dynamAedes

A unified population dynamic modelling framework for invasive *Aedes* species

Daniele Da Re (University of Trento, Edmund Mach Foundation)
Matteo Marcantonio (Joint Research Center)

19th September 2024

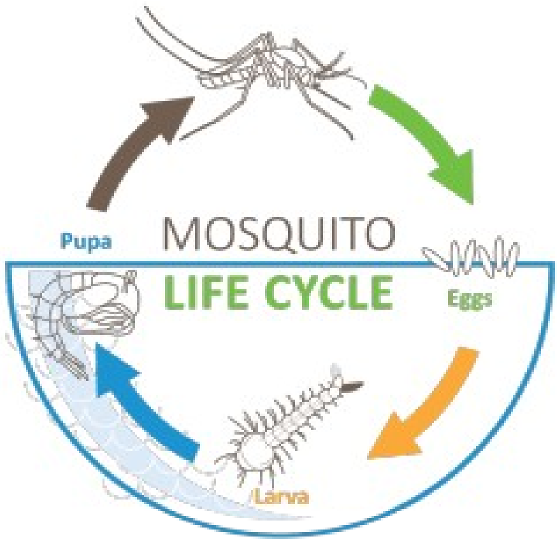
Ae. aegypti

Ae. albopictus

Ae. japonicus

Ae. koreicus

Ph: ECDC 2022



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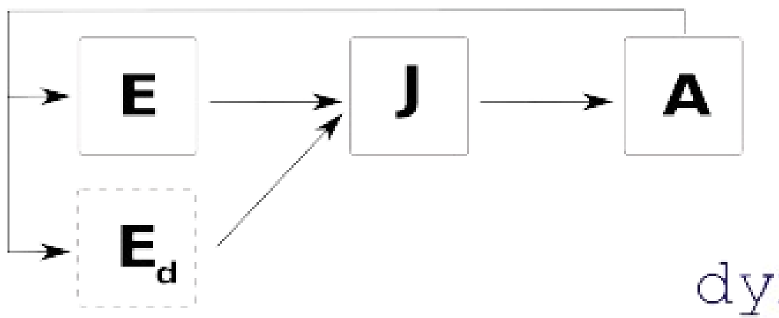
Da Re et al. 2022, *Parasite&Vectors*

Model structure



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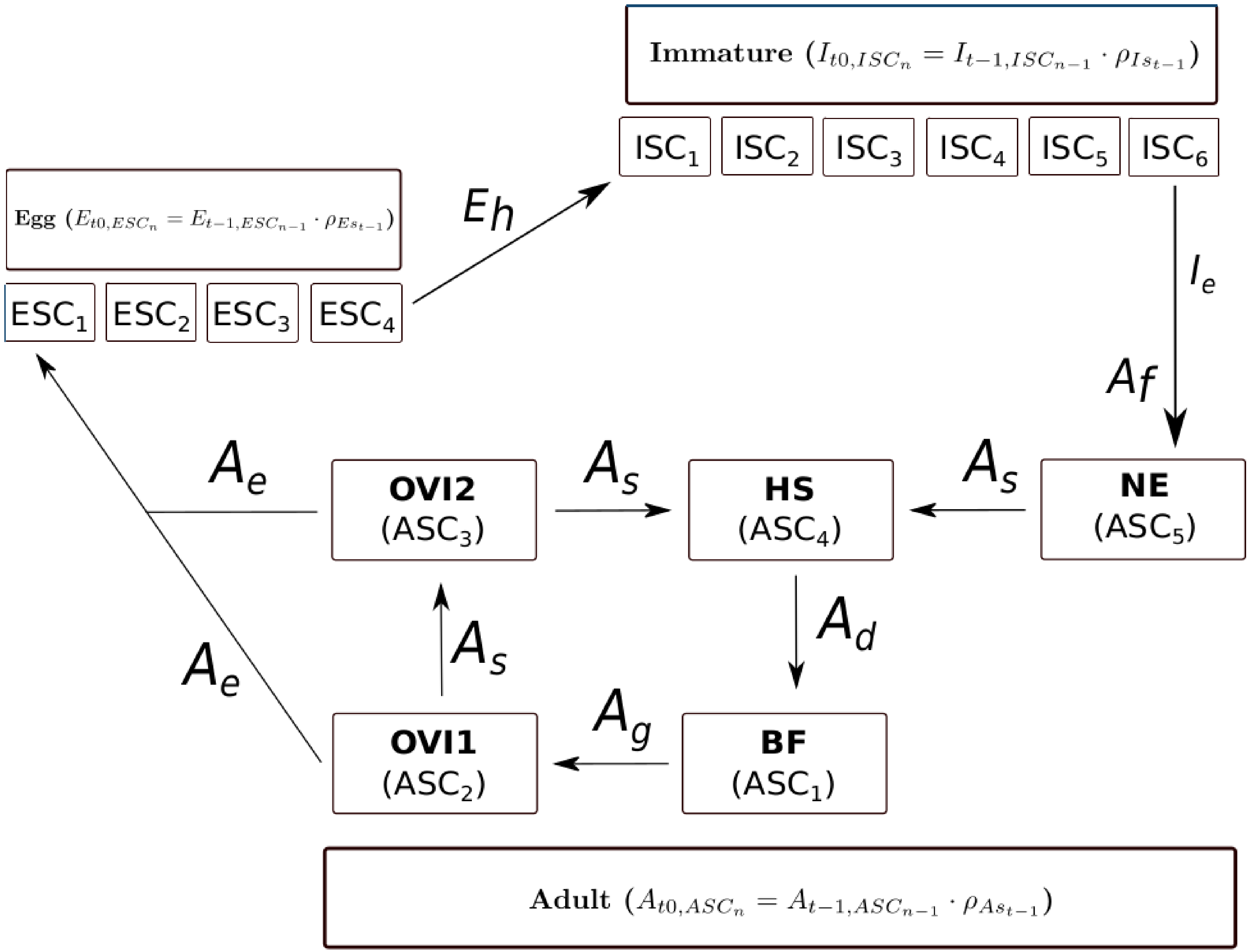
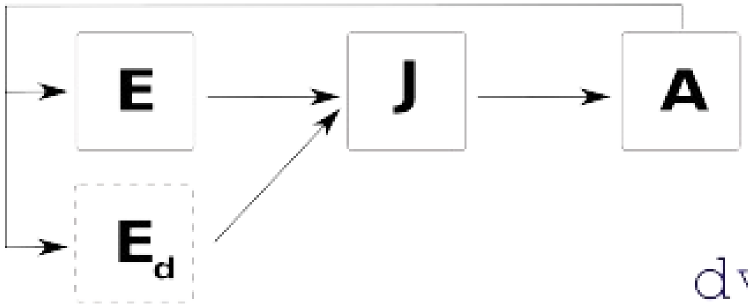


Immature $(I_{t0,ISC_n} = I_{t-1,ISC_{n-1}} \cdot \rho_{Is_{t-1}})$
ISC_1 ISC_2 ISC_3 ISC_4 ISC_5 ISC_6
Egg $(E_{t0,ESC_n} = E_{t-1,ESC_{n-1}} \cdot \rho_{Es_{t-1}})$
ESC_1 ESC_2 ESC_3 ESC_4
E_h
I_e
Af
A_e
OVI2 (ASC_3)
A_s
HS (ASC_4)
A_s
NE (ASC_5)
A_d
A_s
A_e
A_g
OVI1 (ASC_2)
BF (ASC_1)
Adult $(A_{t0,ASC_n} = A_{t-1,ASC_{n-1}} \cdot \rho_{As_{t-1}})$

Model structure



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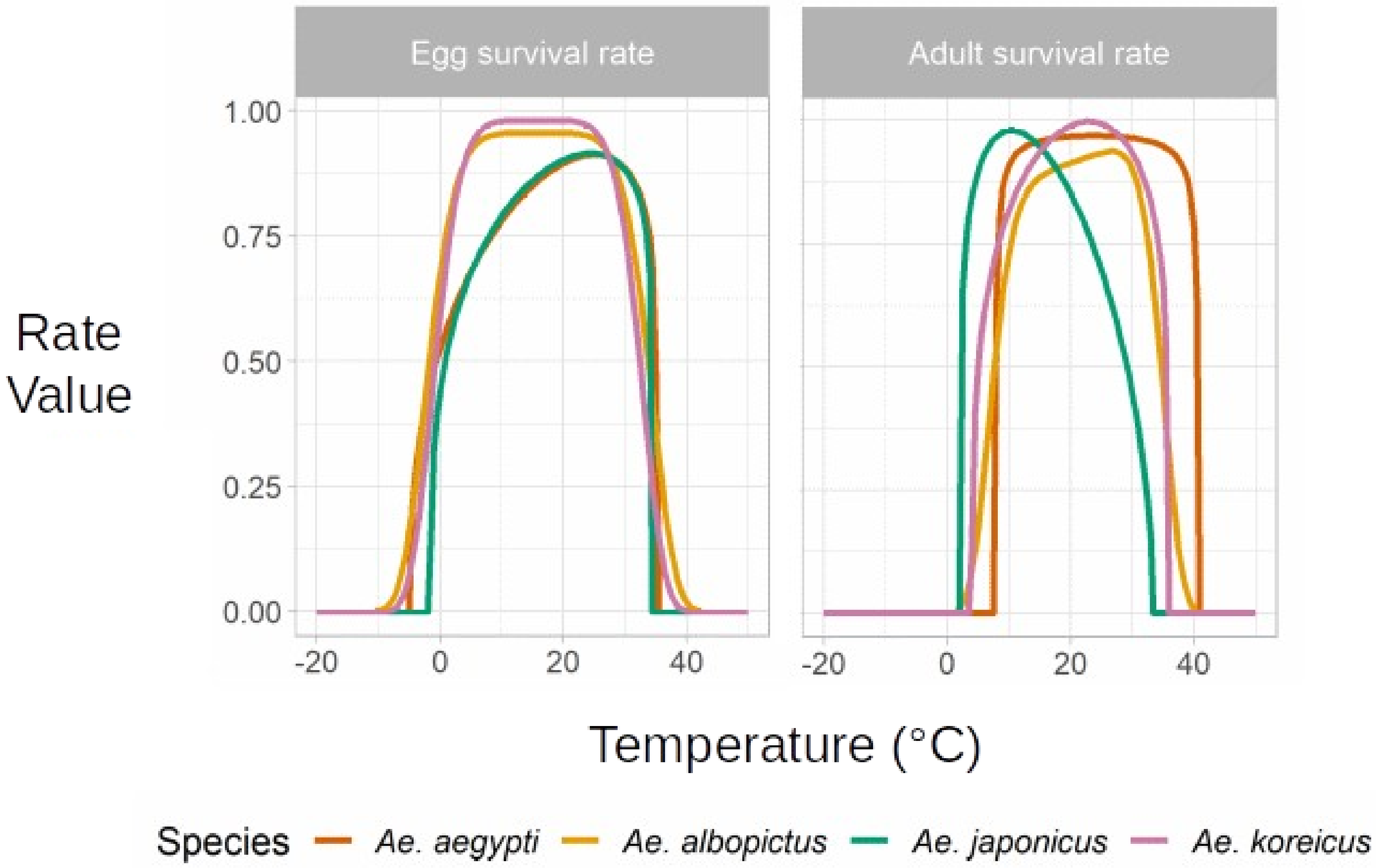
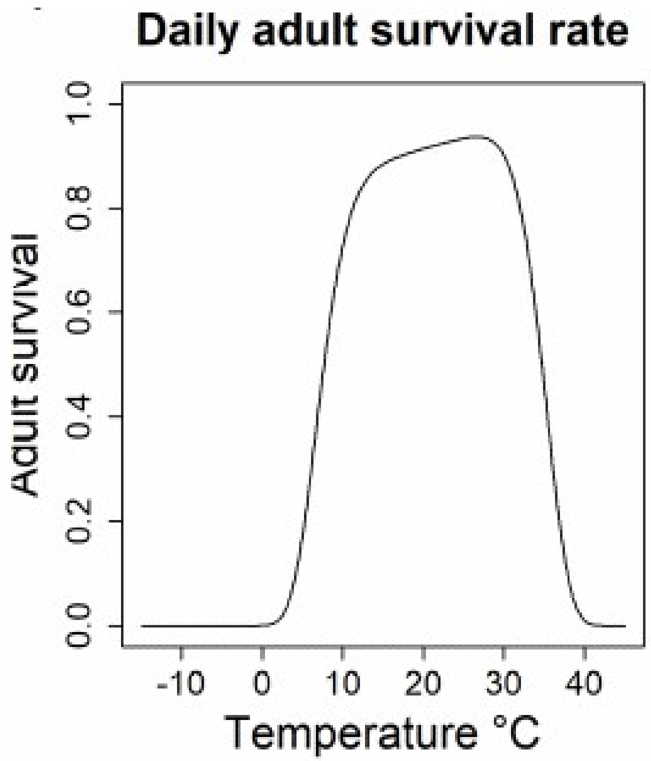
Mortality and **hatching** rates:
- Temperature-dependent
- Density dependent
- Photoperiod-dependent


