

# Epidemiological modelling with behavioural considerations and to inform policy making

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UK Research  
and Innovation



**JUNIPER**

<https://maths.org/juniper/>



@JuniperConsort1

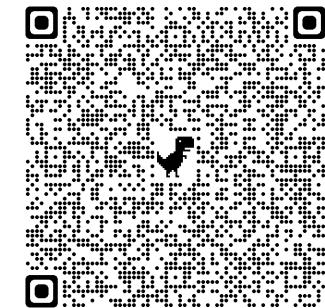
# **1. Modelling the epidemiological implications for SARS-CoV-2 of Christmas household bubbles in England in December 2020**

## **2. Incorporating heterogeneity in farmer disease control behaviour into a livestock disease transmission model**

# Structure of the COVID science to policy path



List of participants of SAGE and related sub-groups:



# How SPI-M-O worked



SPI-M-O provided:

- Multiple independent groups
- Rapid responses to commissions and rapid peer review
- R values / Medium term projections / Reasonable worst-case scenarios
- Consensus statements
- A route for non-commissioned insights

# How SPI-M-O worked

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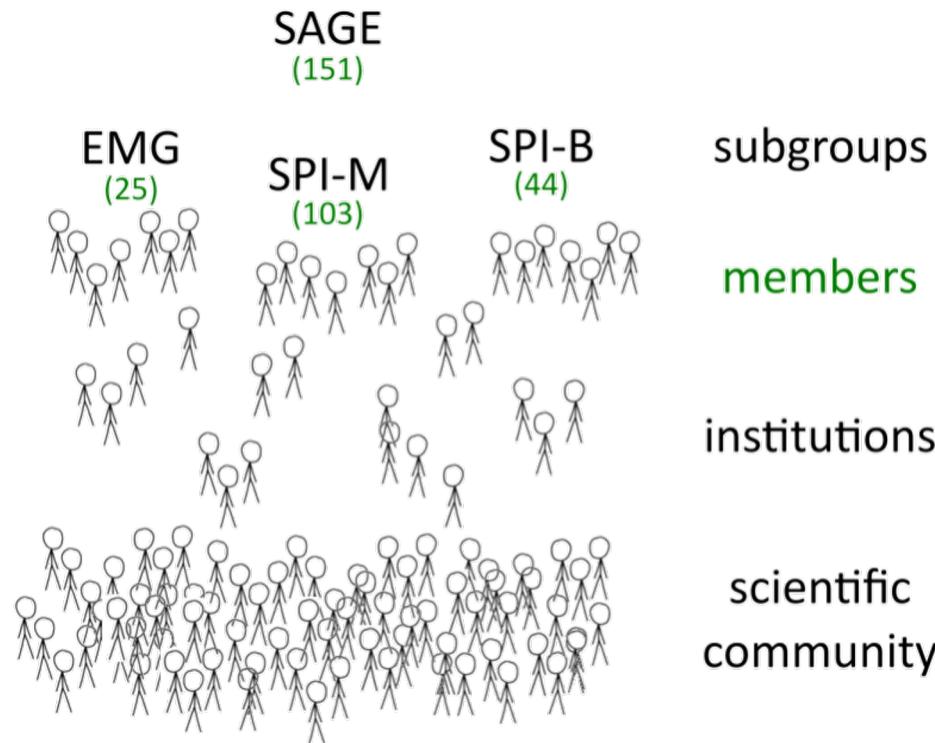


Supported by:

- An incredible secretariat
- Data provision through UKHSA (PHE) and DSTL

# Structure of the COVID science to policy path

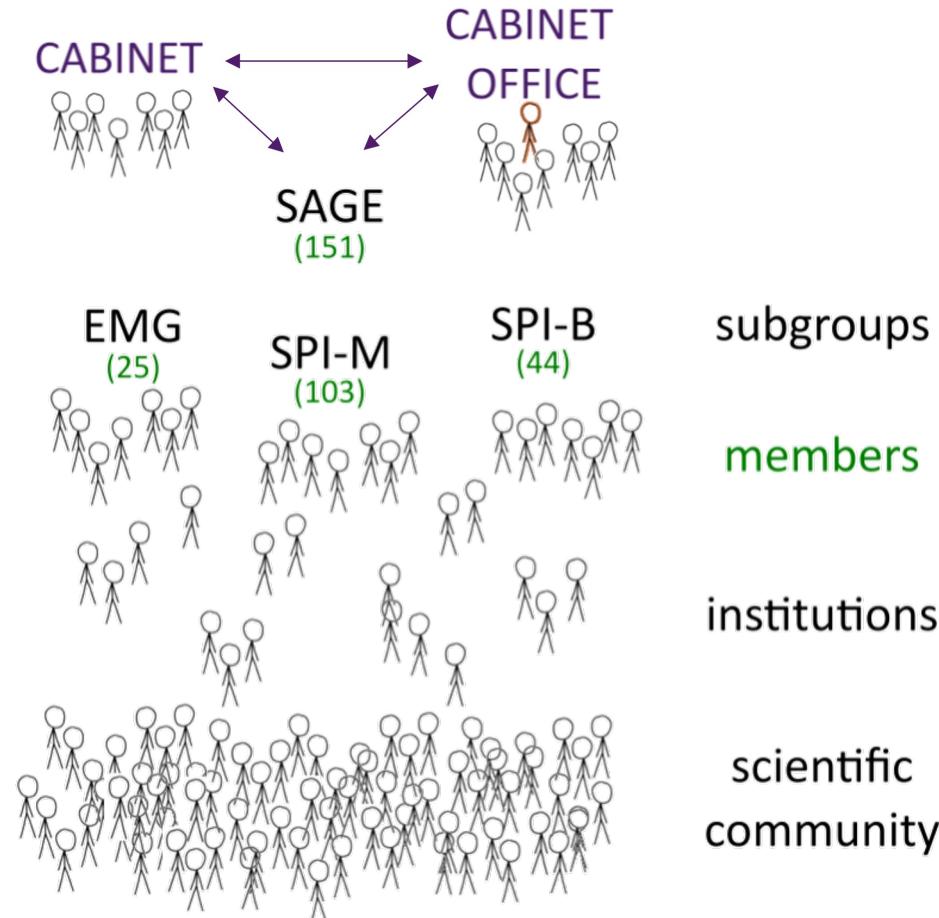
A massive team effort!



# Structure of the COVID science to policy path

## Feeding into policy

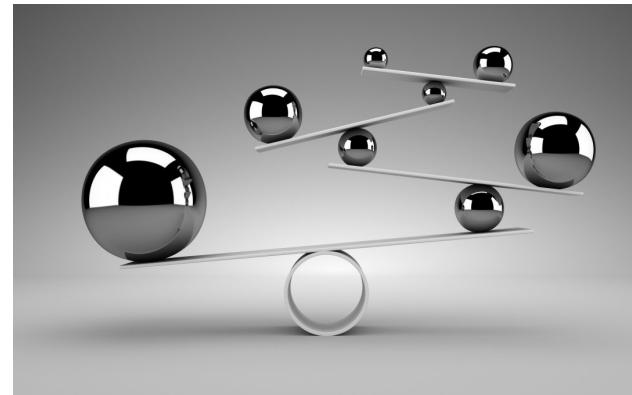
- Chief Medical Officer (Chris Whitty) & Chief Scientific Advisor (Patrick Vallance)
- Secretariat
- Observers
  - UKHSA (also some participants)
  - Cabinet office
  - Treasury
  - No. 10
  - Devolved administrations

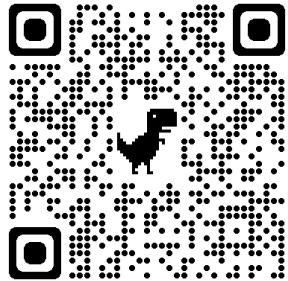


# Potential tensions

There are inherent tensions in the system **to be balanced**:

- Short deadlines vs careful science
- Privacy concerns vs data requirements
- Open science vs information control
- Rapid communication vs clarity and accuracy





Modelling the epidemiological implications for SARS-CoV-2 of  
Christmas household bubbles in England  
EM Hill. (2023)  
*Journal of Theoretical Biology*. **557**: 11131.  
doi: [10.1016/j.jtbi.2022.111331](https://doi.org/10.1016/j.jtbi.2022.111331)

Guidance

## Making a Christmas bubble with friends and family

How may short-term changes to household bubbles influence infectious disease dynamics?

# Methods

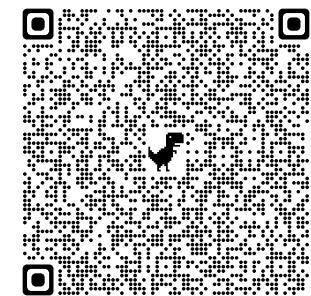
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- 1. Household model**
- 2. Epidemiological model**
- 3. Testing and isolation**
- 4. Christmas bubble scenarios**
- 5. Simulation overview**

# Methods: (1) Household model

- Considered a population containing **100,000 households**.
- Approximate overall population of **310,000**, with a three-class age structure: 0–19 yrs, 20–64 yrs, 65+ yrs.
- Household sizes and the proportion of households with a given age composition from 2011 census data for England and Wales.

