

Recursive simulation and experimental frame for multiscale simulation

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Keywords: Multiscale Modeling and Simulation, DEVS, recursive simulation, VLE

Abstract

In this paper, we present a formal and operational framework for multiscale modeling and simulation. We focus on scale transfer viewed as the coupling between two models of the same system, one at the microscopic scale and the other at the macroscopic scale. We consider that some parameters of the macroscopic model are the result of microscopic processes described in the microscopic model. The main idea is to use an "experimenter model" which performs experiments on the microscopic model during the simulation and compute these parameters in line. To formalize the experimental design of the experimenter model, we define an experimental frame of transfer based on Discret Event System Specification. As an example, we present a multi scale model in epidemiology. We specify it using our framework, and we implement and simulate it within the Virtual Laboratory Environment. Finally, we discuss some of the scale transfer issues and how we want to use the developed framework to address them.

1. INTRODUCTION

1.1. Multiscale modelling and simulation

Multiscale modeling and simulation consists in the modeling of a single source system with several models, each one considering a particular time and/or spatial resolution of the source system [4]. The need for multiscale modeling comes from issues related to the understanding of complex systems dynamics, where the microscopic levels of a particular system interact with the macroscopic levels and *vis versa*. For example, in epidemiology we are interested in understanding the role of humans and animals individual behaviors in the spread of a disease. For disease like flu, for instance, one way to study the influence of individual behaviors is to model and to simulate an epidemiological system where individuals behave and spread the disease through proximity contacts. One of the difficulties in such an Individual Based Model (IBM)

remains in the size of the system. Indeed, the number of individuals implied in a disease spread can be huge and the time and spatial resolution of behaviors (movements, contact durations, etc.) compared with the evolution of the disease within the whole population can be very different. We can argue that if we simulate all the individuals, then we have implicitly the population. Unfortunately, even if we run models on more and more powerful computers, the problem remains the same as we are prone to add more and more individuals and complex behaviors in models (the scalability issue). Furthermore, the simulation duration of IBMs must be as short as possible to use them in the never ended modeling cycle.

1.2. Related works in ecology and epidemiology

A first approach commonly used in ecology and epidemiology to consider the interactions between two scales, is to parametrize macroscopic models using microscopic models [7, 18]. In [15, 6] for example, the authors first define a model at a lower scale [15], and then build a parametric meta-model of this model which is used in a second model defined at an upper scale [6]. Such parameterization can have a less straightforward purposes like the determination of the level of details required to reproduce specific functions of an ecosystem [12]. Hence, several methods coming from other research fields are already used in ecology, such as linear regression, non-linear methods based on least square principle, or mean field approximation, which are the ones used in the papers quoted. As a closer example, in [2] an interesting hybrid epidemic model is built. The formalism changes from individual based to equation based model during a simulation depending of the size of the population to simulate which evolves along the simulation.

1.3. Recursive simulation and experimental frame for multiscale modelling

In agreement with [9], we think that complex systems modeling, and more particularly ecological modeling, needs

new methodologies and tools. In this paper we want to couple models at different scales including up and down scaling within simulations. Our work is inspired from [4] and from discussions taking place within the Virtual Laboratory Environment (VLE) development team¹. Starting from these works, we propose a general method for multiscale simulation based on recursive simulation [8] (see figure 1.3.).

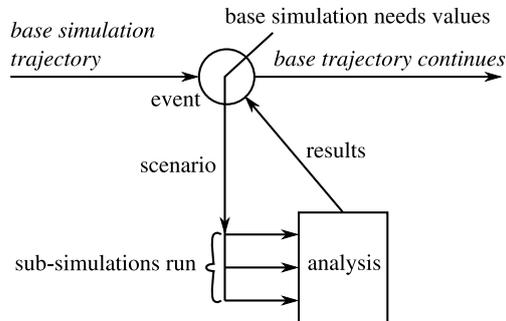


Figure 1. Recursive simulation principle (adapted from [8]). Embedded simulations (or sub-simulations) are launched while a base simulation is running. Sub-simulations can then be used to compute values useful for the base simulation.

To perform multiscale simulations, recursive simulation is not sufficient. Indeed, the dichotomy between scales not only implies to couple models with different time and space resolution. It also implies to exchange microscopic and macroscopic properties between models. To do that, we embed the concept of experimental frame [19] within the recursive simulation method. Indeed, the experimental frame defines the context of using a model (experimental design) and, at the same time, the way the model is observed and synthesized through observation variables. Then, as the recursive simulation technique realizes the control of simulators by another one, the sub-simulations can be embedded in an experimental frame.

