Diffusion and Social Networks: Revisiting *Medical Innovation* with Agents

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Abstract

In this paper, we reanalyze *Medical Innovation*, the classic study on diffusion of a new drug *Tetracycline*, by Coleman, Katz and Menzel (1966). *Medical Innovation* and the subsequent reanalyzes of the original data failed to capture the complexity of events involved in the diffusion process. In this paper, for the first time, we address this limitation by combining Agent-Based Modelling (ABM) and network analysis. Based on the findings of Coleman et. al. (1966) study, we develop a diffusion model, *Gammanym*, in which Doctors' adoption thresholds are decremented by information from their social and professional networks as well as pharmaceutical company supplying Tetracycline. The cumulative adoption curves are derived for three sets of initial conditions, based on which network topology and evolution of uptake are analyzed. 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.

SECTION 1: Introduction

In this paper we reanalyze Medical Innovation by Coleman, Katz and Menzel (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 Modelling (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.

We describe the original study and the rationale for our study in the following section. Section 3 describes the modelling framework, modelling sequences and methods. Simulation results under different scenarios are analysed in Section 4. The structure of the social networks depicted in our model, and its evolution are analysed in Section 5. The paper concludes with discussions and a review of the implications of the simulation results.

SECTION 2: Diffusion and Networks

2.1 Diffusion of Tetracycline

Tetracycline was launched in November 1953. The success of its release was uncertain for the pharmaceutical companies because of an already established market for broad-spectrum antibiotics. Four US Midwestern cities: Peoria, Bloomington, Quincy and Galesburg, were selected for the original study. The authors wanted to set the study in a group of three or four cities in one contiguous area that was not in the shadow of a large medical centre, but where the cities differed from each other in terms of available hospital facilities: the number of teaching hospitals and general hospitals and population. The sample constituted 148 general practitioners, internists, and paediatricians 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. In order to measure the time of adoption, a prescription audit in the local pharmacies were carried out for 125 doctors (121 general practitioners, internists, and paediatricians 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, Katz and Menzel 1966: 194).

In our analysis of the Coleman et. al. study, we identify two broad categories of variables influencing the diffusion process. The first category represents personal traits or i*ndividual variables*, affecting individual receptivity. Individual variables, based on which innovators or early-adopters of Tetracycline are: 1. type of practice, 2. medical background, 3. contacts with out-of-town institutions, 4. media behaviour, and 5. orientations and attitudes. The second category defines *social variables* influencing the adoption process as a result of social or professional ties to other members of the community. The influences of *professional networks* were evaluated on the basis of four factors that enable exchange of information in professional settings: 1. hospital affiliation, 2. shared office, 3. advice seeking, and 4. discussion. The friendship structure, on the other hand, emerged from the informal discussion among doctors in a social setting and doctors were asked to name three doctors whom they see most often socially.

The study revealed strong evidence for social contagion, i.e. doctors' decisions to adopt Tetracycline were strongly influenced by the people they are connected to either socially or professionally. It appeared that the integrated doctors differed very little from their isolated colleagues at the beginning of the introduction of Tetracycline, but their rate of adoption accelerated to produce an increasing gap between 'integrated' and 'isolated' doctors (Coleman, Katz and Menzel 1966).

2.2 Social Contagion vs. Media Exposure

We want to verify if the diffusion process depicted in the original study is better captured by ABM, and also analyze the network structure governing the adoption of new drug.

Burt (1987) used Coleman et al. (1966) study to derive three major conclusions: 1. where contagion occurred, its effect was through structural equivalence[i] not cohesion; 2. regardless of contagion, adoption was strongly determined a physician's personal preferences, but these preferences did not dampen or enhance contagion; 3. there was no evidence of a physician's network position influencing adoption when contagion is properly specified in terms of structural equivalence.

Strang and Tuma (1993) apply an event-history framework at the Coleman et al. (1966) data to analyze a class of diffusion models incorporating spatial and temporal heterogeneity. Their result contradicts Burt, as their models indicate that, "Contagion in medical innovation is not a simple product of structural equivalence. 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. The T/CM model requires a threshold measure and a determination of the critical mass, a system level measure of the minimum number of participants needed to sustain a diffusion process (Valente 1995: 79). The study 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 (2001) provides strong support for external influence in the diffusion of tetracycline by incorporating a data set on advertisement volume. As the empirical results were unable to detect statistically significant contagion effect once advertising effect is controlled for, 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).