CT0820\_2011 Census - household type,  
household size and age of usual residents  
(people) - England and Wales



# Methods: (2) Epidemiological model

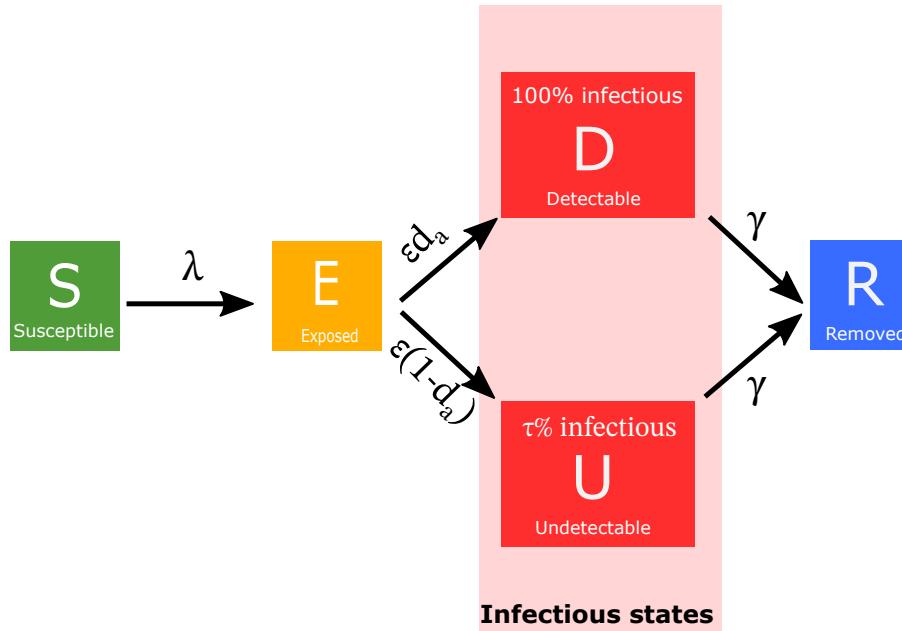


Table 1

Description of epidemiological parameters. The stated distributions are as reported in the cited sources, with additional context provided in the associated subsections of the main text.

Description	Distribution	Source
Incubation period	Erlang(6, 0.88)	Lauer et al. (2020)
Infectiousness profile	Infectivity profile over 14 days: [0.0369, 0.0491, 0.0835, 0.1190, 0.1439, 0.1497, 0.1354, 0.1076, 0.0757, 0.0476, 0.0269, 0.0138, 0.0064, 0.0044]	He et al. (2020) and Ashcroft et al. (2020)
Proportion of cases asymptomatic (0–19 yrs)	Uniform(0.20, 0.35)	Buitrago-Garcia et al. (2020)
Proportion of cases asymptomatic (20+ yrs)	Uniform(0.05, 0.20)	Buitrago-Garcia et al. (2020)
Relative infectiousness of an asymptomatic	Uniform(0.30, 0.70)	Buitrago-Garcia et al. (2020) and McEvoy et al. (2020)
Relative susceptibility of 0–19 yrs age class	Uniform(0.40, 0.60)	Davies et al. (2020a)

# Methods: (2) Epidemiological model

For an infectious individual  $j$  on day  $t$  of their infectious state, the probability of transmission to each susceptible contact  $k$  in household bubble  $h$ :

$$p_{j,k,h}(t) = r_h a_j s_k i_j(t)$$

- Sampled household attack rate in household  $h$

Household attack rates

Size 2: Normal(0.48,0.06)  
Size 3: Normal(0.40,0.06)  
Size 4: Normal(0.33,0.05)  
Size  $\geq 5$ : Normal(0.22,0.05)

Bernal et al. (2022)

- Relative infectiousness of individual  $j$
- Relative susceptibility of individual  $k$
- Value of the infectiousness temporal profile on day  $t$  for individual  $j$

# Methods: (2) Epidemiological model

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$$p_{j,k,h}(t) = \textcolor{blue}{r}_h a_j s_k i_j(t)$$

## ➤ Sampled household attack rate in household $h$

Household attack rates	Size 2: Normal(0.48,0.06) Size 3: Normal(0.40,0.06) Size 4: Normal(0.33,0.05) Size $\geq 5$ : Normal(0.22,0.05)	Bernal et al. (2022)
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## ➤ Relative infectiousness of individual $j$

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- Relative infectiousness of individual  $j$
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# Methods: (2) Epidemiological model

- **Initial conditions:** Intentionally had **no symptomatically infected individuals** at the start of the simulated time horizon, meaning no households began in isolation.

**Table 3**

Percentage of each age group initialised in each infection status.

	Age (years)		
	0–19	20–64	65+
Susceptible	73%	74%	84.5%
Latent infected	1%	0.5%	0.25%
Asymptomatic infected	0.3%	0.1%	0.05%
Presymptomatic infected	0.7%	0.4%	0.2%
Recovered	25%	25%	15%

# Methods: (3) Testing and isolation

Table 2

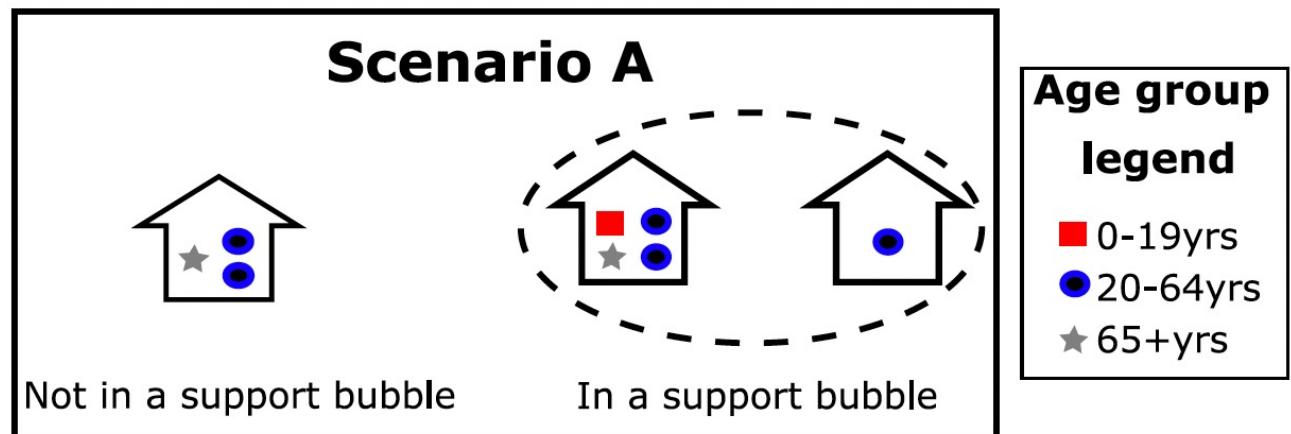
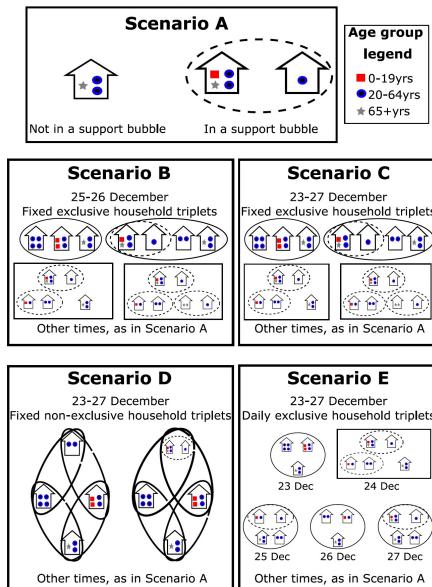
Description of testing and isolation related parameters.

Description	Value	Source
Adherence	70% (30% in adherence sensitivity analysis)	<a href="#">Office for National Statistics (2020a)</a>
Test specificity	100%	<a href="#">Office for National Statistics (2020b)</a>
Test sensitivity	87%	<a href="#">Holborow et al. (2020)</a>
Duration of self-isolation if symptomatic	10 days	UK government guidance in November 2020 ( <a href="#">Public Health England, 2020b</a> )
Household isolation period	14 days	UK government guidance in November 2020 ( <a href="#">Public Health England, 2020b</a> )
Duration of isolation if contact traced	14 days (beginning from the day the index case first displays symptoms)	UK government guidance in November 2020 ( <a href="#">Department of Health and Social Care, 2020</a> )

- Assumed all individuals within a household (or extended household/support bubble) had the **same adherence status**.
- Those that adhered would both follow **isolation guidance** and engage with **test and trace**.
- Assumed an adherent individual household member took a **PCR test** if they displayed symptoms, with **same day** return of result.

# Methods: (4) Bubbling scenarios

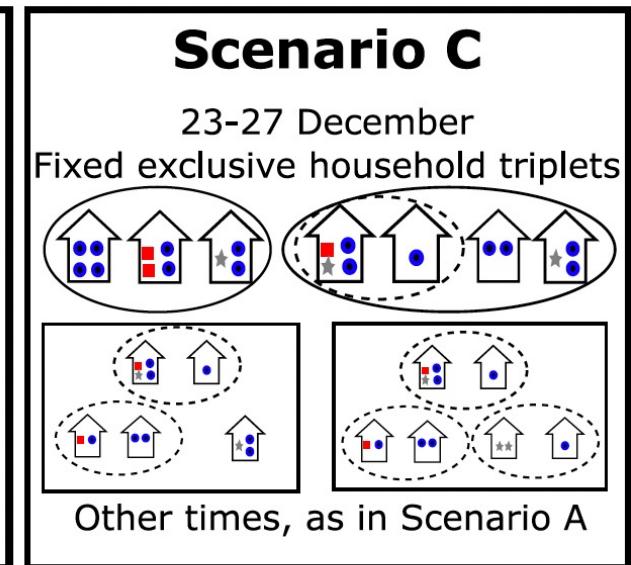
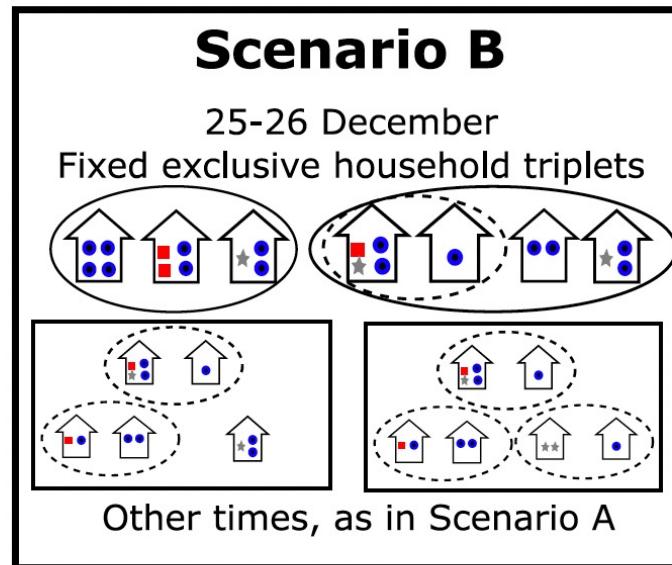
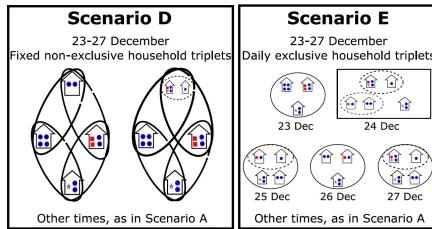
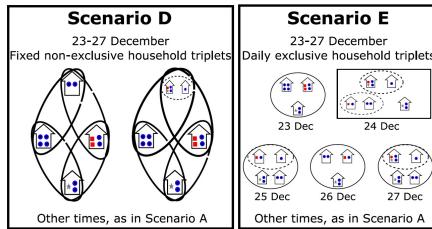
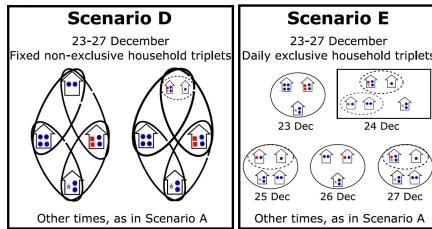
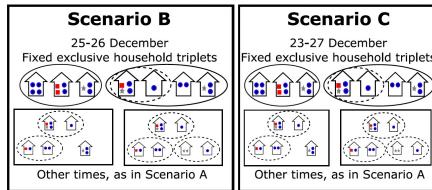
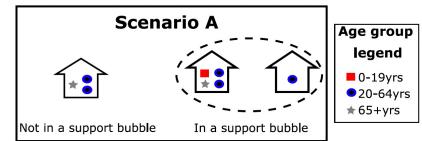
**Figure:** Illustrative examples of the five bubbling scenarios.