Egg survival rate
Adult survival rate
Rate Value
1.00
0.75
0.50
0.25
0.00
-20
0
20
40
Temperature (°C)
Species
Ae. aegypti
Ae. albopictus
Ae. japonicus
Ae. koreicus

Binomial draws informed by temperature-dependent functions



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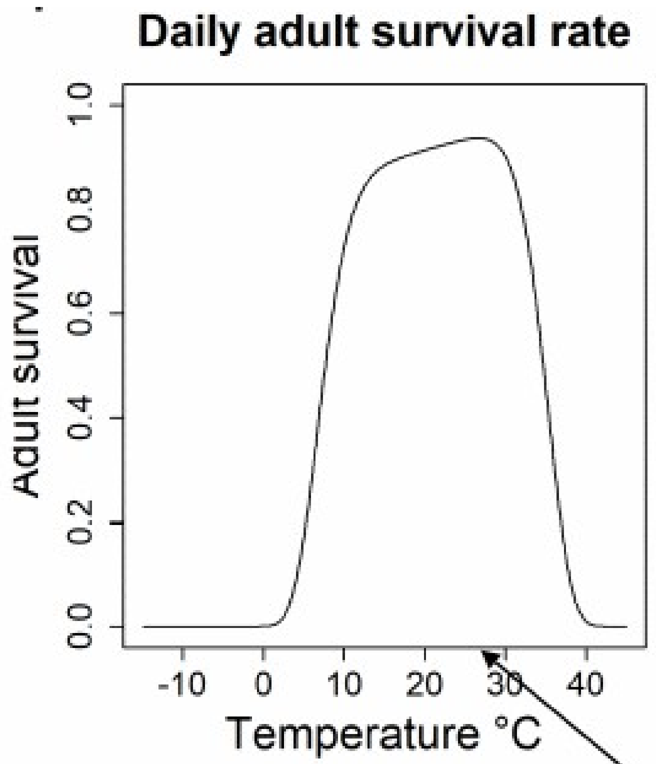

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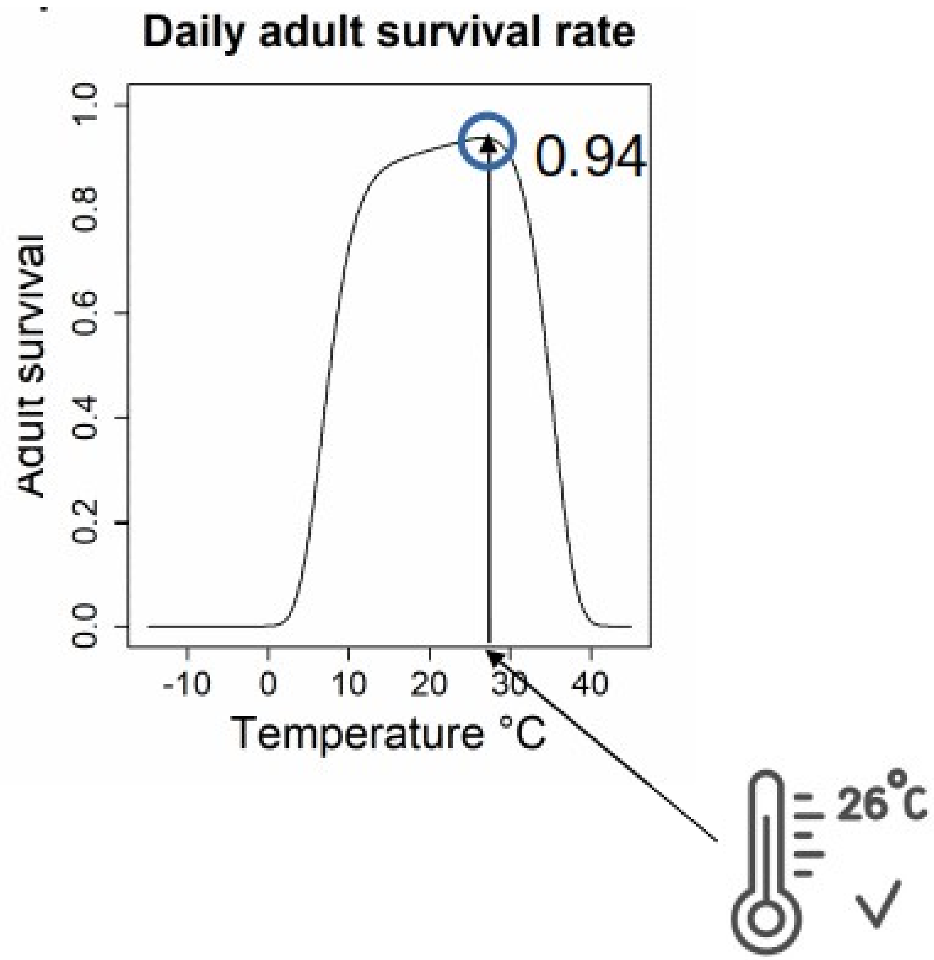

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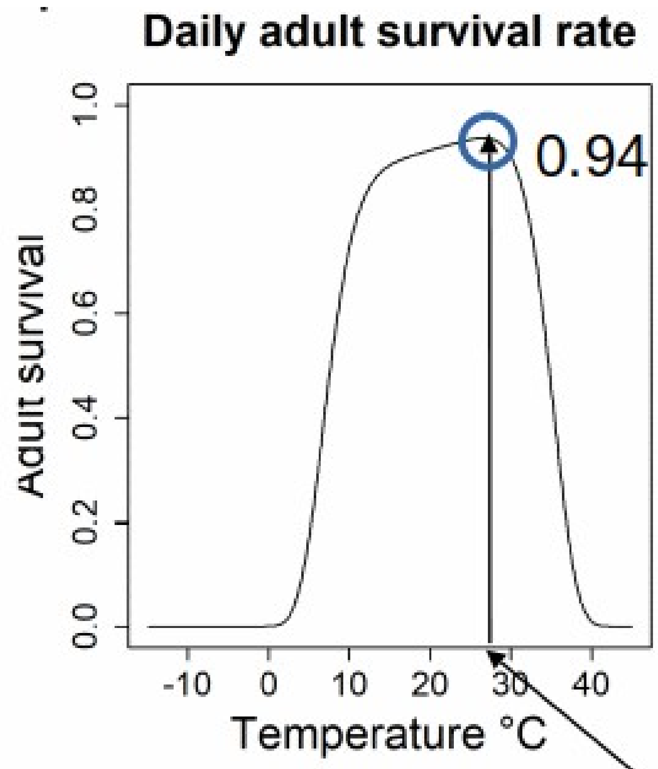
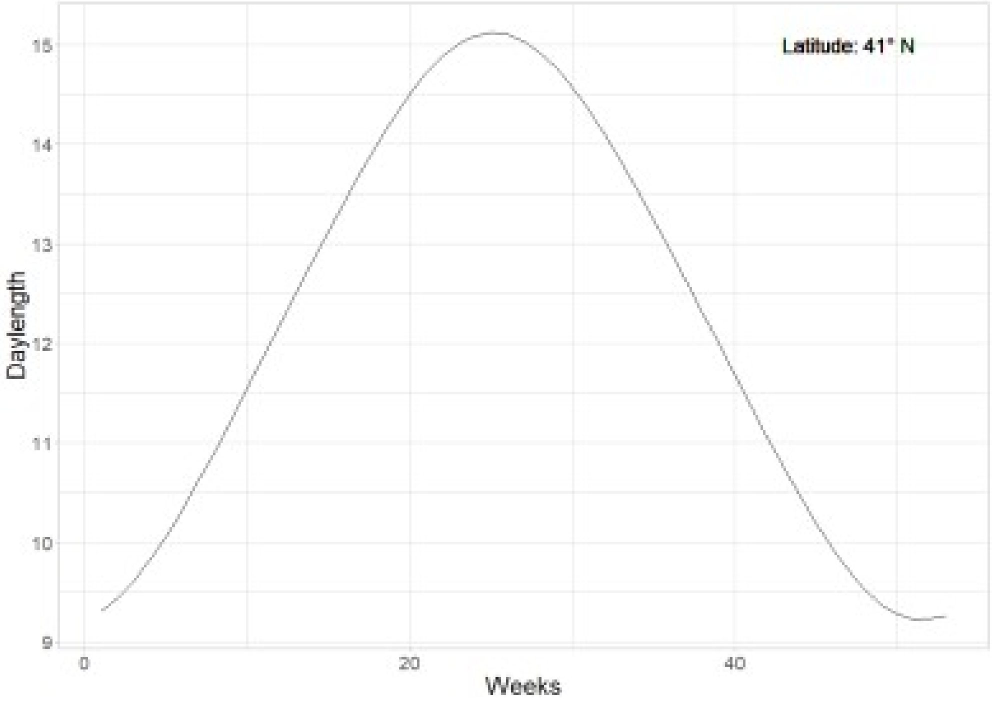



```
rbinom(PopulationSize=500, prob=0.94)

466
```

Diapausing eggs and photoperiod



Lacour et al., 2015, *PlosOne*

Krupa, Henon & Mathieu et al., 2021, *Parasite*

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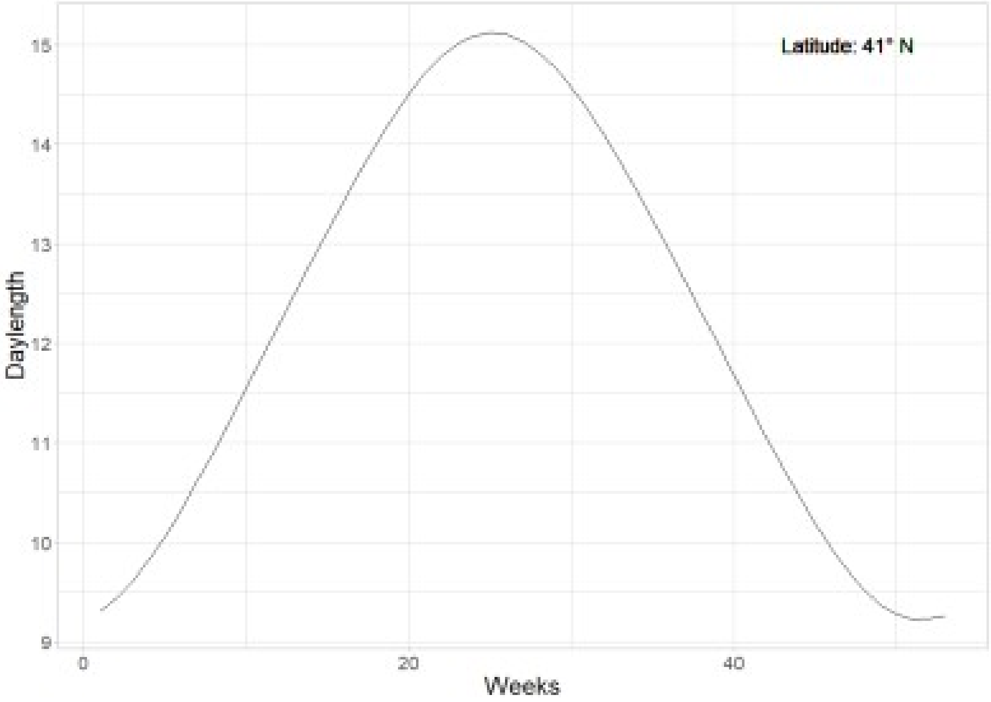