2.3 Rationale for *Gammanym*

We reanalyze the *medical innovation* study by applying ABM for two principal reasons: non-inclusion of dynamics of network structure and complexity in any of the previous studies, and a limited exploration of the impact of external influence or media exposure from previous reanalyses of the Coleman et al. (1966) data.

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 the evolving structure of the network itself such as the making and breaking of network ties. The other set of dynamics refers to '*Dynamics on the network*', created due to the actions taken by individuals. The outcome of their individual actions is influenced by what their neighbors are doing and, therefore, the structure of the network. In the real world, both kinds of dynamics exist simultaneously (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 discrete/disjointed pairs. Given the existence of overlapping networks and consequent influences on doctors' adoption decisions, the complexity of actual events can not be captured by pair analysis. Indeed, the authors themselves considered that analyzing in pairs was the major limitation of the study[ii]. ABM enables us to address this limitation in previous studies by considering the whole network as a unit of analysis.

Apart from the study by Van den Bulte and Lilien (2001), external influence in the diffusion process has also not been analyzed rigorously for the *medical innovation* data set. External influence is created from different forms of advertising and intensive coverage by representatives from the drug companies. In the *medical innovation* study, doctors acknowledged that a 'detailman' or a pharmaceutical representative, and also direct mail from the drug companies, as the major source of initial information about Tetracycline. The original study however did not contain any information on marketing effort by drug companies. An attempt to collect data on marketing effort was constrained by the fact that back issues of Journal of American Medical Association (JAMA) did not have any advertising supplement, as they were removed before binding for storage (Van den Bulte and Lilien 1999). In our study, we examine the impact of external or media influence by performing sensitivity analysis. The simulation results allow us to explore the behaviour of the pharmaceutical companies, which has not been examined in a MAS (Multi-Agent System) setting.

SECTION 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 an 8 X 8 spatial grid. The unit cell captures three different locations for professional interactions: *Hospitals*, *Practices* and *Conference Centre*, which are created as Passive objects. *Gammanym* has sixty-one practices, two hospitals and one conference centre, 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*[iii]; *Private (alone in office)*, *Center (shared office with two partners)* and *Clinic (working with four colleagues)*. The doctors in Gammanym model are thus distributed among 46 private, 11 centers and 4 clinics.

Gammanym specifies two hospitals, as all the cities, on average, have two hospitals. Conference centre, the third passive entity, provides the context in which a much larger group of professionals can interact with each other. *Planning* captures the time steps for three conferences, either randomly chosen by the model or specified by the modeler. 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 centre, do not depend on the location of their practices; as the grid does not incorporate any Geographic Information System (GIS) specifications. Their 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/knowledge 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. An 8 x 8 spatial grid, therefore, is considered succinct to represent the medical community depicted in the original study.

3.1.2. Social agents

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

3.1.2.1 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, Katz and Menzel 1966: 92). Thus, we explore if all the doctors are homogenous in terms of their individual attributes or 'degree of predisposition to adoption' (Burt 1987), to what extent does integration matter for adoption decision? In our model, a random friendship network and professional networks are created through discussions with office colleagues, or through hospital visits or conference attendance, or all of the above.

The friendship network is random in nature as the doctors are initialized with random number of friends and counter for friends; both ranging from 0-3. In the original study, indices of similarity[iv] of pairs were analyzed in order to identify the attributes the doctors share with the colleagues they choose as friends, discussion partners or advisors. We treated the indices with reservation, because of their limited statistical relevance with only 111 friendship pairs (Coleman, Katz and Menzel 1966: 143).

Professional interactions are spatially defined, based on which Gammanym builds discussion networks[v]. 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. Office partnership is central to professional networks as the doctors made most of their interactions in their practices. After each visit to hospital or conference centers, doctors return back to their practices.

3.1.2.2 Communicating Agents: Laboratory

In *Gammanym*, we incorporate one pharmaceutical company as a communicating social agent, termed the *Laboratory* (LAB from hereon). 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.

57% of the doctors asked to reconstruct their stages of diffusion, identified detailman as the first source of information. Hence, we opt for a blanket exposure of all doctors to detailman. In *Gammanym* the *detailman* visits all the doctors at their practices. In the original study, drug house mails or direct mail advertising was identified as the second major source of information. Assuming similar influences by direct mail advertising and journal insertions, we specify *journals* as the second option for the LAB.

