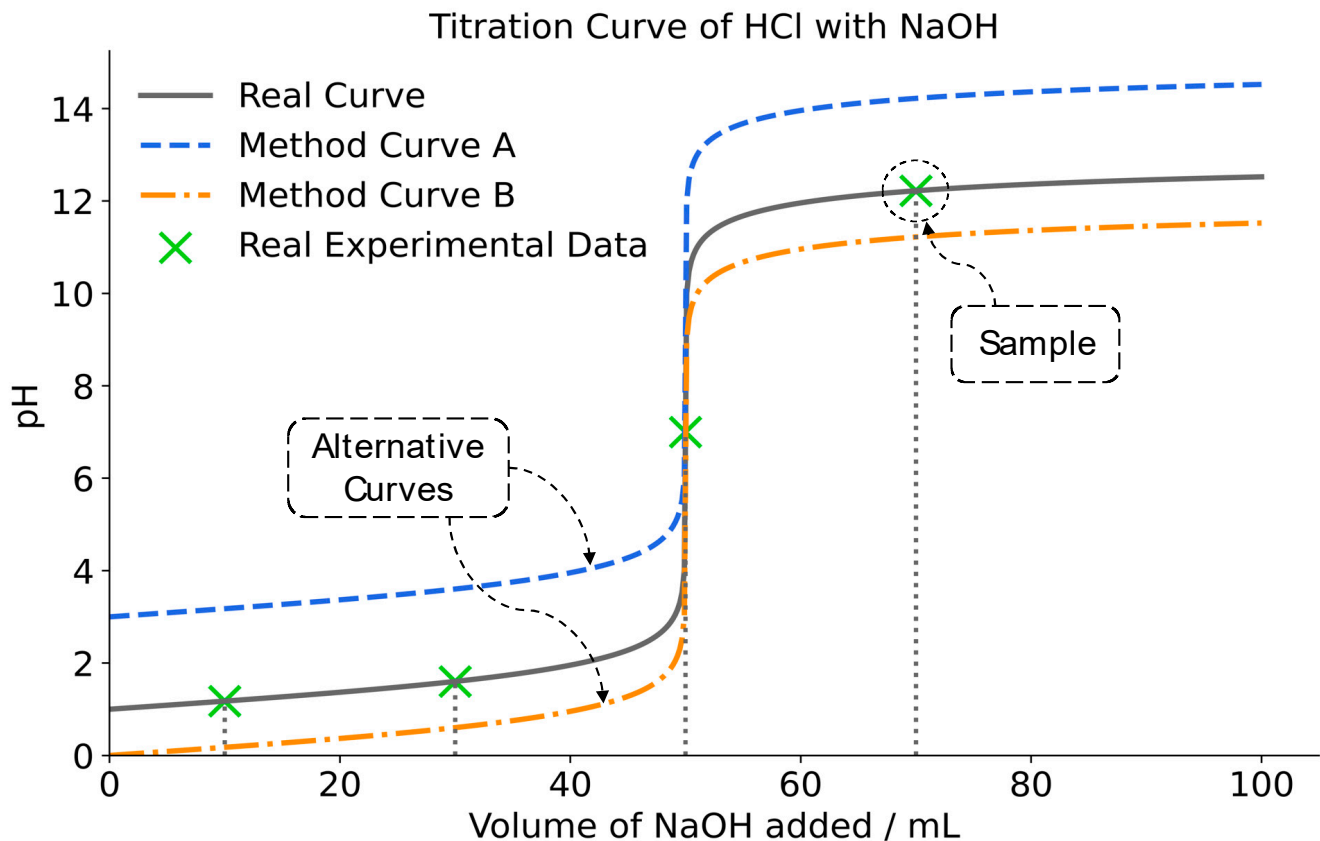


Figure 3. Two-dimensional graphical representation of pH variation with NaOH volume in a solution. The “real curve” represents the actual experimental values, while “method curves” represent models that aim to replicate the “real curve” based on real data¹⁵.

At the start of the simulation, scientists are not exposed to any method. Then, each method is introduced to a different scientist. Using experimental data, each method produces a different curve according to its complexity. Scientists routinely compare these model curves to determine which method yields the most accurate result, defined as the one closest to the “real curve”. For example, in Figure 3, scientists compare each method’s titration curve, assessing which one most closely resembles the real one. This comparison can involve statistical evaluation metrics such as the mean absolute error or other measures that quantify the deviation between the predicted values and the observed reality. By using these metrics, scientists can objectively determine the most rigorous method to best represent the experimental data.

Method accuracy is recorded over time by calculating the prediction error relative to the real curve. This evaluation produces a chronologically recorded degree of accuracy, which is tracked in the model’s simulations. When scientists compare their results, if their neighbor’s method shows a lower error, they copy and adopt it. This process continues until the community reaches a stable state, where no further changes occur.

In this model, complex methods with more variables to refine their results will generate a more accurate representation of the real curve. It is assumed that all tested methods can capture reality to some extent, but only the more complex methods yield the most accurate results. This reflects the “Salicylation” case, where competing methods described reality with varying levels of complexity. Since complex methods may take longer to gain traction and deliver the ideal response, simpler methods may temporarily provide the better option. If this persists for an extended period, scientists may develop resistance to adopting more complex methods, mirroring real-world scenarios where dense theories face initial skepticism and take longer to gain acceptance. While I acknowledge that over-complexity can lead to issues like overfitting, this model is primarily designed to explore theoretical trends in scientific method adoption.

Complexity is defined, in this context, by the number of parameters or samples used within a method, as these elements encode the model’s complexity. This reflects the depth of understanding, and the amount of data required for method validation, allowing for the assessment of each method’s mathematical sophistication¹⁶. Methods become more complex when they involve extensive equations or higher-order mathematics¹⁷. In the model’s code, each method is assigned a complexity value, with higher values indicating increased complexity, simulating how methodological complexity influences scientific consensus within the community.

In all simulations, the performance of each method is recorded over time to track which one best represents reality at a given moment. To model this, the concept of the Performance Ratio (PR) is introduced. The PR serves as a real-time indicator of the relative effectiveness of each method, based on its accuracy in reflecting reality. The accuracy of all methods combined is expressed as a value between 0 and 1, with more accurate methods having a higher PR, indicating superior accuracy in predicting the real curve. Equation (1) represents the overall difference between the real and calculated values, while Equation (2) rationalizes the overall performance of all methods¹⁸. At any given time, the method with the highest PR is considered the best one available, as the sum of all methods’ PRs must equal 1.

$$P_{\text{Method A}} = 1 - \frac{(\text{Real Value} - \text{Value A})^2}{(\text{Real Value})^2} \quad (1)$$

$$\text{Performance Ratio}_{\text{Method A}} = 1 - \frac{P_{\text{Method A}}}{\sum P_{\text{All Methods}}} \quad (2)$$

In both equations, “real value” refers to the real experimental value that encodes the curve’s behavior at a given time, while “Value A” represents the experimental value predicted using “Method A” (the model’s code calculates each sample value based on its complexity and accuracy). “All methods” refers to the combination of methods being tested. The PR of “Method A”, as shown in Equation (2), compares how that method performs relative to the sum of all available methods. Since PR is a dynamic measure, it changes as different methods are tested. A simpler method that requires fewer data may initially seem ideal, but it could be outperformed by a more complex one as more data are collected.

