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Computer Simulation Models of Infectious Diseases: Advantages and Limits

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ABSTRACT

Several researches based on computer science techniques (Artificial Intelligence (AI), Cellular Automata (AC), Agent-based Systems (ABS), etc.) and mathematics (mainly Partial Differential Equations (PDE)) have been carried out to simulate infectious or non-infectious diseases. Results from these researches are very important for better disease management (disease control, prediction, prevention, diagnosis and treatment). Through this article, a study of some existing works based on computer techniques for simulating of infectious diseases is presented. The objective is to carry out a critical analysis of these models there by identifying their advantages and limitations. The results of the adaptation of an already existing infectious diseases simulation model confirm the existence of certain limits. The main limitation is the easy use of simulation tools or systems by the actors. These limits constitute an obstacle to the digitalization of medical data related to infectious diseases and patients. Taking these limits into account will make it possible to improve, in the future, the design of infectious disease simulation systems by integrating other functionalities. This will lead to massive use of decision support tools in the field of health and thus contribute to better management of infectious diseases in Africa for the sustainable development of its States.

INTRODUCTION

Computer simulation tools can be used to improve the performance of diseases management system. Several actors are involved in this care task. For example, health decision-makers and investors need to assess the impact of policies to combat diseases in general; health workers, for their part, can use the services offered by computer simulation systems to improve disease management in terms of diagnosis and treatment. Thus, the ideal would be, for the designers of disease simulation models, to take into account the majority of user needs while guaranteeing a certain level of easy accessibility to their systems.

In fact, several researchers, mostly in mathematics and computer science, are increasingly interested in the development of simulation models for diseases, especially infectious ones. In September 2010, Rosemary Thomas published a state of the art of agent-based systems (ABS) that simulate the prediction and prevention of infectious diseases [1]. According to the author, multi-agent system became popular in healthcare because it could mimic real-life scenarios and simulate an urban or primitive society. Agent-based tools, when combined with visualization tools, open up a new way to analyze and monitor a disease outbreak. The paper in question presents a review of past and ongoing research on multi-agent systems for the prediction and prevention of infectious diseases.

In their article, Smith *et al* argue that much of the extensive research regarding malaria transmission has been supported by mathematical modeling for over a century. However, modelers are increasingly adopting agent-based approaches. They model hosts, vectors and/or their interactions at the individual level. The authors review 90 articles (published between 1998 and May 2018) that characterize agent-based models (ABM) relevant to malaria transmission [2].

Furthermore, the objective of disease simulation systems (in general) is to predict (in the short, medium or long term) the behavior of concerned diseases. This is the case of works presented in [3], [4], [5], [6], etc. Other systems are designed as medical decision support (diagnostic) services. Works presented in [7], [8] and [9] are illustrative.

The main objective of this document is to talk about computer techniques for simulating infectious diseases, through the analysis of existing work according to the following aspects:

- Their ability to predict infectious diseases;
- Their accessibility to users (ease of use);
- The possibility of using them to simulate the same disease (for which they were designed) in a context other than that used by their authors. More precisely, using data other than those of the authors. It should be noted that simulation systems are very often applied on data;
- The possibility of using them to simulate other infectious diseases;
- Their ability to offer a diagnostic and medical treatment assistance service.

A study of existing work is presented in section 2. In section 3, a summary table of the study of this work is presented and discussed. Through section 3, an existing model is presented (in more or less detail). The adaptation of the model as well as the results obtained and the discussions are presented in section 4. A conclusion ends this document (section 5).

2. SOME SIMULATION WORK ON INFECTIOUS DISEASES USING VARIOUS COMPUTER TECHNIQUES

Cissé [3] performed an agent-based modeling (as part of his thesis work) of a mathematical system (based on PDEs) developed by Gao et al [10]. The system simulates the spatial dynamics of schistosomiasis (bilharzia) transmission in Senegal. The agents are humans and molluscs. The latter are the intermediate hosts of parasitic worms (schistosoma) with their phase evolutions (miracidiums and cercariae). They are divided into the following groups: I_1 (group of infected individuals), S_1 (group of susceptible individuals), I_2 (group of infected molluscs), S_2 (group of susceptible molluscs), M (group of miracidiums), P (cercariae group). These agents are placed in an environment in which they are influenced by parameters such as: the birth rate of humans, the birth rate of molluscs, the elimination rate of molluscs, the elimination rate of cercariae, the treatment rate of infected humans, the quantity of eggs accompanying the feces of an infected individual, the rate of miracidium released by an egg after hatching, the rate of cercariae released by an infected mollusc, the rate of humans natural mortality (which does not depend on disease),

the natural mortality rates (which do not depend on treatment) of molluscs, miracidia and cercariae, the mortality rate (from disease) of infected individuals and infected molluscs, the probability of transmission when a mollusc comes into contact with a miracidium. The disease control policies taken into account are: the elimination of molluscs and cercariae as well as the treatment of infected individuals (humans). According to the results, the most effective policy was the elimination of molluscs. The model performs a long-term simulation of the disease (100 days for bilharzia) but does not take into account diagnostic assistance and does not have a user interface. Based on a model designed from PDEs, the adaptation of this system to other data (to simulate the same disease in another context) and to other infectious diseases requires a reformulation of the model.

Espindola et al [11] presented a model based on ABS which simulates the spread of tuberculosis as well as the resistant nature of the disease due to the use of antibiotics by patients. The system works according to the algorithm described below. In [12], Espindola et al modified the algorithm (presented in [11]) to simulate the spread of tuberculosis in a context where individuals undergoing treatment may be infected by drug-susceptible or drug-resistant strains. The L_S and L_R groups (from the algorithm below) represent individuals who carry the pathogen but are asymptomatic. The results of the model presented in [12] (an annual simulation of the disease) were satisfactory because they were close to the real data. As for the basic model (the one presented in [11]), the results indicated that the number of infected individuals tends towards zero (0) after a simulation over a period of 300 years. In addition to the lack of aid in the diagnosis of tuberculosis, their flaws remain the fact that they lack a reusable interface and that they were only designed for the simulation of tuberculosis.

Algorithm gave by Espindonla et al in [11]

- either an individual $I \in \{X, L_S, L_R, T_S, T_R\}$ with X: the group of susceptible people; L_s *and* L_R: the groups of latent and T_s *and* T_R : the groups of infected people (T_S for those who carry the type of bacteria sensitive to antibiotics, and T_R, for those who have the type of bacteria resistant to antibiotics).

