Modelling disease spread when the host distribution is unknown, with an application to African Swine Fever

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The challenge

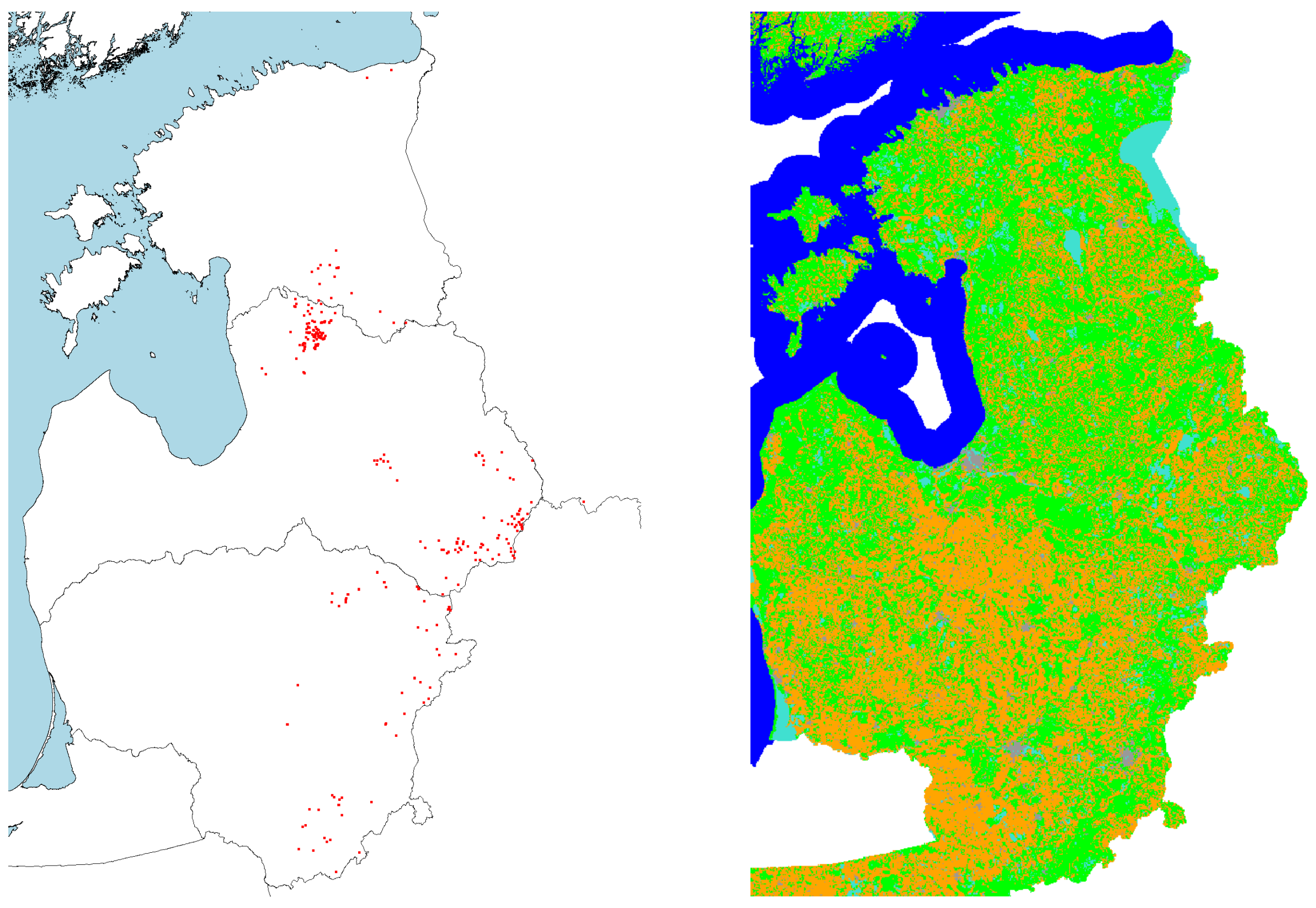
- Animal disease outbreak data typically comprise ONLY cases with times/locations
- However, most data analysis methods also require knowledge of the host spatial distribution
- We have developed methods that allow us to make use of outbreak data when the host distribution is unknown…
- …and enable prediction of spread and control
- The methods are generic and can be applied to a wide range of infectious diseases
- Case study: application to ASF (African Swine Fever) case data for wild boar in the Baltic States

Methods

- First, aggregate case data to grid of cells covering the study area
- Assemble covariate data potentially related to host distribution
- Our method simultaneously estimates:
    - *suitability* of each cell in terms of covariate data, this can be interpreted as an estimate of *host density*
    - the transmission kernel at the aggregated grid cell level
- Analysis enables prediction of spread and control
- Simulations suggest that, if the grid cells are reasonably small, then spatial aggregation has little impact on the estimate of the transmission kernel or suitability

