Supplementary material for

Data-driven models of foot-and-mouth disease dynamics: a review.

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Materials and methods.

Literature Search

We performed the literature search on March 22, 2015 using Web of Science. We searched over all years with

> foot and mouth disease
>
> AND model OR dynamic* OR simulat* OR mathematic* OR stochastic* OR determinis* OR compartmental OR transmission OR reproducti* OR R0 OR estimat* OR sensitivit* OR epidemi* OR endemi*
>
> NOT hand OR mouse OR quasispecies

in the *topic* heading of the search tool. Search terms were motivated, in part, by Lloyd-Smith et al. (2009).

We compare counts of FMDV dynamical models with total counts of all publications on FMDV (Fig. S1). To find all publications, we searched each year between 1976 and 2012 with

> foot and mouth disease
>
> NOT hand

in the *topic* heading.

Categorizing the models

We use five features to categorize models:

1. How the model represents host species diversity.
2. How the model represents farm location and connectivity.
3. How the model represents transmission: within farm, between farm, considering unreported cases, and/or considering carrier animals.
4. How the model represents control: none, unspecified, movement restrictions, vaccination, and/or culling.
5. Types of data used with the model.

Results are tabulated in the database (Table S1-S2), summarized in the figures (S1-S5).

FMDV models represent transmission on two spatial scales: among farms and within farms. Alternatively, some models represent within farm transmission in proxy, using time-varying levels of infectiousness for a farm (Chis Ster et al., 2009). Since models with time-varying infectiousness do not explicitly model within farm dynamics, we did not score them as such in Figure S3 and Table S2.

Models represent three strategies for FMDV control: animal movement restrictions, vaccination campaigns, or culls of infected and possibly susceptible animals. Some models explicitly incorporate one or more method of control. Yet, many models implicitly incorporate control by making inference on data collected during control campaigns. We designated implicit control by an asterisk (*) in both Figure S4 and Table S2.

As a criterion for inclusion in this review, models use data on host abundance and/or distribution, disease incidence or prevalence, or both. In Table S2, we attempt to distinguish between more and lest robust national measures of host abundance by classifying more robust measures as “national registries” and less robust measures as “national censuses” (Tables S1 and S2). Admittedly, this classification is subjective, so graphical analysis of data usage collapsed the two categories and represented both types of data as “host registry” (Figure S5).

Note

Interspread, AusSpread, and NAADSM are three modeling frameworks in which users can include variables by choosing from supported options. We summarize publishing output in Table S3. While publications detail which variables and data are included in the model, relationships among variables are not clearly stated, preventing understanding of methodology for modeling farm connectivity. Therefore, models using Interspread, AusSpread, and NAADSM have been excluded from the database of references (Table S2). However, locations modeled in references using Interspread, AusSpread, and NAADSM are included in Figure 3.

References

Chis Ster, I., B. K. Singh and N. M. Ferguson, 2009: Epidemiological inference for partially observed epidemics: the example of the 2001 foot and mouth epidemic in Great Britain. *Epidemics,* 1, 21-34.

Lloyd-Smith, J. O., D. George, K. M. Pepin, V. E. Pitzer, J. R. C. Pulliam, A. P. Dobson, P. J. Hudson and B. T. Grenfell, 2009: Epidemic Dynamics at the Human-Animal Interface. *Science,* 326, 1362-1367.