- Sampled the propensity to form a support bubble from a Uniform(0.5,0.75) distribution.

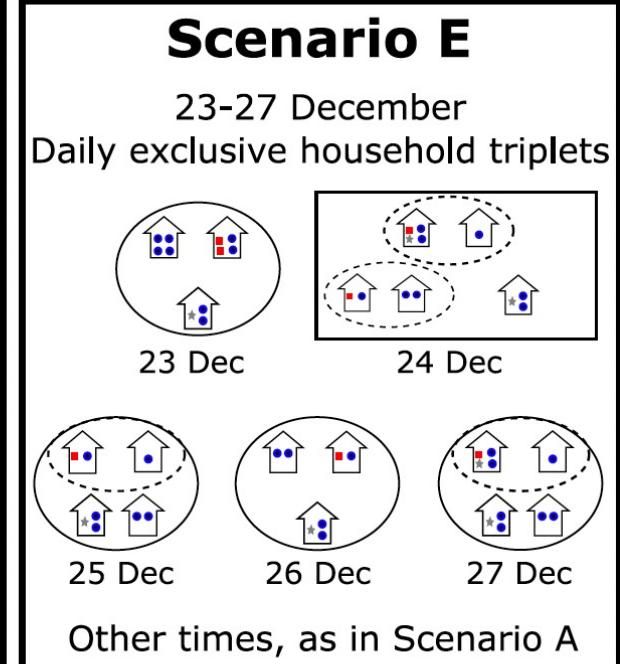
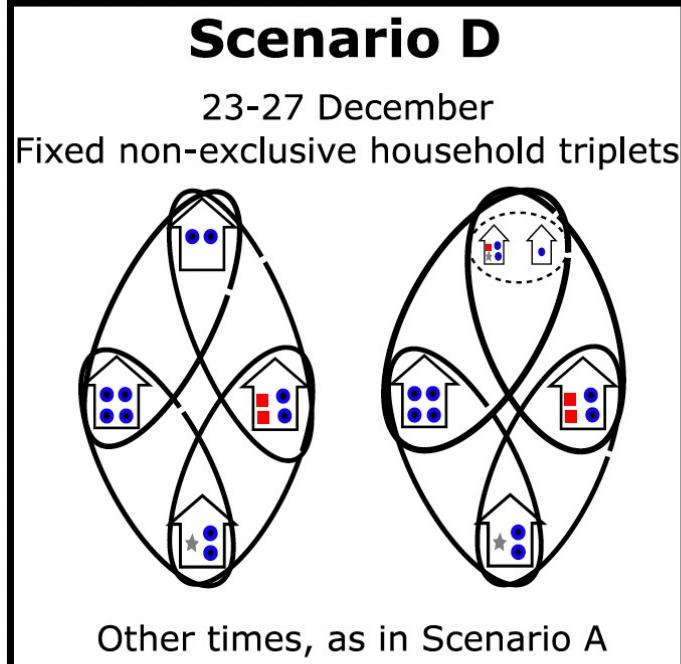
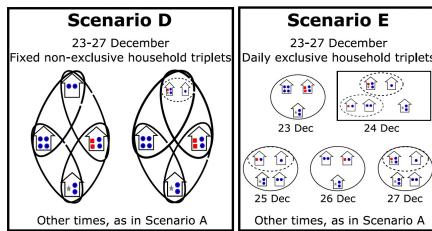
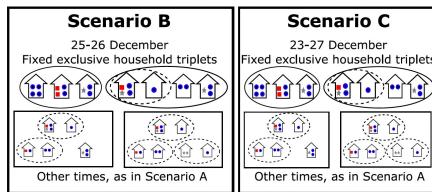
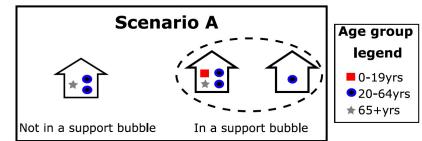
# Methods: (4) Bubbling scenarios

**Figure:** Illustrative examples of the five bubbling scenarios.



# Methods: (4) Bubbling scenarios

**Figure:** Illustrative examples of the five bubbling scenarios.



# Methods: (5) Simulation overview

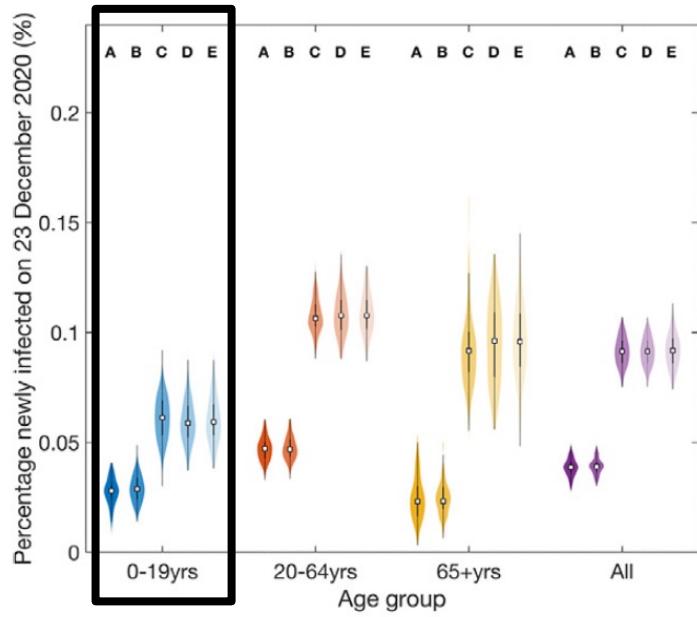
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- Study evaluated **five** different household bubble scenarios.
- **Bubbling period:** 23-27 December 2020
- **Simulated time horizon:** 23 December 2020 – 06 January 2021
- Performed **100 model simulations** for each scenario
- Assessment comprised **incidence** and **cumulative infection** metrics

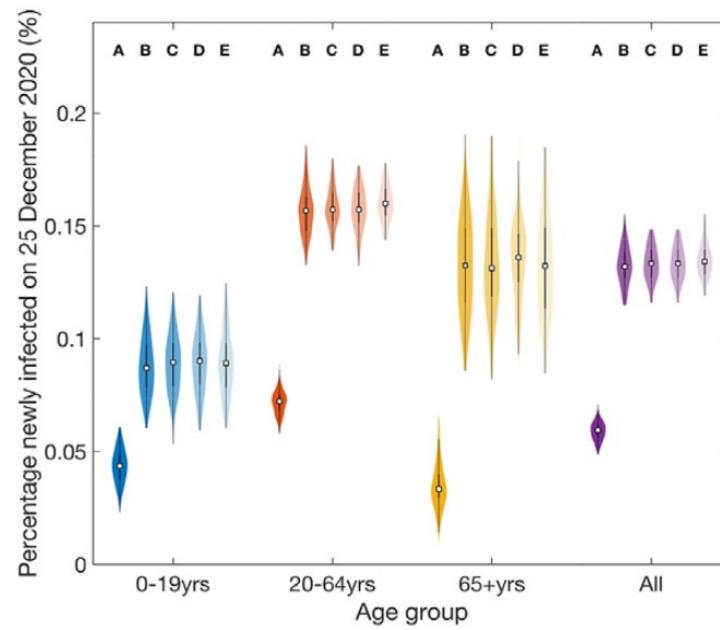
# Inspection of daily incidence

**Figure:** Distributions for the daily incidence under each Christmas bubble scenario. **(a)** 23 December 2020; **(c)** 25 December 2020.

