

Towards a Generic Agent Based Vector-Host Model

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Towards a Generic Agent Based Vector-Host Model

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Abstract The aim of our work is to develop a conceptual generic agent-based model to formalize the interaction of vector and host given climate change. The model consists in creating a hypothetical example of a vector-host system. It simulates the vector's life cycle while considering interactions with hosts and the temperature. It is presented following the ODD protocol and based on parameters and processes to conceptualize the vector-host complexity. It could accommodate a broad spectrum of vector species and different biogeographic regions. Our model can be extended to more ecologically complex systems with multiple species and real-world landscape complexity to test different host and / or vector-targeted control strategies and identify practical approaches to managing vector population and movement patterns.

Keywords Agent based models · Vector-host system · ODD protocol · tick

1 Introduction

Ectoparasites are vectors of pathogens that cause vector-borne diseases. Most ectoparasites are hematophagous species, such as insects and acarians. Ectoparasitic acarians (*i.e.* ticks) of vertebrates (*e.g.* Cattle, sheep, etc.) are vectors of pathogens responsible for zoonoses and significant economic losses for livestock [1,2]. Understanding the role of vectors in transmitting pathogens involves studying their population dynamics [3,4]. In this regard, the study

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of vector population dynamics and their interactions with the environment seems essential to surveillance vector-borne diseases [5,6,7]. The most important factor is climate change [8,9]. In fact, variations in climate and temperature induce great alterations in the distribution of vectors in nature and, in particular, in ticks [9,10,11,12,13].

The use of computer simulations to address complex ecological systems with explicit details while implementing individual-level interactions and spatial structure is promising [14]. Moreover, mathematical and simulation models were developed to further understand the ecological mechanisms and processes underlying the vector-host systems and had shown efficiency in answering problems that controlled experiments or field observations solely cannot fully address [9,15]. In fact, these models give a new degree of knowledge to support public health strategies for disease and vector control (*e.g.* [11,16,17]).

Simulation models as the Agent-based models (ABM) models are prominent tools to predict the relationships between biological processes, the environment, and ecological patterns across different scales, both for population dynamics and evolutionary scales [17,18,19,20,21,22].

Many ABM models have been developed to tackle whether host-vector (*e.g.* [16,23], host-vector-pathogen (*e.g.* [20,24,25,26]), or host-pathogen systems (refer to [27]). Simulation models are increasingly being used to solve problems and aid in decision-making in agricultural systems [28] and veterinary epidemiological systems [16] as well as in public health systems [14]. Our work aims to develop a generic agent-based model to formalize the interaction of vector and host with explicit consideration of temperature when describing the vector's life cycle since ABMs can integrate several scales, unlike ODE mathematical models (*e.g.* [15]). The distinguishing feature of our model is that it explicitly incorporates all the life stages of the vector, as well as temperature as an environmental factor in the development of the vector's life cycle. In addition, the integration of host movement and interactions with the vectors. Our objectives are (1) to develop an agent-based model that simulates the host-vector relationships while considering vector development as a temperature-dependent process, (2) to study the effects of host movement patterns (random versus herd movement) on vector population dynamics, and (3) study the effect of carrying capacity of the host on vector population dynamics.

This paper is organized as follows: In section 2.1, we describe the background knowledge and modeling assumptions we considered. In section 2.2, we explain our model using the overview, design concepts, and details (ODD) protocol [29,30]. Then, in section 3 we present our simulation's results by comparing two movement approaches of Cattle agents. Finally, in section 4, we discuss our results and pinpoint some limits and perspectives to generalise and promote our model to fill in the gap between understanding the ecology of the vector and hosts on the one hand and host movement effects on the ecology on the other hand.

2 Material and methods

2.1 Background

Our model creates a hypothetical example of a semi-intensive livestock production system. This closed system comprises only three entities: ticks, Cattle and Rodents. We consider that Cattle are grazing and then return to a barn. We do not consider in our model the diurnal activity of ticks nor that of Rodents. The host population is closed, while the tick population is an open monospecific population whose recruitment is done through egg laying. It is stratified in cohorts of biological life stages: egg, larva, nymph and adult. Interstadial development ticks are temperature-dependent processes [3, 4]. A blood meal is the only interaction between the hosts and the ticks.

The vector model in this study is a species of hard ticks. Ticks have four developmental stages: an egg and three active obligatory haematophagous ectoparasitic stages characterized by only one larval and nymphal stage before reaching the adult stage and discontinuous feeding, single blood meal to get through the next life stage.

At the end of the embryo's development, the eggs hatch into larvae [1, 31]. The larva begins to seek a host. All instars can enter a behavioural quiescence state called "diapause" where development is paused. In our model, we consider diapause as a temperature-dependent state, which is activated when the temperature of the environment reaches a stage-dependent threshold [32, 33, 34]. Two known host-finding strategies are described in literature [35, 36]: a passive strategy called *questing* where the tick waits on vegetation for the passing-by of a possible host and an active seeking host strategy where the ticks move actively looking for a host.

2.2 The conceptual model

The description of the model follows the "Overview, Design Concepts, and Details (ODD)" protocol developed by [30] to standardize the use of ABMs.

2.2.1 Overview

2.2.1.1 Purpose and patterns

The purpose of the model is to reproduce the tick life cycle, considering temperature-dependent processes and host movement patterns.

Entities, state variables, and scales:

The model is made up of agent types: the vector agent and host agents. The vector agent represents the hard tick; the host is either a Cattle or a Rodent. The interactions between agents are ruled by two ecological processes: (1) vector-host interaction and (2) host movement.

The vector agent:

The *vector* agents are characterized mainly by the life stage attribute *state* respectively: egg, larva, nymph, and adult. The activity status of the vector agents is characterized by three behavioural states (1) *questing*: This is a generic term to designate the activity of the vector before attaching to a

possible host and while it is waiting for the passing-by of a host or the actively seeking the host, (2) feeding: while the vector attaches to the host for taking the blood meal and finally (3) moulting: the behavioural state of the after completing the blood meal and detaching from the host (Figure 2 and 1).

