ModAH 2024

Risk of *Culicoides* dispersal by the wind

CASE STUDY WITH EPIZOOTIC HEMORRHAGIC DISEASE VIRUS IN FRANCE

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INRAE

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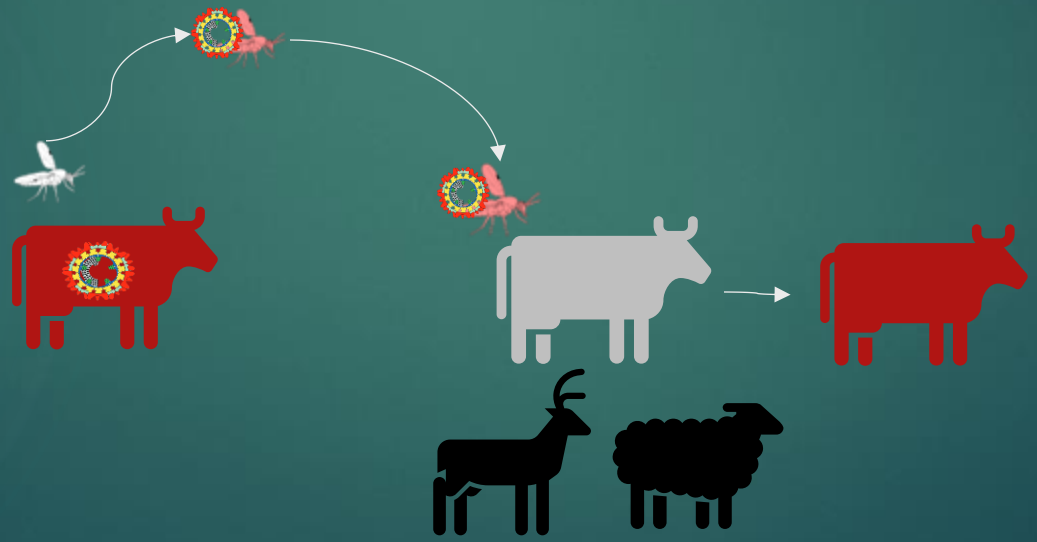
FRANCE RELANCE

EHDV: an arbovirus transmitted by *Culicoides*

- Hemorrhagic fever affecting domestic & wild ruminants
- 90% mortality in deer ; variable in cattle according to serotypes
- High economical & animal health impacts (WOAH-listed disease)
- Transmitted by *Culicoides* midges
- No EU-licensed vaccine available

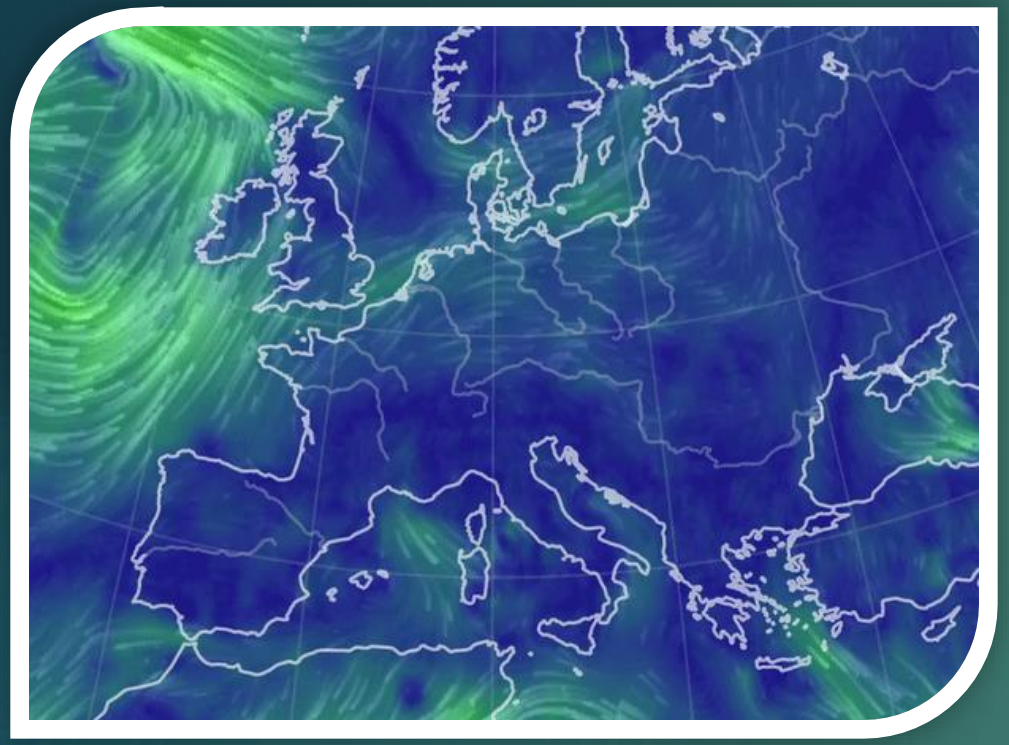
First animal infected by EHDV-8 in Italy (Alessio Lorusso, IZST)



Biting midge (Culicoides glabrior), female. Extracted from Mullen, 2019

Historical emergence EHDV-8 in Europe

- Tunisia : 2021
- Sardinia & Sicily: October 2022
- Southern Spain : November 2022
- Portugal : July 2023
- France: September 2023
- Pathways of introduction : long-distance dispersal by the wind & trade of live animals



How to predict Culicoides wind dispersal in Europe?

