

# Geographical pattern of farms and distance dependent transmission of disease



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## Background

There is a need for general frameworks for models of spread of disease between farms where the spatial aspect is considered. Traditionally models have disregarded the spatial aspect completely or treated it too simple, i.e. assuming farms to be randomly distributed in space. In reality there are spatial patterns both regionally and locally that deviates from random distribution (see Figure 1).

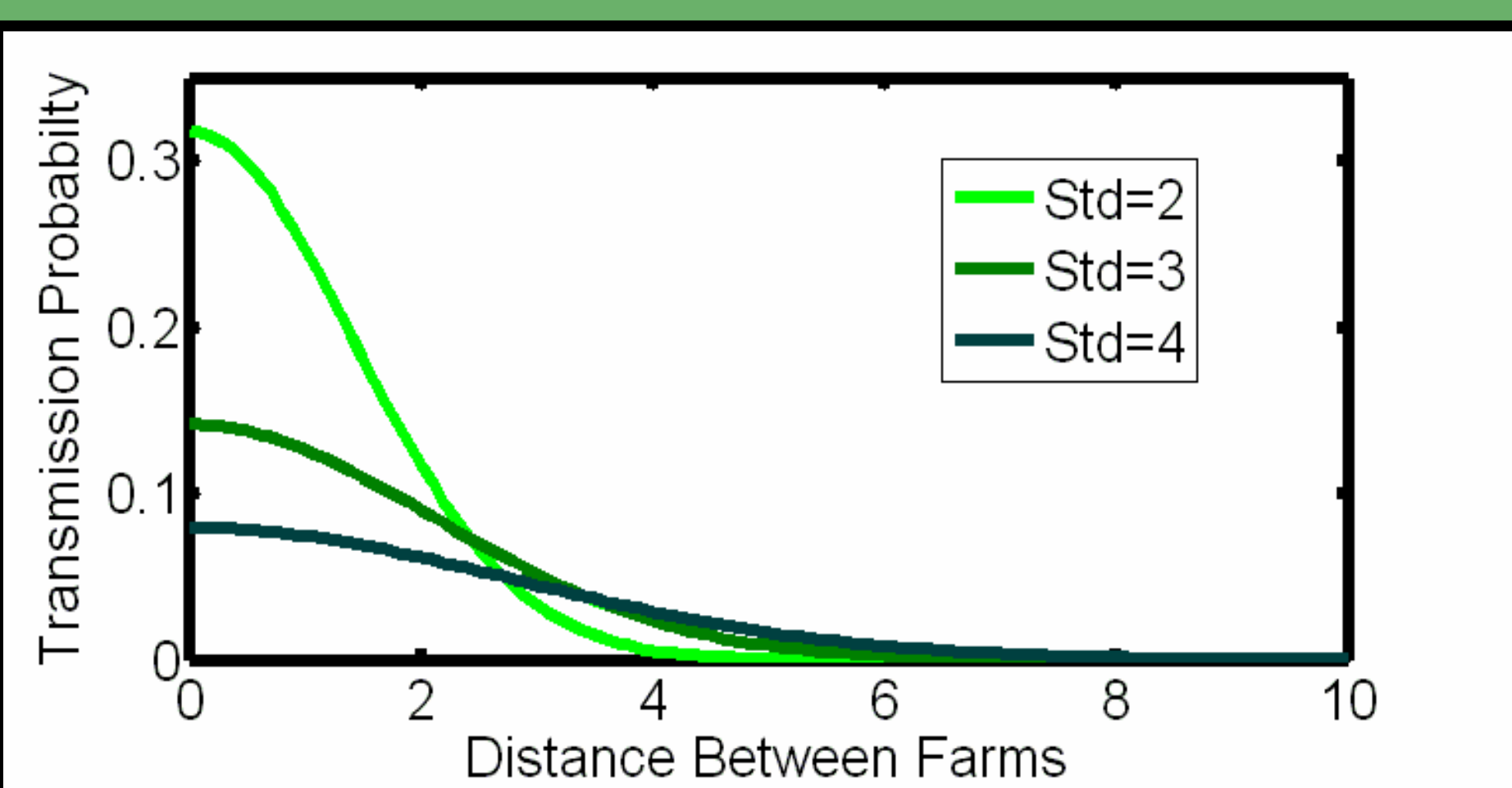
Diseases can be transmitted between farms by an immense number of possible pathways. The complex nature of the process demands too many parameter estimations to make good quantitative predictions. A general model framework can however give insight in to outbreak dynamics.