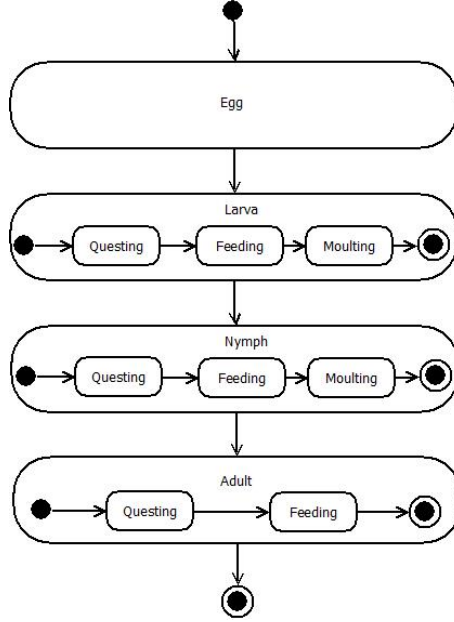


Fig. 1: Conceptual view of the vector life stages (*state*) and behavioural states *BehState* attributes. In every *state*, the vector agent can have, at one time, a sole behavioural state. The egg state has no behaviour. The adult state has only two behavioural states. The larva and the nymph state can have the behavioural state, respectively, questing, feeding and moulting.

The host agent:

The *Host* agent includes two sub-agents (Figure 2): *Cattle* and *Rodent* agents: Rodent agents have a random movement in the environment characterized by a velocity randomly fixed at the beginning of the simulation. The Cattle agent moves following two behaviours. In the first movement behaviour, Cattle agents are endowed with random movements. In the second movement behaviour, Cattle agents abide by a herd movement pattern and follow a dominant Cattle agent considered a leader. In both behaviours, Cattle are characterized by diurnal activity, whether active or resting, by regaining the barn.

Table 1: Summary of attributes and variables with definitions and periods of update

Attri.	Typ.	Dim.	Desc.	Peri.
Vector				
location	\mathbb{R}^2	—	Position	1 H
speed	\mathbb{R}^2	km/h	Speed of vector agent	1 H
BehState	Category	—	Behavioural state	1 D
State	Category	—	Life stages;egg, larva, nymph,adult	1 D
AttachDetachDate	Date	-	attachment/detachment date	1 D
LayDate	Date	-	Date of egg hatching	1 D
QuestDate	Date	-	Questing start date	1 D
NeighHosts	List	-	Neighbouring hosts	1 H
TargetHost	Host	-	Target host	1 H
LayingEgg	Boolean	-	Fitness of adults to lay eggs	1 H
Diapause	Boolean	-	Diapause	1 D
LaidToIncubation	\mathbb{R}	-	Incubation duration	1 D
PreoviToOvi	\mathbb{R}	-	Preoviposition duration	1 D
MoultingDuration	\mathbb{R}	-	Moulting duration	1 D
oviposition	Boolean	-	Oviposition	1 D
moulted	Boolean	-	True to change the life state	1 D
incubation	Boolean	-	incubation	1 D
ProbIndAttach	\mathbb{R}	-	Probability of attachment	1 H
counter	\mathbb{R}	-	Counter for development rate	1 D
Hosts				
location	\mathbb{R}^2	-	Position of the agent	1 H
speed	\mathbb{R}^2	km/h	Speed of host agent	1 H
VectorOfParasite	\mathbb{N}^n	-	List of vectors	1 H

The environment

The environment is set up as a hypothetical square world with a dimension of 1 km x 1 km with unwrapping boundaries movement and does not cause Host agents to jump to the other side of the world.

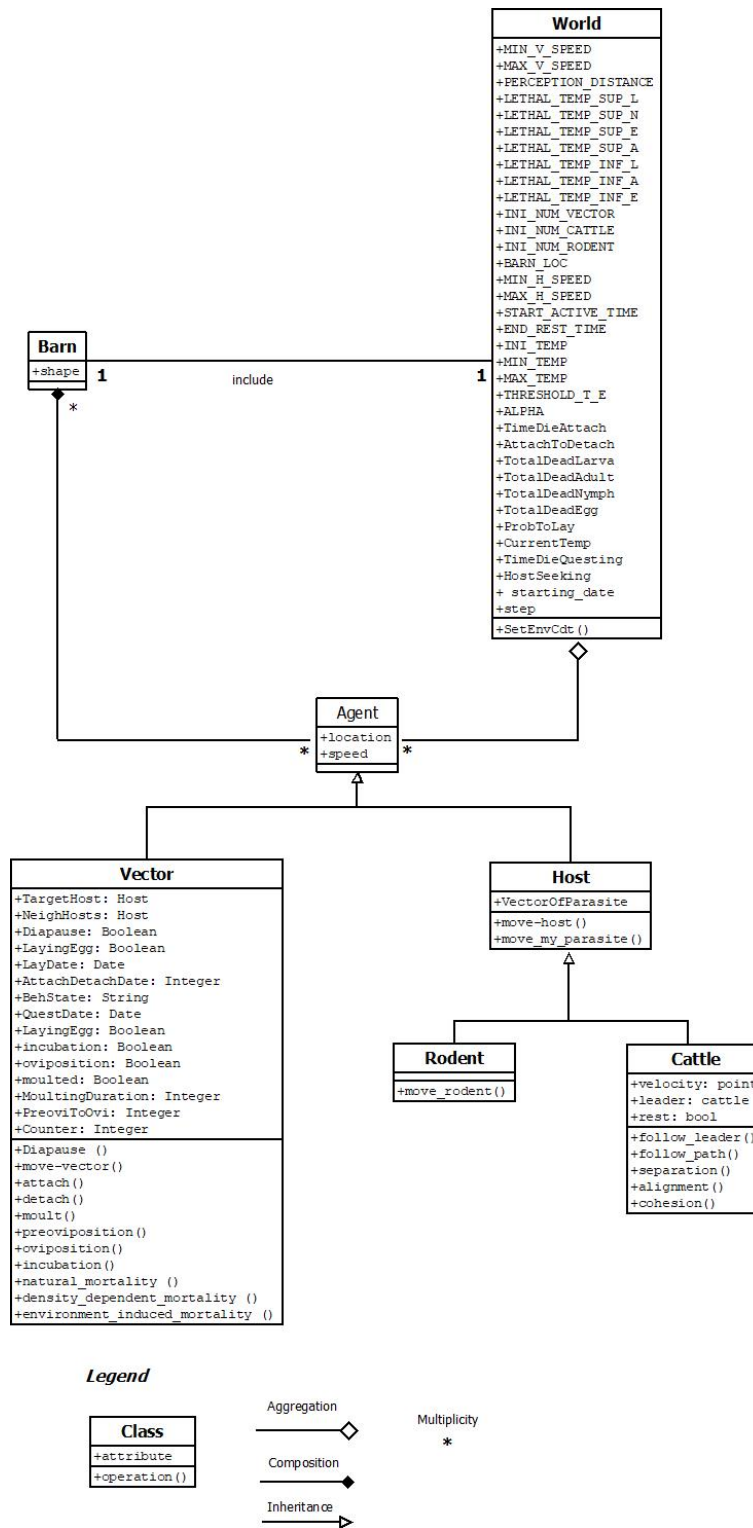


Fig. 2: UML (unified modelling language) class diagram represents our ABM, with two types of agents: Vector agent and Host agent. Both agents are located in the World.