Data for case study

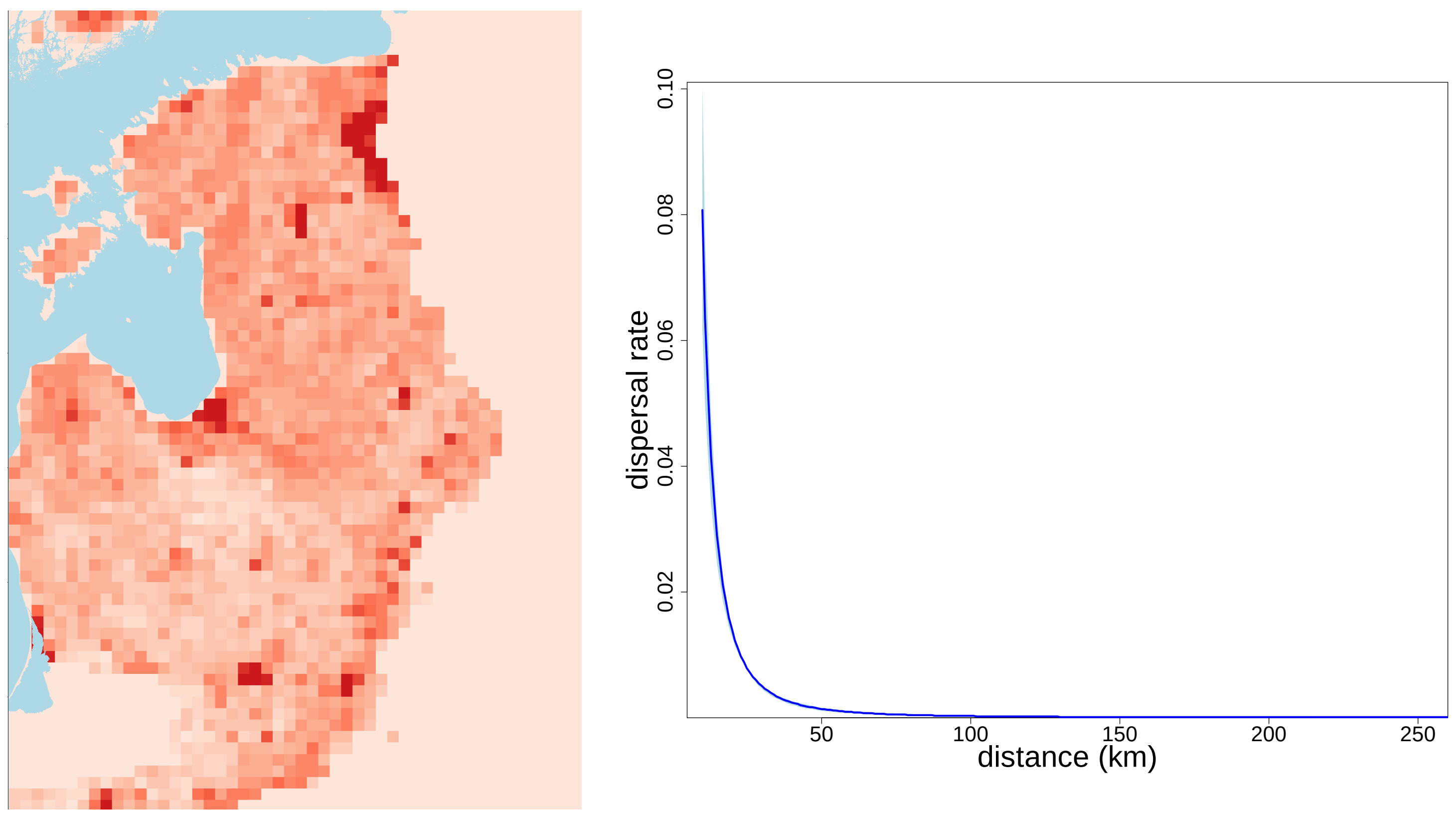
- Study area: rectangular region covering Estonia, Lithuania and Latvia (The Baltic States)
- Case data (time and location) for wild boar infected with African Swine Fever up to May 2015 within study area
- Land use data from Corine CLC2012 land cover map
- Data spatially aggregated to 10km by 10km grid cells



Inputs: wild boar ASF cases and land use data

Left: cases of ASF in wild boar up to April 2015

Right: land use in the study area, with orange=agricultural land, green=forest, grey=urban, turquoise=inland waters, blue=sea, white=no data



Outputs: wild boar density and transmission kernel

Left: estimated suitability (host density), with darker colours corresponding to higher suitability. Inland water and forest had the highest suitability estimates.

Right: estimated transmission kernel, which shows how far the disease typically spreads. Most transmission is estimated to be over distances of <40km, but with rare very long distance dispersal events.

Discussion

- We have developed new methods that enable prediction of spread and control using disease outbreak data when the host distribution is unknown
- We have tested these methods on simulated data and in the case study above
- This is work in progress, and further testing is required to determine the potential and limitations of these methods
- Nevertheless the methods are generic and should be applicable to a wide range of diseases
- **These methods open up new datasets for analysis, ultimately extracting greater value from available outbreak data**