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Coupling equation based models and agent-based models: example of a multi-strains and switch SIR toy model

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Abstract

Modeling in ecology or epidemiology generally opposes two classes of models, Equation Based Models and Agent Based Models. Mathematical models allow predicting the long-term dynamics of the studied systems. However, the variability between individuals is difficult to represent, what makes these more suitable models for large and homogeneous populations. Multi-agent models allow representing the attributes and behavior of each individual and therefore provide a greater level of detail. In return, these systems are more difficult to analyze. These approaches have often been compared, but rarely used simultaneously. We propose a hybrid approach to couple equations models and agent-based models, as well as its implementation on the modeling platform Gama [8]. We focus on the representation of a classical theoretical epidemiological model (SIR model) and we illustrate the construction of a class of models based on it.

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1. Introduction

Agent Based Modeling and Equation Based Modeling are two common modeling approaches for dynamical systems. Equation Based Models (EBMs) usually describe the dynamical processes at the global scale (at the population level in ecology) while Agent Based Models (ABMs) describe the same processes at the local scale (at the individual level in ecology). Each approach offers different advantages and drawbacks. The scale at which the processes are represented determines the way the model is constructed: global processes, a small number of parameters and no individual variability for the EBMs; individual processes, high level of detail for ABMs. EBMs do not take into account individual variability, assuming that mean fied approximations conveniently describe the dynamics at the global level. ABMs are relevant when this individual variability has strong effect on the dynamics emerging at the global level. Additionally they allow explicit representations of the interaction network of individuals when its topology has consequences on the dynamics of the system and the emergence of properties at the global level. ABMs also offer the possibility of an easy integration of GIS and social network information.

Apart from conceptual aspects, the community of the modeler has a strong influence on which approach will be chosen. A strong knowledge in mathematics is needed to understand and build equations for the EBM approach. As a counterpart, mathematics offer powerful tools to analyse EBMs, providing a lot of in-depth information about the dynamics, such as equilibria and

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long term dynamics. ABM approach is more intuitive, and platforms such as Netlogo or Gama propose modeling tools aiming at a wide audience. A few papers have been devolved to the comparison or the coupling of both approaches. As an example of a coupling of EBMs with ABMs, we refer to some particle transport models [10] based an oceanic current model based on physics and Partial Differential Equation, which output is used in a ABM that describes the dispersal of fish larva. However, to our knowledge, there are very few models of strong coupling of an ABM with an EBM, in the sense that both models use the outputs of the other. Such a model has been developed by [1] for a model of pedestrian movements. The model is based on an ABM describing the movements of individuals in the streets of a city. Each road segment between two crossroads can be replaced by a mathematical transport model in order to reduce the amount of resources needed for the simulations. At each intersection, the ABM feeds the EBM with the number of individuals entering the road segment, then the EBM generates agents at its end.

In this article, we illustrate the benefit of hybrid models embedding equations inside agents with a specific class of models: epidemiology models with multiple strains for the virus. Epidemiology models describe the evolution with time of epidemics within a host population. Usually, the host population is divided in several categories: susceptible individuals (hosts without disease but which can get infected), infected individuals, recovered individuals (hosts immune to the disease). Many categories can be added depending on the disease and the model requirement, such as quarantined individuals, infected but still not infectious, etc. Both classes of models are commonly used: the first and most famous, the SIR model by Kermack & McKendrick [9] being an EBM. Epidemiology EBMs consider the population at the global scale: they are compartment models, each compartment corresponding to a variable representing the population size in a given category, or the density at a given location. Evolution of the population size (demography and transition from one compartment to another, such as newly infected individuals being transferred from the susceptible compartment to the infected compartment) in a compartment is governed by differential equations. Such continuous models also have discrete equivalents. ABMs represent each host individually. Hosts can change state (e.g. susceptible to infected) over time, given probabilistic and algorithmic rules.

In epidemiology, EBMs often relate to biological or theoretical studies and have been used to model potential public health outcomes before testing strategies directly on populations. As an example, Shulgin et al. [17] discuss the benefit of a pulse vaccination using a classical SIR model. ABM focus more on studies with sociological aspects using graphs theory: they allow examining the role of social networks, transportation systems, and responses to changing contexts on the evolution of epidemics [11]. As an example, we refer to Auerbach et al. [2] study the propagation of HIV in a sexual contact network of 40 men. Usually, both approaches are used separately. In this article, we focus on a particular class of epidemiology models: models with strain-polymorphic pathogens. Multi-strains models with evolutionary processes and interactions are a major concern in epidemiology. EBM and ABM approaches have both been used: as an example, Roche et al. [16] propose an ABM of influenza with strain-polymorphic pathogens, based on an EBM model. Roche et al. decided to use an ABM because the original EBM fails to follow co-infections and consequently to incorporate re-assortment. One of the main challenges is to define properly the nature of strains space [20]. A common approach is to consider a linear space of parameters. Evolution can be continuous, in which case the possible of strain is infinite or discrete. In the later case, models found in the literature use a finite number of strains. This approach is relevant for pathogens for which the different strains can be enumerated. In EBMs, the number of strains is usually constrained by the nature of systems of differential equations, which use a fi and finite number of equations. But evolution and polymorphism can give rise to unforeseen types of strains, which can change the number of possible strains. In order to release this constraint, we introduce a simple epidemiology model with dynamical change of the number of strains.

