

A Tool for Simulating the Spread of Invasive Mosquitoes

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Abstract

There are many concerns about the spread and establishment of exotic mosquito species in Europe, some of which are highly competent to transmit pathogens. The fast spread of some invasive mosquito species, e.g. the Asian bush mosquito, might be explained by a combination of natural dispersal and human transport. Therefore, the aim of this study was the development of a software tool that is capable to model the local spatial-temporal spread of invasive mosquitoes through natural dispersal and their transportation through human transport via cars. The evaluation of the tool shows that it is capable to simulate the spread but also reveals the need for more biological data about invasive mosquito species.

1. Introduction

Mosquitoes can cause significant nuisance and are important vectors of several pathogens [8]. Therefore, this group of insects was and is subject of research all over the world, but especially in areas with health concerns due to mosquito-borne diseases, e.g. Africa [5]. Nevertheless, in view of the worldwide range expansion of several mosquito species, some of which are highly competent to transmit pathogens, the interest in this research topic is also increasing in other geographical areas [2]. Especially climate change and globalisation are considered to facilitate the spread and establishment of these species [2,27].

There are many concerns about the introduction and establishment of exotic mosquito species in Europe, some of which are highly competent to transmit pathogens [16]. The worldwide most important invasive mosquito species is the Asian tiger mosquito (*Aedes albopictus*). The species is known to be a highly competent vector of several pathogens and is considered to be the vector, which caused the autochthonous transmission of Chikungunya virus [6,19] and Dengue virus [4,14,20] in Southern Europe. Surveillance studies at potential introduction sites in Germany identified motorway service stations as important gateways [1,10,18,26]. Individuals of the Asian tiger mosquito are considered to enter cars or trucks in Southern Europe, where the species is established since several years and transported by transit traffic.

The fast spread of another invasive mosquito species in Germany, the Asian bush mosquito (*Ochlerotatus japonicus*), highlighted the necessity of dispersal analyses and the demand for modelling tools to predict the spread of invasive mosquito species. The species was firstly detected in the year 2008 in Southern Germany at the border to Switzerland. During the following years, the species was found to spread fast in Southern Germany and additional populations were detected in Northern Germany (reviewed by [11]). The fast spread of the Asian bush mosquito might be explained by a combination of natural dispersal and human transport [25]. The distribution and habitat preference of invasive mosquitoes were analysed in several studies in Europe. At least for the Asian tiger mosquito there are several habitat models on the basis of climate data and landscape parameters, which give information on the actual and potential distribution in Europe [3]. However, there are only few studies on the spatial-temporal spread of invasive mosquito species via traffic

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[23]. This applies in particular to the small scaled, regional spread through natural dispersal and human transport (e.g. cars). Information on the potential spread of invasive species especially can help to develop an adequate surveillance program and control strategies.

Therefore, the aim of this study was the development of a software tool that is capable to model the local spatial-temporal spread of invasive mosquitoes through natural dispersal and their transportation through human transport via cars.

2. Mosquito Tool

A software tool for predicting a possible exposure of mosquitoes has to take the passive transport by vehicles as well as the active dispersal of mosquitoes into account. These two processes take place on different scales in time and space. Such multi-scale modelling is often used to model physical phenomena [24]. Hoekstra et al. [7] studied the modelling of complex automata by coupling cellular automata with different temporal and spatial scales. A framework for modelling ecological systems as multi-scale models has already been proposed [21,22]. The theoretical background of this framework models complex spatial processes on different scales by so-called hierarchical asymmetric cellular automata, which allow the coupling of cellular automata (layers) with different spatial and time scales as well as restricted interactions between layers. The *Mosquito Simulation Tool (MoSiTo)* presented here follows this approach. It consists of two automata: the *MosquitoCA* on a spatial fine-scale layer and the Tool *VASim*, which models the dissemination of mosquitos by traffic on a coarse spatial level.

Both components of *MoSiTo* have been prototypically implemented in Python as a Plugin for the geographic information system QGIS (version 1.8 and 2.x, resp.) and can also be used independently from each other.

2.1. Traffic network Tool *VASim*

Tourist traffic from regions with established mosquito populations are considered as a potential reason for mosquito dispersal. The traffic network tool *VASim* ([17]) models this transport.

