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Migration Pattern As Threshold Parameter In The Propagation of The COVID-19 Epidemic Using An Actor-Based Model for SI-Social Graph

Arnold Adimabua Ojugo[a,*], Rume Elizabeth Yoro[b]

[a]*Department of Computer Science, Federal University of Petroleum Resources Effurun, Delta State 32001, Nigeria*
[b]*Department of Computer Science, Delta State Polytechnic Ogwashi-Uku, Delta State 32001, Nigeria*

Abstract

Despite the benefits inherent with social interactions, the case of epidemics cum pandemic outbreaks especially the case of the novel corona virus (covid-19) alongside its set protocols employed to contain the spread therein - has continually left the world puzzled as the disease itself has come to stay. The nature of its rapid propagation on exposure alongside its migration spread pattern of this contagion (with retrospect of other epidemics) on daily basis, has also left experts rethinking the set protocols. Our study involved modelling the covid-19 contagion on a social graph, so as to ascertain if its propagation using migration pattern as a threshold parameter can be minimized via the employment of set protocols. We also employed a design that sought to block or minimize targeted spread of the contagion with the introduction of seedset node(s) using the susceptible-infect framework on a time-varying social graph. Study results showed that migration or mobility pattern has become an imperative factors that must be added when modelling the propagation of contagion or epidemics.

Keywords: Cancer; reinforcement algorithm; spectral-cluster; epidemiology; Nigeria; deep learning.

1. Introduction

Disease in whatever form, is a disorder of the structure or function in any human, plant or animal – that produces specific symptoms, or that affects a specific location and is not simply a direct result of physical injury. At its primitive stage, disease (or disorder) can exists in four dimension/types: infectious, deficiency, hereditary and non-hereditary diseases. Diseases are harmful deviation(s) from the normal functional or structural state of an organism or system that is generally associated with certain symptoms, and differing in nature from a physical injury. Thus, a diseased organism commonly exhibits signs or symptoms indicative of its abnormal state or condition (Ojugo and Otakore, 2021; Ojugo and Eboka, 2021). Disease or disorder (contagion) are propagated or spread from a system to another through medium such as direct contact, fomites, oral (injection), vectorborne and aerosol (WHO, 2019; Adegboye et al, 2020). Propagated from a system to another, they can result in either regular spread, epidemic or pandemic – which can also easily result in contagions that impacts directly on the society (Martinez-Alvarez et al, 2020; Gilbert et al, 2020). Thus, today many such tasks can be modeled with the society represented as a graph network of interconnected nodes (actors/actors) with their corresponding relations as edges (Ojugo and Oyemade, 2020; Worldmeters, 2020; NCDC, 2020). The movement of actors, continues to play significant role in the transformation and change process that has often escalated local disease outbreaks into global pandemics (Soriano-Panos et al, 2019). Thus, necessitating inclusion of human migration into epidemic models so as to help effectively design simulated outbreak episodes as well as to help implement efficiently, a sure and dependable preventive policies (Kim et al, 2020; Jung et al, 2016).

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[*] Corresponding author.

E-mail address: ojugo.arnold@fupre.edu.ng (Arnold Adimabua Ojugo)

1.1. Social Graph With Nodal Interactions / Activities

A social graph is a network that consists of actors that interact amongst each other. With interaction, learning occurs causing a change in these actors as they are exposed to a contagion (Ojugo et al, 2015). Succinctly explained, a social graph consists of tie relations that bind actors together via a structure that helps us analyze social entities and help to explain the observed patterns within. It thus, propagates local feats, which emerge as global patterns as actors interact – to result in connection convergence (Valente, 1996; Wasserman and Faust, 1994).

A powerful role of the social graph is that it helps to bridge local feats as they blossoms into global patterns; while, it forms theories to explain how nodal ties impacts a ripple through a population system. Each node and its corresponding relations helps to shape the graph in time, with learning occurring as the node adapt via interaction activities. The social graph is denoted as $G = (V,E, w)$ – where each node $i \in V$ with a set of ties $m \in E$ that is either self-linked (loop), single-linked or multi-link. Each node has a set of node(s) they are isolated from or linked to. These links are denotes the relation between such nodes, and measured through dyads D (Ojugo et al, 2014). Thus, a social graphs aims at two points: (a) to understand how graphs evolve, and (b) study dependent social processes that specifies how such local interaction of actors' feats are explored. With society viewed as social graph, movement by various actors becomes of great concern aimed at provisioning measures to combat contagion alongside weighing the costs cum penalties therein (Ojugo and Okobah, 2018; Yoro and Ojugo, 2019a; 2019b).

