

# One for all: a generic risk framework for all pathways of disease introduction

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We develop a risk assessment framework that is generic and applicable to a wide range of pathogens. The aim is to improve hotspot identification of exotic disease incursions. The framework will need to cope with spatial variation, diverse sources of input data at different scales, various transmission routes and distributions of both wild animals and livestock.

## What is the risk of infection and spread of a pathogen in Area B due to the presence of that pathogen in Area A?

Our framework for the above risk question is outlined in Fig. 1. Major transmission pathways that we consider are:

- Legal live animal trade
- Trade in food products
- Terrestrial movement of wild animals
- Human transportation
- Vector flight
- Bird migration

**Risk of Infection:** the probability of one or more initial infections in a native species in Area B.

**Risk of Spread:** the probability of one or more infections at a different location in Area B.

### Risk of Infection Calculation

**1. Entry** The number of infected hosts,  $I(g)$ , entering location  $g$  of Area B is defined as

$$I(g) = \sum_q Bin(N_q(g), p_q)$$

where  $N_q(g)$  is the number of hosts entering location  $g$  from sub-region  $A_q$  in Area A and  $p_q$  is the prevalence of infected hosts in  $A_q$ .

**2. Detection** The number of infected hosts passing any detection controls is

$$J(g) \sim Bin(I(g), 1 - p_D(g))$$

where  $p_D(g)$  is the probability of detection in location  $g$ .

### 3, 4 & 5. Survival, Contact and Transmission

We use  $R_0$  to represent these 3 steps. We use different equations for  $R_0$  depending on the disease and transmission pathways.

Overall our risk of infection  $R_I(g)$  at location  $g$  is:

$$R_I(g) = 1 - e^{-R_0(g)J(g)}$$

**Risk of Spread:** Calculated using a similar methodology.

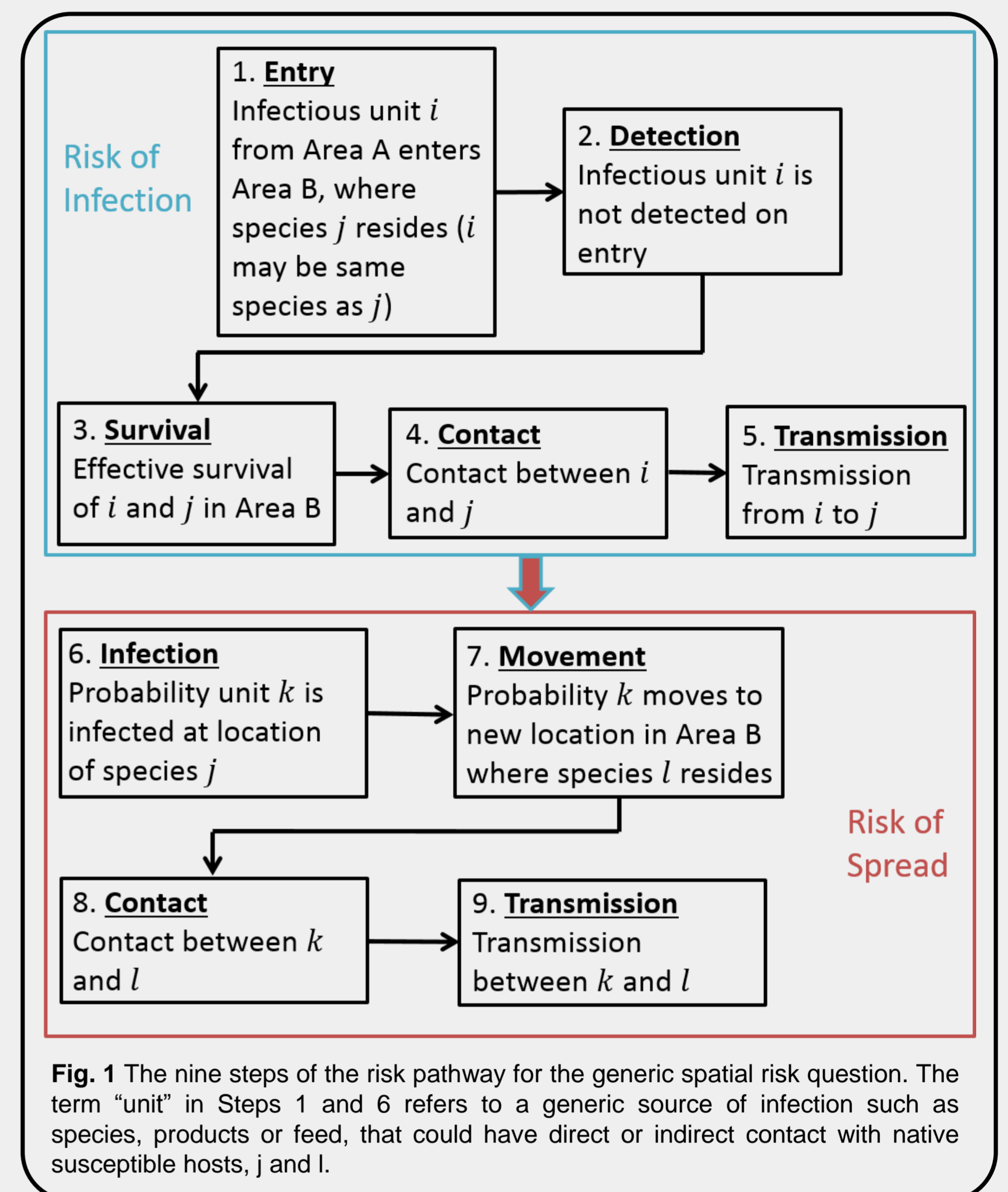


Fig. 1 The nine steps of the risk pathway for the generic spatial risk question. The term "unit" in Steps 1 and 6 refers to a generic source of infection such as species, products or feed, that could have direct or indirect contact with native susceptible hosts,  $j$  and  $l$ .

## Risk of Infection: African Swine Fever (ASF) - PRELIMINARY RESULTS

We predict the risk of infection of ASF in Europe in 2018.

We consider three risk pathways:

1. Trade in Pig Meat Products (Fig. 2)
2. Live Pig Trade (Fig. 3)
3. Terrestrial Movement of Wild Boar (Fig. 4)

We use data on:

- Boar and pig density maps and estimated numbers of backyard pigs
- Boar habitat suitability maps – to determine direction of boar movement (Alexander et al. 2016)
- Eurostat Comext trade data
- Prevalence in 2017 (Simons et al. 2017 and EMPRES-i data)

