



Supporting Online Material for

Epidemic Dynamics at the Human-Animal Interface

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METHODS

Pathogens to be reviewed

We aimed to survey dynamical studies of all significant zoonotic microparasites. To establish a master list of pathogens in our review, we began by merging three comprehensive lists from academic and governmental sources:

- All pathogens designated as zoonotic in the pathogen list from Jones et al. (*S1*), “Global trends in emerging infectious diseases”.
- All pathogens from Wolfe et al. (*S2*), “Origins of major human infectious diseases”
- All pathogens from the US NIAID Category A,B,C Priority Pathogens (*S3*).

This set of 193 pathogens was then restricted to include only zoonoses that satisfy the following criteria:

1. Pathogen is transmitted from vertebrate animals to humans (as opposed to pathogens shared by animals and humans because of common exposure to an environmental source).
2. Pathogen is a microparasite, i.e. a virus, bacterium, protozoan, or prion.
3. Pathogen is an obligate parasite (i.e. no environmental bacteria and fungi that also happen to cause infections).
4. Transmission from animal reservoirs to humans is thought to play an important epidemiological role for the pathogen. This includes pathogens that cannot be maintained in human populations, and those for which zoonotic transmission adds significantly to human transmission in some settings (e.g. yellow fever virus or dengue virus serotype 2, for which sylvatic transmission initiates epidemics in some regions). Pathogens for which humans are a definitive host, with animals as spillover hosts, are excluded.
5. Pathogen strains that are distinct from others in the database only in their drug-resistance profile are excluded.

The Pan American Health Organization volumes on “Zoonoses and Communicable Diseases Common to Man and Animals” (*S4*) were used as the primary reference to judge these criteria, with additional information derived from pathogen-specific review articles.

Pathogens were grouped at the species level, except where there were compelling reasons to use finer systematic resolution:

- We distinguished *Trypanosoma brucei rhodesiense* from *T. brucei gambiense* (the agents of East African and West African sleeping sickness, respectively). These pathogens exhibit markedly different epidemiology, and appear separately in the list of Wolfe et al. (S2). Humans are considered the definitive host for *T. b. gambiense*, and on this basis, papers focusing specifically on this subspecies were excluded.
- We divided *E. coli* into two groups, O157:H7 and all other strains. This division reflects the intensive research effort devoted to O157:H7.

In the course of the survey, the pathogen list was revised slightly for the following reasons:

- Addition of important zoonoses that were not found on other lists (e.g. HIV-2 (origins only), St. Louis encephalitis virus, Louping ill virus).
- Addition of other species from genera that were included in the review (e.g. *Leishmania braziliensis*, *L. mexicana*).
- Changes to taxonomic organization, reflecting recent systematic revisions, or sometimes to add a ‘generic’ category for modeling studies that named particular diseases without specifying the exact species they were addressing (e.g. models of “leishmaniasis”).

This process yielded a master list of 85 zoonotic pathogens (Table S2). Each pathogen was classified according to the following categories:

- Pathogen class: virus, bacteria, protozoa, or prion.
- Zoonotic stage: II, III or IV. Pathogens that can cause human-to-human transmission only under extraordinary circumstances (e.g. organ transplants or blood transfusions) were classified as stage II. To classify a pathogen as stage III, we required evidence of transmission chains with more than one generation of transmission. Note: HIV-1 and HIV-2 were classified as stage V, but only studies addressing their zoonotic origins were eligible for our review.
- Dominant transmission mode: direct contact, vector-borne (via mosquitoes, flies, ticks, fleas, or bugs), or food-borne.

The breakdown of included pathogen species across these categories is shown in Table S1.

Literature survey

Overall scientific effort

As a simple measure of perceived importance and background knowledge for each zoonotic pathogen, we counted the total number of scientific publications in the ISI Web of Science (<http://apps.isiknowledge.com>) that name the pathogen in their title. To ensure that we found publications describing the public health and sociological aspects of the pathogen as well as the biomedical aspects, we searched using all known scientific and common names for both the agent and the diseases or syndromes it causes in humans or animals. We used the Pan American Health Organization volumes (*S4*), Google searches, and Wikipedia to detect those pathogens whose names or classifications may have changed over time; if these changes were confirmed by the primary scientific literature then all variants were included in the same search. These searches were conducted at the species level, and contributions from species that have been modeled were added together to get the genus-level values used in Figure S1C.

Modeling effort

We aimed to find all published articles that included population dynamical models of the 85 zoonotic pathogens on our master list. To achieve this goal, we conducted two rounds of searches on Web of Science using standardized search terms. We augmented these results by tracing citations in modeling studies that were found via our standardized searches, and by expert knowledge (among the authors, colleagues at their institutions, and audience members at workshop presentations of the preliminary results) of studies that had been excluded. We further augmented the results by searching the online archives of *PLoS ONE* for all pathogen name variants; we did this because *PLoS ONE* is not indexed in Web of Science, but our citation-tracing and expert knowledge led us to realize that a significant number of zoonotic dynamics studies had been published there.

These searches were conducted in September 2008, and studies published since that time were not included in our review.

Standardized search terms

Round 1: Searches were conducted using Web of Science, using all available years (1900-2008) and all databases. As above, we included all scientific and common names for both the pathogen and the diseases or syndromes it causes. Note that for non-vectorized pathogens, we required that the pathogen be named in the article title to consider it to be a paper focusing on a given pathogen. For vectorized pathogens, we also considered articles that name the vector (to the genus level) in the title and name the pathogen in the abstract. To select dynamical models from the broader literature on each pathogen, we extended the search terms to include a set of model-related terms and a set of terms related to epidemiological dynamics.

This search strategy was refined via successive iterations using different search terms on a representative sub-set of pathogens for which the authors had some familiarity with the literature. The final set of terms was optimized with greatest emphasis on complete coverage of modeling studies, and secondary emphasis on reducing ‘false-positive’ search results. The standardized search terms were as follows:

For non-vectorized pathogens:

TI=(\langle all variants of pathogen name \rangle) AND TS=(model* OR dynamic* OR simulat*) AND TS = (mathematic* OR stochastic* OR determinis* OR compartmental OR transmission OR reproducti* OR R0 OR reservoir OR estimat* OR sensitivit* OR epidemi* OR endemi* OR epizooti* OR enzooti* OR spillover OR cross-species OR zoono* OR sylv*)

For vectorized pathogens:

TI=(\langle all variants of pathogen name \rangle OR \langle all variants of vector name \rangle) AND TS=(\langle all variants of pathogen name \rangle) AND TS=(model* OR dynamic* OR simulat*) AND TS = (mathematic* OR stochastic* OR determinis* OR compartmental OR transmission OR reproducti* OR R0 OR reservoir OR estimat* OR sensitivit* OR epidemi* OR endemi* OR epizooti* OR enzooti* OR spillover OR cross-species OR zoono* OR sylv*)

Examples of name variants:

e.g. SARS: TI=(SARS* OR "severe acute respiratory syndrome")

Lyme: TI=(Lyme OR Lyme's OR Borrelia OR Ixodes OR Amblyomma OR Dermacentor OR "deer tick*" OR "Lone star tick*" OR "black-legged tick*")
AND TS = (Lyme OR Lyme's OR Borrelia)

Marburg hemorrhagic fever: TI=(Marburg hemor* OR Marburg virus OR marburgvirus OR green monkey disease)

Round 2: Because older entries in Web of Science often do not have abstracts, we employed a less stringent second round of searches to find older papers. In particular, we searched with the following search string for dates up to 1995:

TI=(\langle all variants of pathogen name \rangle) AND TI=(model* OR dynamic* OR simulat* OR transmission)

Refining the search results

These searches returned huge numbers of publication records. By reviewing their titles, abstracts, and full text when necessary, these results were refined to our final list of 445 studies of the population dynamics of zoonotic infections. Studies matching the following descriptions were **included** in our review:

- Population dynamical models of zoonotic infections, i.e. those which represent the population(s) using state variables related to disease status (S,I,R, etc), and track temporal changes or calculate epidemiological parameters.
- Models that were chiefly statistical in intent, but were founded on mechanistic principles incorporating transmission. If the derivation of the statistical model included the notion of an infectious individual and a susceptible individual and transmission of infection between them, then the study was included (Se.g. 5).
- Review articles were included only if they presented new models satisfying the above descriptions (in which case only the new material was included in our review).
- Models of zoonoses that are capable of endemic human circulation were included only if they focused on zoonotic aspects of the dynamics. For influenza A, we focused only on the dynamics within animal populations (e.g. avian and swine) and outbreaks initiated by animal-to-human transmission (i.e. pandemics); for yellow fever and dengue-2 we

focused only on outbreaks initiated by sylvatic transmission; for HIV-1 and HIV-2, we restricted our search to models of the zoonotic origins of the pathogen.

Studies matching the following descriptions were **excluded** from our review:

- Statistical models that were not founded on mechanistic principles, e.g. regression, clustering analysis, ARIMA models, etc.
- Statistical models that estimated epidemiological quantities but did not include transmission, e.g. estimators for case mortality or incubation period.