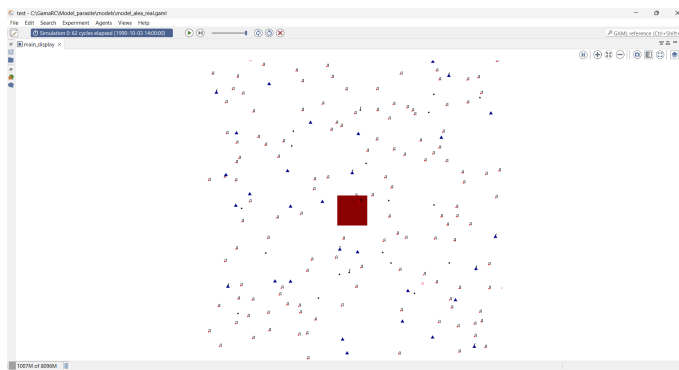


Fig. 3: Screenshot of the Environment on Gama Platform. The central cell (in dark red) represents the barn. Triangles (in blue) represent the rodent agents. Circles (in red) represent the vector agents. The letter designs the behavioural state of every vector agent (q: questing, f: feeding, m: moulting).

The environment is considered a grazing area where all Host agents can move around. In the centre of the environment, a hypothetical barn of square geometric shape and a dimension of 50m x 50m (refer to Figure 3). As for the climatic parameters, only the temperature is considered a climatic factor influencing the vector agents.

2.2.1.2 Process overview and scheduling

The model simulates the interactions between the vector (tick) and the hosts (Cattle and Rodents) agents on the one hand and between environmental (temperature) and vector agents on the other hand. We consider six submodels (Figure 4):

Host agents (Cattle and Rodents) move according to the *move_host* submodel every hour. Questing vector (tick) agents are stationary, waiting for the passing-by of a possible host within a specific distance *PERCEPTION_DISTANCE*. When finding a host (Rodent or Cattle), vector (tick) attach to the host based on the *attach* submodel and start a blood meal. Each day, vectors detach from hosts following the *detach* submodel after completing the blood meal. Furthermore, the life cycle processes of the vector population are the result of the *development* submodel compiled of the following five submodels that occur every day: *preoviposition*, *incubation*, *moulting*, and finally the *diapause* submodel. The *death* submodel is also composed of two submodels: *natural_mortality* and *environment_induced_mortality*.

The temperature is updated every day based on the *SetEnvCdt* submodel.

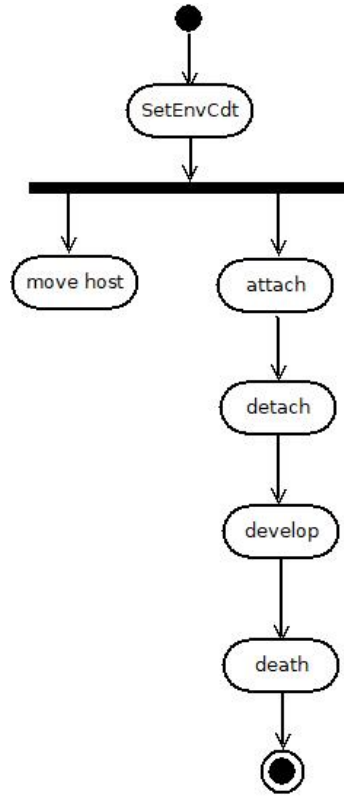


Fig. 4: Conceptual view of the submodels: the diagram represents an outline of the sequence of processes and the schedule of interactions between *Vector* and *Host* agents at each discrete time step.

2.2.2 Design concepts

2.2.2.1 Basic principles

The model considers that the life cycle of ticks consists of four stages, the duration of which depends on temperature. Moulting between stages depends on blood meals and is, therefore, closely linked to the presence of hosts. Adult vectors are all females and would give offspring, and mating is implicitly included in our model. We have considered the host population a closed system with a constant host population. Both scenarios do not include trophic resources for *Host* agents.

2.2.2.2 Emergence

Abundance and stage distribution emerge from the properties of the relationships between temperature and moulting duration and also from host location and probability of attaching to a possible host, permitting the fulfilment of the

transition into the next behavioural stage and life state. The host agents' and vector's combined actions and states in response to the environment produce the total number of vectors questing, feeding, or moulting in any particular location at any given moment.

2.2.2.3 Sensing

Moulting and diapause behaviours are temperature-dependent processes, *vector* agents sense the temperature variation and enter diapause when the daily temperature reaches a stage-dependent threshold. *larva* and *nymph* states sense the temperature when moulting. *Egg* state vector agents sense the temperature when incubating, as for *Adult* state vector sense it when, either in preoviposition or oviposition phase. Intraspecific interactions are not taken into account in our model; *Vector* agents perceive the *host* agent within the range of their distance of perception (refer to tab 2) and do not sense each other or communicate. Both *Cattle* and *Rodent* agents do not sense the temperature. Rodents do not sense each other nor sense Cattle agents. In the first scenario (S1), Cattle do not sense each other; meanwhile, in the second scenario (S2), they sense the movement of each other and move in a herd pattern while following a leader Cattle agent.

2.2.2.4 Interaction

Vector agents interact with both *Cattle* and *Rodent* agents through blood meals, the result of the *attach* submodel. *Host* agent, through a blood meal, can be a limiting factor as it is necessary for the moulting from one stage to another.

The *larva* state of the *vector* agent can only attach and have a blood meal from a *Rodent* agent. *Nymph* and *adult* state can attach to both *Rodent* and *Cattle* agents.

2.2.2.5 Stochasticity

Stochasticity plays a crucial role in three submodels within the system. Firstly, in scenario (S1), the movement of Rodents and Cattle is governed by randomness. Their velocity direction is randomly determined at each time step.

