

The use of ecological connectivity as a tool for predicting African Swine Fever spread: the Italian outbreak as case of study.

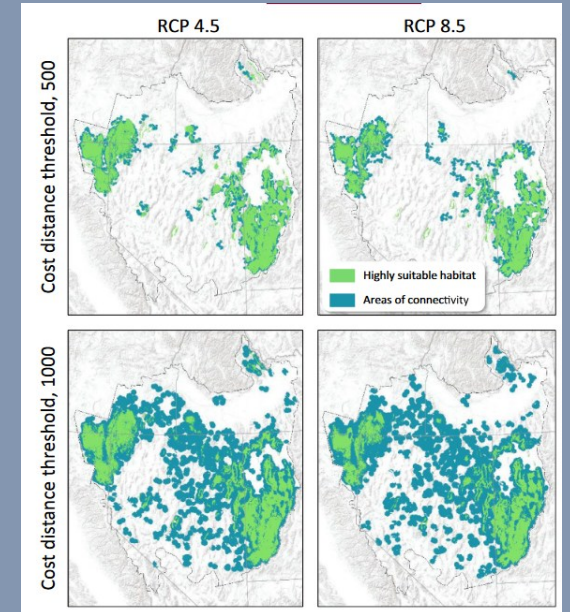
Sonia Illanas, Javier Fernández-López, José Antonio Blanco-Aguilar, Ezio Ferroglio, Marco Scandura, Marco Apollonio, Stefania Zanet, Rachele Vada, Kamila Plis, Tomasz Podgorski, Jim Casaer, Patrick Jansen, Graham Smith, Simon Croft, Oliver Keuling, Ramón C. Soriguer, Joaquín Vicente, Pelayo Acevedo, and *ENETWILD Consortium*



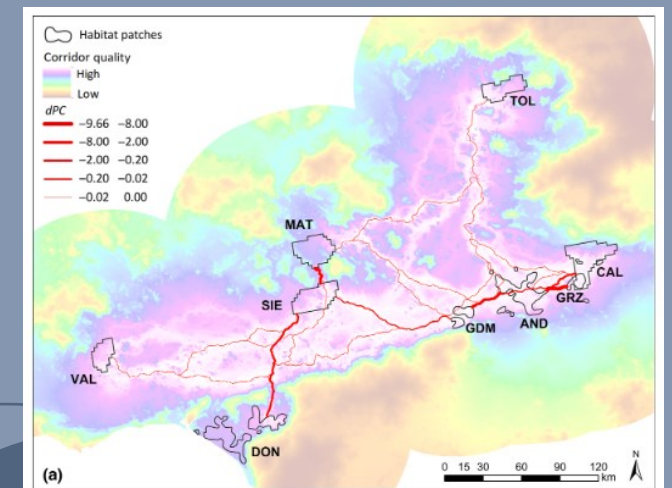
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Ecological connectivity is frequently used in species conservation to detect bottlenecks that hinder movement among populations and could isolate them.

It is based on animal movement, but it is not usually used for predicting disease spread.

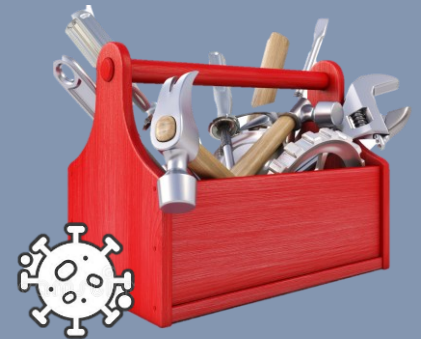


Zeller et al. 2021, *Diversity and Distributions*



Blázquez-Cabrera et al. 2019, *Animal Conservation*

The aim of this study was to determine if ecological connectivity can be used as a tool for predicting the spread of African Swine Fever (ASF) from wild boar density models and, if so, to be integrated into the epidemiology management toolbox.