The updating procedure works by comparing the PRs of different methods¹⁹. Scientists periodically evaluate their current method’s PR against that of their neighbors. If a neighboring method has a higher PR, indicating better accuracy in predicting the real curve, the scientist adopts that method. This process continues iteratively, allowing the most accurate methods to spread throughout the network²⁰.

3.4. Model Simulation Setup

Model simulations were implemented using the “Project Mesa” ABM framework in Python 3.9²¹. These simulations were designed to address specific aspects of method selec-

tion within scientific communities, serving two primary purposes: conducting robustness checks to ensure the model's stability across different scenarios and exploring the dynamics of method adoption with varying levels of method complexity and network structures. The model aims to clarify the logic behind these variations and provide insights into the dynamics of method selection, highlighted in the historical case.

The model ran simulations with $N = 10, 20, 30, 50, 75$, and 100 scientists in two scenarios: one with two methods and the other with three methods to describe reality. In both situations, the methods were tested with increasing complexity, with the most complex being considered the ideal one. Method complexity was set as Method A < Method B < Method C. The choice of N and the number of methods was designed to reflect a scenario similar to the historical case. To account for randomness and variability in the model, 20 simulations of each scenario were recorded to capture a wide outcome range and better depict method adoption dynamics.

The simulation time, sampling, and error assessment were recorded for each method, and the PR was calculated to determine which method performed best. All the methods were introduced at the start of the simulation ($t = 0$), with each one being assigned to a different scientist. The data from each method were recorded until $t = 400$. Scientists compared methods at specific time intervals²², and three fractions of the total simulation time were analyzed²³: 0.050, 0.125, and 0.200 of $t = 400$. Scientists evaluated methods at $t = 20$ for fraction 0.050, at $t = 50$ for 0.125, and at $t = 80$ for 0.200. As the fraction increases, the intervals between method comparisons are extended.

The simulations operationalize dynamic interactions between networked scientists. Consider two scientists connected in a network. At each time step, they gather data, and the model translates these data into a belief state represented by a PR, which is a probability between 0 and 1 (indicating the accuracy of their method compared to others). When the scientists reach a designated sharing time fraction, they compare their methods' PR values. If one scientist's PR is higher than the other's, the scientist with the lower PR adopts the method with the higher one. This iterative process continues until the simulation reaches a stable state.

Figure 4 illustrates PR evolution during a simulation testing two or three methods. The chart shows how PR values change over time for three different methods (A, B, and C), demonstrating how methods compete and evolve based on their performance. The simulations are based on randomly drawn model parameters from a uniform distribution, as outlined in the Simulation Setup steps²⁴. The operability of this PR evolution shows how different methods perform within the scientific community during the simulation.

Throughout the simulation, certain methods exhaust the sampling parameters required for their respective models, as each model's complexity dictates the number of parameters available for testing. In each round, scientists sample one parameter, and if the number of runs exceeds the complexity value, no additional parameters are left to sample. This explains why simpler methods initially perform better: they require fewer samples to make accurate predictions in the early stages of testing. However, as the simulation progresses, these simpler methods are eventually surpassed by more complex ones, which continue to gather samples and improve their accuracy. In subsequent simulations, the evolution of the PR across different parameters is tracked. This consistency is crucial for ensuring comparability and assessing how methods compete, regardless of specific parameters²⁵.

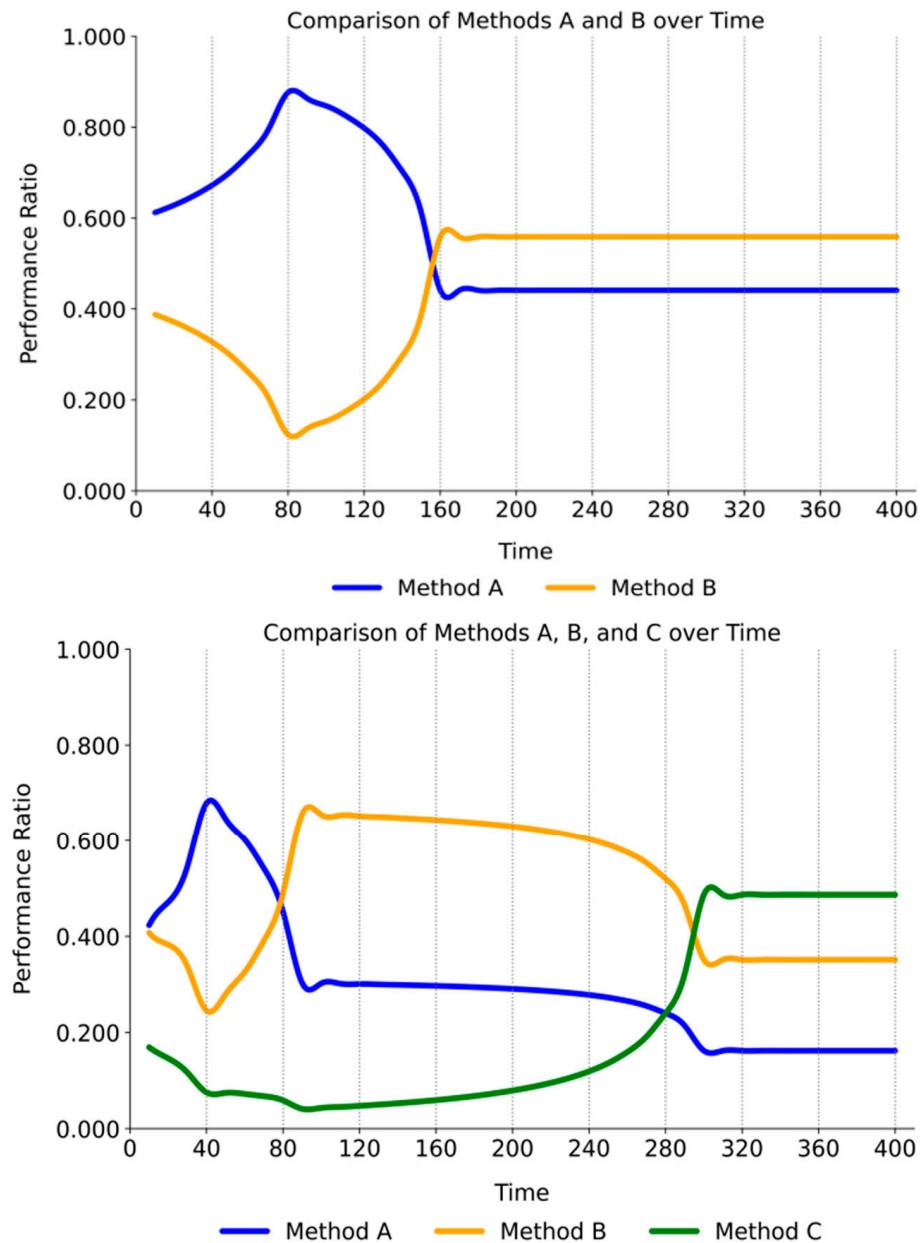


Figure 4. Graphic representation of real-time evolution of method Performance Ratio in a network of scientists testing two methods (**up**) or three methods (**down**).