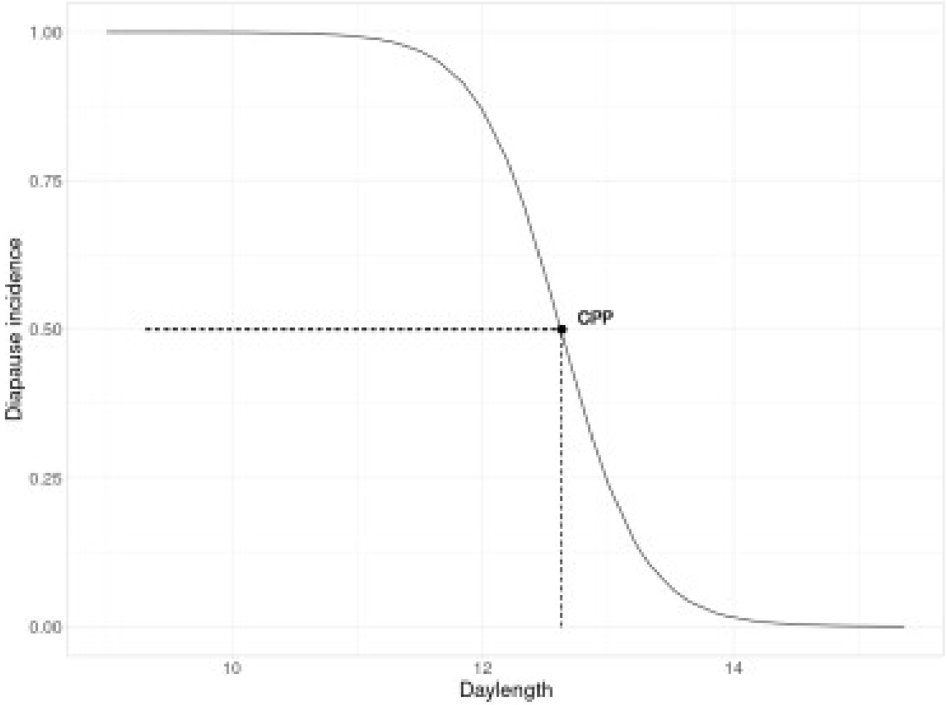

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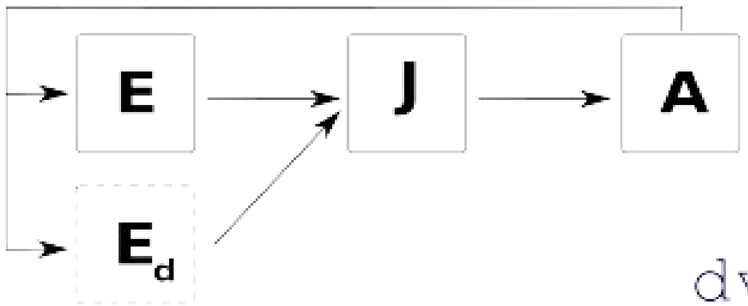

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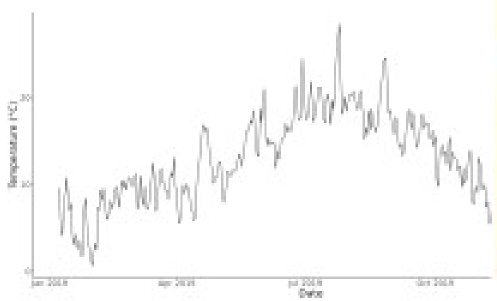
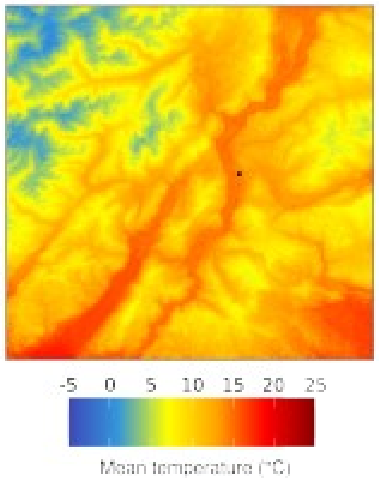
Input temperature datasets

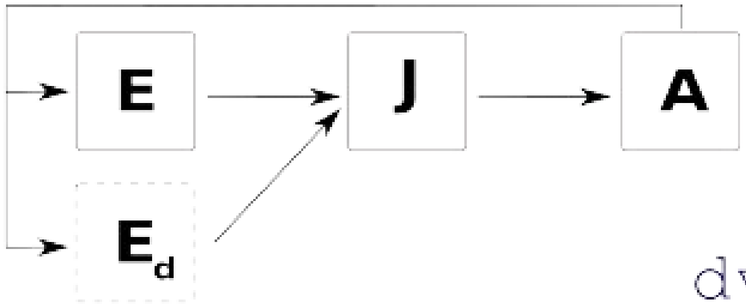
Temporal



Spatial



Model structure



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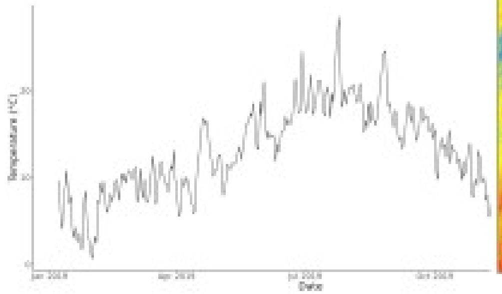
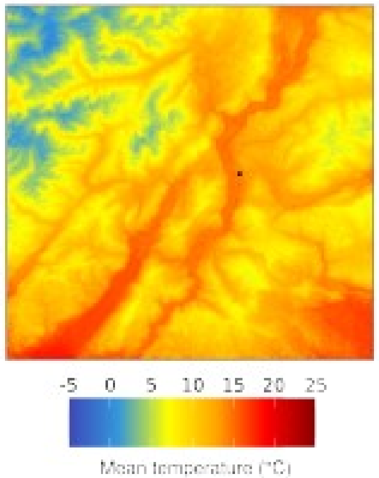
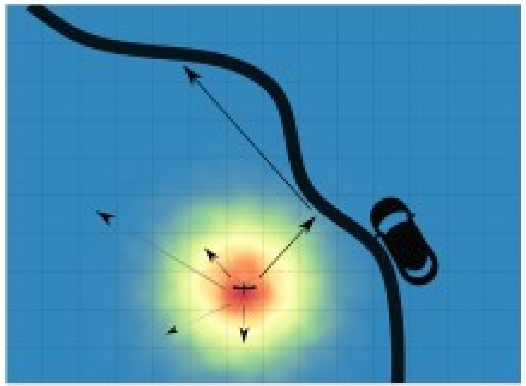


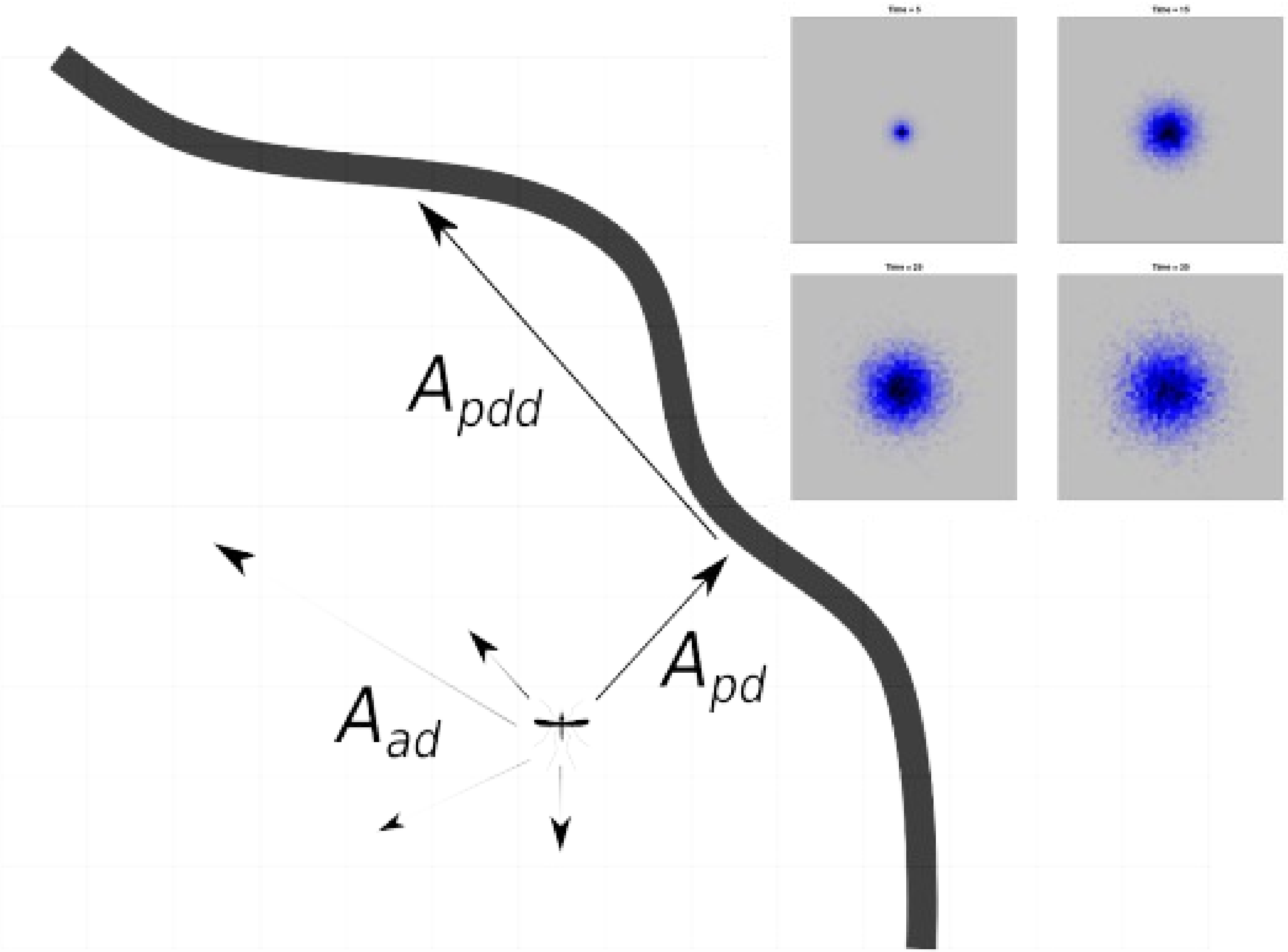
Spatial



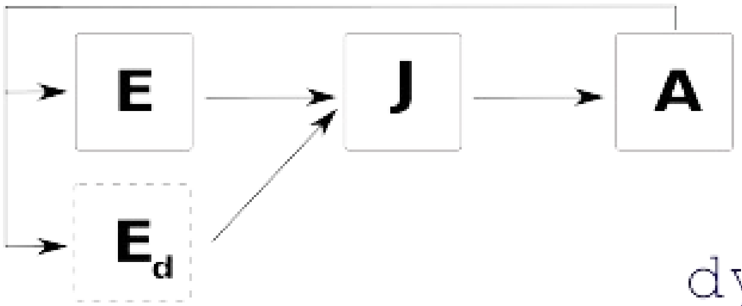
Adults' active and passive dispersal



Active and passive dispersal



Model structure



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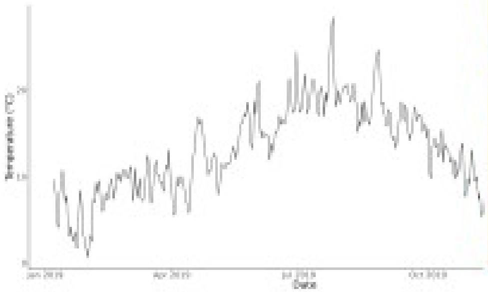
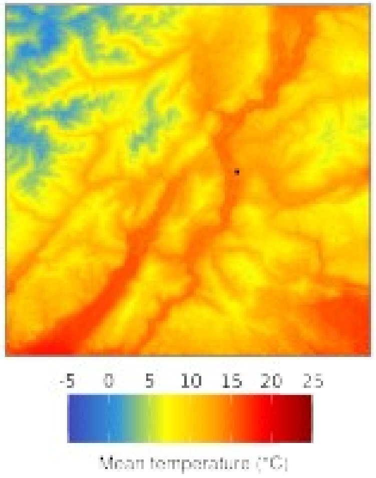
Temporal



Spatial



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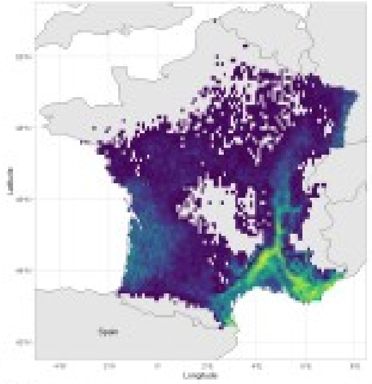
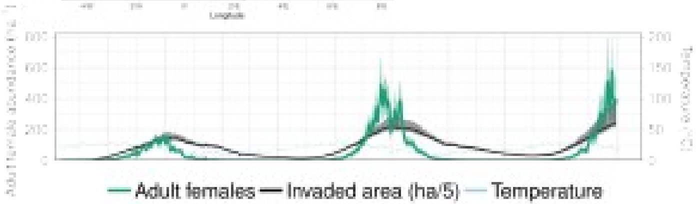
Outputs