**(a)**



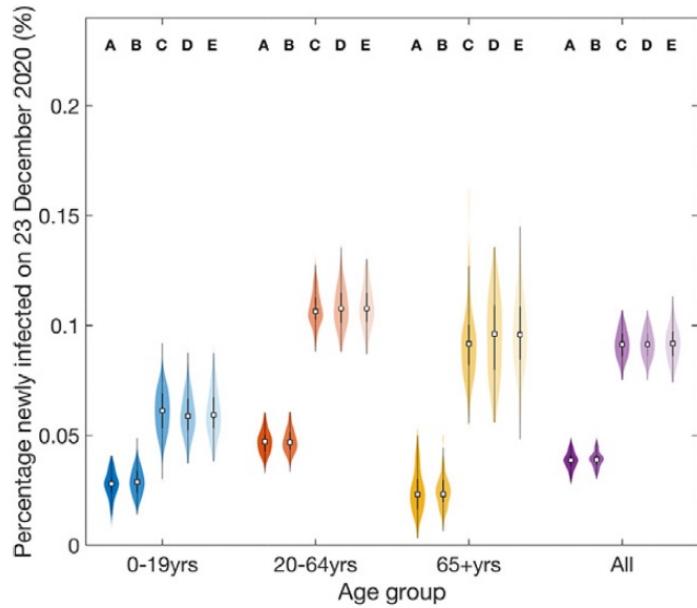
**(c)**



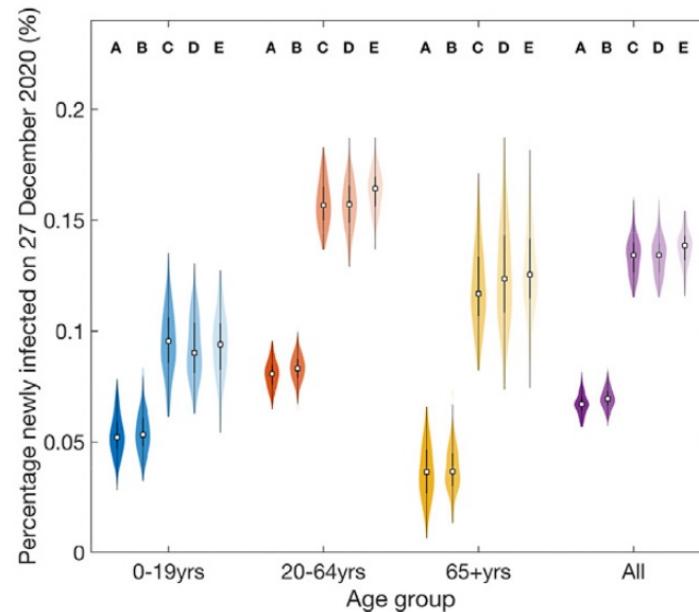
# Inspection of daily incidence

**Figure:** Distributions for the daily incidence under each Christmas bubble scenario. **(a)** 23 December 2020; **(e)** 27 December 2020.

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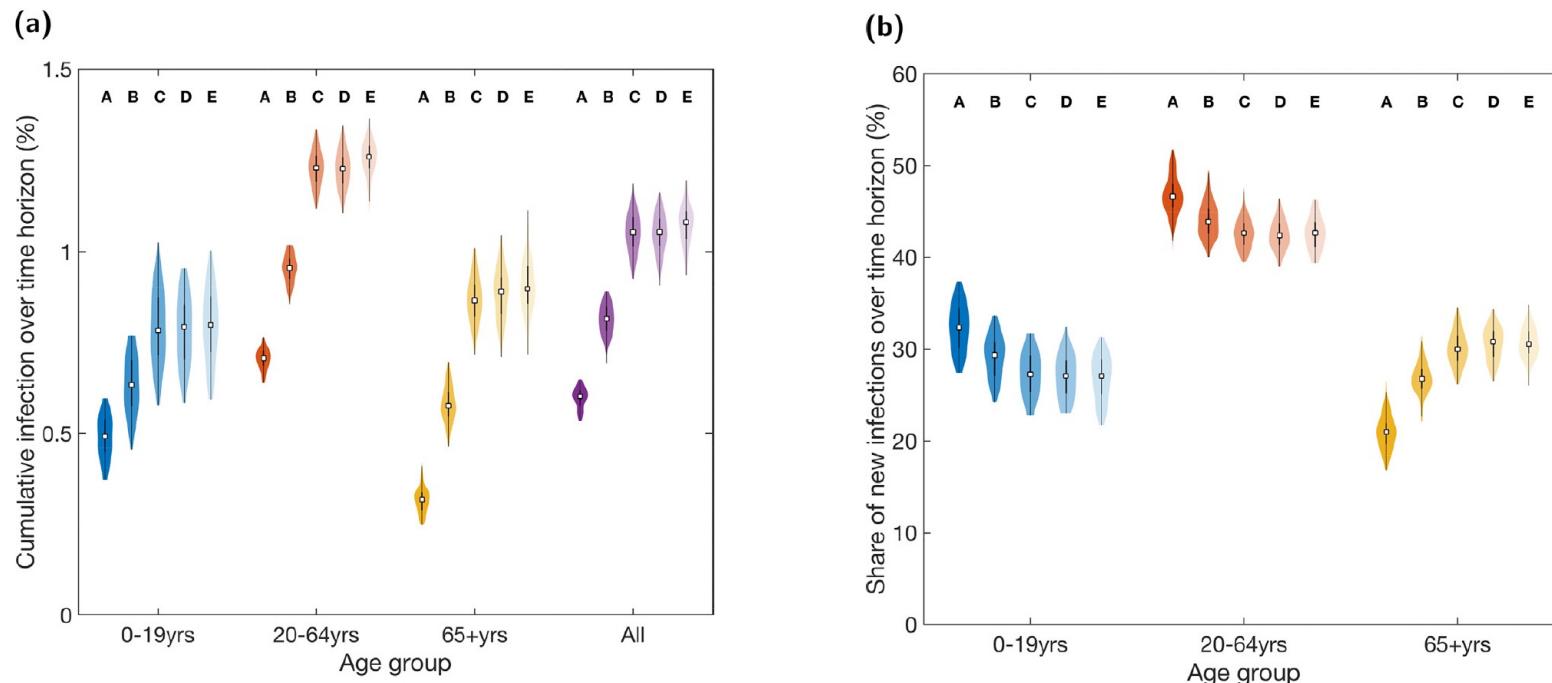
**(e)**



- Appreciable decline in daily incidence for a **shorter duration** and/or **smaller group** gatherings (Scenarios A & B).

# Heightened risk of infection with age

**Figure:** Cumulative infection distribution for the entire 15-day time horizon (23 Dec 2020 – 06 Jan 2021): **(a)** Percentage of each age group infected; **(b)** Percentage share of new infections over the time horizon attributed to each age group.



- Increase in infection from greater amounts of social mixing disproportionately impacted the eldest.

# Limitations

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- Assumptions regarding **bubble formation** were a **simplified representation** of the real-world social system.
- Whilst the model considered infection resulting from person-to-person interactions due to household mixing, it **did not consider** transmission arising from **other settings**.
- Findings may be **sensitive** to alternative epidemiological model structures and intervention assumptions, particularly **adherence** to isolation and test-and-trace measures.

# Implications

**Shows potential use of stochastic individual-based models representing synthetic population of households.**

**When needing to assess the epidemiological impact of extending contacts beyond the immediate household, provides a methodology that is swift to develop & deploy.**

# Acknowledgements

- Zeeman Institute: Systems Biology & Infectious Disease Epidemiology Research (SBIDER)



- JUNIPER consortium



<https://maths.org/juniper/> @JuniperConsort1



Modelling the epidemiological implications for SARS-CoV-2 of  
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**SBIDER COVID-19 webpage:**

<https://tinyurl.com/warwickCOVID19>

**Personal webpage:**

<https://edmhill.github.io>

**Email:**

Edward.Hill@warwick.ac.uk

1. Modelling the epidemiological implications for SARS-CoV-2 of Christmas household bubbles in England in December 2020
2. Incorporating heterogeneity in farmer disease control behaviour into a livestock disease transmission model

# Approaches to control infectious disease outbreaks in livestock

## Direct action of farmers

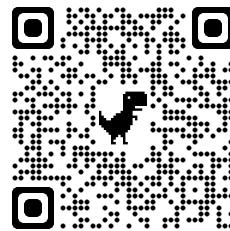
The BVDFree England Scheme

### What is BVD?

Bovine Viral Diarrhoea or BVD is a highly contagious viral disease of cattle. It is one of the biggest disease issues facing the UK cattle industry. BVD has been estimated to cost between £13 and £31 per cow in Great Britain. The national cost could be as high as £61M per year. (Bennett and Ijpelaar, 2005)

### What is the BVDFree Scheme?

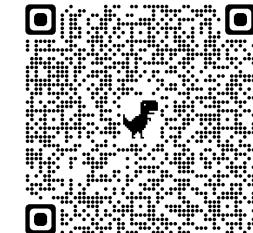
BVDFree England is a voluntary industry-led scheme, working to eliminate Bovine Viral Diarrhoea (BVD) from all cattle in England. The key to success is to identify and remove all animals persistently infected (PI) with the BVD virus from the English cattle herd.