Without prior specification in any of the previous studies, we introduce *flyers* at the conference centers. From the perspective of the LAB, inclusion of flyers is crucial as it adds another dimension to the marketing mix by targeting a large group of doctors at the same time. 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, Katz and Menzel 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 Modelling 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 centre, 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 centre based on number of previous conference attendees. Journals are incorporated in *Gammanym* as the third strategy. 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.

SECTION 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:

1. Baseline Scenario; with one 'seed' or initial adopter, one detailman and one journal ;
2. Heavy Media Scenario; with one initial adopter but different degrees of external influence, by increasing the number of

detailman to five and the number of journals to four ;

3. 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.

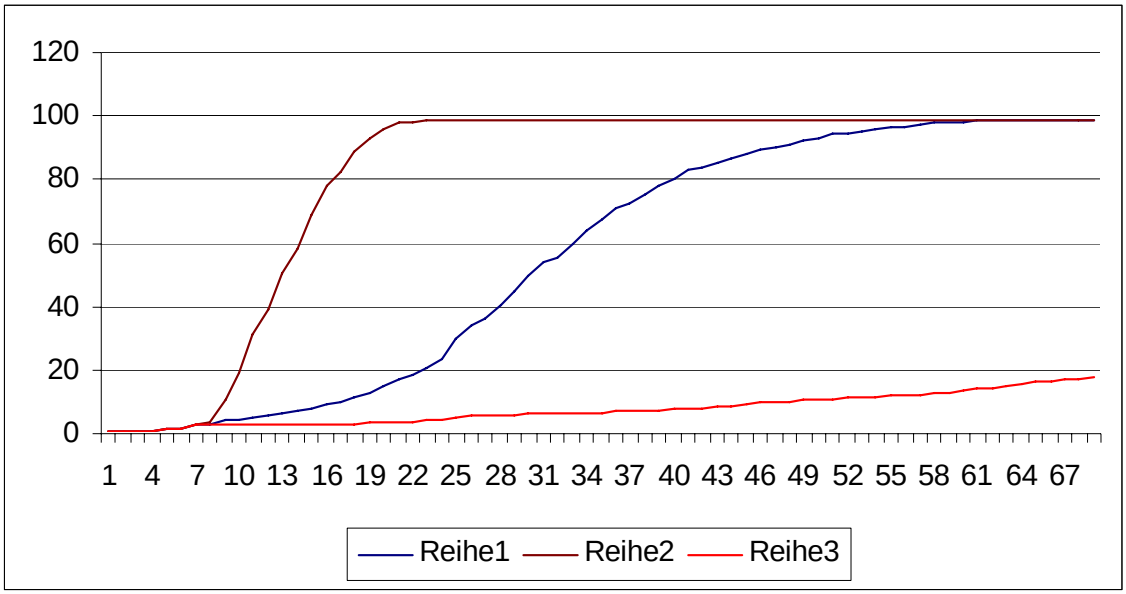

Figure 1: Cumulative Diffusion Curves for three scenarios: Baseline(Series 1), Heavy Media(Series 2) and Integration (Series 3)

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. Overall, 92% of doctors adopted the new drug by the end of 48 weeks, or within 12 months. With one innovator in the system, diffusion seeds through the system as the doctors' adoption decisions are simultaneously influenced by their exposure to the new drug through actions by LAB as well as interpersonal communication.

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 time steps.

SECTION 5: Network Analysis

In this section we will examine: (1) the topology of the interaction networks that are generated by the agent based simulations; (2) how the networks evolve over time; and (3) the way the uptake evolves across these networks.

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).

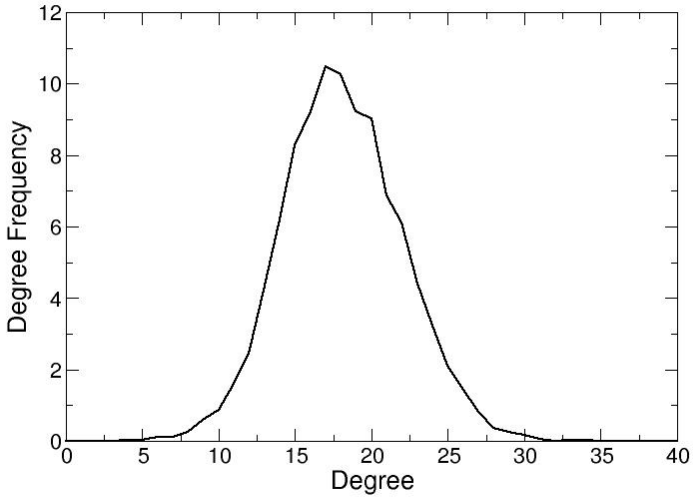

Figure 2: Degree distribution created of the interaction networks in *Gammanym*

Many social systems display two statistical properties;