Analysis of references

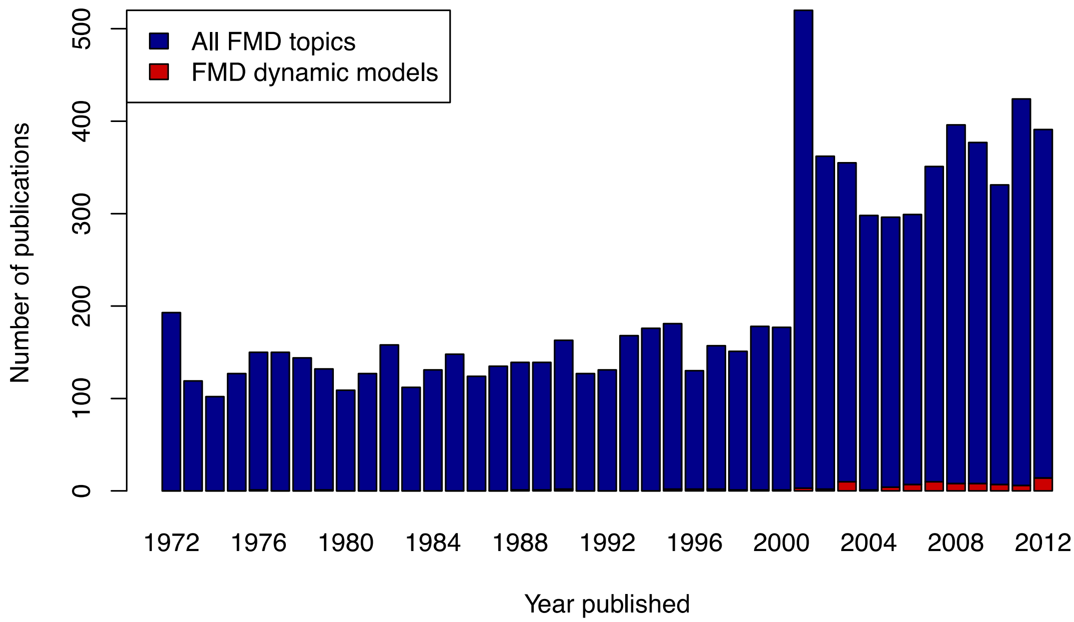

Figure S1. Historical publishing effort of articles relating to FMDV. Articles on FMDV dynamic models are represented in red, while publications on all other FMDV topics are represented in blue. Years of high effort in FMDV dynamical models publishing include 2003, 2007, and 2012 with 10, 10, and 14 articles published, respectively. Publication effort of FMDV models has increased over time, in proportion with the increase in publication effort for all FMDV studies across disciplines.