2. Related Work

In this part, we present the current state of the art of coupling the Agent-Based Modeling approach and Equation-Based Modeling approach. Although these two approaches aim at a common objective, they are distinct by their modeling formalism. The necessity of coupling and comparing the two approaches has been raised in several research studies. They use a common methodology: exploration is always done by implementing an agent-base model beside an equation-based without the support of an agent-based modeling framework neither an equation-based framework.

2.1. Equation-based model

The equation-based models [5] predict the long-term dynamics of the studied systems. they use mathematical formalism based on Ordinary Differential Equations or Partial Differential Equations. The modelling approach is generally driven by the principle of parsimony (or *Occam's razor*), which means that the model should be kept as simple as possible, with as few parameters as possible. Although, if a stochastic

approach is possible, a deterministic approach is preferable when possible. In addition, processes are considered at a global scale (e.g. in ecology: at the population level instead of the individual level), assuming that the processes that govern the system at such a scale can be determined (often using mean field approximation). For example, the demographic dynamics of a population can be described at the global level using a parameter call *population growth rate*, which can be derivated from the mean of offsprings per individual per time unit. Due to such approximations, the variability between individuals is difficult to represent, making these models more suitable for large and homogeneous populations. Mathematics often provide useful analytical tools to find the properties of ODE models, such as equilibria and asymptotic dynamics. The evolution of the system can be determined from mathematical proofs, which are more robust than just simulations. For those reasons, such models can be easily analysed and are useful for making predictions. On the contrary, translating the studied processes into equations requires a good knowledge of similar physics or mathematical models. Processes also have to be sufficiently smooth in order to find their mathematical description. As a summary, such models require a large amount of work upstreams, but they offer conceptually good possibilities of analysis downstreams (the technical issues that could be encountered in mathematical proofs is not discussed here).

EBMs have been widely used for epidemiology modeling. A pragmatic reason is that mathematical analysis methods were the only available methods, as computers and EBM were not available to Kermack and McKendrick in 1927. However, there are many conceptual reasons why EBM are a reasonable choice for modeling epidemics. Firstly, epidemics arise in large populations, and the transmission and remission rates variability among individuals can be easily represented according to familiar distribution laws, making such processes easy to describe at the population level using mean field approximations. Secondly, the analysis of the equations provide useful prediction tools for epidemiology: one can determine conditions on the parameters for which the epidemics will arise or not. For example, the basic reproduction number R_0 can be computed with the parameters of the model, based generally on transmission and remission rates. Values greater than one mean that an epidemics outbreak will occur, such an event can be then predicted without simulations.

2.2. Agent-based model

Agent-based models [7] are used to represent the attributes and behavior at the individual level, and therefore to provide a greater level of detail. They can describe strong individual variability, not only for the attributes of the individuals of a same population, but also for their behavior. They are often associated to small time scales, which correspond to the individual processes time scales. In return, these systems may be more difficult to analyze and prediction almost rely on simulations (apart from some ABMs which are actually probabilistic mathematical models that can be analysed with mathematical tools). Because of the large number of parameters, it can be difficult to test the model sensitivity to one of them. A large amount of analysis, dependent on simulations and on the assumed prior distribution of parameters has to be performed in order to provide synthetic results. ABM use a specific language to describe in detail the aspects of agents: perception, action, belief, knowledge, goals, motivation, intention, reflexion etc. Processes can be written as algorithms, offering more freedom to the modeler, as complex decision structures can be used (e.g. if the behaviour of individuals depends on some condition, an *if-then-else* construct can be used). The ABM approach also proposes a more intuitive way to build the model: processes can be represented as close to the perception of the modeler. As a summary, such approach proposes an easy and intuitive work upstreams, but requires a large amount of work downstream to provide relevant results. In addition, the large number of parameters combined with the often large size of population considered means that such a model may need a very important amount of resources to run simulations.

Interest of epidemiologists in ABMs relies on the ability to give a detailed description of the network of transmission, and such models have been developed alongside graph theory. Such models are useful to represent singular events (one infected individual entering a large susceptible population) and the stochasticity associated to such events. Such models are used to represent the worldwide propagation of infection due to air travel. Depending on the disease, a detailed behavior of the infection vector can be given.