1.2. The Society And Actor-Based Modelling

Local features will continue to break forth as global patterns. Modeling human interactions and migration in spread patterns has become imperative as such insight (data), will help society plan future conditions of such spread, its scale alongside other dependent events (Macy and Miller, 2002). Such prediction(s) will help us make informed decisions about the future from observed values and made manifest via models. Thus, models are tools that yield knowledge statement of the future, provide real-time prediction that helps us plan in time, the magnitude of a probable event as it reaches optimal (Ojugo and Yoro, 2021). The reliability of the results generated by these model, can be questioned as either myths or fictions, as its results are viewed as prophesies; rather than prediction (Marin, 1981).

Actor-based models (ABM) is best be described with a flock of bird, flying in tight formation as a single organism. Yet, they choreograph in such grace with no leader. Instead, each reacts to the movement of its immediate neighbor, to result in hypnotic rhythm of highly-nonlinear pattern. This, is easily modelled as an aggregation of local feats using 3-simple rules: (a) separation – each bird does not get too close to another, (b) alignment – each bird matches its direction and speed to nearest bird, and (c) cohesion – each bird stores in memory the perceived center of the flock and its immediate neighbor (Reynolds, 1987). Thus, each bird is modelled as an actors with local feats interaction to yield a realistic flight formation (Ojugo and Nwankwo, 2021; Ojugo and Eboka, 2020; Tiovonen et al, 2009; Reynolds, 1987).

ABM as applied in a social graph involves highly self-organized, nonlinear, dynamic and complex actors that emits local feats and learns via interacting in response to various influences received – to result in a global pattern (Epstein and Axtel, 1996). We continue to harness the merits of ABM with a focus on emergent structure thus: (a) it posits a dynamic graph shaped via actor interactions, and (b) it tests social learning by manipulating its feats such as its topology, stratification etc (Kaufman, 1996; Macy and Willer, 2002; Durkheim, 1982; Friedkin, 1980; Gilbert et al, 2008).

2. Literature Review: The Social Graph Framework

Human activities have often advanced globalization. As a demerit therein – is its acceleration of epidemic processes and its geographical expansion that multiplies and escalates local outbreaks into global epidemics. These factors have also been driven by frontier features namely: (a) migration activities from one place to another, and (b) effects of climate change (Soriano-Panos et al, 2019). As a direct consequence of these two factors above, we have assisted in the spread of the Ebola outbreak as well as the current corona virus (covid-19). Thus, it has become imperative that the inclusion and modeling of actor migration and interaction activities in the well-formulation of an epidemic propagation model has become mandatory as well as critical to achieving accurate description of any epidemic scenario. Many algorithms and models have been posited leveraging on graph theories as their backdrop – as means to address these growing and ever-increasing concerns. Popular heuristics include: (a) susceptible-infect diffusion models, (b) Markovian models, (c) movement interaction return model – to name a few.

2.1. The Susceptible-Infect (SI) Diffusion Model

A graph G consists of a set of actors $i \in$ V, connected to other actors on the network via a set of corresponding edges $e \in$ E so that interactions between two/more actors can take place. For a social network, a typical SI-case has that an idea or innovation is allowed to diffuse through the network using a seed-node. The seed-node (seedset) is the node that is already exposed to the innovation and has adopted such an innovation. Thus, other nodes in the graph yet to adopt are initialized as: (a) susceptible – implies that the node is active and exposed to the innovation; and depending on its threshold – can either adopt or reject the innovation, (b) infected – it implies that the actor/node has been exposed and adopted the innovation. Thus, it is now a carrier of the innovation and will influence others to adopt also, (c) removed – implies that the node was exposed to the innovation, accepted it (and may have also influenced other nodes to also try to adopt the innovation) and is currently recovered or has now rejected the innovation. This continues till a stop criterion is met or there are no more inactive vertices (Schnettler, 2009).

The two basic SI-diffusion models: (a) SI-Remove and (b) SI-Susceptible (Ojugo et al, 2015) are explained thus:

a. SI-Remove – At discrete-time at t = 0, the graph is inserted with actors, infected with the innovation. Removed nodes are immunized, and unable to propagate such innovation again as they can no longer be infected. Thus, if actor x is exposed and has adopted the innovation at time t, it has single chance to influence its immediate neighbor y. Thus, node y is exposed but not-infected or yet to adopt. We have then that the probability x succeeds with y is P_{xy} – so that if x succeeds, y is infected and adopts the innovation at t+1. Else, x tries again in the future (and y may adopt via another actor). This process continues and stops at n-steps (t – 1) at which point there are no more active actors to be exposed. Thus, every actor is exposed exactly once (Handcock and Giles, 2009; Haythornwaite, 2002). A graph G of size M, and d-copies of seedset actors given by M_d is placed on the graph. At its end, $S(M_d,G)$ is the expected number of final adopters, expected to exceed all random choices depending on diffusion model and nature of graph in use. Eq. 1 describes maximum expected number of adopters.

