Diffusion and Social Networks: Revisiting Medical Innovation with Agents

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EXTENDED ABSTRACT

In this paper, we reanalyze *Medical Innovation*, the classic study on diffusion of *Tetracycline* by Coleman, Katz and Menzel (1966). *Medical Innovation* articulates how different patterns of interpersonal communications can influence the diffusion process at different stages of adoption. In their pioneering study, individual network (discussion, friendship or advice) was perceived as a set of disjointed pairs, and the extent of influences were therefore, evaluated for pairs of individuals. Given the existence of overlapping networks and consequent influences on doctors' adoption decisions, the complexity of actual events was not captured by pair analysis. Subsequent reanalyses (Burt 1987, Strang and Tuma 1993, Valente 1995, Van den Bulte and Lilien 2001) failed to capture the complexity involved in the diffusion process and had a static exposure of the network structure. In this paper, for the first time, we address these limitations by combining Agent-Based Modeling (ABM) and network analysis.

Based on the findings of Coleman et. al. (1966) study, we develop a diffusion model, *Gammanym*. Using SMALLTALK programming language, *Gammanym* is developed with CORMAS platform under Visual Works environment. The medical community is portrayed in an 8 X 8 spatial grid. The unit cell captures three different locations for professional interactions: practices, hospitals, and conference centers, randomly located over the spatial grid. Two social agents- *Doctor* and *Laboratory* are depicted in the model. Doctors are the principal agents in the diffusion process and are initially located at their respective practices. A doctor's adoption decision is influenced by a random *friendship network*, and a *professional network* created through discussions with office colleagues, or hospital visits or conference attendance. A communicating agent, *Laboratory*, on the other hand, influences doctors' adoption decisions by sending information through multiple channels: medical representatives or *detailman* visiting practices, journals sent to doctors' practices and commercial flyers available during conferences. Doctors' decisions to adopt a new drug involve interdependent local interactions among different entities in *Gammanym*.

The cumulative adoption curves (Figure 1) are derived for three sets of initial conditions, based on which network topology and evolution of uptake are analyzed. The three scenarios are specified to evaluate the degree of influences by different factors in the diffusion process: *baseline scenario* with one seed (initial adopter), one detailman and one journal; *heavy media scenario* with one seed but increasing degrees of external influence, with five detailman and four journals; and *integration scenario* with one seed, without any external influence from the laboratory.

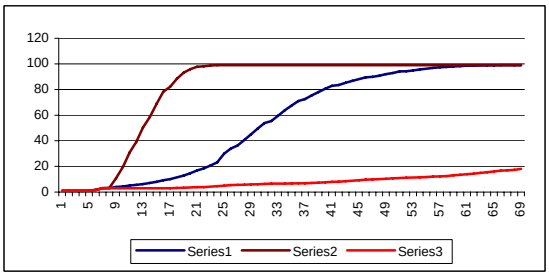

Figure 1: Cumulative Diffusion Curves for three scenarios: Baseline (Series 1), Heavy Media (Series 2) and Integration (Series 3)

Averaged over an ensemble of 100 runs, clustering coefficient and average shortest path length indicate that social networks depicted in *Gammanym* are random graphs. Evolution of uptake suggests that although the degree of external influence in terms of marketing strategies adopted by the pharmaceutical company does not have impact on the network structure, the speed of diffusion is largely determined by it.

1. INTRODUCTION

In this paper we reanalyze *Medical Innovation* by Coleman et. al. (1966), the classic study on diffusion of *Tetracycline,* which at that time was a newly introduced antibiotic. Their pioneering study elaborated on how different patterns of interpersonal communications can influence the diffusion of a medical innovation in four medical communities in Illinois. The motivation for our reanalysis is to capture the complex interactions involved in the diffusion process by combining Agent-based Modeling (ABM) and network analysis. Based on the findings in *Medical Innovation*, we develop a diffusion model called *Gammanym*. The topology of networks generated in *Gammanym*, and its evolution, are analyzed to evaluate how, and to what extent, network structure influences the diffusion process.

