Risk assessment of BTV incursion in Europe from Sardinia by Culicoides spp. wind dispersal

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Risk assessment of BTV incursion in Europe from Sardinia by *Culicoides spp.* wind dispersal

Sardinia island (Italy) experiences regular **orbiviruses incursions** like serotype 3 of **BlueTongue Virus (BTV)** in 2018, or Epizootic Hemorrhagic Disease Virus (EHDV) in 2022. Once the disease is established in Sardinia, what is the risk of introduction for the other regions in Europe?

Long-distance dispersal of the *Culicoides* vectors through the wind is a major disease **introduction pathway** but remains rarely considered in quantitative risk assessment models. However, combination of epidemiological and meteorological models can provide useful insights on risk estimations. A methodological framework and its first application for Sardinia as the infection source, are hereby presented.

Model Framework

1 BTV Infection in vector population in source i

✖

2 Probability of *Culicoides spp.* to reach destination j from i

✖

3 BTV establishment in j (R0)

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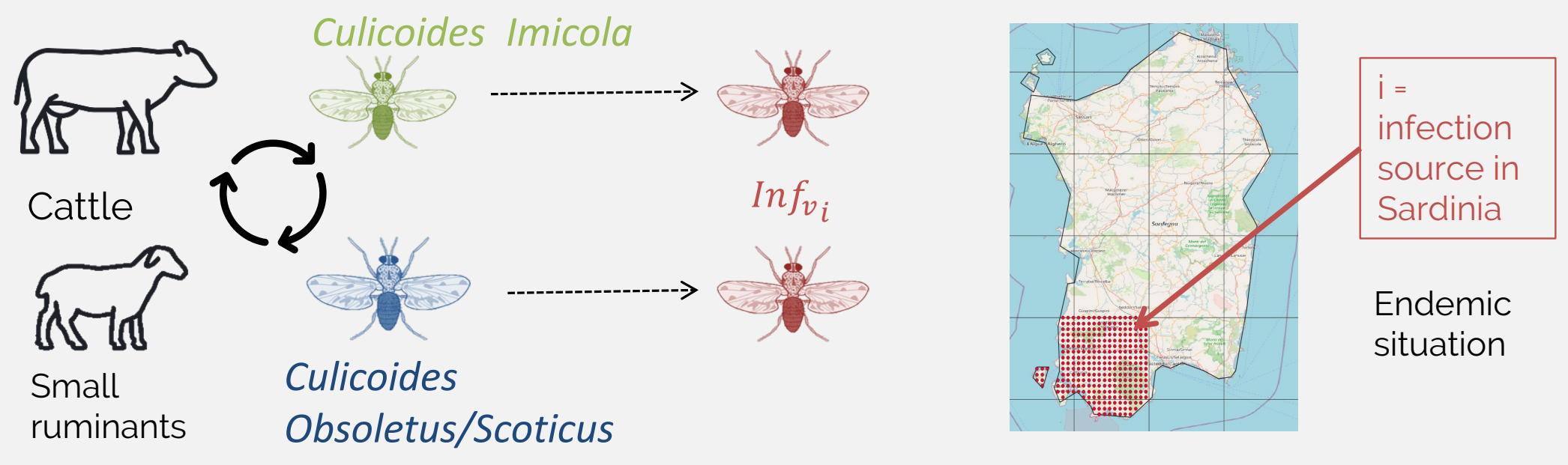
4 Risk = BTV Number of local infections in j