$$S_d(G) = \max_{M_d} S(M_j, G) \quad (1)$$

Subset $A_d = arg \max_{M_d} S(M_d, G)$ correspond to choices made by an adaptive seednode. $S_d(G)$ is epidemic spread in G. Eq. 2 is the epidemic spread with randomize seednode – denoting expected epidemic spread as expectation takes over all possible positions of the d innovations placed on the network and given by (Ojugo and Otakore, 2021):

$$S'_d(G) = \mathrm{E}_{\mathrm{M_d}}[S(M_d, G)] \quad (2)$$

b. SI-Susceptible (SIS): At discrete time t = 0, G has inserted copies of infected actors. Also, an infected actor x at time t has a single chance to convince its immediate neighbor y. The probability x succeeds with y is P_{xy}. If x succeeds, y is infected and adopts at time at t+1; Else, x tries again in the future (even if y adopts via another actor's neighbor). Also, actor y can reject at another time. The process continues and stop after n-steps (t–1) – where there are no more actors to be exposed. It requires an actor to be exposed more than once (Wilson et al, 2009). A graph G of size M with d-seedset actors M_d placed on the network, at completion – we have that $S(M_d,G)$ denotes the expected number of final adopters. This process evolve in time to either propagate or eventually die. Actor x adopts with a rate $\frac{\beta}{\delta}$ and probability of β. An actor may reject adoption after previous adoptions with probability δ; while, the threshold $\frac{\beta}{\delta} < \frac{1}{\lambda_1(T)}$ is sufficient for quick recovery (Yoro and Ojugo, 2019; Ojugo and Okobah, 2018).

2.2. Traditional Markovian Clustering Model

The Markov Model is a double embedded chain that seeks to model complex chaotic processes as a chain of state sequences with probabilities associated to transition between states. For an *n*-order Markov, its transition probabilities depend on current and n-1 previous states, and used to determine states generated for each state observation in a series. A variant of the Markov model is the Hidden Markov and Profile Hidden Markov – both of which seeks to address the fundamental issues of Markov by: (a) makes explicit use of positional (alignment) data contained in sequences, and (b) it allows null transitions, where necessary so that the model can match sequences that includes insertion and deletions (Ojugo and Eboka, 2021). With state transition and probability distribution of nodal observations, the Markovian Equation expressed as $\lambda = (A,B,\pi)$ and depending on task (Ojugo and Eboka, 2014; 2015). It is best suited for these tasks (Ojugo and Otakore, 2021):

a. **Problem 1**: Given observations and parameters N and M, determine model $\lambda = (A,B,\pi)$ that best fits sequence. We train model to fit data. HMM training requires no *aprior* assumptions about the model other than outline parameter N and M, which specifies the size of the model.

b. **Problem 2**: Compute probability that the given model produces an observation sequence if given the model λ – (A,B,π) and an observation sequence O, compute $P(O/\lambda)$.

c. **Problem 3**: Uncover HMM $\lambda = (A,B,\pi)$ and observation sequence O to determine most likely sequence of states $X = (x_1, x_2, \ldots, x_T)$ that could have produced the sequence.

2.3. The Movement-Interaction-Return Model: An Extended Markovian Clustering Model

Soriano-Panos et al (2019) proposed this extended Markovian movement-interaction-return model as in figure 1. It first, notes that every time-step consists of three (3) stages namely:

a. Stage 1 – Movement: Actors can move across social graph with a probability *p* – and each subgraph can be populated with actors from different geographical regions – so that the graph is etched with behavioral feats accompanying visitors and residents in a small-world graph as they possess very different migration pattern. Thus graph, introduces an object or parameter to govern migration flow – more complex than Origin-Destination matrices termed M_j^i – a 3-D tensor that describes the probability with which an actor *i* moves from subgraph *j* to subgraph *k* as in Eq, 1. This parameter imposes that only actors located at their residence are allowed to move to other neigbourhood areas. Thus, visitors staying out of their residence are forced to stay at their temporal node until coming back home. Once these movements takes place – actors initiate interaction and then learning can occur.

$$M_j^i k = \delta_j^i R_k^j + (1 + \delta_j^i)\delta_k^j \quad (1)$$

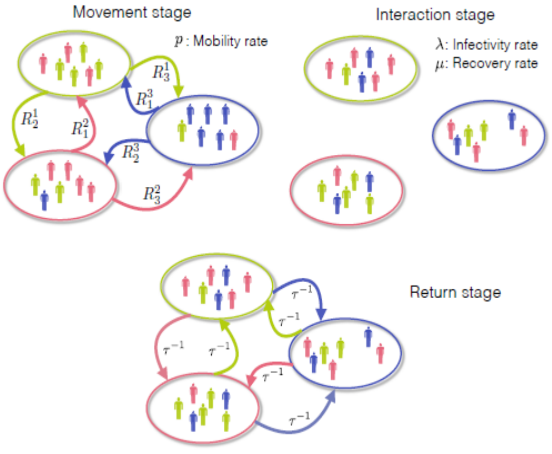

Fig. 1. Movement-Interaction-Return Schematic diagram

b. Stage 2 – Interaction: With the SI-Susceptible model for disease propagation, social graph assumes that all actors are well-mixed as actors interact with those in their immediate neighborhood. Thus, an actor/node x has several chances of exposing itself to another node y and has exactly one chance of infecting the node y. Thus, the probability that an infected actor x transmits the innovation (in this case, the disease pathogen) to a susceptible node actor y is given by λ; while, the probability that an infected actor overcomes the disease (that is, the disease dies out and the node is unable to propagate and not become susceptible again) is μ.

