Evaluating control measures against Highly Pathogenic Avian Influenza spread between Dutch poultry farms: preventive culling and bucket sampling

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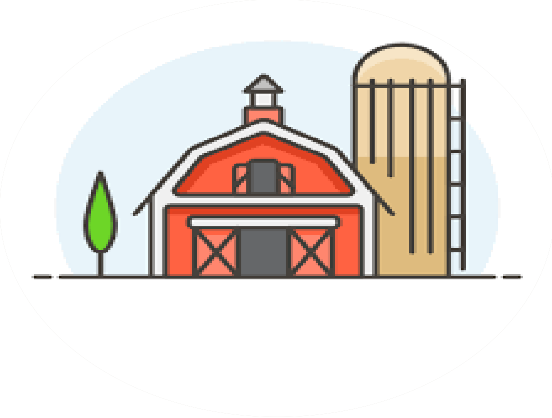


Ideas on proper use of modelling to support veterinary policy making

- Dubé et al. The use of epidemiological models for the management of animal diseases. Conf. OIE 2007, 13-23:
- ‘Models need to be fit for purpose and appropriately verified and validated’

What is ‘appropriately validated’?

- ‘…the value of epidemiological models lies in their ability to study ‘what if’ scenarios … impact of control scenarios’.

Spatial spread in the 2003 HPAI epidemic

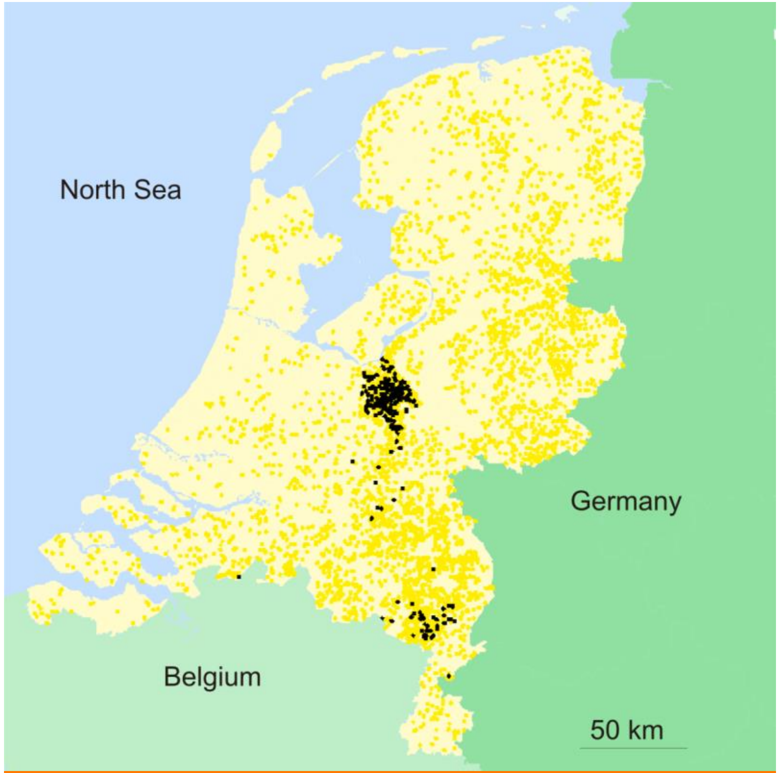
Control measures:

EU base-line + 1-km ring culling

Epidemic duration: 2 months

Epidemic size:

- 241 infected farms
- 1255 culled farms

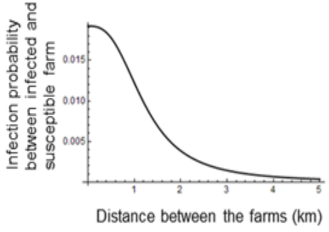


Black dots: Poultry farms infected
Yellow dots: Poultry farms not infected

Boender et al. (2007). PLoS Comput. Biol. 3, e71.