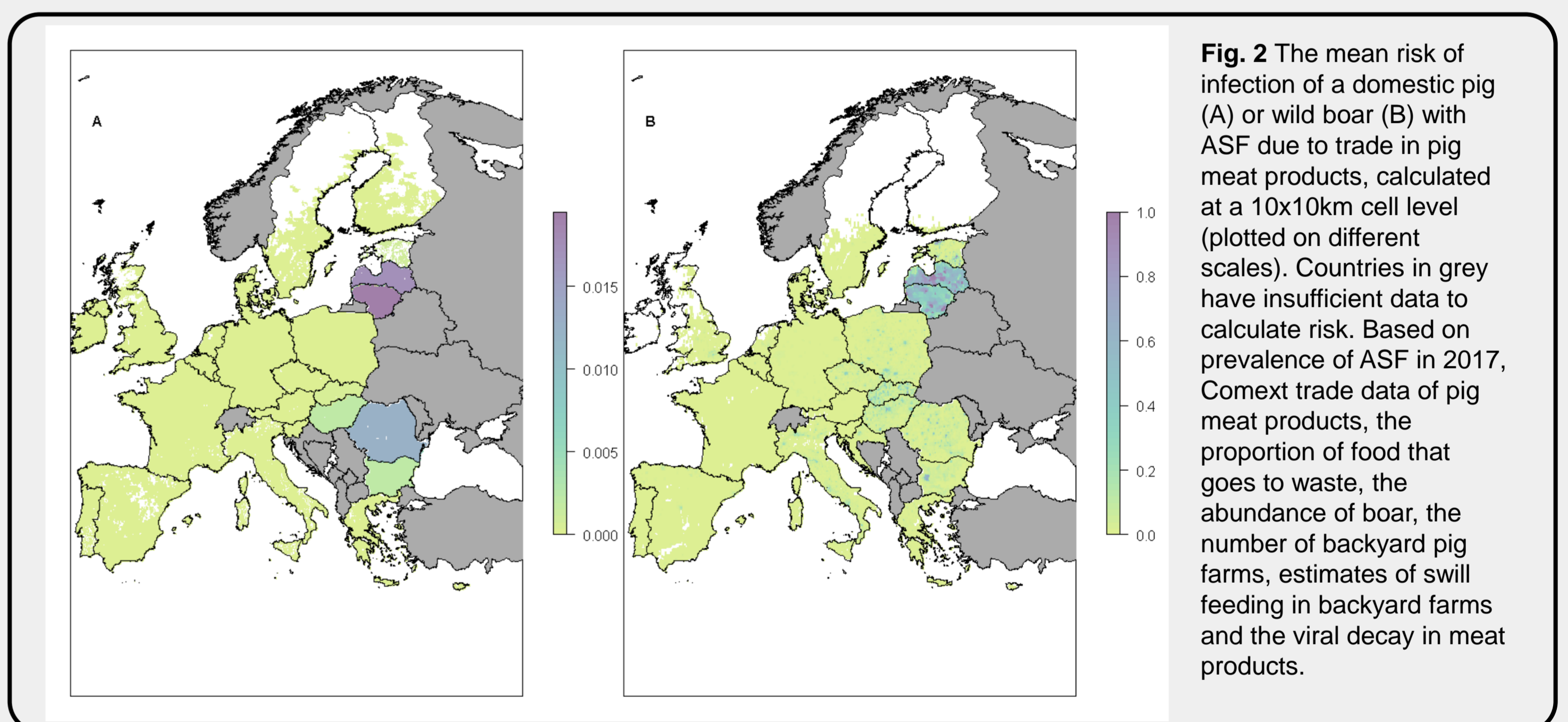


Fig. 2 The mean risk of infection of a domestic pig (A) or wild boar (B) with ASF due to trade in pig meat products, calculated at a 10x10km cell level (plotted on different scales). Countries in grey have insufficient data to calculate risk. Based on prevalence of ASF in 2017, Comext trade data of pig meat products, the proportion of food that goes to waste, the abundance of boar, the number of backyard pig farms, estimates of swill feeding in backyard farms and the viral decay in meat products.