2. DIFFUSION AND NETWORKS

2.1. Diffusion of Tetracycline

Tetracycline was launched in November 1953. Four US Midwestern cities: Peoria, Bloomington, Quincy and Galesburg, were selected for the original study. The sample constituted 148 general practitioners, internists, and pediatricians in active practice, of which 126 (85% of the sample) were interviewed. In an attempt to evaluate the importance of social networks, each of them was asked about their close associates (e.g., friends, colleagues and advisors) in the medical community. A prescription audit in the local pharmacies was carried out for 125 doctors (121 general practitioners, internists, and pediatricians and 4, listed as surgeons or proctologists) over a 16-month period following the release of Tetracycline for general sale. Prescriptions were edited for three successive days at approximately monthly intervals (Coleman et. al. 1966: 194).

Their study identifies two broad categories of variables influencing the diffusion process. First category describes personal traits or *individual variables,* affecting individual receptivity: 1. type of practice, 2. medical background, 3. contacts with out-of-town institutions, 4. media behavior, and 5. orientations and attitudes. Second category defines *social variables* influencing the adoption process as a result of professional ties created through hospital affiliation and shared office, or social ties to other members of the community. Their analyses revealed that doctors' decisions to adopt *Tetracycline,* the new drug, were strongly influenced by the people they are connected with, either socially or professionally.

We have reviewed four reanalyses of *Medical Innovation*. The authors differed in terms of their methods as well as their perspectives on the process of diffusion. Burt (1987) argues that where contagion occurred, its effect was through structural equivalence not cohesion. Strang and Tuma (1993) apply an event-history framework incorporating spatial and temporal heterogeneity. Their results contradicts Burt, as they opine, "Cohesive ties based on advice giving and discussion also contribute to diffusion, as do structures of similarity in physicians' orientation towards their work (Strang and Tuma 1993: 638)." Valente (1995) tests his threshold/critical mass (T/CM) model on medical innovation data and indicates that the opinion leaders, who have greater exposure to external influence, play a dominant role in the diffusion process. A study by Van den Bulte and Lilien (1999, 2001) provides strong support for external influence in the diffusion process by incorporating a data set on advertisement volume. The authors conclude that the data do not show that diffusion was driven by contagion operating over social networks, and that earlier analyses confounded social contagion with the effect of marketing effort (Van den Bulte and Lilien 2001).

2.2. Rationale for *Gammanym*

The major limitation of all the previous studies is their static exposition of network structure, which falls short of representing the evolving process. These dynamics can be described by the *Dynamics of the network,* or *Dynamics on the network* (Watts 2003). Until now, however, neither medical innovation study nor the subsequent reanalyses of the original dataset incorporated any of those dynamic features. Our study, therefore complements the extant work.

Our study also makes contribution in that the complexity generated in the diffusion process has not been examined by any previous studies. In *Medical Innovation*, the extent of influence was evaluated for pairs of individuals. Individual network (discussion, friendship or advice) was, therefore, perceived as a set of disjointed pairs. Given the existence of overlapping networks and consequent influences on doctors' adoption decisions, the complexity of actual events was not captured by pair analysis. ABM enables us to address this limitation in previous studies by considering the whole network as a unit of analysis.

3. MODELLING FRAMEWORK

Using SMALLTALK programming language, we develop *Gammanym* with the CORMAS platform (Common-pool Resources and Multi-Agent Systems, **http://cormas.cirad.fr**) under Visual Works environment.

3.1. Spatial Representation and Passive objects

We portray the medical community in a 8 X 8 spatial grid. The unit cell captures three different locations for professional interactions: *Hospitals*, *Practices* and *Conference Center*, which are created as Passive objects. *Gammanym* has sixty-one practices, two hospitals and one conference center, randomly located over the spatial grid. In the original study, on average 47% of doctors were alone in office, 20% were in clinics, 17% were working with two colleagues and 15% were sharing office with one colleague. We captured the categories of office partnership into three *practice types: Private (alone in office), Center (shared office with two partners)* and *Clinic (working with four colleagues)*. The doctors are thus located among 46 private, 11 centers and 4 clinics.