2.3. Coupling EBM and ABM

In [19], the authors study the difference between agent-based modeling and equation-based modeling in a industrial supply network project in which network's domain supply are modeled with both agents and equations. They also summarize the resemblance and variety of two approaches with a suggestion to use one or another. Their study is part of the DASCh project (Dynamical Analysis of Supply Chains). DASCh includes three species of agents: Company agents, PPIC agents and Shipping agents. It also integrates a fixe set of ordinary differential equations (ODE).

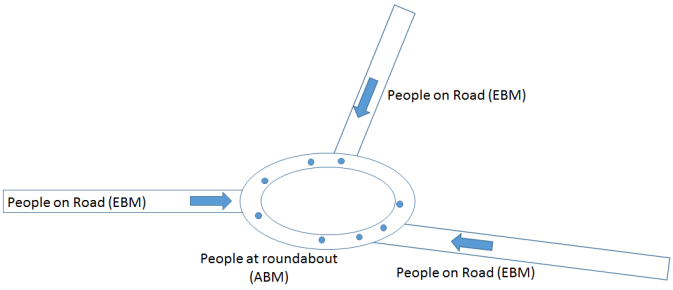

Figure 1. Coupling approach example: people moving on the road are represented in the form of equation, and in form agents at the crossroads

Coupling and comparing agent-based and equation-based is also found in [15] where Rahmandad et al. examine in contrast the dynamic of well-know SEIR model which describe the common and important context of the spread of contagious disease. They compare and validate an ABM and EBM for epidemiological disease-spread models, as well as in [18] in which an ABM and an EBM of the 1918 Spanish flu are compared. In this publication, a model validation framework for choosing ABM or EBM is proposed.

In [13], it is proposed to use only one appropriate modeling formalism instead of two approaches, and infer an EBM from an ABM SIR model by exploring the deducible parameters like number of individual in population, rates of interactions base on dimension of environment. They have done a study with the measure based on disk graph theories [12] to link ABM with EBM dynamical systems applied to theoretical population ecology.

Another coupling approach is proposed in [14], [1] or [4]. In the simulation of emergency evacuation of pedestrians in case of a tsunami in Nhatrang City, Vietnam, people move along the road networks as agents. The agent based model of individuals movements are replaced by equation models for the roads with higher traffic. This transformation give the model an addition of time and resource for such evacuation model which usually take into account huge populations.

All these approaches provide mechanisms that allow interaction between several models but they still have the following disadvantages:

- In general, these approaches are not generic and are difficult to be re-implemented in different domains and contexts.

- There are no consideration of the differences in spatial and temporal scales.

- There are no framework that support coupling of heterogeneous models between equation-based modeling and agent-based modeling paradigm.

3. Description of the epidemiology model

In the present paper, we discuss the concept of integrating EBM inside ABM. We build a model composed of several sub-models. Each sub-model refers to an EBM or ABM. Instead of choosing between an ABM or EBM approach as in previous works for the global models, sub-models are integrated in a framework that allows using both paradigms at the same time.

As a demonstration, we introduce a mathematical epidemiology model with dynamical change of the number of strains. The epidemiology dynamics for a given strain is described by a classical EBM, while the strain evolution dynamics is described by an ABM.

The equations of the mathematical model will be embedded into agents, each agent representing a different strain. Each strain is characterized by different values of the parameters. In order to illustrate the benefit of the hybrid approach, the mono-strain mathematical epidemiology model has to verify two conditions:

- the model must be as simple as possible, with very few parameters. This condition allows a good tractability of the model. Because each strain corresponds to particular values, it is easier to monitor the dynamics of evolution of strains with a low number of parameters;

- epidemics outbreak does not fade away with time. This condition ensures that the evolution of strains can be monitored over an infinit period of time. Such a condition is not met with the classical SIR model [9] and thus a slightly different class of compartment models must be chosen.

3.1. Mono-strain models

We base our study on a common mono-strain SIS model, which is a compartment model with two compartments S, I which are respectively the number of susceptible and infected individuals at a given time. The evolution of the S and I populations is governed by a system of differential equations, which reads:

$$\begin{cases} \frac{dS}{dt} &= -\beta IS + \gamma I \\ \frac{dI}{dt} &= \beta IS - \gamma I \end{cases} \quad (1)$$

where the total population $I + S$ is constant over time and normalized to 1. In presence of infected individuals, the number of susceptible individuals infected per unit of time is proportional to the to size of the infected population and the proportion of susceptible individuals in the total population. The coefficient of proportionality is written β and is called the *infection transmission rate*. Finally, constant γ corresponds to the recovery rate, the rate at which

infected individuals recover from the disease and become susceptible again. Such a model corresponds to diseases for which there is no long term immunity, such as common cold and influenza. The SIS model has an explicit analytic solution and its dynamics is well known. Let us introduce the *basic reproduction number* $R_0 = \beta/\gamma$. A well know result is that if $R_0 < 1$, the epidemic dies out, while if $R_0 >$, the epidemics spreads and the system tends toward an equilibrium with a infected population of size $1 - 1/R_0$. Therefore, such a model verifie the two previous conditions: there are only two parameters (β and γ), and the dynamics tends toward a steady state with a persisten t infected population.