## Government action



Department  
for Environment  
Food & Rural Affairs



## Contingency Plan for Exotic Notifiable Diseases of Animals in England

Including Foot and Mouth Disease, Avian Influenza, Newcastle Disease and all other exotic notifiable diseases of animals

Updated on 18 July 2022

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

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FEED project webpage: <https://feed.warwick.ac.uk>

## Project motivation

- A knowledge gap on the different factors that drive farmer behaviour in response to an emerging disease.
- Mathematical modelling approaches traditionally treat farmers as passive bystanders & omit variation in disease management behaviours

# The Team

## Infectious disease modelling



**Mike Tildesley**

**Matt Keeling**

(University of Warwick)

## Veterinary epidemiology



**Naomi Prosser    Martin Green    Jasmeet Kaler**  
(University of Nottingham)

## Scientific software



**Paul Brown**

(University of Warwick)

## Behavioural psychology



**Eamonn Ferguson**

(University of Nottingham)

## Stakeholders



Animal &  
Plant Health  
Agency

# 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 fast-spreading 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

# Study aims

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

**1**

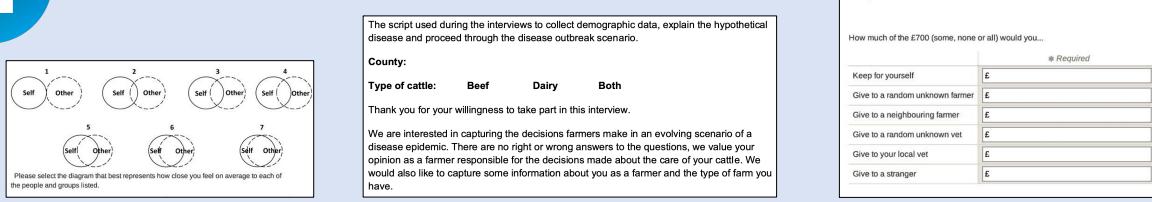
Design of a Graphical User Interface (GUI) to act as a core, interactive component of the interview exercise

Visit <https://feed.warwick.ac.uk>



**2**

Development and usage of an interview script to elicit farmer disease vaccination behaviours



**3**

Grouping of farmer vaccination behaviours in the elicitation exercise



# Elicitation methods - GUI

**Home details**

County: Nottinghamshire

**Scenario details**

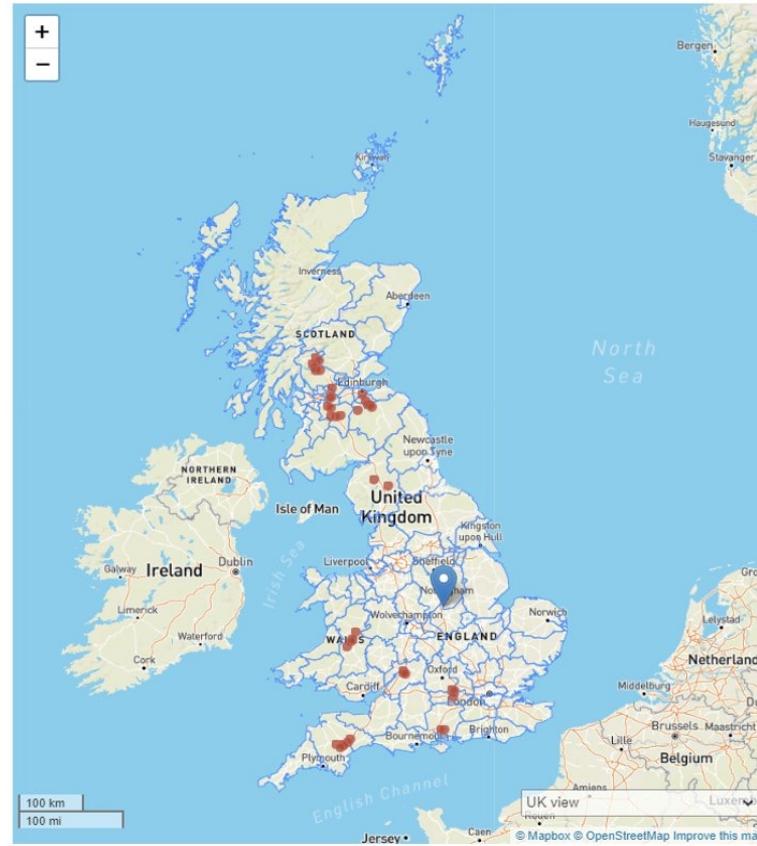
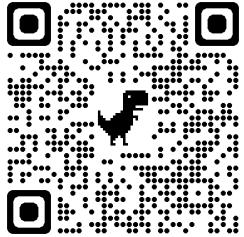
Week:  1 2 3 4 5 6 7 8

National view  Local view

Distance to nearest case: 100 miles

Cumulative number of cases: 40

Number of clusters: 10



<https://feed.warwick.ac.uk/map.html>

- Gave a common outbreak experience in terms of distance to the nearest infected herd for all farmers.

# Elicitation methods - Questionnaire

## Other people and groups

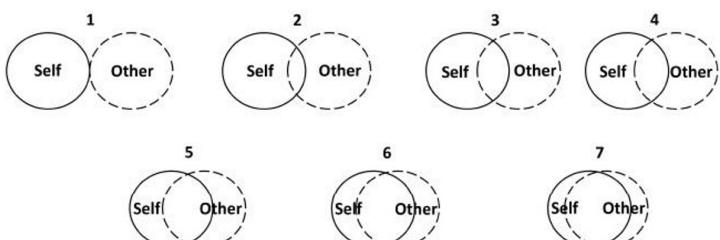
Please indicate how well you agree with each of the following statements.

	* Required				
	Strongly agree	Agree	Neither agree nor disagree	Disagree	Strongly disagree
When dealing with farmers it is better to be careful before you trust them	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I feel respected by the government	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I trust other farmers nationally to be controlling infectious diseases in their herds	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I trust other farmers I meet for the first time	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
When dealing with vets it is better to be careful before you trust them	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
When dealing with strangers it is better to be careful before you trust them	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
In general, one can trust people	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>
I feel respected by my vet	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>	<input type="radio"/>

Imagine you have **won £700 in a lottery**. Imagine you had the option to divide some, none or all of this £700, between yourself and the others listed below. You can split the money in any way you see fit, you don't have to give anyone any money or give everyone the same amount. You can decide who gets what, if anything, of the £700. Please indicate how you would like to split the £700 between yourself and these groups (the total divided must equal £700).

How much of the £700 (some, none or all) would you...

* Required	
Keep for yourself	£
Give to a random unknown farmer	£
Give to a neighbouring farmer	£
Give to a random unknown vet	£
Give to your local vet	£
Give to a stranger	£



Please select the diagram that best represents how close you feel on average to each of the people and groups listed.

	1	2	3	4	5	6	7
Your vet	<input type="radio"/>						
The veterinary community in general (i.e. all vets nationwide)	<input type="radio"/>						
Your neighbouring farmers	<input type="radio"/>						
The farming community in general (i.e. all farmers nationwide)	<input type="radio"/>						
The Government	<input type="radio"/>						
Your cows	<input type="radio"/>						
Dairy farmers in general (i.e. all dairy farmers nationwide)	<input type="radio"/>						
Beef farmers in general (i.e. all beef farmers nationwide)	<input type="radio"/>						

# Elicitation results – GUI simulation

Table: Number of infected herds, distance of the nearest infected herd from the interviewee's herd and number of farmers that vaccinated each week during the disease epidemic scenario.

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

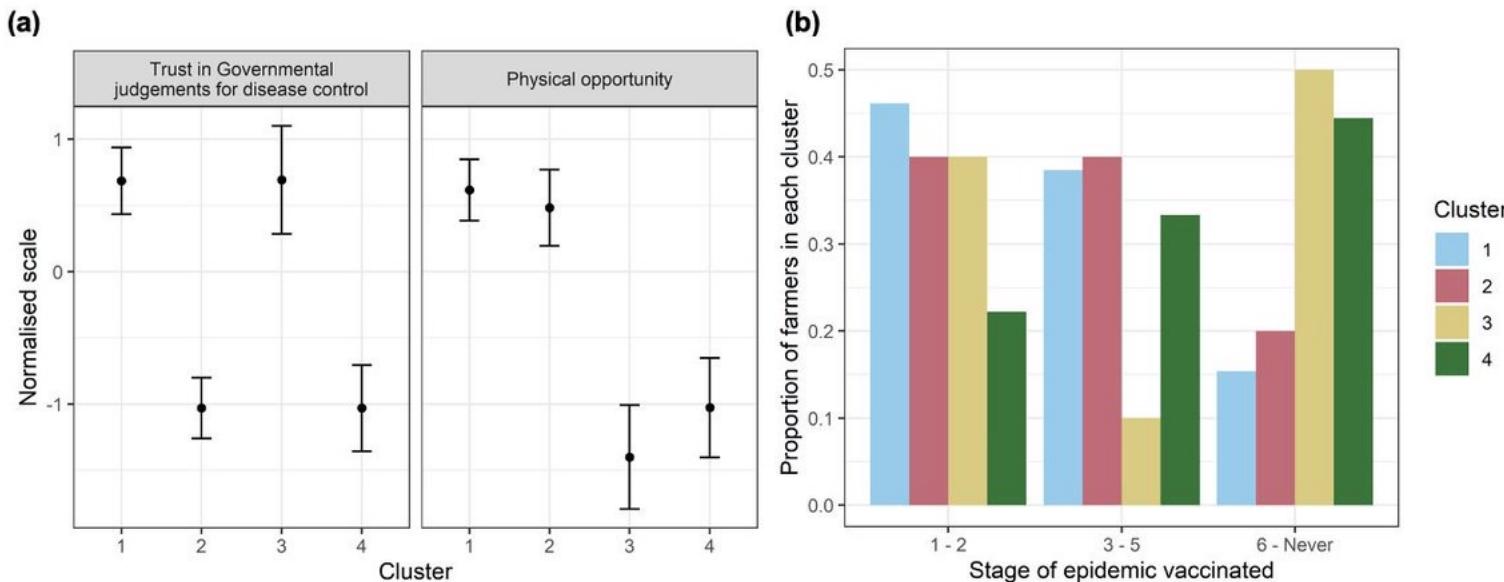
\*Epidemic confined to southern-central France

- Sixty farmers (39 beef & 21 dairy) participated, with variability apparent 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)

**Figure: Farmer groups from k-means clustering conducted on the two most stable covariates.**  
**(a)** Mean and 95% confidence interval scores of the covariates for each group. **(b)** Proportion of farmers in each group that vaccinated in different stages of the outbreak.