Review of dynamical models

Our literature search returned 445 modeling studies of zoonotic pathogens (Table S3). All of these papers were retrieved and read by at least one member of our team. Each paper was classified according to a range of criteria describing:

- Pathogen species modeled and associated characteristics (Table S2).
- Zoonotic phases included in model.
- Level of detail in depiction of spillover (see caption to Figure S2).
- Use of data to estimate individual-level parameters or to fit model output to population-level outcomes. Note that ‘parameterization’ was scored positive if the paper borrowed data-derived parameters from an earlier study, or even if certain rate parameters were assigned values based on cited sources (e.g. ‘the incubation period for SARS is 3-5 days [reference]’). Similarly, ‘model-fitting’ entailed everything from complex time-series methods to comparing model trajectories to a few point estimates of prevalence. Positive scores for data usage thus encompass a broad range of sophistication and completeness in data use; negative scores indicate no use of data whatsoever at the individual or population scale.
- Topics addressed by modeling analyses. For each of eight broad topics (see Figure S3), studies were scored positive if they presented modeling results that addressed these topics directly; studies that only mentioned the topics in discussion were scored negative

RESULTS

A partial summary of our literature review is given in the main text. For clarity, we expand upon those remarks here, and show the full results and raw data.

Zoonotic dynamics—the broad overview

The study of zoonotic dynamics has escalated rapidly over the last decade, with increasing emphasis on viral pathogens (Fig. S1A). Breaking down the results by pathogen genus, however, shows that effort has been heavily skewed toward a few agents, notably influenza A, SARS-Coronavirus, and rabies virus (genus: *Lyssavirus*) (Fig. S1B). Furthermore, vector-borne and food-borne zoonoses have been neglected relative to those transmitted directly, and protozoan pathogens are under-represented compared to viruses (Fig. S1B). Considering particular pathogen species (Table 1 in main text), we see that many zoonotic diseases of great public health concern have been minimally modeled (e.g. leptospirosis (*Leptospira* spp.), Japanese encephalitis, monkeypox, and yellow fever) or not modeled at all (e.g. tularemia (*Francisella tularensis*), epidemic typhus (*Rickettsia prowazekii*), and sylvatic dengue). Indeed, 40 of the 85 species of zoonosis in our database had never been modeled (25/44 for viruses, 12/28 for bacteria, 3/12 for protozoa, 0/1 for prions).

To derive an objective assessment of the distribution of modeling effort, it is necessary to control for differences in perceived importance of pathogens. Thus, we examined the ratio of the total number of scientific publications to the number of modeling studies (Fig. S1C). Pathogen genera that are clearly under-served relative to their knowledge base include arenaviruses; the bacteria *Bacillus*, *Leptospira*, *Campylobacter*, *Brucella*, and *Salmonella*; and the protozoans *Toxoplasma*, *Trypanosoma*, and *Leishmania*. At the other extreme, with relatively intense modeling activity, are recently-emerged pathogens such as SARS-CoV, transmissible spongiform encephalitis (TSE), and hantaviruses. Rabies and bovine tuberculosis (*Mycobacterium bovis*) also stand out as widely modeled, perhaps due to their status as modeling case studies with great applied importance in some regions. It is noteworthy that the huge modeling literature on pandemic influenza is not disproportionate to the broader research focus on this pathogen.

We next sought to characterize *how* zoonotic pathogens have been modeled, with particular reference to their multi-host ecology. Models of directly-transmitted zoonoses have focused almost universally on a single phase of the zoonotic process (Fig. S2A). For stage II and III zoonoses this focus has predominantly been on dynamics in the reservoir, while for stage IV the focus has almost entirely been on human outbreaks (Fig. S2B). We identified a glaring deficit in modeling of the spillover process: only 6% (17/282) of models of directly-transmitted zoonoses had any representation of cross-species transmission. Because of the central importance of this process to zoonotic dynamics, we probed further by distinguishing different degrees of mechanism incorporated in the models (Fig. S2C). Only 6 of 17 models treated the spillover process explicitly, which we defined as modeling infection in the reservoir and human populations with a transmission term connecting them. The remainder included only an implicit representation of spillover, by including primary infections in humans but not considering their animal source. Thus a mere 2% (6/282) of dynamical studies of directly-transmitted zoonoses actually incorporated a mechanistic model of spillover transmission, while the vast majority dealt with one host species at a time.

For vector- and food-borne zoonoses, modeling studies were less numerous but also less skewed in their focus. Models of vector-borne zoonoses were more likely to integrate several zoonotic phases (Fig. S2A). Roughly 34% (30/88) of these models addressed spillover transmission, of which a clear majority represented spillover explicitly (Fig. S2B,C). Strikingly few studies addressed the dynamics of human outbreaks for vector-borne zoonoses—a particularly surprising finding given that the majority (9/15) of the stage IV pathogens in our database are vector-borne. Models of food-borne zoonoses showed similar patterns to vector-borne disease models overall, with more studies integrating several phases and almost 40% (27/72) of models incorporating spillover transmission (Fig. S2A,B). The representation of spillover was more mechanistic, with roughly one third of spillover models addressing pathogen dynamics in carcasses during food processing and the resulting risk to humans (a pathway we termed food-borne spillover) and another third explicitly representing reservoir and human populations (Fig. S2C).

For all three transmission modes, we identified a further gap in modeling the dynamics of inefficient stuttering chains of transmission—even among stage III pathogens for which this

process is most relevant (Fig. S2B). Stuttering transmission was modeled in just 3.6% (16/442) of all studies in our data base, and just 8% (10/125) of models of stage III zoonoses. In contrast to spillover dynamics, stuttering chains have received greater attention for directly-transmitted zoonoses.

Patterns by pathogen

The aggregate view is informative, but masks important differences among pathogens that can be unduly influential when modeling effort is extremely skewed towards a small number of pathogen species. To gain insight into the idiosyncrasies of research into particular pathogens, we undertook detailed case studies of the six most-modeled genera of zoonoses (Fig. S3). We characterized the dynamical scope of the studies, the use of data to estimate parameter values and fit model output, and the broad topics and goals addressed by each study.

Consistent with trends in the aggregate data, the most frequently modeled pathogens show a near-absolute focus on a single zoonotic phase (Fig. S3A); examples include SARS, rabies, and *Mycobacterium bovis*. Models of influenza have encompassed more phases (owing to active concern about circulation in poultry flocks as well as potential pandemic strains) but most studies (94%) have focused on a single phase of transmission. Work on bovine spongiform encephalopathy (BSE) has been notably diverse in focus, encompassing both reservoir dynamics and intensive efforts to understand spillover and possible secondary transmission in the wake of that pathogen's discovery. Studies of flaviviruses, despite including models of seven different species, are still dominated by work on reservoir dynamics, with a proportion also treating spillover. Consideration of the less widely modeled zoonoses reinforces the pattern identified for flaviviruses and BSE: models of vector-borne and food-borne zoonoses are generally more diverse in scope and more likely to encompass spillover transmission. The dominant pattern overall, though, is that dynamical studies of most pathogens have tended to be relatively restricted in scope. Expanding on this work to develop more integrative models is an essential priority for advancing our ability to understand and control zoonoses.

Patterns in data use (Fig. S3B) and scientific questions addressed by studies of zoonotic dynamics (Fig. S3C) are described fully in the main text.

Dynamics of response by the modeling community

For six zoonotic pathogens that either were discovered or made significant range shifts in recent decades, we constructed temporal profiles of the scientific literature to characterize the dynamics of the modeling community's response (Fig. S4). As noted in the main text, the response for SARS was almost immediate, with numerous modeling studies published within a few months of discovering the pathogen (S6-S9). A more complex story emerges for influenza, for which research has been maintained at a high level throughout the past century, with a small fraction of studies focusing on 'pandemic' or avian influenza. Research activity on pandemic and avian influenza rose following the emergence of the H5N1 subtype in Hong Kong in 1997, and increased dramatically following its re-emergence in 2003. Modeling effort on pandemic influenza followed suit with a few years' delay, rapidly becoming the largest literature for any zoonotic pathogen (Fig. S1B). We note with interest the first stirrings of a modeling epidemic focusing on the current H1N1 influenza threat (S10, S11); based on considerations outlined in the main text we predict a swift and robust surge in modeling activity.

Dynamical studies of avian influenza have arisen much more slowly than those of pandemic influenza, perhaps because of the complex and previously under-studied ecology of the virus in wild and domestic bird populations (S12). Other complex or under-studied pathogens have shown similar lags, including *Borrelia burgdorferi* with its multi-host sylvatic cycle and BSE with its status as a newly-discovered prion infection. Chikungunya virus echoes the pattern shown for West Nile virus in the main text, where scientific interest is relatively low while the infection is circulating only in endemic, developing world settings, then picks up dramatically when the pathogen invades the US or Europe. In both instances, modeling activity rises within a few years of the broader increase in research.

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FIGURE CAPTIONS

Figure S1. Summary of literature on zoonotic modeling. (A) Increasing trend in published studies of zoonotic dynamics over time, with colors indicating the class of pathogen. (B) Number of modeling studies found for each genus, taxonomic group, or transmission mode, using the same color scheme. Symbols indicate the dominant mode of transmission for the genus: direct contact (handshake), vector-borne (insect), or food-borne (meats). Numbers (X/Y) indicate the number of pathogen species in each category, where X is the number for which we found population dynamic models, and Y the total number of species in our list of significant zoonoses. (C) The ratio of the total scientific literature to the modeling literature for each category. The total publications were tabulated by pathogen species, and only species that have been modeled were included in the genus totals used here. See Supplementary Information for details on methods.

Figure S2. Scope of models for zoonotic infections, organized by dominant mode of transmission. (A) Number of zoonotic phases (reservoir dynamics, spillover, stuttering chains, or outbreaks in human population) included in models. (B) Zoonotic phases included in models for pathogens in stage II, III or IV. Note that not all phases are biologically relevant for all pathogens (e.g. stage II pathogens do not exhibit outbreak dynamics), but in some cases these were included in models due to speculative or incorrect assumptions and have been tabulated accordingly. (C) Approach to modeling spillover transmission: explicit spillover is a model incorporating both reservoir and human populations with transmission between them; implicit spillover is a model where primary (zoonotic) cases appear in humans but there is no mechanism depicted; food-borne spillover is a model that considers the pathogen abundance during food processing and the resulting risk to humans. Note that entries in pie-charts are mutually exclusive, but those in the bar-plots are not (i.e. a model including reservoir dynamics and spillover transmission is counted in both bars).