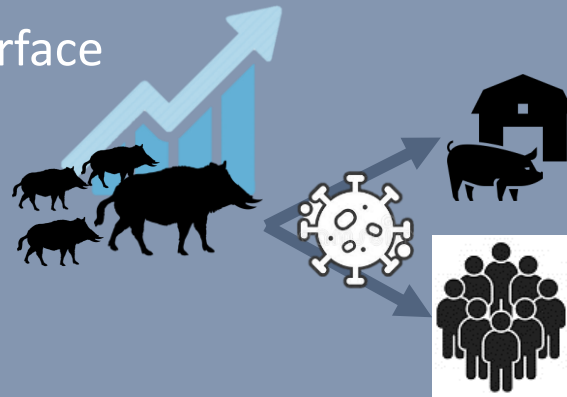


From 2018 to 2023



Main aims of the project:

- 1) Guidance for estimating wildlife populations.
- 2) Data harmonization.
- 3) Estimation of the distribution, abundance and density of wildlife species.
- 4) Wildlife- livestock interface



- Spatial modeling of the maximum hunting bag and project models in a 2x2km grid.
- Hunting yield statistics are the main source of information widely distributed and potentially comparable at European scale.

Thanks to the project it has been possible:

1. to collect more than 300.000 wild boar hunting bags in Europe (9 HS), and
2. establish a net of collaboration at continental scale.

First ASF outbreak in
Italy: January 2022

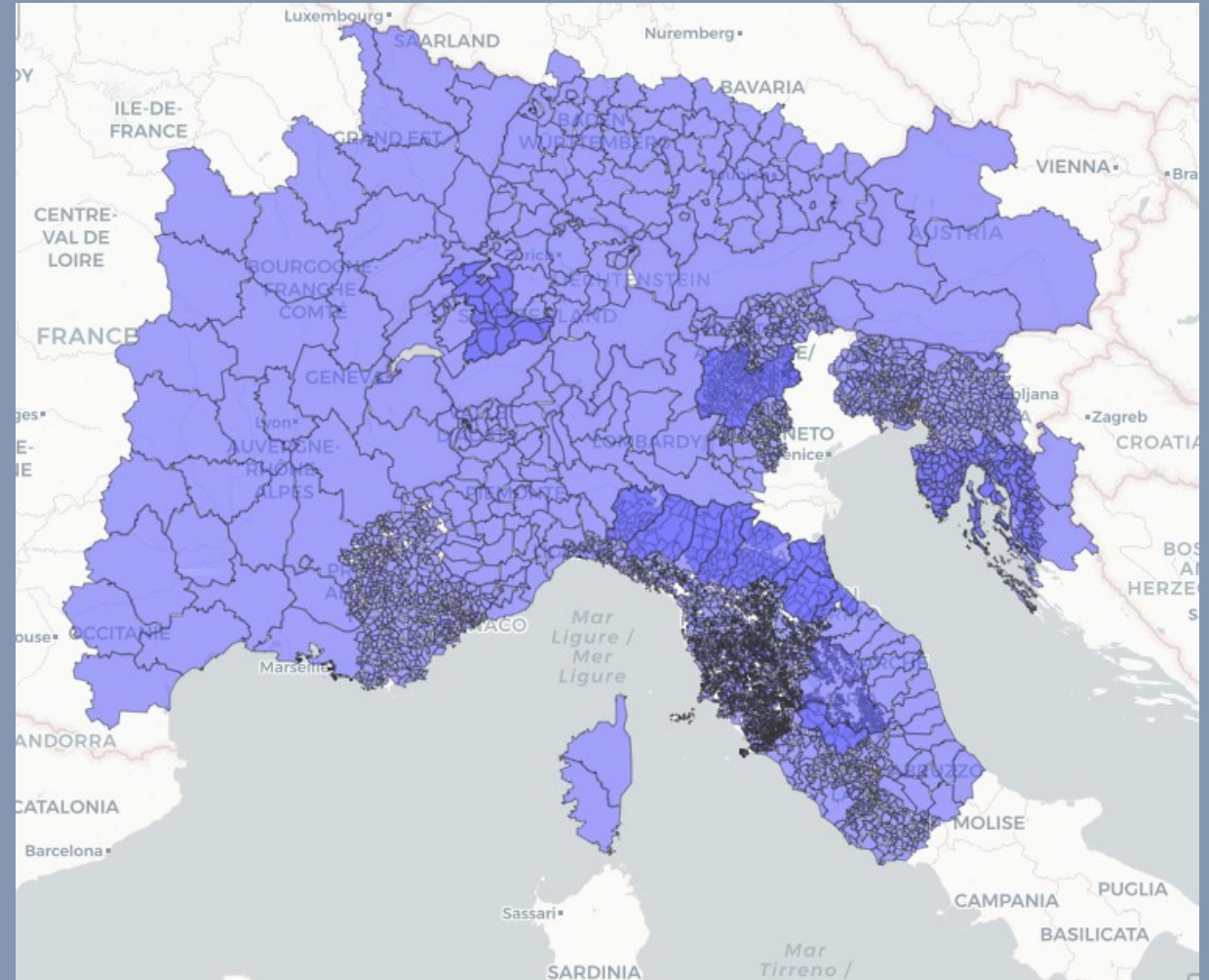
Hunting bags data were
rapidly updated with the last
hunting season and higher
spatial resolution available.