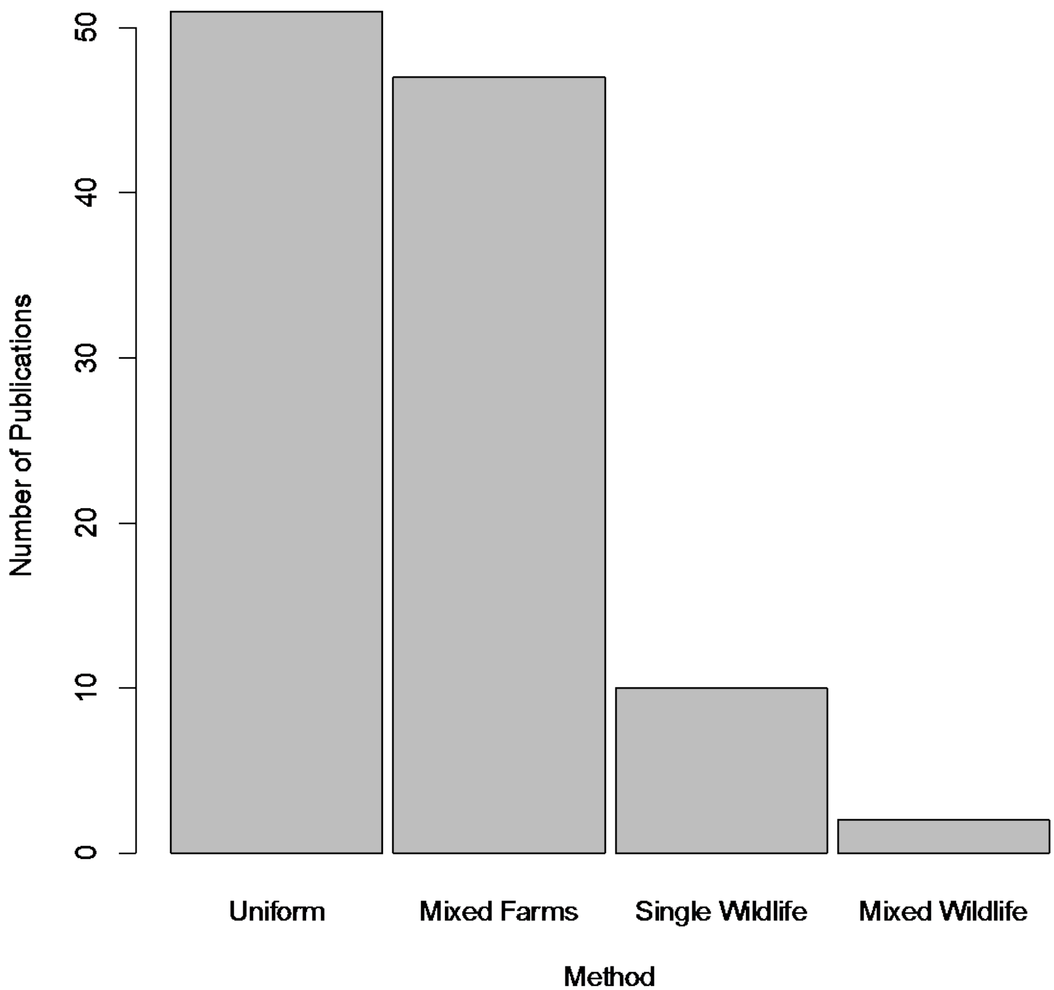

Figure S2. Species diversity in FMDV models. Host species diversity has been depicted in FMDV models as mixed farms, single wildlife species, or mixed wildlife species, or is absent with a uniform representation for all hosts. Frequency of use differs among methodologies.

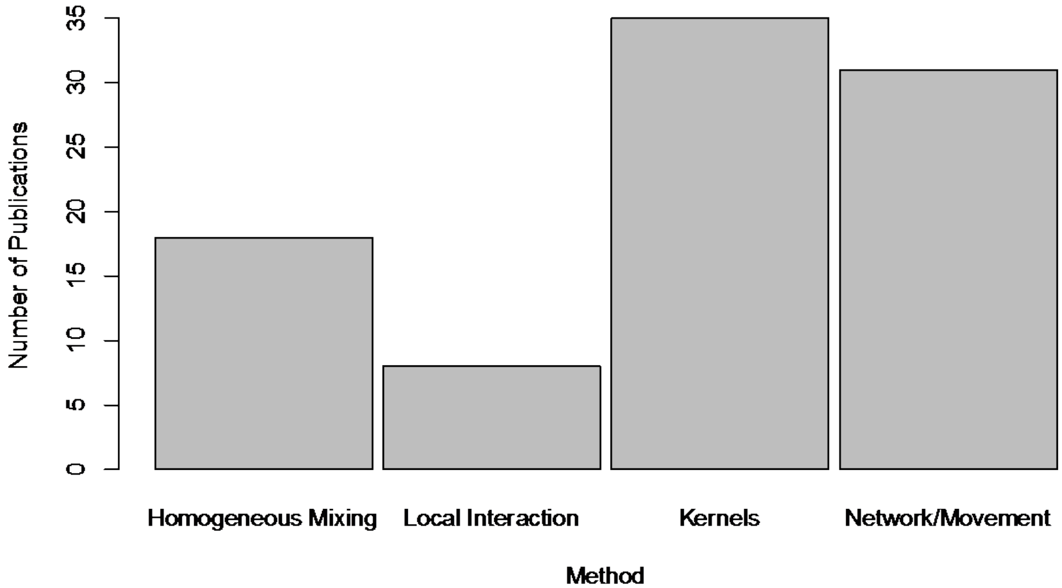

Figure S3. Transmission in FMDV models. Models reviewed here represent six methods to represent of FMDV transmission: (1) homogeneous mixing, (2) local interactions, (3) distance-based transmission kernels, and (4) network or host movement models. Frequency of use varies, with kernels being the most frequently employed methodology.