c. Stage 3 – Return: A visitors may decide to stay off their residence, or to travel with a probability of γ^{-1}. This feat accounts for permanence time in destination node. Also, $\gamma^{-1} = 1(\gamma = 1)$ recovers the original MIR model. But, $(\gamma^{-1} = 0)$ – the actor loses data about their residence. Thus, are steadily redistributed across the neighboring area.

2.4. Rationale for Using ABM on Social Graph

We use ABM to model actors in such large graphs for these (Goldbeck, 2013; Ojugo et al, 2015) as thus:

a. ABM-modeled graphs often assumes certain dispositions for certain actors and then observes patterns as they emerge from interactions between such actors.
b. ABM involves elaborate experiment to learn about complex adaptive systems rather than build valid representation of a real-world system (Axelrod, 1997; Holland, 1995). ABM serves as a black-box to unveil unexpected consequences of the interactions in themselves of such simple processes.
c. People may not know why they undertake certain decisions. Behaviour can help reveal true motivations/intentions of certain actors, and thus, ripple through society. Empirically investigating preferences, disposition and other feats and the consequence of these acts, is quite tedious and difficult.
d. Need to collect longitudinal data on entire social network over a period of time often complicates empirical studies, and particularly for such complex patterns of interactions in these small world-graphs.
e. Previous studies posit that local emergent feats are often biased. ABM can fully harness the potentials modeled by such complex feats in a social systems via data analysis.

The experiment seeks to explore the covid-19 epidemic ripple effects across a social graph using migration/mobility pattern as threshold parameter for nodal adoption/rejection of innovation. Thus, we seek to find the expected number of final adopters via network parameters with the actors' position in a social graph as they locally interact over-time. The study is more interested in the local emergent feats emanating from large-scale effects of such interacting actors of the entire supply network.

3. Materials and Methods

3.1. Data Gathering

Graphs and the science of networks, have continued to impact our knowledge on many of the tasks we perform today as well as impact on the corresponding processes therein. Many of today's tasks can be adequately represented as graphs in a social system. Disease propagation and diffusion as contagion is not left behind in these scenes as relevant phenomenon, paradigms and theories emerge when investigating biological theories and social impacts on many of such tasks or events. The study uses as its innovation – the covid-19 contagion. The study was initiated at the beginning of the Lockdown enacted by the Delta State Government in starting from April 1, 2020 through to the end of the lockdown and furthermore till January 31, 2021. We use small-world graph, population of 45-Wards (clusters) generated from 4 Local Government Areas namely: Aniocha North, Aniocha South, Oshimili North and Oshimili South respectively. See table 1 for the dataset parameters.

Table 1. Dataset as Pre-Analyzed on Social Network

Network Features	**Corona Virus Contagion**
Clusters in each Community	45wards (cluster)

Network Features	Corona Virus Contagion
Targeted Number in Age range	456,342 persons / contacts
Seedset Phase	5-seedset nodes per ward
Time of Diffusion	9months
Graph Probability Distribution	$\mu = 0.5346$ and $\delta = 0.34$
Average time of Adoption	2months
Lowest/Highest Saturation (Final number of Adopters)	36% / 80% at $t > 0$ and $t = t - 1$ respectively

3.2. Problem Formulation

The evolution of covid-19 epidemic size is a function of both the migration and epidemiological parameters. The epidemic size here is a fraction of entire population who remains infected once the epidemic has reached stationary state (i.e. no more actors to infect or conclusion of the project). As in table 1, we can compute this fraction using seedset node(s) as introduced into the framework and clusters (Soriano-Panos et al, 2019). Events modeled on social graphs never treats actors as equal. We distinguish residents from visitors via relations to provide the requisite *ties.* Visitors have *weak ties* with others actors in the graph; while, residents have *strong ties*. Their relations is a function of ***ties*** that exists in actors as they form clusters, cliques and communities. Thus, the cluster ties are measured via *dyads* (which measures all pair of interactions between *n*-actors with *m*-ties – for m×n binary matrix in G.

