

A spatial entry assessment model framework for incursion of exotic disease into the European Union (SPARE)



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Introduction: Disease incursion and transmission modelling can play an important role in elucidating important pathways and dynamics of transboundary diseases. It is an important pre-requisite for preparedness and rapid response. A model framework has been developed which makes use of global datasets to predict the probability of entry of exotic animal pathogens to European Union (EU) member states (MSs) via some of the most likely routes of introduction: legal trade of livestock and meat products, illegal trade of red meat, wild animal dispersion, windborne vector dispersion and human introduction of pets. The model was designed to be applicable for a wide range of pathogens, many of which have limited data. We demonstrate its application through four case study pathogens: African swine fever (ASF), Classical swine fever (CSF), Bluetongue virus (BTV) and classical rabies.

Methodology: The generic model framework consisted of two modules (Figure 1). Module 1 utilised historical input data such as pathogen incidence and animal demographics to derive an estimate for country level pathogen prevalence by animal species. Module 2 combined these prevalence estimates with data specific to the route of entry, such as type of trade products and pathogen survival rates, to estimate the probability of introduction to EU MSs.

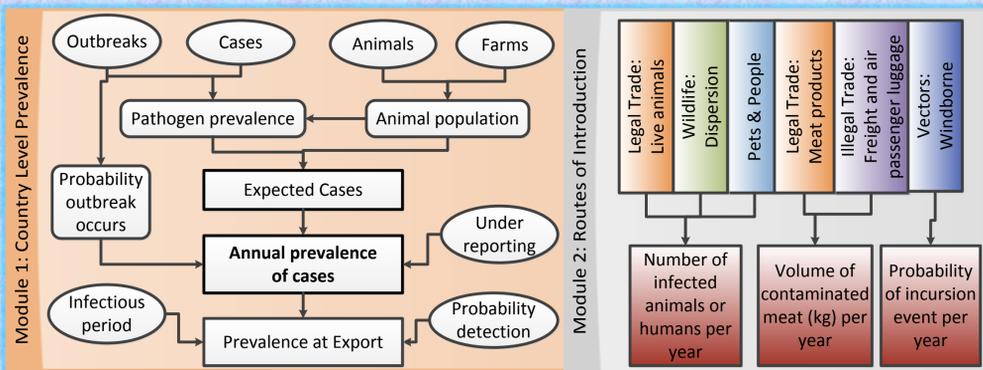


Figure 1: Model Framework diagram; country level prevalence (left) and routes of introduction (right)

The main outputs of the baseline model were estimates for the expected annual introduction to each EU MS, from each route and pathogen, as detailed in Figure 1. The model also provided interim results, by specific countries of export and species. Key parameters are shown in Table 1.

Table 1: Key parameters and data sources

Parameter	Data Source
Country Prevalence	
Species considered in the model	OIE, WAHIS annual & weekly reports: www.oie.int/wahis_2/public/wahid.php/Wahidhome/Home
Number of outbreaks, cases, animals and establishments by species, country and year	
Probability of an outbreak occurring	
Legal Trade (meat products)	
Legal trade products considered in the model	Comext (Eurostat): epp.eurostat.ec.europa.eu/newxtweb/
Volume of legal trade between country and MS	
Illegal trade (red meat)	
Number of legal consignments of type (maritime container, air freight, passenger luggage)	Eurostat databases: www.ec.europa.eu/eurostat/data/database
Average kg of illegal red meat seizures	Assumed by author based on unpublished data
Proportion consignments containing illegal meat	
Pets	
Number pets moved between country and MS	TRACES: webgate.ec.europa.eu/sanco/traces/
Vectors (windborne dispersion)	
Proportion of country's livestock population in area close enough to EU MS for vectors to travel	FAO livestock density maps: fao.org/ag/againfo/resources/en/glw/home.html
Probability of a vector surviving the journey between the country and EU MS	Model calculation based on shape files of the world
Wild animal dispersion	
Wild animals species considered	ASF,CSF: wild boar, BTV: N/A, Rabies: red fox
Wild animal density & habitat suitability	Based on raster maps from published data

Results: The model predicts the pathogen with the greatest probability of entry for infected live animals is ASF in Lithuania and Poland and BTV in Italy and Greece (Figure 2). Poland imports pigs from Lithuania, one of the EU MSs with the highest prevalence of ASF, and Italy imports a very high number of cattle from France which has a non-zero prevalence of BTV. Thus, for Poland the risk is higher due to trading with a relatively high prevalence country, while for Italy it is simply just the high volume of trade from a country with a non-zero prevalence that leads to an increased probability. Note, results also provided for Switzerland.