Risk map

Estimated kernel

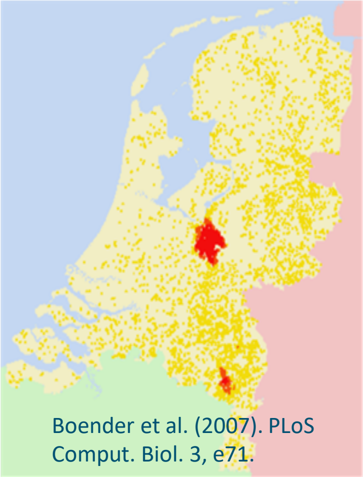


Farm population data:
- Farm locations
- Farm types
- Farm sizes

Calculate risk map

Risk: calculate $\bar{R}$ for all farms in NL

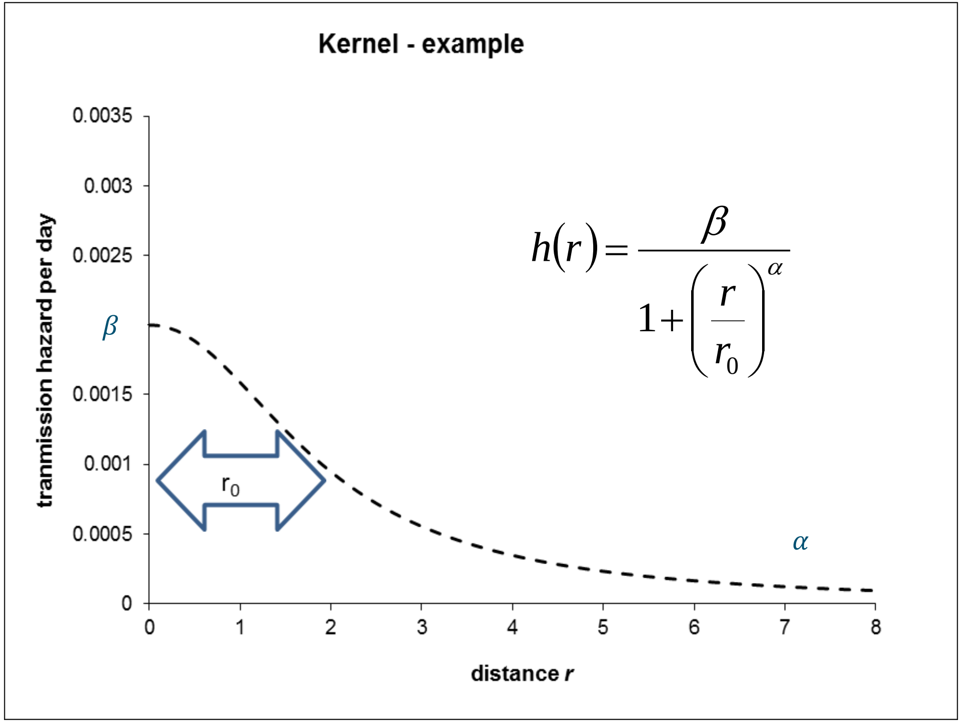
Map: plot on NL map using colour scale



Boender et al. (2007). PLoS Comput. Biol. 3, e71.

Quantifying between-farm transmission through estimation of the transmission kernel

- Parameter estimation: maximum likelihood + likelihood-ratio test
- Model fit: AIC