Ojugo et al (2015) notes that measuring ties can be along the lines of 7-dimensions that manifest in various forms to include: (a) time structure, (b) emotional intensity, (c) mutual intimacy and (d) reciprocal services, (e) topology of the environ in which study is being carried out, (f) emotional support, and (g) social distance as embodied in socio-economic status, education, race etc of an actor. Gilbert and Karahalois (2009) and Ojugo et al (2015) notes that using tie as a threshold predictor helped actors to overcome the issue of retrospective data accuracy as well as act as potential feedback in ways that benefit users as in Eq. 3. Thus, *ties* are modeled as a linear combiner, where R_i is number of predictive variables in task, e_i is error term, D_i is dyads pairs, N_i is network structure and EI_i are external influences.

$$S_i = \propto + \beta R_i + \gamma D_i + N_i + EI_i + e_i \quad (3)$$

3.3. Network Structure: A Linear Combiner

Acemolgu et al (2012) A cluster is a strong candidate of a cohesive set or clique by itself due to large number of ties amongst members. As clusters increase, actors form more cliques with others in close proximity, which also decreases the set cardinality and increase the number of sets in graph. High-clustered graphs have short-path length, large number of cliques with small cardinality. It results in large expected number of final adopters, introduces a close knit relationship between clustering coefficient and bound for number of final adopters. Such graphs are quite beneficial for complex diffusion process (contagion) to reinforce adoption of the innovation as they are more likely to be exposed to multiple adopters and overlapping influences via such short path-lengths during diffusion. Its merit is, in the existence of a seed set adopter inside the cluster. In contrast, with no *seed-set* adopter in a locally dense cluster, it is highly stable and may resist adoption of innovation. Thus, while clustering reinforces adoption if the innovation penetrates, it also weakens adoption – making penetration more difficult for small cluster coefficient *k* (Gilbert and Karahalois, 2009; Ojugo et al, 2014; Acemoglu et al, 2012). N_i encodes an idea that its structure is dependent on the structural predictive variable in tie-strengths with respect to: (a) tie history, (b) reciprocity, and (c) cohesive clusters and its coefficients. A major reason in using clustering includes: (i) there is a direct relationship between cohesiveness and clustering, and (ii) clustering has been used extensively in many studies to capture graph network structure as it also allows for easy comparison of result (Acemoglu et al, 2012) given as thus:

$$N_i(G) = P_{\theta,G} + \lambda_0 \mu_L + \lambda_1 Med_L + \sum_{t=0}^{t-1} \sum_{i \in L} \lambda_t (s - \mu_L)^t + \lambda_5 Min_L + \lambda_6 Max_L \quad (4)$$

where L = S_j and i,j are mutual friends. N_i uses the parameters: (a) $P_{\theta,G}$ to encode graph's probability distribution of actors via lower/upper bounds of actor positions, (b) μ / Med are actor's and system thresholds, (c) $\sum_{t=0}^{t-1}\sum_{i\in L}\lambda_t(s-\mu_L)^t$ encodes nodal learning as its convergence in time, and (d) Max/Min values are upper/lower bounds of final adopters. Each node *i's* neighbour has potentially unique set of mutual friends, we use 5-feats to describe ties distribution in relation to graph's structure, which agree with Gilbert and Karahalois (2009).

3.4. Threshold: A Parameter To Path Decision

A social graph is modeled as ties to bind loosely connected actors, and is required to impact a proposed learning outcome via diffusion of an innovation in a social system (Granovetter, 1978). It provides a structure that allow actors form opinions of the innovation as well as reflects how actors' interactions and local feats can influence the consideration of adoption or its consequent rejection (Krackhardt, 1990; Newman, 2003a; 2003b). As ties are formed, actors vary from one another – in their willingness to risk in adoption of a new innovation, product, ideas and behaviour. Thus, most actors are quite reluctant as they will rather wait until others have adopted such innovation first. Measuring the willingness to adopt is *threshold value* of an actor for the innovation (Valente, 1996).

Threshold is collective behaviour where an actor considers adoption based on the proportion of mutual friends that have already done so in the social system (Granovetter, 1983). An actor thus, adopts based on the behaviour of other actors in his immediate neighbourhood (personal network of actors that can influence him to adopt). Actor of low-threshold for a specific innovation will engage before many others; those of high-threshold only engage after many have done so; while actors of same threshold adopts at different times depending on the nature of influences received (Marsden and Campbell, l990).