Additionally, the environmental-induced mortality is a stochastic process. At every time step, a probability of death is computed based on the life state and the temperature, both of which contribute to the stochastic nature of the model.

Moreover, the *attach* submodel relies on the probability of attachment, and the selection of the host is determined randomly at each time step. The probability of attachment is influenced by the number of hosts within the perception distance of the vector agents.

2.2.2.6 Observation

The main target observations are the vector's population and per-stage abundance. Additionally, we tracked the life-stage behavioural state (questing, feeding, moulting, and diapause).

We denote the total abundance of the tick population, at time t , $N(t)$ and $\bar{N}(t)$ the mean over the replication of the population abundance and $N_{state(i)}(t)$, the life stage population abundance, where i is, respectively to "egg", "larva", "nymph" and "adult" stage.

$$\bar{N}(t) = \sum_i \bar{N}_{state(i)}(t) \quad (1)$$

2.2.3 Details

2.2.3.1 Initialization

Each simulation starts with an environment wherein Cattle are situated in the centre of the barn. In the second scenario (S2), the leader *Cattle* agent is selected randomly. *Rodent* agents are located randomly in the environment. All vector agents are adults on day zero of the preoviposition stage. The initial date of the simulation is October 1st, 1990. The initial daily temperature corresponds to that of the initialization date. The initial values of all parameters are in table 2.

Table 2: Global Parameters and input values of the vector agent and host agent attributes. For the dimension, the following symbols are used: “-” indicates no dimensions.

Param.	Sym.	Val.	Dim.	Uni.	Ref.
World					
The current daily value of T°	CurrentTemp	-	\mathbb{R}	°C	[37]
Maximum T°	MAX_TEMP	40	\mathbb{R}	°C	-
Minimum T°	MIN_TEMP	-30	\mathbb{R}	°C	-
Coeff.of Environment-induced mort.	ALPHA	0.2	\mathbb{R}	-	-
Time step	step	2	\mathbb{R}	hour	-
World size	shape	1	\mathbb{R}	km	-
Posi. of the barn	BARN_LOC	(500,500)	\mathbb{R}^2	m	-
Vector					
Initial num. of vectors	INI_NUM_VECTOR	150	N	-	-
Distance of perception	PERCEPTION_DISTANCE	7	N	m	-
Larva max. Lethal T°	LETHAL_TEMP_SUP_L	40	\mathbb{R}	°C	[3]
Nymph max. Lethal T°	LETHAL_TEMP_SUP_N	45	\mathbb{R}	°C	[3]
Egg max. Lethal T°	LETHAL_TEMP_SUP_E	32	\mathbb{R}	°C	[3]
Adult max. Lethal T°	LETHAL_TEMP_SUP_A	35	\mathbb{R}	°C	[38]

Table 2: Global Parameters and input values of the vector agent and host agent attributes. For the dimension, the following symbols are used: “-” indicates no dimensions.

Param.	Sym.	Val.	Dim.	Uni.	Ref.
Nymph min. Lethal T°	LETHAL_TEMP_INF_N	-18	\mathbb{R}	°C	[39]
Adult min. Lethal T°	LETHAL_TEMP_INF_A	-20	\mathbb{R}	°C	[39]
Larva min. Lethal T°	LETHAL_TEMP_INF_L	-18	\mathbb{R}	°C	[40]
Egg min. Lethal T°	LETHAL_TEMP_INF_E	-30	\mathbb{R}	°C	[34]
Threshold T° of diapause for L.	THRESHOLD_T_L	8	\mathbb{R}	°C	[40]
Threshold T° of diapause for N.	THRESHOLD_T_N	11	\mathbb{R}	°C	[39]
Threshold T° of diapause for E.	THRESHOLD_T_E	8	\mathbb{R}	°C	[34]
Threshold T° of diapause for A.	THRESHOLD_T_A	8	\mathbb{R}	°C	[38]
Proba. to lay eggs	ProbToLay	1	[0, 1]	-	-
Larva Nat. Mortality Proba.	P_NAT_MOR_N	0.006	[0, 1]	-	-
Nymph Nat. Mortality Proba.	P_NAT_MOR_L	0.006	[0, 1]	-	-
Adult Nat. Mortality Proba.	P_NAT_MOR_A	0.006	[0, 1]	-	-
Egg Natural Mortality Proba.	P_NAT_MOR_E	0.006	[0, 1]	-	-
Proba. of attachment	P_ATTACH	0.9	[0, 1]	-	-
Duration of attachment	AttachToDetach	7	\mathbb{R}	day	[41]
Time to die when questing	TimeDieQuesting	167	\mathbb{R}	day	-
Host					
Initial num. of Cattle	INI_NUM_Cattle	50	N	-	-
Initial num. of Rodents	INI_NUM_Rodent	100	N	-	-
Min. Host speed	MIN_H_SPEED	0.02	\mathbb{R}^2	km/h	-
Max. Host speed	MAX_H_SPEED	0.5	\mathbb{R}^2	km/h	-
Cattle’s activity start time	START_ACTIVE_TIME	9	\mathbb{R}	hour	-
Cattle’s activity end time	END_ACTIVE_TIME	16	\mathbb{R}	hour	-
New position of boid movement	velocity	(0,0)	\mathbb{R}^2	-	-
Resting status	rest	False	Boolean	-	-
Min. distance of perception	minimal_distance	50	N	meter	-
Carrying capacity	parasite_max	-	N	-	-
Movement behaviour	movement_beh	["R", "H"]	list	Cat.	-

2.2.3.2 Input data

The model is parameterized for the species *Ixodes scapularis*. Climate data used in this model are the Climatic Research Unit (CRU) TS Time Series datasets 4.04 [37]. This dataset is monthly estimates of Temperature recorded between the years 1990 and 2000 with a spatial resolution of (0.5x0.5 degree) grids for the region of Wisconsin. Fitting data points generate the daily estimates to a polynomial function of the order 3.

The parameters used in this model come from bibliographic data and/or the modeller's expertise, as detailed in table 2.