Gammanym specifies two hospitals, as all the cities, on average, have two hospitals. Conference center, the third passive entity, provides the context in which a much larger group of professionals can interact with each other. Random allocation of these practices over the grid reflects that spatial representation is not sensitive to distances. In other words, the doctors' decision to go to hospitals or the conference center, do not depend on the location of their practices; as the grid does not incorporate any Geographic Information System (GIS) specifications. This inclusion was not possible, as we do not have the original data set. GIS specifications, on the other hand, would add little to our analysis in the sense that the significance of physical distance in diffusing a new idea can, and is, well captured by our definition of discussion networks. Without GIS specifications real distance between cells have no impact on the doctors decision to move from office to hospitals or conference centers.

3.2. Social agents

Gammanym depicts two kinds of social agents- *Doctor* and *Laboratory*. Initially located in their respective practices, 99 doctors are created. A laboratory (LAB from hereon), on the other hand, influences doctors' adoption decisions by sending information through multiple channels: medical representatives, journals and commercial flyers.

3.2.1 Located and Communicating Agents: Doctors

In Gammanym, *Doctors* are specified with the attributes generating network effects only. Individual traits have impacts on the adoption decision. Nevertheless, we opt for this simplification on the basis of the correlation coefficient estimated in *medical innovation*. Four network variables, shared office, advice seeking, discussion and friendship, showed a strong association to the date of first use of *Tetracycline* than any other individual variables, with the single exception of total volume of prescriptions for the class of drugs. Holding the volume of prescriptions constant, the association between integration and adoption increased (Coleman et. al. 1966: 92). Thus, we explore if all the doctors are homogenous in terms of their individual attributes, to what extent does integration matter for adoption decision?

Professional interactions are spatially defined, based on which Gammanym builds discussion networks. We do this to signify the importance of tacit knowledge or non-codified knowledge, which requires face-to-face contacts for its transmission. The doctors, therefore, consider the others as discussion partners if they are situated in the same cell. After each visit to hospital or conference centers, doctors return back to their practices. The friendship network, on the other hand, is random in nature as the doctors are initialized with random number of friends and counter for friends; both ranging from 0-3. We treated the indices of similarity derived in the original study with reservation, because of their limited statistical relevance for only 111 friendship pairs (Coleman et. al. 1966: 143).

3.2.2. Communicating Agents: Laboratory

LAB adopts a mixed marketing strategy with three different channels to send information about the new drug: *i. Detailman* (pharmaceutical representative) visiting practices; *ii. Flyers*, available at the conferences; *iii. Journals*, sent to doctors' practices.

In *Gammanym* the *detailman* visits all the doctors at their practices. Assuming similar influences by direct mail advertising and journal insertions, we specify *journals* as the second instrument for the LAB. We introduce *flyers* at the conference centers as an additional marketing tool. To avoid the notion of blanket exposure to all doctors, we specify the criterion that LAB sends flyers based on the number of previous conference participants.

3.4 Adoption Process/Decision-making process

Doctors' decisions to adopt a new drug involve interdependent local interactions among different entities in *Gammanym*. Diffusion scholars have long recognized that individual's decision about adoption is a process that occurs over time, consisting of several stages (Coleman et. al. 1966; Rogers 1995). We specify five stages of adoption: 1. *Awareness* or *knowledge*, 2. *Interest*, 3. *Evaluation/mental trial*, 4. *Trial*, and 5. *Adoption/acceptance*. In our model *readiness* is specified as the attribute signifying the above stages of adoption. All doctors are initialized with readiness 4. Readiness is decremented when they receive an *alert* from different sources. Discussions with other doctors, either friends or colleagues at practices, conferences, or hospitals generate an alert when the mean adoption rate is 0.50 or above. In case of the LAB, on the other hand, an alert is created each time a doctor received information from the detailman, flyers or journals. Doctors' readiness is gradually reduced with alerts from all the aforementioned sources. When the readiness reaches zero (Adoption/acceptance stage), doctors adopt the new drug.