4. Model Simulation Results

To analyze the simulation results, an integrated chart is constructed that incorporates various data sets recorded when each simulation reaches a stable state. These charts capture data such as the number of methods, the ratio of different population beliefs, the network type (e.g., complete, wheel, small-world, and cycle), the number of scientists, specific time intervals, and the sharing ratio. For example, Figure 5 shows how belief in different methods (neutral, Method A, Method B, and Method C) evolves over time in a small-world network of 75 scientists with a 0.125 sharing ratio. This comprehensive approach ensures that the visualizations effectively capture the dynamics within the simulated scientific community, highlighting how methods are adopted. To avoid overwhelming the reader, the complete simulation data and visualizations are available in the article's online repository²⁶ and in Figures S1–S6 of the Supporting Information.

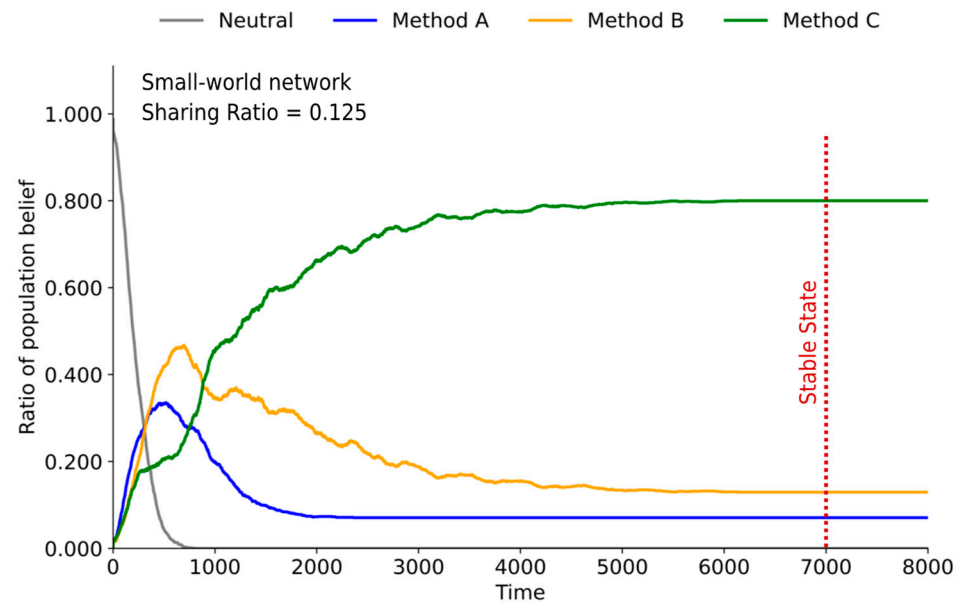


Figure 5. Real-time development of method preference in a small-world network with $N = 75$ on a 0.125 sharing ratio, highlighting a stable state. The yy axis represents the fraction of the population adopting a method or maintaining a neutral belief over the course of the simulation, depicted on the xx axis.

Figure 5 presents the average results of 20 different simulations with the same characteristics²⁷. Multiple simulations are conducted to account for the randomness in network disposition and distribution inherent in its features. When the stable state is reached (indicated by the red dotted line), two key pieces of data are recorded: (i) the ratio of the population that adopts a certain method and (ii) the time required to reach the stable state. These data are then transposed to the charts presented in the upcoming results section, where the evolution of parameters is recorded across different population sizes.

The analysis begins by examining the results for small-world networks, as these closely resemble the structure of the case study. Following this, the findings from small-world networks are compared with those from other network types²⁸. This comparative approach helps us understand how different network structures impact the dissemination and adoption of scientific methods. Analyzing small-world networks first provides a relevant baseline, ensuring that subsequent comparisons are rooted in a context that mirrors the “Salicylation” case.

4.1. Small-World Networks

Small-world network models are generated according to the Watts and Strogatz method [35]. The algorithm produces a network where each scientist is connected to their K -nearest neighbors, and these connections are rearranged according to a predefined probability²⁹. With this configuration, the network becomes closer to a lattice when more rewiring occurs, while less rewiring results in a more random network. This creates an intermediate representation between these two organizational states.

During the “Salicylation” quarrel, scientists operated within closely connected local groups while maintaining long-range connections, facilitating the spread of information. The chosen parameters for the Watts and Strogatz method were $(k, p) = (8, 0.1)$, as they capture this balance of combining local clustering with the potential for widespread information dissemination through occasional long-range links. This configuration models an intermediate organization state, providing a realistic simulation of how beliefs evolved and the dynamics of scientific communities in the historical context.

4.1.1. Two-Method Simulations

The results of the two-method simulations are presented in Figure 6. In the small-world network simulations with two methods, a clear pattern of belief evolution emerges, influenced by the network size and sharing timeframe. Initially, in smaller networks (fewer than 30 scientists), there is a strong preference for Method A across all sharing timeframes, with population belief ratios ranging from 0.800 to 0.950. This indicates that in smaller, more interconnected networks with localized clusters and sporadic long-range connections, simpler methods are preferred. This preference could be attributed to the ease of dissemination of simpler methods within tightly knit groups.