Figure S3. Analysis of the six most-modeled genera of zoonoses (with corresponding pathogen species shown in parentheses; note that 5 of 6 genera are represented by only one species) and all other modeled pathogens by mode of transmission. (A) Distribution of zoonotic phases

incorporated in models of each pathogen genus (R = reservoir dynamics, Sp = spillover transmission, St = stuttering transmission among humans, O = outbreaks among humans). (B) Use of data in zoonotic models. Parameterization refers to the estimation of individual-level parameters such as infectious period or case mortality; model-fitting refers to fitting model output to population-level data on incidence, prevalence or similar measures. (C) Topics addressed by analyses of zoonotic dynamics. Again, entries in pie-charts are mutually exclusive, but those in the bar-plots are not.

Figure S4. Temporal profiles of total research effort and modeling effort for recently-emerged zoonoses. Figure panels have different y-axis scaling, but in each instance the scaling for number of modeling studies (right axis) is 10-fold smaller than that for the total number of research papers (left axis). Traces for influenza show several subsets of research and modeling effort, indicated by different colors. Most profiles are truncated in 2007 to avoid a partial-year effect, but Chikungunya virus was extended to 2008 so that recent modeling effort (in response to the virus's recent expansion) would be visible. Note that the panels for SARS, BSE and West Nile virus appear in Figure 3 of the main text, but are repeated here for ease of comparison.

FIG S1

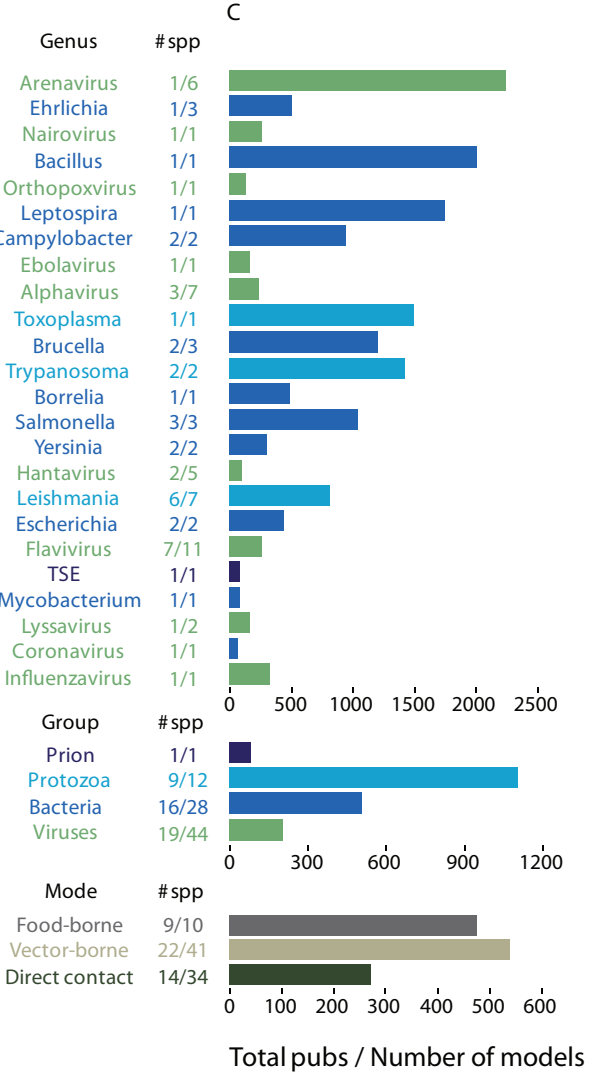
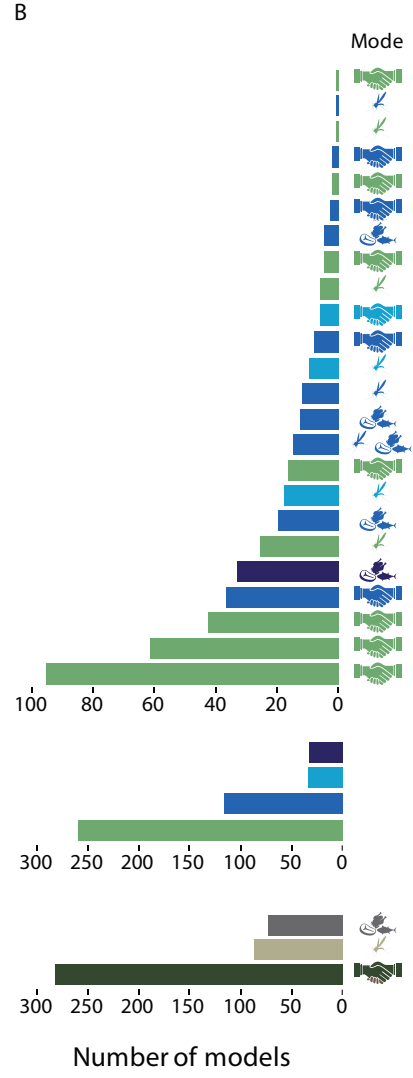
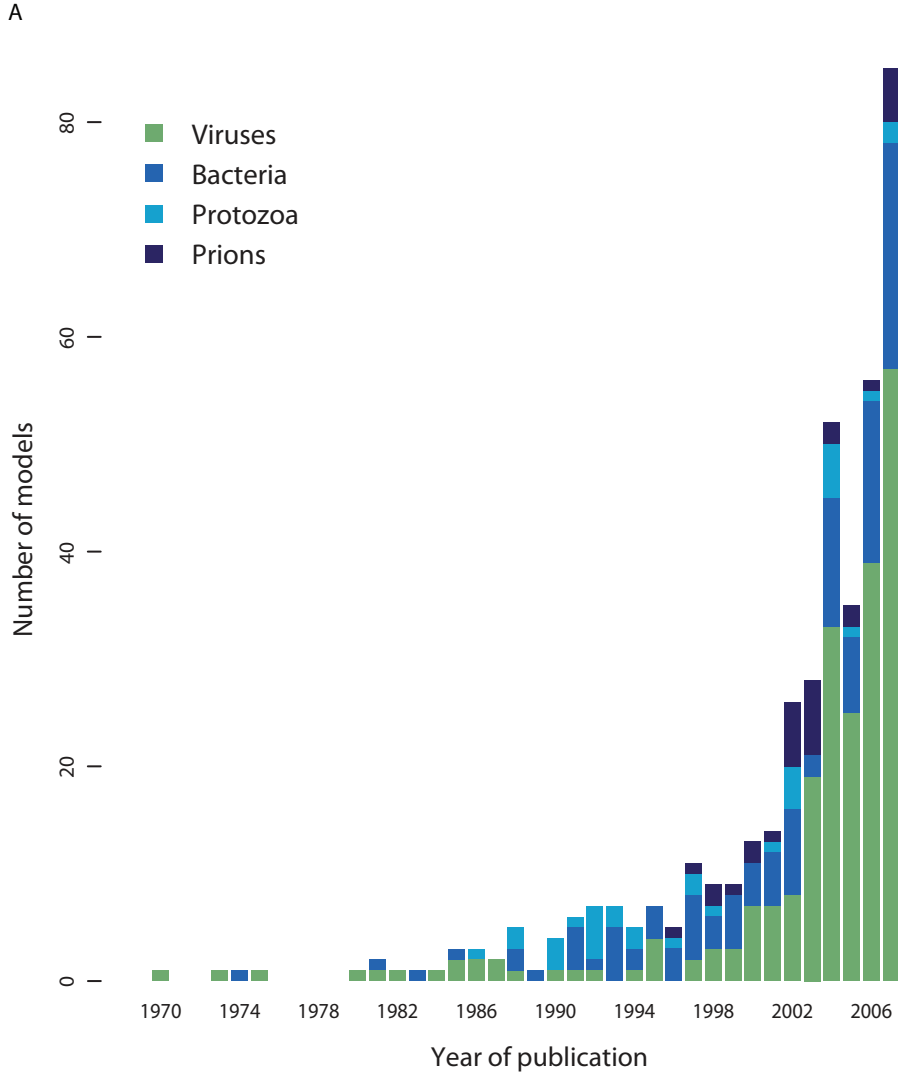