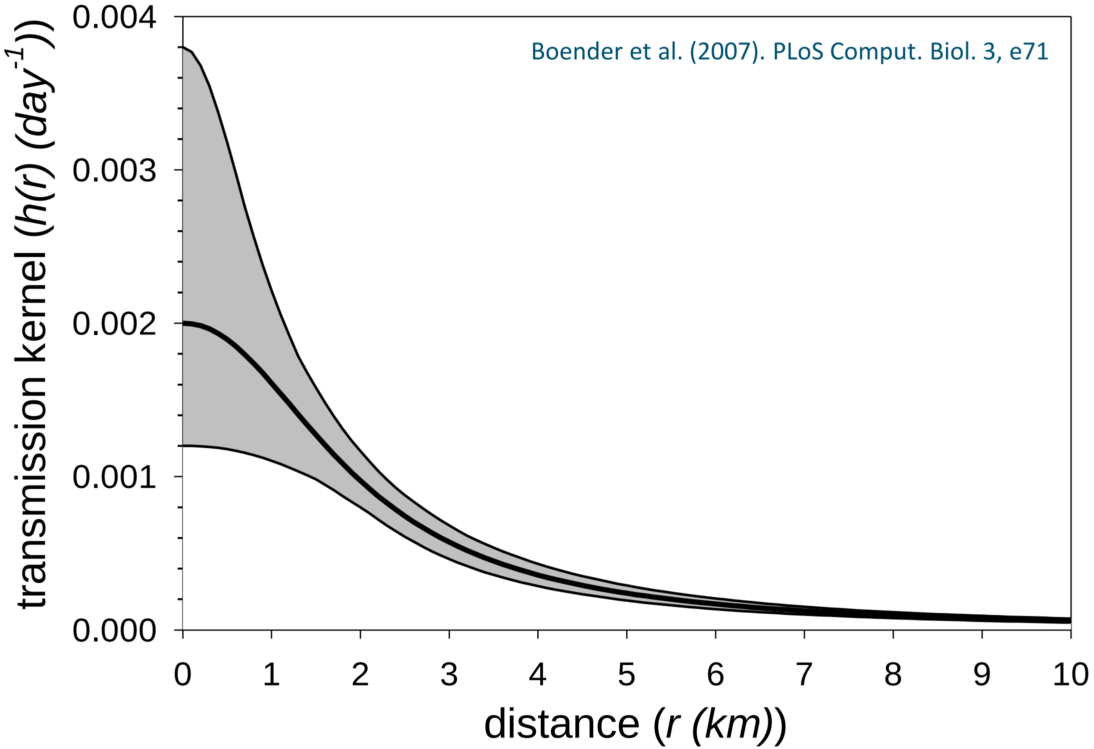


$$h(r) = \frac{\beta}{1+\left(\frac{r}{r_0}\right)^{\alpha}}$$

Boender et al. (2007). PLoS Comput. Biol. 3, e71.
Boender and Hagenaars. (2023). Scientific Reports 13:3550.

Kernel from the 2003 H7N7 HPAI epidemic

This kernel quantifies the between-farm transmission in the presence of base-line control measures



Estimation of transmission kernel from epidemic data

Quantitative importance of specific routes is unknown

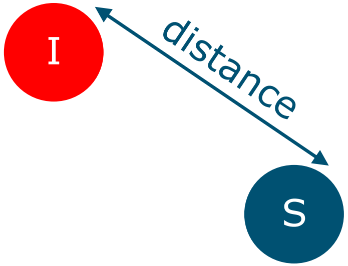
→ *Therefore quantify indirect transmission by fitting a single "transmission kernel" to the epidemic data*

Epidemic data

↓ *Statistical analysis*

Transmission probability per day between an infectious farm and a susceptible farm