In this paper we propose a way of using recursive simulation and experimental frame concepts for scale transfer and we illustrate the effectiveness of the method by an example in the field of epidemiology.

2. METHOD

2.1. Principle

A first step for multiscale modeling is to know how to link one scale to another. The work presented here is limited to this problem. Therefore, this method shows the coupling between two models defined at two different spatio-temporal scales. Furthermore, we restrict our study to the case where the first scale characterizes slow processes occurring at the

¹Simple models using recursive simulations are available on VLE web site: http://vle.univ-littoral.fr/fr/index.php/Simulation_recursive

macroscopic level and the second scale characterizes fast processes occurring at the microscopic level.

For the coupling of these two levels of study, we interpret the interactions between the two levels in the following way:

- The processes described at the macroscopic level determine the context for the processes described at the microscopic level.
- Some properties viewed as simple functions at the macroscopic level are the consequences of complex processes occurring at the microscopic level

Considering these interactions, we use recursive simulation to couple the models and perform the scale transfer. To do this we will use the experimental frame concept developed by Ziegler [19]. The experimental frame defines the use to be done of the model in the experimental design and at the same time the circumstances under which the source system is to be observed.

Ziegler distinguishes two different views of the experimental frame which either can be viewed as "a definition of the type of data elements that will go into the database", or as "a system that interacts with the system of interest to obtain the data of interest under specific conditions". In this last case, the frame is characterized by its implementation as a measurement system or observer, and must contain three elements: the generator, which generate input segments of the system; the acceptor, which monitors experiment to see if the desired experimental conditions are met; and the transducer, which observes and analyses the system output segments. In [16], Traore and Muzy consider that these two views are the representation of an experimental frame at two different levels of specification. Here, we consider a simulation which simulate the macroscopic models and another simulation which simulate the microscopic models. These simulations are independent (simulations times are totally disconnected) and the experimental frame is the link between them. We need to define it at different levels of specification. We will use the term "experimental frame of transfer" to refer to the frame viewed as a set of data and "experimenter model" to refer to the frame viewed as an active observer. In fact, the experimenter model will evolve in the base simulation (where the macroscopic model is simulated) and maintain the link between the macroscopic level and the microscopic level by triggering simulations of the microscopic model within the experimental frame of transfer and update some values of the macroscopic model (see figure 2).

2.2. The experimental frame of transfer and the experimenter model

Traore and Muzy, in [16], propose a formal definition build from Zeigler's description of an experimental frame viewed

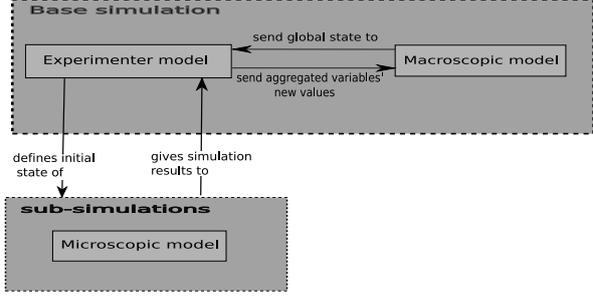


Figure 2. Recursive simulation for scale-transfer

as an observer. Furthermore, they propose several levels of specification for this experimental frame. In order to explain how we use experimental frame concept for scale transfer, we will adapt the definitions given in [16] and explain, for each specification level the role it has in our work.

The reason why we must modify the frames' definition proposed by Traore and Muzy is that they designed it to be computed in the same simulation as the model it frames, meaning that in Traore and Muzy, frame "experimenters" and model simulators are indistinguishable from superior coordinator that manages the simulation. For that reason, they share the same simulation time and time base. In our work, the experimenter model and the microscopic model have to be simulated in different simulations managed by different coordinators. In practice the experimenter model must be included in the base simulation because some variables of the macroscopic model have to be evaluated at run time. As an answer to this evaluation, sub-simulations can be triggered to feed the base simulation with new values. Hence, two different time base are necessary (see figures 1.3. and 3).