FIG S2

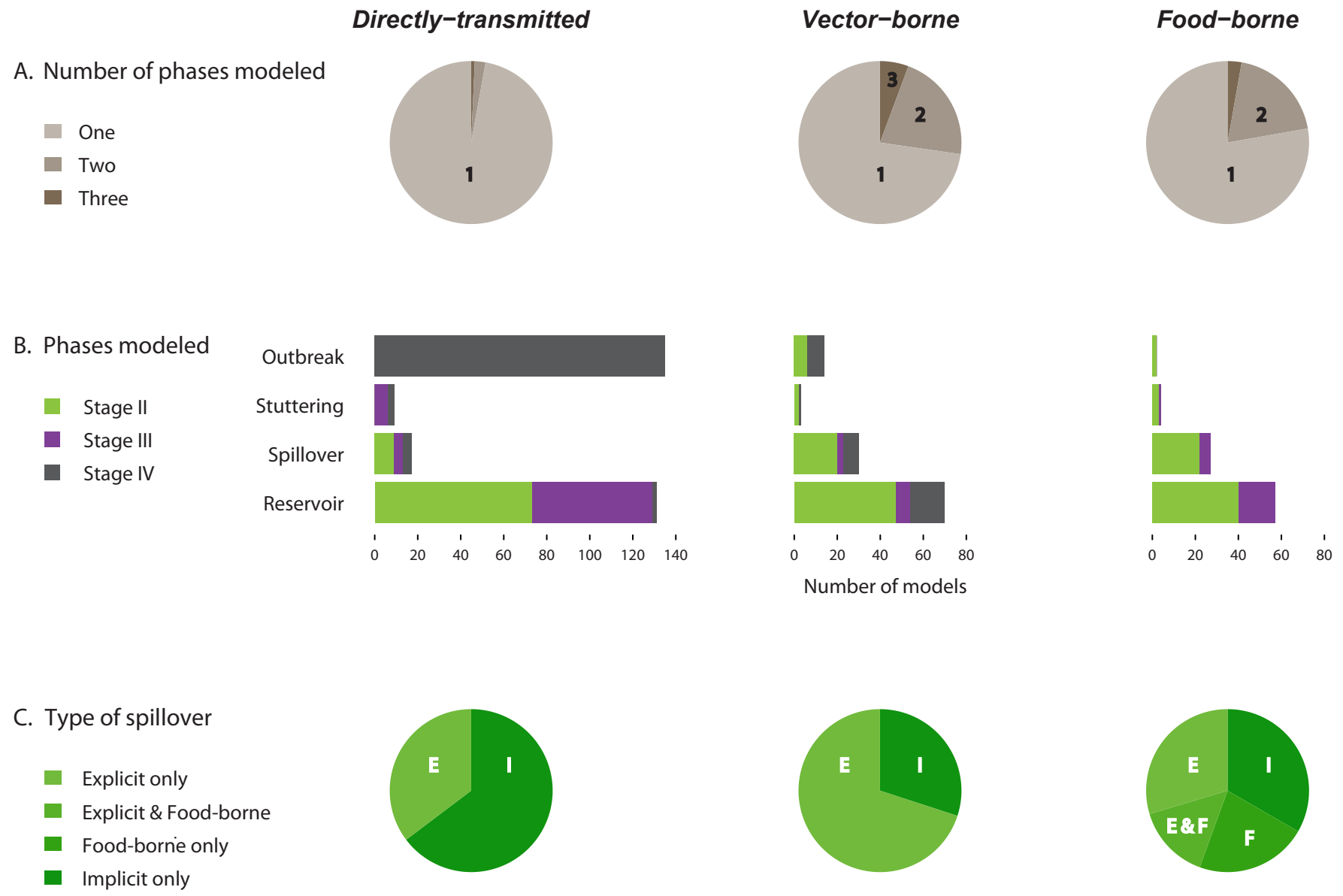
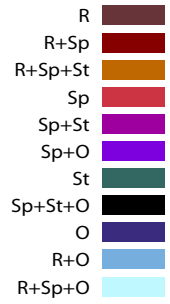
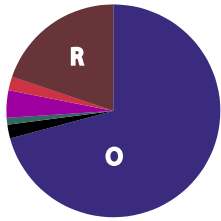


FIG S3

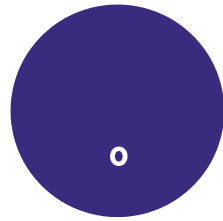
A. Scope



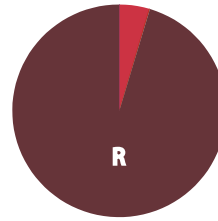
Influenzavirus
(influenza A)



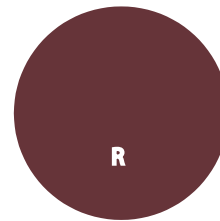
Coronavirus
(SARS-CoV)



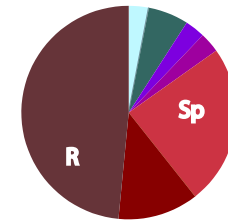
Lyssavirus
(rabies)



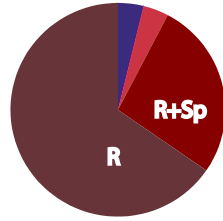
Mycobacterium
(bovine TB)



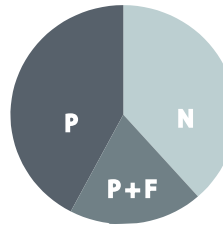
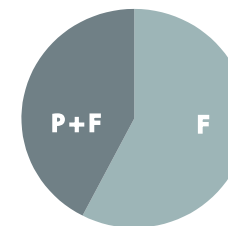
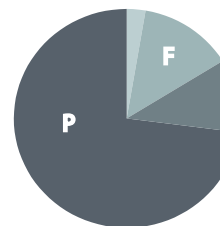
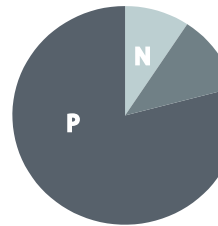
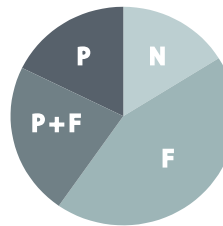
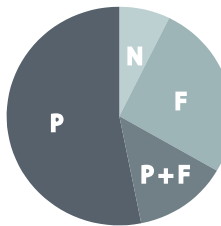
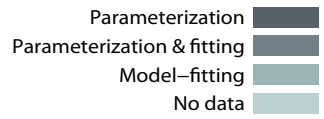
TSE
(BSE/vCJD)



Flavivirus
(7 species)

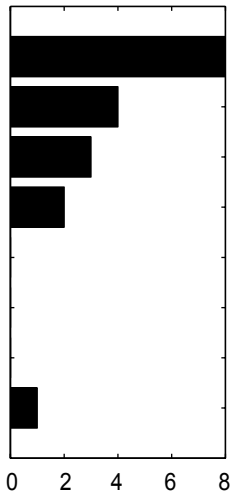
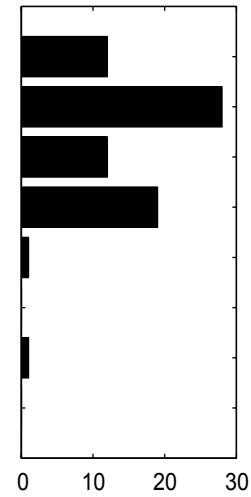
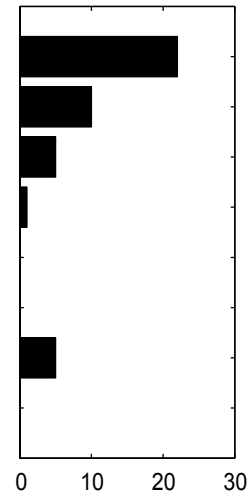
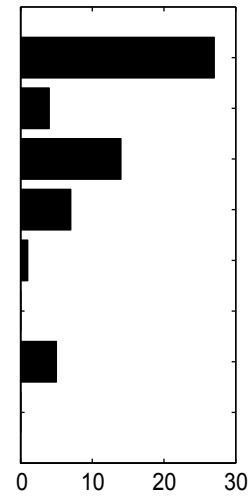
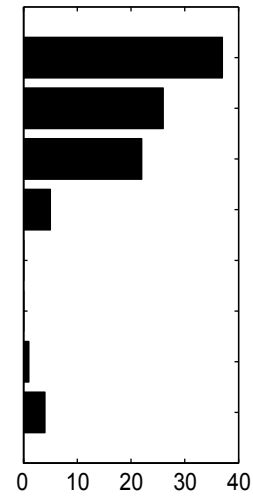
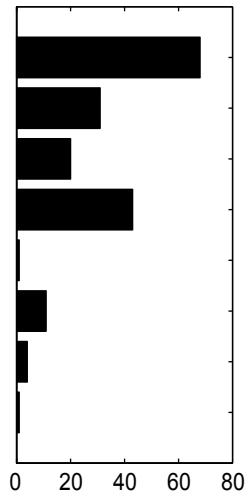


B. Use of data



C. Topics addressed

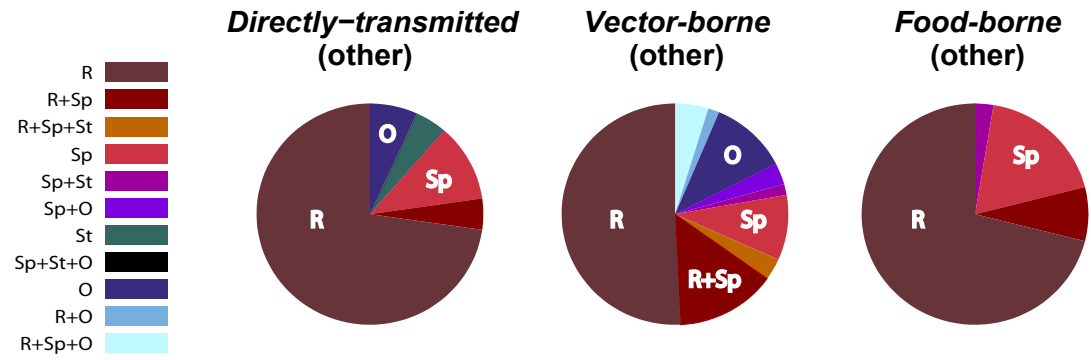
Study control measures
Parameter estimation
Explain patterns in data
Prediction of future trends
Within-host dynamics
Pathogen evolution
Economic aspects
Pathogen interactions



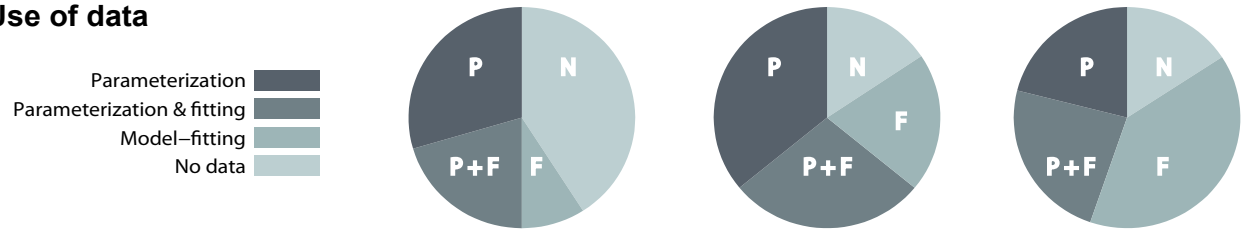
Number of models

FIG S3 (cont.)