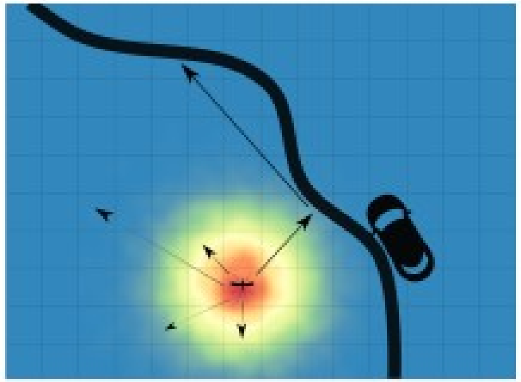


% of successful introduction



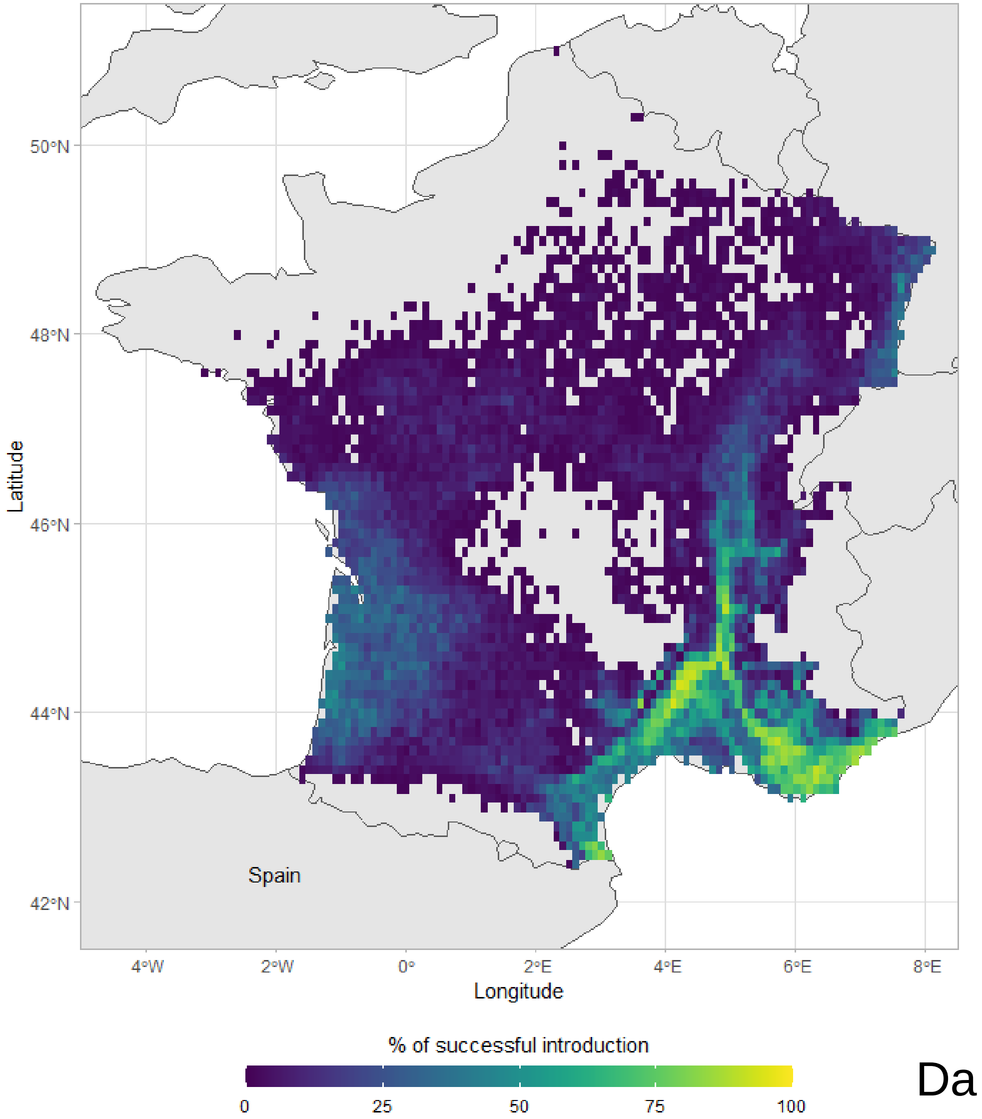
Population dynamics

Adults' active and passive dispersal



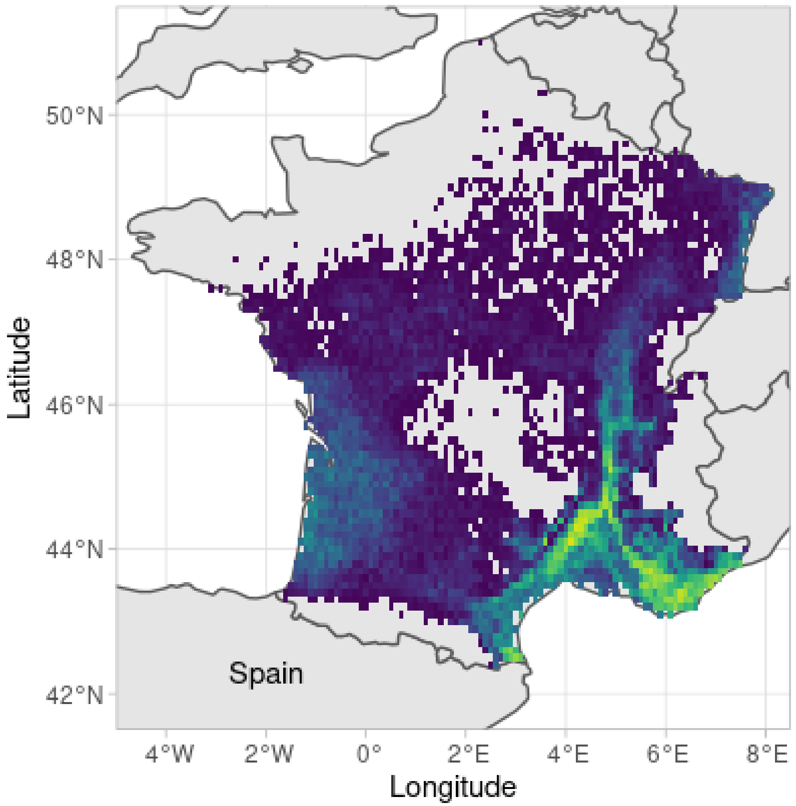
Parametrised from MRR and literature review

Ae. albopictus regional 2015-2020 model: percentage of successful introductions



Da Re et al. 2022, *Parasite&Vectors*,

Percentage of successful introductions out of 50 iterations of the model



AUC: 0.874 (0.867-0.880)

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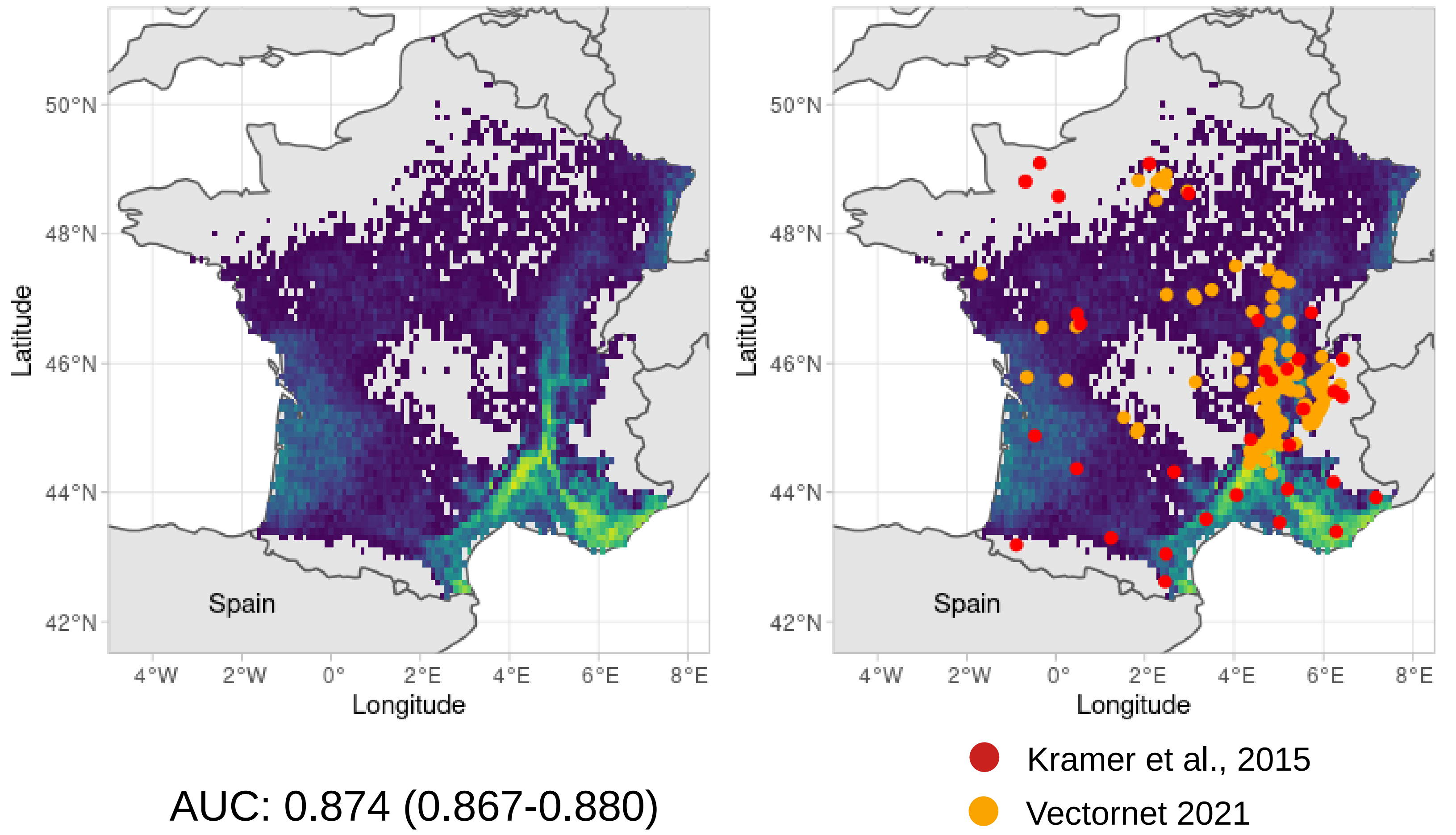

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88% of the occurrences fall on a pixel having > 1 % successful introduction

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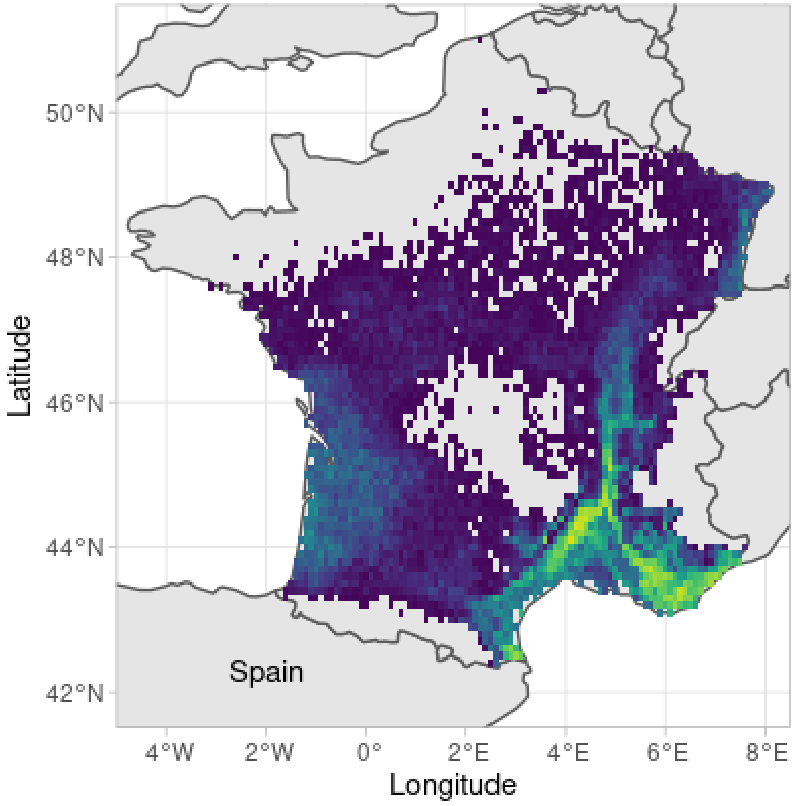