A SIR model modify so as incorporate vital dynamics can be used. Such a model use a third compartmen t R which represen ts the recovered individuals, who are free from the disease and who cannot be infected again. The model reads:

$$\begin{cases} \frac{dS}{dt} &= \mu - \mu S - \beta IS \\ \frac{dI}{dt} &= \beta IS - (\gamma + \mu)I \\ \frac{dR}{dt} &= \gamma I - \mu R \end{cases} \tag{2}$$

Constan t μ is the population renew al rate, which means that populations S, I ad R suffer from a natural mortality rate of μ, while new individuals are produced with the same fertility rate μ. The basic reproduction number is $\beta/(\mu + \gamma)$. If $R_0 > 1$, the dynamics tends toward a steady state with a infected population density of $\mu/\beta(R_0 - 1)$. This model also verifie the two conditions. The model has three parameters, however parameter μ is not related to the disease and won't affect the strains monitoring.

3.2. Multi-strains models, with a constant number of strains

Usually, multi-strains models are static, meaning that N is constan t over time and there is no new strain that was not presen t at time t=0. Such approach is consisten t with the mathema tical approach of dynamical systems: the number of equations is the same once and for all. We propose a dynamics approach where strains can be created or removed. The previous models are modifie in order to consider n differen t strains, the strain i being characterized by a couple of parameters (β_i, γ_i), n being constan t. The infected population density is denoted I_i.

The modifie SIS models reads:

$$\begin{cases} \frac{dS}{dt} &= -\sum_{i=1}^{n} \beta_i I_i S + \gamma_i I_i \\ \frac{dI}{dt} &= \sum_{i=1}^{n} \beta_i I_i S - \gamma_i I_i \end{cases} \tag{3}$$

A straightf orward analysis of the system shows that appart from the disease free equilibrium (DFE) $(1, 0, \ldots, 0)$, there exist n equilibria

$$E_i = (1 - \gamma_i/\beta_i, 0, \ldots, 0, \gamma_i/\beta_i, 0, \ldots, 0)$$

where the non-zero elemen t corresponds to the population infected by strain i. If $R_0 > 1$, all those equilibria are unstable but the one that maximizes γ_i/β_i. Let us denote i^* the number of the strain corresponding to the stable equilibrium. The systems tends towards this equilibrium, with a non-null infected population density, with individuals infected only by the strain i^*. Therefore this model illustrates the competitiv e exclusion among the strains: only the strain with the highest fitnes survives.

Similarly, the SIR model with vital dynamics and n differen t strains reads:

$$\begin{cases} \frac{dS}{dt} &= \mu - \mu S - \sum_{i=1}^{n} \beta_i I_i S \\ \frac{dI}{dt} &= \sum_{i=1}^{n} \beta_i I_i S - (\gamma_i + \mu) I_i \\ \frac{dR}{dt} &= \gamma_i I_i - \mu R \end{cases} \tag{4}$$

Similar results can be obtained, with only one strain surviving in the long term. One should notice that such a model introduces simple competition between the strains as cross-immunity is not considered. Therefore there is only one global compartmen t for recovered individuals, which is common to all strains. In this model, we only take into account virus strains mutations. Host ecosystem, evolutionary processes and host variability impose selection on virulence [6]. Evolutionary ecology epidemics models could benefi for such approach, mixing agents and equations.

3.3. Multi-strain models, with varying number of strains

We now consider models in which the number of strains varies with time: strains are removed when the corresponding population is too low, and a new strain is created when a random mutation occur in an existing strain. Formally, the models can be described by the systems of equations 3 and 4, except that two rules are added:

- when the population of strain i drops below a threshol d σ, strain i is removed from the system.
- for each strain i, a mutation can occur with a probability p. When the mutation occurs, a density m of individuals is removed from the population infected by strain i. A new strain $n + 1$ is created, with an initial infected population density $I_{n+1} = m$. New parameters β_{n+1} and γ_{n+1} are randoml y chosen with regard to old values β_i and γ_i.

In our study, we decide to chose the values β_{n+1} and γ_{n+1} according to a uniform distribution on the respectiv e intervals $[0.7\beta_i, 1.3\beta_i]$ and $[0.7\gamma_i, 1.3\gamma_i]$.

4. Hybrid concept and implementation

Mathema tical models often do not consider systems of equa tions with a varying number of equa tions. Here we propose to use ABM with agents embedding equa tions in order to buil d a system of equa tions that can evolve with time. Strains are represen ted by agents which can comm unica te with each other. For each strain, there is one equa tion describing the evolution of infected individ uals corresponding to that strain. Such a system is an ABM and an EBM in the same time: each strain is considered as an individ ual, but the popula tion of susceptible and infected is considered at the global lev el. Each strain is an entity that embeds an equa tion. The inter action betw een individ uals form a larg e dynamics set of equa tions. It can be seen either as:

- an ABM com posed of strains, each individ ual embedding an equa tion. Inter actions betw een the individ uals giv e rise to a non-sta tic system of equa tions, and so to an EBM that evolves with time.