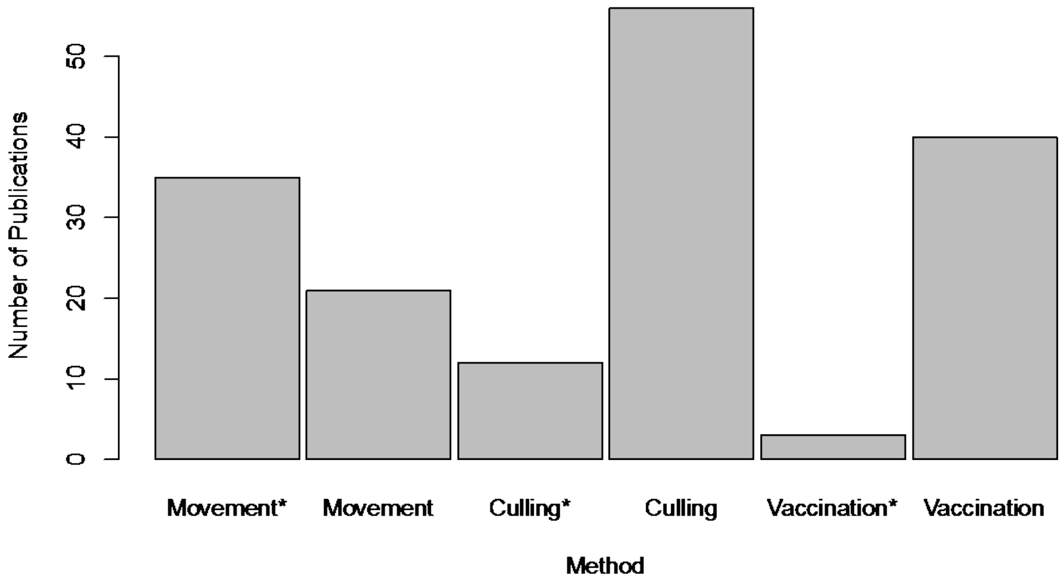

Figure S4. Control in FMDV models. Models reviewed here represent movement restrictions, vaccination campaigns, and animal culls. We distinguish between explicit and implicit (*) models of control; the latter indicating inference made on disease data collected during control campaigns. Frequency of use in models differs among control strategies as shown.

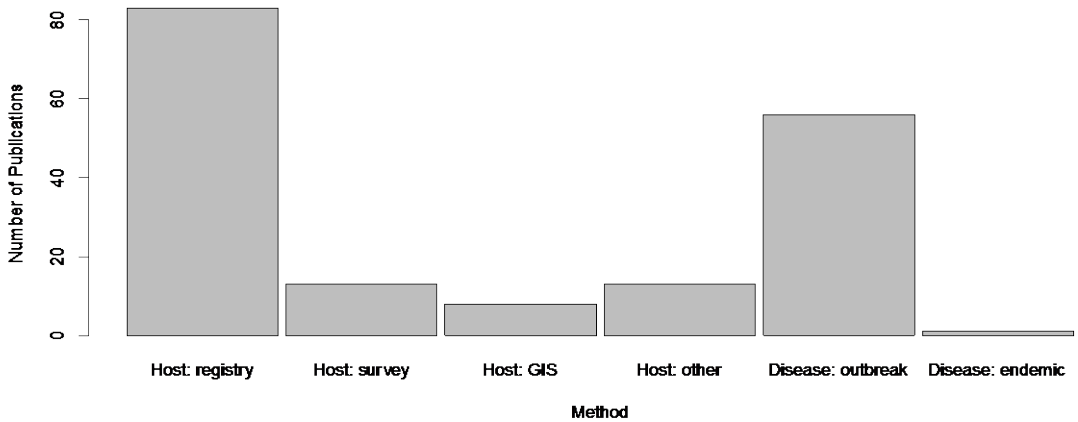

Figure S5. Use of data in FMD models. Host abundance and disease incidence or prevalence data can parameterize models of FMDV transmission or control. Sources of data on host abundance include national databases, registries, or census, investigator directed surveys, land-use or geographical information systems (GIS) data, or other sources. Sources of disease data include incidence time-series from outbreaks or endemic case reports. Frequency of use in models differs among data sources as shown.

Table captions.

Table S1. Notation and codes used in the database of references. Descriptions model methods, with codes used in the database of references. Note that various methods of control are implicitly modeled (*) by performing inference on disease data collected simultaneously with control campaigns.

Table S2. Database of references. Ninety-five references are listed, categorized on methods used to incorporate species diversity, farm location and connectivity, FMDV transmission and control, and use of data.