3.5 Modeling Sequence

Gammanym is divided into four phases: i) managing professional interactions; ii) external influence; iii) decision making process; and iv) networks formation. At each time step, *Gammanym* resets the attributes of the practices. Thus, the doctors are at their respective practices at the beginning of each simulation.

Phase I entails the methods for doctors' professional interactions. Primarily, the doctors interact with the office colleagues at their practices. Hospitals are another location for professional interactions, where they have their monthly visits. The third location for information exchange is the conference center, as the doctors move from their practices to there after receiving invitations. Phase II depicts the mixed marketing strategy adopted by the LAB. At each time step, the LAB targets practices from the unvisited ones and send the detailman if the doctors are available. After receiving an invitation for a conference from the conference center, the LAB sends flyers to the conference center based on number of previous conference attendees. LAB issues journals only when the number of newly adopted doctors in the previous time step, i.e., the last increment, is less than half of the average number of adopted doctors. Phase III is the decision-making process based on readiness. Phase IV constitutes the methods for network formation. At each time step, the network matrices for professional networks and friendship networks contain the number of interpersonal interactions for each doctor. The adoption matrix, on the other hand, specifies the adoption status at each time step for all the doctors.

4. SIMULATION RESULTS

In this section our discussion traces through the shape of the cumulative diffusion curves under three scenarios. The three scenarios are specified to evaluate the degree of influences by different factors in the diffusion process: i. *Baseline Scenario*; with one 'seed' or initial adopter, one detailman and one journal; ii. *Heavy Media Scenario*; with one initial adopter, five detailman and four journals; iii. *Integration Scenario*; one initial adopter, without any external influence from the LAB. All three scenarios have been run over a 68 weeks or 17 months which was the time length for original study. As several random functions are included in the algorithm, each scenario is repeated 100 times in order to estimate the output's variability. For each of the cases, the seed or the innovator is chosen among the doctors who are practicing at centers, i.e. doctors who have two colleagues.

The cumulative diffusion curve (CDC), representing the total number of adopted doctors at each time step is shown in Figure 1. All three curves are derived after averaging over 100 simulations. Baseline scenario (Figure 1: Series 1) with one innovator and one detailman generated a logistic or S-shaped curve, similar to those found in cases of mixed influence diffusion models (Ryan and Gross 1943; Mahajan and Peterson 1985; Rogers 1995; Valente 1993). In this scenario, our model reveals an adoption curve with an initial phase of slow diffusion until the first inflection point at the 24-time step where 23% of doctors have adopted the new drug. Thereafter, the rate of adoption speeds up as more doctors are exposed to someone who has already adopted and gradually begins to level off as fewer doctors remain in the population who are yet to adopt.

The steepest diffusion curve (Figure 1: Series 2) represents a heavy media scenario, where 50% of the population adopts the new drug at the end of 12 weeks. The rate of diffusion increases up to 16 time steps and decreases afterwards as only 18% of doctors at that time have failed to adopt and remain unaffected. At the 25 time step, the CDC levels off as all the doctors have adopted the new drug. The integration scenario represents an extremely slow diffusion process (Figure 1: Series

3). As the only means to have an alert is to be in contact with the initial adopter, only 18% of the population adopt the new innovation at the end of 68 times.

5. NETWORK ANALYSIS

5.1. Network Topology

We first calculate the degree distribution to identify the class of networks the ABM interaction networks from four possible alternatives: (1) regular lattices; (2) random graphs (Erdös and Rényi 1959) (3) small world networks (Watts and Strogatz 1998); and (4) scale-free networks (Barabási 2002). Our simulations produce a degree distribution (Figure 2) that conforms to a binomial distribution, which suggests that the networks are most likely either a random graph, or a small world network (Watts 1999).