Acemoglu et al (2012) Stochastic threshold of actor *i* from a linear threshold model and collective point of diffusion is: If M = {1,2,3,…N} actors of a graph has V-vertices, E-edges and w-weighted probabilities for its nodal feats denoted by G(V,E,w). With no self-loops in graph, (i,j)∈E is directed from i to j and its weight w(i,j) = 0 only if (i,j)∉E. w(i,j) = [0,1] as $\sum_{i\in J} w(i,j) \leq 1$. Thus, an actor's network has a neighbour set of the actor i∈M given by Pi(G) = {j | (j,i) ∈ ε} to consist of actors who can potentially influence actor *i* in G. If at iteration time t = {0,1,2,…,n), a subset of actors Φ(0) ⊆ M is selected as *seed* set, known as group of innovators exposed with threshold randomly uniform between [0.5,1] to reflect our lack of knowledge of the actor's true threshold (see Kempe et al, 2005). If the *seed* set adopts innovation at t = 0, at t > 0 – actor i ∈ M \ Φ(0) will adopt innovation if at least ϕ_i ∈ Φ [0,1] fraction of the actor's neighbors are in the seed set. and the expected number of final adopters are given by Eq. 5:

$$FA_d = \frac{|\Phi(0) \cap P_i(\mathrm{G})|}{|P_i(\mathrm{G})|} \geq \phi_i \Rightarrow i \in \Phi([0,1]) \quad (5)$$

Set $\Phi([0,1])$ are actors not exposed; But, will consider adoption as persuaded by their personal network and seedset node. At t ≥ 0, we generalized that: A node i∈M \ $\cup_{l=0}^{t-1}\Phi(l)$will adopt at *t* of linear threshold of Eq. 6.

$$FA_d = \frac{|\{\cup_{l=0}^{t-1}\Phi(l)\} \cap P_i(G)|}{|P_i(G)|} \geq \phi_i \Rightarrow i \in \Phi(t) \quad (6)$$

It is quite powerful to capture the role of backstage actors and interpersonal influences in adoption – with insight into the dynamic, complex relationship in network connectivity with respect to its seed set and threshold values. It fails to capture path dependence amongst other feats/parameters.

Acemoglu et al (2012) Path dependence is the idea that a few minor shocks, insignificant events along the way within the network can alter history's course. Diffusion has been argued to be an extremely fragile task with respect to such small shocks, which in turn goes to imply that the diffusion of innovation process is highly, path-dependent. Two ideas of similar feats, functions, seeding strategy and perceived quality may diffuse differently on the same network due to the different realizations of these minor shocks. Ties help include an actor as a member of another actor's network with a *seed* set – to allow for faster diffusion and yield cohesive clusters. External influence are factors that influence an actor to consider adoption as they are not from within the system. These include cosmopolitan actions, media influence, campaign, parallel innovation and initiatives etc – as reflected in the model (Ojugo et al, 2015).

If we denote the state of an actor at iteration t as $x_i(t)$, so an actor *i* takes one of 3-possible values: {0,1,-1} as not-yet-adopted, adopted and rejected respectively. At t = 0, the seed set of actors $\Phi(0) \subseteq M$ selected will adopts innovation. Thus, at t > 0, actor $i \in M \setminus \{\cup_{l=0}^{t-1} \Phi(l)\}$ will adopt if atleast $\phi_i \in [0,1]$ fraction of the actor in actor's personal 's network are members of *seed* set based on Bernoulli trial probability $p \in [0,1]$. For each $i \in \Phi(1)$, $x_i(1) = 1$ with *p* and $x_i(1) = -1$ with probability 1 – *p*. Feat *p* (or FA_d) determines likelihood of adoption conditioned upon its consideration and exposure – so that the larger the value of *p*, more likely an actor will adopt the innovation when such innovation is considered. Thus, set of actors who have adopted at *t* = 1 forms two sets given as: $A(l) = \{i \in V | i \in \Phi(1), x_i(1) = 1\}$, comprise of actors *seed* set and those that have adopted; while, the other set: $R(l) = \{i \in V | i \in \Phi(1), x_i(1) = -1\}$ comprise actors that are considering rejection. We generalize that at t ≥ 0, expected number of final adopters from modified stochastic threshold model that take into account path dependence, tie strength, and external influences is given by (Ojugo et al, 2015):

$$FA_d = \frac{|\{A(l) \cup_{l=0}^{t-1} \cup \Phi(o)\} \cap S_i(P_i(G))|}{|P_i(G)|} \geq \phi_i \Rightarrow i \in \Phi(t) \quad (7)$$

An actor adopts if: (a) a member of his network has been exposed, (b) members of his network forms a cohesive set, (c) where members of his network is not a cohesive set, then such members that has adopted are mavens, and (d) if one initializes an innovation from a set $\Phi(t)^*$whose complement is a cohesive set, then such innovation will not be adopted. Main difference between linear and stochastic threshold model is that an actor does not necessarily adopt if fraction of its neighbours that have adopted is above their threshold. At p < 1, actor can reject with a non-zero probability (due to minor shock and external influences); while at p > 1, actor can accept adoption also as case is.