There is little legal importation of live animals from outside the EU by any MS (Figure 3). The highest risk region(s) of import can differ by pathogen and route; for illegal trade, Africa is the highest risk for ASF, but it is the Caribbean for CSF.

Conclusion: The model proposed here provides valuable information for risk assessors, providing detailed quantitative comparisons to indicate which pathogens are most likely to enter the EU, by which route and into which areas within Europe. The model can be a useful quantitative complement to current qualitative early warning systems, to highlight a change in probability due to factors such as changing trade patterns or new outbreaks of disease. Such results are of particular value in the first instances of a disease outbreak where, typically, information on imports and routes of entry are investigated on a case-by-case basis. We believe that considering the results from multiple models will best inform stakeholders to respond in a rapid and risk appropriate manner to drive risk-based surveillance activities.

Acknowledgements: This work had funding agreed through the Animal Health and Welfare ERA-NET consortium (<https://www.anihwa.eu/>) under SPARE ('Spatial risk assessment framework for assessing exotic disease incursion and spread through Europe'). Funders are acknowledged as the Department for the Environment, Food and Rural Affairs (Defra) - UK, Ministry of Health - Italy, Spanish National Institute of Agriculture and Food Research and Technology - Spain, and Federal Food Safety and Veterinary Office (FSVO) - Switzerland. **Contact details:** robin.simons@apha.gov.uk.

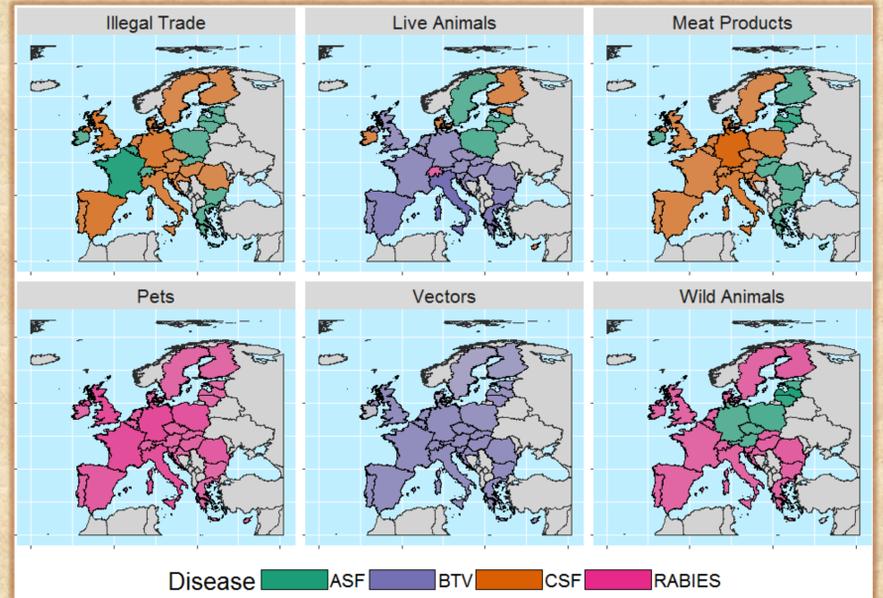


Figure 2: Maps showing highest risk pathogen for each MS and route. Darker shading signifies higher risk relative to other MSs (absolute values not presented).