The transport can be viewed as a generalized (asymmetric) cellular automaton [21] where the cells represent *starting points*, *stops* (at resting places, motorway stations), and *destinations of vehicles*. The neighbourhood relation is determined by a traffic route from the starting point to the destination with stops in between.

The movement of cars on a traffic route and the release of mosquitos at stops is modelled by the cells' state: The cell at the starting point of the route is initialized with a *vehicle object*. Each *vehicle object (VO)* represents a set of cars, which traverse the same route. It is characterized by parameters to describe its behaviour:

- The minimal distance between *stops* (d_{min}) and its *mileage* determine where the *vehicle object* will *stop* and possibly release mosquitos.
- The distribution of the number of mosquitos inside the *VO* at the start of the simulation and the probability for *mosquitos leaving* the vehicle at every single *stop* determine how many mosquitos will be initially in the *VO* and leave it at a *stop*.

Beside the information about the *VO*, the cell stores the distance to the prior cell (attribute *length*) and the number of mosquitos, which have been released (attribute *mosquitos*). The behaviour is modelled as transfer step and update step:

- The transfer step moves the *VO* information to the next cell:

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cell[i+1].VO = cell[i].VO
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- The update step describes the release of mosquitos inside a cell:

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cell[i].VO.mileage += cell[i].length
If cell[i].VO.mileage > random_km(cell[i].VO.dmin):
    mosquitos_out = random_Mosquitos(cell[i].VO.inside)
    cell[i].mosquitos += mosquitos_out
    cell[i].VO.inside -= mosquitos_out
    cell[i].VO.mileage = 0

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The random-functions allow random deviations from the minimal distance between stops of a vehicle and from average number of mosquitos released.

Hence, a traffic route defines a one-dimensional cellular automaton. As it is possible to assign an arbitrary number of routes to one simulation scenario, a more complex neighbourhood relation is possible.

For initialization of *VASim* at least one traffic route between arbitrary starting points and destinations and a list of possible *stops* along the route (rest areas, service stations) must be specified as xml-documents. *VASim* extracts the cell attributes and topology from these inputs. The documents can be generated by the web services OpenRouteService (<http://openrouteservice.org>) and the Overpass API (<http://www.overpass-api.de/>), which are based on OSM XML OpenStreetMap data. The vehicle objects at the starting position of each route are initialized according to user-specified probability distributions for the initial number of mosquitos inside and the release of mosquitoes.

So far *VASim* does not model time explicitly. In one simulations step the *VO* is transferred from one cell to the following - the real time, which corresponds to this transition, depend on the distance between the *stops*, i.e. *length* of the cells.

2.2. MosquitoCA

The *MosquitoCA* [13] models the autonomous dispersal and the possibility of establishing a population as a fine-scale 2-dimensional cellular automaton with a regular grid of cells. The dynamic is based on the static data about the area using the Corine landcover information (<http://www.eea.europa.eu/>) and integrates climatic information about the regional temperature.

Each cell is characterized by its habitat quality factor ($hab \in [0,1]$), the number of its adult mosquitoes (*adults*) and mosquito larvae (*larvae*), which vary during the simulation. The maximum mosquito or larvae capacity of cells depends on the habitat quality. Hence the optimal capacities of adult mosquitos (A_{max}) or larvae (L_{max}) are reduced by the habitat quality factor. The size of the cells depends on the flying range of the mosquito species in the given time step.

The dynamics of the number mosquitoes per cell depends on the mortality rate (m), reproduction rate (r), the length of a gonotrophic cycle (u), i.e. the time span of alternate feeding and laying of eggs, and the larvae's development rate d . u and d depend on climatic factors (temperature) and are defined as in [15]. The variable P describes the length of a time step in the simulation and corresponds to one day.

The default dynamic of the cellular automaton is based on rules for reproduction, mortality, and dispersion based on the MALCAM model published by [15] with some minor improvements concerning the different habitat qualities. The dynamic of adults and larvae inside each cell is determined by

$$larvae(t) += P \cdot (adults(t-1) \frac{r}{u} - d \cdot larvae(t-1)) \cdot hab \cdot \left(1 - \frac{larvae(t-1)}{L_{max} \cdot hab}\right)$$

$$adults(t) += P \cdot (d \text{ larvae}(t - 1) - m \text{ adults}(t - 1)) \cdot hab \cdot \left(1 - \frac{adults(t - 1)}{A_{max} * hab}\right)$$

Alternatively to this predefined dynamics inside each cell, user specified rules can be specified and used in *MosquitoCA*.