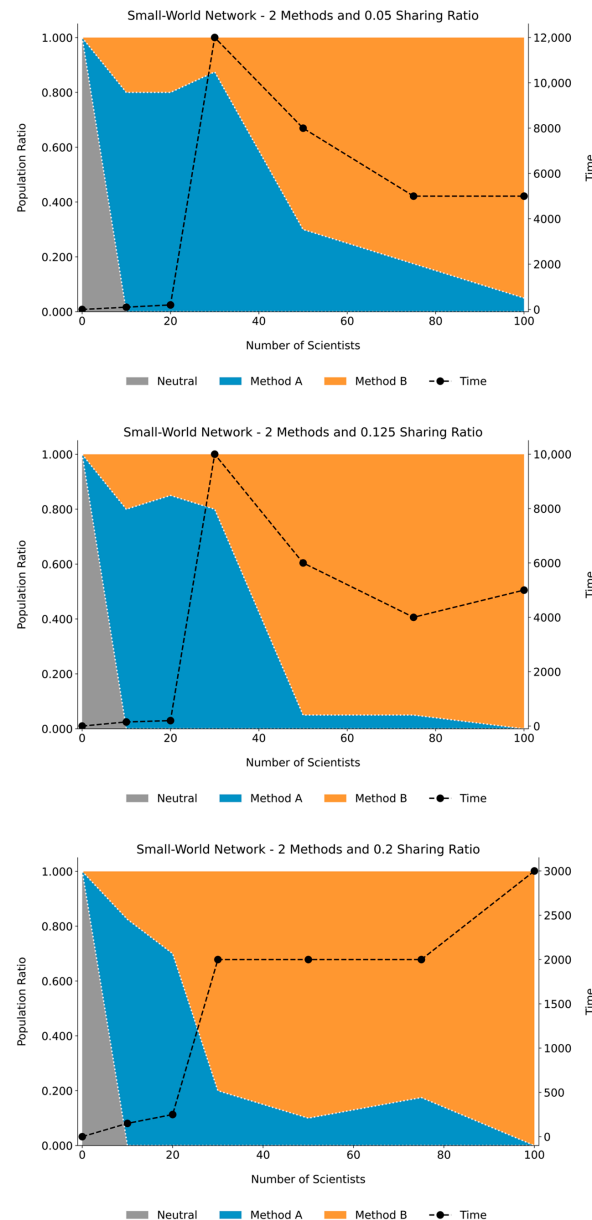


Figure 6. Result chart for population ratio belief, number of scientists, and the time to reach a stable state for a scenario with two methods on a small-world network (with time-sharing ratios of 0.050, 0.125, and 0.200).

As the network size increases, there is a noticeable shift toward Method B. For instance, in a 50-scientist network, the population belief in Method B ranges from 0.700 to 0.950. In networks with more than 60 scientists, Method B becomes predominant. In a 75-scientist network, belief in Method B reaches 0.825 in a 0.050 sharing timeframe and 0.950 in a

0.125 sharing timeframe. By the time the network size reaches 100 scientists, Method B completely dominates, with population belief ranging from 0.950 to 1.000 across various sharing times. This suggests that in larger small-world networks, where information can spread beyond immediate clusters, more complex methods are favored. The interconnected nature of these networks facilitates the acceptance of complex methodologies.

Additionally, in the longest sharing timeframe (0.200), larger networks eventually shift toward the more complex method, although they initially show a preference for Method A (up to approximately 70 scientists). This highlights the influence of extended deliberation and peer-to-peer interactions in the adoption of new methodologies. The gradual transition from Method A to Method B in larger networks underscores the central role of network structure and information-sharing dynamics in shaping the scientific community's consensus.

By analyzing method adoption within small-world network simulations, an interesting observation emerges regarding the influence of sharing frequency on complex method selection. While it might seem intuitive that more frequent sharing (0.050 ratio) would lead to quicker adoption because of constant peer-to-peer interactions, the data show that Method B is selected faster in networks with a lower sharing frequency, particularly in larger networks (over 50 scientists). In fact, Method B is adopted faster with a 0.200 sharing ratio than with a 0.050 ratio, despite the latter involving frequent sharing.

This phenomenon can be explained by the nature of interactions and the depth of deliberation allowed by longer sharing intervals. In scenarios with a 0.200 sharing ratio, scientists have more time between interactions to evaluate methods based on the data they have gathered. Such an extended period allows for deeper consideration and reduces potential noise from constant updates because of more frequent sharing. Longer intervals provide scientists with sufficient time to critically assess the performance of complex methods, leading to a more stable consensus on their predominance. In larger networks, the ability to engage in thorough deliberation appears to outweigh the benefits of constant updates, resulting in a shift toward Method B. While frequent sharing facilitates ongoing updates, longer sharing intervals create a more conducive environment for thoughtful evaluation, ultimately leading to a faster consensus on complex methodologies. This counterintuitive finding underscores the importance of interaction dynamics in the dissemination of new scientific methods.

4.1.2. Three-Method Simulations

The results of the three-method simulations are presented in Figure 7. As the sharing window widens in small-world network simulations, there is a clear evolution of preference involving three methods. In shorter sharing timeframes (0.050 and 0.125), smaller networks (fewer than 30 scientists) show a strong initial preference for Method A. For example, in a 10-scientist network with a 0.050 sharing timeframe, the population belief in Method A stands at 0.900. Similarly, in a 20-scientist network with the same sharing timeframe, Method A holds a belief of 0.450. This suggests that simpler methods, like Method A, are favored in smaller communities due to the ease of dissemination.

However, as the network size increases, preference shifts toward Method B and eventually Method C. In a 30-scientist network with a 0.050 sharing timeframe, belief in Method B rises to 0.550, while Method C starts gaining traction with a population belief of 0.300. By the time the network size reaches 50 scientists, Method C's belief significantly increases to 0.600. This trend continues in a 75-scientist network, where Method C dominates with a belief of 0.850, and in a 100-scientist network, Method C reaches full population belief at 1.000.