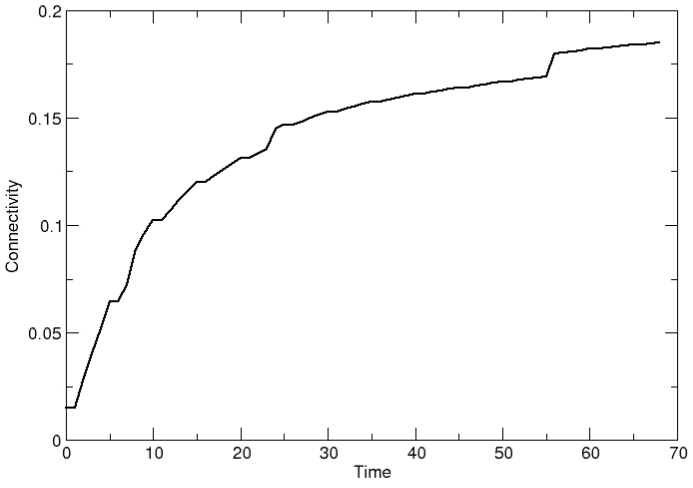

Figure 3. Evolution of connectivity within professional and friendship networks.

first they display a high degree of clustering when compared to random graphs; second they have an average shortest path-length *similar* to that found in random graphs. These two properties are known as the small-world properties. The clustering coefficient (*CC*) is a measure of the number of friends of friends type relationships found within the network. For a given node N_i, with k_i neighbors, E_i is defined to be number of links between the k_i neighbors. The clustering coefficient is the ratio between the number of links that exist between neighbors (E_i) and the potential number of links $(k_i(k_i-1))/2$ between the neighbors. The average clustering coefficient is:

$$CC = \frac{1}{N}\sum_{i=1}^{N}\frac{2E_i}{k_i(k_i-1)}$$

The average shortest path length (*PL*) is defined as:

$$PL = \frac{1}{N(N-1)}\sum_{i=1}^{N}\sum_{j=i+1}^{N} PL_{\min}(i,j),$$

where PL_{min} is the minimum distance between nodes *i* and *j*.

A network is said to have small world properties if, compared to an Erdös-Rényi random graph, the following conditions hold: $PL \approx PL_{rand}$ and $CC >> CC_{rand}$. 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* can be 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. Figure 3 shows the evolution of connectivity between agents within the simulation. The connectivity is defined as $L/N(N-1)$, where L is the total number of interactions within the system and N is the total number of agents within the simulation. Connectivity values were averaged over an ensemble of 100 runs. From Figure 3, it can be seen that the connectivity within the system grows as a function of *n log n* over time. An interesting property in Figure 3, are the sudden jumps in connectivity associated with conference events. The most notable of these occurs at time step 55 and appears to capture an element of many real world 'networking' events, where people come together to exchange ideas and experiences.

Initially the agents are only connected to doctors that they interact with, within their practices. This means that system consists of a set of disconnected groups of agents or clusters[vi]. This means that the flow of information within the system is limited to only small isolated pockets of interactions. However, as

connectivity increases, the size and the nature of these clusters changes.

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 4 shows how the clusters of agents evolve over time.