Method

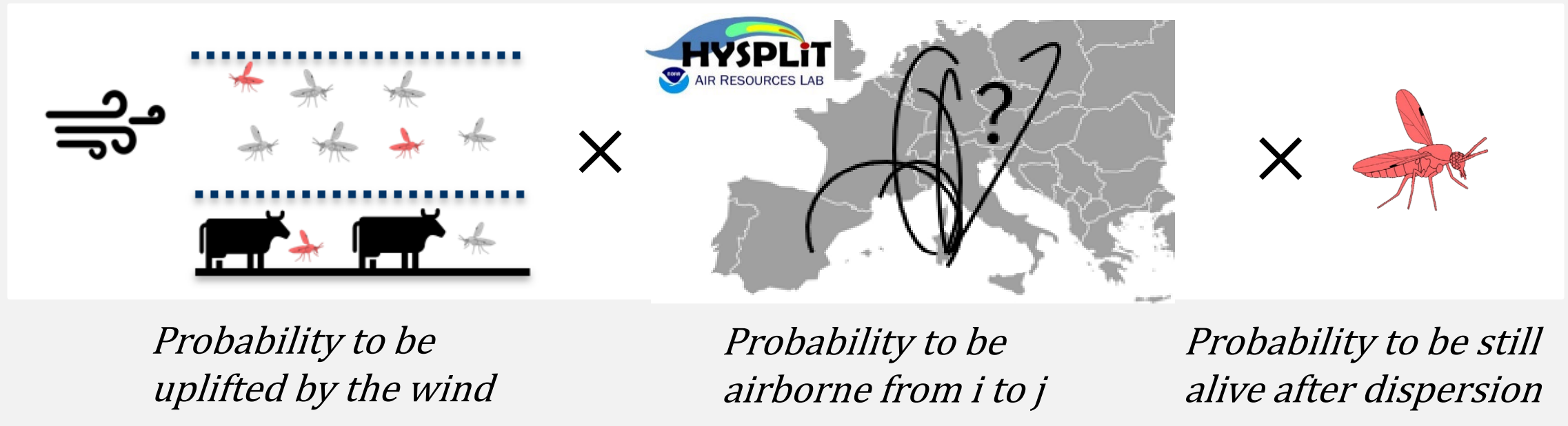
1 BTV infection of vector population in west southern Sardinia : Inf_{v_i}



$Inf_{v\,i}$ ~ Disease prevalence in hosts, vector abundance [1], weekly presence probability [2], livestock abundance [3], vector competence [4] and other vector specific parameters

2 Probability of long-distance dispersal : P_{LDWD_j}

1. Simulate **HYSPLIT® aerial trajectories** from source area (i) to destination cells (j) :
   - daily from Week 11 (mid March) to Week 46 (mid November), named « study period »
   - at sunrise & sunset
2. Filter trajectories according to **survival conditions** of the *Culicoides*:
   - Max duration of aerial transport : scenarios for 24, 48 and 72 hours
   - Trajectory below planetary boundary layer
   - Temperature >10°C
3. Calculate **frequency of trajectories reaching j** as a proxy for the probability to be dispersed from i to destination j by the wind
4. Calculate **probability of long distance dispersal** considering ecology & biology of the *Culicoides spp.*



Probability to be uplifted by the wind × *Probability to be airborne from i to j* × *Probability to be still alive after dispersion*

3 First local establishment at destination : R_{0_j}

R_0 = **Basic Reproduction Number**

R_0 = Average number of secondary infections in destination produced by one exogenous infected vector

Disease can be established at destination only if $R_0 > 1$

R_0 formula from Turner et al. [5] consider :

- **different hosts** populations and **vectors** populations
- potential **cross infections** between vector populations

4 Introduction Risk

Introduction risk in j is a combination of the 3 previous steps

Risk = **Number of local infections in destination j** per unit of time

References: [1] https:/ /doi.org/10.5334/ohd.33 ; [2] 10.1046/j.1439-0450.2003.00632.x; [3] 10.1038/sdata.2018.227; [4] https://doi.org/10.1038/s41597-020-00587-y; [5] 0.1371/ journal.pone.0053128 ;