- an EBM, in which each equa tion is represen ted by an agent corresponding to a strain which is dynamicall y linked to the others. The EBM is a non-classical one, in the sense that it can be dynamicall y be chang ed.

The model has been implemen ted on the Gama pla tform [8], which all ows embedding equa tions. In an equa tion associa ted to an agent, it is possible to refer to the variable and equa tions embedded in other agents, in order to buil d dynamicall y a set of equa tions.

The strains are susceptible to muta tions, and so to evolution through com petition for resources (popula tion susceptible to the disease). From time to time, a strain is randoml y selected for muta tion, a new strain of one individ ual being crea ted, and the par ameters beta and gamma for the new strains being chosen randoml y with values close to the ones of the old one. The set of equa tions is upda ted dynamicall y, and the new strain joins com petition for resources.

4.1. Dynamics of the model

The model we buil t illustr ates a phenomenon of genetic drifts. According to excl usiv e com petition principle, the strains with the smaller fitnes final y get discarded from the pool. Depending on the frequency of the muta tion events and on random aspects, it happens that sev eral strains coexist for a short period (up to 20 in our sim ula tion with par ameters ...) According to expecta tion, the drift tends tow ards par ameter rang e where beta is larg e and gamma is small.

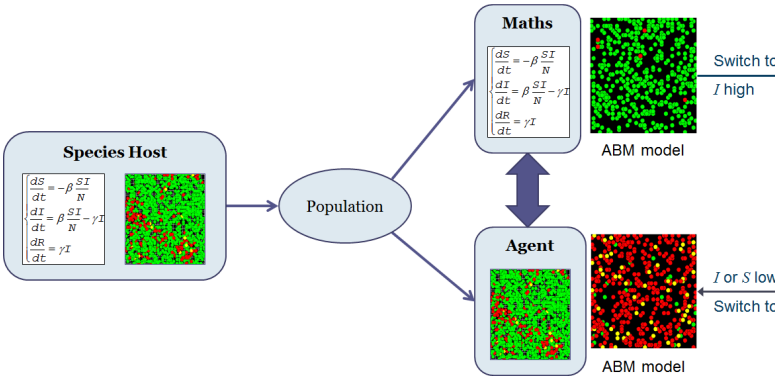

Figure 2. Representation the dynamic of "Switch" model

4.2. Model "Switch"

We illustr ate our coupling methodol ogy by implemen t-ing a hybrid model, called Switch, combining equa tions and agents on the modeling pla tform Gama. We buil d a class of SIR model based in both ABM and EBM (figur 2), in which people are represqen ted by agents when the density is low, and by equa tions if the density is higher , a til ting mechanism for moving from an approach to another .

Both models are based on the same assum ptions. They involve two processes: contamina tion and recov-ery. The ABM model also adds spa tial inter actions and dispersal. The ma thema tical model is indeed a mean fie d approxima tion of the ABM and represen ts the dynamics at the global scale, while ABM shows the dynamics at local scale. The contamina tion and recov ery processes happen frequen tly with a "unif orm distribution " over time.

- Assum ption i) implies that processes can be represen ted at a con tinuous time;

- Assum ption ii) all ows to replace probabilities of processes occurrences by expectancies; final y assum ption iii) all ows to consider that all individ ual have the same number of neighbors.

- Assum ption iii) popula tions are considered to be at sufficien tly high density; popula tions are considered as homog eneous for spa tial distribution of individ uals, as well as for the distribution of each type of individ uals (S, I and R).

Considering that assum ption i) hol ds is rather natu-ral, as processes occur al ong constan t time steps. Epi-demiol ogical models usuall y assume that popula tion densities are high, thus condition for assum ption ii) seems to be natur all y fulfilled How ever, in a larg e popula tion, the density of infected (or even suscep-tible) individ uals may be very low. Indeed, a usual condition for such kind of model is the intro duction of a small group of infected inside a disease free popula tion. Mathema tical model are deterministic and ignore the variability due to stochasticity which al ter

the dynamics: if one infected individual is introduced in the population, if basic reproduction rate R0>1, and epidemic outbreak will be predicted by the mathematical model. However, in real cases or for ABM, there is a chance to avoid epidemic outbreak as contamination may not occur thanks to the stochasticity of infection process. Assumption iii) may not be possible for spatially explicit ABM, as spatial distribution does not remain constant and spatial patterns could appear, like contamination waves. Assumption iii) makes that the EBM, as mean-field approximation of ABM, is also the the "limit" (in the mathematical sense) of the EBM when spatial process tends to spatial homogeneity, which is achieved by letting the neighborhood of an individual tend to cover the whole environment, or by increasing the speed of movement of individuals (well mixed populations).