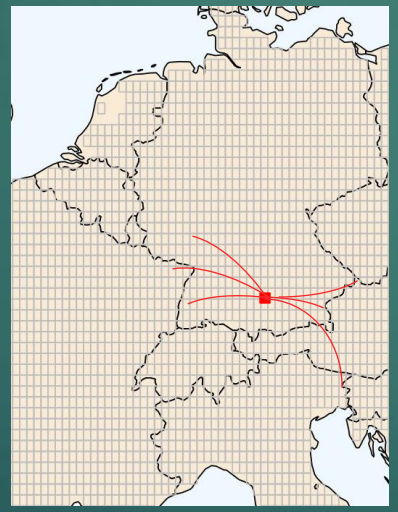
Atmospheric Dispersion Model

HYSPLIT Model

- HYSPLIT simulates the dispersion and trajectory of particles in our atmosphere, at local and global scales.
- Originally developed for nuclear explosion and volcano eruption
- Adapted to the specific biological & ecological limits of *Culicoides* spp.

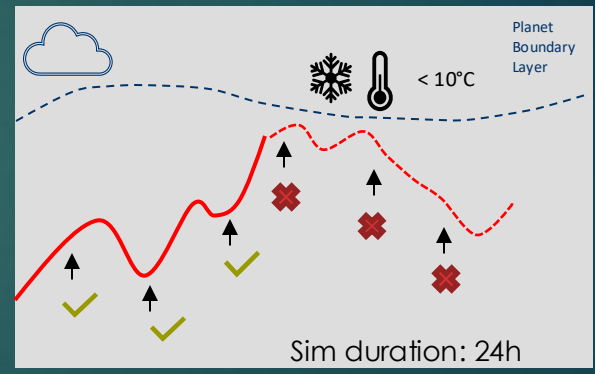
1 Define the starting point(s)

2 Initiate trajectories from it



- **2 starting time** per day (sunset & sunrise)
- **36 weeks** of simulations (mid March – Mid Nov)
- **Historical data of 2020-2021-2022-2023**

3 Filter suitable trajectories according to midges survival conditions



H_{ij} ~ probability to reach destination from starting point

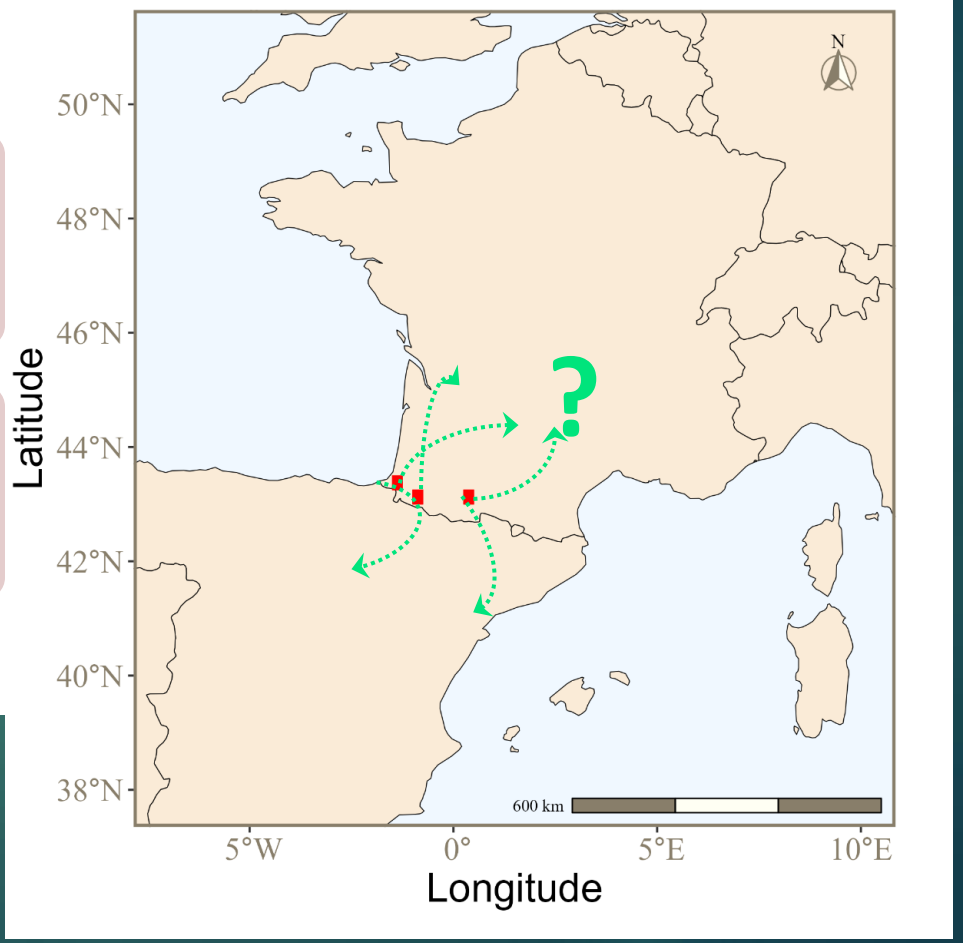
Stein A F, Draxler R R, Rolph G D, Stunder B J B, Cohen M D and Ngan F 2015 NOAA's HYSPLIT Atmospheric Transport and Dispersion Modeling System *B Am Meteorol Soc* **96** 2059–77