A. Scope



B. Use of data



C. Topics addressed

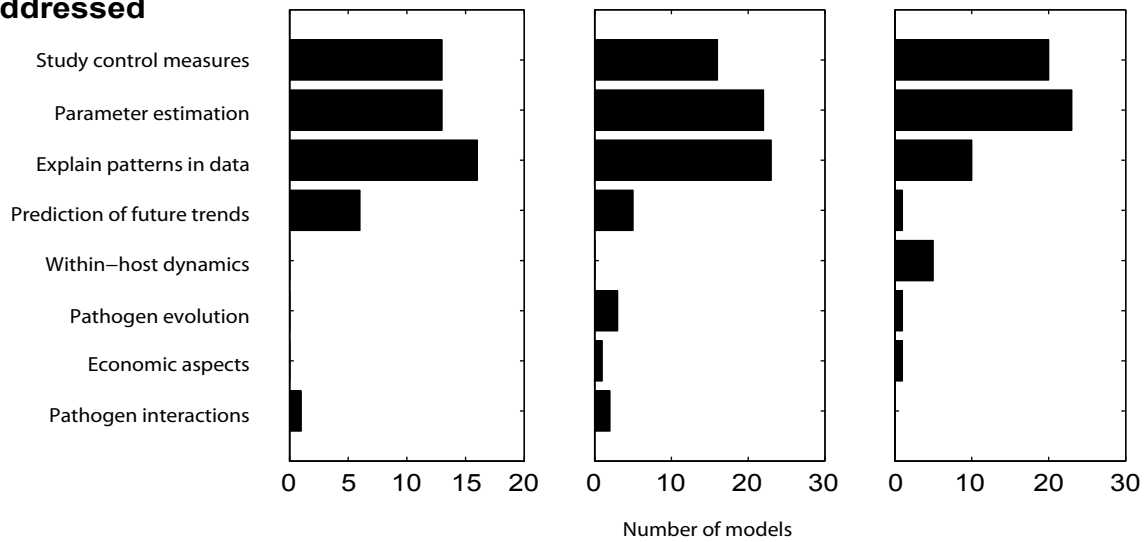
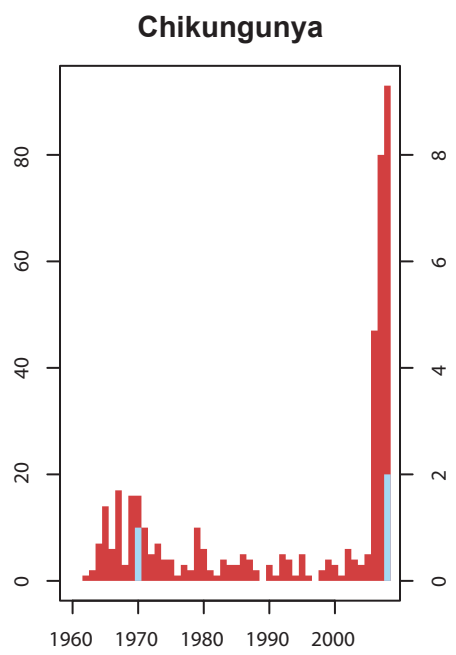
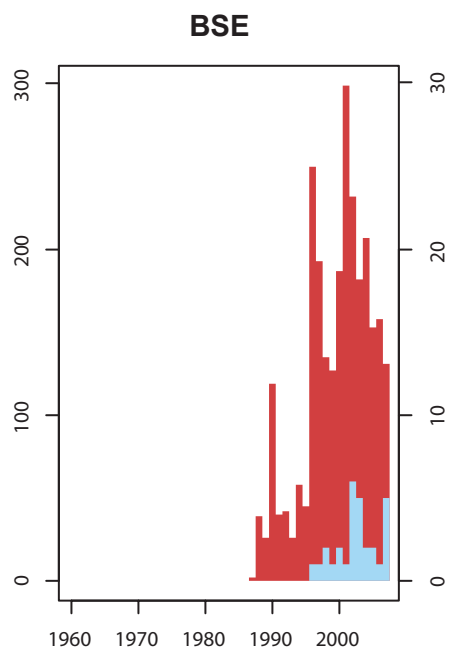
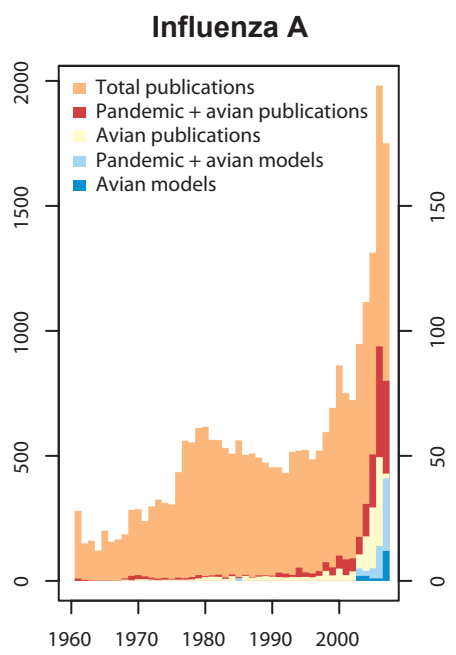
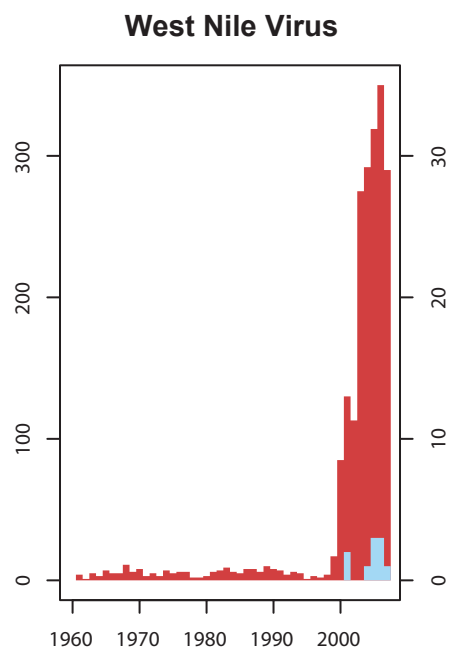
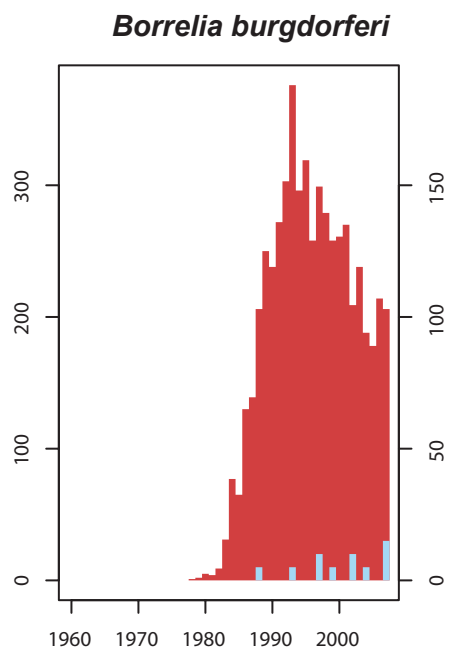
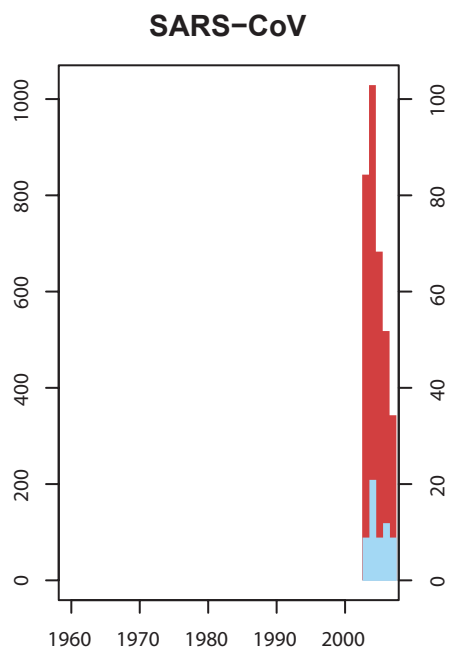


FIG S4

Number of research papers



Number of modeling papers

TABLE CAPTIONS

Table S1. Distribution of pathogen species included in review, by pathogen stage, transmission mode and taxonomy. Note that two species included in the review are not included in these totals (HIV-1 and HIV-2, which are stage V pathogens but only their zoonotic origins were included in our review).

Table S2. List of pathogen species included in review.

Table S3. List of dynamic modeling studies included in review.

Table S1. Distribution of pathogen species included in review.