- an individual from group X can be infected by individuals from groups T_S,T_R.

- individuals from L_S, L_R groups carry the pathogen but are not infectious.

- a proportion n_L of individuals from L_S, L_R is randomly chosen to receive treatment by chemoprophylaxis. During treatment, the chosen individuals can: either heal with probability $\boldsymbol{\sigma}$ and thus become susceptible (join group X); either leave the latent groups (L_S, L_R) for the infected groups (T_S,T_R) with probability υ; or remain latent.

- latent individuals who have not received chemoprophylaxis treatment continue to remain in their state with probability $1\text{-}\upsilon$ or cease to be latent to become infectious with probability υ.

- a proportion n_T of individuals from T_S,T_R is randomly chosen to receive treatment with antibiotics. During treatment, chosen individuals can either heal or finish treatment without healing.

All individuals are in an environment and are influenced by the following parameters: natural mortality rate, probability of death due to tuberculosis, probability of developing tuberculosis, probability of disease progression in latent individuals, etc.

In her thesis, Dalila [4] presented an approach based on decision trees, association rules and data segmentation to propose two models which, each, simulate an infectious disease. The author presented in [13] a first model which simulates the dynamics of tuberculosis in Algeria. The model in question is a Bio-PEPA implementation, a language for modeling and analysis of biochemical systems (see [14]) of the Espindola et al [11] model presented in the previous paragraph. The model, therefore, simulates tuberculosis. She considered that the results of the implementation are compatible with those of the basic model (that of Espindola et al [11]). As for her second proposed model, it concerns the simulation of mumps in France [4]. The model, also implemented under Bio-PEPA, is based on a compartment system of seven groups of individuals who are:

- the group of naturally susceptible individuals, named S_1;

- the group of individuals (children aged 9 to 12 months) having received the first dose of vaccination against the disease (MMR1: first dose of vaccine against measles, mumps and rubella in France), named V_1;

- the group of individuals (children aged 12 to 15 months) who received the second dose of vaccination against the disease (MMR2), named V_2;

- the group of individuals who have lost their immunity after being vaccinated. They have, therefore, become susceptible again. This group is named S_2;

- the group of latent individuals (named E);

- the infected group, named I;

- and the group of recovered individuals who acquired immunity after being infected, named R.

The interaction between these groups is a function whose parameters are: population growth rate, immigration rate, vaccination rate, transmission rate, susceptibility, recovery, latency and immunity loss rates. The results obtained confirmed the persistence of the epidemic (mumps) in France. However, it should be noted that the two models (that of tuberculosis and that of mumps) do not have a reuse interface. Moreover, they are not applicable to other infectious diseases and do not offer a support service for diagnostic. The proof is simply the fact that the author was forced to propose two models, in the same thesis work, for the simulation of two different infectious diseases, although the first (which concerns tuberculosis) is an adaptation of another tuberculosis simulation model. The latter does not carry out a long-term simulation because tuberculosis can be modeled over more than a year.

In [5], Miralles-Pechuán et al implemented an epidemiological model using two approaches (one based on Deep Q-Learning (DQL) and the other based on Genetic Algorithms (GA)) to simulate the evolution of COVID-19 virus and optimize the best sequences of actions that governments can take. In other words, it was a question of evaluating the impact of the application (or non-application) of barrier measures (isolation, social distancing, confinement, etc.) on the spread of the disease and the economy. The model in question updates the groups in the following way:

$$S_i = S_{i-1} - \delta_i \beta S_{i-1} I_{i-1}$$

$$E_i = E_{i-1} + (\delta_i \beta S_{i-1} I_{i-1} - \alpha E_{i-1})$$

$$I_i = I_{i-1} + (\alpha E i_{-1} - \gamma I_{i-1})$$

$$R_i = R_{i-1} + \gamma I_{i-1}$$

With:

i: index updated. If the total number of days over which the simulation is carried out is N, then $i \in [0..N]$; S: the group of susceptible people; E: the group of exposed people; I: the group of infected people; R: the group of recovered people; α: the inverse of the incubation period on average. For example if the latter is 12, then $\alpha = 1/12$; β: the contact rate which allows the disease to be transmitted; γ: the inverse of the time (in days) for an infected person to become infectious in turn; $\delta_i \in \{0,1\}$: the weight associated with the contact rate β in the case of an action $A_i \in \{1,...,M\}$ which is the possible confinement level.

The model as presented does not have a reuse interface but can simulate the disease (COVID-19) in other contexts (with other data). The system cannot simulate other infectious diseases and does not offer diagnostic support services. In the context of COVID-19, the model performs a medium and long term simulation.

Savi et al [6] illustrated the complexity of malaria transmission and its persistence in a case study in Accra, Ghana through a Causal Loop Diagram (CLD). The authors showed that beyond simple biological and environmental processes, people's behavior plays an important role in the transmission and persistence of malaria. The authors identified a list of determinants explaining the transmission and persistence of malaria and obtained a cause and effect map based on the interactions between the determinants. A cause in the CLD represents a determinant from which the arrow emerges, and the effect is a determinant which receives the arrow. The positive or negative sign of the arrow explains the type of association, that is to say that a cause *A* implying an effect *B* with a positive sign must be read: The increase in *A* implies an increase in *B*. Conversely, *A* implying *B* with negative sign must be read: An increase in *A* leads to a decrease in *B*. According to the results, the model involves 56 interactions between 45 determinants. It shows three sub patterns that a reinforcement loop triggers, namely:

- transmission related to urbanization and resistance to insecticides acquired by anopheles: Deficient urban planning, inadequate housing conditions, poor management of waste and

wastewater, digging of wells for urban and peri-urban agriculture as well as precipitation leads to the proliferation of anopheles breeding sites;

- the infectious behavior of humans: At individual and family levels, awareness of the risk of malaria leads to the reduction of nocturnal activities, the use of protection and prevention measures against mosquito bites (the use of anti-insect nets on doors and windows, impregnated mosquito nets). The more these measures are accepted and used, the lower the infection;

- and the effectiveness of care and resistance to plasmodium: Malaria carriers can be asymptomatic. Due to the fact that the Ghanaian health system is often unable to detect them, they often remain untreated and thus continue to spread the disease. Knowledge of malaria symptoms and sufficient family income lead to more visits to health centers. If health workers are well trained and patients comply with prescribed treatment, the reinforcement loop will work and trust in the health system will increase. Otherwise, the use of inappropriate medications as well as self-medication increase the resistance of the plasmodium parasite (to preventive and curative medications).