Emergence of EHDV-8 in France

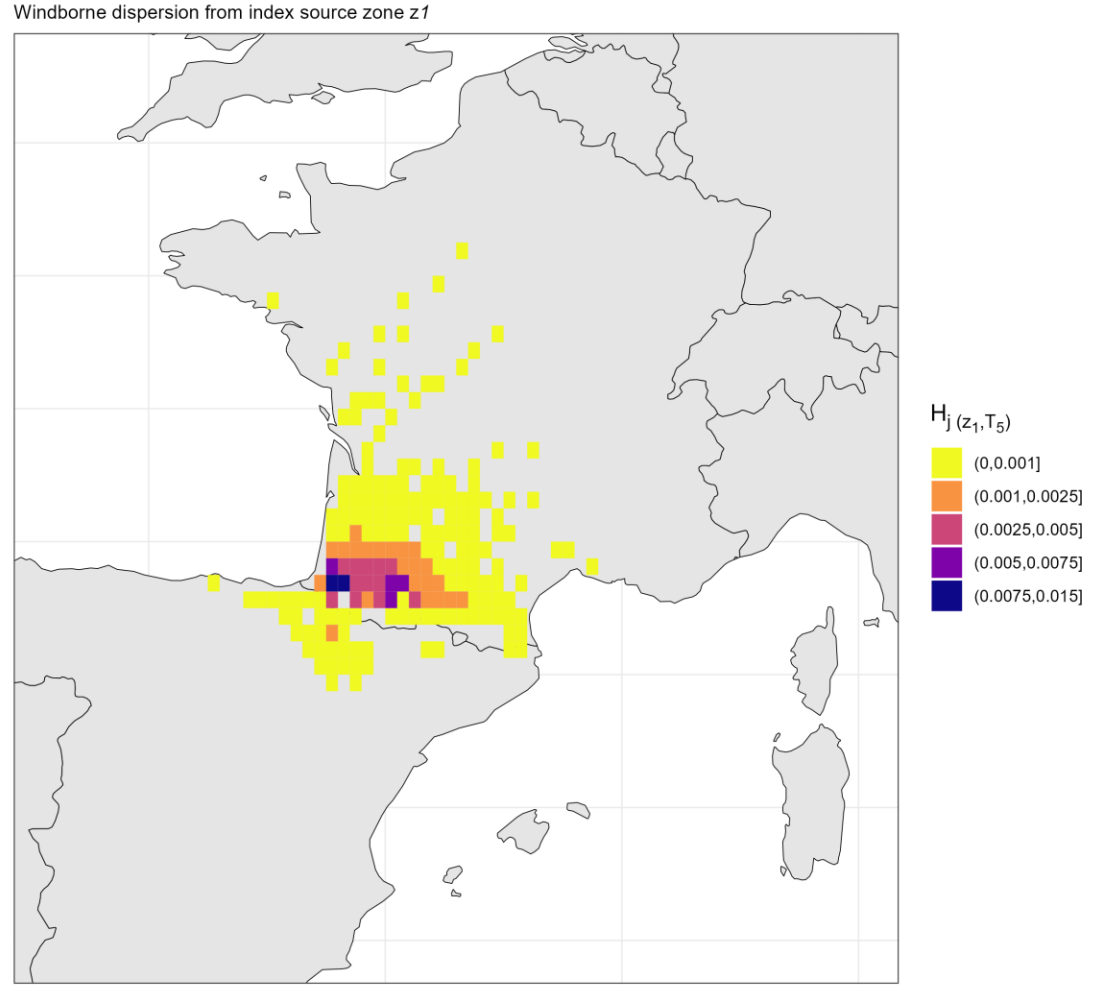
- First detection in Pyrénées-Atlantiques department early September 2023

What is the magnitude of the long-distance dispersal zone from the first index cases?

Is this zone predictive for emerging outbreaks?



Predicted risk zone averaged over 5 week-period



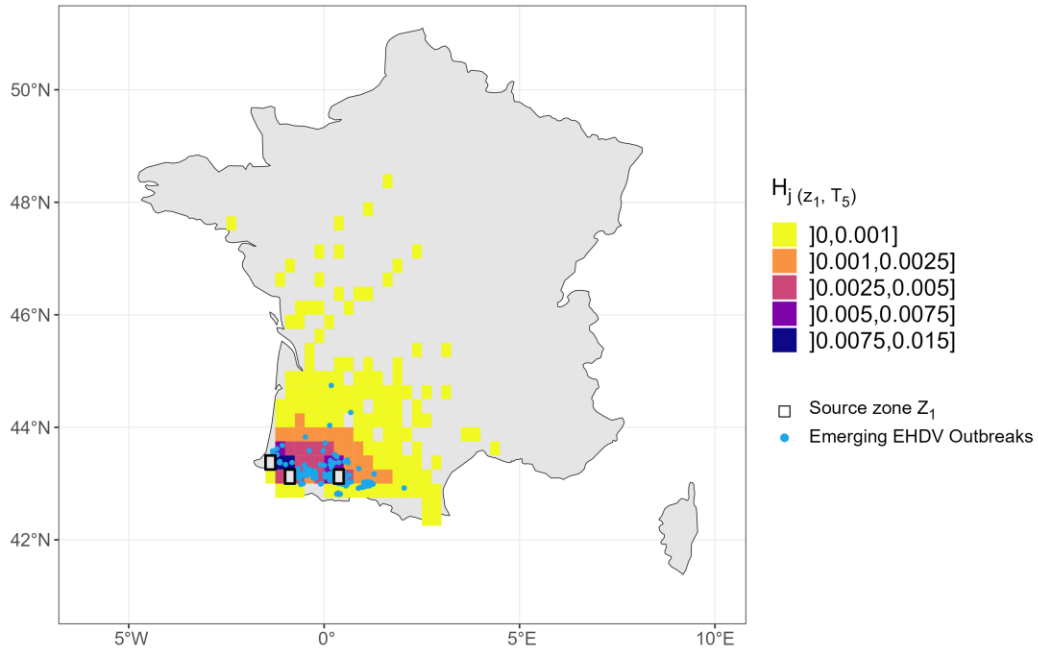
- Risk averaged from mid September to mid October (2023 only)
- High-risk zone mostly in the south western region ; (if H_j >10^{-3} ~25 000 km²)
- Full risk zone (~103 000 km²)
- Limited risk of incursion in SP

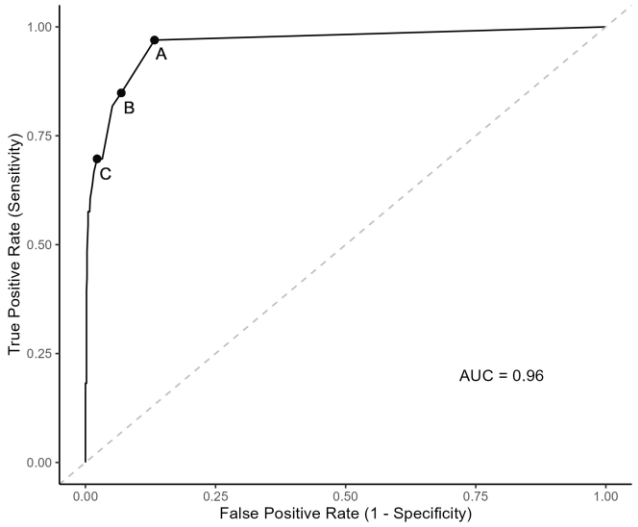
Very good predictability of the model

- 99.9% locations with at least 1 outbreak were predicted at risk
- BUT 26.3% Ob remain within the source zone > under estimation of the short range dispersion