## The aim

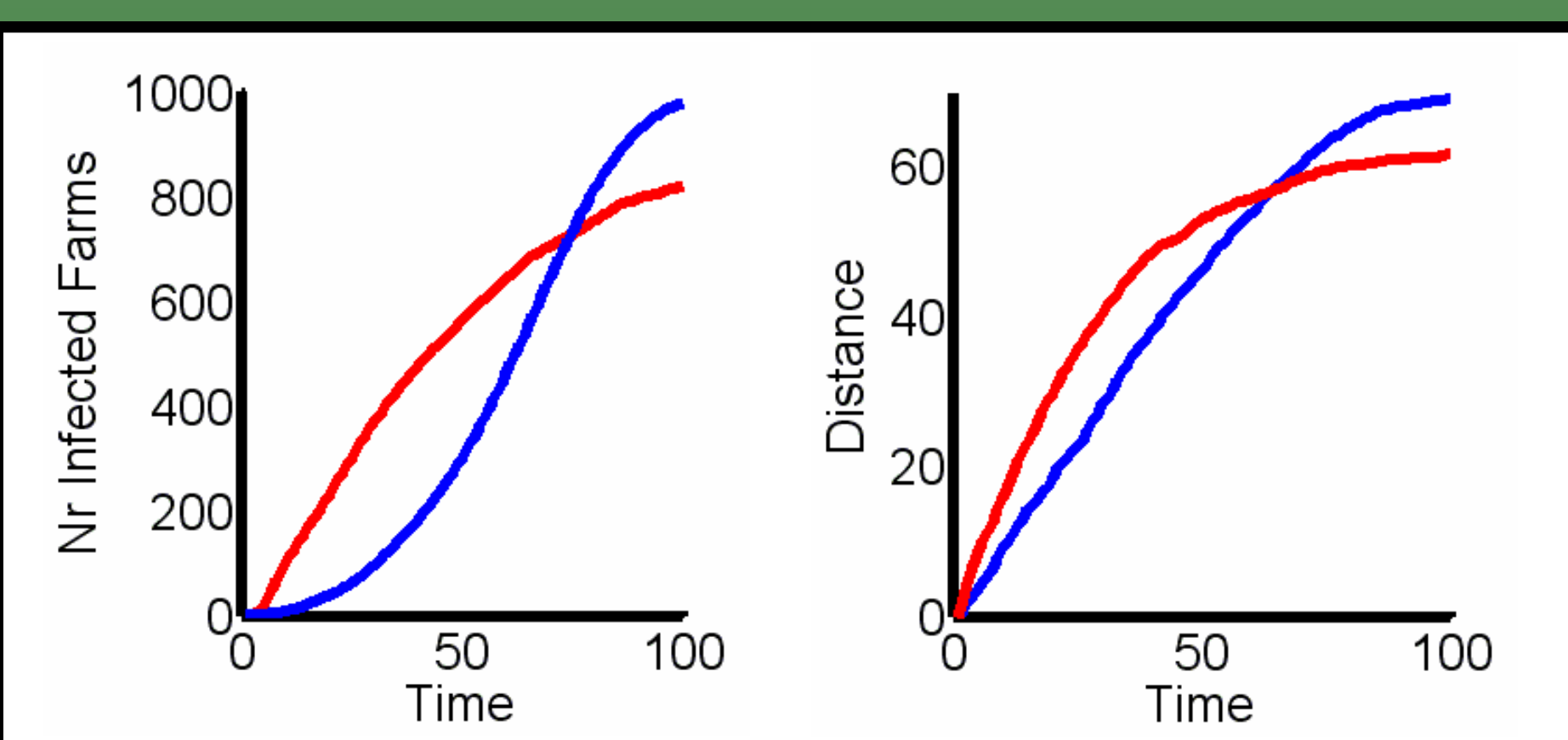
We want to show the importance of including spatial characteristics for modeling spread of disease. We hypothesize that neglecting the spatial component will lead to erroneous predictions about the behavior of an outbreak. With a general method of describing aggregation patterns beyond just looking at local densities we can estimate the importance of the spatial aspect.