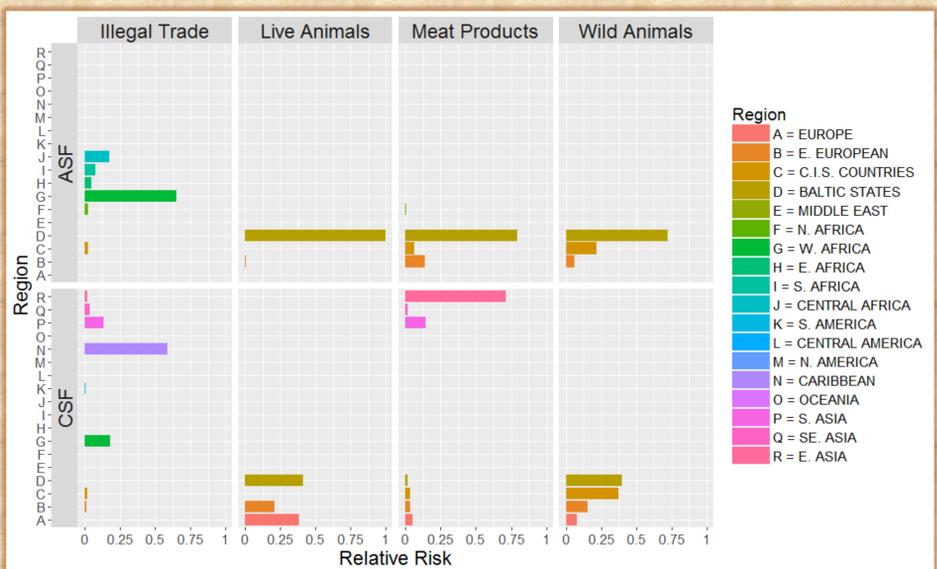


Figure 3: Risk of introduction to EU MSs, relative to geographical region, for ASF and CSF. Results split by route of introduction and pathogen.

A scenario analysis considering parameters with high uncertainty suggested that in general there was not a huge impact on the model results (Figure 4). The main exception was the scenario where it was considered that there was zero risk from any EU MS, which has a much lower risk. This is not surprising as there is little trade of live animals from non EU countries and most of the risk from wild animal introduction comes from within the EU.

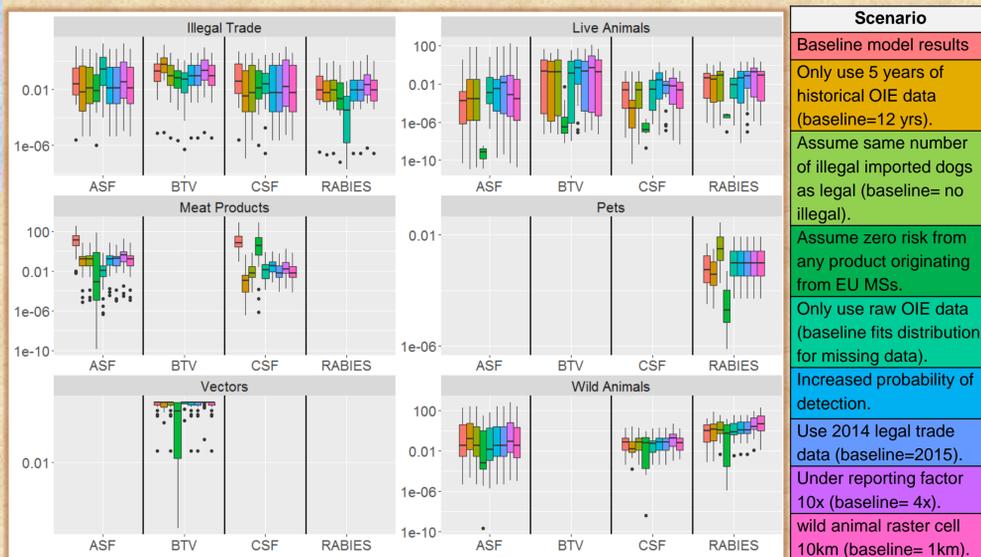


Figure 4: Boxplots for results of scenario analyses. The legend details the order the scenarios appear on the x axis and the colour