- ROC curve of 0.96 (Se:97%, Sp:86,7%)
- Reducing the risk threshold leads to a significant drop in sensitivity

Situation	θ	TPR	FPR	Area (km²)	Proportion
A	1.10^{-4}	97%	13.3%	103,125	100%
B	3.10^{-4}	84.8%	6.9%	60,625	58.8%
C	9.10^{-4}	69.7%	2.2%	28,750	27.9%

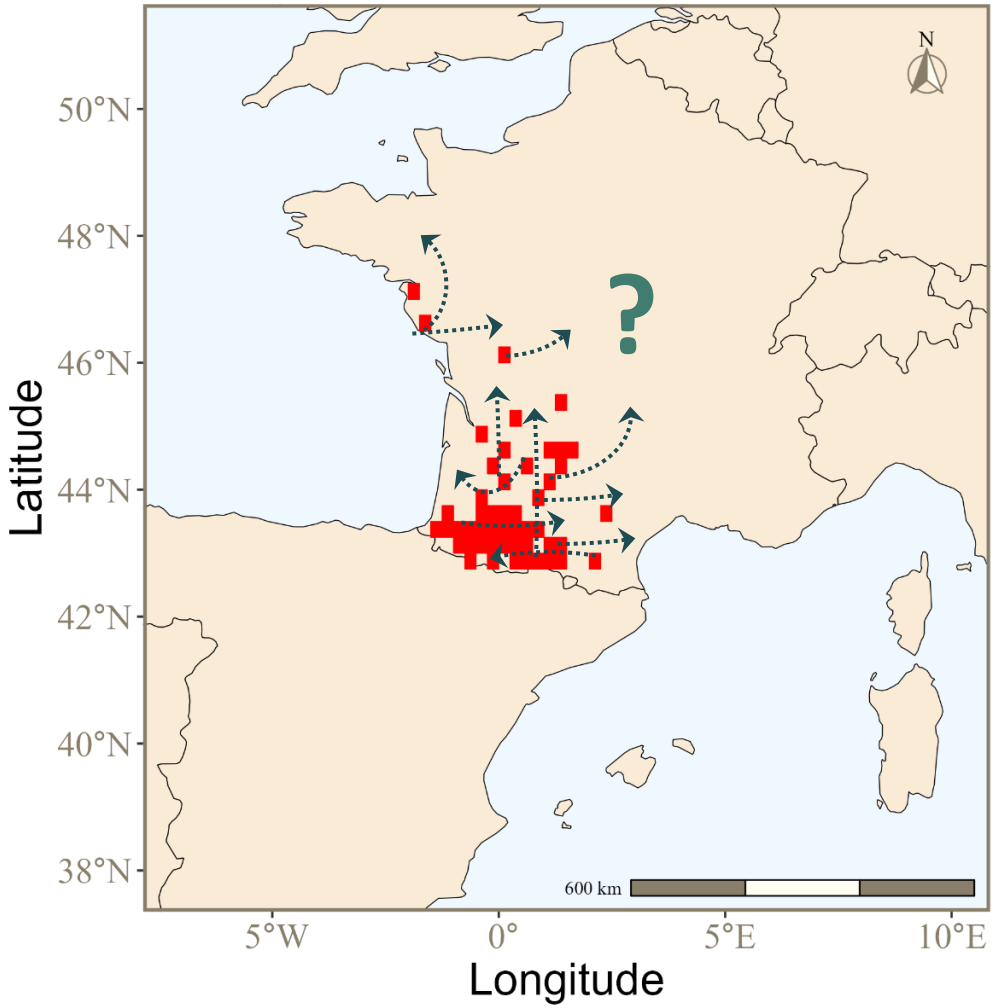