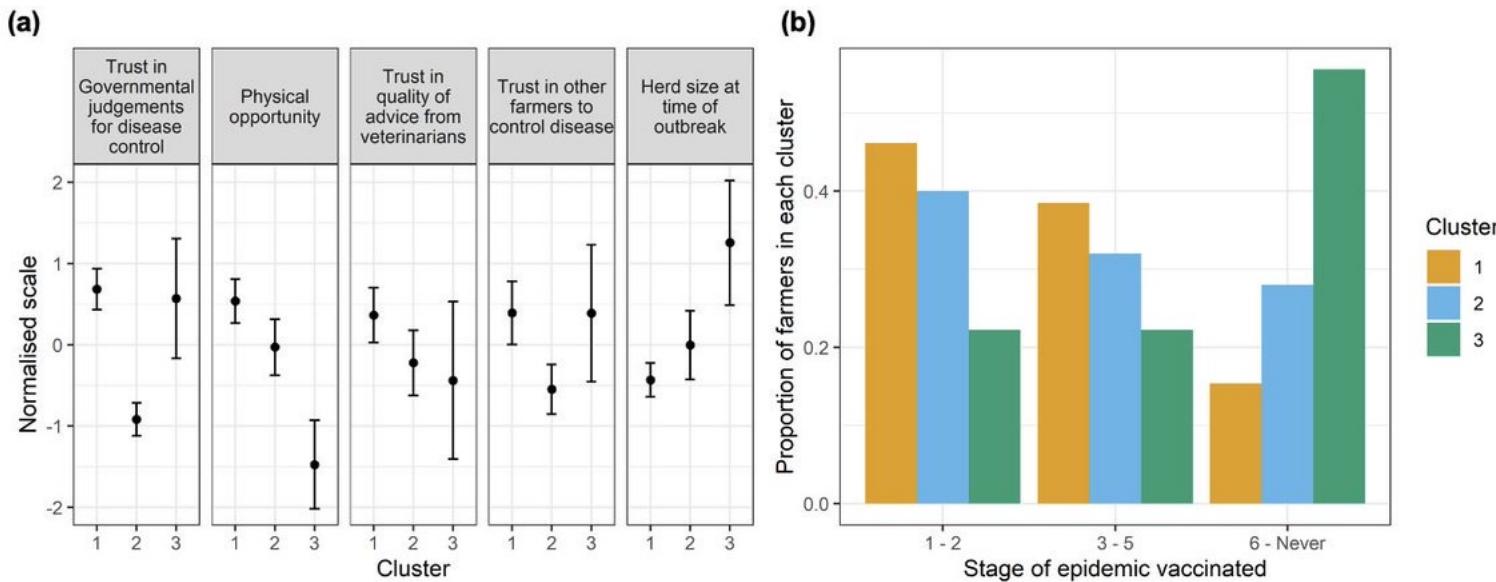


# Elicitation results – Farmer groupings

- Grouping using five most stable covariates, three groups gave best fit.
- Additional covariates: Trust in vet advice, trust in other famers to control disease, herd size.

**Figure: Farmer groups from k-means clustering conducted on the five most stable covariates.**

(a) Mean and 95% confidence interval scores of the covariates for each group. (b) Proportion of farmers in each group that vaccinated in different stages of the outbreak.



# Study aims

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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**

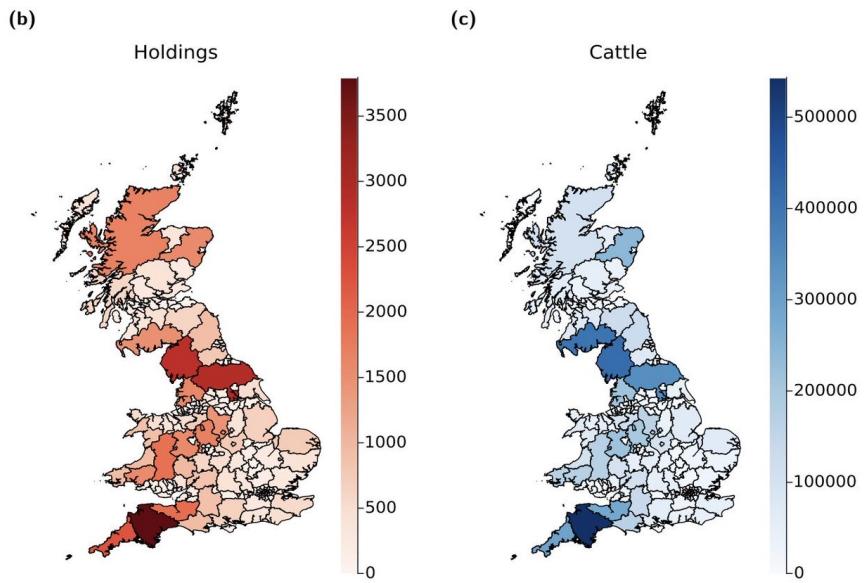
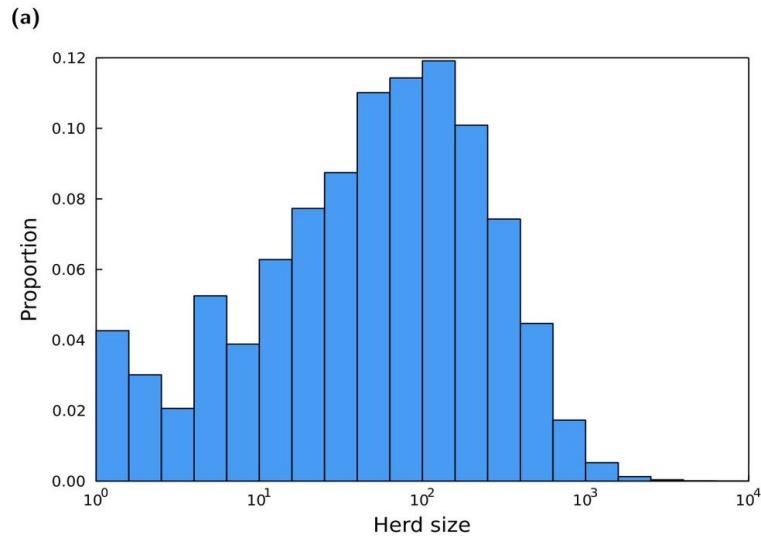
Data-driven model framework with epidemiological and behavioural layers.

3. Assess how psychosocial & behaviour change factors impact epidemiological outcomes given a fast-spreading livestock disease

# Modelling methods - Cattle data

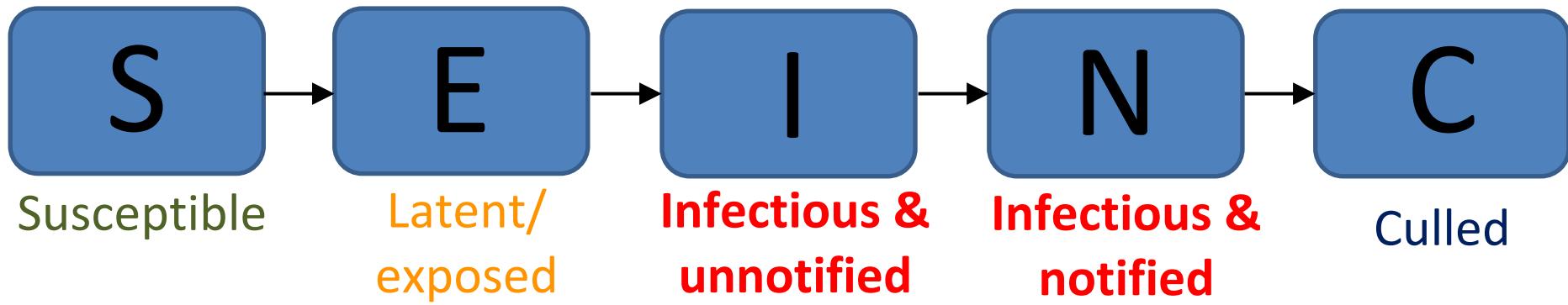
- Average 2020 cattle herd sizes from the Cattle Tracing System.

**Figure:** (a) Distribution of cattle herd sizes. (b) Number of holdings with cattle per region. (c) Number of cattle per region.



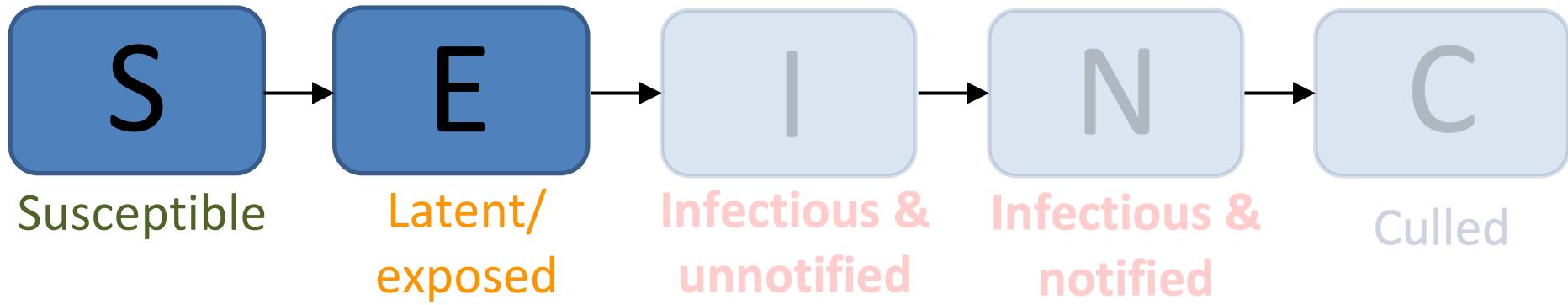
# Modelling methods – Disease states

- Epidemiological unit: Premises.
- 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 – Force of infection

---

Force of infection on premises i from premises j:  $\lambda_{ij} = t_c N_{c,j}^q N_{c,i}^p K(d_{ij})$

- Infected premises contribution: Dependent on herd size
- Susceptible premises contribution: Dependent on herd size
- Transmission kernel: Force of infection between premises dependent on the distance between them.