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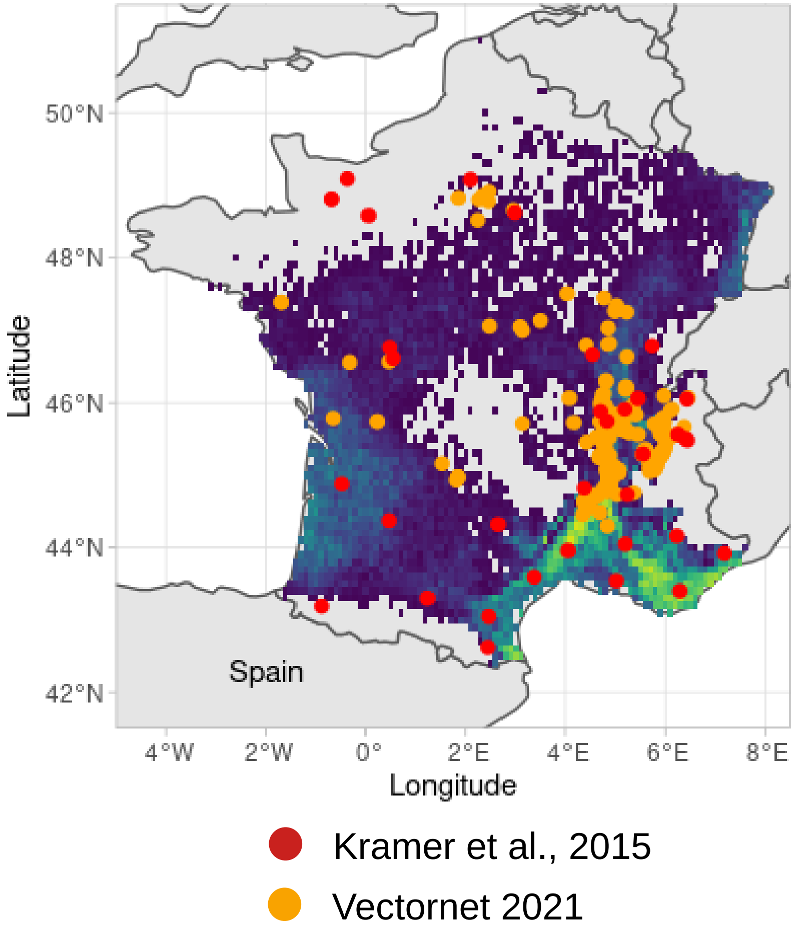

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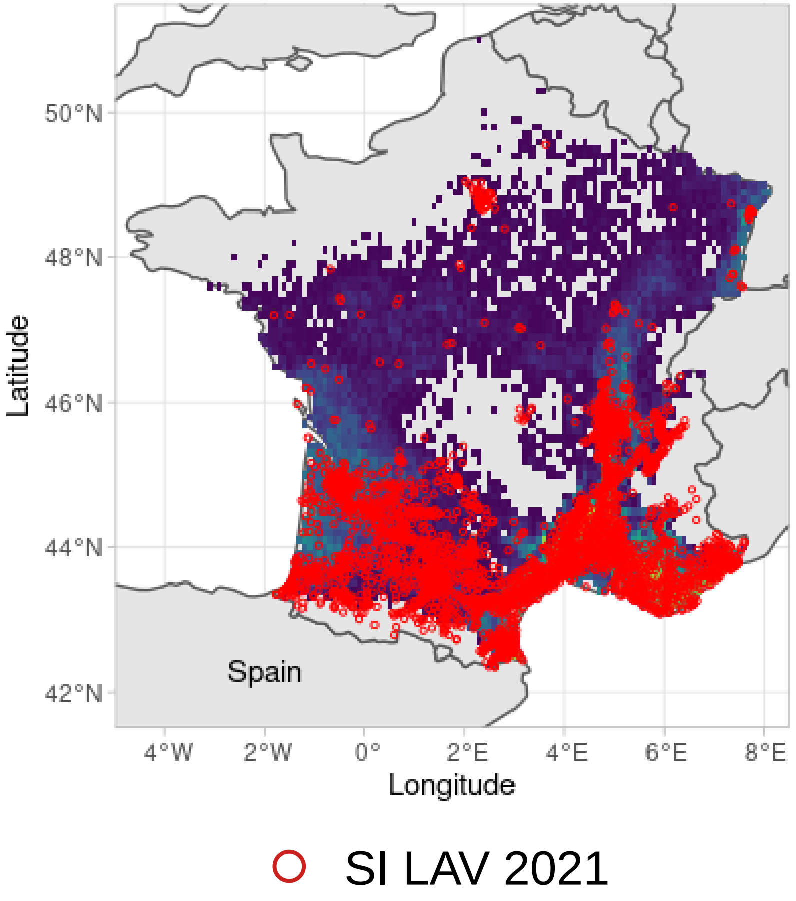
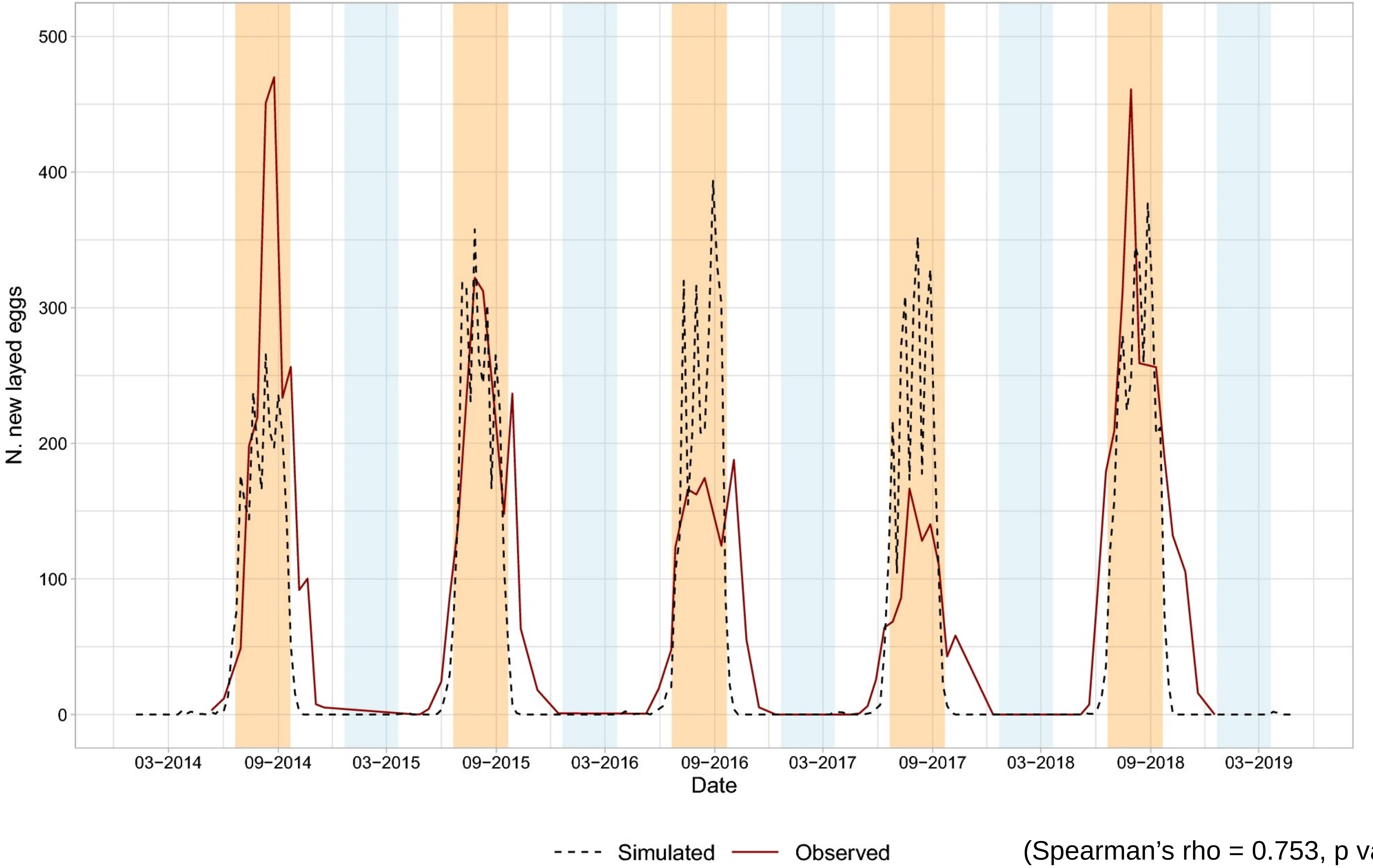


84% of the occurrences fall on a pixel having > 1 % successful introduction

Temporal trend reporting simulated and observed new-laid eggs of *Ae. albopictus* in Nice (France, 2014–2018)



(Spearman's rho = 0.753, p value <0.001)

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Overview

dynamAedes is a stochastic, time-discrete and spatially-explicit population dynamical model for four invasive *Aedes* mosquito species: *Aedes aegypti*, *Ae. albopictus*, *Ae. japonicus* and *Ae. koreicus*.

The model is driven by temperature, photoperiod and intra-specific larval competition and can be applied to three different "spatial scales": punctual, local and regional. These modes consider different degrees of spatial complexity and data availability, for example by accounting for active and passive dispersal of mosquitoes or for specific input temperature data (weather station vs. gridded remotely-sensed temperature data).

The main features of **dynamAedes** are:

- It allows to simulate the active and passive dispersal of adult mosquitoes (when *scale="local"*).
- It's a stochastic model, thus the distribution of its output metrics (e.g., number of adults) integrates "random" variation and can thus differ slightly between different model runs.
- It provides four functions (*psi*, *adci*, *dici* and *icci*) to easily derive summary metrics (i.e., based on user-defines quantiles) on the space-time trend of the simulated population dynamics, e.g., the 95% CI of the population dispersal in a given period or the number of cells colonised.

Installation

```
# Install the released version from CRAN
install.packages("dynamAedes")
# Or the development version from GitHub:
# install.packages("devtools")
devtools::install_github("mattmar/dynamAedes")
```

Links

View on CRAN

Browse source code

Report a bug

License

GPL(>=2)

Citation

Citing dynamAedes

Developers

Matteo Marcantonio
Author, maintainer

Daniele Da Re
Author

Dev status

CRAN 2.2.9

Essentially, how does it work?

```r
#---- 1. Inputs ----
# define a two-column matrix of coordinates to identify each cell in the lattice grid.
cc <- df_temp[,c("x","y")]
#get temperature matrix for modelling
w <- sapply(df_temp[,-c(1:2)], function(x) as.integer(x*1000))

## Define the day of introduction (January 1st is day 1)
str <- "2022-05-01"
## Define the end-day of life cycle (December 31st is the last day)
endr <- "2023-12-31"
## Define the number of eggs to be introduced
ie <- 10000
## Define the number of model iterations
it <- 10 # The higher the number of simulations the better
## Define the number of liters for the larval density-dependent mortality
habitat_liters <- 1000
## Define the number of parallel processes (for sequential iterations set nc=1)
cl <- 5
```

```r
#---- 2. Run the model ----
#subset w to get the first column of the matrix matching the day of introduction
w<-w[,as.numeric(format(as.Date(str),"%j")):ncol(w)]

#run the model
simout <- dynamAedes.m(species="albopictus",
                       scale="rg",
                       jhwv=habitat_liters,
                       temps.matrix=w,
                       cells.coords=as.matrix(cc),
                       startd=str,
                       endd=endr,
                       n.clusters=cl,
                       iter=it,
                       intro.eggs=ie,
                       compressed.output=TRUE,
                       seeding=TRUE,
                       verbose=FALSE)
```

```r
##---- 3.2  adult female abundance ----
# Compute a raster with the median female adult abundance (type "N" derives a spatial time series)
ad.r <- adci(simout, eval_date=1:dd, breaks=c(.5),#extract only the simulated median
             stage="Adults",
             n.clusters = 5,
             type="N")

ad.r<-ad.r$q_0.5
```

What can you do with dynamAedes?

