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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?

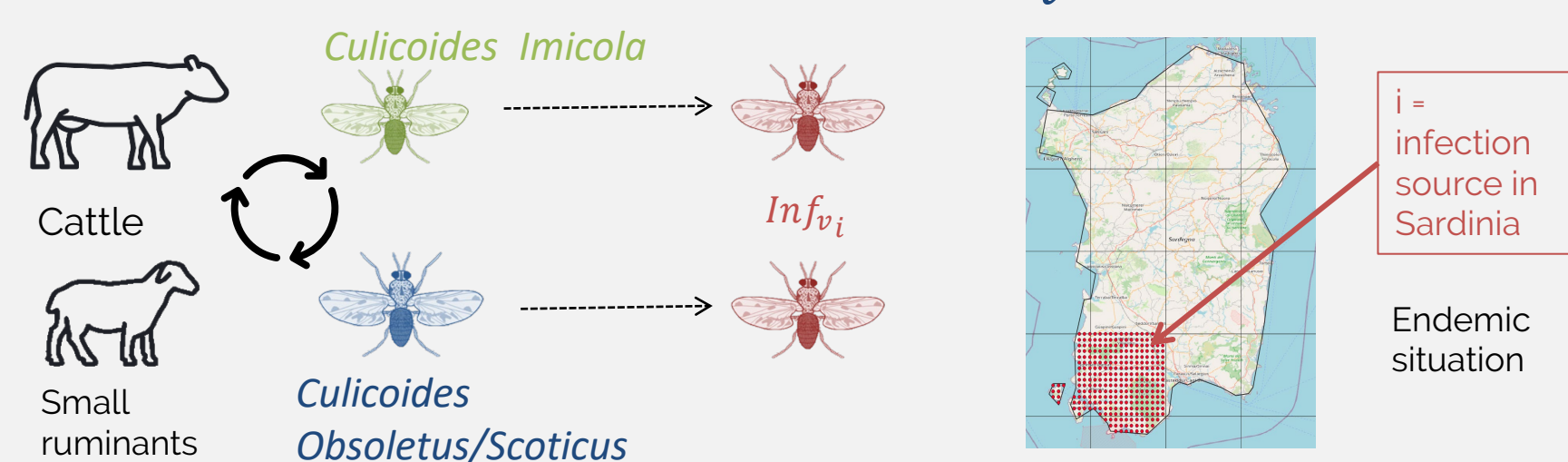
Long-distance dispersal of the *Culicoides* vectors through the wind is a major disease introduction pathway but remains rarely considered in quantitative risk assessment models. However, combination of epidemiological and meteorological models can provide useful insights on risk estimations. A methodological 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 (R_0)
- 4 Risk = BTV Number of local infections in j

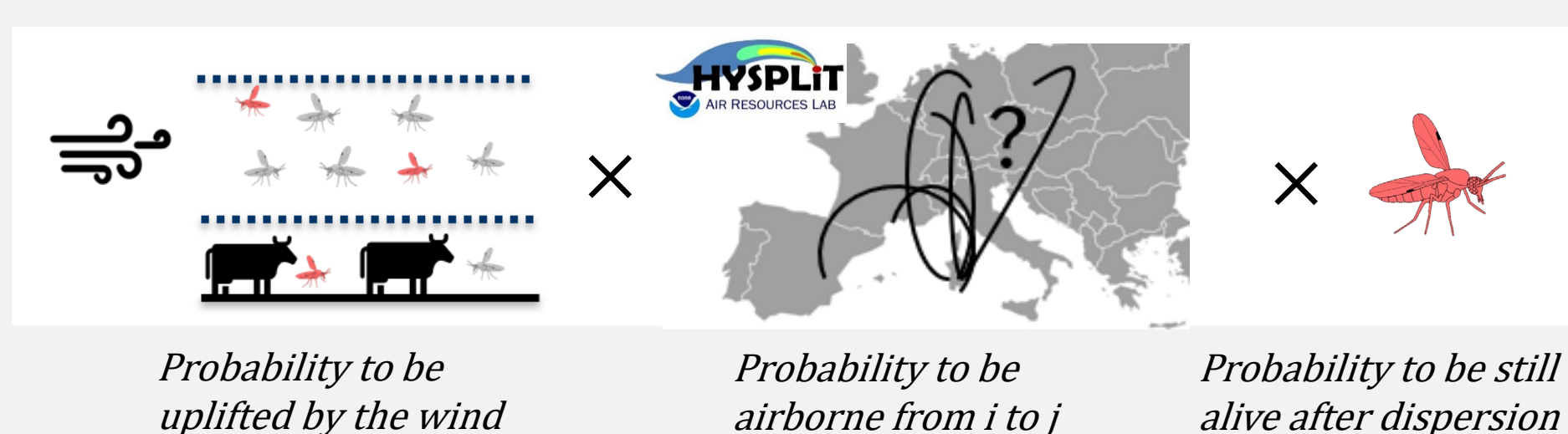
Method

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



- 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*.
 - o Max duration of aerial transport : scenarios for 24, 48 and 72 hours
 - o Trajectory below planetary boundary layer
 - o 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.*