Wild boar density model

Response variable

More precise hunting bags inside a region delimited by a 500km buffer from the first positive ASF reported.

- Date: 2018 and 2021,
- Different spatial resolution: 4478 hunting administrative units (68 NUT2, 1634 NUT1, 2776 HG).



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Explanatory variables

- WorldClim (19 bioclimatic variables) 
- CCI Land cover classes (ESA) 

$VIF < 2$
(variable selection)

Calibration plot

Model framework developed by ENETWILD: GLM with Negative Binomial distribution.

MESS

Results were projected to 2x2km grid.

Resistance model

Density model was transformed using the mean of the 8 neighbor adjacency cells.

Cumulative Cost

ASF wild boar positives were used as disease spread locations.

Connectivity

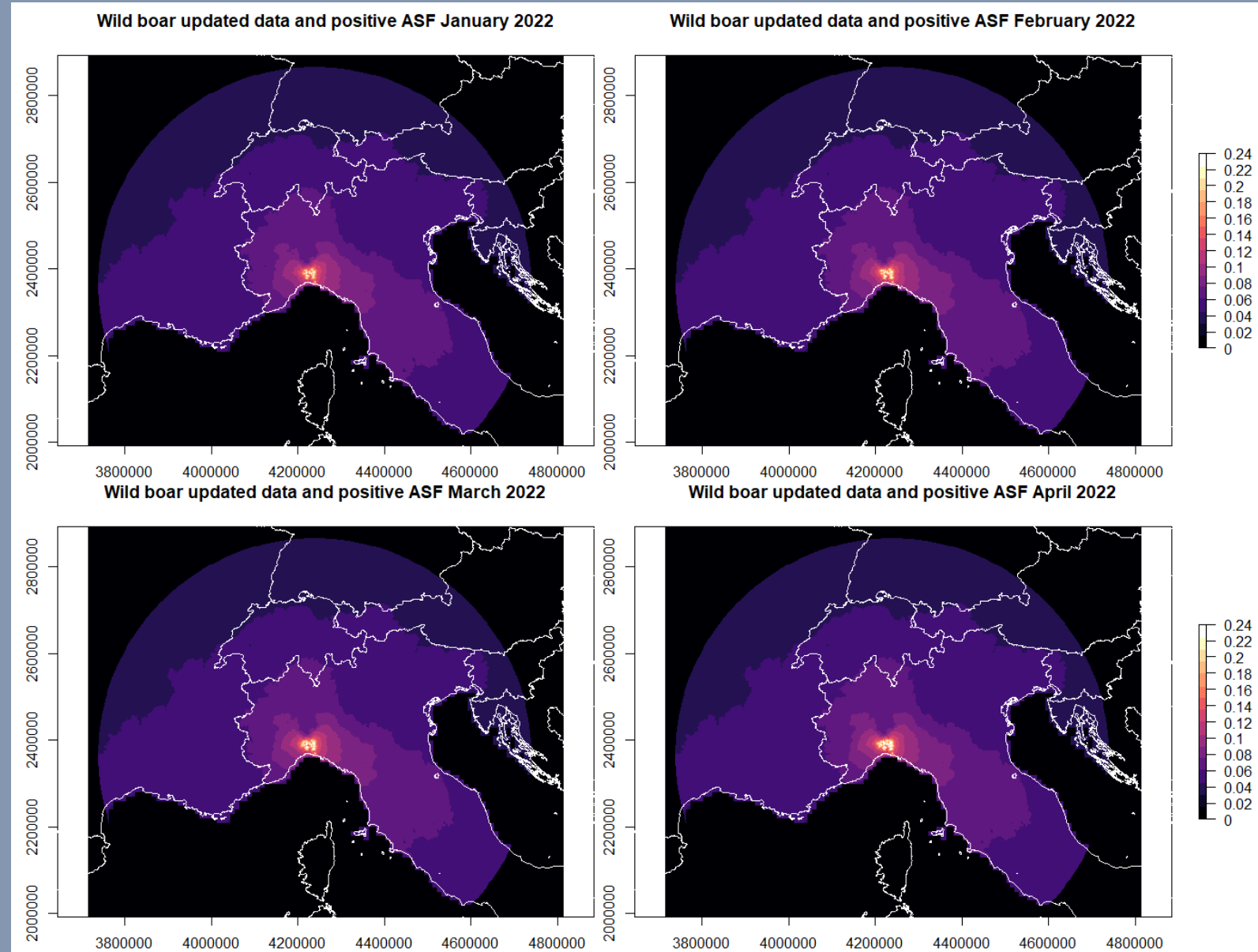
Easier disease displacement where higher abundances.