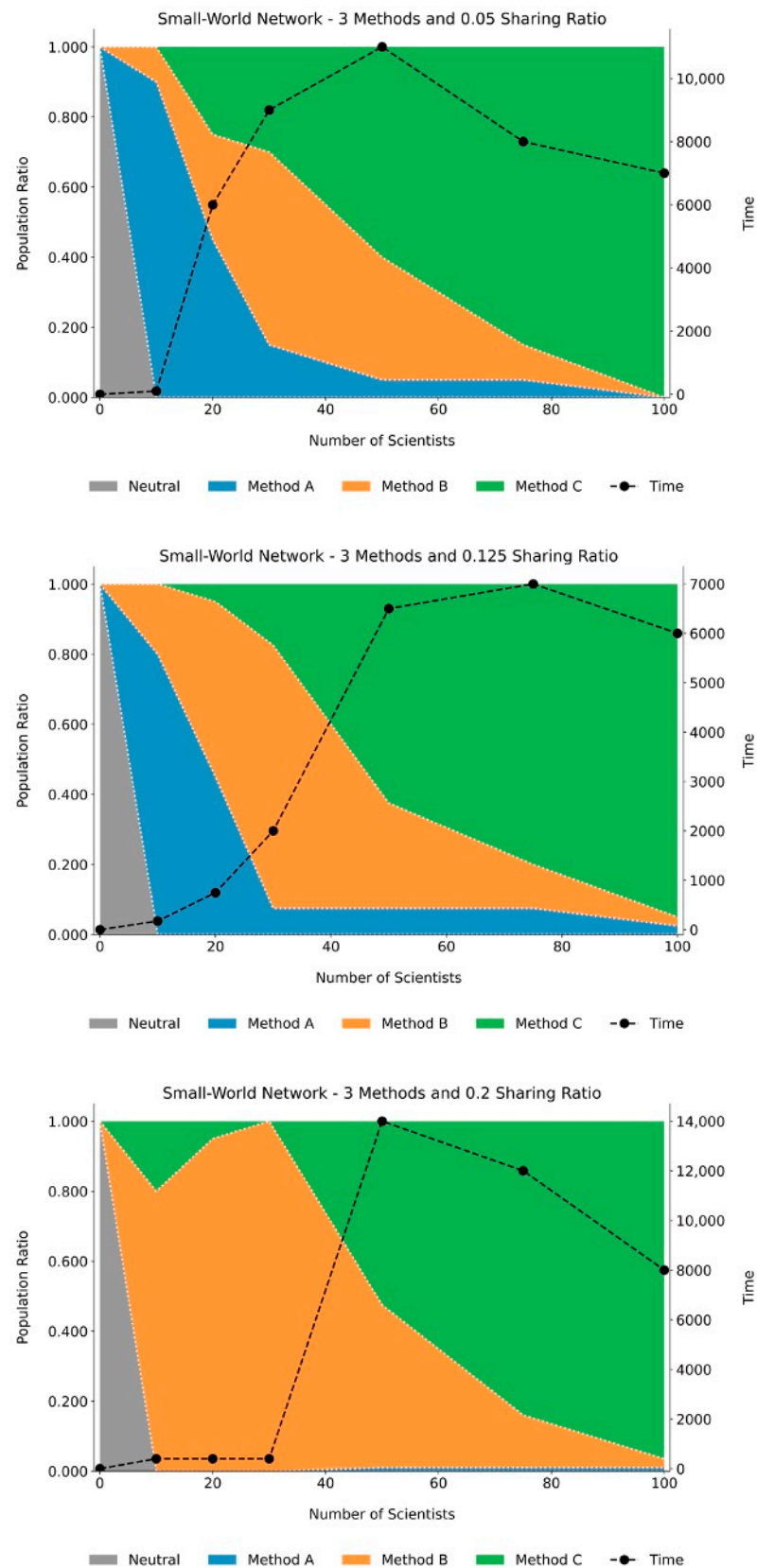


Figure 7. Result chart for population ratio belief, number of scientists, and the time to reach a stable state for a scenario with three methods on a small-world network (with time-sharing ratios of 0.050, 0.125, and 0.200).

For the 0.125 sharing timeframe, the pattern is similar but with a slightly quicker shift. In a 10-scientist network, Method A holds a population belief of 0.800. As the network size

increases to 30 scientists, Method B becomes more dominant, with a population belief of 0.750, while Method C begins to rise with a belief of 0.175. In larger networks, ranging from 75 to 100 scientists, Method C becomes predominant, with beliefs of 0.800 and 0.950, respectively. In the longest sharing timeframe (0.200), there is a distinct preference for Method B and Method C, even in smaller networks. For example, in a 10-scientist network, Method B holds a population belief of 0.800. While Method A seems to disappear entirely, it is still present but barely noticeable due to its limited penetration under the given simulation constraints.

As the network size increases to 20 scientists, Method B's belief rises to 0.950. However, Method C gains more traction in larger networks. In a 50-scientist network with a 0.200 sharing timeframe, Method C's belief reaches 0.525, surpassing Method B's 0.465. This trend continues, with Method C becoming more dominant in networks of 75 to 100 scientists, achieving population beliefs of 0.840 and 0.965, respectively.

In these three-method simulations, the time required to achieve consensus varies significantly based on the network size and the sharing timeframe. For shorter sharing timeframes (0.050), smaller networks reach a relatively quick consensus, often favoring simpler methods, like Method A. As the network size increases, the time to consensus also increases, and preference shifts toward more complex methods. In larger networks, Method C becomes dominant, but it takes longer to reach full population agreement.

For medium sharing timeframes (0.125), the transition toward more complex methods is more pronounced. Smaller networks still initially favor simpler methods, but the shift to Methods B and C happens more quickly compared to the shortest sharing timeframe. Method C becomes dominant even faster in larger networks, with a 100-scientist network reaching a population belief of 0.950 in 6000-time steps. There is also a noticeable trend toward the rapid adoption of complex methods in smaller networks with the longest sharing timeframe, as Method C's dominance becomes more evident as the network size increases.

Overall, longer sharing timeframes expedite the dissemination and adoption of more complex methods. In contrast, shorter sharing timeframes lead to faster consensus in smaller networks but tend to initially favor simpler methods. Medium sharing timeframes strike a balance, promoting a quicker transition to complex methods without the extended deliberation period required for longer sharing timeframes. This indicates that while sporadic sharing times help the broader dissemination of complex methodologies, network size plays a crucial role in determining the time needed to achieve consensus.

4.2. Result Discussion

The simulation results highlight the pivotal role of network structure, size, and information-sharing dynamics in the adoption of scientific methods. While larger networks generally tend to favor more complex methods over time, the rate and pattern of this adoption vary depending on the network's characteristics. These insights underscore the complexity of scientific consensus and the significant impact that different dissemination methodologies have on it. But how can these results be interpreted considering the historical case that inspired this research?

4.2.1. Small-World Networks and the "Salicylation" Quarrel

The results of the small-world network simulations align with the historical reports from the "Salicylation of Port Wines" case, demonstrating how both localized clustering and occasional long-range connections influenced the spread and acceptance of scientific methodologies. Initially, in smaller clusters within the network, simpler methods were rapidly adopted due to their ease of dissemination. For example, in a 10-scientist network with a 0.050 sharing timeframe, the population's belief in Method A was 0.900, reflecting the

initial spread of the erroneous “Salicylation” test within the Brazilian scientific community. This mirrors how the flawed belief in the Pellet Method became entrenched because of its rapid acceptance within localized groups.

Figure 8 summarizes the adoption dynamics of different scientific methods within small-world networks. As the network size increased, the simulations showed a gradual shift toward more complex methods. In a 50-scientist network with a 0.050 sharing time-frame, the population belief in Method C rose to 0.525, while in a 75-scientist network with a 0.200 sharing ratio, belief in Method C reached 0.840. This shift required extended sharing periods, reflecting the real-world delay in overturning the established erroneous beliefs about the “Salicylation” test. The Pellet Method faced significant challenges, requiring considerable time to validate the correct findings (mirroring the simulation results), which showed how complex methodologies gradually acquired traction.