- 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

Results

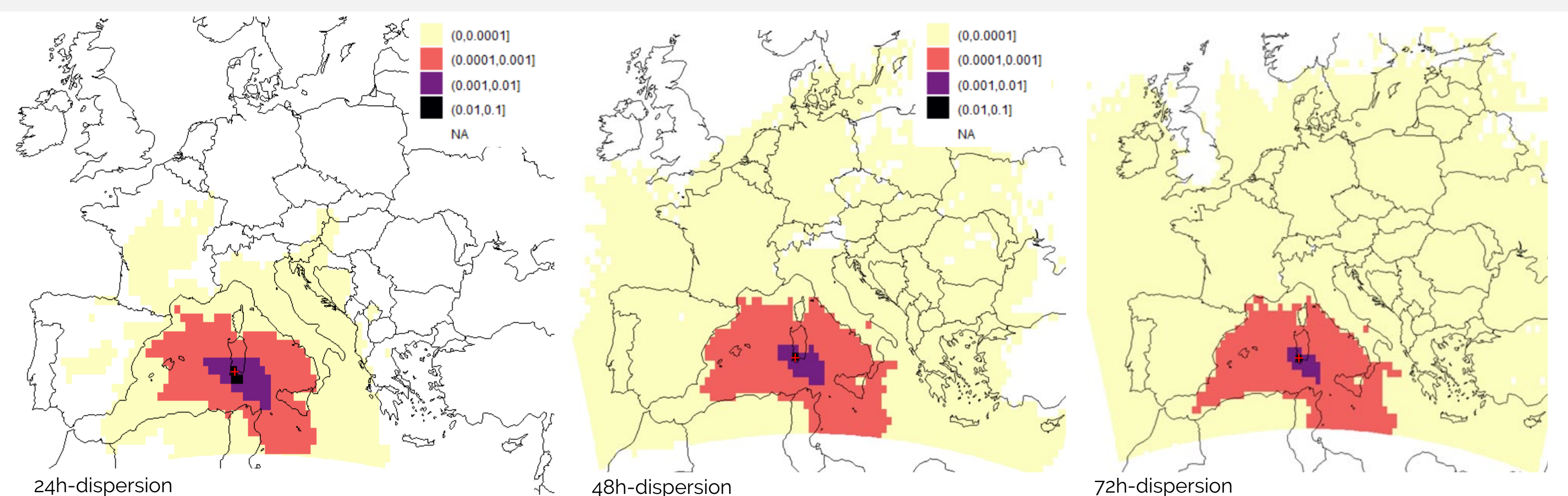
- 1 Infection in i

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

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

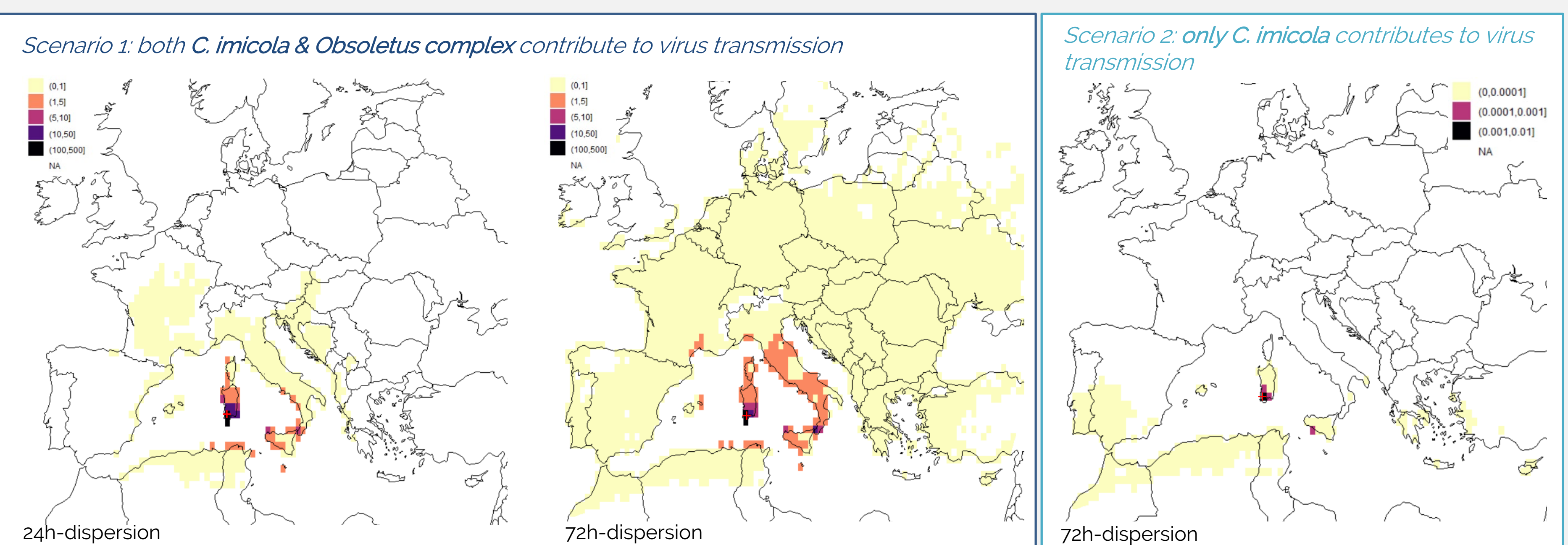
- 2 Long distance dispersal to destination j by wind

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)

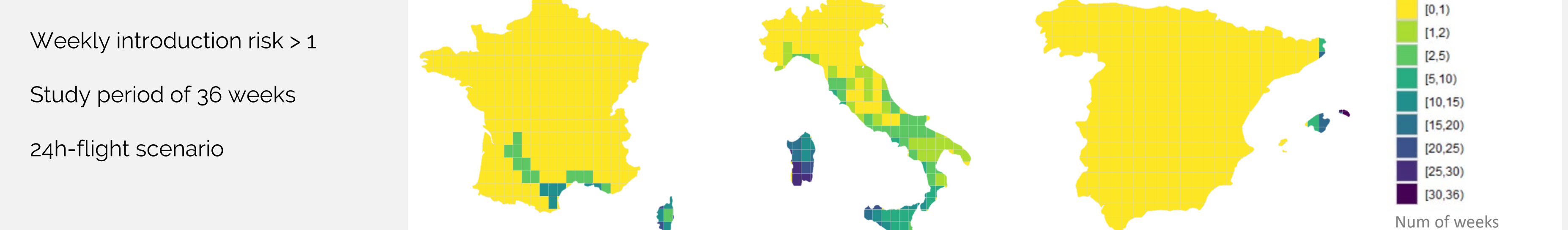


- 4 Yearly risk of introduction at destination

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



- 4' Number of weeks at risk for 3 neighbouring countries