It has been calculated using a negative exponential transformation:
 $\text{Conductance} = \text{CumulativeCost}^{-1}$.

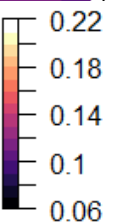
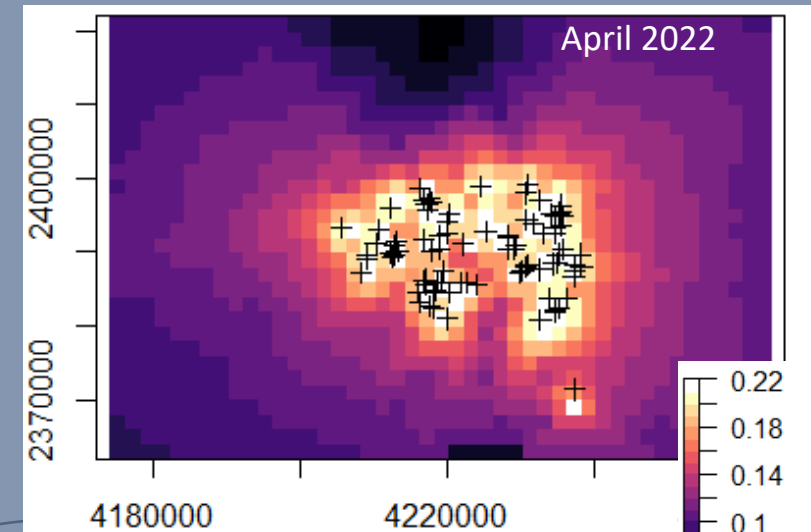
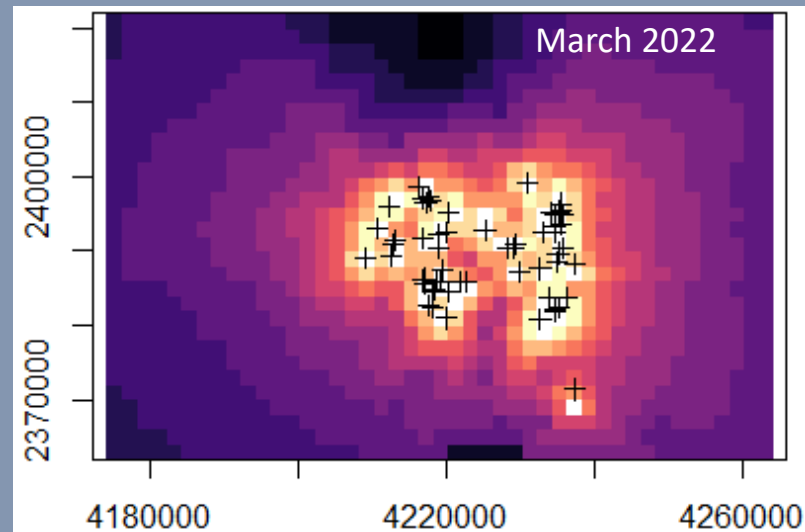
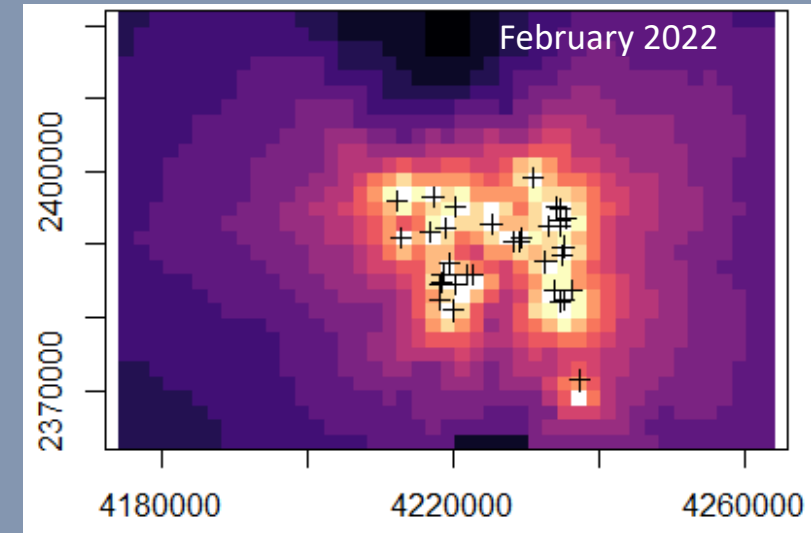
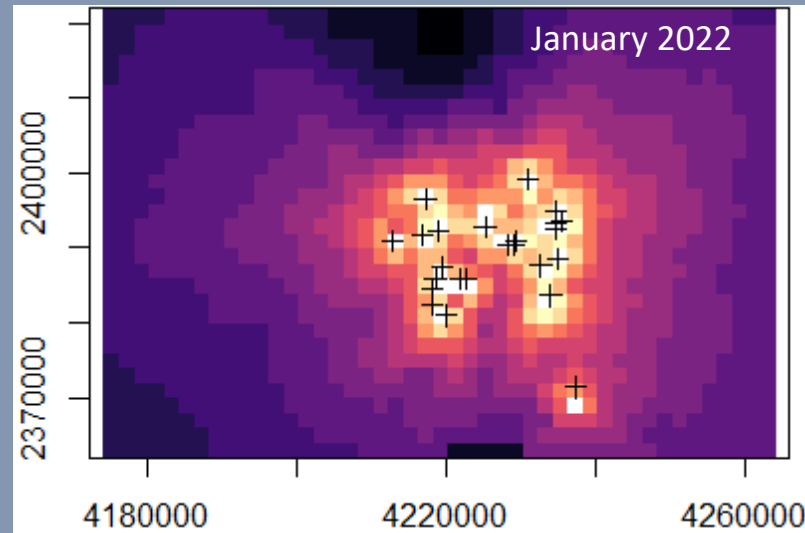
Zoom out

Connectivity maps indicated a plausible spread through the South of Italy instead of crossing the French border.



Zoom in

Within the first four months since ASF outbreak in Italy, the spread of the disease seemed its expansion range more plausible towards the West than the East.



Pros and Cons of using ecological connectivity as a tool for disease expansion.

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- Few parameters are needed to determine plausible expansion range of the disease, and
 - it is fast and easy method for being applied.

- 
- Cumulative cost values are dependent on the frame window.
 - Connectivity validation from one period to the next one needs a systematic search of positive and negative carcasses reported.

Useful tool for determining **expansion range of the disease** and then it could be useful to **integrate** it into the epidemiology **management toolbox**, especially at the first stages of the outbreak as ecological connectivity results are fast to obtain and could help to species management for controlling the expansion wave.

This study has been possible thanks to:

- ENETWILD consortium, project financed by EFSA.
- The contract PRE2020-095091 associated to I+D+i HAWIPO project (PID2019-111699RB-I00), which is funded by the Spanish Ministry for the Science (MCI).



Thanks very much for your attention!



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