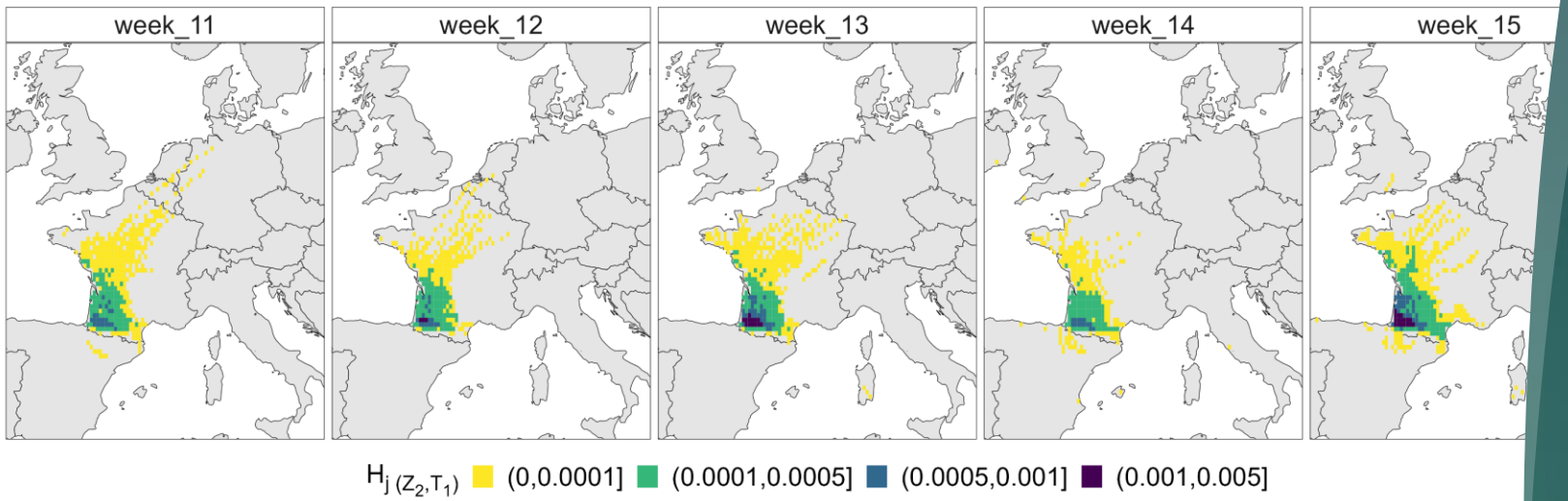
Prospection of future expansion

- Last available infected zone (early December 2023)
- Assumption of virus overwintering

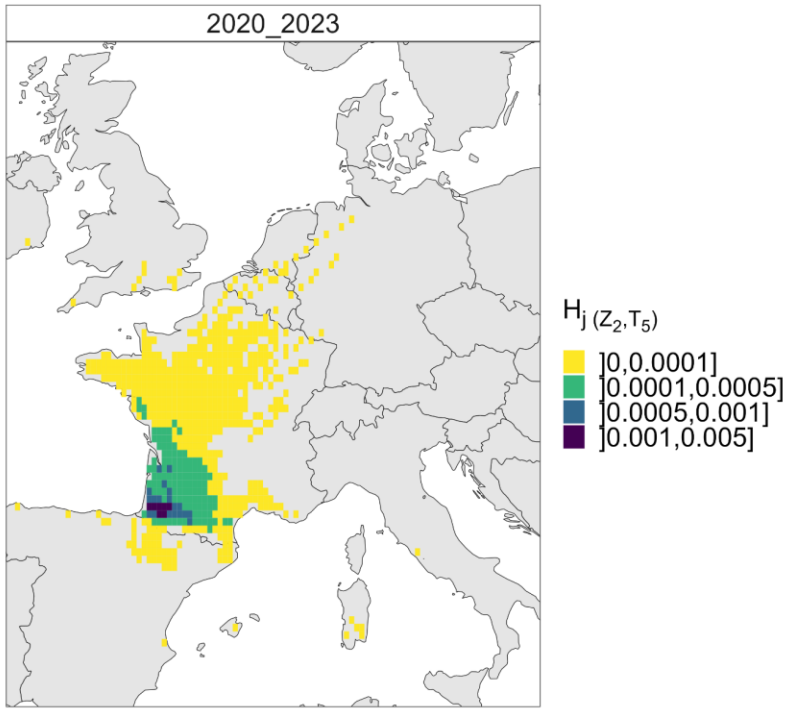
What is the zone at risk of wind-dispersal in 2024, at the re-start of the season?



(A)



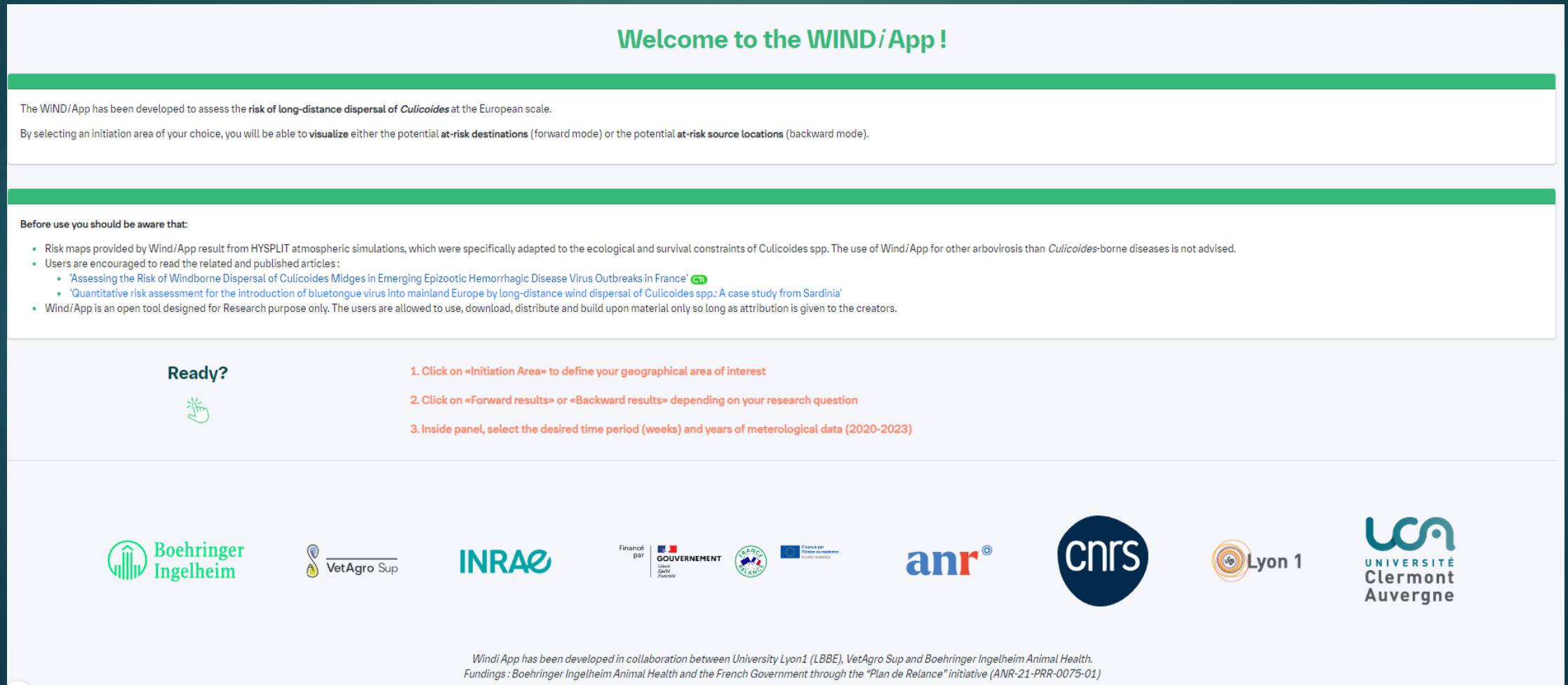
(B)