Results

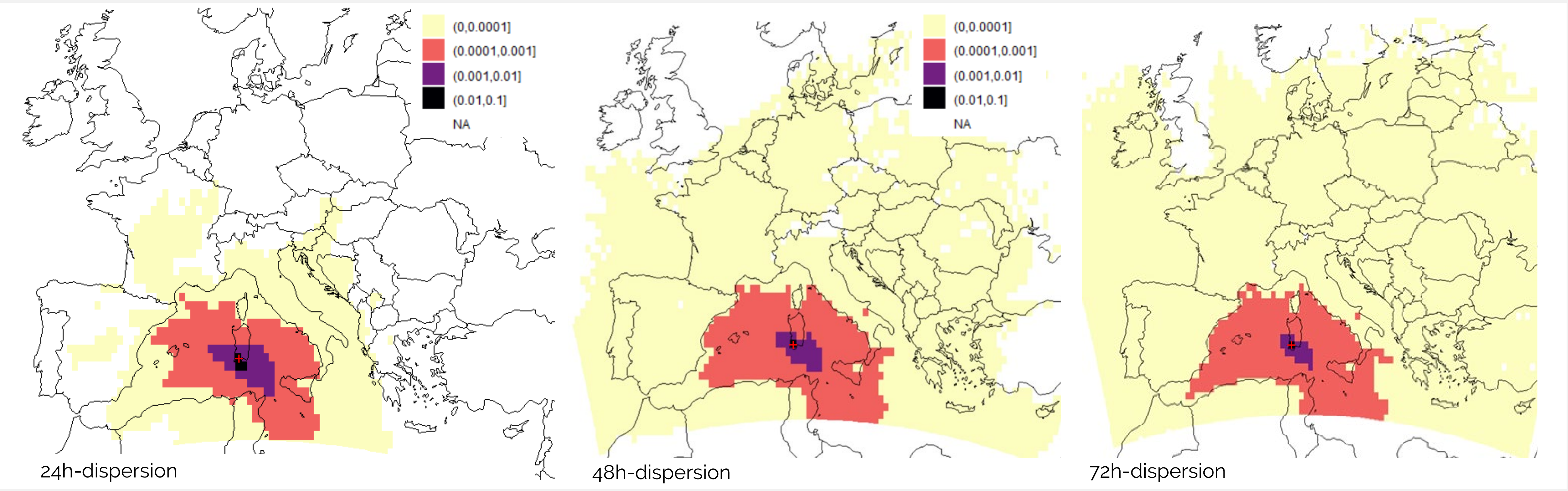
1 Infection in i

Prevalence arbitrary set in source:
50 cattle cases <=> $prev_c = 0.66\%$
200 small ruminant cases <=> $prev_s = 0.06\%$

Vector infection starts end of April and ends mid of November
C. imicola: [0,5 - 1,9] infected midges / week
C. obsoletus/scoticus : [45 – 2500] infected midges / week

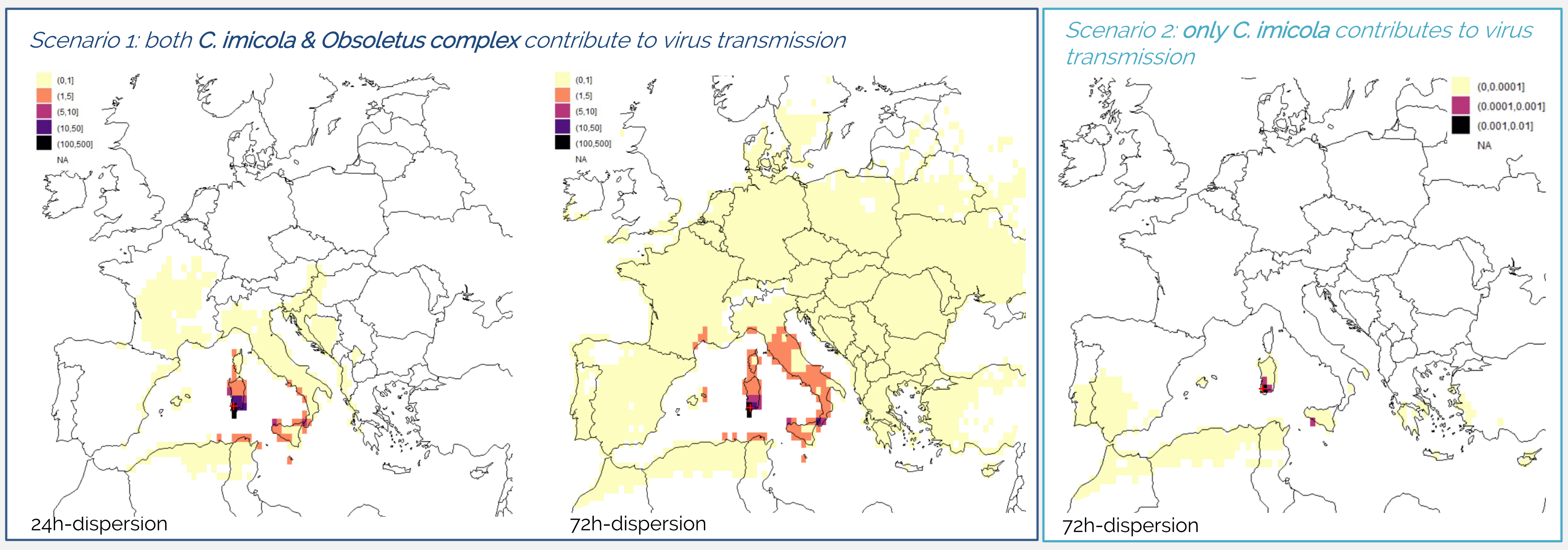
2 Long distance dispersal to destination j by wind