The lowest level of specification of the experimental frame of transfer (which corresponds to "frame Interface" in [16]), is defined as a structure: $\langle T_1, T_2, I_M, I_E, O_M, O_E \rangle$ where: T_1 and T_2 are time bases; I_M and O_M are respectively the sets of input and output variables of the model; I_E and O_E are respectively the sets of input and output variables of the experimental frame. Here, the elements of this structure have specific meanings. T_1 and T_2 are respectively the microscopic and macroscopic simulations' time bases. The I_E set is the context given by the macroscopic model. The I_M set is the list of initial conditions of the microscopic model. The O_M set is the list of outputs of the microscopic model for these conditions. Finally, the O_E set is the list of macroscopic level aggregated variables representative of microscopic behaviours.

At an upper level of specification, we still are very close from the "frame behaviour" proposed by Traore and Muzy. We define the experimental frame of transfer as the structure: $\langle T_1, T_2, I_M, I_E, O_M, O_E, \Omega_E, \Omega_M, \Omega_C, SU \rangle$ where $T_1, T_2, I_M, I_E, O_M, O_E$ are the same as defined earlier, $\Omega_E \subset T_2 \times I_E$ is the set of Timed possible inputs for the experimen-

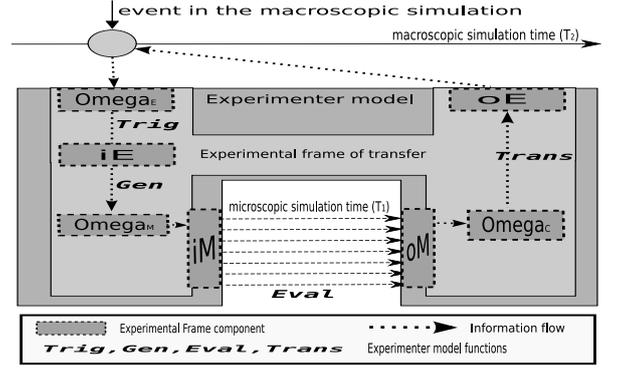


Figure 3. Management of recursive simulations by the experimenter model through the experimental frame of transfer. The experimental frame of transfer (light gray) is embedded in the experimenter model (dark gray)

tal frame of transfer, $\Omega_M \subset T_1 \times I_M \times \mathfrak{X}$ is the set of triplets: $i_M \in I_M$ the initial conditions, $t \in T_1$ the time segment to simulate ($[initial_time, simulation_end_duration]$), and $n \in \mathfrak{X}$ the number of replicas of the same experiment. $\Omega_C \subset T \times O_M$ is the set of pairs time segments over the cross-product of O_M variables, telling when and what to observe during the sub-simulations, and $SU \subset T_1 \times I_M \times O_M$ is the summary mapping of sub-simulations results.

Finally, the experimenter model, which corresponds to the highest level of specification of the experimental frame of transfer, is very different from the "frame system" described in Traore and Muzy and is defined as a particular DEVS model. This DEVS model is specified by a *parallel DEVS* model as follows: $\langle T, X, Y, S, \delta_{ext}, \delta_{int}, \delta_{con}, \lambda, ta \rangle$ (Zeigler [19]) and implements the experimental frame of transfer. T corresponds to the macroscopic simulation time base T_2 , X corresponds to the frame inputs set I_E and Y to the frame outputs set O_E . Then the realisation of the experimental design is situated in the transition functions δ_{ext} and δ_{int} . They are composed of four functions *Trig*, *Gen*, *Eval* and *Trans* which are used within the experimental frame of transfer structure (see figure 3) and defined as follows:

- *Trig* : $I_E^2 \times T_2 \rightarrow \{true, false\}$ is the trigger condition function where we can test if sub-simulations are needed, knowing the new value of the macroscopic state, the value at the last estimation, and time spent between both
- *Gen* : $I_E \rightarrow \Omega_M$ is the generator function which generate the microscopic initial states from the macroscopic context
- *Eval* : $\Omega_M \rightarrow SU$ is the evaluation function that computes $\omega_C \in \Omega_C$ from any $\omega_M \in \Omega_M$ and computes $su \in SU$.

