# arbocartoR: An R package for *Aedes*-borne disease risk assessment and vector preparedness

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Summary

Aedes-borne diseases such as dengue, Zika, and chikungunya are expanding globally in both tropical and temperate regions (Hedrich et al., 2025; A. Lim et al., 2025). Effective risk assessment and preparedness requires modelling tools that integrate mosquito ecology, human behavior, epidemiological processes, environmental conditions, and spatial heterogeneity (A.-Y. Lim et al., 2023). In this context, decision-makers and field operators increasingly rely on operational tools that can translate complex scientific knowledge into actionable information (Brown et al., 2025).

arbocartoR is an R package providing a mechanistic and spatially explicit modelling framework for *Aedes aegypti* and *Aedes albopictus* populations and for the transmission of major arboviruses. It implements a coupled SEIR (human) / SEI (mosquito) metapopulation model using the `SimInf` R package (Widgren et al., 2019, 2025), which is well suited for metapopulation compartmental models in epidemiology.

Stochastic epidemiological transitions are simulated using a Gillespie-type algorithm, while mosquito population dynamics are modelled deterministically through a detailed life-cycle representation implemented in compiled C code. This explicit representation of mosquito life stages allows the exploration and comparison of a wide range of vector-control scenarios targeting specific biological processes.

arbocartoR provides a vector- and disease-specific implementation of this framework, exposed through user-oriented functions for data preparation, simulation, and analysis. It is intended for both research and operational public health applications, with a specific focus on risk assessment, preparedness, and vector-control planning. Unlike some complementary platforms, arbocartoR does not model health system characteristics such as detection capacity or case management.

Statement of need

Operational management of *Aedes*-borne disease risk requires models that are spatially explicit, mechanistic, and computationally efficient, while remaining accessible to non-specialist users such as public health agencies and vector-control services. In particular, operational actors need tools that allow the exploration of alternative vector-control strategies and their effects on mosquito populations and disease transmission dynamics at a spatial resolution appropriate to

the vector management. Existing tools often lack either the flexibility to represent intervention-specific biological mechanisms or the usability required for routine operational use (Eisen & Lozano-Fuentes, 2009).

arbocartoR addresses this need by building on both the broader ARBOCARTO modelling projects and the SimInf framework for stochastic compartmental modelling in metapopulations. While SimInf provides a performant and flexible simulation engine, it requires advanced expertise to define model structure, parameters, and data formats. arbocartoR bridges this gap by providing a ready-to-use SEIR/SEI model tailored to *Aedes*-borne diseases and by automating the construction of SimInf-compatible inputs from epidemiological, environmental, and spatial data.

A key feature of arbocartoR is its explicit and detailed representation of the mosquito life cycle, which enables the simulation and comparison of vector-control scenarios targeting specific stages or processes of mosquito development. In contrast to platforms such as the ECDC AedesRISK tool, arbocartoR does not yet incorporate health system components (e.g. surveillance performance, reporting delays, or healthcare capacity), and focuses on vector dynamics, transmission processes, and intervention mechanisms.

The package complements existing tools from the ARBOCARTO ecosystem, including the ARBOCARTO Java application focused on vector population dynamics (Marti et al., 2025). It prioritizes modularity, transparency, and reproducibility, and is designed to serve as a modelling backbone for R-based decision-support tools used by researchers, public health authorities, and vector-control practitioners.

Model implementation

arbocartoR is based on a detailed mosquito life-cycle dynamics model (Tran et al., 2013) coupled with an epidemiological model that explicitly accounts for human mobility between spatial units (based on Soriano-Paños et al., 2020). This coupled framework has been implemented using the SimInf package, which provides a high-performance engine for compartmental disease models in a metapopulation context.

Mosquito population dynamics are modelled deterministically through a biologically detailed life cycle, including aquatic and adult stages, driven by environmental conditions. These deterministic processes are implemented within SimInf using compiled C code, allowing efficient simulation alongside the stochastic epidemiological components.