The model is applicable to other data although it does not have a reuse platform. The model does not aid in medical diagnosis and cannot simulate other infectious diseases other than malaria.

Sharma et al comparatively used two data mining classification algorithms (Support Vector Machine (SVM) and Artificial Neural Network (ANN)) for malaria prediction using a dataset, from 2011 to 2014, from 35 districts of the state of Maharashtra in India. Samples were collected (a total of 1680) for this study through the National Vector-Borne Disease Control Program and the Indian Meteorological Department. Support Vector Machine is a supervised learning model with associated learning algorithms. Given a set of training examples, each marked to belong to one of two categories, an SVM algorithm constructs a model that classifies new cases into one category or the other. The model uses parameters like average monthly precipitation, temperature, humidity, total number of positive cases, total number of plasmodium falciparum. Without having explicitly given, through their paper, the algorithms, the authors recalled a formal description of the techniques applied (SVM and ANN). The authors used a classification according to the following input parameters: average maximum temperature (of each health district), average minimum temperature, average precipitation, average humidity, number of

positive cases, number of cases per month. The results obtained allowed the authors to note that the performance of the model developed using SVM is more accurate than that of ANN because the SVM model can predict malaria epidemic 15 to 20 days in advance. A test of accuracy (of SVM and ANN) against the output field "Epidemic" with a YES or NO value was provided. The SVM-based model produced a mean square error of 0.12 and an overall performance of 0.89, while the ANN-based model produced a root mean square error of 0.47 and an overall performance of 0.77. The basic simulation system being Weka, it is up to the user to develop the reuse interface and integrate a diagnostic support service if necessary and this requires advanced skills. The models of Sharma et al [15] cannot be applied to other data and other diseases.

Ziyadi [16] (in his doctoral thesis) used the Object-oriented concept to implement a multi-agent system which materializes the computer modeling of a mathematical system designed by the same author with the aim of simulating sheep scrapie. The author considered the agents Sheep (who died) and Herd which he placed in an environment called MyModel. The characteristics of the Sheep agent are: sex, genotype, date of birth, date of death, scrapie diagnosis h (equal to 0 if scrapie is not detected in the animal, 1 otherwise), the force of infection (the power of contamination of the herd by an infected individual at a specific time) and the incubation period (the date of death due to scrapie minus the date of contamination). The Herd class is a set of sheep (Sheep agents) to which the dynamics of disease transmission is applied, which boils down to the following algorithm:

- each iteration of the execution corresponds to the simulation of the behavior of the disease for a time Δt;
- initialize the parameters (herd and disease characteristics) and $t=\Delta t$;
- For a total duration $N\Delta t$ do $N-1$ times:
    - $t = t + \Delta t$;
    - for all living animals, make age $a = a + \Delta t$;

- for all infected animals, change the force of infection from $\theta \; to \; \theta e^{c_g \Delta t}$ (this means that the longer the incubation period, the more contagious the animal becomes). c_g is the growth rate of an animal's infection strength based on its genotype;
- apply the parameters to live and uninfected animals (to determine dead, newly infected);
- update the values;
- show the results.

According to the results, animals less than one year old are the least exposed to the disease. One observes a small variation in the incubation period depending on the individuals and their genetic heritage (the genotype). The system has a graphical interface that allows the disease to be simulated using other data. However, it cannot simulate other infectious diseases in animals and does not offer diagnostic support services. The simulation can be carried out over a long period of time because it is up to the user to determine the overall time.

In [17], the authors made a comparative study (before and after the confinement between India and the United States) of the behavior of COVID-19 using machine learning methods such as the algorithm of linear regression and the XGBoost algorithm (see [18] and [19]). Sowmya et al [17] simulated the cases such as the numbers of infected people, people who died due to the virus and people who recovered. They represented by R_0 the average number of people transmitting the disease to people who were not previously affected. According to the authors, if $R_0 < 1$, there is no risk of infection spreading. If $R_0 = 1$, then the existing infection will spread to a new person, but it will not be an epidemic or pandemic. If $R_0 > 1$, the infection affects more than one person and there will be an outbreak leading to a pandemic. It is found that even though USA has less population as compared to India and total days of lockdown were more, USA has the highest number in terms of infected people, dead people and recovered people. The parameters considered, for the two countries, are: temperature (minimum and maximum), days of confinement and non-containment, administration of the BCG vaccine (anti-tuberculosis vaccine), the population of the country and the reproduction factor of the disease R_0. For an application to COVID-19, without a reuse interface and without the medical diagnosis assistance service, one can talk about long-term simulation (8 to 9 months). Application of the model to

other data is possible while it is impossible to use the system to simulate other infectious diseases.

Pizzituti et al [20] presented an agent-based model to simulate malaria transmission at a local scale. The model reproduces the environment of a typical riverine village in the northern Peruvian Amazon, where malaria transmission is highly seasonal and apparently associated with the flooding of large areas caused by the overflow of the nearby river. Agents representing humans, mosquitoes and the two species of plasmodium (falciparum and vivax) are simulated in a representation of the environment around the village. The model environment includes: climate, house positions and altitude. A representation of changes in the expansion of mosquito breeding areas caused by river flooding is also included in the simulation environment. The results gave monthly malaria incidence as calculated by the model (based on SMA), total malaria incidence, Plasmodium vivax malaria incidence and Plasmodium falciparum malaria incidence. The simulated malaria incidence curves are compared to the monthly malaria incidence from the study by Bautista et al [21] at the Nanay River (in Padre Cocha, Loreto and Peru) during the period from the beginning of 1996 to the end of 1998.

Pizzitutti et al [22] presented another model to study the influence of the mobility of humans (mobile agents) on the local transmission of malaria. The agents considered are:

- the environment essentially composed of the study area (a spatial domain), parameters linked to mosquitoes (capacity to smell the odor of humans, reproduction, method of searching for blood, survival time depending on temperature and rainy days) and the presence of domestic animals that can serve as targets for mosquitoes;

- and humans through their age structure (0 to 5 years, 6 to 12 years, etc.), their number, their distribution according to each household, their activity (driver, office worker, farmer, etc.), the probability of exposure (of humans) to mosquito bites and their asymptomatic nature due to falciparum or vivax Plasmodium.