Comparing both EBM and ABM is exhibiting the differences due to approximations done for the ABM model due to assumptions ii) and iii). Assumption ii) is at the heart of the model switch problematic: EBM should not be used when the conditions for this assumption are not fulfilled Assumption iii) also add a challenge to model switching, as corrections have to be made in order to represent into the ABM the effects of spatial structures that have been hidden by the approximation made with this assumption. Furthermore, switching from EBM to ABM introduces an explicit spatial distribution of individuals, for which assumption iii) doesn't have to be made. The spatial distribution, hidden in the EBM, may have to be generated.

The two models are based on SIR models assumptions. Individuals can be in three different states: susceptible individuals (S): the individual is disease-free and can be contaminated by contact with an infected individual (I). After some time, infected individuals recover from the disease (or die). They are assumed to be in a recovered state (R): they are immune to the disease and do not take part anymore in the infection dynamics. The models involve the following processes:

- infection: transmission of the disease from infected individuals. This depends on the contact rate between susceptible individuals and infected individuals;
- recovery: infected individuals heal and recover from infection;
- movements: individuals are assumed to move within the considered environment. There are two type of movement, one is random walking and other is not random, (figur 3).

Hypothesis found in both models:

- Recovery rate: the remission rate is very similar in the agent-based model and the equation-based model. In the ABM, parameter gamma is the probability to recover per time unit. In the EBM model, the parameter gamma is a mean-field approximation, which means

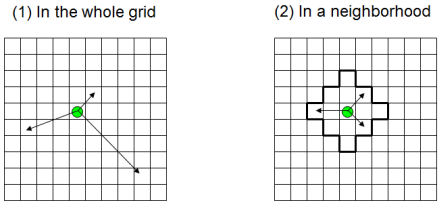

Figure 3. Two type of deplacement of agent in an environment

that the number of recovered individuals given by the EBM model is exactly the expectancy of the number of recovered individuals given by the ABM model (provided that there is no infection occurring at the same time). Stochasticity of recovery rate appears at low I populations, otherwise both models fit

- Contact rate: in the present models, contact are define in a similar way for the mathematical model and the agent-based model. In the agent-based model, two individuals are considered to be "in contact" if they are in each other's vicinity for one time step. In mathematical model, space is not explicitly represented, but the average number of neighbours can be determined. Stochasticity of contact rate appear because of size of neighbourhood (strong variability in number of hosts neighbours) and speed of hosts (low speed means no mixing, neighbourhood proportion of R and I may greatly vary).

We compare this model with existing models and present a method to determine the parameters for transitions between models. In particular, we establish a link between the parameters of the mathematical model, and the representation of contacts and travel agents in a spatial environment.

We are also interested in how to compensate for the loss of information on spatial structures when we move an agent model to a mathematical model. Currently, we save the attributes, especially the location and the status, of all agents and re-assign to agents when they need. We are also interested in how to compensate for the loss of information on spatial structures when we move an agent model to a mathematical model. Currently we have implemented two following method of creation new distribution after the switch from EBM to ABM.

5. Experiments

5.1. Objective, Data and tools used

In this part, we do experiment to prove the capabilities of coupling framework that we have proposed to compose the ABM and EBM. The experiments will have three scenarios, each scenario The data used in the "Switch" model is bring in the real data of SIR model. The epidemiology's parameters are the spread of the fu and measles.

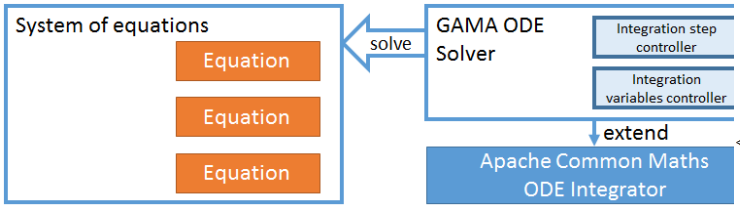

Figure 4. an ODE solver structure inside a modeling and simulation platform

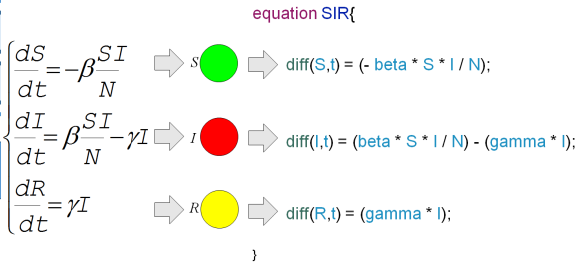

Figure 5. Representation of an equation-based model in an simulation platform.