Pathogen stage	<u>Number of pathogen species</u>			<u>Number of pathogen species</u>			
	Direct transmission	Vector-borne transmission	Food-borne transmission	Viruses	Bacteria	Protozoa	Prions
II (spillover only)	22	28	6	25	23	8	0
III (spillover + stuttering chains)	6	4	4	7	4	2	1
IV (spillover + possible outbreaks)	4	9	0	10	1	2	0

Table S2. Pathogen species included in review

Pathogen genus	Pathogen species	Pathogen class (1=virus, 2=bacteria, 3=protozoan, 4=prion)	Pathogen stage (2=spillover, 3=stuttering chains, 4=outbreaks)	Transmission mode (0=direct contact, 1=vector-borne, 2=food-borne)
<i>Alphavirus</i>	<i>Barmah forest virus</i>	1	4	1
<i>Alphavirus</i>	<i>Chikungunya</i>	1	4	1
<i>Alphavirus</i>	<i>Eastern equine encephalitis virus</i>	1	2	1
<i>Alphavirus</i>	<i>Mayaro virus</i>	1	4	1
<i>Alphavirus</i>	<i>Ross River virus</i>	1	4	1
<i>Alphavirus</i>	<i>Venezuelan Equine Encephalitis virus</i>	1	2	1
<i>Alphavirus</i>	<i>Western equine encephalitis virus</i>	1	2	1
<i>Anaplasma</i>	<i>Anaplasma phagocytophilum</i>	2	2	1
<i>Arenavirus</i>	<i>Guanarito</i>	1	2	0
<i>Arenavirus</i>	<i>Junin virus</i>	1	2	0
<i>Arenavirus</i>	<i>Lassa virus</i>	1	3	0
<i>Arenavirus</i>	<i>Lymphocytic choriomeningitis virus</i>	1	2	0
<i>Arenavirus</i>	<i>Machupo virus</i>	1	3	0
<i>Arenavirus</i>	<i>Sabia virus</i>	1	2	0
<i>Babesia</i>	<i>Babesia microti</i>	3	2	1
<i>Bacillus</i>	<i>Bacillus anthracis</i>	2	2	0
<i>Bartonella</i>	<i>Bartonella henselae</i>	2	2	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	2	2	1
<i>Brucella</i>	<i>Brucella abortus</i>	2	2	0
<i>Brucella</i>	<i>Brucella melitensis</i>	2	2	0
<i>Brucella</i>	<i>Brucella suis</i>	2	2	0
<i>Campylobacter</i>	<i>Campylobacter fetus</i>	2	2	2
<i>Campylobacter</i>	<i>Campylobacter jejuni</i>	2	2	2
<i>Chlamydia</i>	<i>Chlamydia psittaci</i>	2	2	0
<i>Coronavirus</i>	SARS	1	4	0
<i>Coxiella</i>	<i>Coxiella burnetii</i>	3	2	0
<i>Ebolavirus</i>	<i>Ebola virus</i>	1	4	0
<i>Ehrlichia</i>	<i>Ehrlichia canis</i>	2	2	1
<i>Ehrlichia</i>	<i>Ehrlichia chaffeensis</i>	2	2	1
<i>Ehrlichia</i>	<i>Ehrlichia ewingii</i>	2	2	1
<i>Escherichia</i>	<i>E. coli (non O157:H7)</i>	2	3	2
<i>Escherichia</i>	<i>E. coli (O157:H7)</i>	2	3	2

Pathogen genus	Pathogen species	Pathogen class (1=virus, 2=bacteria, 3=protozoan, 4=prion)	Pathogen stage (2=spillover, 3=stuttering chains, 4=outbreaks)	Transmission mode (0=direct contact, 1=vector-borne, 2=food-borne)
<i>Flavivirus</i>	<i>Japanese encephalitis virus</i>	1	2	1
<i>Flavivirus</i>	<i>Kyasanur forest disease virus</i>	1	2	1
<i>Flavivirus</i>	<i>Louping ill virus</i>	1	2	1
<i>Flavivirus</i>	<i>Murray Valley encephalitis virus</i>	1	2	1
<i>Flavivirus</i>	<i>Omsk virus</i>	1	2	1
<i>Flavivirus</i>	<i>St. Louis encephalitis virus</i>	1	2	1
<i>Flavivirus</i>	<i>Sylvatic dengue virus</i>	1	4	1
<i>Flavivirus</i>	<i>Tick Borne Encephalitis virus</i>	1	2	1
<i>Flavivirus</i>	<i>West Nile Virus</i>	1	2	1
<i>Flavivirus</i>	<i>Yellow fever virus</i>	1	4	1
<i>Flavivirus</i>	<i>Zika virus</i>	1	3	1
<i>Francisella</i>	<i>Francisella tularensis</i>	2	2	1
<i>Hantavirus</i>	<i>Andes virus</i>	1	3	0
<i>Hantavirus</i>	<i>Hantaan</i>	1	2	0
<i>Hantavirus</i>	<i>Puumala virus</i>	1	2	0
<i>Hantavirus</i>	<i>Seoul virus</i>	1	2	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	1	2	0
<i>Henipavirus</i>	<i>Hendra virus</i>	1	2	0
<i>Henipavirus</i>	<i>Nipah virus</i>	1	3	0
<i>Influenzavirus A</i>	<i>Influenza A (avian influenza,</i>	1	3	0
<i>Influenzavirus A</i>	<i>Influenza A (pandemic flu,</i>	1	4	0
<i>Influenzavirus A</i>	<i>Influenza A (past pandemics,</i>	1	4	0
<i>Influenzavirus A</i>	<i>Influenza A (swine flu)</i>	1	4	0
<i>Leishmania</i>	<i>Leishmania braziliensis</i>	3	2	1
<i>Leishmania</i>	<i>Leishmania chagasi</i>	3	3	1
<i>Leishmania</i>	<i>Leishmania donovani</i>	3	4	1
<i>Leishmania</i>	<i>Leishmania infantum</i>	3	3	1
<i>Leishmania</i>	<i>Leishmania major</i>	3	2	1
<i>Leishmania</i>	<i>Leishmania mexicana</i>	3	2	1
<i>Leishmania</i>	<i>Leishmania peruviana</i>	3	2	1
<i>Lentivirus</i>	<i>Human Immunodeficiency Virus 1 (origins only,</i>	1	5	0
<i>Lentivirus</i>	<i>Human Immunodeficiency Virus 2 (origins only,</i>	1	5	0
<i>Leptospira</i>	<i>Leptospira interrogans (sensu lato)</i>	2	2	0
<i>Lyssavirus</i>	<i>Australian bat lyssavirus</i>	1	2	0
<i>Lyssavirus</i>	<i>Rabies virus</i>	1	2	0

Pathogen genus	Pathogen species	Pathogen class (1=virus, 2=bacteria, 3=protozoan, 4=prion)	Pathogen stage (2=spillover, 3=stuttering chains, 4=outbreaks)	Transmission mode (0=direct contact, 1=vector-borne, 2=food-borne)
<i>Marburgvirus</i>	<i>Lake Victoria marburgvirus</i>	1	4	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	2	3	0
<i>Nairovirus</i>	<i>Crimean-Congo Hemorrhagic Fever</i>	1	3	1
<i>Neisseria</i>	<i>Neisseria weaveri</i>	2	2	0
<i>Orientia</i>	<i>Orientia tsutsugamushi</i>	2	2	1
<i>Orthobunyavirus</i>	<i>California encephalitis virus</i>	1	2	1
<i>Orthopoxvirus</i>	<i>Monkeypox</i>	1	3	0
<i>Phlebovirus</i>	<i>Rift Valley fever virus</i>	1	2	1
<i>Rickettsia</i>	<i>Rickettsia prowazekii</i>	2	2	2
<i>Rickettsia</i>	<i>Rickettsia typhi</i>	2	2	1
<i>Salmonella</i>	<i>Salmonella dublin</i>	2	2	2
<i>Salmonella</i>	<i>Salmonella enteritidis</i>	2	2	2
<i>Salmonella</i>	<i>Salmonella spp.</i>	2	2	2
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	2	2	2
<i>Streptococcus</i>	<i>Streptococcus suis</i>	2	2	0
<i>Toxoplasma</i>	<i>Toxoplasma gondii</i>	3	2	0
<i>Transmissible Spongiform Encephalitides</i>	<i>Bovine spongiform encephalitis</i>	4	2	2
<i>Trypanosoma</i>	<i>Trypanosoma brucei rhodesiense</i>	3	2	1
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	3	2	1
<i>unclassified Paramyxoviridae</i>	<i>Menangle virus</i>	1	2	0
<i>Yersinia</i>	<i>Yersinia enterocolitica (O:3, O:5, O:9)</i>	2	3	2
<i>Yersinia</i>	<i>Yersinia pestis</i>	2	4	1