The simulation results show that human movements have a strong influence in determining where mosquito-to-human and human-to-mosquito transmission events occur, and thus

determine an increased risk of malaria for certain categories of individuals as in the case of farmers.

For the models presented in [20] and [22], one can speak of short-term simulation in the context of malaria. Each of the models is missing a re-use interface as well as the diagnostic assistance service in addition to the fact that their application to other diseases is not possible.

In [23], Burman et al proposed an ABS model to study the dynamics of COVID-19 by manipulating different parameters in a population. The input to the model includes the characteristics of each individual in the human population. The model shown works according to the following principle:

- one considers a dispersion in the plane of infected and uninfected people. Uninfected people are susceptible people represented by set S and have coordinates *(x, y)*. the infected people are represented by set I and have coordinates (x_0, y_0);

- in a healthy community (where no individual is infected), when the first infected person enters, all others are susceptible;

- the spread of the disease is simulated based on the proximity of infected individuals. A susceptible individual is in the vicinity of an infected individual if the distance $\sqrt{(x - x_0)^2 + (y - y_0)^2}$ is less than a threshold l_0 defined by the user;

- one classifies, in the group of infected people, a susceptible individual based on their characteristics (age, sex, work status, compliance with barrier measures) and their belonging to the neighborhood of an infected individual.

The results show that the model can be considered as a guide in identifying measures to control the epidemic in a community. It is flexible to adapt to different parameters such as incubation period, test yield, socio-economic strata, daily commute, awareness level, population density, social distancing, confinement, etc. However, the model does not include a medical diagnosis assistance service and does not carry out a long-term simulation. Adaptation is needed to study other infectious diseases with a similar transmission pattern to COVID-19.

Codella et al [24] developed an agent-based simulation model to study the factors controlling the transmission of clostridium difficile (an infectious disease whose main consequence is diarrhea in the patient[25]) in a hospital. In this model, the agents are patients, health workers and visitors. The input parameters of the system are disease information (from medical literature) and patient data (obtained from Wisconsin Hospital Association in the United States). The operating rules of the system are:

- the conditions of a patient (admitted to hospital for a disease other than clostridium difficile) are: Susceptible (*S*), Exposed (*E*), Colonized (*C*), Ill (*D*), Recovered (*CL*), Clinically colonized resolved (*CR*), Relapsed Disease (*R*), Dead (*X*) and Not Susceptible (*NS*);

- each patient agent has a dynamic status linked to clostridium difficile (disease bacteria) which is updated every 6 hours;

- When a susceptible patient comes into contact with an infectious patient, they become exposed. So the Exposed state (*E*) represents patients who have been exposed to clostridium difficile through interaction within the last 6 hours;

- a patient in the Colonized state (*C*) is infected asymptomatically and can infect other people;

- a patient in the Sick state (*D*) has received a positive diagnosis (he is infected) and may expose other people (patients, health workers and visitors);

- a patient in the Cured (*CL*) state has already had an infection. He is now cured and is no longer contagious;

- a patient in the state of clinically resolved colonization (*CR*) has already been infected, but the symptoms have lessened although he or she still remains infected;

- a patient in the Relapsed Ill (*R*) state has already been infected but is experiencing a recurrence of the previous infection;

- a patient in the Dead state (*X*) died from complications linked to the infection;

- finally, a patient in the Non Susceptible (*NS*) state cannot be infected and does not expose (does not contaminate) other people.

To validate the model, a comparative study is made between the simulation results and the reference values found in the literature. Results indicated that regularly disinfecting patient rooms with bleach provided the greatest reduction in disease transmission (21.8 to 42.8%). Treatment with vancomycin (an antibiotic for the disease) provides the greatest reduction in relapses (41.9%), mortality (68.5%), and total patient length of stay (21.6%). The model does not offer a reuse interface but can be applied to other data. It performs a short-term simulation and does not offer a diagnostic assistance service.

In [26], Hunter and Kelleher adapted a model presented in [27] (which is presented in the section 3 of this document) to simulate the spread of COVID-19. To adapt the measles model to the dynamics of COVID-19, the authors adjusted the disease parameters (COVID-19 instead of measles). The parameters of society (of humans) and those of the environment (cities, schools and workplaces) remain the same as in [27]. The main parameters adjusted are the incubation period, the infection period and the basic reproduction number R_0 (this is the estimate of how quickly the disease spreads). In the case of COVID-19, the incubation period ranges from 1 to 14 days. The infection period is estimated at 2 weeks for mild cases and 3 to 6 weeks for severe cases and R_0 is estimated at a value between 2 and 2.5. R_0 is used to determine the probability that human agents will infect each other when they meet.

The results of the models presented in [27] and [26] highlight the number of infected people, the duration of the epidemic (in number of days) and the maximum number of infections as well as the corresponding day. The systems ([27] and [26]) do not have a reuse interface and do not offer a diagnostic support service. They can be applied to other data in the case of the same infectious disease (measles and COVID-19 respectively). The models can do long-term simulation because they simulate measles and COVID-19 respectively for the time each disease can take in the event of an epidemic.

Diemier [28] used Causal Loop Diagrams to progressively simulate the behavior of covid-19 in Wuhan (China) and on the Asian continent in general. The simulation concerns the period from January 3 to March 31, 2020. The system takes into account the disease parameters (infection

rate, incubation period, lethality, mortality, etc.) as well as some population attributes (density, contact rate, age, prevention measures, etc.). According to the author, the older the population, the more people there are infected (or dead). This was the case for Italy and Japan. The system can only simulate Covid-19. The simulation period is very short even if it was a continent. Diagnostic assistance and the user interface were not taken into account in the modeling.