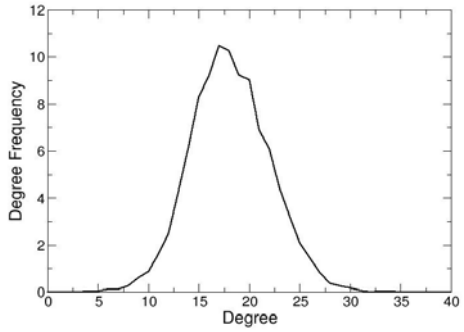

Figure 2: Degree distribution created of the interaction networks in *Gammanym*

A network is said to have small world properties if, compared to an Erdös-Rényi random graph, the following conditions hold: the average shortest path length, $PL \approx PL_{rand}$; and clustering coefficient, $CC >> CC_{rand}$. The comparison between the interaction networks generated by the simulation model, and an ensemble of random graphs reveals that $PL_{model} \approx PL_{rand}$ and $CC_{model} \approx CC_{rand}$. This suggests that the networks depicted in *Gammanym* are random graphs.

5.2 Evolution of Networks

The evolution of social networks in Gammanym has been analyzed to gain an understanding of the diffusion process. As agents interact with each other, new connections (relationships) form between agents, while others are reinforced. In order to study the nature and structure of clusters, we define a *cluster* as a set of agents that are connected. That is, there exists a path from any agent to any other agent within that cluster. At each time step within the simulation we count the number of groups of agents and calculate the maximum, minimum, average cluster size, standard deviation in cluster size and the average shortest path length between agents within the system. All statistics were averaged over an ensemble of 100 runs. Figure 3 shows how the clusters of agents evolve over time.

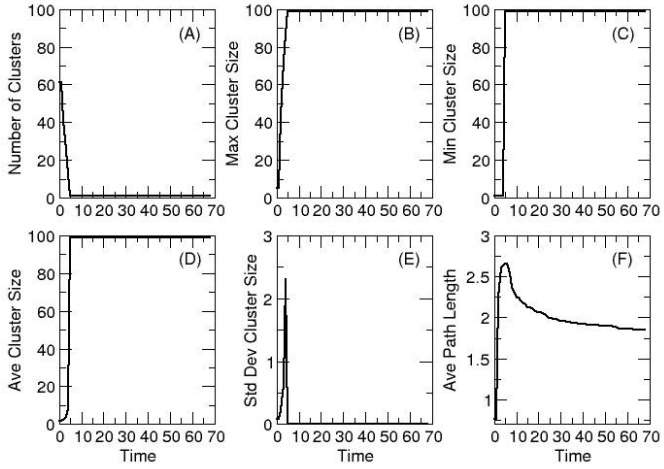

Figure 3: Network statistics. (A) Number of clusters; (B) Maximum cluster size; (C) Minimum cluster size; (D) Average cluster size; (E) Standard deviation in cluster size; (F) Average shortest path-length.

From Figure 3, we see that initially the simulation contains approximately 60 clusters of agents (Figure 3A). As new interactions occur, the number of clusters quickly decays. Similarly, the maximum cluster size grows rapidly (Figure 3B). The minimum and average cluster sizes quickly explode as the agents become consumed by the giant cluster (Figures 3(C–D)). The system begins to behave as one giant cluster after about 7–10 time steps. The standard deviation in cluster size is maximized just before the emergence of a fully connected system (Figure 3E). We note that the average shortest path length between nodes initially increases rapidly, as more and more nodes become connected to the giant cluster. When the system becomes connected, such that there exists a path between all agents, the average shortest path-length between any two nodes is on average is relatively long. This is because of the sparsity of interaction matrices and the network containing many long paths. However, as the system increases in connectivity the path-lengths become smaller until there is approximately two degrees of separation between any two agents within the system (Figure 3F). In short, the system initially consists of a number of disconnected components, but quickly evolves to form a single connected component

5.3 Evolution of Uptake

To analyze the differences in the speed of diffusion depicted in Section 4, we can look at how Tetracycline uptake evolves under three scenarios. We, therefore, define an *uptake cluster* as a set of agents who are connected to each other and each agent has adopted *Tetracycline*. In this context the uptake cluster can be thought of as a cluster commonly encountered in percolation studies (Stauffer 1979). Figure 4 shows how the uptake of Tetracycline evolves through time. In the base scenario, starting from one seed (innovator) the average number of uptake clusters increases up to 1.6 at time step 15 (Figure 4A). Then, it decreases to one giant cluster (time step 30) as the size of the existing clusters increases gradually before merging. In Figure 4 (A) we also observe that the number of uptake clusters explodes rapidly under the heavy media scenario (Figure 4A). Under integration scenario, one average, only one uptake cluster is formed during 68 time steps (Figure 4D) and its maximum size (Figure 4B) barley reaches 20 at the end of simulation.