Table S3. Citations for Interspread, AusSpread, and NAADSM model use. While publications that use Interspread, AusSpread, or NAADSM cannot be included in the database of references due to insufficient information for categorization, they are listed here along with the outbreak they represent.

Table S1. Notation and codes used in the database of references

Heading	Notation	Definition
Location: Farm connectivity	kernel (1)	Spatial transmission kernel estimated by DEFRA using data from contact tracing post-movement ban during the UK 2001 FMDV epidemic
	kernel (2)	Spatial transmission kernel estimated using incidence from the entire duration of the UK 2001 FMDV outbreak
	kernel (3)	Multiple spatial transmission kernels estimated using incidence data from the entire duration of the UK 2001 FMDV epidemic; kernels were estimated pre/post movement ban and pre/post increased culling
	kernel (4)	Spatial transmission kernel estimated using incidence from the entire duration of an epidemic other than 2001 UK
	kernel (5)	Exponential distance-based decay
	kernel (6)	kernel (1) with probability equal to 1 at very short distances
	kernel (7)	Geometric change point kernel plus additional infections
	kernel (8)	Inverse distance for local contacts with a fixed probability of infection from long-range contacts
	kernel (9)	Cauchy-type kernel
	kernel (10)	Radial function
	metapopulation	Spatial patches of hosts with transmission among patches
	mvmt	Based directly on records of host movement between farms
	mvmt. model	Spatial host movement model based on production type, herd size, distance, and contact probabilities
	local interaction	Specified distance-based interactions at a local scale; commonly used in cellular or geographic automata models
	pair approximation	Spatial structure imposed implicitly as pairwise clusters of are defined over which transmission may occur
	network-opinion	Contact network with probability of disease transmission over edges determined by expert opinion
	network	Network of all means of contact that could cause FMDV transmission
	homogeneous (1)	Homogeneous mixing among entire study population
	homogeneous (2)	Multiple geographic regions defined with homogeneous mixing within each region and no connection among regions
	route	Milk tanker routes connecting geographically distinct farms with the potential to transmit infection between farms
Transmission: unobserved cases	1	Exposed (latent) state or time delay to infectiousness: explicitly defined or determined by sensitivity analysis
	2	Undetected infected farms culled as a part of the contiguous or ring culls (in UK)
	3	Silent spread before detection of infected farm

Heading	Notation	Definition
Control	X	Explicitly modeled
	X*	Implicitly modeled as a byproduct of making inference on data collected while the control measure was practiced
	1	Reduction in cases
	2	Reduction in carriers
	3	Explicit economic costs
Data: Host	1	Data from a national registry
	2	Data from a national census
	3	Investigator-directed survey
	4	GIS land cover data
	5	Other
	unk	Unknown
Data: Disease	1	Epidemic time-series data used in parameter estimation
	2	Endemic case reports data used in parameter estimation
	3	Endemic serology data used in parameter estimation
	4	Parameter estimates (originally obtained from outbreak data in another population) used for simulation
	5	Other

Table S2. Database of references.