2.2.4 Submodels

2.2.4.1 Host's agent submodels

move_my_parasite submodel

We assume that the hosts will move the attached hosts on themselves following their position according to the *move_my_parasite* submodel. This submodel is common for both *Rodent* and *Cattle* agents. *Vector* agents attached to a *Host* agent change their location as per the host they are fixed on until they detach.

move_Cattle submodel

The *move_Cattle* sub-model simulates the movement and activity patterns of Cattle sub-agents. Two movement behaviours are considered in the *Cattle* and *Rodent* agents move randomly according to the *move_host_random* sub-model. Unlike the first scenario, *Cattle* agents follow a leader agent according to the *follow_leader* process, which itself follows a predefined path according to the *follow_path* sub-model starting from the centre of the barn and returning to it. *Cattle* agents, besides the leader, are moving in a herd cohesion according to a boid movement composed of the "separation", "alignment", and "cohesion" processes as described by [42], *Cattle* agents flocks to the centre of a mass of agents within the *minimal_distance*, and avoiding other agents while trying to match the position of other *Cattle* agent. If a current hour of the day is in the grazing time range, the *leader* will move with a random speed following the path. Otherwise, the *leader Cattle* agent will move to the centre of the barn *BARN_LOC*.

2.2.5 Vector's agent submodels

The attach submodel

The *attach* submodel describes the attachment of the vector to a host agent within the *PERCEPTION_DISTANCE* when its behaviour stage is questing. Vectors which have their life *sate* equal to "larva" attach to *Rodent* agent, *nymph* and *adult* attach both *Cattle* and *Rodent*. The *attach* submodel does not apply to *egg* since it is a free life stage.

The process of attachment has a probability *ProbIndAttach* dependent on the number of neighbouring hosts *NeighHosts* within the *PERCEPTION_DISTANCE*,

computed as follows:

$$ProbIndAttach = 1 - (0.8)^{NeighHosts} \quad (2)$$

Since the vector is more likely to attach to one of its hosts, the probability of attachment success “ProbIndAttach” is determined by the number of host in the range of the vector’s perception distance (refer to Equation 2). When applying a carrying capacity for the host, we assume that every host agent (both Cattle and Rodent agents) have a maximum number of vectors that can be attached to them *parasite_max*. The *attach* submodel is modified in a way that if the attribute *VectorOfParasite* is more or equal *parasite_max*, the vector agent will not attach to the host

detach submodel

This sub-model describes the detachment of vectors from the host after a successful blood meal. A successful blood meal is controlled by a fixed duration of the blood meal: *AttachToDetach* (refer to table 1). When this occurs, the *vector* detach from the *host* agent at a random proximate location, and its behaviour state, *BehState* updates to “moulting”.

develop submodel

The *develop* submodel considers the life stages transitions and diapause process. In this submodel, we consider the development of the vectors as daily temperature functions (Figure 5). Also, the *develop* submodel is itself organized into five processes, respectively, *diapause*, *moulting*, *preoviposition*, and finally *incubation*. The transition between each life state is the result of the success of the *attach*, *detach*, and *moult* submodels.

moult, preoviposition and incubation submodels

Based on the work of Ogden et al.,2004 [3], moult , preoviposition and incubation are temperature-dependant processes (refer to Figure 6). The development is incremented every day. We denote $f(t)$ the duration function for every life state , respectively, $m_{larva \rightarrow nymph}$, $m_{nymph \rightarrow adult}$, (Figure 6 and equations 3) and each behaviour is structured by life state i , respectively i_{moult} and $i_{preoviposition}$.

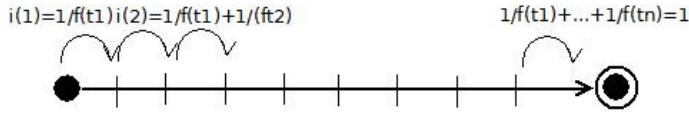


Fig. 5: A schematic diagram for the duration incremental function f .

We assume at every time step, the duration of moulting, respectively for larva into a nymph and nymph into an adult, the preoviposition and the incubation are computed according to, respectively, the equations 3, where m is, respectively, the moulting duration respectively for larva and nymph, preoviposition duration, and $T_{current}$ is the daily temperature (Figure 5,Equation 3).

$$\begin{aligned} m_{j(state1 \rightarrow state2)} &= aT_{current}^{-b} \\ i_{j(state1 \rightarrow state2)} &= i_{j(state1 \leftarrow state2)} + f(t) \end{aligned} \quad (3)$$

where

$$f(t) = 1/m_{j(state1 \rightarrow state2)}$$

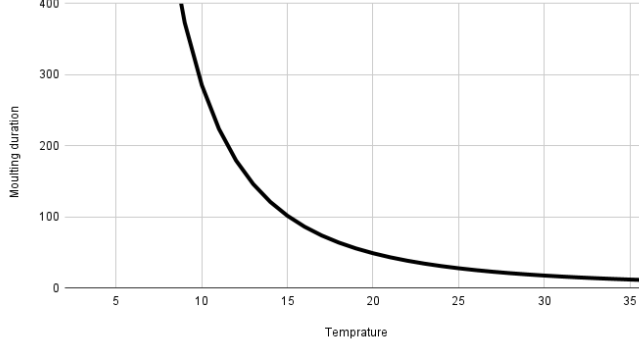


Fig. 6: The curve of the relationship of larva moulting duration with temperature variation.

diapause submodel

The *diapause* submodel describes the temperature-dependent process of the diapause. The diapause state is activated when the daily temperature reaches a life state-dependent threshold temperature (refer to table. 1). When the diapause state is activated, the development incremental function f approaches infinity $f \rightarrow \infty$, the *develop* submodel is paused until the daily temperature surpasses the diapause temperature threshold, then the *diapause* submodel is deactivated, and the *develop* submodel in its turn is activated.

death submodel

The *death* submodel describes mortality processes. Two types of mortality are considered in this submodel *natural mortality*, *environment-induced mortality*.

Natural mortality

Every day at the end of the day, each *vector* agent had a daily probability of mortality for every life state (refer to table 1). Also, all adult agents die after laying eggs.

Environment-induced mortality process

the *Environment-induced mortality* process is temperature-dependent. Every life state has a daily probability of death if the current daily temperature reaches the state-dependent lethal temperature threshold (refer to table 1).

3 Results

The objective of our simulations is to study the effects of host movement patterns on vector population dynamics as well as the effect of the carrying capacity of the host on vector population dynamics. Simulations were performed using the Gama 1.8.2 [43] platform. All simulations reproduce a duration of ten from October 1st 1990 until September 30th 2000.