- $Trans : SU \rightarrow O_E$ is the transducer function which uses simulation results to calculate the value of the macroscopic variable to update

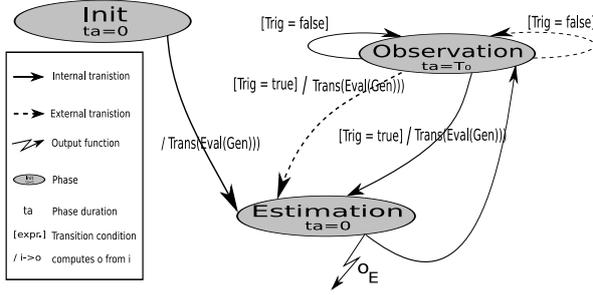


Figure 4. Experimentier model DEVS state machine: phases dynamics

The dynamics of the experimenter model is illustrated Figure 4, by a DEVS state machine diagram and formally described as follows:

- T , the time base, corresponds to the macroscopic simulation time base (T_2 in the above text)
- S , the set of sequential states,

$$S = \{(state, phase) | state \in state_set \text{ and } phase \in phase_set\}$$

with:

$$state_set = \{(i_E^{old}, i_E^{act}, o_E) | (i_E^{old}, i_E^{act}) \in I_E^2 \text{ and } o_E \in O_E\}$$

and

$$phase_set = \{INIT, OBS, EST\}$$

Where i_E^{old} and i_E^{act} are used to store respectively the macroscopic state at the last estimation and at the actual time, and the phases OBS and EST stand for observation phase and estimation phase.

- The set of admissible input events is: $X = I_E$
- The set of admissible outputs events is: $Y = O_E$
- The external transition is:

$$\delta_{ext} : I_E \times state_set \times phase_set \times T \rightarrow state_set \times phase_set$$

$\forall phase \neq OBS$

$$(i_E, state, phase, t) \mapsto (\{i_E^{old}, i_E, o_E\}, phase)$$

for $phase = OBS$

If $Trig(i_E, i_E^{old}, t) = true$

$$(i_E, state, OBS, t) \mapsto (\{i_E, i_E, Trans(Eval(Gen(i_E)))\}, EST)$$

Else

$$(i_E, state, OBS, t) \mapsto (\{i_E^{old}, i_E, o_E\}, OBS)$$

- The time advance function is:

$$ta : phase_set \rightarrow \mathfrak{R}_0^+ \cup \infty$$

$$\forall phase \neq OBS, phase \mapsto 0$$

$$OBS \mapsto T_0$$

where T_0 is the maximum period without control.

- The internal transition is:

$$\delta_{int} : state_set \times phase_set \rightarrow state_set \times phase_set$$

$$(state, INIT) \mapsto (\{i_E^{init}, i_E^{init}, Trans(Eval(Gen(i_E^{act})))\}, EST)$$

$$\forall state, (state, EST) \mapsto (state, OBS)$$

if $Trig(i_E^{old}, i_E^{act}, ta) = true$

$$(state, OBS) \mapsto (\{i_E^{act}, i_E^{act}, Trans(Eval(Gen(i_E^{act})))\}, EST)$$

else

$$(state, OBS) \mapsto (state, OBS)$$

Where i_E^{init} is the initial state of the coupled model given at macroscopic scale.

- The output function is:

$$\lambda : state_set \times phase_set \rightarrow O_E$$

$$\forall phase \neq EST, (state, phase) \mapsto \emptyset$$

$$(\{i_E, o_E\}, EST) \mapsto \{o_E\}$$

- The confluent transition is:

$$\delta_{con} = \delta_{int} \circ \delta_{ext}$$

With this formal definition of the experimenter model, we specify how recursive simulations are performed by the experimenter model using the experimental frame of transfer. In the next section, we illustrate the effectiveness of the method through an example in epidemiology.

3. APPLICATION

Our application consists in the coupling of two epidemiological models. The microscopic model is defined at the individual level and the macroscopic model is defined at the population level. We call them the IBM model (Individual Based Model) and the SIR model (Susceptible, Infectious and Recovered) respectively. Originally, the aim of this coupling is to measure the impact of different individual behaviors on the global dynamic of the population. In this work, we do not insist on such a study rather than on the method we use to achieve the modeling and simulation of the scale transfer.

3.1. Macroscopic model: SIR

The SIR model is formally described by the following system of differential equations defining the dynamics of three state's variables (equations 1, 2 and 3).

$$\frac{dS}{dt} = -\beta IS \quad (1)$$

$$\frac{dI}{dt} = \beta IS - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

Where:

- S is density of individuals susceptible to infection.
- I is the density of infectious individuals.
- R is the density of recovered (or removed).
- β is a constant parameter reflecting the combined effect of all the processes affecting the transmission rate.
- γ is the recovering rate.

The SIR model is one of the simplest model used in epidemiology. It has been widely developed and is still of a high interest of study and use in more complex forms [3]. In this model, the number of individuals is stationary. The individuals are supposed to be uniformly distributed and to move and interact within a continuous toroidal space. Let c and t be respectively arbitrary surface unit and time unit. Then the unit of S , I and R is *individual.c⁻¹*, the unit of β is *individual⁻¹.c.t⁻¹*, and the unit of γ is t^{-1} .