5.2. Tools used: An ODE-integrated environment

We tackle the problems of differences modeling formalism with our proposition of coupling by integrating these two approaches in a modeling and simulation platform, GAMA [8], in which the equation-based model is declared as an attribute of the agent. It has two famous examples of equation-based modeling which are the Lotka and Volterra [24] modeling of prey-predator dynamics or the Kermack and McKendrick [3] SIR model to represen t epidemic dynamics.

We have introduced in GAMA the possibility to describe the dynamics of agents using a differential equation system and to integrate this system at each simulation step. With the enhancement of GAMA modeling language (GAML), modelers have possibility to write equations linking agentsâĂŹ attributes and to integrate equation-based system with agent-based system. The GAML syntax permit to write an system of equations of most EBM based on the implementation with Commons Mathematics Library.

To figur out the coupling problem of different temporal scale, we introduce the controller of integration steps and simulation steps beside the two current integration method Runge-Kutta 4 and Dormand-Prince 8(5,3). This controller is main tain in the solve statement of GAML and would be call at each simulation step. In the figur 4, an equation-based model in form of algebrics is represen ted into GAML syntax that are called Equation. Set of equations make a System of equations. This type of entity will be integrated by our GAMA ODE (Ordinary Differential Equation) Solver package.

5.3. Represent classical SIR model in EBM and ABM formalism.

The firs experimen t show that we can easily modeling the classical SIR in form of equation-based and also agent-based. As in the figur 5, an differential equation can be declare with two expression. The firs one on the left of "=" is the keyword diff followed by the name of integrated variable and the time variable t:

```
diff( <integrated variable>, t )
= <calculating expression>;
```

An EBM is then represen ted as a attributes of agent with a block of equations:

```
equation <name_identifier> {
    diff(...) = ...;
    diff(...) = ...;
    ...
}
```

6. Results

6.1. Discussion on the methodology

The EBM submodel describes the dynamics of the epidemic at the global scale: host population is considered at global population through density measuremen ts. The ABM submodel describes the dynamics of strain evolution at the individual level: at each momen t, one can describe which strains are active and which have been removed. One should notice that the global level for EBM is indeed embedded in the individual level for strains: to each individual strains corresponds a density of infected population.

6.2. Adjust the parameters to calibrate EBM and ABM

The ABM simulation result is a stochastic result, instead of EBM'result s are deterministic. Our proposition allow modeler to calibrate the SIR model in ABM fi with EBM. We launch the simulation with following parameter: N = 500; I = 1.0; S = N - I; R = 0.0; beta = 1/2.0; gamma = 1/3.0. After 100 simulations, the SIR model and agent model presen t significa t differences from (figur 6):

- popula tion initial (N)
- effect of size grid (grid size)
- effect of topologies (neighborhood size)

The transition beta from EBM to ABM is then adjust an amoun t alpha. We relaunch the simulation 100 times to explore the value of alpha. We found the fixes alpha = 0,45 (figur 7). We have also found several criterias that would be effect the fitnes betw een SIR EBM and ABM are: difference of synchronous/asynchronous

$$\beta_m = \beta \frac{\text{neighborhood size}}{\text{grid size}} N \times a \quad , a \text{ adjustment parameter}$$

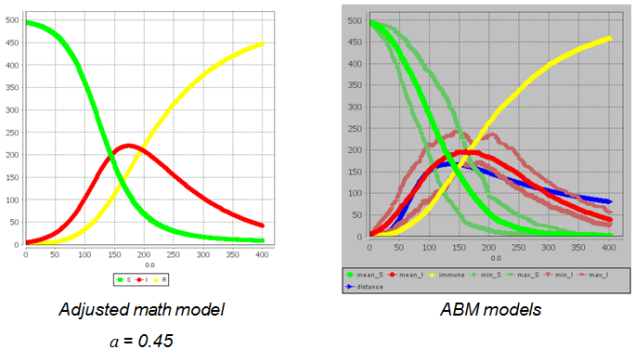

Figure 6. Adjust the beta parameter of SIR model to calibrate EBM with ABM result.

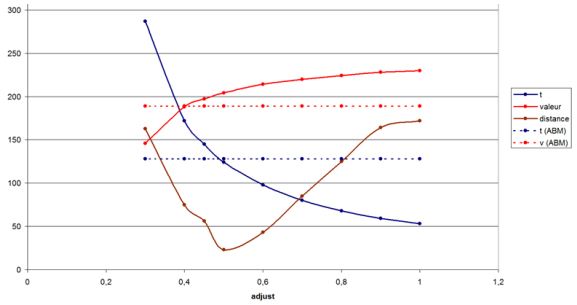

Figure 7. Adjust the beta parameter of SIR model to calibrate EBM with ABM result.

(infect others vs is infected); random walk; effect of beta; dispersion; effect of movement speed.

6.3. Study of the dynamics of multi-strains epidemiological model

with our proposed coupling methodology, modeler can easily study the multi strain epidemiological model by the implementation like in the figur 8. agent strain can be created an removed dynamically in time of simulation.