For each cell the number of leaving mosquitos is computed as in [15] by

$$leaving(t) = adults(t) \cdot \frac{P}{u}$$

We simplified the MALCAM model for the entering of cells: the flow of mosquitos from cell[i] to cell[j] is computed by cell[i].leaving(t) weighted by the normalized habitat quality factor of cell[j]:

$$cell[j].entering(t) = cell[i].leaving(t) \cdot \frac{cell[j].hab}{\sum_{k \text{ neighbor of } i} cell[k].hab}$$

The simulation of *MosquitoCA* results in a map, which shows the distribution and abundance of mosquitoes in the cellular automaton.

2.3. Coupling

MosquitoCA and *VASim* are only loosely coupled: In a first step, *VASim* computes the *initial occurrences of mosquitos* at the *stops* along the routes for a given set of routes and *vehicle objects*. These *stops* comply with cells of the *MosquitoCA*. This allows to check, whether the suspected traffic flows are able to transport mosquitos that far. Starting from these *stops* as initial places, *MosquitoCA* computes the *dispersal* of mosquitoes.

In the next version of *MoSiTo*, we plan to integrate a refined time concept: as the survival rate of transported mosquitos and the behaviour of the mosquitos depend on the time of the day, in future version *VASim* cells will transfer mosquitos numbers tagged with a time stamp information.

Evaluation scenarios

For ensuring the correct implementation of the underlying models, the *MoSiTo* layers *MosquitoCA* and *VASim* have been successfully tested separately with virtual scenarios. Due to the limited availability of data about the detailed behaviour of neozoa and their spread, we based our real world evaluation on existing publications.

2.4. Scenario 1: Spread of Mosquitos

The fast spread of the invasive Asian bush mosquito (*Ochlerotatus japonicus*) in Germany highlights the necessity of dispersal analyses and the demand for modelling tools to predict the spread of invasive mosquito species. The species was firstly detected in the year 2008 in Southern Germany at the border to Switzerland. During the following years, the species was found to spread fast in Southern Germany (reviewed by [11]). This spread is probably due to natural dispersal and, therefore, is a good case study to evaluate the *MosquitoCA* tool.

Huber et al. [9] presented a map where the Asian bush mosquito has been found in 2011. Their study only included punctually data. Therefore, raster grids cells in a resolution of a topographic map (1:25.000, 18km×10km) were defined as colonized, if at least one positive point lay in the respective grid cell. As this scale is much too coarse for a detailed simulation, we initialized the automaton with 135×55 cells of size approx. 0.01×0.01 square degree (1.1km×1.1km) and focused to the infested area in the south of Baden-Württemberg, using a daily rates of 0.1 (mortality *m*) and 1.0 (reproduction rate *r*), and a constant temperature of 20°C. The habitat qualities of the cells were derived from the Corine landcover data 2006 on a 250m×250m grid. Based on expert knowledge

the landcover types were classified as “not suitable”, “medium suitable” and “very suitable” and each cell was assigned a habitat quality of 0.01, 0.5 or 10, resp. As the cell size of *MosquitoCA* and the Corine grid differed, the landcover in the centre of the cell determined its habitat quality.

In order to start *MosquitoCA* with the map of 2011, about 20 cells in the infested area were initialized with 1000 mosquitoes and 5000 larvae and (pre-)simulated for 25 time steps (days). Figure 1 shows the occurrence of mosquitoes and after the pre-simulation phase with 2011 distribution data [9]. The infested areas from 2011 show a medium to high occurrence of mosquitoes. Below the simulated occurrence after about 120 time steps can be seen with a map section of the 2014 distribution.