Kersting et al [29] used ABS to evaluate COVID-19 prevention policies in South Africa. The agents of the system are humans who form a population of 114,346 individuals living in 32,597 households. They are divided according to their age using the age pyramid. They move within a virtual network generated from OpenStreetMap data (a free geographic database). During an iteration of the simulation, each agent carries out one or more activities distributed in the following places: home, work, school (primary, higher), market, leisure places and other. The containment levels that apply to the activities of human agents are:

- level 1: All activities are authorized. The use of masks and social distancing are mandatory. Public gatherings are prohibited. Shops are open;

- level 2: All businesses are authorized, restaurants operate in home delivery mode (the customer orders from home) and takeaway (the customer orders on site and takes their dish away). Interprovincial travel is authorized. Personal travel (personal vehicle for example) is authorized for essential activities. Schools remain open part-time for 57 days;

- level 3: No restrictions on daily workload in major industries, services and public sectors. Other industries and sectors are limited to 50% of their daily workload. Travel (via public land and air transport) is prohibited unless proof of necessity to travel is presented. Personal travel is authorized for essential activities (individual sport for example). Schools are fully open for 57 days;

- level 4: Some industries are partially open. Public Transport is authorized on demand under appropriate conditions (wearing a mask, social distancing) and only for authorized activities. Physical exercises (sport) are authorized under strict conditions. Gyms or sports clubs are prohibited. Schools remain closed;

- level 5: Critical work such as the production of essential goods (food, water, electricity, logistics, medical and social services) is authorized. Only the transport of goods is authorized, public transport services are exceptionally authorized for authorized activities only. Citizens are ordered to stay at home, except for certain purposes (purchase of essential goods, funerals, medical emergencies). Schools remain closed. The retail sale of alcohol or street food is prohibited.

The results underline that from an epidemiological point of view, strict and long confinement (level 5) is the best policy to fight the pandemic. The system does not have an interface to carry out other simulations and lacks flexibility to take other data or simulate other infectious diseases. It does not offer a diagnostic assistance service.

Layie et al [30] demonstrated, through an SMA type model, the possibility of stopping the transmission of malaria by destroying mosquito development environments (stagnant water) around homes. According to the authors, Africans pour dirty water around their houses which constitutes aquatic habitats (AH) sought by mosquitoes for larval development. The model, whose compartments (susceptible, exposed and infected) of mosquitoes and humans are represented as a UML state diagram, evaluates the impact of population awareness campaigns (on the harmful effects of aquatic habitats around houses) on malaria transmission. The environment in which the agents find themselves (mosquitoes and humans) is constructed from satellite images of the village of Demgoya in Cameroon. Around thirty houses are targeted. Around each house, 30 AH are located in a radius whose distance varies between 1 to 400 meters. The main parameters of the simulation are:

- the daily rate of egg development;
- the daily development rate of the larvae;
- daily mortality of larvae at immature stages;
- the rate of successful blood meals for questing vectors;
- the natural mortality rate of vectors;

- the human birth rate;
- the rate (for humans) to move from the exposed state to the infectious state;
- the rate (for humans) to move from the infectious state to the cured state;
- the rate of loss of immunity in humans;
- the probability of transmission of a mosquito infectious agent to a susceptible human if contact between the two (mosquito and human) occurs;
- the probability of transmission of infection from a human (asymptomatic carrier) to a susceptible mosquito if contact between the two occurs;
- the probability of transmission from an infectious human to a susceptible mosquito when contact between the two occurs;
- the daily human mortality rate;
- the human mortality rate induced by the disease.

According to the results, the number of infected people only begins to decrease (to tend very quickly towards 0) when AHs are 100% eliminated. In other words, as long as there is only one AH around a house, malaria transmission will continue without any mitigation. However, the authors cited other researchers (such as Gu et al [31]) who believe that malaria transmission decreases as AHs are eliminated. The system can be applied to other data but not to other diseases. It does not offer a diagnostic assistance service or a reuse interface. The simulation is done over 1441 iterations of 6-hour intervals, i.e. 360 days. One can affirm that the model does not carry out a long-term simulation (in the case of malaria).

Sarumi et al [32] used the Gammaitoni and Nucci [33] model (called GN model) to perform an agent-based simulation of the potential for measles transmission in a confined space. The GN model is a mathematical system developed in 1997 to simulate and evaluate tuberculosis control measures. The system runs in 1800 iterations (representing 30 minutes of average waiting time) by varying the volume of the room and the number of people there. The infection property is

simulated for susceptible agents according to the distance that separates them from the infected agent. According to the results, the infection rate increases when the volume of the room decreases. The proposed system performs a short-term simulation (30 minutes) but can be applied to other data. It cannot directly simulate (without major modification) other diseases whose parameters differ from those of the disease the authors reported on (measles). Diagnostic assistance is not taken into account.

Staffini et al [34] evaluated the transmission and control policies of COVID-19 in four countries (Italy, Germany, Sweden and Brazil) through a multi-agent system. they used statistical data, information related to the disease and the barrier measures of each of the countries considered. These are: age (over 65), number of people who are not critically ill, number of critically ill people, number of beds provided for critically ill patients, recovery rate (recovery), the case fatality rate, and the hospitalization rate. For each country, one considers a sample of 1000 individuals (including 6 infected) among which one applies the percentage of people aged over 65 years. One considers that this sample takes into account the characteristics of the entire population. The barrier measures considered are wearing a mask and social distancing. The simulation is done in 365 iterations (corresponding to one year). The system has an interface that allows you to define the parameters and the corresponding country. The simulation is guided by the following equation: $P(I) = 1 - (1 - TR)^n$. $P(I)$ is the probability applied to each susceptible individual so that they become infected. This probability is linked to an already infected individual (among the *n* infected individuals in total in the vicinity of the susceptible individual) with a transmission rate (*TR*) of the disease. According to the results, the curves resulting from the simulation are close to those of real cases. This model has the advantage of having a reuse interface to take, as input, data from another simulation (for another country for example). Additionally, the simulation can be considered long-term for the case of COVD-19 (365 days). However, the system does not provide diagnostic assistance and does not allow other infectious diseases to be simulated.

In [35], the authors used satellite images to classify land occupation by mosquitoes with the aim of studying the risk of re-emergence of malaria in the Camargue (France). Using eCogniton 2, they performed supervised object-oriented classification of the data. The tool in question

performs semi-automatic classification of very high resolution imagery according to the following algorithm:

- The image is considered to be a set of pixels;
- One considers each pixel as an object;
- Similar neighboring objects are grouped using a heterogeneity criterion;
- One calculates the increase in the overall heterogeneity criterion. The latter is calculated on the basis of correlations in shape and color of neighboring objects;
- If this increase is lower than the threshold defined by the scale factor, the grouping is accepted, otherwise the procedure returns to the step of grouping similar objects.

The results show an important heterogeneity criterion for rice fields, bulrush marshes and reed beds which are the main hosts for Anopheles mosquitoes. This really constitutes a risk of spreading malaria. The method can only be reused on image type data and in the case where the living environment of the vector agent can be photographed. There is no precision on the duration of the simulation.