Reference	Species diversity				Location		Transmission				Control						Data	
	Uniform	Mixed species farms	Single wildlife	Mixed wildlife	Country	Farm connectivity	Within farm	Between farm	Unobserved cases	Carriers	None	Unspecified / other	Mvmt. Restriction	Vaccination	Culling	Metrics for impact	Host	Disease
Ap Dewi et al., 2004	X				UK	homogeneous (1)		X	3			X				1	1	5
Arnold et al., 2008		X			UK	kernel (2)		X	1	X			X*	X	X*	1,2	1	0,4
Backer et al., 2012		X			Netherlands	kernel (4)	X	X	1,3				X*	X	X	1	1,3	0,4
Bajardi et al., 2012	X				Italy	mvmt		X				X				1	1	0
Bates et al., 2003a	X				US	network-opinion	X	X	1				X	X	X	1	2,3	0
Bates et al., 2003b	X				US	network-opinion	X	X	1				X	X	X	1	2,3	0
Boender et al., 2010		X			Netherlands	kernel (4)		X					X*	X	X	1	1	1
Bokland et al., 2013		X			Denmark	network-opinion		X	1			X	X	X	X	1,3	1	0
Bouma et al., 2003	X				Netherlands	homogeneous (1)		X					X*	X*	X*	1	1	1
Buhnerkempe et al., 2014	X				US	mvmt model		X	1				X			1	3	0
Carpenter et al., 2007	X				US	network-opinion	X	X	1		X					1	2,3	0
Carpenter et al., 2011	X				US	network-opinion	X	X	1				X	X	X	1,3	2,3	0
Chis Ster et al., 2007		X			UK	kernel (3)		X	1				X*		X*	1	1	1
Chis Ster et al., 2009		X			UK	kernel (3)		X	2				X*		X*	1	1	1
Chis Ster et al., 2012		X			UK	kernel (3)	X	X	1,3				X*		X*	1	1	1
Chowell et al., 2006	X				Uruguay	kernel (5), metapopulaton	X	X	1,3				X	X		1	5	1
Deardon et al., 2010		X			UK	kernel (7)		X	1				X*	X	X	1	1	1
Deardon et al., 2012		X			UK	kernel (5)		X	1				X*	X	X	1	1	1
Dexter, 2003			X		Australia	n/a	X		1							1	5	0
Dickey et al., 2008	X				US	network-opinion		X	1,3			X	X		X	1	2,3	0
Diggle 2006		X			UK	kernel (2)		X	1				X*		X	1	1	1
Dijkhuizen, 1989	X				Netherlands	homogeneous (1)		X						X	X	1,3	unk	0
Doran & Laffan, 2005		X	X		Australia	local interaction		X	1		X					1	1, 2	0
Durand & Mahul, 1999		X			France	homogeneous (2)	X	X	1,3					X	X	1	2	0
Estrada et al., 2008	X				Peru	homogeneous (1)		X			X					1	0	1

Reference	Species diversity				Location		Transmission				Control						Data	
	Uniform	Mixed species farms	Single wildlife	Mixed wildlife	Country	Farm connectivity	Within farm	Between farm	Unobserved cases	Carriers	None	Unspecified / other	Mvmt. Restriction	Vaccination	Culling	Metrics for impact	Host	Disease
Ferguson et al., 2001a	X				UK	pair approximation		X	1				X*	X	X	1	1	1
Ferguson et al., 2001b		X			UK	pair approximation		X	1				X*		X	1	1	1
Garner & Lack, 1995a		X			Australia	homogeneous (2)		X	1					X	X	1,3	1	0
Garner & Lack, 1995b	X				Australia	homogeneous (2)		X	1					X	X	1,3	1	0
Gerbier et al., 2002	X				UK	kernel (8)		X							X	1	1	1
Gilbert et al., 2005		X			Turkey	kernel (5)		X						X*		1	1	1
Green et al., 2006	X				UK	mvmt, kernel (5)		X	1,3*				X			1	1,2	0
Halasa et al., 2013		X			Denmark	network-opinion		X	1			X	X		X	1,3	1	0
Halasa et al., 2014 (March)		X			Denmark	network-opinion		X	1			X	X		X	1,3	1	0
Halasa et al., 2014 (July)		X			Denmark	network-opinion		X	1			X	X		X	1,3	1	0
Handel et al., 2011		X			UK	kernel (2)		X	1,3		X		X*		X*	1	1	4
Hayama et al., 2013		X			Japan	kernel (4)		X					X*	X	X*	1	1	1
Haydon et al., 1997	X				UK	homogeneous (1)		X			X					1	1	1
Heuer et al., 2007		X			New Zealand	n/a	X		1,3			X				1	1,3	0
Highfield et al., 2008			X		US	local interaction		X	1		X					1	4,5	0
Highfield et al., 2009			X		US	local interaction		X	1		X					1	4	0
Highfield et al., 2010a			X		US	local interaction		X	1		X				X	1	4,5	0
Highfield et al., 2010b			X		US	local interaction		X	1		X				X	1	4,5	0
Hone & Pech, 1990			X		Australia	n/a	X		1,3			X				1	5	0
Hosseinkashi et al., 2012		X			UK	network		X								1	1	1
Howard & Donnelly, 2000	X				Taiwan, UK	homogeneous (1)		X	1				X*		X	1	1	1
Hughjones, 1976	X				UK	route		X	1		X					1	1	0
Hutber et al., 1996	X				Saudi Arabia	n/a	X		1					X		1	1	5
Hutber et al., 1998	X				Saudi Arabia	n/a	X		1					X		1	1	5
Jewell et al., 2009		X			UK	kernel (9)		X					X*		X	1	1	1
Kao, 2003		X			UK	kernel (2)		X	1,3				X*		X	1	1	1
Kao et al., 2006	X				UK	mvmt		X			X					1	1	0
Kao et al., 2007	X				UK	mvmt		X			X					1	1	5