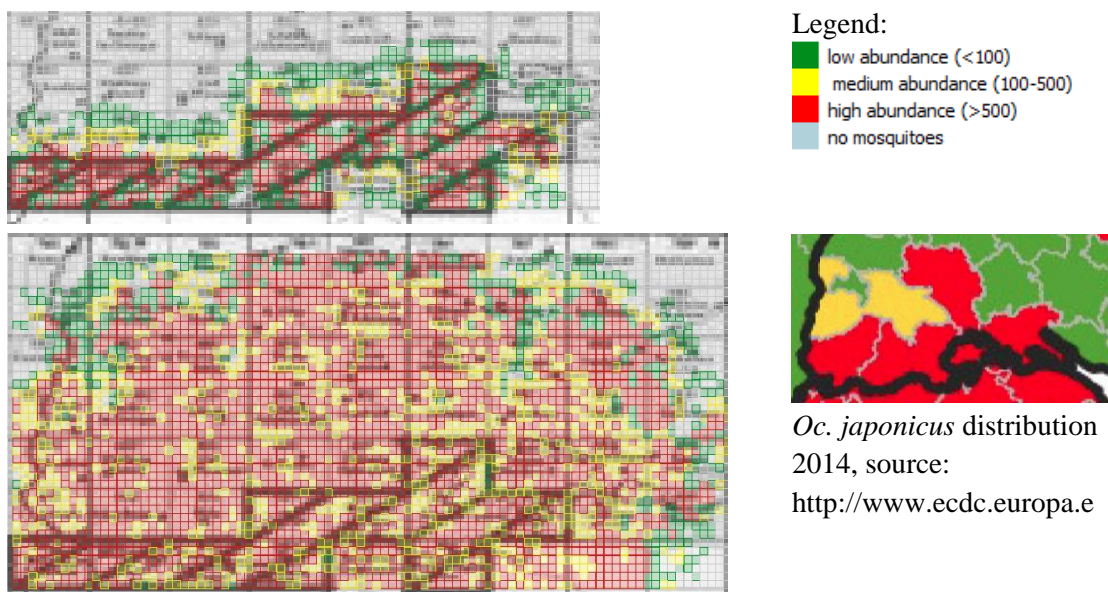


Figure 1: Simulated mosquito occurrences after pre-simulation (left, upper) and after 120 timesteps (left, lower). Positive *Ochlerotatus japonicus* raster grids in 2011 [9] in a resolution of a topographic map (1:25.000, 18km×10km) are edged dark gray (left, upper). Small sketch in the right show the observation from *Ochlerotatus japonicus* in this region from 2014.

Our modelling results showed a much faster spread of *Ochlerotatus japonicus* compared to the observed spread in the real-world. This might be explained by different reasons: 1) the input data do not have a very good quality and are only based on a very broad meshed mosquito survey. Colonized areas with very low *Ochlerotatus japonicus* might be not detected. Therefore, the currently published distribution maps might not reflect the actual distribution of the species. 2) Furthermore, our model use several assumptions and simplifications, e.g. each cell have the same, relatively high temperature (20°C) and there are no temperature variations in space and time, which significantly accelerate the spread in our model. Therefore, the incorporation of upper and lower development temperature thresholds might give a more realistic picture.

2.5. Scenario 2: Transport and Spread

Further *Ochlerotatus japonicus* foci were detected in Northern Germany (reviewed by [11]), which appeared to be too far away to be explained by natural dispersal, but might be explained by human transport via car traffic [25]. Therefore, this scenario 2 was used to evaluate the *VASim* tool in the first place. Beyond that, subsequent simulation of the spread with the tool *MosquitoCA*, starting from service stations might explain findings of the main traffic routes.

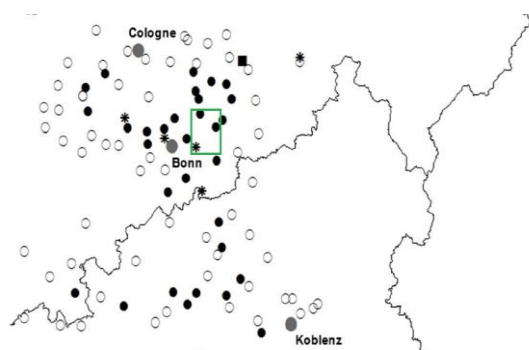


Figure 2: Mosquito findings in [12], dark points: presence of *Ochlerotatus japonicus*. Green frame: location of scenario 2

In scenario 2, the object of investigation was the possibility of an introduction of mosquitoes from southern Germany by traffic which is passing the motorway junction Weilheim (nearby Heilbronn and the most northern point of *Ochlerotatus japonicus* observation in the federal state Baden-Württemberg [9]) and going north in direction to motorway junction Hilden (nearby Düsseldorf). North bound motorway routes in this area were generated by OpenRouteService and service stations along the routes were determined by the web service Nominatim. The “fastest route” via the motorways A67 and A3 crosses the north eastern region of further *Ochlerotatus japonicus* foci [12].