- Mostly the western half of France
- Extreme destinations at very low probability (UK, Belgium, Sardinia..)
- Pyrénées & Massif Central mountains act as orographic barriers

Windi App

RShiny application for rapid assessment of the zone at risk of wind dispersal
https://windiapp.univ-lyon1.fr/windi_app/



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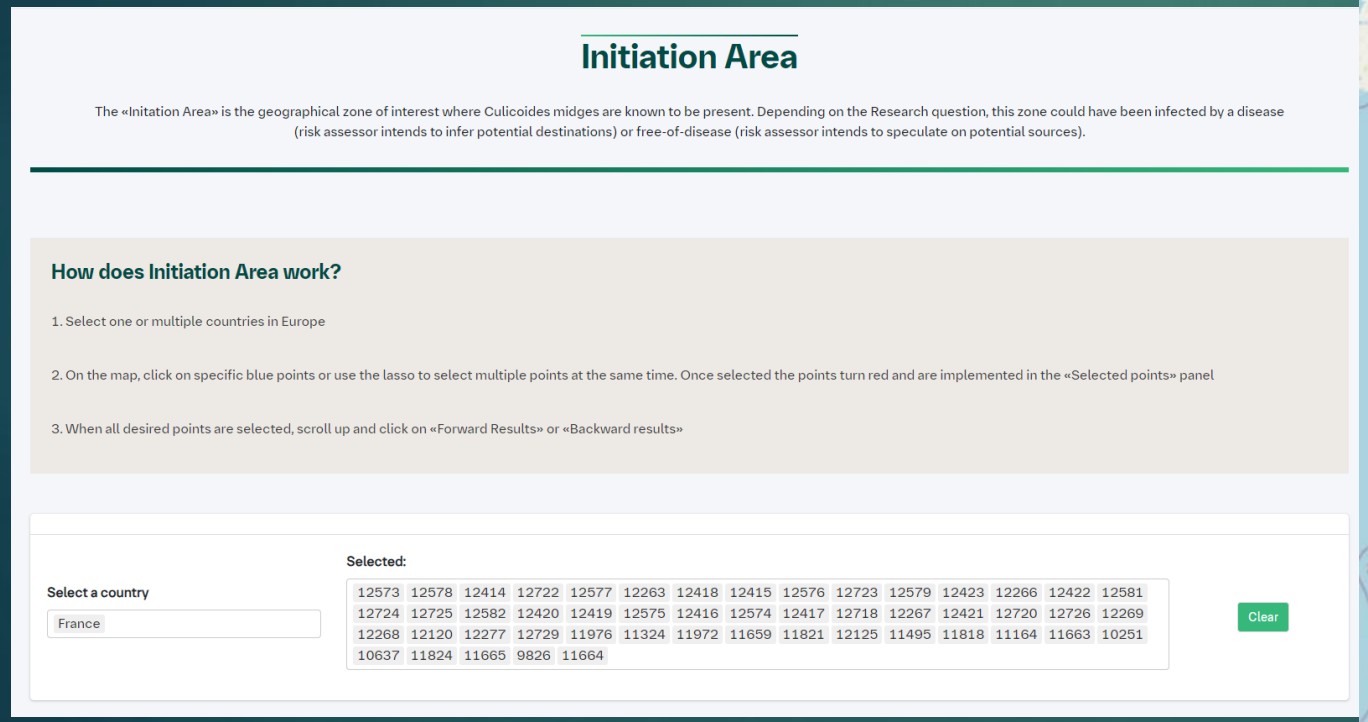
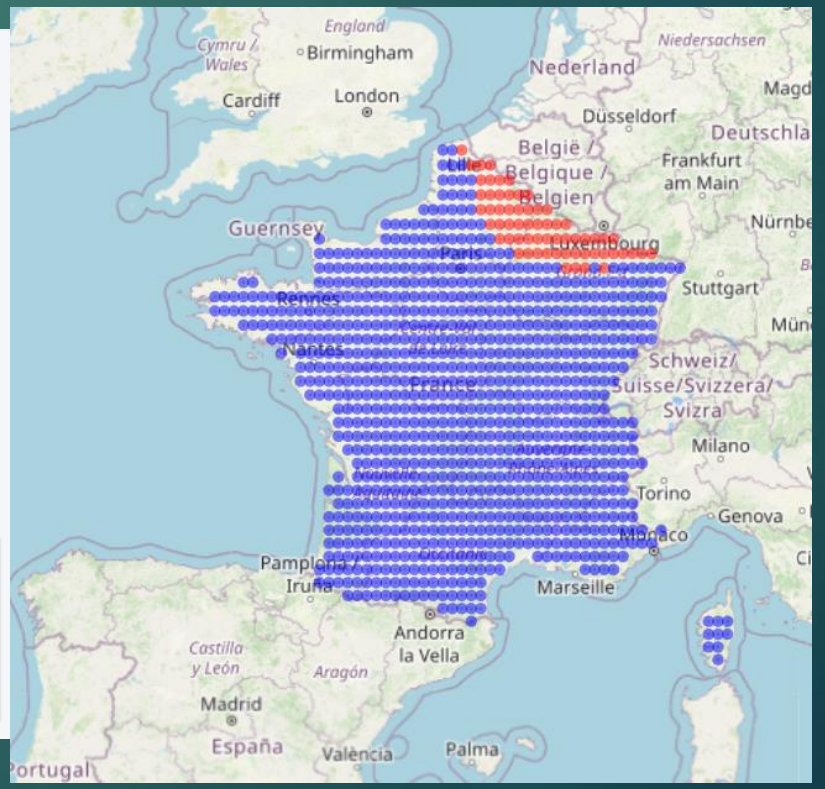
1 Select your 'Initiation Area' (starting point for atmopsheric simulations)