3.2. Microscopic model: IBM

The IBM is specified within the DEVS formalism [19] and associated extension as proposed by [5]. It is composed of:

- An explicit space (a lattice of cells) formalized as a Cell-DEVS [17]

Table 1. scale transfer summary

| properties | IBM scale | SIR model scale |
|--------------------|-----------|---------------------------|
| time unit | tu_1 | tu_2 |
| simulated duration | t_1 | t_2 (with $t_1 < t_2$) |
| space unit | c | c |
| space size | a | <i>undefined</i> |
| population density | d | d |

- A set of individuals each one formalized as an atomic DEVS model
- A model of individual movements on the space formalized as a DS-DEVS [1].

We invite the reeder to refer to the literature we cite for the definition of space and movement. Due to a lack of space we will not present here the formal definition of individuals DEVS models but we can give its main features. The state of an individual model contains an "infection state" (S, I or R), an infectious period (corresponding to the time spent in the infectious state "I", before switching to "R") and an individual time step. Its dynamics consists in moving at each time step and to change its infectious state. Firstly, the infectious state is switched from "S" to "I" (with a fixed probability "infection probability") if it is on the same cell as an individual of state "I". Then, it is switched from "I" to "R" if it has been infected since the duration of its infectious period. The initial conditions are defined as the number of susceptible, infected and recovered individuals. At initialisation, the individuals are randomly distributed over the space.

3.3. Coupling macro and micro levels

In order to illustrate the method, we choose a simple, but expressive enough, scale transfer. To perform the scale transfer, we consider the parameter β of the SIR model as a variable computed at run time with the IBM. To do that, the IBM is simulated according to an experimental frame described in the experimenter model (see section 2.). The IBM has the same density $d = \frac{n \text{ individuals}}{\text{surface}}$ as the SIR model but the space considered in the SIR model is not represented when the IBM is simulated on an area a expressed in the unit cell ("c"). Different time units are used for both models. Table 1 summarizes the scale transfer to perform.

We give here the complete specification of the experimenter model which perform this computation.

- $I_E = \mathfrak{R}_0^{+3}$, corresponding to values of the S, I and R state variables of the SIR model, expressed in *individuals.c⁻¹*
- $T_1 = \mathfrak{R}_0^+ \cup \infty$, the IBM time base expressed in tu_1
- $T_2 = \mathfrak{R}_0^+ \cup \infty$, the SIR model time base expressed in tu_2

- $O_E = \mathfrak{R}_*^+$: $o_E \in O_E$ corresponds to the value of the variable β of the SIR model, expressed in $individuals^{-1} \cdot tu_2^{-1}$
- $I_M = \mathfrak{R}_0^{+3}$: $i_M \in I_M$ corresponds to initial values of the S, I and R variables of the IBM, expressed in *individuals*
- $O_M = \mathfrak{R}_0^{+3}$: $o_M \in O_M$ corresponds to values of the S, I and R state variables of the IBM, expressed in *individuals*
- $\Omega_M = \{([0, t_1], IBM_init, N) | IBM_init \in I_M \text{ and } N \in \mathfrak{N}\}$: $\omega_M \in \Omega_M$ corresponds to N simulations of same duration $t_1 tu_1$, with the same initial conditions IBM_init
- $\Omega_C = \{(t, IBM_state) | t \in [0, t_1] \text{ and } IBM_state \in O_M\}$
- $SU = \{(t, i_M, o_M) | t \in [0, t_1], i_M \in I_M \text{ and } o_M \in O_M\}$
- The *Trig*, *Gen*, *Eval* and the *Trans* functions are defined as follows:

$$Trig : I_E^2 \times T \rightarrow true, false$$

$$\{(s^{old}, s^{act}) | s^{old} - s^{act} > \Delta S_{max}\} \mapsto true$$

$$\{(s^{old}, s^{act}) | s^{old} - s^{act} \leq \Delta S_{max}\} \mapsto false$$

$$Gen : I_E \rightarrow \Omega_M$$

$$(s, i, r) \mapsto ([0, t_1], s \times a, i \times a, r \times a, N)$$

$$Eval : \Omega_M \rightarrow SU$$

$$\omega_M \mapsto sim_res$$

$$Trans : SU \rightarrow O_E$$

$$su \in SU \mapsto -\frac{tu_1}{tu_2} \times \frac{a}{N} \sum_{k=1}^{k=N} \frac{1}{\bar{i}_k \times \bar{s}_k} \times \frac{\Delta s_k}{t_1}$$