3.4. Probability Distribution For Small-World (Barabasi and Albert) Graph

The study employs a stochastic social graph using ABM to test the role of migration pattern (for both external and internal influences) as shocks on either the adoption or rejection therein of the covid-19 epidemic as innovation for the social graph. It seeks to compute as clarified via threshold parameter so as to measure and estimates the expected number of final adopters within the timeframe for the project. This classification permits specifications of how these shocks influences flows through the system to govern diffusion process for the covid-19 epidemic. The nature of the problem determines that we use a small world (Barabasi and Albert graphs), and ascertain cum test the extent of local/nodal exogenous and dependency endogenous feats as contained therein. These in no time ripple throughout the social graph as observed global pattern of path dependence, shared tie, cluster coefficient etc – as captured via nodal attributes (Ojugo et al, 2015). Thus, a graph G with *n* nodes and *m* possible ties between nodes i and j, with random seedset nodes G_{ij} placed therein – its *Probability Distribution* is defined thus in Eq. 4:

$$P_{\theta,G}(G = g) = \frac{\exp[\theta^t u(g)]}{c(\theta, G)} \quad (4)$$

u(g) is vector statistics of graph realization G, C(θ,G) is a normalization function to ensure distribution sums up to 1, and θ is vector parameters of particular graph, found via Maximum likelihood in Markov Chain heuristics for the social graph via distribution $P_{\theta,G}$ (Sala et al, 2010).

Tie measurement often metamorphose into nodal network as actors often vary in their willingness to take risks in adopting new ideas cum innovations especially where the innovation in question is exposure to an epidemic of negative consequence. Thus, most actors are reluctant to do adopt as they will rather wait till the contagion dies out (Ojugo et al, 2014; 2015). Thus, the quantity *threshold* consists of 4-major feats: (i) actor $i \in M$ with $P_i(G) = \{j \mid (j,i) \in \mathcal{E}\}$ to indicate immediate neighbours node *i* can influence to adopt, (b) $\Phi(l)U_{l=0}^{t-1}$ is the rate at which actor *i* has neighbours who are also members of *seed*-set node that enables actor *i* to engage in considering if adoption is worth it or not, (c) $|N_i(G)|$ - is the network of actors who can influence actor *i* to adopt, and (d) set $A(l)$ as number of actors that will adopt innovation. Set $\Phi([0,1])$ have actors yet to be exposed at *t* = 0; But, who on exposure are persuaded by their immediate neighbors to adopt (consequent upon which they may adopt or reject) as in Eq. 5. The algorithm is thus:

```
Algorithm Local Emergent Feats {n, m, M, P}:
Initialize number of nodes n; number of Ties m
Set Initial Ties = 10+, Cluster Structure = 25+; Initialize Graph with actors via PD of $P_{\theta,G}(G = g) = \frac{\exp[\theta^t u(g)]}{c(\theta,G)}$
Set Actor position with Max/Min bounds of expected number of final adopters as a function of Motion or Movement M.
Randomly select nodes for seedset choice
While Node are yet to be Exposed
Choose actors position in seedset as best position in graph
Initialize current Actor position = {$M_{min}$ + rand($P_{max}$ – $P_{min}$)}
Compute Threshold for all nodes in Graph
Set Pairwise Variables Interactions (+$D_i$)
Set Predictive Variables for task (+$R_i$)
Compute Actor's Tie Strength as function {+$R_i$, +$D_i$, +$N_i$G, +$El_i$)
    For Each Actor, Node or Actor i
    Do {
      If seedset is member of an actor's personal network
        Then node.list.append(seedset node)
      End If    }
    End For Each
Compute Network Structure $N_i(G) = P_{\theta,G} + \lambda_0\mu_L + \lambda_1 Med_L + \sum_{t=0}^{t-1}\sum_{i\in L}\lambda_t(s - \mu_L)^t + \lambda_5 Min_L + \lambda_6 Max_L$
Compute Actor's new disposition from exposure at t ≥ 0 as: $M_{new} = w * M_{old} + c_1 * rand() * [(P_i)/T] + c_2 * rand() * [(P_n)/T)]$
Updating actors' positions as $P_{new} = (P_{old} – M_{new})$ //continue till all nodes are exposed, implies stop criterion is met.
```

4. Result Findings and Discussion

4.1. Result Presentation and Discussion

As propagation is enacted at t ≥ 0, actors are exposed to nodes (seedset with innovation covid-19). In time, as more actors are exposed due to migration pattern as shocks – it influences their capability to withstand adoption and their threshold parametric value shifts towards ***positive*** (as the nodes showcase a stronger resolve to reject), or ***negative*** (as they adopt) forming cliques via structured learning. These ties help the actors to better retain data in memory overtime as the system continues in its search for optimality. The random exchange in nodal network allows for knowledge swap – and yield in time, actors with a new set of disposition. With mode adoption and more exposure, more actors will continue to learn and retain contents to better their personal network via community-based influences.