Mean of weekly probabilities for long distance dispersal from source area i (+) according to 3 scenarios of maximal duration of aerial transport (1, 2 or 3 days)



4 Yearly risk of introduction at destination

Mean of weekly secondary infections at destination according to vector contribution to transmission

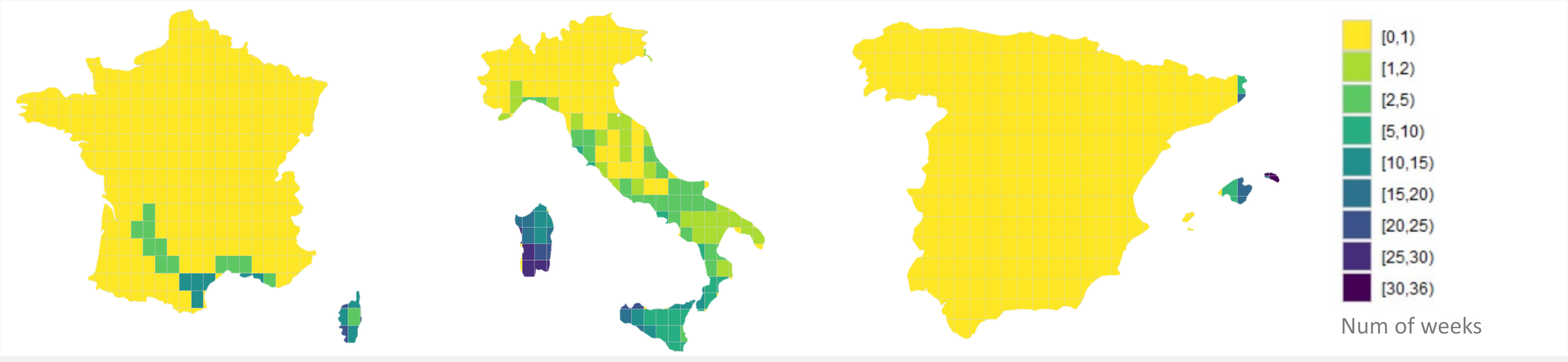


4' Number of weeks at risk for 3 neighbouring countries

Weekly introduction risk > 1

Study period of 36 weeks

24h-flight scenario



- The vector dispersion halo from Sardinia mostly points to the **southeastern direction**. It **expands to the west** as the vector flight duration increases but very rarely to the north.
- Risk of new introduction remains mostly **limited to Sicily, continental Italy and Corsica**. Annual risk for continental France (southwest) and Spain (Baleares islands) was only evidenced considering 72h of flight and **competence of both vector types.**
- If only *C. imicola* contributes to the disease transmission, there is no significant risk of further introduction to neighbouring countries.
- Mediteranean islands are exposed almost the entire period whereas continental areas are **exposed during only few weeks, at most 3 months.**

Next steps:

- Finetune estimations of vectors abundance data
- Perform sensitivity analysis
- Make the model generic for any combination of source and destination

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