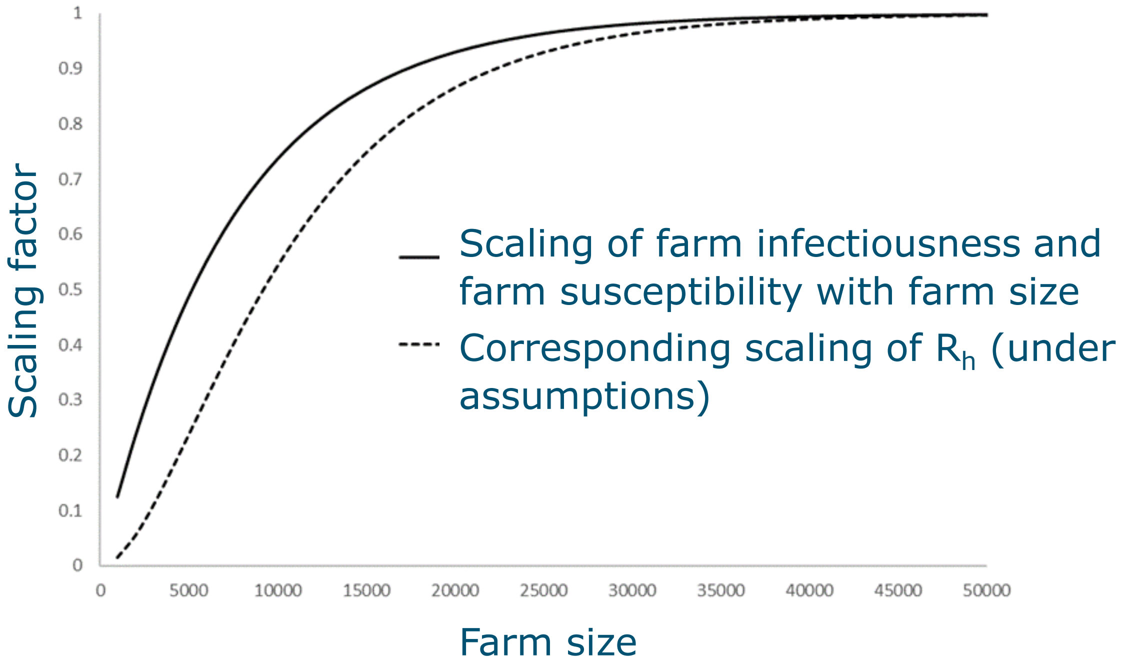
as a function of the distance between the two farms



or if the epidemic data is informative enough:

Also include dependence on ***the production types*** *and/or* ***the sizes*** *of the two farms*

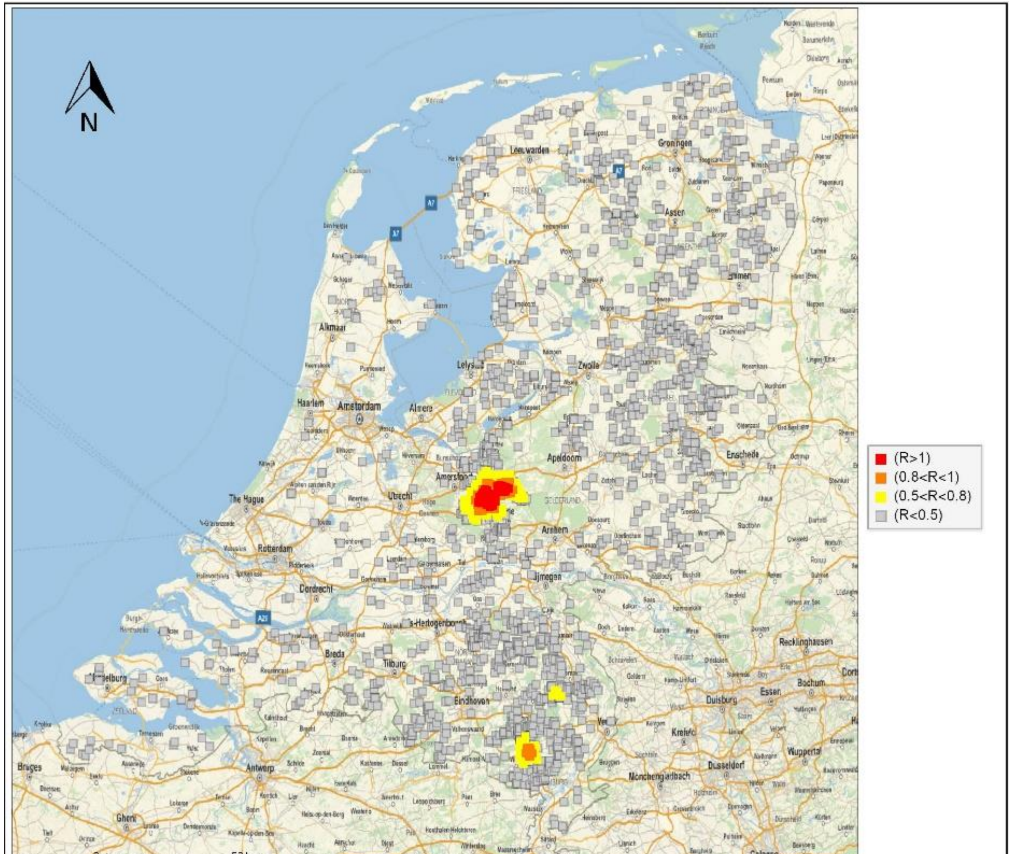
Farm-size dependence of transmission risk