Daudé et al [36] carried out multi-agent modeling to simulate the transmission of dengue fever in Bangkok (Thailand). The agents of the system are mosquitoes and humans placed in an environment representing the geographic location and breeding grounds for mosquitoes. The influences are the disease control factors which mainly consist of the reduction of hosts for mosquitoes, the use of insecticides and the control of human movement. The results give a distribution, over 38 days, of infected humans on one hand and a distribution of infected mosquitoes on the other. The model is not directly reusable on other data, does a short-term simulation (in the case of dengue fever). It does not allow other infectious diseases to be simulated because it directly takes into account the parameters of the disease that was the subject of the study.

Table 1 provides a summary of the analysis.

Table 1: Summary of the analysis of some existing works

✓ Yes	☒ No	✍ Maybe

Model	Short and/or Medium term prediction	Long term prediction	Diagnosis of the disease	Reuse interface	Reuse on other data	Reuse on other diseases
CHEN et al [9]	☐	☐	☐	☐	☐	☐
Papa Alioune CISSE [3]	✓	✓	☒	☒	☒	☒
Espindonla et al [11]	☐	☐	☐	☐	☐	☐
Espindonla et al [12]	☐	☐	☐	☐	☐	☐
HAMAMI D. (Tuberculose) [4]et [13]	☐	☐	☐	☐	☐	☐
HAMAMI D. (Oreillons) [4]	☐	☐	☐	☐	☐	☐
Miralles-Pechuán et al [5]	☐	☐	☐	☐	☐	☐
Savi et al [6]	☐	☐	☐	☐	☐	☐
Sharma et al [15]	✓	✓	☐	☐	☐	☐
ZIYADI Najat [16]	✓	✓	☒	✓	✓	☒
Sowmya et al [17]	✓	✓	☒	☒	✓	☒
Pizzituti et al [20]	✓	✍	☒	☒	✓	☒
Pizzitutti et al [22]	✓	✍	☒	☒	✓	☒
Burman et al [23]	✓	☒	☒	☒	✓	☒
Codella et al[24]	✓	☒	☒	☒	✓	☒
Hunter et al[27]	✓	✓	☒	☒	✓	☒
Hunter et Kelleher [26]	✓	✓	☒	☒	✓	☒
Arnaud IEMER[28]	✓	☒	☒	☒	✓	☒
Kersting et al[29]	✓	✓	☒	☒	☒	☒
Paul Layie et al[30]	✓	☒	☒	☒	✓	☒
Sarumi et al [32]	✓	☒	☒	☒	✓	☒
Staffini et al[34]	✓	✓	☒	✓	✓	☒
MARTI et al [35]	✓	☒	☒	✓	✓	☒
Daudé et al [36]	✓	☒	☒	☒	☒	☒
Total	24/24	11/24	1/24	3/24	21/24	1/24

The advantages of the models are mainly:

- They provide an idea of the future behavior of the diseases they simulate and/or make it possible to evaluate the impact of policies to combat infectious diseases (this is the case for all the models analyzed);

- Most of the models studied (with the exception of those presented in [3], [29] and [37]) can be applied to other data to simulate the same disease;

- Others offer a medical diagnosis assistance service ([9]).

The limits are:

- Most of these systems can only simulate a single disease. The simulation of other infectious diseases, even similar to the one for which they were designed, is not possible. This is the case of all the systems analyzed (except the one presented in [9] and perhaps the one presented in [23]);

- All the models analyzed (except those presented in [16], [35] and [36]) do not have an interface to facilitate users (other than the authors) the application of the system to test data. The systems may only be used by users who have a certain level of knowledge of computer simulation techniques. This is due to the lack of a flexible user interface;

- All systems (with the exception of that of Chen et al [9]) do not allow the simulation of an infectious disease while offering a medical diagnosis assistance service as well as the appropriate treatment depending on the patient (infant, child, adult, level of severity of the disease, standard of living of the patient, etc.).

3. IMPLEMENTED MODEL

In [26], Hunter et al presented an ABS model to simulate the spread of airborne infectious diseases in an Irish city. The model was tested by simulating a measles outbreak that occurred in 34 towns in Ireland in 2012 and was used to examine the correlation between the results and town characteristics. This made it possible to determine whether the model results are affected by the interaction of the characteristics of a specific city on the agents. The simulation begins with the creation of the environment. These include cities, as well as primary and secondary

schools, households and workplaces. They are created according to geographical layout using data from the Irish Department of Education and Statistics. Each patch (square which makes up the grid of the NetLogo platform) corresponds to 111 m² in the representation of cities. Then, people are distributed across cities based on their demographics: age, gender, single, couple, couple with children, economic status (worker or student), etc. Adults are added first and have an age and sex based on the distributions (percentages of statistical data) of age and sex. Then, households probably receive children (with their age and sex). The percentage of each age group that has received a measles vaccination is determined using vaccination data. To simulate the dynamics of measles transmission, agents (humans) are classified by status (susceptible, exposed, infected or cured). When an infectious agent comes into contact with a susceptible agent (this implies that both agents are in the same patch), the susceptible agent is exposed based on the probability of contagion. When an agent enters an exposed state, it is assigned an exposure period (10 days on average) which corresponds to the length of time it will remain exposed before becoming infectious. The agent is then assigned a period of time during which he will remain contagious (8 days) before curing. The results presented in [26] highlight the number of infected people, the duration of the epidemic (in number of days) and the maximum number of infections as well as the corresponding day. The updating of groups (susceptible people, exposed people, infected people and recovered people) is done according to the following system [37]:

$$\begin{cases} S_{t+1} = S_t - \dfrac{\beta I_t S_t}{N} \\ E_{t+1} = E_t + \dfrac{\beta I_t S_t}{N} - \sigma E_t \\ I_{t+1} = I_t + \sigma E_t - \gamma I_t \\ R_{t+1} = R_t + \gamma I_t \end{cases}$$

With:

S_t: the number of people susceptible in the previous iteration;

S_{t+1}: the number of people susceptible in the current iteration;

E_t: the number of people exposed from the previous iteration;

E_{t+1}: the number of people exposed in the current iteration;

I_t: the number of infected people from the previous iteration;

I_{t+1}: the number of infected people in the current iteration;

R_t: the number of people recovered from the previous iteration;

R_{t+1}: the number of people recovered in the current iteration;

β: the probability that a susceptible person will be exposed when they come into contact with an already infected person;

N: the total number of people;

$\boldsymbol{\sigma}$: the probability that an exposed person will become infected;

γ: the healing rate.