- model the population dynamic at punctual or regional scale
- model the species dispersion at local scale
- simulate species introductions into new areas or climatic conditions

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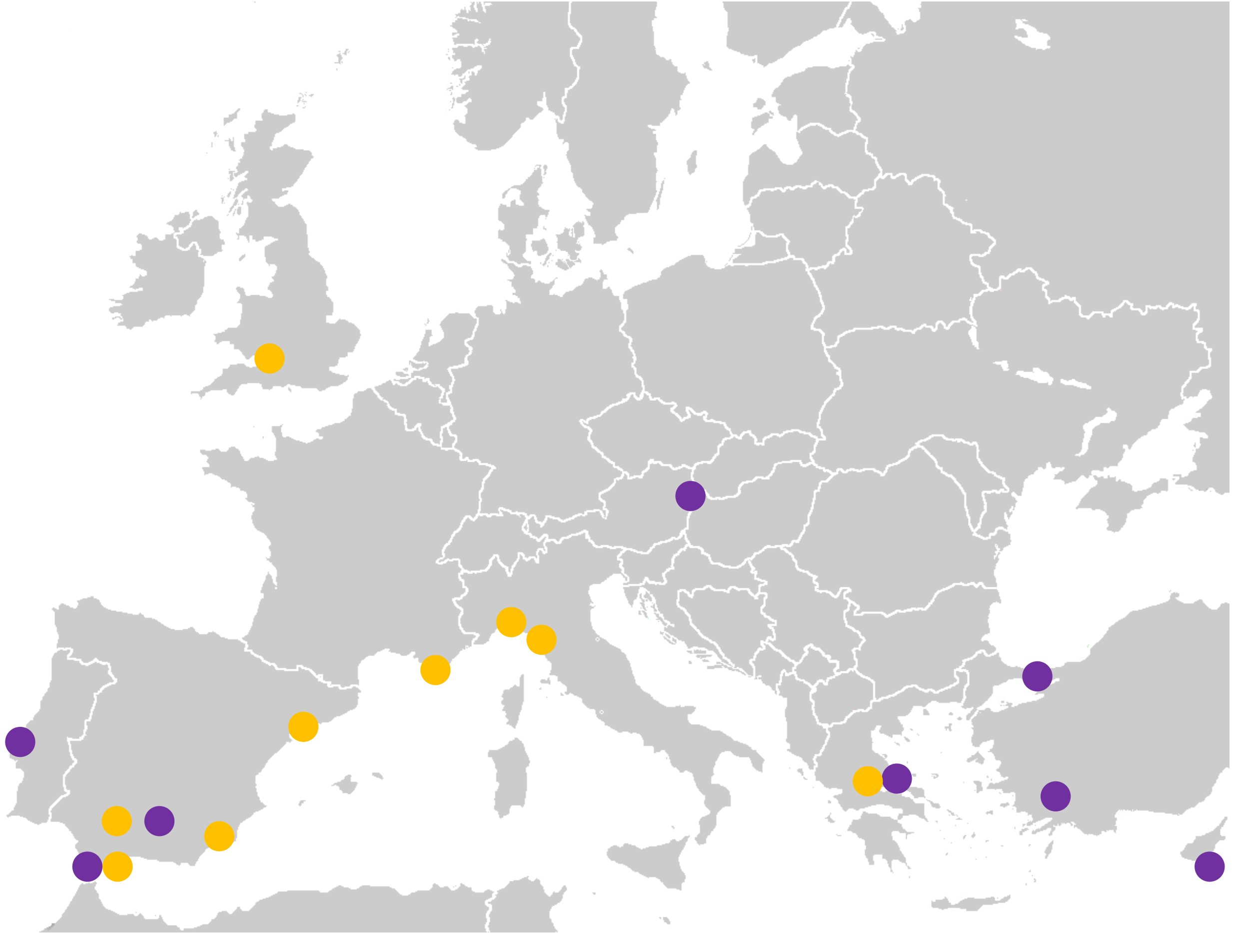
Can *Ae. aegypti* successfully establish in Europe?

Multiple outbreaks during the XIXth and mid-XXth centuries

	Location	Notes
1784, 1788, 1793	Cadiz, Seville (Spain)[9,10]	End of first pandemic, 1779–84
1861	Cyprus[11]	--
1863, 1867	Cadiz (Spain), then Jerez, Seville, and other places in Andalusia[10,11]	Imported from the West Indies by troops
1865	Canary Islands (Spain)[10]	--
1881	Crete (Greece)[11–13]	Half of the inhabitants affected
1887	Gibraltar[10]	Fifth pandemic, 1887–89
1888–1889	Cyprus[10]	--
1889	Athens, Piraeus, Salonica (Greece),[13,14] Greek Islands (Rhodes, Chios, and others), southern Turkey,[10,11,16] Izmir,[15] Manisa to Istanbul, Trabizon (Turkey), Varna*(Bulgaria), Lisbon (Portugal), Israel[10,11,16]	Around 80 000 cases in Izmir (80% of the inhabitants)
1889–1890	Istanbul, Izmir (Turkey), Napoli (Italy)[9,11,17]	--
1895–1897	Athens (Greece)[14]	--
1899	Antalya (Turkey)[11]	--
1910	Athens, Piraeus (Greece)[12,16,18]	--
1912	Israel[19]	--
1913	Cyprus[11]	--
1916	Dardanelles, Trabizon (Turkey)[11,20]	--
1921	Vienna*(Austria)[21]	--
1927	Malta[16]	--
1927–1928	Piraeus, Athens, Euboea, Gulf of Aegina (Greece), Izmir to south of Rhodes (Turkey)[10,13,21], Israel[16], Greece: DEN-1 and DEN-2 confirmed by retrospective serological study[22,23]	More than 1 million of people affected (90% of the population in Athens); 1000–1500 deaths
1928	Cyprus, Andalusia[24,25]	--
1929	Izmir[25]	--
1929–1933	Greece[22,26]	Confirmed by retrospective serological study
1945	Turkey, Israel (and other Middle East countries)[27]	--
2010	Croatia;[3,5] three DEN-1 clinical cases (including one reported in Germany) plus 15 recent infections	Virus probably introduced from Indian subcontinent
2010, 2013	France;[4,6] DEN-1 cases (2010), one DEN-2 case (2013)	Viruses probably introduced from West Indies
2012–13	Madeira;[7,8,28] more than 2200 DEN-1 cases from October, 2012, to January, 2013, plus 74 cases reported from Portugal mainland[8] and 12 other European countries	Virus probably introduced from Venezuela[29]

DEN-1=dengue virus serotype 1. DEN-2=dengue virus serotype 2. *Not clear whether data refer to a dengue outbreak or imported cases only, as there is no indication for the presence of *A aegypti* in Varna and Vienna.

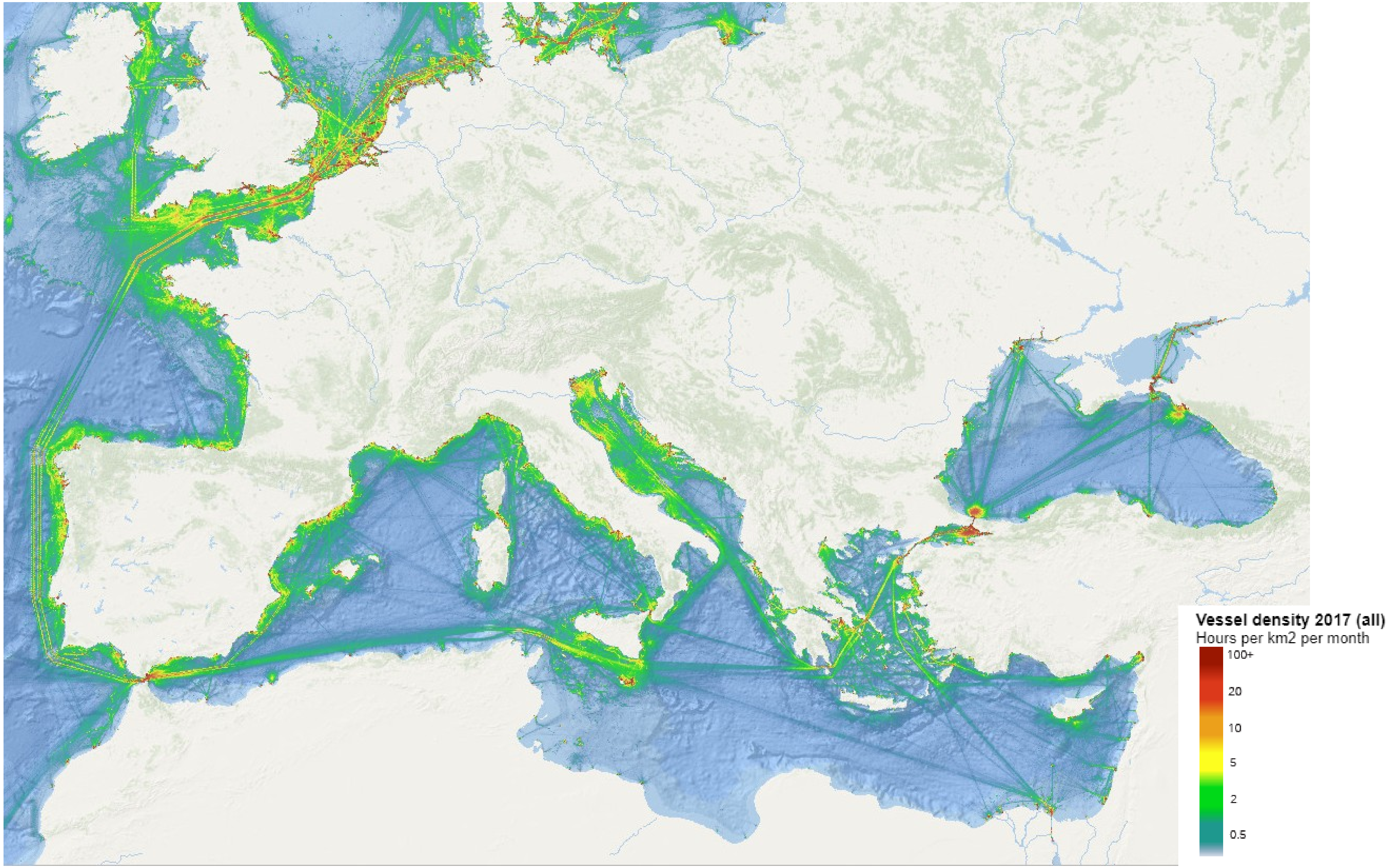
***Table:* Historical and contemporary outbreaks of dengue in the WHO European region**