Model extrapolation: Risk maps for 2022 in comparison to 2003

2003

2022



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Genetic clusters of HPAI outbreaks in poultry

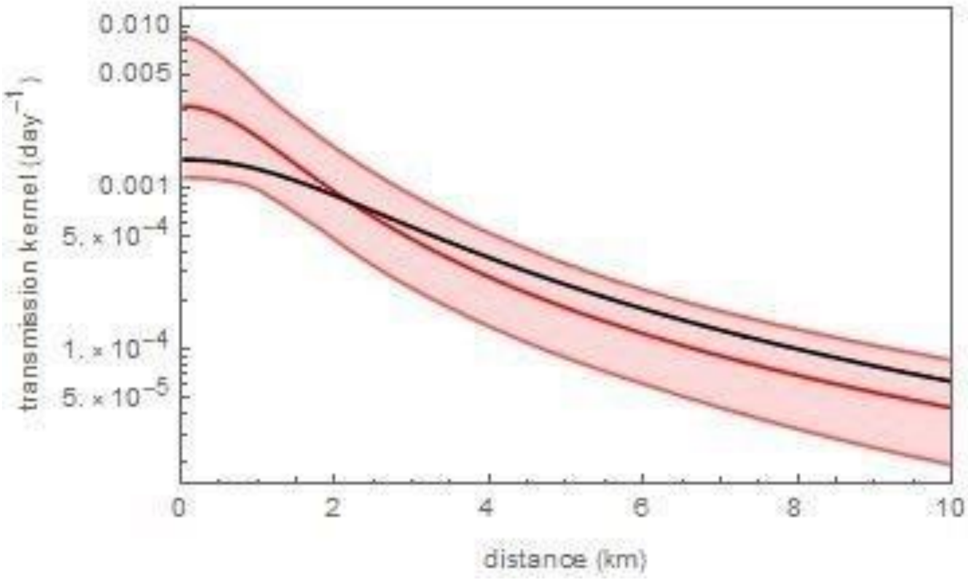
Netherlands, 1 Oct 2021 - 1 Sept 2022: a total of 57 outbreak farms; 14 in Densely Populated Poultry Area (DPPA) and 43 elsewhere

	DPPA	Elsewhere	Anywhere
#clusters	3	6	9
#singletons	1	23	24

Compare kernel estimated based on 14 outbreaks in DPPA (in red)