As in the case of a constant number of strains, competitive exclusion prevails: the strains with lowest fitnes eventually disappear, while the one with the highest remains. As mutations allow the appearance of new strains, strains with higher fitnes appear (higher $R_0 = \beta/\gamma$ ratio), and it is possible to exhibit a genetic drift. In figur 9, it is shown that evolution favours an increase of β (better contamination ability) and a decrease of γ (longer infection duration).

```
species S
{
    equation evol simultaneously : [Strain]
    {
        diff(first(S).Ssize, t) = mu - mu * self.Ssize -
            sum(Strain accumulate (each.beta0 *
                (1 + each.beta1 * cos_rad(2 °pi * t)) * each.Isize
            )) * self.Ssize;
    }

}

species Strain
{
    reflex mutation when: (flip(mutation_probability))

    equation evol simultaneously : [S]
    {
        diff(self.Esize, t) = (self.beta0 *
            (1 + self.beta1 * cos_rad(2 °pi * t)) *
            first(S).Ssize * self.Isize)
            - (self.alpha + mu) * self.Esize;
        diff(self.Isize, t) = self.alpha * self.Esize
            - (self.gamma + mu) * self.Isize;
    }
}
```

Figure 8. Multi-strain SIR model declared in Gama platform

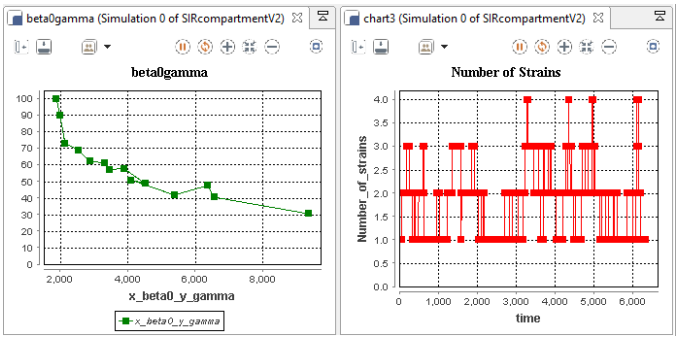

Figure 9. The result of

6.4. Regenerate spatial information from EBM to ABM

In this experiment (figur 10), we save the attributes, especially the location and the contamination status of all agents when we do a switch from ABM to EBM model. Then when re-assign to agents. The image represent the regeneration algorithm in figur 10 is two example results. With the same manner, we have do 100 times of simulation and compare the state of population with and without a switch in the table 11 to see the efficient of algorithm.

7. Conclusion

This paper has proposed a hybrid approach combining modeling equations and agents, as well as its implementation on the modeling platform Gama. We are interested in the representation of this approach theoretical epidemiological models. We illustrate the construction of a class of models based on a SIR model in which people are represented by agents when their density

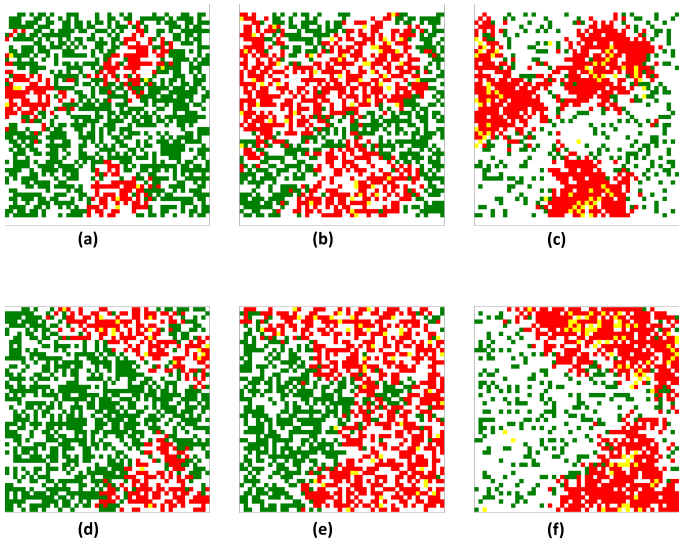

Figure 10. Regeneration of spatial information algorithm, the example result: (a),(d) population before the switch, (b)(e) population at threshold without a switch, (c)(f) population regenerated from (a)(d) after a switch

Random seed	Number S	Number I	Switch threshold	Number of simulation	Spatial Regeneration Percentage
0.5	1950	5	500	100	49%
1.0	1950	5	500	100	43%
3.14	1950	5	500	100	46%

Figure 11. Average result by simulate 100 times the spatial regeneration algorithm.

is low, and equations with higher density, a tilt mechanism for moving from an approach to the other. We compare this model with existing models and present a method to determine the parameters during transitions between models. In particular, we seek to establish a link between the parameters of the mathematical model and representation of contacts and travel agents in a spatial environment. We are also interested in how to compensate the loss of information on spatial structures when moving an agent model to a mathematical model.

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