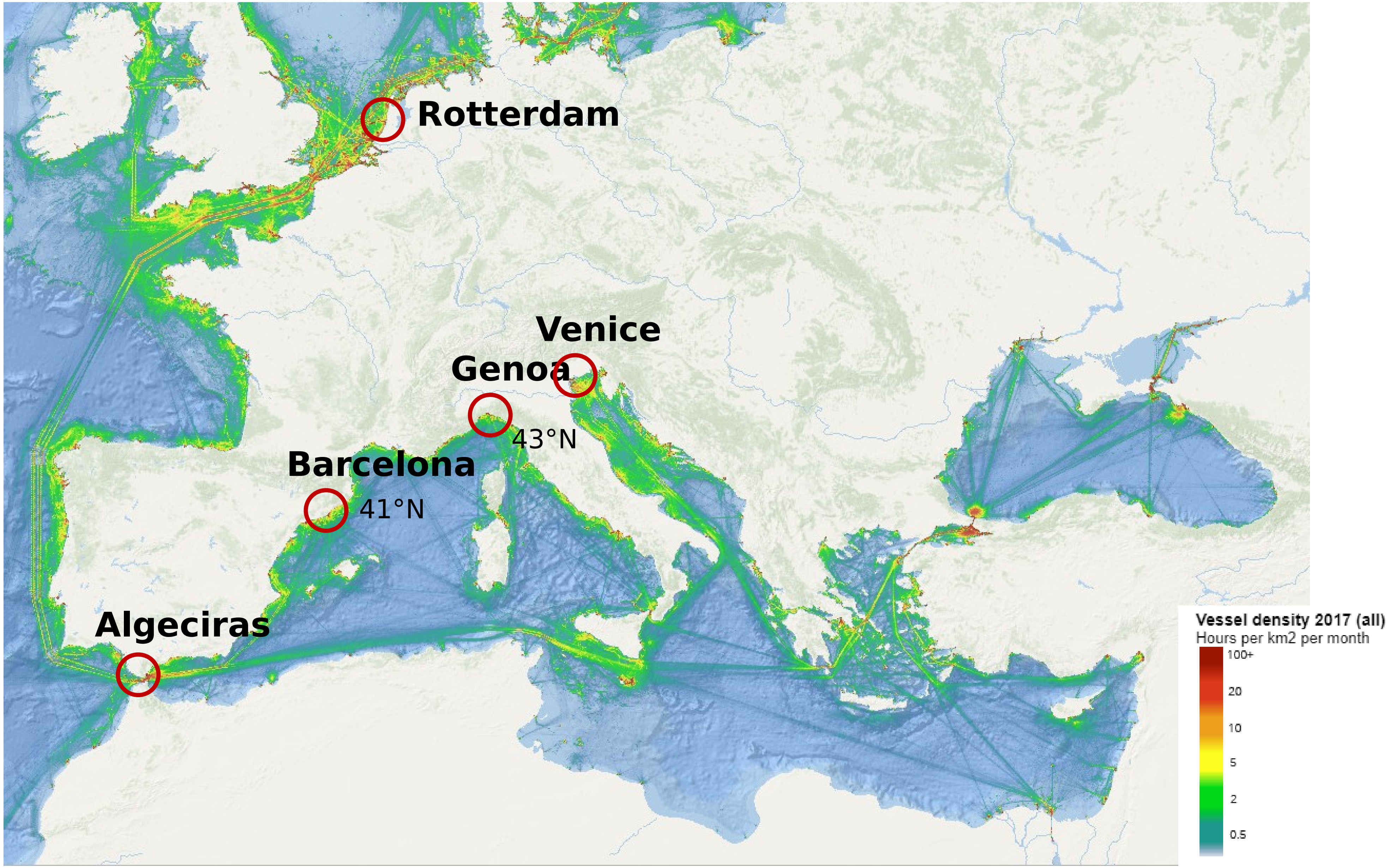
Yellow Fever

Dengue

Schaffner & Mathis 2014, *The Lancet*



Source: https://ec.europa.eu/maritimeaffairs/atlas/maritime_atlas/



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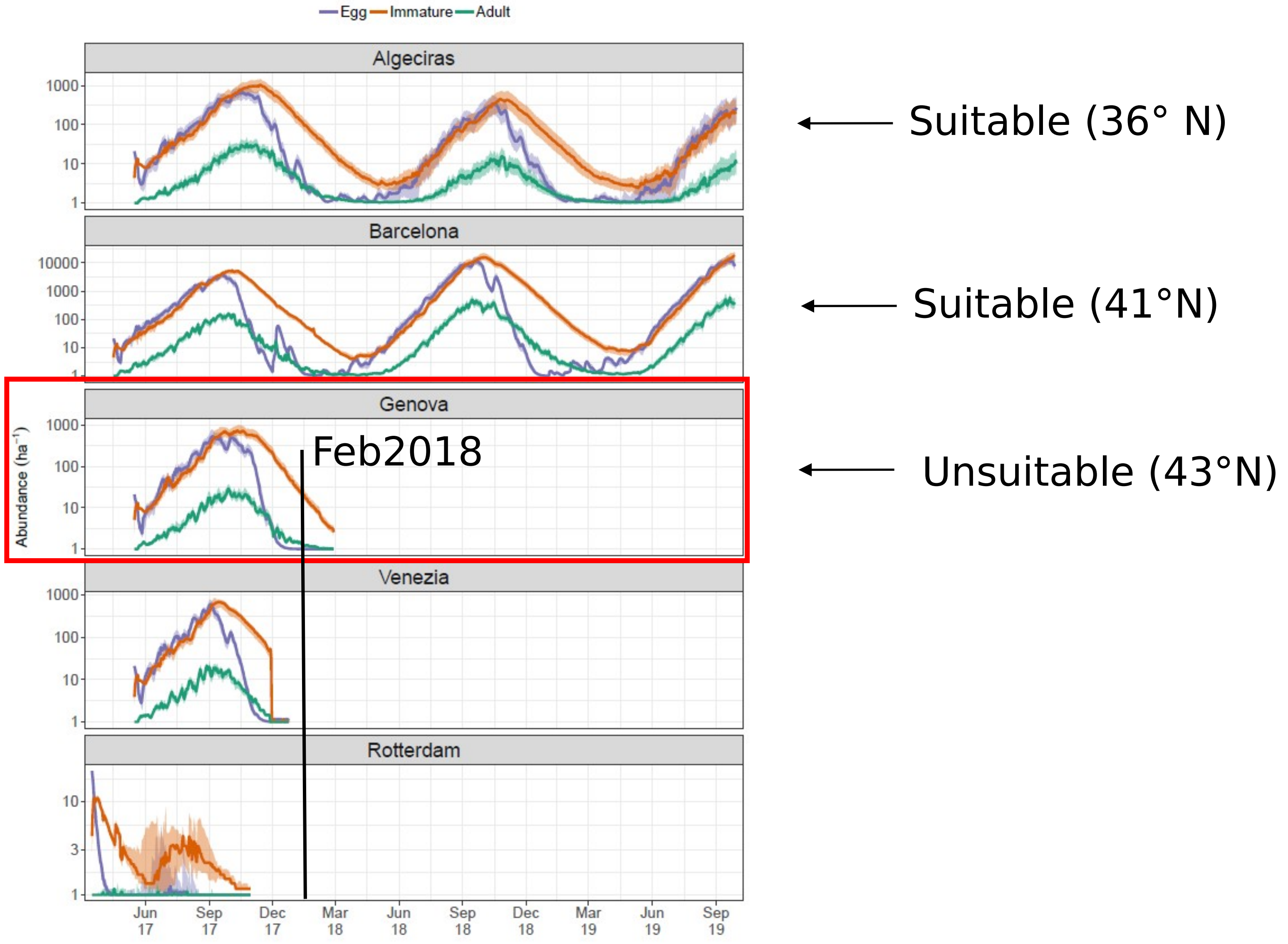
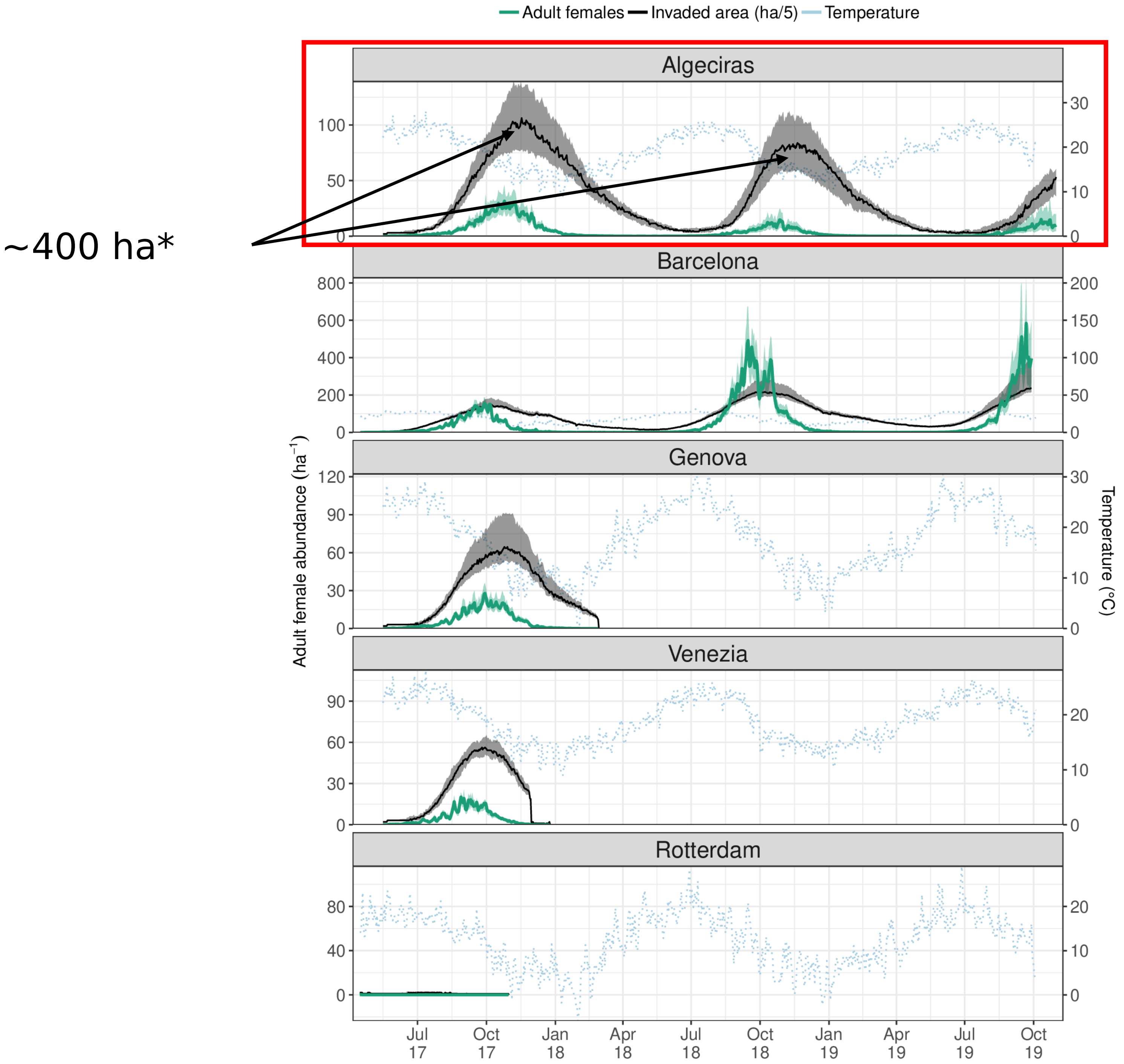


Da Re et al. 2020, *Ecol. Inf.*



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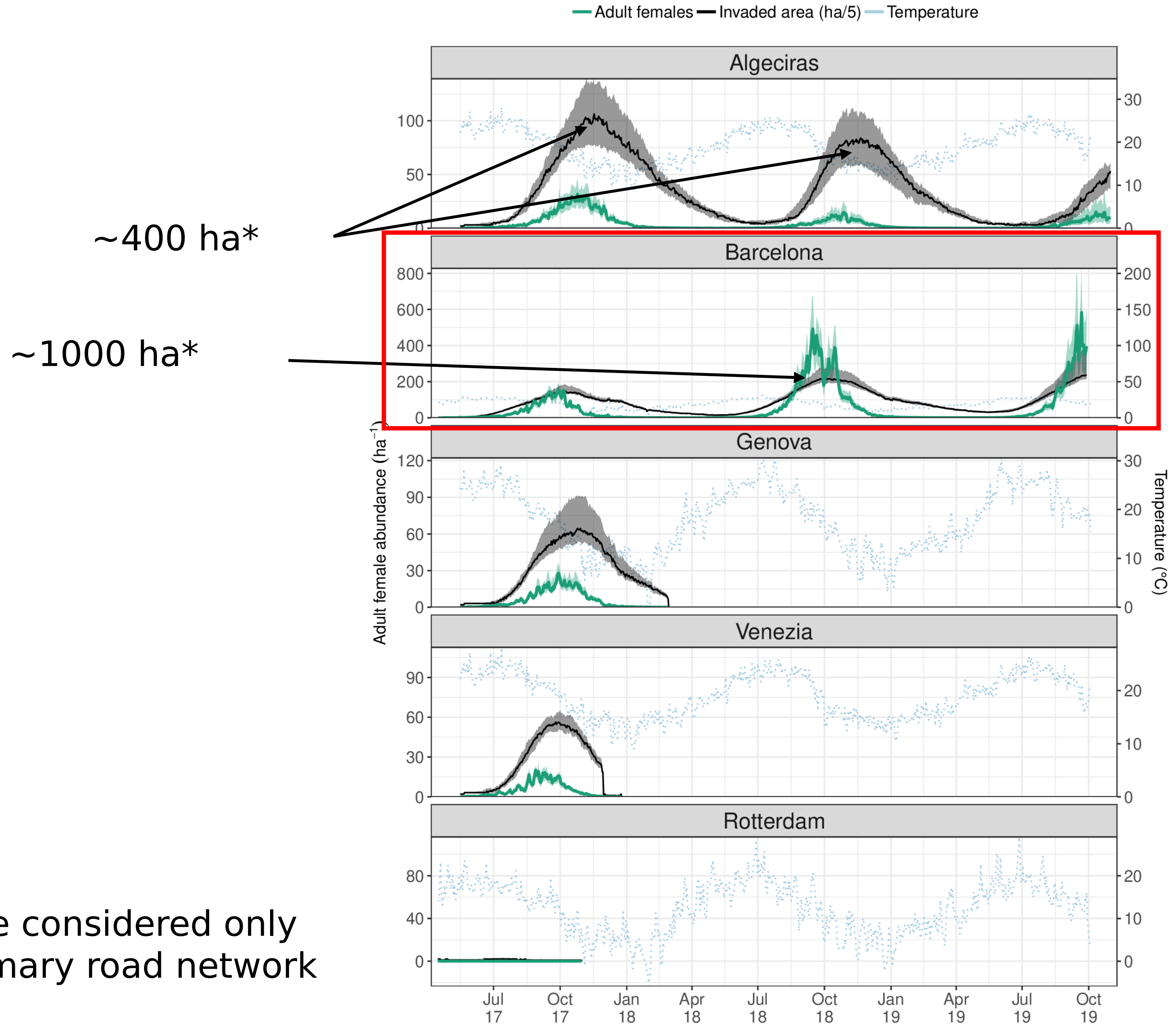

*NB: we considered only the primary road network

Da Re et al. 2020, *Ecol. Inf.*

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- model the <u>population dynamic</u> at punctual or regional scale
- model the <u>species dispersion</u> at local scale
- <u>simulate species introductions</u> into new areas or climatic conditions
- Hindcasting and forecasting