The epidemiological core of arbocartoR corresponds to a coupled SEIR (human host) and SEI (mosquito vector) model. Stochastic epidemiological transitions, including infection, incubation, and recovery processes, are simulated using a Gillespie-type algorithm as implemented in SimInf. Human mobility between spatial units is represented through movement matrices, produced using TDLMpackage (Lenormand, 2023), that modulate contacts and pathogen transmission across the metapopulation.

arbocartoR does not reimplement the simulation engine. Instead, it defines a vector- and disease-specific model structure and provides user-oriented functions that translate user inputs into the core SimInf objects:

- gdata, containing global biological and epidemiological parameters (specific to the vector species and virus);
- ldata, describing spatial heterogeneity across sub-populations;
- pts_fun, encoding the deterministic mosquito life-cycle processes, as well as the time-dependent variables.

These objects are generated automatically by functions such as build_gdata(), build_ldata(), and iniState() from environmental data, vector species, pathogen characteristics, human mobility information, and optional intervention scenarios. The assembled model is executed

89 via run_arbocartoR(), which passes the complete specification to SimInf for simulation. This
90 design leverages the computational efficiency of SimInf while providing an accessible and
91 reproducible interface for applied and operational users.

Package installation and use

93 The package can be installed either from CRAN or directly from its development repository on
94 GitLab. On Windows systems, installation from source requires Rtools.

```r
install.packages("remotes")
library(remotes)
remotes::install_gitlab("astre/arbocartoR", host = "https://gitlab.cirad.fr")
```

95 After installation, arbocartoR provides 10 user-facing functions, three example datasets, and
96 complete documentation. Three vignettes are included to guide users through the modelling
97 workflow, from data preparation to simulation and output visualization.

98 The main entry point of the package is run_arbocartoR(), which executes simulations of
99 mosquito population dynamics and disease transmission. The function returns demographic and
100 epidemiological trajectories that can be explored using the built-in plotting function plot_TS()
101 or standard R visualization tools.

Functional overview

103 Most other functions are dedicated to preparing inputs, constructing model parameters, and
104 defining simulation scenarios:

function	description
filter_meteo	Validate and optionally subset meteorological datasets
estim_K	Draft spatial carrying capacities from expert knowledge (non-validated inputs)
iniState	Construct the initial state of the metapopulation
build_gdata	Assemble the list of global parameters
build_ldata	Build the matrix of local parameters
build_E_random	Generate optional pathogen introduction events for epidemiological simulations (optional)
build_mMov	Build the contact-probability matrix (optional; based on TDLM package ; Lenormand (2023))
build_prev_control	Define vector-control actions to include in the simulation (optional)

105 The overall workflow of the package is summarized in Figure 1. The central simulation function
106 run_arbocartoR() is surrounded by data checking and formatting steps, model construction,
107 optional scenario components, and output visualization.

Figure 1: Function network of the arbocartoR package.

Key arguments of run_arbocartoR()

run_arbocartoR() requires four main inputs:

- **parcels** local characteristics of each spatial unit.
- **meteo** daily meteorological data (temperature in degree and accumulated rain in millimeters) for each spatial unit and simulation day.
- **vector** specification of the *Aedes* species of interest.
- **virus** specification of the pathogen to simulate.

Further details are provided in the documentation of run_arbocartoR(), parcels, and meteo.

The function returns a list of data.table objects containing the outputs of each simulation.

Simulated demographic and epidemiological trajectories can be plotted directly using plot_TS().

Example

```r
library(arbocartoR)

traj <- run_arbocartoR(parcels = parcels,
                       meteo = meteo,
                       vector = "Ae. albopictus (D)",
                       virus = "DEN")

plot_TS(traj, stage = "newEggs")
```

Code availability

arbocartoR is available on CRAN (https://cran.r-project.org/web/packages/arbocartoR) and the full source code, including documentation and vignettes, is openly available on GitLab (https://gitlab.cirad.fr/astre/arbocartoR).

Acknowledgements

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