Table S3. Dynamic modeling studies included in review

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
<i>Alphavirus</i>	<i>Chikungunya</i>	DeMoor & Steffens (1970)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Alphavirus</i>	<i>Chikungunya</i>	Dumont et al (2008)	0	0	1	0	0	1	1	1	0	0	0	0	0	0	1	1
<i>Alphavirus</i>	<i>Chikungunya</i>	Massad et al (2008)	0	0	1	0	0	1	1	0	0	0	0	0	0	1	1	1
<i>Alphavirus</i>	<i>Eastern equine encephalitis virus</i>	Unnasch et al (2006)	1	0	0	0	0	0	0	1	0	1	0	0	0	0	1	1
<i>Alphavirus</i>	<i>Ross River fever</i>	Choi et al (2002)	1	1	0	0	1	0	1	0	1	0	0	0	0	0	1	1
<i>Alphavirus</i>	<i>Ross River fever</i>	Glass (2005)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Arenavirus</i>	<i>Junin virus</i>	Porcasi et al (2005)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Bacillus</i>	<i>Bacillus anthracis</i>	Furniss & Hahn (1981)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Bacillus</i>	<i>Bacillus anthracis</i>	Hahn & Furniss (1983)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Ginsberg (1988)	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Ginsberg (1993)	0	0	1	0	0	0	1	0	1	0	0	0	0	0	1	0
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Mount et al (1997a)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Mount et al (1997b)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Porco (1999)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Caraco et al (2002)	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Schauber & Ostfeld (2002)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Ghosh & Pugliese (2004)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Ding (2007)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Ogden et al (2007)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Rosa & Pugliese (2007)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Borrelia</i>	<i>Borrelia burgdorferi</i>	Hartemink et al (2008)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Brucella</i>	<i>Brucella abortus</i>	Almeida & Louza (1988)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
<i>Brucella</i>	<i>Brucella abortus</i>	Peterson et al (1991a)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	1
<i>Brucella</i>	<i>Brucella abortus</i>	Peterson et al (1991b)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
<i>Brucella</i>	<i>Brucella abortus</i>	Gonzalez-Guzman & Naulin (1994)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Brucella</i>	<i>Brucella abortus</i>	Dobson & Meagher (1996)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1
<i>Brucella</i>	<i>Brucella abortus</i>	Cantrell et al (2001)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Brucella</i>	<i>Brucella abortus</i>	England et al (2004)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Brucella</i>	<i>Brucella melitensis</i>	Zinsstag et al (2005)	1	1	0	0	0	0	1	0	1	0	0	0	0	0	0	1
<i>Campylobacter</i>	<i>Campylobacter fetus and jejuni</i>	Hartnett et al (2001)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
<i>Campylobacter</i>	<i>Campylobacter fetus and jejuni</i>	Rosenquist et al (2003)	0	1	0	1	0	0	0	0	1	0	0	0	1	0	1	1
<i>Campylobacter</i>	<i>Campylobacter fetus and jejuni</i>	Van Gerwe et al (2005)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Campylobacter</i>	<i>Campylobacter fetus and jejuni</i>	Conlan et al (2007)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Campylobacter</i>	<i>Campylobacter fetus and jejuni</i>	Nauta et al (2007)	0	1	0	1	0	0	0	0	0	0	0	0	1	0	1	1
<i>Coronavirus</i>	<i>SARS Coronavirus</i>	Choi & Pak (2003)	0	0	0	0	0	1	1	0	0	1	0	0	0	0	1	0
<i>Coronavirus</i>	<i>SARS Coronavirus</i>	Chowell et al (2003)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	1	1
<i>Coronavirus</i>	<i>SARS Coronavirus</i>	Lipsitch et al (2003)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
<i>Coronavirus</i>	<i>SARS Coronavirus</i>	Lloyd-Smith et al (2003)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
<i>Coronavirus</i>	<i>SARS Coronavirus</i>	Ng et al (2003)	0	0	0	0	0	1	0	1	0	1	0	0	0	1	0	1

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
Coronavirus	SARS Coronavirus	Riley et al (2003)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Shi (2003)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Wang et al (2003)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Zhou & Yan (2003)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Chowell et al (2004a)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Ding et al (2004)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Fang et al (2004)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Gumel et al (2004)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Hsieh et al (2004a)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Hsieh et al (2004b)	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Huang et al (2004)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Li et al (2004a)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Li et al (2004b)	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Li et al (2004c)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Masuda et al (2004)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0
Coronavirus	SARS Coronavirus	Nishiura et al (2004)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Coronavirus	SARS Coronavirus	Small et al (2004)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Wallinga & Teunis (2004)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Wang & Ruan (2004)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Webb et al (2004)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Yu et al (2004)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Zhang et al (2004)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Zhou & Yan (2004)	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Zhou et al (2004)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Becker et al (2005)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Coronavirus	SARS Coronavirus	Gjorgjieva et al (2005)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Khan et al (2005)	0	0	0	0	0	1	0	0	1	0	1	0	0	1	0	0
Coronavirus	SARS Coronavirus	Massad et al (2005)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Meyers et al (2005)	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0
Coronavirus	SARS Coronavirus	Nishiura et al (2005)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Coronavirus	SARS Coronavirus	Small & Tse (2005a)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Small & Tse (2005b)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Zhang & Hao (2005)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Coronavirus	SARS Coronavirus	Zhang et al (2005)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Bombardt (2006)	0	0	0	0	0	1	0	1	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Cauchemez et al (2006)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Chen et al (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	1	1	0
Coronavirus	SARS Coronavirus	Drake et al (2006)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Glass & Becker (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Coronavirus	SARS Coronavirus	Gumel et al (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Hsu & Hsieh (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
Coronavirus	SARS Coronavirus	McBryde et al (2006)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	McLeod et al (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Coronavirus	SARS Coronavirus	Ruan et al (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Coronavirus	SARS Coronavirus	Small et al (2006)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Wang et al (2006)	0	0	0	0	0	1	0	1	1	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Colizza et al (2007b)	0	0	0	0	0	1	0	1	0	1	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Fukutome et al (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Coronavirus	SARS Coronavirus	Hsieh et al (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Hsu & Roeger (2007)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
Coronavirus	SARS Coronavirus	Jiang (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Coronavirus	SARS Coronavirus	Kwok et al (2007)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Pitzer et al (2007)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Zeng et al (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	1	1	1
Coronavirus	SARS Coronavirus	Zhang (2007)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	1	1
Coronavirus	SARS Coronavirus	Chen et al (2008)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1
Coronavirus	SARS Coronavirus	Yan & Zou (2008)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Ebolavirus	Ebola virus (Zaire)	Chowell et al (2004b)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	1
Ebolavirus	Ebola virus (Zaire)	Caillaud et al (2006)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1
Ebolavirus	Ebola virus (Zaire)	Lekone and Finkenstadt (2006)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	0	1
Ebolavirus	Ebola virus (Zaire)	Legrand et al (2007)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	1	1
Ebolavirus	Ebola virus (Zaire)	Rizkalla et al (2007)	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Ehrlichia	Ehrlichia chaffeensis	Gaff & Gross (2007)	1	1	0	0	0	0	0	1	1	1	0	0	0	0	1	0
Escherichia	E. coli (non O157:H7)	Davis & Gordon (2002)	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
Escherichia	E. coli (non O157:H7)	Geenen et al (2004)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
Escherichia	E. coli (non O157:H7)	Geenen et al (2005)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Escherichia	E. coli (non O157:H7)	Liu et al (2005)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1
Escherichia	E. coli (non O157:H7)	Dopfer et al (2006)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Escherichia	E. coli (non O157:H7)	Liu et al (2007b)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1
Escherichia	E. coli (O157:H7)	Jordan et al (1999a)	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0
Escherichia	E. coli (O157:H7)	Jordan et al (1999b)	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0
Escherichia	E. coli (O157:H7)	Laegreid & Keen (2004)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Escherichia	E. coli (O157:H7)	Ahmadi et al (2006)	0	0	0	1	0	0	0	0	1	0	0	0	0	0	1	0
Escherichia	E. coli (O157:H7)	Matthews et al (2006a)	1	0	0	0	0	0	1	1	1	0	0	0	0	0	1	1
Escherichia	E. coli (O157:H7)	Matthews et al (2006b)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1
Escherichia	E. coli (O157:H7)	Turner et al (2006)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
Escherichia	E. coli (O157:H7)	Wood et al (2006a)	1	0	0	0	0	0	0	0	1	0	0	0	1	0	1	1
Escherichia	E. coli (O157:H7)	Wood et al (2006b)	1	0	0	0	0	0	0	1	0	0	0	0	1	0	1	1
Escherichia	E. coli (O157:H7)	Ahmadi et al (2007)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Escherichia	E. coli (O157:H7)	Liu et al (2007a)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1
Escherichia	E. coli (O157:H7)	Seto et al (2007)	0	0	1	0	1	0	1	1	1	0	0	0	0	0	0	1
Escherichia	E. coli (O157:H7)	Stacey et al (2007)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
<i>Escherichia</i>	<i>E. coli</i> (O157:H7)	Wood et al (2007a)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
<i>Flavivirus</i>	<i>Japanese encephalitis virus</i>	Mukhopadhyay & Tapaswi (1994)	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>Japanese encephalitis virus</i>	Tapaswi et al (1995)	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>Japanese encephalitis virus</i>	Ghosh & Tapaswi (1999)	1	1	0	0	0	0	0	0	1	1	0	0	0	0	1	0
<i>Flavivirus</i>	<i>Louping Ill virus</i>	Hudson et al (1995)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>Louping Ill virus</i>	Norman et al (1999)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>Louping Ill virus</i>	Laurenson et al (2000)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1
<i>Flavivirus</i>	<i>Louping Ill virus</i>	Gilbert et al (2001)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Flavivirus</i>	<i>Louping Ill virus</i>	Laurenson et al (2003)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Flavivirus</i>	<i>Louping Ill virus</i>	Norman et al (2004)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>Murray Valley encephalitis virus</i>	Kay et al (1987)	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>St Louis encephalitis virus</i>	Lord & Day (2001a)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>St Louis encephalitis virus</i>	Lord & Day (2001b)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>Tick Borne Encephalitis</i>	Lindgren (1998)	0	0	1	0	0	0	0	0	1	1	0	0	0	0	1	0
<i>Flavivirus</i>	<i>Tick Borne Encephalitis</i>	Rosa et al (2003)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>Tick Borne Encephalitis</i>	Foppa (2005)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Lord & Day (2001b)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Thomas & Urena (2001)	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Wonham et al (2004)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Bowman et al (2005)	1	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Cruz-Pacheco et al (2005)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Kenkre et al (2005)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Lewis et al (2006)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Flavivirus</i>	<i>West Nile Virus</i>	Lewis et al (2006b)	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Liu et al (2006)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>West Nile Virus</i>	Hartemink et al (2007)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Flavivirus</i>	<i>Yellow fever virus</i>	Massad et al (2001a)	0	0	0	0	0	1	1	0	1	0	0	0	0	1	0	1
<i>Hantavirus</i>	<i>Puumala virus</i>	Sauvage et al (2003)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Hantavirus</i>	<i>Puumala virus</i>	Wolf (2004)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Puumala virus</i>	Sauvage et al (2007)	1	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Abramson & Kenkre (2002)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Aguirre et al (2002)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Abramson & Kenkre (2003)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Allen et al (2003)	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Buceta et al (2004)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Escudero et al (2004)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Kenkre (2005)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Allen et al (2006)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Chen & Clemence (2006a)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Chen & Clemence (2006b)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Peixoto & Abramson (2006)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Kenkre et al (2007)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Adler et al (2008)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Hantavirus</i>	<i>Sin Nombre virus</i>	Camelo-Neto et al (2008)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	van der Goot et al (2003a)	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	van der Goot et al (2003b)	1	0	0	0	0	0	1	0	0	0	0	1	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Ferguson et al (2004)	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Stegeman et al (2004)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	van der Goot et al (2005)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Le Menach et al (2006)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Bos et al (2007)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Busani et al (2007)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Garske et al (2007)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Guan et al (2007)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Guberti et al (2007)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Mannelli et al (2007)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Small et al (2007)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Tiensin et al (2007)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Truscott et al (2007)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	van Boven et al (2007)	0	0	1	0	1	0	1	1	1	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	van der Goot et al (2007)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Yang et al (2007)	0	0	1	0	1	0	1	1	0	0	0	0	0	0	0	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Bettencourt & Ribeiro (2008)	0	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Elbakidze (2008)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Rao (2008)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Sharkey et al (2008)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Avian influenza</i>	Upadhyay et al (2008)	1	0	0	0	0	0	0	1	0	1	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Rvachev & Longini (1985)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Ferguson et al (2003)	0	0	0	0	0	1	0	1	0	0	0	1	0	1	1	1
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Grais et al (2003)	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Sattenspiel & Herring (2003)	0	0	0	0	0	1	0	1	1	0	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Longini et al (2004)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Mills et al (2004)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Ferguson et al (2005)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Gani et al (2005)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Longini et al (2005)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Patel et al (2005)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Bansal et al (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Carrat et al (2006)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Chowell et al (2006a)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Chowell et al (2006b)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	1	1
<i>Influenzavirus A</i>	<i>Influenza A virus</i>	Cooper et al (2006)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	1