4. APPLICATION OF THE MODEL, RESULTS AND DISCUSSIONS

To adapt the model to the context of measles in Niger, it is necessary to adapt the distribution of humans according to their characteristics. For the case of Niger, the economic statuses are: student, looking for work, in activity (civil servant, employee, farmer, seller in a market, etc.), retired and staying at home (housewives, especially for women).

Representing Niger, which is a very large country (1,267,000 km²) in a set of patches of 111 m² would be very difficult. It should be noted that the basic model was applied to the case of measles in County Leitrim which has an area of 1588 km². Table 2 gives an extract of patch construction in the base model.

Table 2: Some patches for County Leitrim [26]

pxcor	pycor	Nom de la ville	Pays
-7	7	Killarga	Leitrim County
-6	7	Yunga	Leitrim County
-5	7	Yunga	Leitrim County
0	7	Carrigallen	Leitrim County
-2	7	Carrigallen	Leitrim County

This difference in surface area (1,267,000 km² versus 1,588 km²) means that in the adaptation to the case of Niger, a representation of a district of the city of Niamey (capital of Niger) is made on a set of patches as in the model of base. Table 3 gives the example of the creation of some city-related patches by observing Figure 1.

Table 3: List of patches for the city of Niamey

Pxcor	**pycor**	**Nom de la ville**	**Pays**
-5	-1	Niamey	Niger
-4	-1	Niamey	Niger
-5	-2	Niamey	Niger
-4	-2	Niamey	Niger
-5	-3	Niamey	Niger
-4	-3	Niamey	Niger
-3	-2	Niamey	Niger
-3	-3	Niamey	Niger

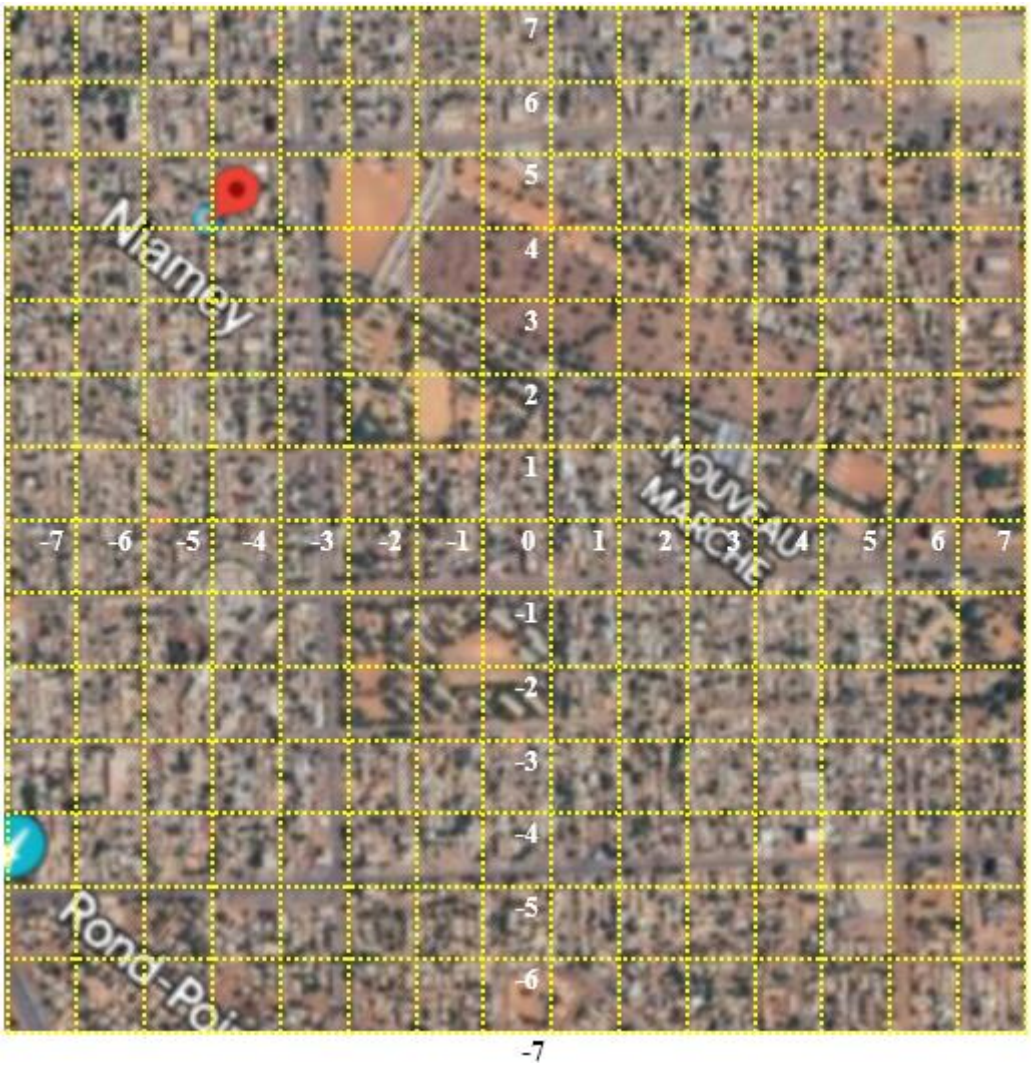

Figure 1: Representation of a neighborhood of Niamey city (called "Nouveau Marché") using an image capture of a view given by Google Earth

Table 4 gives an extract from the adaptation of data from the population of the Nouveau Marché district (and its surroundings) of Niamey considering a sample of 36,550 individuals. This number is the same as that of the test population.