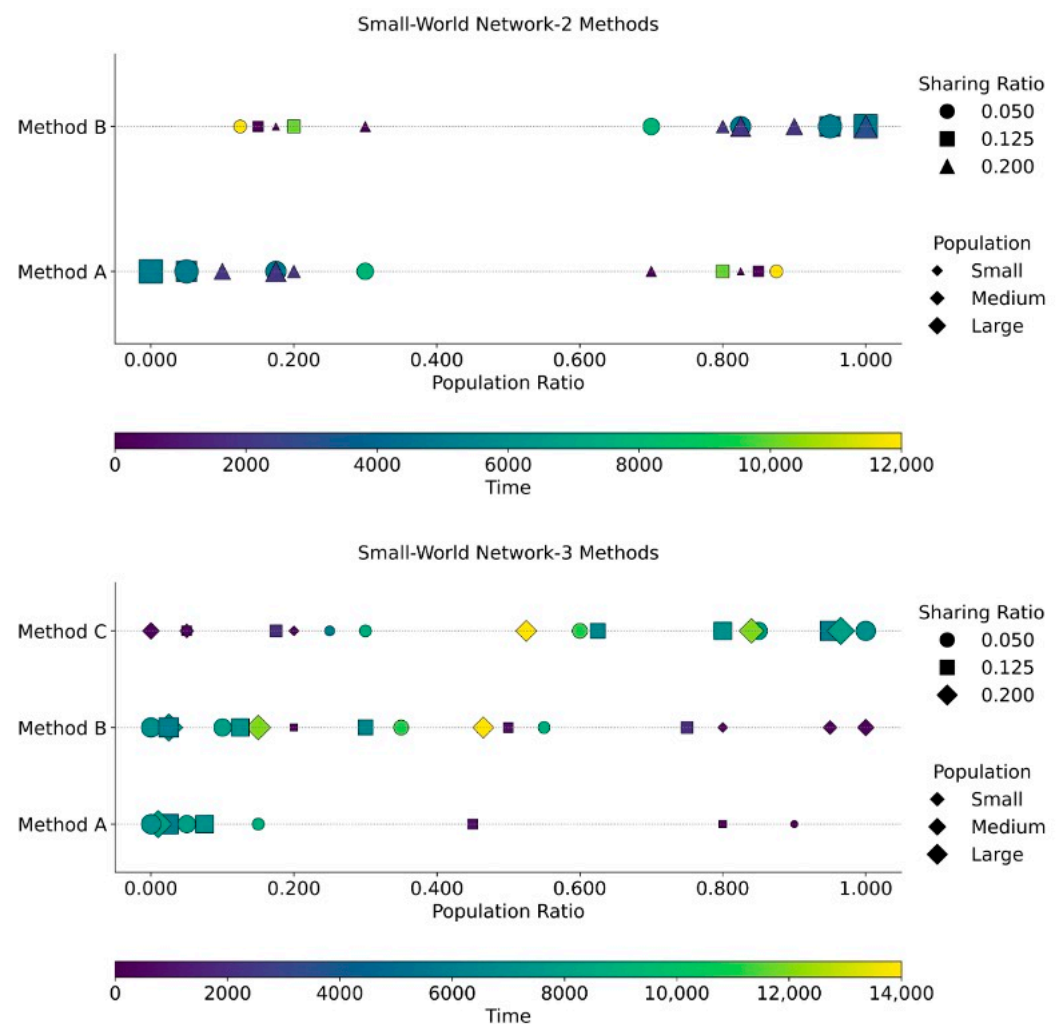


Figure 8. Adoption method dynamics within small-world networks simulations over time. The charts compare the spread of two methods (**top**) and three methods (**bottom**) across population sizes and sharing ratios. The xx axis represents the population proportion that adopted each method, while the color gradient shows the time progression. The shape sizes correspond to the different population sizes, and the shape forms reflect the sharing ratio.

While it might raise the question of what timeframe best suits this situation, even in larger networks, a less resourceful network may be less inclined to adopt more complex methods. If the correct method for the “Salicylation” test had provided the better outcome from the start, this would not have posed a problem. However, as is often the case in

science, the discovery of the best method can be difficult, especially within a community, reflecting the complexity seen in both the simulations and the historical case.

The small-world network's balance of local interactions and long-range connections facilitated the eventual acceptance of the correct method. For instance, in a large 100-scientist network with a 0.200 sharing ratio, Method C achieved a population belief of 0.965. The historical case saw the Portuguese scientists' accurate findings gradually gaining acceptance through international dissemination, analogous to the long-range connections that supported the adoption of complex methods. These interactions and the time required for peer evaluations align with the prolonged process of achieving scientific consensus in the "Salicylation" quarrel³⁰.

Another important takeaway is revealed when the community must choose between two or three methods. In most cases, the complex method prevails with a larger proportion of scientists in two-method simulations. However, there are situations—particularly in smaller populations with three methods—where exposure to previous incorrect methods can override the accumulation of evidence for the better method. Like the "Salicylation" case, some small-world network simulations demonstrate a population window where, even with different timeframes, the most believed method is not the most complex. Although this is a partial finding considering the diverse network aspects, it still draws an interesting parallel in method selection.

Mathematical complexity played a major role in the "Salicylation" case, influencing both the dissemination and acceptance of scientific methods. This dynamic is reflected in the small-world simulations, where smaller networks with high local clustering more readily adopted simpler methods. This mirrors the initial spread of the Pellet Method, which was easier to disseminate within the Brazilian scientific community, as simpler methods tend to gain rapid acceptance even if they are less accurate (Figure 8). The persistence of such methods in the face of emerging complex ones highlights the challenge of overturning established beliefs. The simulations demonstrated that larger networks and longer sharing timeframes are necessary for complex methods to gain traction. In the historical case, the more complex method proposed by Portuguese scientists faced significant resistance and took considerable time to be accepted, mirroring the simulations.

The simulations also highlight that longer sharing timeframes facilitate the adoption of complex methods. This was evident in the "Salicylation", where only after prolonged scientific validation and extensive international communication was the accurate testing method finally accepted. In medium sharing timeframes (0.125), the transition toward more complex methods is more pronounced (Figure 8). While smaller networks initially favor simpler methods, the shift to Methods B and C happens faster compared to the 0.050 sharing timeframe. For the longest timeframe (0.200), there is a trend toward the rapid adoption of more complex methods, even in smaller networks (Figure 8). This parallels the historical case, where Portuguese scientists' findings gradually gained traction and eventually dominated the consensus, much like the dominance of Method C in the simulations with longer sharing timeframes. This reflects the historical period when international scientific discourse and increased scrutiny began to favor the more accurate method proposed by Portuguese scientists.

However, the simulations also reveal a tendency for localized information spread through neighboring interactions, reflecting how historical scientific communities operated. With multiple methods in play, the model shows the difficulty of reaching consensus amid methodological diversity, particularly in larger communities. It also demonstrates the trade-offs of limiting scientists' exposure to diverse ideas, balancing broad exposure with the risk of fixation on certain methodologies. This trade-off between sharing speed and

scientists' exposure underscores the challenge of balancing beliefs and model complexity: an incorrect method can spread regardless of the sharing timeframe.

This trend, where longer sharing timeframes ease the acceptance of complex methods, is not new to the literature. Some argue that decreasing communication helps particularly difficult problems, where data alone do not easily clarify the truth. The "Salicylation" quarrel supports this view, showing that even with initially obscure methods, continuous communication allows for more gradual acceptance of the best methodologies. Rather than decreasing communication, scientists may benefit from a structure that allows for both the rapid initial dissemination of ideas and slower, thorough evaluations. This aligns with Rosenstock's argument that promoting diversity in scientific approaches may be more effective than simply reducing communication [20].

Communities often settle on a belief based on the frequency and nature of their exposure to peer evidence, regardless of how accurately it represents reality. While method accuracy can sway more scientists toward adoption, the simulations reveal that the duration of exposure and community size play critical roles in achieving consensus. This aligns with the concept of transient diversity, where balancing rapid dissemination with thorough evaluation is key [36]³¹. The simulations show that, despite various degrees of network interconnectivity, communities rarely achieve 100% consensus on a single method, reflecting the explore/exploit trade-off in learning (Figure 8). Even with strong evidence supporting a superior method, resistance to change persists, highlighting the importance of maintaining diversity in scientific exploration to prevent premature convergence on suboptimal methods.