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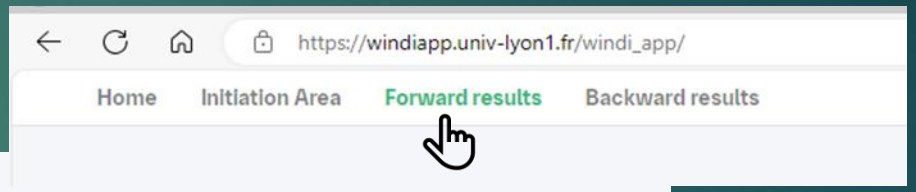
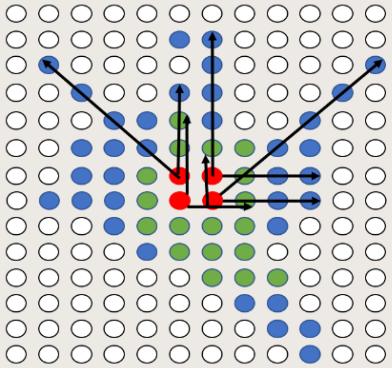
2 Get to the Forward Risk Map



Forward Results

«Forward» probability : infering destinations from source

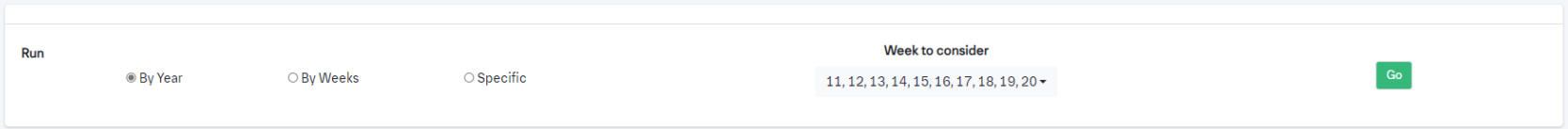


The Foward probability of long-distance dispersal (H_j) is the probability for a Culicoides to reach the destination cell j knowing that it started from the source cell i

- (ID_i : source cell i selected by the risk assessor
- (ID_j with 1 connection (1 trajectory went through)
- (ID_j with 2 connections (2 trajectories went through)
- (ID_j not connected

$$H_j(Z_i, T_y) = \frac{1}{(s_i y_n t_m \alpha)} \sum_{y=1}^{y_n} \sum_{i=1}^{s_i} \sum_{t=1}^{t_m} D_{ijt}$$

D_{ijt} is the number of connections between the source cell i and the destination cell j at day t;
s_i is the number of source grid cells i in the source zone Z_i;
y_n is the number of historical years of meteorological data considered (between 1 and 4 from 2020 to 2023);
t_m the total number of days in the period T_y , with T_1 for a period of 1 week (T_m=7 days) and T_5 for a period of 5 weeks (T_m=45 days); and α is the maximal number of possible destinations reached in a day from a given source cell i, such as α=48 (24 potential deposition spots per trajectory, 2 trajectories started per day)



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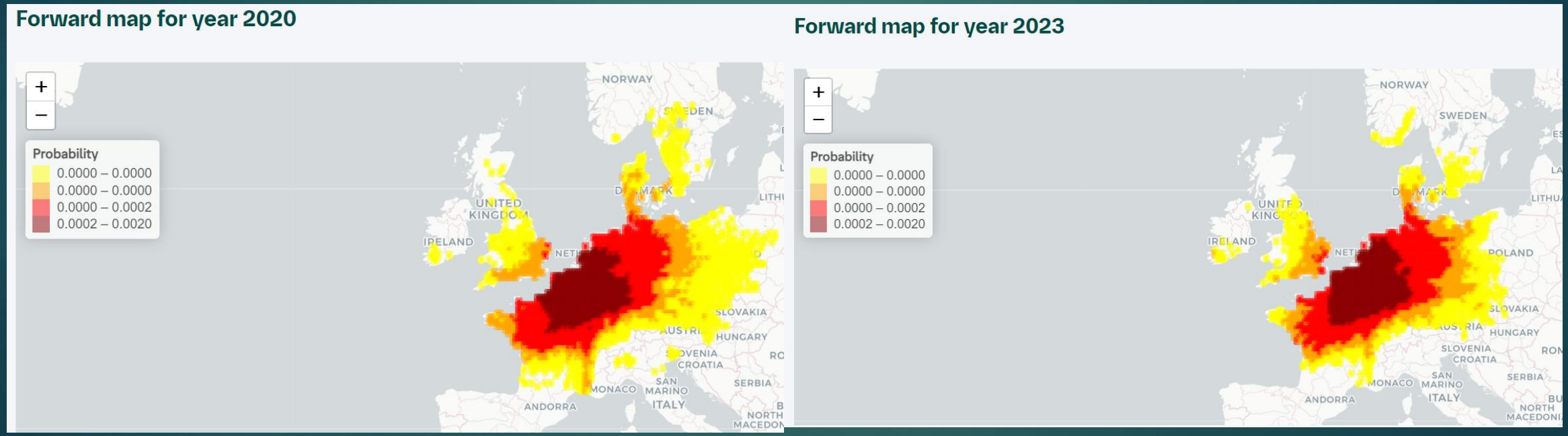
Display the mean probability per year (mean over mid March to mid of November)