Each exposure yields an updated number of final adopters as its optimal solution in time with recomputed threshold based on exposed actors. We note that: (a) actor position is normalized between ranges [0-1], (b) each position randomly determines swap type needed for adoption rate, and (c) positions are reset and recomputed values eventually reflects new graph threshold. With each solution found, model restarts with another randomly selected point for the planted seed-set choice in the graph space. Actors with threshold value above 0.5 are chosen. Process continues till all actors are exposed time ≥ t – 1 at which all actors will have a threshold of 1 for the diffusion process or the nodes are continuously re-evaluated till an actor is found of threshold lesser than or equal to start-off threshold value (these form the stopping criterion for the model). At which point the solution is reached. Table 3 shows percentages for adopter categories in relation to the nodal personal network and the social graph with a 90% significance.

Table 3. Tie strength on Time of adoption

No.	Dependent Variables	**μ**	**+R_i**	**+N_i**	**+D_i**	**EL_i**
1	Duration	0.67	0.94	0.87	0.89	0.21
2	Intensity	0.47	0.87	0.78	0.89	0.10
3	Social Distance to Nodes	0.23	0.42	0.34	0.43	0.19

No.	Dependent Variables	μ	$+R_i$	$+N_i$	$+D_i$	EL_i
4	Emotional Support	0.43	0.90	0.92	0.95	0.21
5	Recency and Intimacy	0.28	0.81	0.65	0.78	0.10
6	Reciprocity	0.38	0.81	0.76	0.72	0.13
7	Structural Distance	0.31	0.80	0.82	0.86	0.34

Results shows that the introduction of *seedset* actors allows for a uniformly distributed adoption of covid-19 contagion across the graph. This suggests that a highly clustered graph with more seedsets will also allow for easier propagation. High clustering coefficients promotes propagation ease along the lines of nodal personal network. Conversely, such tightly cohesive graph also are dfficult to penetrate if no initial seed-set. However, use of Markovian clustering allows for targeted diffusion; though, it may generate some errors – even with such migration pattern (and shocks). It will alter the diffusion outcome significantly. The use of migration has become imperative to be used as threshold parameter. We note that a node's time-of-adoption is associated with proportion of adopters in the graph and the shock's influence in proportion to an actors' network. We observed that with seedset nodes, over 80% of active nodes were exposed and adopted the covid-19 epidemic (i.e. in the early, early and late majority). These were also reflected in both the nodal and system thresholds – and was found to represent the proportion of actors that easily adopted the covid-19 disease (i.e. easily infected from exposure). A high threshold implies that the node has high tolerance against the disease and vice-versa. All the node in the *laggard* group were found to have (very) high tolerance threshold.

Table 4. Convergence of Expected Final Adopters

Adopter Category	Ext. Infl.	Personal network: direct ties μ	δ	Low	Ave	High	System Total
Early	4.1	0.76	0.31	1.6	12.7	9.9	24.2%
Early Majority	20.1	0.57	0.23	8.8	11.2	10.6	30.6%
Late Majority	12.1	0.46	0.21	13.7	10.1	10.0	33.8%
Laggards	6.5	0.32	0.20	1.9	6.1	3.4	11.4%
Personal Network Total	42.8			27.3	30.1	42.6	100%

Actors that fall within the laggard resulting to about 11.4% are not innovation either to their personal network or to the entire social system. Laggards skewed from a considerable proportion of non-adopters in relation to the datasets used and accounts for about 11.4% of population. A reason for this skewness is projected that all actors will eventually adopt after a given time, or as we reach stop-criterion t = t – 1 and adoption of covid-19 even with the protocols set up in place and its adherence. This is because, residents cannot dessert their homes and visitors (infected) cannot be allowed to get back to their homes also. However, some actors will remain indifferent and thus, are classified as *laggards* as they will not adopt the innovation due to high threshold.

4.2. Theoretical Implications

With agent-based modeling on social graphs, there are still a lot more variance to understand such as predictive variables and "behind-the-scenes" data. Though, the addition of more data to the task in hand may not resolve these issue therein raised. But, we can aimed to define the parameters that can help us predict such complexities in a social graph. Thus, there is the critical need to develop standards alongside novel indicator parameters for social-graph models. This will though, in turn – raise new questions like: (a) what parameters are deemed important to be used as threshold predictors?, and (b) what upper and lower boundaries must be set for ties and migration pattern especially in its adoption as predictors? This is in agreement with even real-world data as posited by (Gilbert and Karahalois, 2009; Ojugo et al, 2014; 2015; Ojugo and Eboka, 2020; 2021; Ojugo and Otakore, 2021; Ojugo and Nwankwo, 2021).

5. Summary and Conclusion

We believe our work has made some critical contributions as thus: (a) defined ties as a dimension manifested in all social-graphs, (b) defined network structure as a linear function and used it as a function of probability distribution of actors in the problem space being considered, (c) used mobility/migration pattern as a threshold predictor modeled as a continuous value, (d) our result extends upon the realization that help modulate the graph feats by filtering actor relations via clusters/cliques, and (e) previous works assumed edgewise relations in the graph without recourse to the properties of the link itself. We defined these properties as dimensions in the network structure itself.

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