Thus, these ABM simulations offer more than a technical exercise. They provide a means of uncovering latent dynamics in the "Salicylation". The slow diffusion of the correct method through the scientific community in the simulations mirrors the delays in the acceptance of the Portuguese findings. As the model also reveals that tightly clustered scientific networks can lead to entrenched belief in incorrect methods reflects the real-world persistence of the Brazilian scientists' flawed "Salicylation" test. The ABM highlights the epistemic difficulty of overcoming entrenched beliefs in isolated networks, offering broad implications for understanding the history of scientific discovery.

4.2.2. The "Zollman Effect" and Dynamics of Method Consensus

While the small-world network model connects with the historical "Salicylation" case, examining other network structures is equally important. Different structures (complete, cycle, wheel, and small-world) offer unique insights into the dynamics of scientific consensus and methodology dissemination. By exploring these networks, scientists can better understand how scientific beliefs spread, how errors persist, and how corrections are eventually adopted. This section delves into the relevance of the "Zollman Effect" in understanding these dynamics, both in the model and in the historical context.

The "Zollman Effect" provides a framework for understanding how scientific beliefs spread within different network structures. The simulation results show how varying levels of network connectivity influence the adoption of scientific beliefs. In complete networks, where all scientists are fully connected, the "Zollman Effect" is evident in the rapid dissemination of both correct and incorrect information. Smaller networks initially favored simpler methods, with Method B reaching a population belief of 0.950 in a 100-scientist network with a 0.050 sharing timeframe. This reflects the idea that high connectivity can quickly spread ideas, including erroneous ones. However, this same connectivity allows for rapid correction once robust evidence is presented, as seen in the eventual dominance of more complex methods in larger networks.

Cycle networks, on the other hand, show a slower and more deliberate process of information dissemination. The results indicate a steady but slower shift toward complex methods, with Method C becoming dominant with a belief of 0.900 in a 50-scientist network with a 0.050 sharing timeframe. This highlights how less connected networks can act as buffers against the rapid spread of false information. The step-by-step evaluation process mirrors the extended time required to overturn entrenched erroneous beliefs, emphasizing that less connected networks may delay consensus but also lead to more thorough scrutiny of accurate methods.

Wheel networks, with their central hub structure, illustrate the significant impact of influential figures or institutions on scientific consensus. In a 75-scientist network with a 0.050 sharing timeframe, Method C reached a population belief of 0.650, showing how central hubs can influence the adoption of complex methods. This is similar to the initial rapid adoption of the flawed “Salicylation” test due to endorsement by influential hubs, followed by the gradual acceptance of the correct method as these hubs shifted their support. It underscores the “Zollman Effect” principle that influential nodes can accelerate or hinder the spread of scientific beliefs.

The small-world network results bridge the dynamics observed in other tested networks. The rapid initial spread of simple methods in local clusters, like in complete networks, and the gradual, thorough scrutiny enabled by occasional long-range connections, akin to cycle networks, show how small-world networks embody the “Zollman Effect”. These networks demonstrate that scientific communities can benefit from both localized rapid dissemination and broader, slower evaluation processes, ultimately leading to a more robust consensus on complex methods.

The simulations also demonstrated that smaller networks with high local clustering initially favored simpler methods, like the dynamics of complete networks. This mirrors the initial rapid spread of the erroneous “Salicylation” test, where the flawed method quickly gained acceptance within the Brazilian scientific community. As the network size increased, the presence of long-range connections in small-world networks facilitated a gradual shift toward more complex methods. As reported in earlier modeling studies [37], this aligns with how the Portuguese scientists’ accurate but complex method eventually gained acceptance through international correspondence. It also aligns with the “Zollman Effect”, suggesting that while high connectivity can initially spread incorrect beliefs, the introduction of long-range connections enables the dissemination of robust evidence, leading to the eventual adoption of accurate methods. This comprehensive understanding highlights the importance of network structure in shaping scientific consensus formation.

These insights provide encouraging evidence that the developed ABMs can be powerful tools for analyzing historical events. When social dynamics play a significant role in an event outcome, these models can capture the community landscape described by historians and give it an experimental structure to support their analysis. While they may not fully capture all relevant aspects of real-world systems³², they are useful in reasoning about collaboration and homophily, as supported by recent literature [38]. Models can also illuminate potential issues in diversity initiatives, such as promoting contact that leads to discrimination between identity groups. They offer a helpful framework for thinking about different intervention strategies, allowing researchers to study costly and complex interventions in a low-risk, low-cost way. The results are not definitive but can guide further research into how academic collaborations might be diversified.

The small-world network simulations provided significant insights into the “Salicylation” case, highlighting the challenges of spreading complex methods within a community. Despite solid evidence, disseminating complex methods, like those proposed by the Portuguese scientists, faced resistance, especially in smaller, peripheral scientific networks.

The simulations confirmed that simple but incorrect methods could persist for a long time, just as they did in the historical case. These small-world simulations effectively mirror historical scientific network behaviors, and future studies incorporating influential roles could enhance our understanding of scientific inquiry dynamics.

In follow-up studies, introducing other roles seen in other ABMs (like a propagandist) could improve historical realism and allow for the exploration of influential scientists' role in the direction of scientific discovery. For example, the slow adoption of the Portuguese method in Brazil may have been affected by the socio-political dynamics of the time. Historical tensions could have heightened the perceived epistemic risks associated with adopting a method tied to Portuguese scientists. Future studies could refine these simulations by introducing parameters that account for epistemic risks and political influences. Models could explore how differing risk thresholds impact the dissemination of complex ideas, particularly when the adoption of such methods intersects with socio-political tensions. This asymmetry in risk perception highlights how political values can shape the spread of scientific ideas, not as irrational biases but as rational responses to socio-political contexts. Although there are still intricacies in developing a broad framework for such investigations, this study represents a solid and sustained step in that direction.

5. Conclusions

ABMs can offer valuable insights into the dynamics of method selection in scientific discovery. The presented model help clarify how incorrect methods can persist within a community, given the specific constraints of method complexity. It also underscores the importance of how scientists share information with their peers and the impact of method complexity where a community becomes entrenched in a wrong belief.

ABM simulations confirm key aspects of how scientific communities operate, and the “Salicylation of Port Wines” case provides a compelling historical example. In smaller, tightly clustered networks, the simulations reveal a tendency to favor simpler but flawed methods, similar to the initial acceptance of the incorrect “Salicylation” test in the 19th century. As network size and complexity increased in the model, a shift toward more accurate but complex methods became evident, mirroring the historical progression where the correct method gradually gained acceptance. The timing of this shift, influenced by the network structure and the frequency of information sharing, reflects the historical reality that dissemination of correct scientific methods often depends on the broader communication dynamics within the scientific community.