Reference	Species diversity				Location		Transmission				Control						Data	
	Uniform	Mixed species farms	Single wildlife	Mixed wildlife	Country	Farm connectivity	Within farm	Between farm	Unobserved cases	Carriers	None	Unspecified / other	Mvmt. Restriction	Vaccination	Culling	Metrics for impact	Host	Disease
Keeling et al., 2001		X			UK	kernel (1)		X	1				X*	X	X	1	1	1
Keeling et al., 2003		X			UK	kernel (1)		X	1				X*	X	X	1	1	4
Kiss et al., 2005	X				UK	pair approximation, network		X	1				X		X	1	1	4
Kiss et al., 2006		X			UK	mvmt		X	1,3*		X					1	1	0
Klaring & Timischl, 1979	X				Austria	homogeneous (1)		X						X	X	1	1	1
Klinkenberg et al., 2006	X				UK	homogeneous (1)		X	3			X				1	0	4
Kobayashi et al., 2007a	X				US	homogeneous (1)		X	1				X	X	X	1,3	2,3	0
Kobayashi et al., 2007b	X				US	homogeneous (1)		X	1				X	X	X	1,3	2,3	0
Laffan et al., 2011		X			US	local interaction		X	1		X					1	2	0
Lawson et al., 2011	X				UK	homogeneous (1)		X					X*		X	1	1	1
Le Menach et al., 2005		X			France	kernel (1)		X	1				X*	X	X	1	2	4
Lindstrom et al., 2011		X			Sweden	mvmt. model		X			X					1	1	0
Lindstrom et al., 2012		X			Sweden	mvmt. model		X			X					1	1	0
Martinez-Lopez et al., 2014		X			Peru	network	X	X	1			X				1	2	0
Matthews et al., 2003	X				UK	metapopulation		X	1						X	1	1	5
Mardones et al., 2013		X			US	network-opinion		X	1			X	X		X	1	2,3	0
Orton et al., 2012	X				UK	mvmt, kernel (5)		X	1		X					1	1	0
Parham et al., 2008	X				UK	pair approximation		X	1						X	1	1	0
Pech & Hone, 1988			X		Australia	n/a	X		1						X	1	5	0
Pech & McIlroy, 1990			X		Australia	n/a	X		1							1	5	0
Porphyre, et al., 2013		X			Scotland	kernel (1)		X	1				X	X	X	1	2	0
Pineda-Krch et al., 2010	X		X		US	network-opinion		X	1				X		X	1	2	0
Rautureau et al., 2012		X			France	mvmt, network	X	X	1,3*			X				1	1	0
Rich et al., 2007	X				Argentina Uruguay Paraguay	metapopulation		X	1	X				X	X	1,3	1	5