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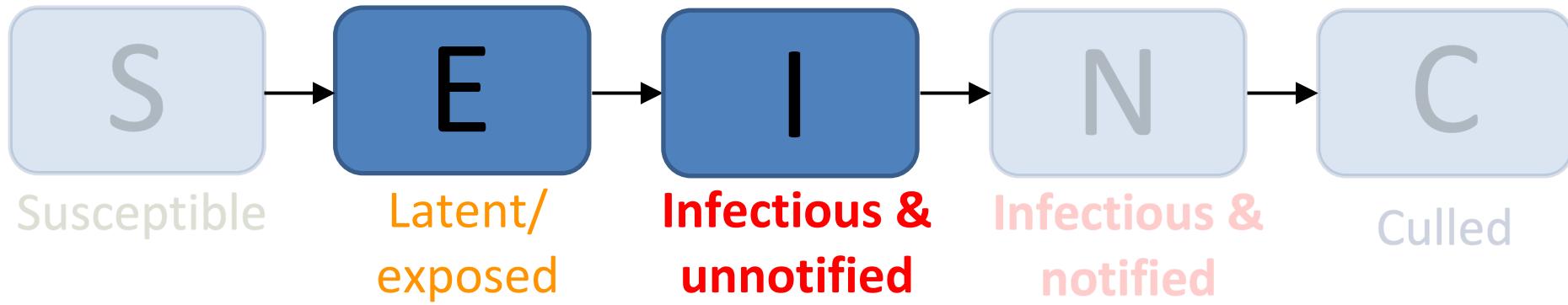
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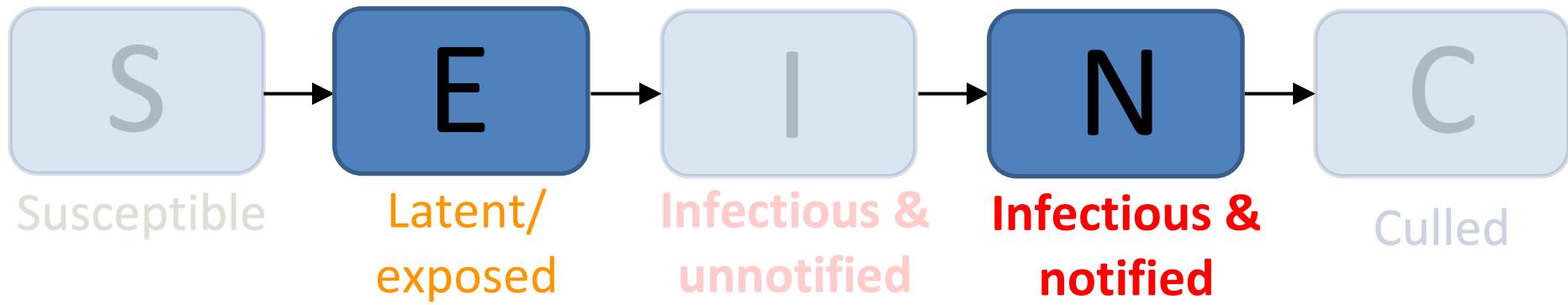
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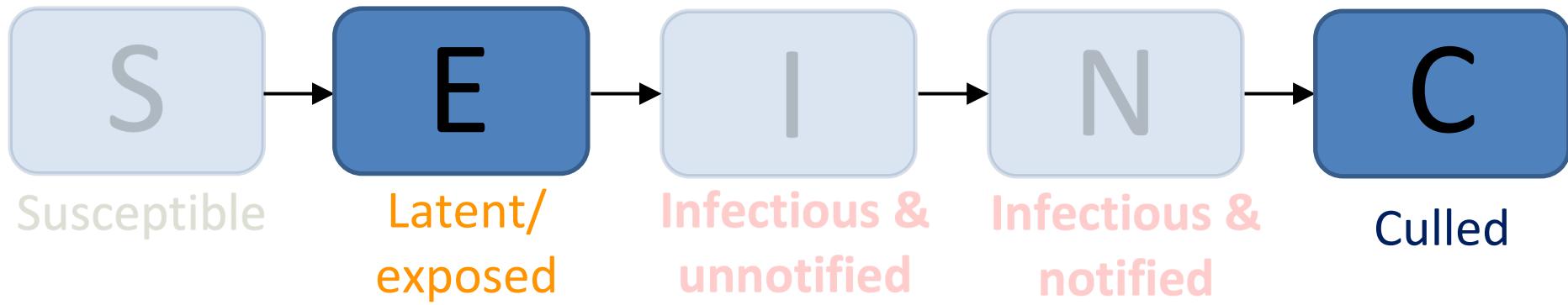
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# Modelling methods – Behavioural configurations

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

## **Homogeneous: Non-data informed**

Farmer vaccinates when infection is within:

- Strong parasitism – 50km
- Weak parasitism – 320km
- Mutual cooperation – Before pathogen emergence

## **Heterogeneous: Non-data informed**

Even split across different groups.

- Coop-Parasitism-Free riders (FR)
- Coop-Parasitism

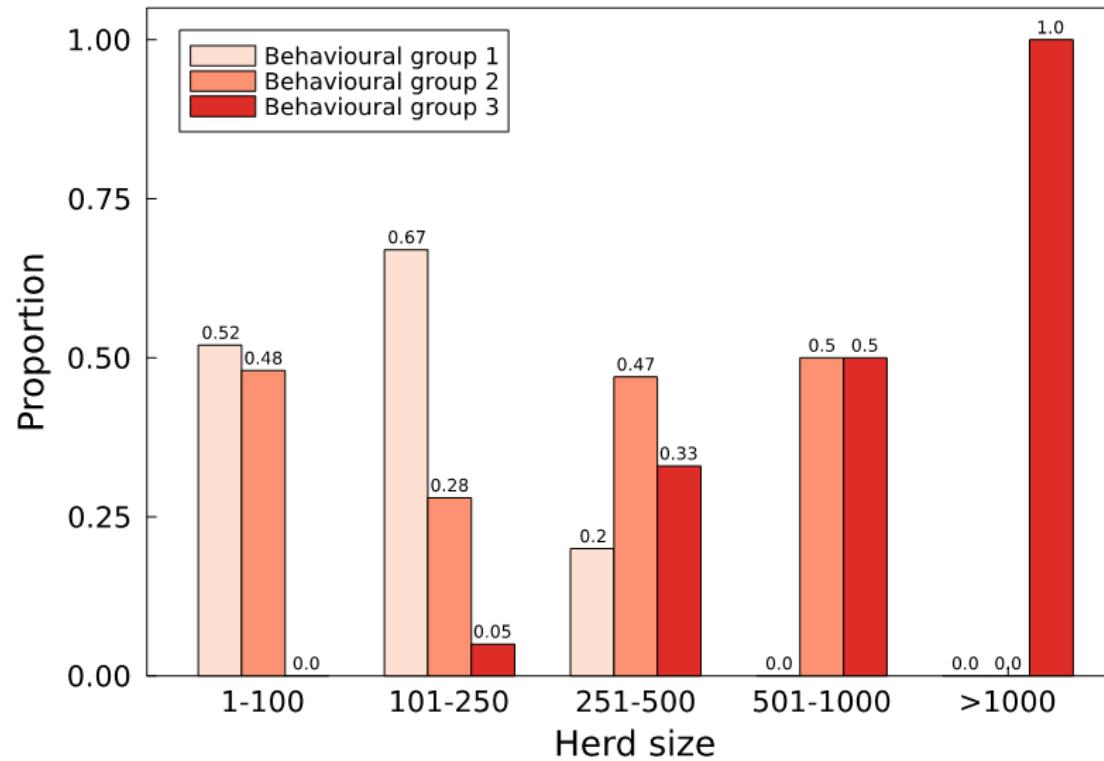
## **Heterogeneous: Data informed**

Parameterised using interview results

- Trust expectancy (two covariate model)
- Herd size dependent (five covariate model)

# Modelling methods – Behavioural configurations

**Figure:** For the “Herd size dependent” behavioural configuration, the probability of a holding being assigned to each of the behavioural groups with respect to the herd size.



# Study aims

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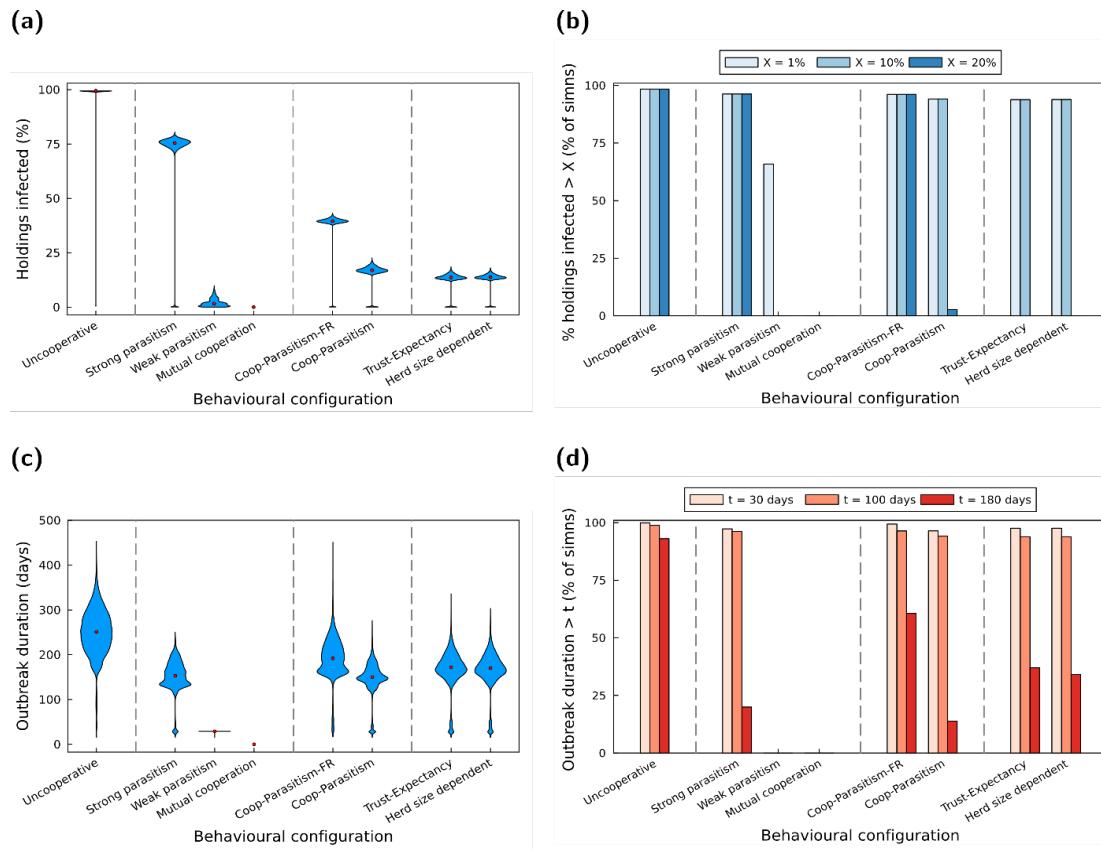
1. Elicit farmers vaccination decisions to an unfolding epidemic and link to their psychosocial and behavioural profiles (within Great Britain)
2. Refine mathematical disease models to capture psychosocial & behaviour change heterogeneities
3. **Assess how psychosocial & behaviour change factors impact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

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

- Per behavioural configuration, ran 500 replicates for each of the 89 seed region locations.
- Per simulation replicate, seeded infection in a 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; **(c&d)** Analogous summary statistics for outbreak duration.

