

Incorporating heterogeneity in farmer disease control behaviour into a livestock disease transmission model

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ttps://edmhill.github.io/

Farmer-led Epidemic and Endemic Disease-management (FEED)



Biotechnology and Biological Sciences Research Council

Project motivation

- Control of infectious disease in livestock can be farmer-led or government-led.
- There is a knowledge gap on the different factors that drive farmer behaviour in response to an emerging disease.
- Mathematical models traditionally treat farmers as passive bystanders and omit variation in disease management behaviours.

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Study aims

- 1. Elicit farmers vaccination decisions to an unfolding epidemic and link to their psychosocial and behavioural profiles (within Great Britain)
- 2. Refine mathematical disease models to capture psychosocial & behaviour change heterogeneities
- 3. Assess how psychosocial & behaviour change factors impact epidemiological outcomes given a fastspreading livestock disease



Incorporating heterogeneity in farmer disease control behaviour into a livestock disease transmission model **EM Hill**, NS Prosser, PE Brown, E Ferguson, MJ Green, J Kaler, MJ Keeling, MJ Tildesley. (2023) *Preventive Veterinary Medicine*. doi:10.1016/j.prevetmed.2023.106019

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Study aim 1: Elicit farmers vaccination decisions

1. Elicit farmers vaccination decisions to an unfolding epidemic and link to their psychosocial and behavioural profiles (within Great Britain)







Elicitation results – GUI simulation

Stage of epidemic	Time since previous stage (weeks)	Number of infected herds (in GB)	Distance to nearest infected herd (km)	Number of farmers vaccinating (/60)
1	2	0	>500*	8
2	2	2	322	16
3	1	10	322	5
4	1	40	161	14
5	1	100	161	1
6	1	150	48	10
7	1	450	16	3
8	1	600	5	1
*Epidemic confined to southern-central France				

Sixty farmers (39 beef & 21 dairy) participated.

Variability in when they would use preventative vaccination.



Elicitation results – farmer groupings

Using k-means clustering, four groups gave best fit when clustering by two most stable covariates (trust in Governmental judgements for disease control, high physical opportunity)

Farmer groups from k-means clustering conducted on the two most stable covariates.



Proportion of farmers in each group that vaccinated in different stages of the outbreak.



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Study aim 2: Refine the livestock disease model

- 1. Elicit farmers vaccination decisions to an unfolding epidemic and link to their psychosocial and behavioural profiles (within Great Britain)
- 2. Refine mathematical disease models to capture psychosocial & behaviour change heterogeneities
- Data-driven spatial model framework with epidemiological and behavioural layers.
- 3. Assess how psychosocial & behaviour change factors impact epidemiological outcomes given a fast-spreading livestock disease



Modelling methods - Cattle data

- > Data from the Great Britain Cattle Tracing System (from 2020 ; approx. 60,000 holdings)
- > Cattle demography: Per holding, average cattle herd size
- > Cattle holding locations: Per holding, easting-northing co-ordinates.



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Distribution of cattle herd sizes



Per region, number of holdings with cattle & cattle population

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- > Epidemiological unit: Cattle holding (farm).
- Spatial model, based loosely on the dynamics of FMD.
 - Force of infection dependencies: Number of livestock, livestock type specific transmissibility and susceptibility, distance between premises.
 - Infection to infectiousness (latent period): 5 days
 - Infection to notification: 9 days
 - Infection to culled: 13 days



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Modelling methods – Behavioural configurations

Uncooperative Only control is cattle being removed at holdings with confirmed infection. i.e. No holdings apply vaccination.

Homogeneous: Non-data informed

Each farmer has same risk threshold - will vaccinate when infection is within a given distance. Heterogeneous: Non-data informed

Even split across different groups.

Heterogeneous: Data informed

Parameterised using interview results

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Study aim 3: Assess impact of behaviour assumptions

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Spatial stochastic simulations of a fast-spreading epidemic in Great Britain cattle holdings:

- Per behavioural configuration, ran 500 replicates per 89 seed region locations.
- Per simulation replicate, seeded infection seeded in randomly selected cluster of three premises.

Modelling results – Epidemiological metrics

Figure: For each behavioural configuration: **(a)** Distribution of percentage of holdings infected; **(b)** Percentage of simulations exceeding the stated final size.



Comparing homogeneity in farmer behaviour vs data-informed heterogeneity in farmer behaviour: Disconnect in outcomes

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Modelling results - Role of seed infection region

Median percentage of holdings infected, dependent on region of outbreak emergence and behavioural configuration. Statistics computed from 500 replicates per scenario.



Study implications

Demonstrated a conjoined epidemiological and socio-behavioural workflow in action!

Encourage consideration of actions of individual farmers in policy frameworks for tackling future livestock disease outbreaks

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