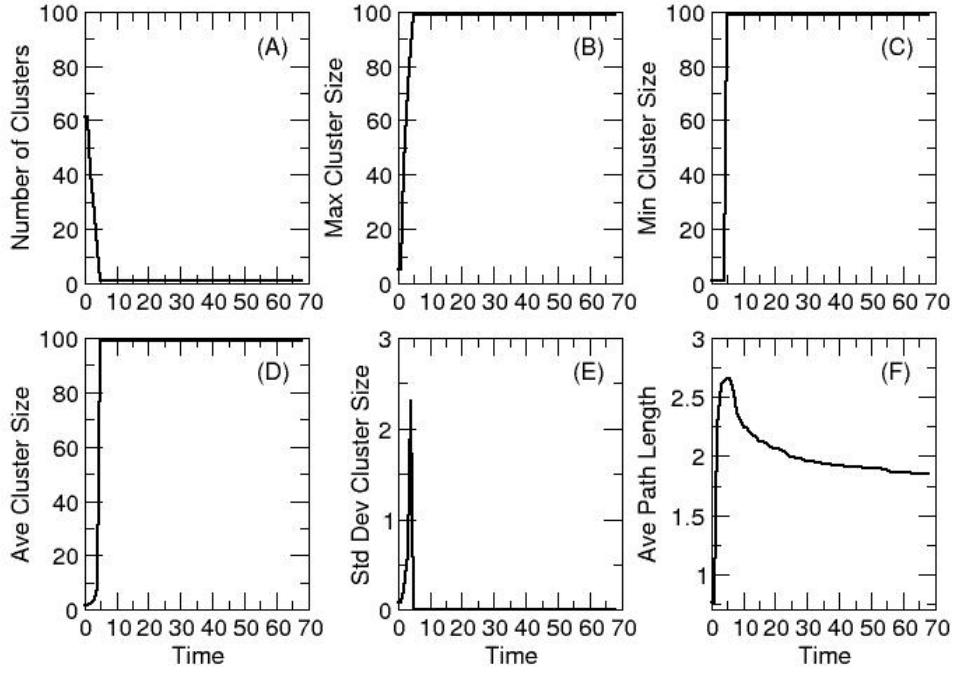

Figure 4: Network statistics. (A) Number of clusters; (B) Maximum cluster size; (C) Minimum cluster size; (D) Average cluster size; (E) Standard deviation in cluster size; (F) Average shortest path-length.

From Figure 4, we see that initially the simulation contains approximately 60 clusters of agents (Figure 4A). As new interactions occur, the number of clusters quickly decays. Similarly, the maximum cluster size grows rapidly (Figure 4 B). The minimum and average cluster sizes quickly explode as the agents become consumed by the giant cluster (Figures 4 (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 4E). 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 4F). In short, the system initially consists of a number of disconnected components, but quickly evolves to form a single connected component. The size and structure of these clusters define how far and how quickly Tetracycline is adopted.

5.3 Evolution of Uptake

To analyze the differences in the speed of diffusion depicted in Section 4.1, 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 5 shows how the uptake of Tetracycline evolves through time.

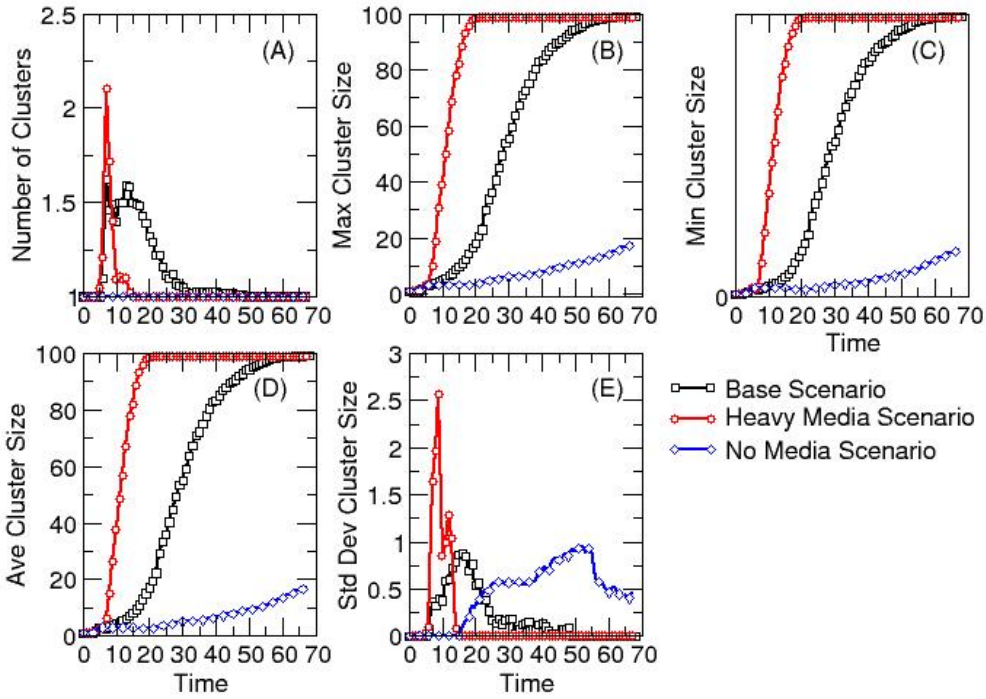

Figure 5: Uptake clusters for three scenarios (A) Number of clusters within the system; (B) Maximum cluster size; (C) Minimum cluster size; (D) Average cluster size; and (E) Standard deviation of cluster size.