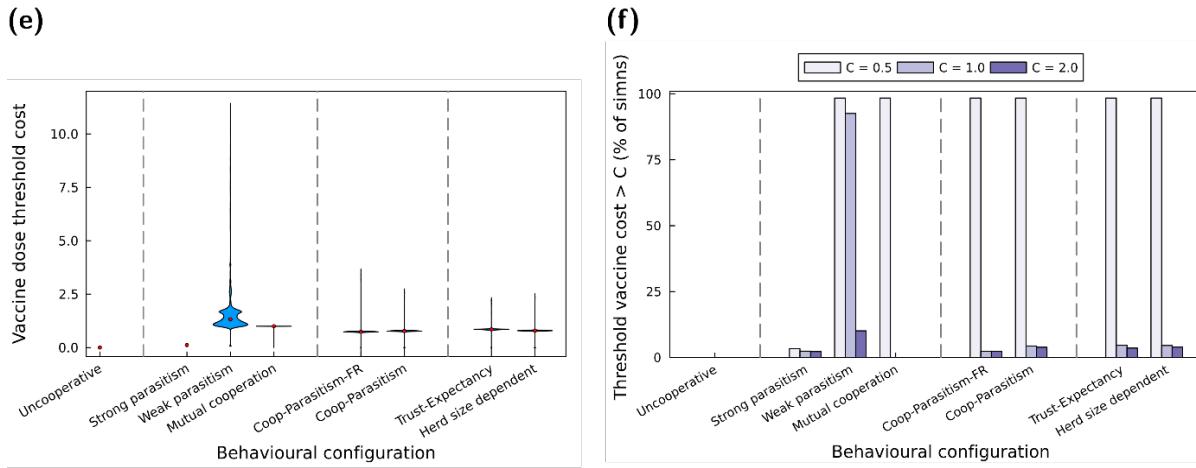


➤ Homogeneity in farmer behaviour vs data-informed psychosocial profile clusters estimates:  
**Disconnect in outcomes**

# Modelling results – Health economic metrics

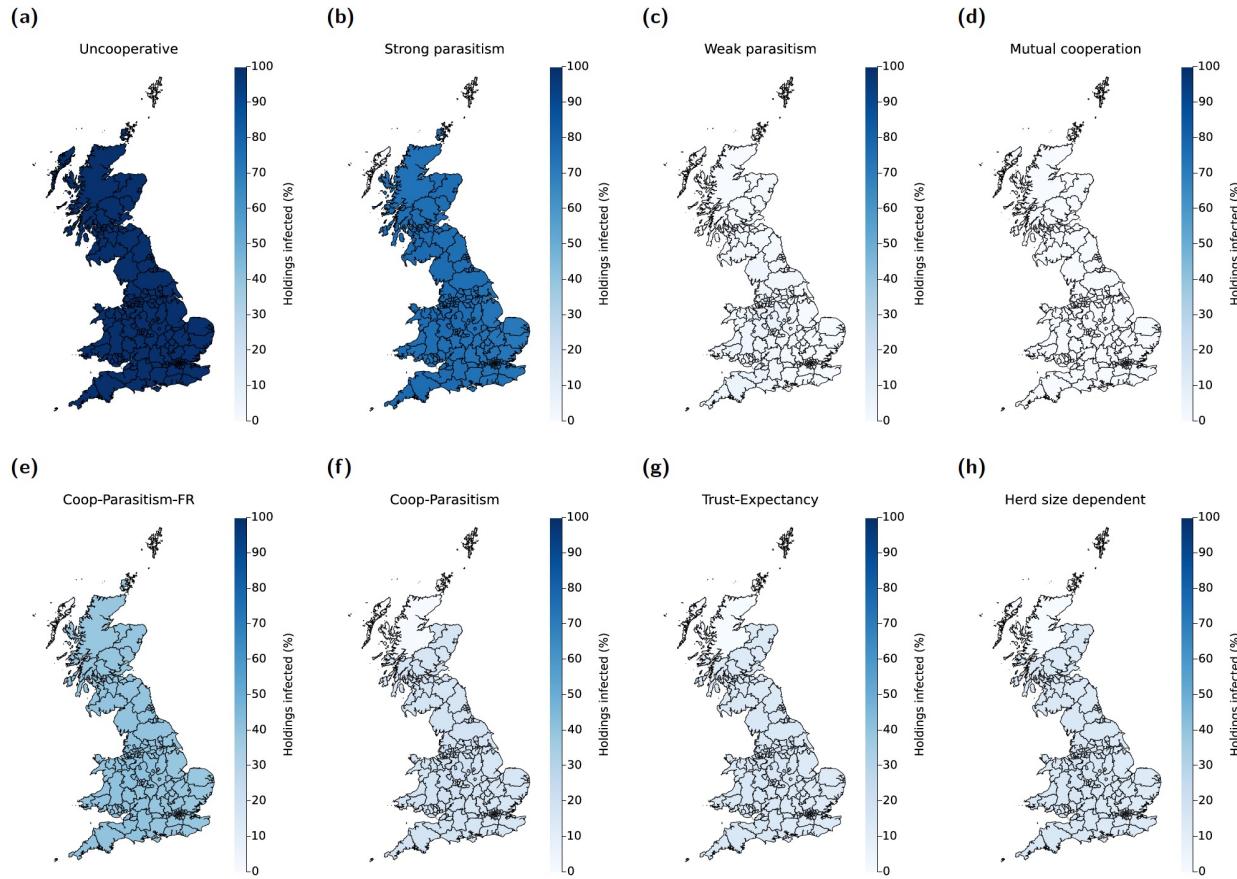
- **Vaccine dose threshold cost:** The maximum amount you can spend on a single vaccine dose where the total monetary cost (across vaccines and losses due to infection) does not exceed the monetary cost of infection incurred in the no intervention scenario (uncooperative configuration).

**Figure:** For each behavioural configuration: (e) Distribution of vaccine dose threshold costs; (f) Percentage of simulations exceeding the stated vaccine dose threshold cost.



# Modelling results – Role of seed infection region

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



# Limitations & further work

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## Elicitation

- Behavioural cluster analysis not feasible at regional level
- Are other intervention practices available to farmers

## Modelling

- Focused on a limited set of interventions
- Considered a single set of epidemiological parameters

## Open questions– what are the next steps?

- Support to establish longitudinal elicitation studies
- Tailored elicitation exercises to instruct behavioural group attributes amongst farmers towards control of enzootic diseases

# Implications

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**A demonstration of 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**

# Acknowledgements

**Mike Tildesley, Matt Keeling, Paul Brown**

Zeeman Institute: Systems Biology & Infectious Disease Epidemiology Research (SBIDER),  
University of Warwick, UK.

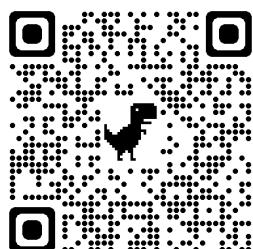
**Naomi Prosser, Jasmeet Kaler, Martin Green,**

School of Veterinary Medicine and Science, University of Nottingham, UK.

**Eamonn Ferguson**

School of Psychology, University of Nottingham, UK.

**Animal and Plant Health Agency (APHA)**



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

**FEED project webpage:**

<https://feed.warwick.ac.uk>

**Personal webpage:**

<https://edmhill.github.io>

**Email:** Edward.Hill@warwick.ac.uk

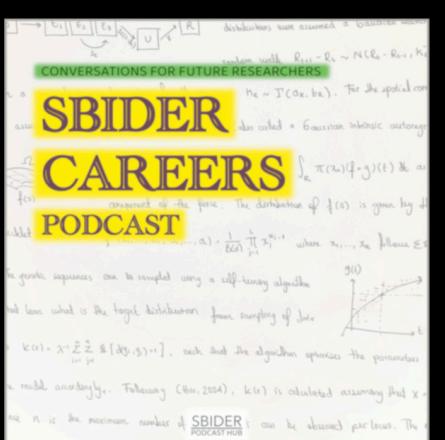


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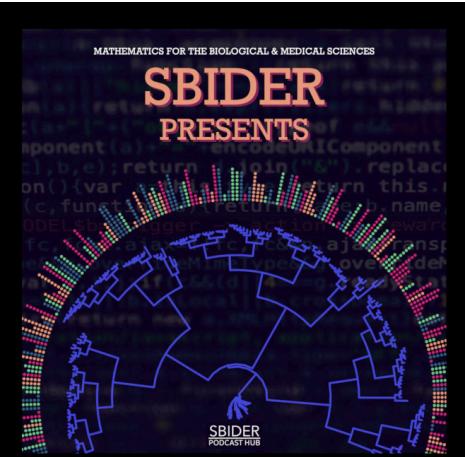
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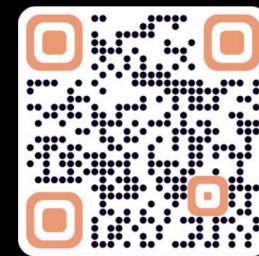
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