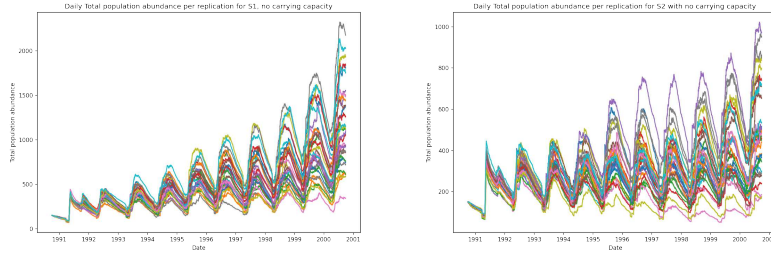
Two scenarios are tested for the movement behaviour of *Cattle* agent (refer to table 3). First, we run the random movement scenario (S1) and then the Herd movement scenario (S2). Both simulation scenarios were run using the same parameter values and initial state. First, we run the simulations with no carrying capacity applied (thereafter, they are defined as, respectively, S1-NC and S2-NC), and then, we fix the carrying capacity for both S1 and S2 (refer to subsection 3.3). We analyze the total and per-stage population and the total population abundance for all simulation sets. We run 30 replicas per simulation set.

Table 3: Experimental plan for the scenarios S1 and S2. For both S1 and S2, we vary the carrying capacity parameter for these different values.

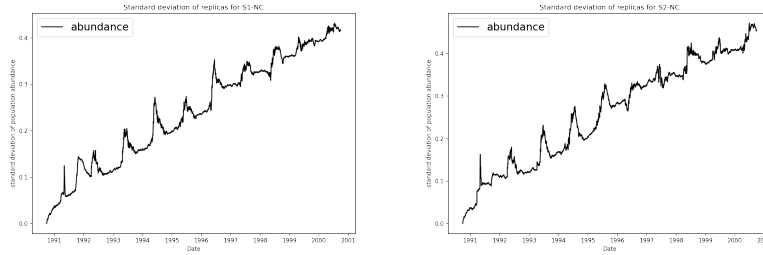
Parameter-Scenario	Scenario 1 (S1)	Scenario 2 (S2)
Host movement behaviour	Random movement	Herd movement
Carrying Capacity	{2, 3, 4, 5, 6, 7, 8, 9, 10}	{2, 3, 4, 5, 6, 7, 8, 9, 10}

3.1 Effect of simulations replication

The replication effect is analyzed for both scenarios (S1 and S2) with no carrying capacity applied (S1-NC and S2-NC), we observe an annual fluctuation in the total population abundance per replication (refer to Figure 7a and 7b). Additionally, there is a noteworthy disparity in the magnitude of fluctuation between both scenarios and within the replications of each scenario, which becomes significant over the last four years of the simulation time. This is confirmed by computing the standard deviation σ_i over the mean between the replication for both S1-NC and S2-NC (Figure 7c and Figure 7d).



(a) Population abundance per replica for the S1-NC (b) Population abundance per replica for S2-NC

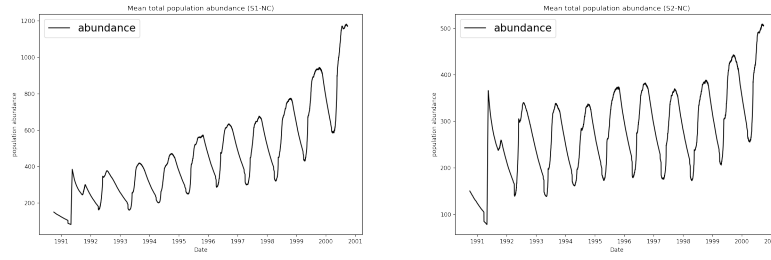


(c) Standard deviation σ over the mean per replica for S1-NC (d) Standard deviation σ over the mean per replica for S2-NC

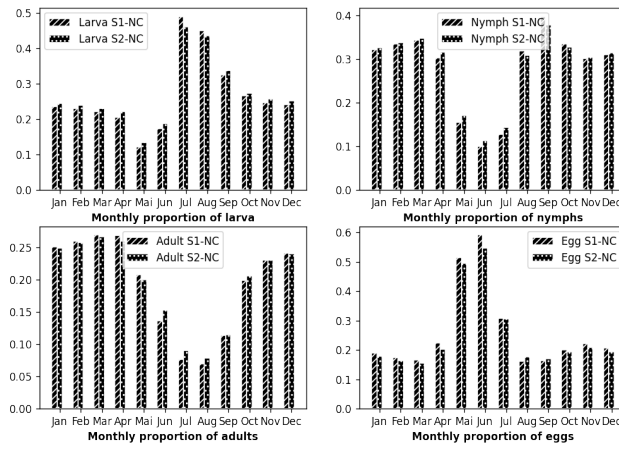
Fig. 7: Total population abundance and standard deviation σ_i , where i the replica index, over the mean, per replica for respectively for the first scenario with no carrying capacity applied (S1-NC) and for the second scenario with no carrying capacity applied (S2-NC).

3.2 Random movement Versus Herd movement patterns

The total population abundance for both scenarios (S1 and S2) increases over time while no carrying capacity is fixed. Specifically in S1-NC (Figure 8 and 8a). The mean population abundance $\bar{N}(t)$ grows exponentially from an initial value of 150 until reaching roughly 1200. In the second scenario, S2-NC, the mean population abundance knows a significant peak in the first year of the simulation, then, it recognizes a slight fluctuation in the yearly maximum, after which it reaches two new peaks, respectively, in the ninth and tenth year of the simulation (Figure 8b). For the first set of simulations (S1-NC and S2-NC), the total population has an increasing trend based on the Mann-Kendall Trend test ($p_{value} < 0.05$).



(a) Mean total population abundance (S1-NC) (b) Mean total population abundance (S2-NC)



(c) Monthly per-stage population abundance

Fig. 8: Mean total population with no carrying capacity (NC) and Monthly per stage population , respectively, for the first scenario with no carrying capacity applied (S1-NC) and for the second scenario with no carrying capacity applied (S2-NC).

Both simulation sets have roughly the same per-stage population distribution (refer to Figure 8c). The egg population knows a peak in early summer as expected [3,4]. Larva population emerged after the rise of the egg population in midsummer, followed by a peak of the nymph population in late summer. The adult population increases in early autumn and stays steadily high until late spring.

3.3 Host carrying capacity effect

We varied the carrying capacity of the host agent for both S1 and S2 and analysed the mean total population abundance over 10 years (Figure 9). For every simulation set, the carrying capacity of host values is fixed.