Download the data if wanted

Windi App

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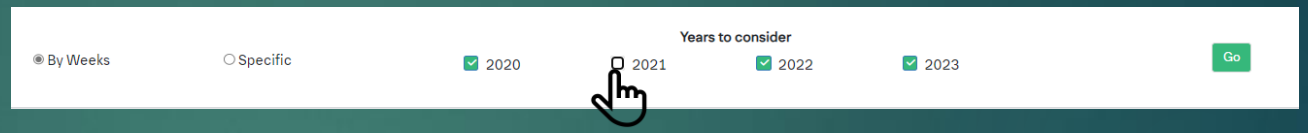
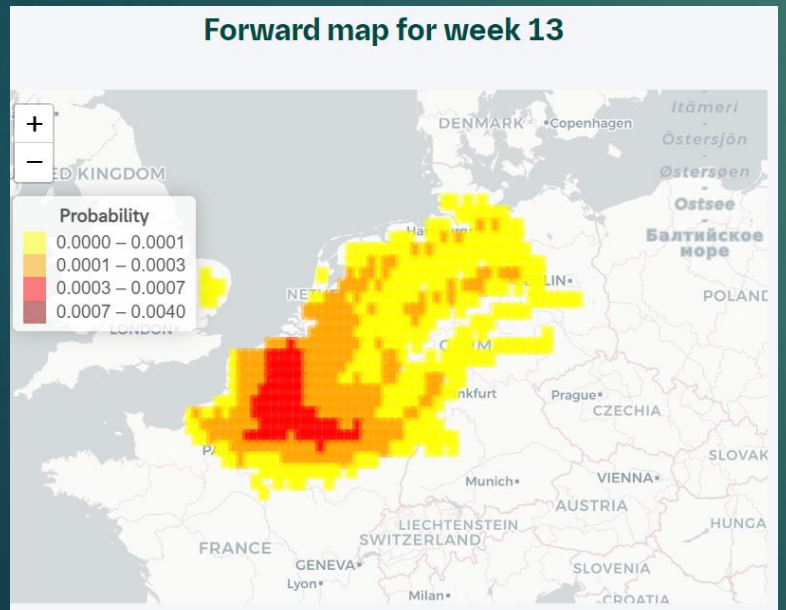
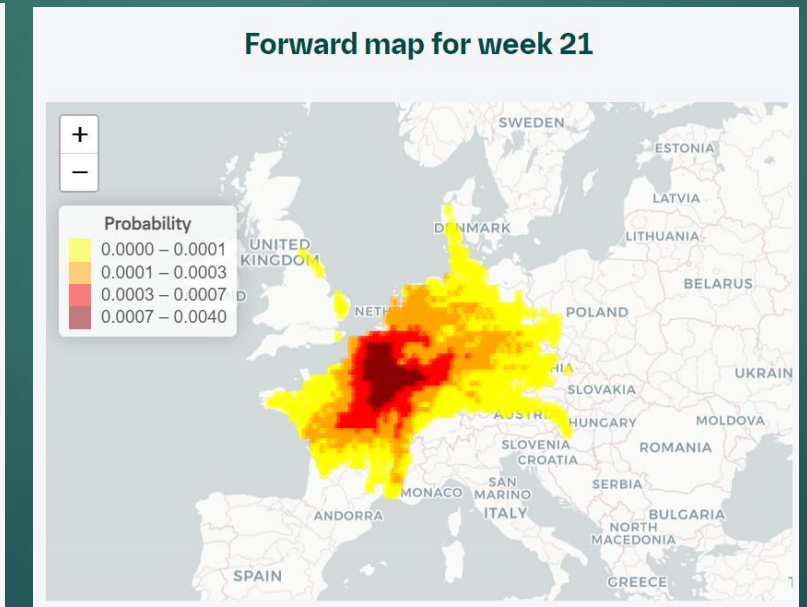
Select the desired years of meterological data (2020-2023)



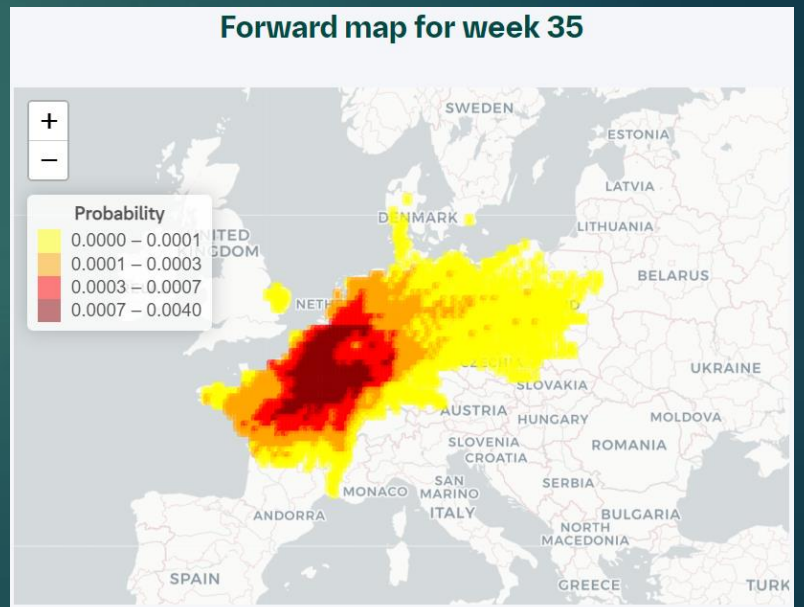
Display the mean probability per week



End March



End May



End August

Conclusions & Perspectives

- Our model is able to **rapidly assess the risk of *Culicoides* long-range dispersal** by the wind
- It considers **historical variations** of wind speed, directions at **large scale** of Europe
- Provides insights to **identify at-risk locations** at risk from a known area with a very **good predictability** (over 5 weeks)
- **Flexible** tool (source locations / *Culicoides* borne disease /time period…)

However…

- Model assumes homogenous vector/host presence in source & destinations
- Under estimates short-range dispersal
- Source area to be updated according to the disease epidemiology

Thank you for your attention

Thanks to all the contributors

Research Article

Assessing the Risk of Windborne Dispersal of *Culicoides* Midges in Emerging Epizootic Hemorrhagic Disease Virus Outbreaks in France

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