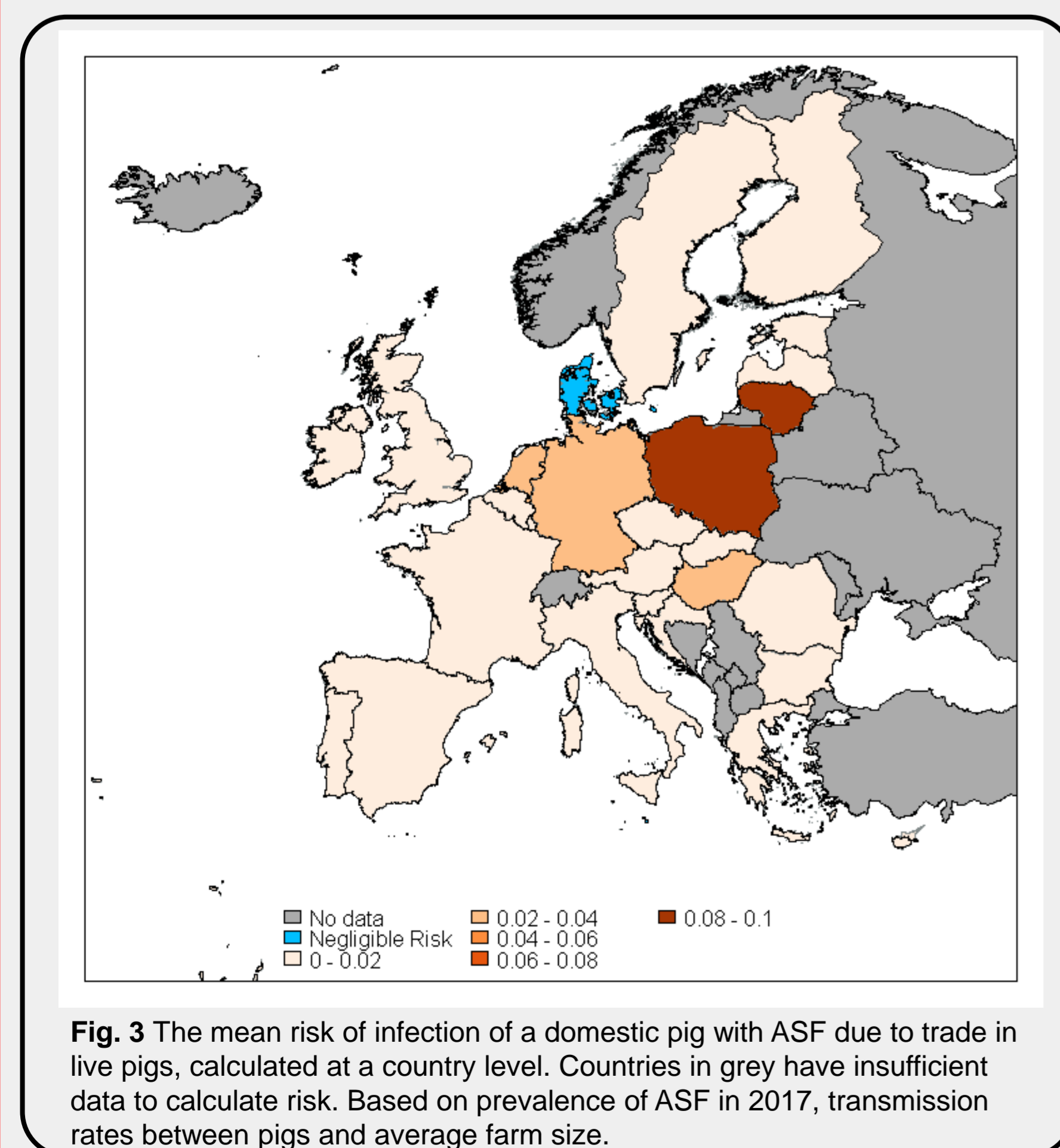


Fig. 3 The mean risk of infection of a domestic pig with ASF due to trade in live pigs, calculated at a country level. Countries in grey have insufficient data to calculate risk. Based on prevalence of ASF in 2017, transmission rates between pigs and average farm size.