VASim was initialized with three routes having each 1000 *vehicle objects*. Each VO was meant to represent a set of cars with an average of 60 mosquitoes per VO, an initial, uniform distributed *initial mileage* of 50 up to 250 km, and a *minimum distance between stops* of 200 km. Figure 3 shows the number of VOs (“Cars”) and the final number of exposed mosquitos per station. The stations have been sorted by their (Euclidean) distance from the start at Weilheim. Figure 3 shows that the number of released mosquitos correlates linearly to the number of cars. Despite the uniform distribution of the initial mileage, waves of resting cars become obvious.

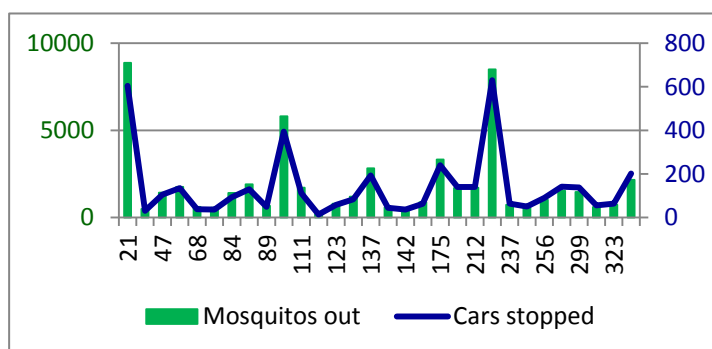


Figure 3: Distribution of stopping cars (right axis) and released mosquitoes (left axis) per stations. The X-axis shows the distance of the stations to the starting point at Weilheim.

The *Ochlerotatus japonicus* observations from [12] were located by manually georeferencing the sketch (Figure 2). The resulting map was validated using Open Street Map data locations of cemeteries.

Figure 4 shows the modelling results of scenario 2 produced with the *MosquitoCA* tool. For the service station Siegburg West at km 299, an exposure of 1460 Mosquitos was computed by VASim and simulated by *MosquitoCA* in order to prove, if the nearby findings at locations in the north, east and south-west can be attributed to exposures at Siegburg West. Each of these positive sites has a distance of about 5 km. With the parameters of the scenario, Corine landcover data with a resolution of 100m×100m and nearly equally sized cells (0.0015×0.0015 square degrees), we

found, that only the observations in the eastern location can be explained. Figure 4 shows the simulation after 100 and 200 simulation steps.

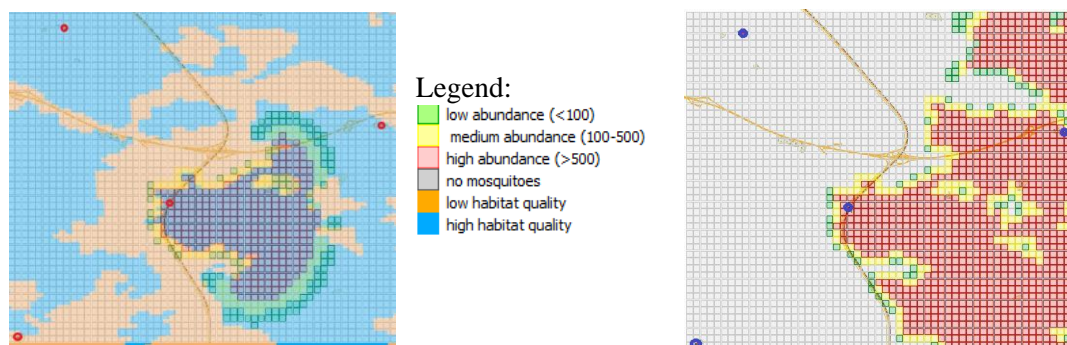


Figure 4: Simulation starting at station Siegburg West after 100 (left) and 200 simulation steps (right). In the left picture, a map of habitat quality is shown in the background. Due to land use barriers, the dispersal is only directed eastwards.