Reference	Species diversity				Location		Transmission				Control						Data	
	Uniform	Mixed species farms	Single wildlife	Mixed wildlife	Country	Farm connectivity	Within farm	Between farm	Unobserved cases	Carriers	None	Unspecified / other	Mvmt. Restriction	Vaccination	Culling	Metrics for impact	Host	Disease
Rich, 2008	X				Argentina Uruguay Paraguay	metapopulation		X	1	X				X	X	1	1	5
Rivas et al., 2003	X				Uruguay	homogeneous (2)		X						X	X	1	unk	1
Rivas et al., 2012	X				Uruguay	network		X				X*				1	unk	5
Savill et al., 2007		X			UK	kernel (6)		X	1				X*		X*	1	1	1
Schley et al., 2009	X				UK	kernel (2)		X					X			1	1	4
Schley et al., 2012	X				UK	n/a	X				X					1	3	0
Schoenbaum & Disney, 2003	X				US	homogeneous (2), network-opinion		X	1					X	X	1,3	2	0
Shea et al., 2014		X			UK	kernel (1)		X	1				X*		X*	1,3	1	4
Thornely & France, 2009	X				UK	kernel (10)	X	X	1,3				X	X	X	1		4
Tildesley et al., 2006		X			UK	kernel (1)		X	1				X*	X	X	1	1	4
Tildesley et al., 2008		X			UK	kernel (1)		X	1				X*		X	1	1	1
Tildesley and Keeling, 2008		X			Denmark	kernel (1)		X	1				X*		X	1	1	4
Tildesley et al., 2009		X			UK	kernel (1)		X	1				X*		X	1	1	4
Tildesley and Keeling, 2009		X			UK	kernel (1)		X	1				X*	X	X	1	1	4
Tildesley et al., 2010		X			UK, US	kernel (1)		X	1				X*	X	X	1	1,2,4,5	4,0
Tildesley et al., 2012		X			US	kernel (1)		X	1				X*	X	X	1	2	4
Tildesley and Ryan, 2012		X			UK	kernel (1)		X	1				X*	X	X	1	4	4
Tomassen et al., 2002	X				Netherlands	network		X	1				X	X	X	1,3	2	0
Traulsen et al., 2010	X				Germany	network, mvmt		X	1			X		X	X	1	2	0
Traulsen et al., 2011	X				Germany	network, mvmt		X	1			X		X	X	1	2	0
Tsutsui et al., 2003	X				Japan	homogeneous (1)	X	X	3				X*			1	2	1
van den Broek et al., 2007	X				UK	homogeneous (1)		X					X*		X*	1	0	1
Vergne et al., 2012	X				Cambodia	n/a					X					1	3	2,3
Vernon et al., 2012	X				UK	mvmt	X	X	1				X*	X*	X*	1	1	0

Reference	Species diversity				Location		Transmission				Control						Data	
	Uniform	Mixed species farms	Single wildlife	Mixed wildlife	Country	Farm connectivity	Within farm	Between farm	Unobserved cases	Carriers	None	Unspecified / other	Mvmt. Restriction	Vaccination	Culling	Metrics for impact	Host	Disease
Ward et al., 2007	X			X	US	local interaction		X	1		X					1	4,5	0
Ward et al., 2009a				X	US	local interaction		X	1		X					1	4,5	0
Woolhouse et al., 1996	X				Saudi Arabia	n/a	X		1					X		1	5	1
Woolhouse et al., 1997	X				Saudi Arabia	n/a	X		1					X		1	5	1
Xiang and Neal, 2014		X			UK	kernel (9)		X					X*		X*	1	1	1

Table S3. Citations for Interspread, AusSpread, and NAADSM model use.

Location and dates of FMD outbreak	Model	Citation
Australia, Simulated outbreak	AusSpread	Garner & Becket, 2005 Roche et al., 2014 East et al., 2014 Ward et al., 2015
Canada, Simulated outbreak	Interspread Plus	Sanson et al., 2014
Denmark, Simulated outbreak	Interspread Plus	Halasa et al., 2014 (March)
Netherlands, 2001 outbreak	InterSpread	Velthuis & Mourits, 2007
Netherlands, Simulated outbreak	Interspread	Ge et al., 2010
New Zealand, Simulated outbreak	Interspread	Sanson et al., 1993 Owen 2011
Republic of Ireland, Simulated outbreak	AusSpread InterSpread NAADSM	Sanson et al., 2011 Sanson et al., 2011 Sanson et al., 2011
Republic of Korea, 2002 outbreak	Interspread	Yoon et al., 2006
Spain, Simulated outbreak	InterSpread	Martinez-Lopez et al., 2010
UK, 2001 outbreak	InterSpread	Morris et al., 2001
USA, Simulated outbreak	AusSpread AusSpread NAADSM	Ward et al., 2009 Hagerman al., 2013 McReynolds et al., 2014
Hypothetical location, Simulated outbreak	AusSpread InterSpread NAADSM NAADSM	Dube et al., 2007 Dube et al., 2007 Dube et al., 2007 Harvey et al., 2007

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