For low values of the parameter (refer to Figure 9a and 9b), representing a low number of vectors able to attach to the host, the average population decreases over the simulation time towards extinction. For higher values (refer to Figure 9c and 9d), the population decreases less steeply. A stabilization begins to take hold for both scenarios when the carrying capacity is equal to 8 (refer to Figure 9e and 9f). For the extreme value of the parameter, the population behaviour is similar to that of the scenario where the host's capacity limit is not applied in the first scenario (refer to Figure 7).

Scenario 1: Random pattern

We notice, as expected that the mean population abundance increases as the *parasite_max* values increase (Figure 10). We fitted the output into a linear least square regression for the 30th replicas for every parameter value (refer to Figure 10a).

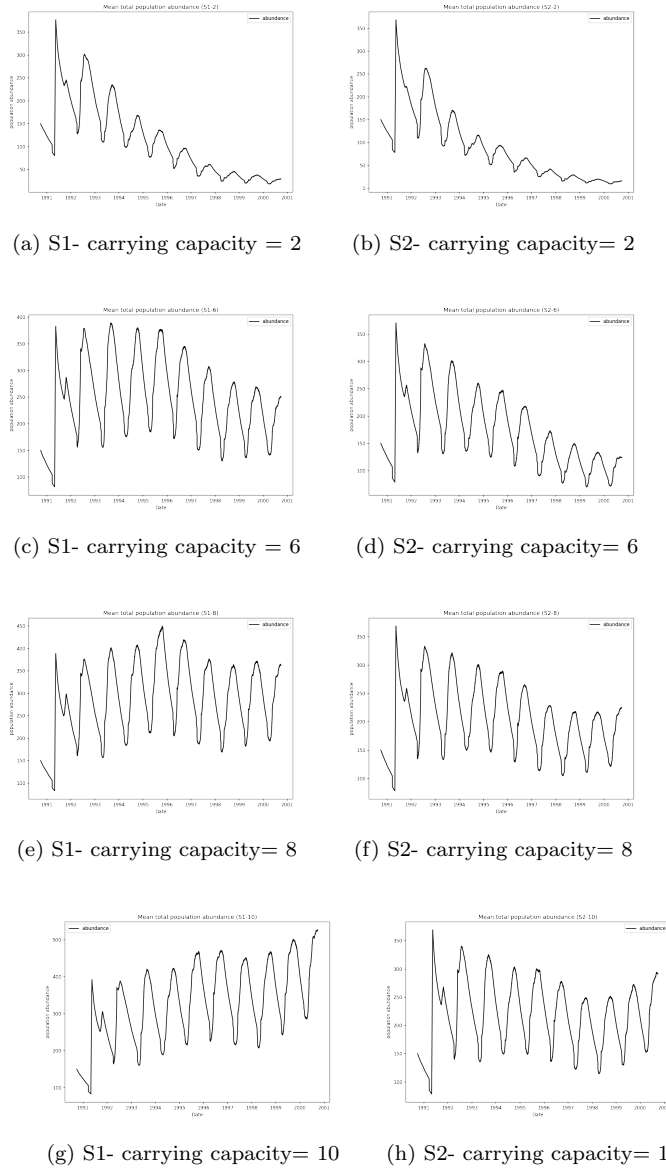
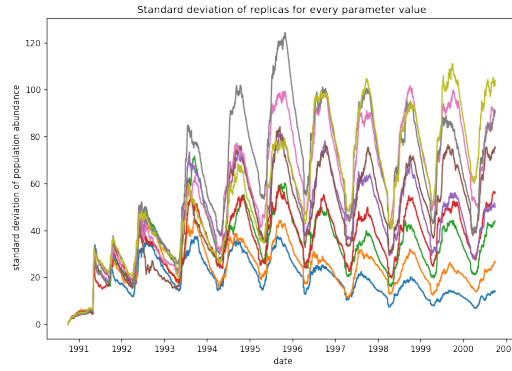
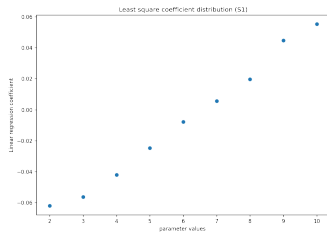


Fig. 9: Mean population abundance for both scenarios S1 and S2 for the different carrying capacity parameter values. The evolution of the mean population abundance is inversely proportional to the carrying capacity.



(a) Standard deviation of replicas for every parameter value



(b) Least square coefficient for S1

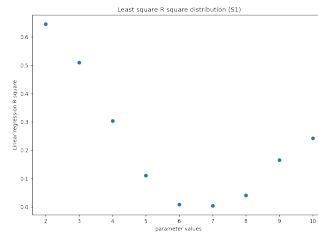
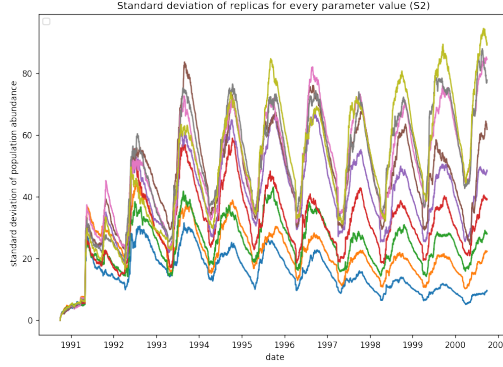
(c) R^2 for S1

Fig. 10: The figure shows the standard deviation and the fitting of replicas for the first scenario S1. (a) Standard deviation of replicas for each parameter value for S1. (c,d) Least square fitting of replicas for each parameter value for S1.

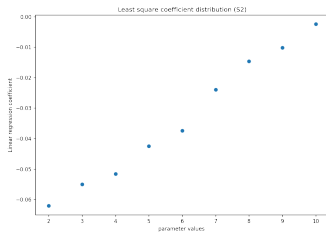
For S1, the least square coefficient increases gradually with the parameter value (refer to Figure 10b). Also, we notice the R^2 is the highest for the simulation set Sim2, as well as for the minor square coefficient, is the lowest for the carrying capacity is equal to 7 ($R^2 = 0.004$), then it is the value that best regulates our vector population (Figure 10c).

Scenario 2: Herd movement pattern

The same approach used for the first scenario, S1, is followed in the second scenario (Figure 10a and 11b). However, for the coefficient R^2 , we notice the best value for the carrying capacity is equal to 10 (Figure 11c).