Known issues

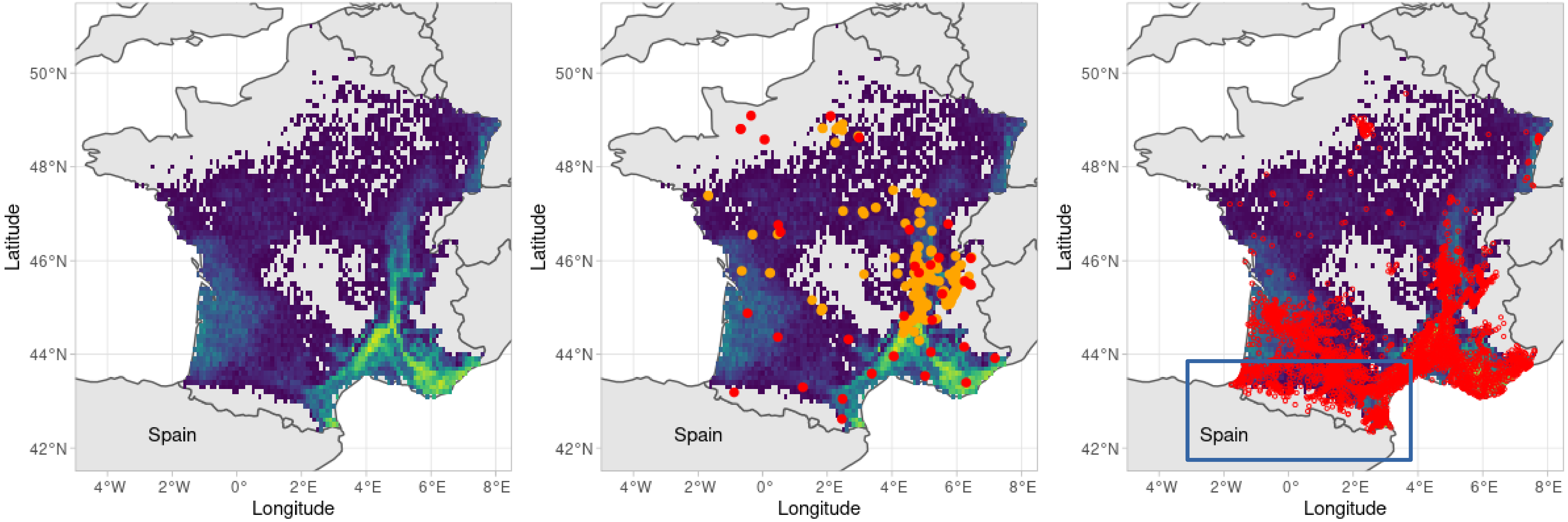
Spatial resolution of the temperature dataset

Burn-in period and stochasticity

Some temperature-dependent functions must be updated (see P. Huxley’s presentation)

Model outputs: crude abudance? What about the effect of breeding sites availability?

Known issues: spatial resolution



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Kramer et al., 2015
Vectornet 2021

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SI LAV 2021

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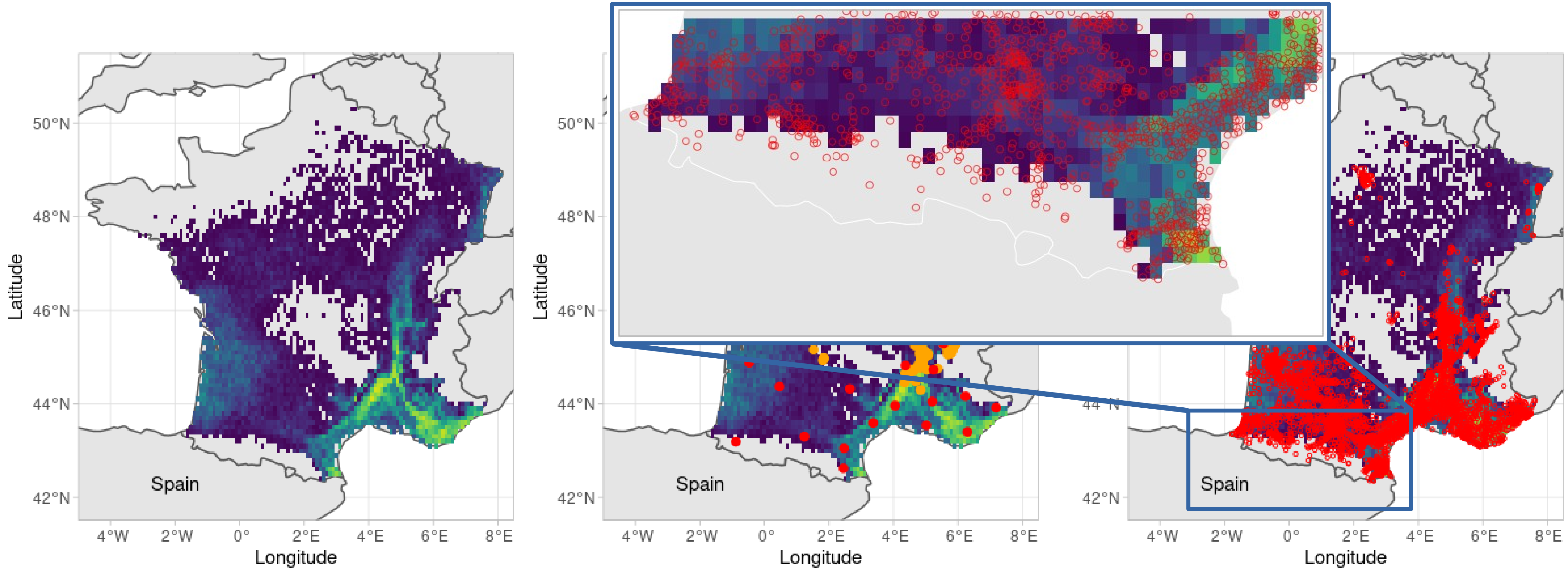

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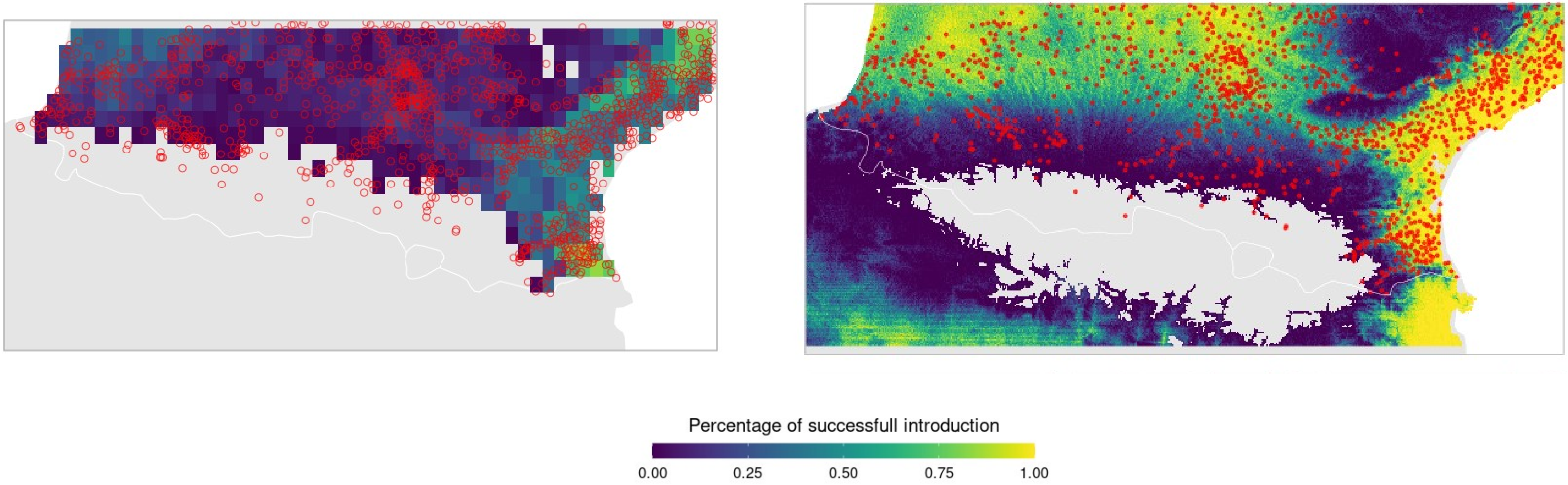
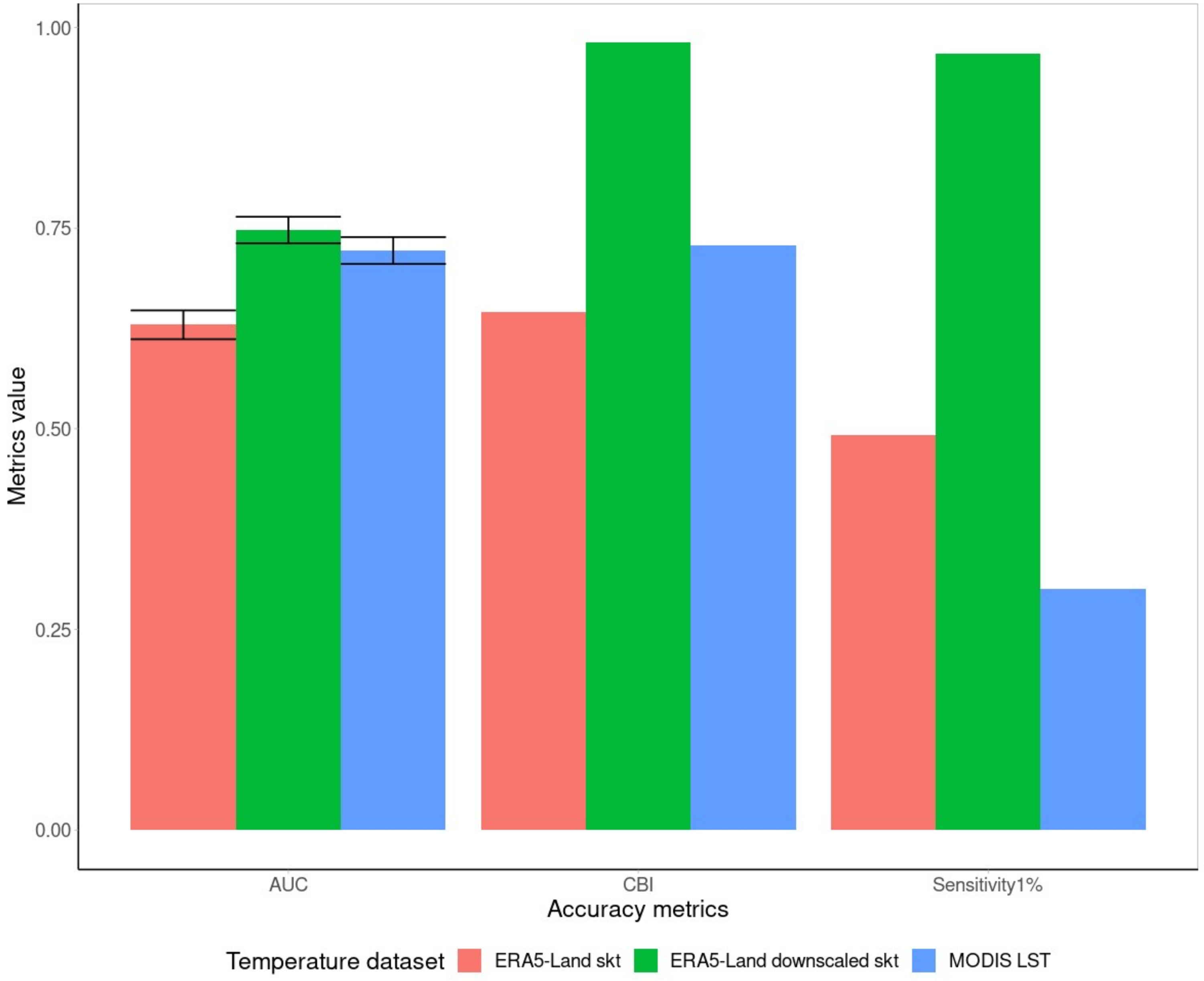
ERA5Land downscaled to 1km




1.00
0.75
0.50
0.25
0.00
Metrics value
AUC
CBI
Sensitivity1%
Accuracy metrics
Temperature dataset
ERA5-Land skt
ERA5-Land downscaled skt
MODIS LST

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Some temperature-dependent functions must be updated (see P. Huxley’s presentation)

Model outputs: crude abudance? What about the effect of breeding sites availability?

Known issues

Spatial resolution of the temperature dataset

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New features soon to be released

Extract sub-stage counts at each pixel

Multiple introductions

R0 module for CHIKV, DENV and ZIKV

Thank you

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