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 5A). Then, it decreases to one giant cluster (time step 30) as the size of the existing clusters increases gradually before merging. In Figure 5 (A) we also observe that the number of uptake clusters explodes rapidly under the heavy media scenario (Figure 5A).

Compared to the base scenario, much faster dynamics is displayed with the giant uptake cluster forming at time step 15 with heavy media exposure. At time step 20, 100% of the doctors have adopted the drug and the size of the uptake cluster equals the size of the social network.

The integration scenario displays a very slow process of diffusion. On average, only one uptake cluster forms during the 68 time steps, and its maximum size barely reaches 20 by the end of the simulation (Figure 5B). Thus, despite a very efficient deployment of the giant social cluster, the uptake cluster struggles to invade the whole network without external influence.

SECTION 6: Concluding Remarks

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, Katz and Menzel (1966). Due to the limited availability of proper technique/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 adoption. In our study, we overcome this limitation using agent-based modelling 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. Network properties like connectivity, clustering, degree distribution and others, are estimated from the interaction matrices generated by agent-based model. On the basis of these 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 the initial starting condition.

Analysis of the evolution of uptake or adoption of Tetracycline enables 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, a much earlier than that with a baseline scenario with much less media exposure. We validate the previous evidence of a dominant media influence by comparing the speed of diffusion for three scenarios: baseline, heavy media and integration. The dominant role of media also suggests there is a trade off between the effort expended in promoting a new drug, and the speed of the diffusion process.

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. To summarize, 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.

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[i] Structural equivalence is the degree two individuals occupy the same position in a social system. A structural equivalence model of diffusion postulates that individuals are influenced to adopt an innovation by imitating the behaviour of others to whom they are structurally equivalent.

[ii] "To analyse pairs of individuals instead of single individuals may seem like only a very modest step towards the analysis of networks of social relations. It would be more satisfactory, and truer to the complexity of actual events, if it were possible to use longer chains and more ramified systems of social relations as the units of analysis. But so little developed are the methods for the analysis of social processes, that it seemed best to be content with the analysis of pair relationships", so writes the authors themselves (Coleman et. al. 1966:114).

[iii] Elaborating on significance of office partnership to generate network effects, the researchers in the original study specified it's three broad categories (Coleman et. al. 1966: 73): alone in office, shared office, clinic. Shared office was further classified on the basis of number of colleagues being one, two, and three or more. Shared office for three or more colleagues are not incorporated as only 3 doctors in City B was identified for this category. We specified 5 doctors to be practiced in a clinic based on the representation of office partnership in City D (Coleman et. al. 1966: Figure 15). Majority of doctors in City A were practicing alone (53%); in contrast to which 50% of doctors were affiliated with clinics in City C. None of the doctors in City B were practicing in a clinic. See Medical innovation (P 73-74) for detailed analysis.

[iv] The index varies from a value of +1, where all doctors choose others like themselves, to -1, where doctors choose only others who are unlike themselves. Based on the indices of similarity (in parenthesis for each factor), the order of importance for choosing friends were: religion (0.403), professional age (0.195), place of growing up (0.146) and medical school (0.167).

[v] Our intension to distinguish among discussion and advice networks was constrained, primarily, by unavailability of original data. The criteria for advice networks, was further complicated by the fact that none of the common background factors seemed to work for choosing the advisor, as the indices of similarity for religion, professional age, place of growing up and medical school are respectively 0.109, 0.042, 0.077, 0.018. Interestingly enough, analyses by Burt (1987) and Stang and Tuma (1993), despite using the original dataset, were not specific in distinguishing the structures of those two networks either.

[vi] This type of clustering is not to be confused with the structural clustering measured by the clustering coefficient. Clusters in this context, simply refers to a connected group of nodes.