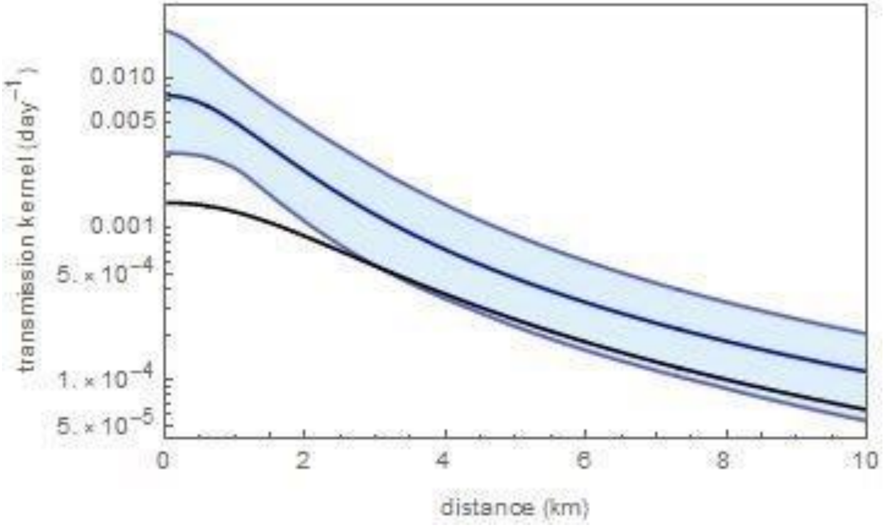
with kernel extrapolated from 2003 epidemic estimates (in black)

Assumption: genetic clusters arise from between-farm transmission



Compare kernel estimated based on 43 outbreaks outside DPPA (in blue) with kernel extrapolated from 2003 epidemic estimates (in black)

Assumption: genetic clusters arise from between-farm transmission

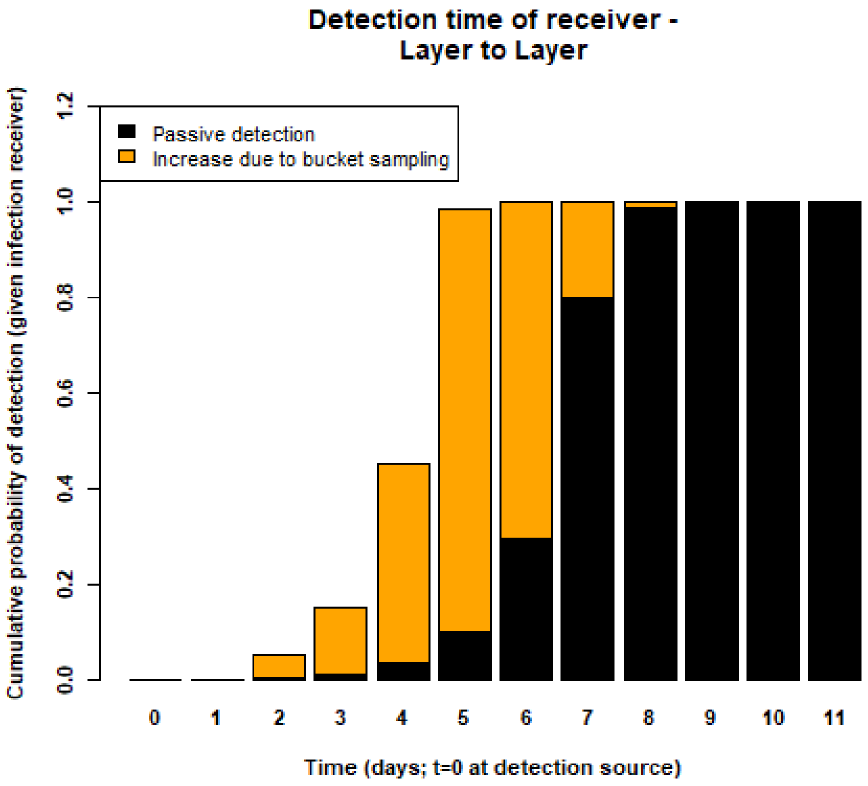


Expected infectious period reduction of a neighboring infected farm when preventively culled?

Under the conservative assumption of constant infectiousness:

Simple modelling arguments lead to an expected 50% reduction of infectious period length

Bucket sampling could replace preventive culling?



The largest R_h is 1.33 according to our model, so under the (conservative) assumption of constant infectiousness:

a 25% reduction of infectious period length is sufficient…

Thanks to

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And many others