- 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 (Balears 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.
- Mediterranean 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

References: ^[1] <https://doi.org/10.5334/ohd.33> ; ^[2] <https://doi.org/10.1046/j.1439-0450.2003.00632.x> ; ^[3] <https://doi.org/10.1038/sdata.2018.227> ; ^[4] <https://doi.org/10.1038/s41597-020-00587-y> ; ^[5] [0.1371/journal.pone.0053128](https://doi.org/10.1371/journal.pone.0053128) ;

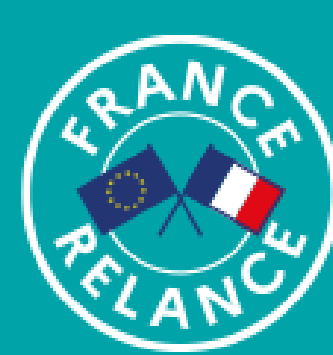
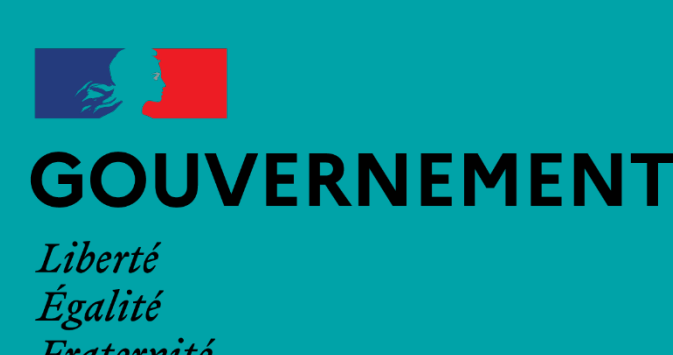
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