Where:

- *sim_res* are the simulation results obtained from implemented DEVS abstract simulators (see subsection 3.4.) and organized as summary results.
- \bar{x}_k stands for the mean number of individuals in state x over the duration of the sub-simulation $([0, t_1])$.
- Δs_k stands for the difference of the number of susceptible individuals between the beginning and the end of the sub-simulation k

- s^{old} and s^{act} correspond to values stored in the experimenter model state (see section 2.) and stand respectively for the density of susceptible individuals in the base simulation, at the last estimation time and at the actual time
- The other notations are those described above in the experimenter model formal definition and in the scale transfer summary table (see table 1)

In the two following sections we present our implementation of this model and then some simulations of the coupled model showing the values of the parameters we used.

3.4. Implementation

In this work, we have implemented all our models in a DEVS framework. To do so we implemented the SIR integrator as a Quantized State System [11] integrator. The experimenter model is a classical DEVS model. The complete implementation is realized within the Virtual Laboratory Environment (VLE) [13], a DEVS based set of tools and application programming interfaces for multi-modeling and simulation of complex systems. VLE proposes an XML representation for experimental frames structures which can be embedded in the state of a model. Moreover, issue of using recursive simulation for scale transfer were addressed within the VLE development team. Thus, the VLE environment allows recursive simulations, meaning that a DEVS simulator can run stand alone simulations with the VLE kernel. Thus, the experimenter model is a DEVS atomic model with two particularities. Firstly, it contains in its state the experimental frame of transfer coded with the VLE XML library. Secondly, it is able to launch another VLE simulation and to get back the associated simulation results.

Staying in a "DEVS world" and using VLE facilitate the implementation of our models. One very important feature of VLE is the possibility to distribute simulations defined in an experimental frame on several processors or computers. It is of the most importance in our case, because several simulations of the microscopic model are required to perform the experimental frame of transfer.

3.5. Simulation

We perform two simulations with two different individual behaviours for the IBM and observed the consequences at the macroscopic level (the SIR model).

We use the same set of parameters for both simulations except for the time step of individuals in the IBM that controls individuals' speed. Table 2 presents the values we used for all the parameters.

The simulation's curves of the two graphics of figure 5 are classical for SIR models. At the beginning of the simulation, there are many susceptible individuals that can be infected

Table 2. Parameters of models

| parameter | value ² |
|--------------------------|--|
| tu_1 | $1 t$ |
| t_1 | $20 t$ |
| a | $80 \times 80 c$ |
| infection probability | 0.5 |
| individual's time step | uniform distribution between $[0.8, 1] t$ (sim 1) between $[0.5, 0.7] t$ (sim 2) |
| mean infectious period | $150 t$ |
| tu_2 | $5 t$ |
| t_2 | $150 t$ |
| γ | $0.0033 t^{-1}$ |
| d | $0.015625 \text{ individuals} \cdot c^{-1}$ |
| nb recursive simulations | 40 |
| ΔS_{max} | $15 \text{ individuals} \cdot c^{-1}$ |
| T_0 | $5 t$ |

by infectious individuals. Hence, the number of infected individuals rises at the same time as the number of susceptible individuals decreases. Then, at a point the number of susceptible individuals to infect becoming too small, the recovering becomes higher than the force of infection and the number of infectious individuals start decreasing. The number of recovered individuals always rises while the infected individuals are recovering.

The interest of taking into account microscopic processes in similar models has already been discussed in the literature ([14],[18],[10]) and is not the question we want to address here. We rather want to illustrate that the dynamics of the coupled model can be parametrized at a microscopic scale. Therefore, the curves of the two charts have similar shapes and one can notice easily that if one changes the value of a parameter in the microscopic model (the speed of the individuals), the behaviour of the coupled model changes. In the simulation with slower individuals (top chart) the whole population has been infected after 25 time units (number of susceptible individuals reaches 0), and in the simulation with faster individuals (bottom chart), the whole population has been infected after only 15 time units.

4. DISCUSSION

In our application, we use a scale invariance (the population density) to link processes at lower scale with processes at upper scale. Anyway, several questions raise here. First, the hypothesis we make choosing this scale invariance can be strong. For instance in our example, it is a strong hypothesis to consider that the density is the same in any place of the macroscopic model. However, it is the hypothesis that allows us computing the value of β with the IBM. Secondly, up-scaling and down-scaling issues are not resolved.