(a) Standard deviation of replicas for every parameter value



(b) Least square coefficient for S2

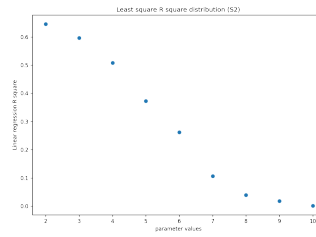
(c) Least square R^2 for S2

Fig. 11: The figure shows the standard deviation and the fitting of replicas for the second scenario S2. (a) Standard deviation of replicas for each parameter value for S2. (c,d) Least square fitting of replicas for each parameter value for the second scenario S2

4 Discussion

We developed an agent-based model to investigate the dynamics of tick populations. The model primarily aims to evaluate host movement patterns on tick population dynamics. We monitored annual and seasonal population fluctuations and population growth tendencies. We tested different host movement patterns while varying the carrying capacity of the host. The outcome of the different simulation scenarios suggests that the movement pattern of the host does not affect the seasonality of the vector agent, although it impacts its population abundance. Since the random movement pattern allows a higher likelihood for the host agent to be located within the perception distance of the vector agent, driving vectors, in a cascade effect, to execute the remaining processes and produce offspring. Furthermore, our model introduces an essential dimension by incorporating resource competition, mainly through host availability, as a significant regulatory factor influencing vector populations.

This approach enhances the generalization and formalizes the intricate relationship between vectors and hosts, making our model adaptable to a broad spectrum of vector and host species across diverse biogeographic regions. The most obvious finding to emerge from analyzing the carrying capacity of the host, on the one hand, is the exponential growth of the population when increasing the capacity of the host to attach vectors approaching the results of S1, and on the other hand, the extinction of the population when low carrying capacity is fixed, limiting the vector agents to continue other processes. Over ten years of simulations, we note that the population abundance shows a decreasing behaviour for both S1 and S2 while applying low carrying capacity parameter values. While the carrying capacity of the host increases, the population knows a gradual increase and tends to stabilize over time for both S1 and S2 until reaching a turning point for the simulation, where the population behaves as the one in S1 when no carrying capacity is applied.

So far, our work has focused on host movement patterns' effect on vector population on the one hand, and on the other hand, it focused on the grooming effect of the host illustrated in our model by the carrying capacity parameter.

This model complements studies *e.g.* [44, 45, 46] by incorporating temperature-dependent vector developmental stages, host-vector interactions, and the influence of host movement on tick species characterized by passive host-seeking behaviour, exemplified by *Ixodes ricinus*. Our model's uniqueness lies in its ability to encompass the entire tick life cycle, representing development as a temperature-dependent process and the sole interaction between vector and host through blood meals. Our model's hypotheses exhibit a robust capacity to replicate the seasonal dynamics of the vector population. Remarkably, this is achieved by considering only temperature as the regulating factor governing transitions between developmental stages. The unique aspect of our model lies in the sole dependence on the temperature as the tick life cycle regulator, as [2, 3] highlighted. While our model's assumptions are straightforward, they have proved essential in reproducing the tick's whole life cycle. Moreover, our model affords us a comprehensive descriptive framework for understanding the tick's life cycle, integrating physiological processes (illustrated by vector life state transitions and behavioural states of each instar) and ecological processes (captured through host availability for blood meals).

Also, our model seeks to explore the tangled mesh between ecological interactions at the individual level and their impact on physiological processes, particularly the development time of each life stage; the individual dependence on the temperature to develop will create a seasonality. This objective aligns with the distinction of various scales in ecology, as the scale of matter, from cellular processes to ecosystems, with individuals as the key link. This illustration of ecological scales facilitates the subsequent delineation of other dimensions, such as temporal and spatial scales ... ([47, 48, 49]).

The issues related to changes in scale levels are relevant, and coupling different scales in modelling is a challenge. Prior studies have underscored the importance of agent-based modelling in elucidating the complexities of vector-host systems (*e.g.* [10, 20, 24]). These studies have predominantly focused on

landscape characteristics, particular tick species, and host-specific models. Unlike its counterparts, our model does not rely on actual landscapes or the real movement of hosts; instead, it delves into a theoretical exploration. In doing so, it allows to examine intriguing ecological phenomena, such as the impact of temperature on developmental processes, in a controlled and hypothetical environment. This distinctive feature sets the stage to extend the model to simulate a wide spectrum of ecological complex systems featuring multiple species and real-world landscape complexities.

In addition to the possibility of extending the model to other tick species, it also has a potential for generalization to include other vector species, such as the *Anopheles* mosquitoes responsible for malaria transmission. The fundamental interactions between *Anopheles* and their hosts closely resemble those observed with ticks. However, a distinctive challenge arises when selecting an appropriate scale representing mosquito movement. When addressing mosquitoes, we can describe them as individual clusters exhibiting synchronous movement, collectively representing a single agent. Alternatively, we can model them as individual mosquitoes acting as individual agents, a concept already outlined in our model.

5 Conclusion

This work introduces an initial model designed to conceptualize the dynamics of the vector-host system, specifically focusing on investigating the impact of both host movement patterns and host carrying capacity on short-term vector population dynamics. The model's hypotheses are aligned within the framework of a hypothetical landscape encompassing host and vector populations while considering the vector physiological development as a temperature-dependent process. The simulation experiments carried out in our work substantiate the importance of host-carrying capacity in the dynamics of the vector population and contribute to our understanding of these complex interactions. One of the more significant conclusions to emerge from this work is that the temperature can regulate vectors' life cycle and keep the vector population dynamics seasonality. Moreover, the host movement behaviour has no effect on the vector dynamics. A natural progression of this model is to validate the findings with empirical data and extend it to cover more environmental factors and include vector-borne diseases since our model possesses the versatility to explore a variety of host- and environment-targeted control strategies, facilitating the identification of practical approaches for managing vector population dynamics in a broader ecological context.

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- Authors' contributions: C.C. co-conceived the conceptualization and methodology and co-performed the computation, writing and the original draft

preparation. N.M.: co-performed the computation, the validation and the reviewing and co-supervised the work S.B.M.: co-conceived conceptualization and methodology, co-performed the writing, reviewing and editing and co-supervised the work. All authors discussed the results and contributed to the final manuscript. All authors reviewed the manuscript

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