## The model

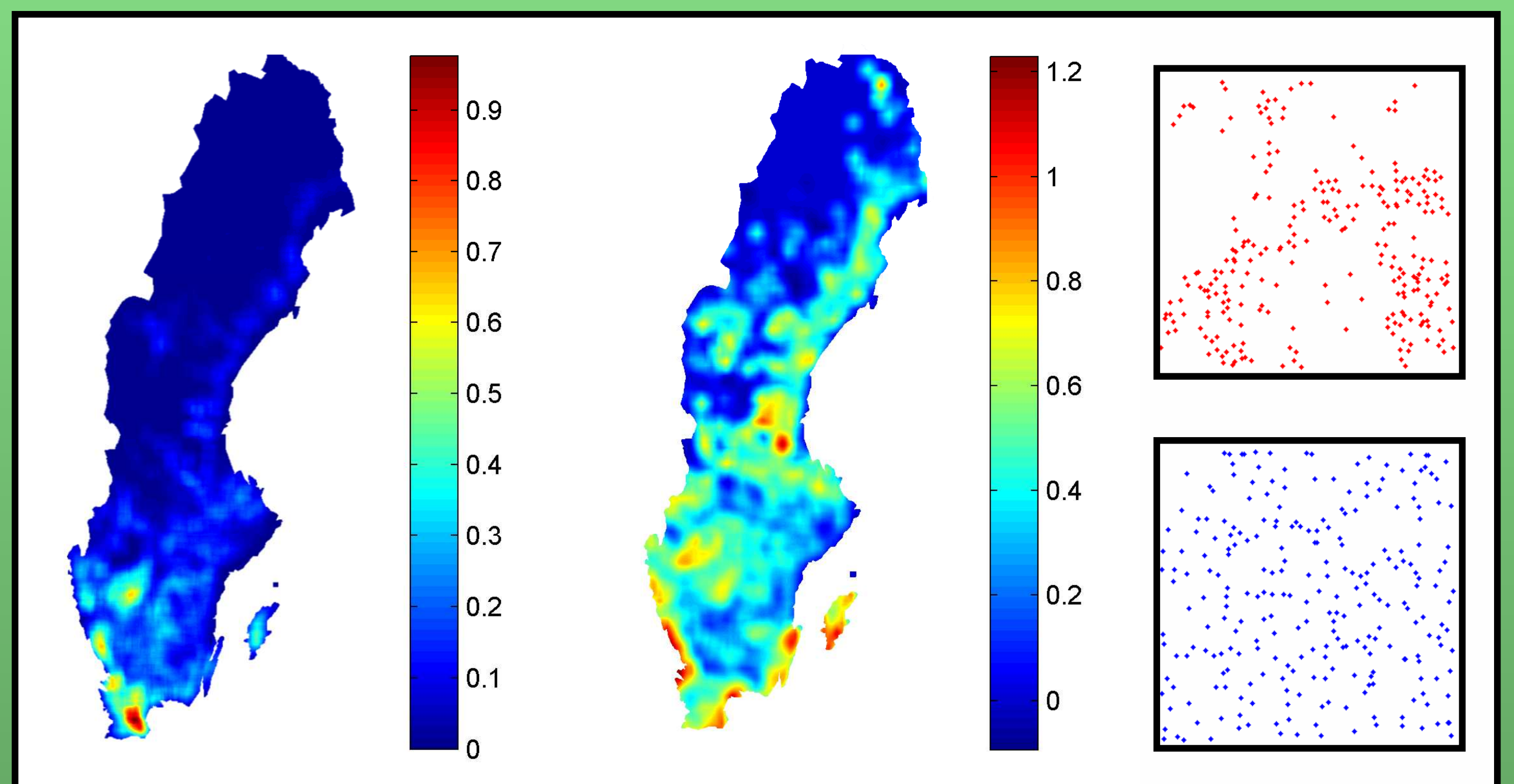
We use spectral density to estimate and model spatial characteristics. This method allows us to find and describe aggregations in real areas. We can also generate replicates with the same spatial features to make general predictions. We use discrete time steps and simulate an outbreak starting at a random farm. Transmission probabilities are assumed to follow a normal distribution and we change the distance dependence by altering the standard deviation (see Figure 2).



**Figure 2.** Modeled probability of transmission between farms. Probability decreases with distance following a normal distribution. Volume under a rotation of the curves are the same.



**Figure 3.** Number of infected Farms (left) distance between the first infected and the one furthest away. The curves show the mean of 100 replicates for farm aggregation 0 (blue curves) and 1 (red curves). The results are from simulations performed with probability of transmission decreasing with Std=4 and density=0.1.



**Figure 1.** Left: Densities of farms in Sweden. Colorbar shows densities as number of farms per km<sup>2</sup>. Middle: Level of aggregation in farms in Sweden. Right: Examples of generated aggregation pattern corresponding to 0 (blue) and 1 (red) in middle figure.

## Results and Conclusions

As shown in Figure 3, both the number of infected farms and maximum distance are influenced by level of aggregation. The effect is very non linear. In the beginning of an outbreak, a high level of aggregation speeds up the outbreak. However, as time goes on, aggregation has the reverse effect. Though not shown in Figure 3, these results hold for other farm densities and distance dependence in transmission probability.

We conclude that the geographical pattern is important for the behavior of an outbreak. Traditionally models have treated the geographical pattern as random (blue in middle and right picture in Figure 1). The difference between the red and the blue curve in Figure 3 points out the flawed predictions that can be made by that assumption. By making general theory where adequate spatial representation is included, better predictions can be made. We argue that this can provide information for decision making for outbreak control.

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