This approach shows how ABMs can test hypotheses about historical cases, providing fresh insights into how and why certain beliefs persisted. By connecting the real-world challenges faced during the “Salicylation” dispute with the model's results, we acquire a clearer picture of the factors that facilitate or hinder epistemic progress, reaffirming the value of combining historical inquiry with computational modeling to better understand method adoption and scientific consensus.

The model simulations revealed that mathematical complexity plays a crucial role in the acceptance of scientific methods. Complex methods faced significant challenges in gaining traction within scientific communities, particularly in smaller, peripheral networks. Despite having solid evidence, disseminating these methods required considerable time. This resistance to complex methods was clear in the historical case, where the accurate but complex “Salicylation” method proposed by Portuguese scientists faced initial skepticism and took time to be accepted.

Given the exploratory nature of these simulations, real-world applications must be drawn carefully, as this work focused on models within an empirical framework [39]³³. As seen in the historical case, scientists can sometimes ignore relevant findings in scientific

forums, selectively using information to support their theses. Method complexity is seldom mentioned in more recent studies, and further work is needed to introduce other variables, such as reasoning biases. Simulating confirmation bias would add depth to these models, enhancing the complexity of each scientist's behavior.

However, there are many valuable conclusions from these simulations. They generate different research hypotheses regarding how scientists converge on a state-of-the-art technique from empirical insight based on method complexity. There is a vast field of study around the historical emergence of scientific methods used to define legal methodologies, whose dynamics have yet to be fully explored. This applies not only in chemistry but also in public health and regulation issues, where there are reports of the misapplication of scientific methods (sometimes even against the most accurate practices). Whether due to scientific misinterpretation, foul play, or political intervention, these models lay a foundation for epistemic research on such scenarios. As a novel study in this area, this article also provides guidance on how to adapt previous and current approaches to epistemic modeling toward the study of scientific communities. While these models are somewhat simplified, they offer various possibilities for integrating different solutions or adjusting them from other traditional models.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/philosophies10010001/s1>, It presents a result analysis of conducted model simulations to explore the adoption dynamics of scientific methods across additional network structures. These results highlight the influence of network type, size, and communication frequency on the spread and eventual dominance of both simple and complex methodologies. Figures S1–S6: Result charts for population ratio belief, number of scientists and the time to reach a stable state for a scenario with two/three methods on a complete/cycle/wheel network (with time-sharing ratios of 0.050, 0.125 and 0.200).

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Data Availability Statement: The full model code and exported results are presented in the online repository of this article at <https://github.com/jfcaetano/ABM-Mod-Innovations>.

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Conflicts of Interest: The author declares no conflicts of interest.

Notes

- ¹ This is relevant when it comes to demystifying generalized considerations about science-making in a social community.
- ² Each simulation considers that scientists have a random probability of choosing each hypothesis, with each one having a given percentage of success.
- ³ If at the beginning of information sharing scientists converge on a wrong hypothesis, which seemed to be the right one, it will be easier for it to spread in a fully connected network (and therefore, more difficult to reverse it in the long run).
- ⁴ It is also the case where there is a misidentification of the chemical product, with a mix-up between traditional and chemical nomenclature used by the experts.

Salicylic acid is the active precursor to aspirin and was widely used during the 19th century for its medicinal properties. Derived from willow bark, it was known for its anti-inflammatory and pain-relieving effects, making it a common treatment for ailments such as fever, rheumatism, and headaches.

Before being labeled as an adulterant, salicylic acid was sometimes used as a wine preservative in the 19th century. This was due to its antimicrobial properties, which helped prevent fermentation issues, maintaining the wine's quality and shelf life. This is argued in detail in [1], notably the echoes from Brazilian press at the time.

Like the case made by [32], how they aptly capture the essence of a historical scientific communities, characterized by clusters of closely collaborating groups interconnected by long-range links.

In the biography of chemist Antônio Ferreira da Silva, who led Portuguese efforts to debunk Brazilians' claims [33], a historical interpretation on how key scientists in this quarrel communicated and disseminated their findings is presented. This network interpretation is largely based on its findings.

Unlike a cycle network, which oversimplifies the interaction dynamics by limiting each scientist to only two connections, or a complete network, which assumes an unrealistically high level of interconnectedness, a small-world network introduces a realistic scenario of scientific collaboration.

Reference [33] lists several historic sources, including transcripts of Portuguese scientific journals that back this information path. Specific source quotes are present on pages 245–263 of the book. A detailed account of the scientific institutionalization of the *Laboratório Químico Municipal do Porto* in this case has recently been published [34].

These two institutions were key in the public scientific debate that occurred, as mentioned in [1].

This resistance can be due to political, social, or economic reasons, which are not directly modeled but are an implicit part of the network dynamics.

Model sample code is available in the following online repository forked from previous work by [22]: <https://github.com/jfcaetano/ABM-Mod-Innovations>. "Project Mesa" online document page can be accessed at <https://mesa.readthedocs.io> (accessed on 1 October 2024).

Method curves represent reality by a mathematical condition, amassed by the plot points taken from experiments.

In the code, each method has a given complexity: they are assigned a number on a 0 to 30 scale, where increasing values mean increased complexity.

The conceptual depth of a method is considered, as methods based on abstract concepts are considered more complex.

Where Value A is the quantitative value of a given point, and the real value is the exact value of the reality curve.

Applied for simulations considering more than two different methods. The operationalization is presented in the model's code. Updating is inspired by the procedure following Kevin Zollman's framework for Epistemic Communities [19].

The focus on evidence sharing emphasizes scientists' sensibility to chance based only on new data, serving a baseline for further network structures with new agents.

Python Software Foundation—Python Language Reference, version 3.9.8. <http://www.python.org> (accessed on 1 October 2024).

Limit sharing time was marked to give time for each simulation to reach a stable state.

Each sharing time is determined by multiplying the testing time by the sharing ratio.

The sample code for the generation of the data for both charts is presented in the article's online repository.

By keeping the PR evolution consistent, it is possible to identify fundamental patterns and trends, providing clearer insights into how methods perform and are adopted over time within the scientific community.

Model sample code is available in the online repository and additional network simulation results are presented in Annex A.

Figure 5 gives a comprehensive read that enables an integrated read out of the results, which will become useful when comparing different network structures.

The complete data and charts gathered for other network simulations are presented in the online repository.

This is performed with a combination of (n_i, n_k) , where k is defined randomly (so that there are no constraints on the definition of links between agents).

This reflects how resource constraints and initial deep-rooted beliefs can obstruct the acceptance of complex methodologies.

A good summary on the concept of transient diversity in scientific community modeling is depicted in Section 4 of [36].

In the model, it is assumed that collaborations are always dyadic, whereas in real scientific communities, collaborations can include many members, or researchers may work alone. Also, there are no costs to breaking old collaborative ties and forming new ones.

Although some of these models have been theoretically developed, they still lack empirical validation [39].

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