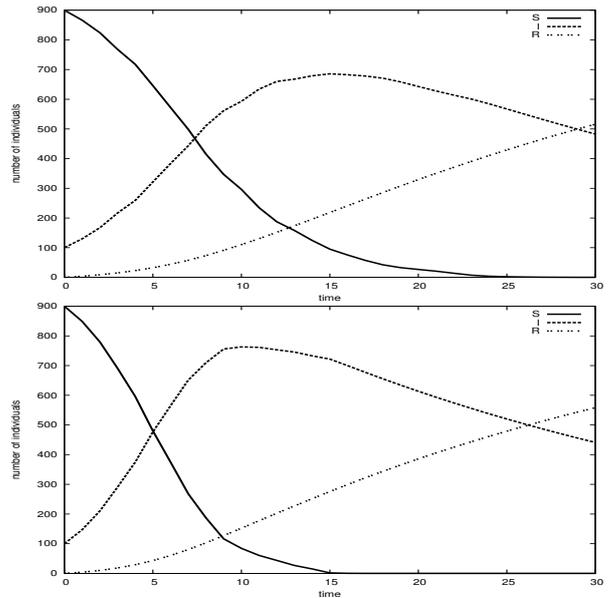


Figure 5. Simulation results. The charts present the evolution of the S, I and R, variables of the macroscopic model in the coupled simulations. The top chart shows the results of simulation 1 (with slower individuals) and the bottom chart shows the results of simulation 2 (with faster individuals).

The transfer from macro to micro seems to be the most problematic. We can consider it starting from our example. An epidemic starts from one place and then spreads over the whole space. Hence, the more it spreads, the more the infectious individuals are surrounded by other infectious individuals and the less they will individually infect susceptible individuals. Therefore, the IBM property of spatial autocorrelation is important. Unfortunately, all spatial information is lost during the transfer to the SIR model which does not have any space representation. For that reason we have to randomly distribute the individuals over the space at each simulation of the IBM. It means that at the level of the coupled model we lose the spatial autocorrelation property, which introduces a bias in our simulation. More generally, down-scaling asks to generate a distributed initial state at the microscopic scale from aggregated variables. We think that for many models, an intermediary statistical model can be necessary to capture this distribution and predict its evolution. In our application, this model could be for instance a statistic on the spatial distribution of the infected individuals over the space.

The transfer from micro to macro seems to be easier. On one hand, it is important and sensitive to choose the right observations and the right expressions to be used by the transducer to compute the new aggregated variables. But on the other hand we can use all previous work already done in sam-

²c and t are respectively surface and time arbitrary units ("c" corresponds to the surface of one cell of the IBM space).

pling methods and parameter estimation in our field of interest. For our application for instance, we use a simple method to compute β because we did not want to address epidemiological questions here, but methods have already been developed and discussed to link population variables (such as β and γ) to some indicators measured in population samples, such as the mean age of infection[3, 10].

Another issue in up-scaling is to evaluate the sub-simulations' durations. The aim of up scaling is to capture the behaviour of the system in a given context, hence it is necessary: either to study the microscopic model to know *a priori* the duration of the sub-simulations (solution adopted here), or to add a control function in the experimenter model, which would limit sub-simulations' duration according to system's evolution. The coupling coherence is then insured by both the trigger function which tells when to compute aggregated variables, and this control function which tells when the observations at the microscopic scale are valuable or not.

Thus our future work in scale transfer, apart from up-scaling and down-scaling issues, will deal with estimating the sensitivity of the experimenter model definition.

5. CONCLUSION

The aim of this paper was to explore the original idea of using recursive simulation for scale transfer in multiscale modeling. To do that, we have built a formal framework for recursive simulation, we have shown how it can be used for scale transfer, and how to implement it in an example. The objective was not to enrich scale transfer theory, but to develop an operational framework allowing to build multi-scale models.

The formal framework we propose for recursive simulation comes from previous work in modeling and simulation, mainly the Experimental Frame concept and Discrete Event System Specification formalism. Our researches on this subject are not limited to the question of scale transfer but consider more generally the use of recursive simulation for other issues such as anticipation or optimisation for instance. Using this framework for scale transfer is a first step and still raises a lot of questions as mentioned in our "discussion" part. However, our definition of an "experimenter model" is destined to be independent of scale transfer issues.