Table 4: Extract of data from the population of Niamey

who	xcor	ycor	home-patch	work-patch	age	sex
0	-6	7	{patch -6 7}	0	66	Female
1	-6	7	{patch -6 7}	0	72	Male
2	-6	7	{patch -6 7}	{patch 3 5}	64	Female
3	-6	7	{patch -6 7}	0	31	Female
4	-6	7	{patch -6 7}	0	30	Male
5	-6	7	{patch -6 7}	{patch -5 5}	39	Female
6	-6	7	{patch -6 7}	{patch 4 -1}	41	Female
7	-6	7	{patch -6 7}	{patch 3 -6}	30	Male
8	-6	7	{patch -6 7}	{patch -7 -1}	45	Female
9	-6	7	{patch -6 7}	0	48	Female
10	-6	7	{patch -6 7}	0	75	Female
11	-6	7	{patch -6 7}	{patch 4 5}	50	Female
12	-6	7	{patch -6 7}	0	75	Male
13	-6	7	{patch -6 7}	0	33	Female

The results of running the model with the test data and with the adapted data are given, respectively, by Figures 2 and 3. The behavior of the curve in gray shows that all individuals (36549 individuals of the 36550 individuals in total in both cases) of the population are considered to be susceptible (this is the curve of susceptible people). After a few iterations (runs), the curve of infected people and that of immune people appear. The latter (the curve of immunized people) increases as infections continue, unlike the curve of susceptible people which decreases and tends towards zero. The simulation stops when there is no longer any possibility of contagion.

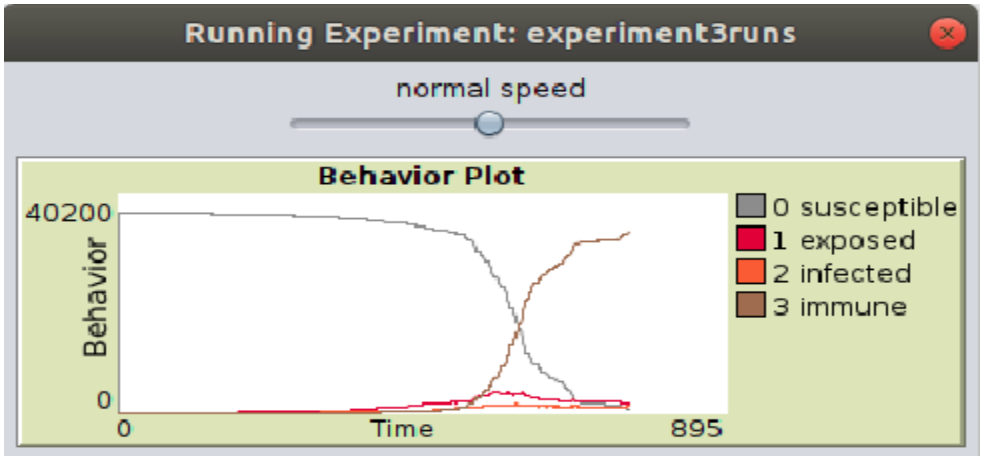

Figure 2: Model result with provided test data

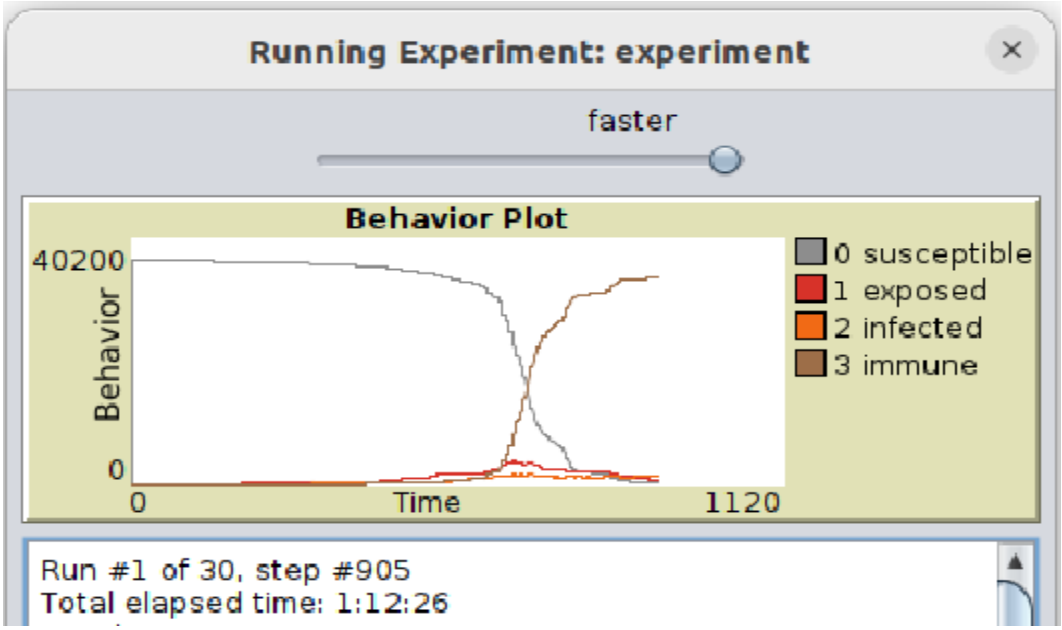

Figure 3: Model adaptation result

Although adaptation of the model was possible, the problems are as follows:

- the difficulty of adapting population data. For each individual to be taken into account in the simulation, it is necessary to specify their age, their gender, their activity, the patches of their home, their workplace and especially the patches of individuals with whom they could often be in contact (colleagues or classmates). Defining population data in accordance with the format

used by the model is surely a blockage for a user in a context where information on individuals is not guaranteed;

- a user without basic knowledge of computer simulation and advanced programming (computer) language will not be able to adapt the model because it was necessary to modify the data path (patches and population) in the nlogo file to carry out the simulation in a Linux environment;

- adaptation of the model to an infectious disease which is not of the airborne type (even for County Leitrim) is impossible. This is due to the fact that the model is based on a mathematical system (see section 2 of the document);

- lack of diagnostic and medical treatment support services.

5. CONCLUSION

This paper made it possible to present the analysis of a certain number of research works that deal with the simulation of infectious diseases (such as malaria, measles, tuberculosis, etc.). Several computer techniques are used in this direction. Simulation models are important in the management, from a public health point of view (prediction, evaluation of the impact of disease control policies), aid in the diagnosis and medical treatment of infectious diseases. The study made it possible to detect limitations in the models that were analyzed. The adaptation of a simulation model for airborne infectious diseases made it possible to justify the existence of these limits. Future simulation systems will be more useful if their design takes into account the limitations that were detected through this study. In other words, if they make it possible to manage several infectious diseases (prevention, diagnostic assistance and treatment) through a flexible user interface, accessible to all. This will lead to massive use of decision support tools in the field of health and thus contribute to better management of infectious diseases in Africa for the sustainable development of its States.

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