As stated above, the tools of *MoSiTo* are only loosely coupled and communicate asynchronously via data files. As a next step, it is planned to allow a tighter and timed coupling between the two layers, which will also allow the integration of seasonal changes in traffic flows as well as in the *mosquitoes' survival* conditions into the model.

Conclusion

The research on invasive mosquito species predominantly focus on static information about the recent and future distribution based on environmental data and lacks studies and tools to predict and understand the spatial-temporal spread especially on the regional and local scale. The tool *MoSiTo* with its layers *VASim* and *MosquitoCA* is the first approach, combining the natural dispersal and the transportation through human transport via road traffic. From the vector ecologist's perspective, the tools can help to understand the historic dispersal of exotic mosquito species. However, the ultimate objective of this project is the establishment of a tool, which allows predicting the future spread and distribution of the exotic mosquito species. This tool offers extensive application possibilities, e.g. an exact geographic definition for the design of mosquito surveillance or control programs. The next steps in this ongoing project are the evaluation of the system by real world scenarios as well as the enhancement of the layers by a refined concept of time.

References

- [1] Becker, N., Geier, M., Balczun, C., Bradersen, U., Huber, K., Kiel, E., Krüger, A. et al., "Repeated introduction of *Aedes albopictus* into Germany, July to October 2012", *Parasitol Res*, vol. 112, no. 4, pp. 1787–1790, 2013.
- [2] Benedict, M. Q., Levine, R. S., Hawley, W. A., and Lounibos, L. P., "Spread of The Tiger: Global Risk of Invasion by The Mosquito *Aedes albopictus*", *Vector-Borne Zoonotic Dis*, vol. 7, no. 1, pp. 76–85, 2007.
- [3] D. Fischer, S. M. Thomas, M. Neteler, N. B. Tjaden, C. Beierkuhnlein, "Climatic suitability of *Aedes albopictus* in Europe referring to climate change projections: comparison of mechanistic and correlative niche modelling approaches", *Euro Surveillance*, no. 19 (4), pp. 1–13, 2014.
- [4] Gjenero-Margan I. (et al.), "Autochthonous dengue fever in Croatia, August-September 2010", *Euro Surveillance*, vol. 16, no. 19805, 2010.
- [5] Godfray, H. Charles J. and Coulson, T., "Mosquito ecology and control of malaria", *J Anim Ecol*, vol. 82, no. 1, pp. 15–25, 2013.
- [6] Grandadam, M (et al.), "Chikungunya virus, southeastern France", *Emerg Infect Dis*, no. 17, pp. 910–913, 2011.