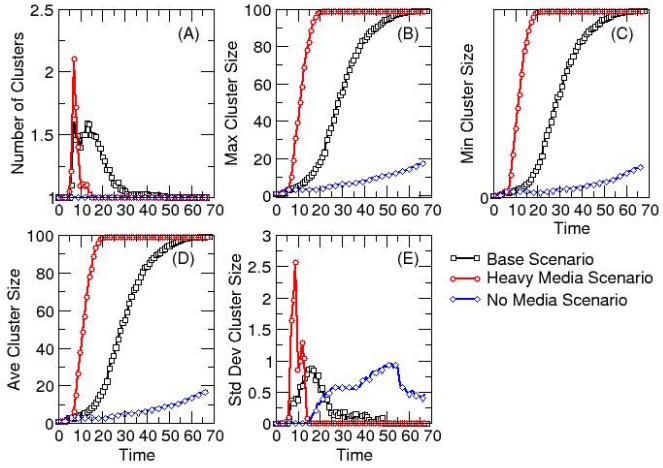

Figure 4: Uptake clusters for three scenarios (A) Number of clusters within the system; (B) Maximum cluster size; (C) Minimum cluster size; (D) Average cluster size; and (E) Standard deviation of cluster size.

6. CONCLUSIONS

We develop an agent-based model, called *Gammanym*, to analyze the diffusion process. This is inspired by the classic Medical Innovation study on the adoption of *Tetracycline* in the Midwestern US in 1950s by Coleman et. al. (1966). Due to the limited availability of proper technique or methods during 1950s, the original study focused on interpersonal influence for pairs of individuals. This approach, however, fails to capture the complexity and dynamics of actual adoptions. In our study, we overcome this limitation using agent-based modeling to consider the whole network as a unit of analysis. Our model brings original features within the existing literature of

diffusion research and also complements the extant work on *medical innovation.*

In our study we also examine the diffusion process by applying the core concepts of network theory. On the basis of network properties we determine that the interaction networks depicted in the model are random graphs. Complexity of the diffusion process is explained by analyzing evolution of networks or dynamics on the networks. We find that initially the system consisted of a number of disconnected components and quickly evolves, after 7-10 time steps, to form a single connected component. The analysis of network topology also indicates that underlying networks evolve in predictable ways, and the uptake is a function of initial starting condition.

Analyses of the evolution of uptake and adoption of Tetracycline enable us to disentangle the extent of different factors affecting adoption. Despite stressing the complementarity between network theory and diffusion research, a large body of diffusion literature has so far failed to examine the dynamic structures of the interpersonal networks and their evolutions over the diffusion process. Our model shows that although the media does not influence the network structure, it does have a major impact in accelerating the diffusion process. Under a heavy media exposure undertaken by the pharmaceutical company to increase sale of Tetracycline, the average size of clusters with agents who have adopted the new drug rise faster than otherwise. Moreover, all the agents adopt the new drug within 25 time steps, much earlier than that with a baseline scenario with much less media exposure.

We also compare the cumulative diffusion curves of Gammanym with those of *medical innovation*. The cumulative diffusion curve under the heavy media scenario with initial speedy diffusion resembles more the one in the original study, compared to that of the typical S-shaped diffusion curve generated under baseline scenario or mixed influence diffusion. In conclusion, our results provide support to the importance of social networks in the diffusion process, but also show that external influences play a dominant role in speeding up the rate of adoption.

7. REFERENCES

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