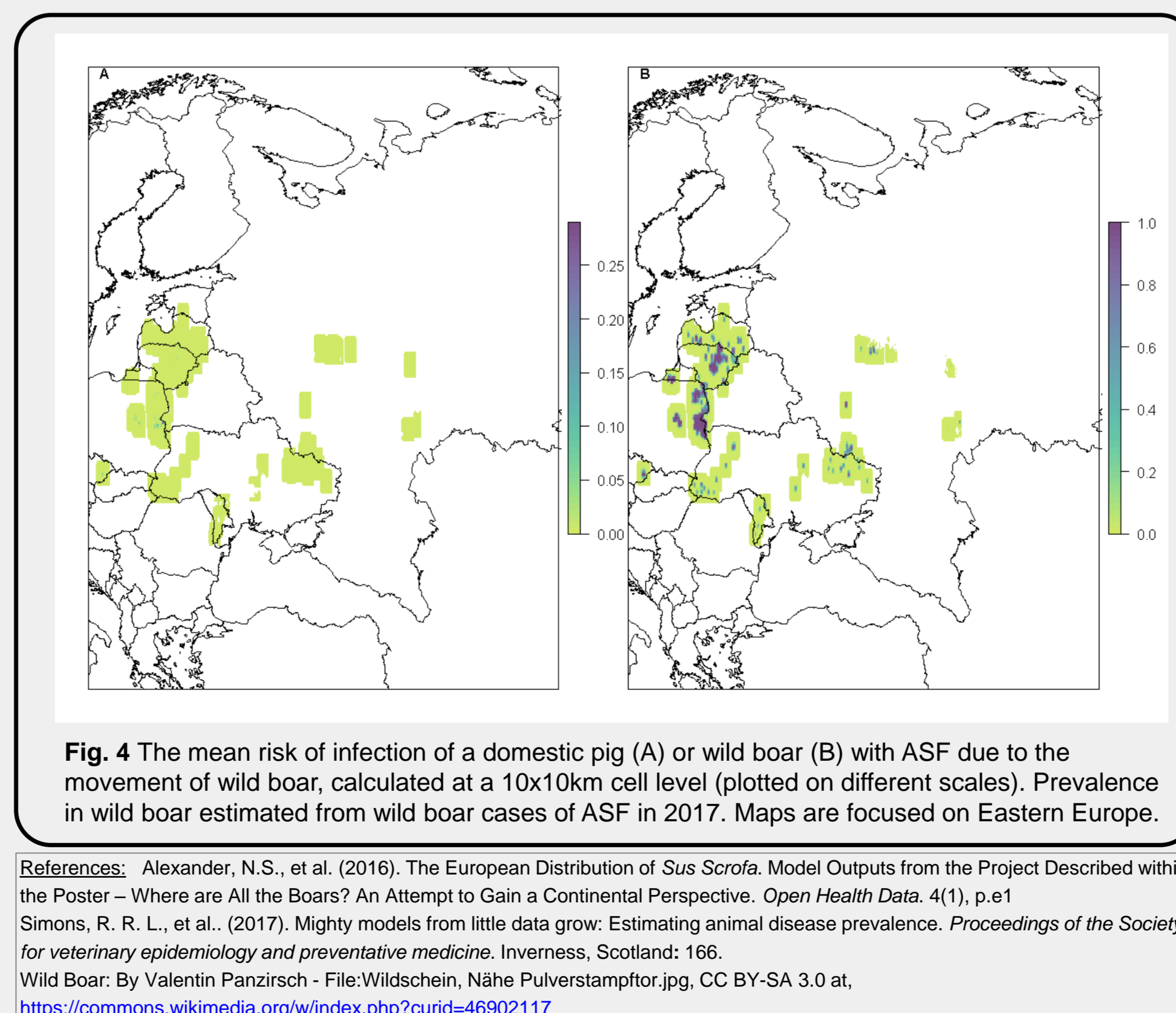


Fig. 4 The mean risk of infection of a domestic pig (A) or wild boar (B) with ASF due to the movement of wild boar, calculated at a 10x10km cell level (plotted on different scales). Prevalence in wild boar estimated from wild boar cases of ASF in 2017. Maps are focused on Eastern Europe.

References: Alexander, N.S., et al. (2016). The European Distribution of *Sus Scrofa*. Model Outputs from the Project Described within the Poster – Where are All the Boars? An Attempt to Gain a Continental Perspective. *Open Health Data*. 4(1), p.e1  
Simons, R. R. L., et al. (2017). Mighty models from little data grow: Estimating animal disease prevalence. *Proceedings of the Society for Veterinary Epidemiology and Preventative Medicine*, Inverness, Scotland: 166.  
Wild Boar: By Valentin Panzirsch - File:Wildschein, Nähe Pulverstampfor.jpg, CC BY-SA 3.0 at <https://commons.wikimedia.org/w/index.php?curid=46902117>

Countries predicted to have higher relative risk in 2018 are those which had cases in 2017 (Lithuania, Latvia and Poland), or have now had outbreaks in 2018, such as Romania, Hungary and Bulgaria. Our three risk pathways did not predict sporadic long-distance spread, such as the recent cases in Belgium. In general, the wild boar movement pathway predicted non-negligible risk only near current cases, indicating that natural wild boar movement is not responsible for long-distance spread. The food trade and movement of wild boar pathways were both more likely to cause cases in wild boar than pigs.