- [7] Hoekstra, A., Caiazzo, A., Lorenz, E., Falcone, J.-L., and Chopard, B., “Complex Automata: Multi-scale Modeling with Coupled Cellular Automata”, 2010. In *Simulating Complex Systems by Cellular Automata*, ed. Jiri Kroc, Peter M. Sloot, and Alfons G. Hoekstra, 29–57. Understanding Complex Systems: Springer Berlin Heidelberg. http://dx.doi.org/10.1007/978-3-642-12203-3_3.
- [8] Hubálek, Z., “Mosquito-borne viruses in Europe”, *Parasitol Res*, vol. 103, no. S1, pp. 29–43, 2008.
- [9] Huber, K., Pluskota, B., Jöst, A., Hoffmann, K., and Becker, N., “Status of the invasive species *Aedes japonicus japonicus* (Diptera: Culicidae) in southwest Germany in 2011”, *J Vector Ecol*, vol. 37, no. 2, pp. 462–465, 2012.
- [10] Kampen, H., Kronefeld, M., Zielke, D., and Werner, D., “Further specimens of the Asian tiger mosquito *Aedes albopictus* (Diptera, Culicidae) trapped in southwest Germany”, *Parasitol Res*, vol. 112, no. 2, pp. 905–907, 2013. <http://dx.doi.org/10.1007/s00436-012-3128-y>.
- [11] Kampen, H. and Werner, D., “Out of the bush: the Asian bush mosquito *Aedes japonicus japonicus* (Theobald, 1901) (Diptera, Culicidae) becomes invasive,” *Parasit Vectors*, vol. 7, no. 1, p. 59, 2014.
- [12] Kampen, H., Zielke, D., and Werner, D., “A new focus of *Aedes japonicus japonicus* (Theobald, 1901) (Diptera, Culicidae) distribution in Western Germany: rapid spread or a further introduction event?”, *Parasit Vectors*, vol. 5, no. 1, 2012.
- [13] Klich, D., Vogel, U., Lühken, R., Kiel, E., “Entwicklung eines Software-Prototypen zur Modellierung des Ausbreitungsprozesses von Mückenarten”, 2013. In *Modellierung und Simulation von Ökosystemen: Workshop Kölpinsee 2012*, ed. Nguyen X. Thinh. Berichte aus der Umweltinformatik. Aachen: Shaker.
- [14] La Ruche G. (et al.), “First two autochthonous dengue virus infections in metropolitan France”, *Euro Surveillance*, vol. 15, no. 19676, 2010.
- [15] Linard, C., Ponçon, N., Fontenille, D., and Lambin, E. F., “A multi-agent simulation to assess the risk of malaria re-emergence in southern France”, *Ecol Model*, vol. 220, pp. 160–174, 2009.
- [16] Medlock, J. M., Hansford, K. M., Schaffner, F., Versteirt, V., Hendrickx, G., Zeller, H., and van Bortel, W., “A Review of the Invasive Mosquitoes in Europe: Ecology, Public Health Risks, and Control Options”, *Vector-Borne Zoonotic Dis*, vol. 12, no. 6, pp. 435–447, 2012.
- [17] Mengelkamp, M., “Mengelkamp, M., (2013): Erweiterung eines Zellularen Automaten-Modells um eine Netzwerkkomponente zur Simulation des verkehrsbedingten Ausbreitungsprozesses von Neozoen,” Bachelor Thesis, University of Oldenburg, 2014.
- [18] Pluskota, B. (et al.), “First record of *Stegomyia albopicta* (Skuse) (Diptera: Culicidae) in Germany,” *European Mosquito Bulletin*, no. 26, pp. 1–5, 2008.
- [19] Rezza, G. (et al.), “Infection with chikungunya virus in Italy: an outbreak in a temperate region”, *Lancet*, no. 370, pp. 1840–1846.
- [20] Schmidt-Chanasit, J. (et al.), “Dengue virus infection in a traveller returning from Croatia to Germany”, *Euro Surveillance*, vol. 15, no. 19677, 2010.
- [21] Sonnenschein, M. and Vogel, U., “Hierarchische asymmetrische Zellulare Automaten zur Modellierung ökologischer Systeme auf mehreren Skalen”, 2001. In *Theorie und Modellierung von Ökosystemen: Workshop Kölpinsee*. ASIM Mitteilungen AMB 80, ed. A. Gnauck, 37–50.
- [22] Speckels, B., Sonnenschein, M., Vogel, U., and Stierand, I., “The ecoscape framework for spatially explicit multiple-scale modelling of environmental”, 2003. In *Proceeding 4th Mathmod Vienna: ARGESIM Report No. 24*, ed. I. Troch and F. Breitenecker. 2 vols.
- [23] Tatem, A. J., Hay, S. I., and Rogers, D. J., “Global traffic and disease vector dispersal”, *PNAS*, vol. 103, no. 16, pp. 6242–6247, 2006.
- [24] Weinan, E., *Principles of multiscale modeling*. Cambridge, New York: Cambridge University Press, 2011.
- [25] Werner, D. and Kampen, H., “The further spread of *Aedes japonicus japonicus* (Diptera, Culicidae) towards northern Germany”, *Parasitol Res*, vol. 112, no. 10, pp. 3665–3668, 2013.
- [26] Werner, D. (et al.), “Two invasive mosquito species, *Aedes albopictus* and *Aedes japonicus japonicus*, trapped in south-west Germany, July to August 2011”, *Euro Surveillance*, vol. 17, no. 20067, 2012.
- [27] Ying Zhang, Peng Bi, and Hiller, J. E., “Climate Change and the Transmission of Vector-Borne Diseases: A Review”, *Asia-Pac. J. Public Health*, vol. 20, no. 1, pp. 64–76, 2008.