REFERENCES

- [1] F. J. Barros. Dynamic structure discrete event system specification: Formalism, abstract simulators and applications. *Winter Simulation*, 13(1):35–46, 1996.
- [2] G. V. Bobashev, D. M. Goedecke, F. Yu, and J. M. Epstein. A hybrid epidemic model: combining the advantages of agent-based and equation-based approaches. In *WSC '07: Proceedings of the 39th conference on Winter simulation*, pages 1532–1537, Piscataway, NJ, USA, 2007. IEEE Press.
- [3] M. Choisy, J.-F. Guegan, and P. Rohani. *Encyclopedia of Infectious Diseases: Modern Methodologies*, chapter Mathematical Modeling of Infectious Diseases Dynamics. John Wiley and Sons Inc, 2007.
- [4] R. Duboz, E. Ramat, and P. Preux. Scale transfer modelling: Using emergent computation for coupling an ordinary differential equation system with a reactive agent model. *Systems Analysis Modelling Simulation*, 43(6):793–814, june 2003.
- [5] R. Duboz, D. Versmisse, G. Quesnel, A. Muzzy, and E. Ramat. Specification of dynamic structure discrete event multiagent systems. In *Agent Directed Simulation (Spring Simulation Multiconference)*, Huntsville, Alabama, USA, April 2-6 2006.
- [6] B. Durand, M. A. Dubois, P. Sabatier, D. Calavas, C. Ducrot, and A. V. de Wielle. Multiscale modelling of scrapie epidemiology: Ii. geographical level: hierarchical transfer of the herd model to the regional disease spread. *Ecological Modelling*, 179(4):515 – 531, 2004.
- [7] P. S. Gilioli Gianni. Use of individual-based models for population parameters estimation. *Ecological Modelling*, 200:109–118, 2007.
- [8] J. B. Gilmer and F. J. Sullivan. Issues in event analysis for recursive simulation. In M. E. Kuhl, N. M. Steiger, F. B. Armstrong, and J. A. J. eds., editors, *Proceedings of the 2005 Winter Simulation Conference*, pages 1234–1241. The Society for Computer Simulation, july 2005.
- [9] A. A. Graig. A methodology for developing simulation models of complex systems. *Ecological Modelling*, 202:385–396, 2007.
- [10] M. J. Keeling and B. T. Grenfell. Individual-based perspectives on r_0 . *Journal of Theoretical Biology*, 203(1):51 – 61, 2000.
- [11] E. Kofman and S. Junco. Quantized state systems. a DEVS approach for continuous systems simulation. In *Transactions of the Society for Computer Simulation International*, volume 18, pages 123–132. Society for Computer Simulation International San Diego, CA, USA, 2001.
- [12] F. A. Picard Nicolas. Aggregation of an individual-based space-dependent model of forest dynamics into distribution-based and space independent models. *Ecological Modelling*, 145:69–84, 2001.

- [13] G. Quesnel, R. Duboz, and E. Ramat. The Virtual Laboratory Environment – An operational framework for multi-modelling, simulation and analysis of complex dynamical systems. *Simulation Modelling Practice and Theory*, 17:641–653, April 2009.
- [14] H. Rahmandad and J. Sterman. Heterogeneity and Network Structure in the Dynamics of Diffusion: Comparing Agent-Based and Differential Equation Models. *MANAGEMENT SCIENCE*, 54(5):998–1014, 2008.
- [15] P. Sabatier, B. Durand, M. Dubois, C. Ducrot, D. Calavas, and A. V. de Wielle. Multiscale modelling of scrapie epidemiology: I. herd level: a discrete model of disease transmission in a sheep flock. *Ecological Modelling*, 180(2-3):233 – 252, 2004.
- [16] M. A. Traore K. Mamadou. Capturing the dual relationship between simulation models and their context. *Simulation Modelling Practice and Theory*, 14:126–142, 2006.
- [17] G. A. Wainer and N. Giambiasi. Application of the Cell-DEVS paradigm for cell spaces modelling and simulation. In *Simulation*, volume 76, pages 22–39, 2001.
- [18] J. W. Waniewski Jacek. Individual based modeling and parameter estimation for lotka-volterra system. *Mathematical Biosciences*, 157:23–36, 1999.
- [19] B. P. Zeigler, T. G. Kim, and H. Praehofer. *Theory of modeling and simulation: Integrating Discrete Event and Continuous Complex Dynamic Systems*. Academic Press, 2000.