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
Influenzavirus A	Influenza A virus	Day et al (2006)	0	0	1	0	0	0	1	0	0	1	0	0	1	0	0	1
Influenzavirus A	Influenza A virus	Ferguson et al (2006)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Flahault et al (2006)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Germann et al (2006)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Glass et al (2006)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Mills et al (2006)	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0
Influenzavirus A	Influenza A virus	Sertsov et al (2006)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1
Influenzavirus A	Influenza A virus	Wu et al (2006)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Alexander et al (2007)	0	0	0	0	0	1	0	0	1	0	0	1	0	0	1	0
Influenzavirus A	Influenza A virus	Bootsma & Ferguson (2007)	0	0	0	0	0	1	0	1	1	0	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Chowell et al (2007a)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Chowell et al (2007b)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Colizza et al (2007a)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Debarre et al (2007)	0	0	0	0	0	1	0	0	1	1	0	1	0	0	1	0
Influenzavirus A	Influenza A virus	Duerr et al (2007a)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Duerr et al (2007b)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Eichner et al (2007)	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Epstein et al (2007)	0	0	0	0	0	1	0	0	1	1	1	0	0	0	1	0
Influenzavirus A	Influenza A virus	Galvani et al (2007)	0	0	0	0	0	1	0	1	1	0	1	0	0	0	1	0
Influenzavirus A	Influenza A virus	Gardam et al (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Glass & Barnes (2007)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Haber et al (2007)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Hall et al (2007)	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Iwami et al (2007)	0	1	0	0	1	1	0	0	1	1	0	1	0	0	0	0
Influenzavirus A	Influenza A virus	Larson (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
Influenzavirus A	Influenza A virus	Lee & Chen (2007)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Lessler et al (2007)	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	1
Influenzavirus A	Influenza A virus	Lipsitch et al (2007)	0	0	0	0	0	1	0	0	1	1	0	1	0	0	1	0
Influenzavirus A	Influenza A virus	Massad et al (2007)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1
Influenzavirus A	Influenza A virus	Mathews et al (2007)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	McCaw & McVernon (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Nuno et al (2007)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Riley et al (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Roberts et al (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Vynnycky et al (2007)	0	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Wood JG et al (2007)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Ajelli & Merler (2008)	0	0	0	0	0	1	0	0	0	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Alexander et al (2008)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Andreasen et al (2008)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Arinaminpathy & McLean(2008)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Atkinson & Wein (2008)	0	0	0	0	0	1	1	0	0	0	0	0	1	0	1	0

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
Influenzavirus A	Influenza A virus	Caley et al (2008)	0	0	0	0	0	1	1	1	1	0	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Cauchemez et al (2008)	0	0	0	0	0	1	1	0	1	1	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Chowell et al (2008)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	1	1
Influenzavirus A	Influenza A virus	Ciofi degli Atti et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Das et al (2008)	0	0	0	0	0	1	0	0	1	1	1	0	0	0	1	0
Influenzavirus A	Influenza A virus	Davey & Glass (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Davey et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Gumel et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Halloran et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Iwami et al (2008)	0	1	0	0	1	1	0	0	1	1	0	1	0	0	0	0
Influenzavirus A	Influenza A virus	Kerneis et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	McCaw et al (2008)	0	0	0	0	0	1	0	0	1	1	0	1	0	0	1	0
Influenzavirus A	Influenza A virus	Miller et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Moghadas et al (2008)	0	0	0	0	0	1	0	0	1	1	0	1	0	0	1	0
Influenzavirus A	Influenza A virus	Mylius et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	Nuno et al (2008)	0	0	0	0	0	1	0	0	1	1	0	0	0	0	1	0
Influenzavirus A	Influenza A virus	White & Pagano (2008)	0	0	0	0	0	1	1	1	0	0	0	0	0	0	0	1
Leishmania	Leishmania (general)	Hasibeder et al (1992)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
Leishmania	Leishmania (general)	Burattini et al (1998)	1	1	0	0	0	0	1	0	1	0	0	0	0	0	1	1
Leishmania	Leishmania braziliensis	Chaves & Hernandez (2004)	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leishmania	Leishmania braziliensis	Rabinovich & Feliciangeli (2004)	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1
Leishmania	Leishmania braziliensis	Chaves et al (2007)	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Leishmania	Leishmania braziliensis	Das et al (2007)	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leishmania	Leishmania chagasi	Courtenay et al (2002)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Leishmania	Leishmania chagasi	Palatnik-de-Sousa et al (2004)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Leishmania	Leishmania infantum	Dye (1988)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Leishmania	Leishmania infantum	Dye et al (1992)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Leishmania	Leishmania infantum	Dye & Williams (1993)	0	0	1	0	0	0	1	1	0	0	0	0	0	0	0	1
Leishmania	Leishmania infantum	Dye (1996)	1	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Leishmania	Leishmania infantum	Quinnell et al (1997)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
Leishmania	Leishmania infantum	Reithinger et al (2003)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
Leishmania	Leishmania infantum	Reithinger et al (2004)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0
Leishmania	Leishmania major	Dye & Davies (1990)	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0
Leishmania	Leishmania major	Garnick (1992)	1	1	0	0	0	1	0	0	0	0	0	1	0	1	1	1
Leishmania	Leishmania mexicana	Kerr et al (1997)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1
Leishmania	Leishmania peruviana	Dye (1992)	1	0	0	0	0	1	1	1	0	0	0	1	0	0	0	1
Leptospira	Leptospira interrogans	Bennett (1993)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Leptospira	Leptospira interrogans	van der Kamp et al (1990)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	0	1
Leptospira	Leptospira interrogans	Caley & Ramsey (2001)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	0
Leptospira	Leptospira interrogans	Holt et al (2006)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Lyssavirus	Rabies virus	Preston (1973)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
Lyssavirus	Rabies virus	Frerichs & Prawda (1975)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
Lyssavirus	Rabies virus	Anderson et al (1981)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	David et al (1982)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Kallen (1984)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Kallen et al (1985)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Garnerin et al (1986)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Murray et al (1986)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0
Lyssavirus	Rabies virus	Coyne et al (1989)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
Lyssavirus	Rabies virus	Gardner et al (1990)	1	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0
Lyssavirus	Rabies virus	Smith et al (1991)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0
Lyssavirus	Rabies virus	Murray & Seward (1992)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Cleaveland & Dye (1995)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	White et al (1995c)	1	0	0	0	0	0	1	0	1	1	0	0	0	0	1	0
Lyssavirus	Rabies virus	Artois et al (1997)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Jeltsch et al (1997)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Rhodes et al (1998)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Tischendorf et al (1998)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
Lyssavirus	Rabies virus	Benyoussef et al (1999)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Childs et al (2000)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
Lyssavirus	Rabies virus	Deal et al (2000)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0
Lyssavirus	Rabies virus	Fowler et al (2000)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Langlais & Suppo (2000)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lyssavirus	Rabies virus	Suppo et al (2000)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Massad et al (2001b)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Allen et al (2002)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
Lyssavirus	Rabies virus	Bohrer et al (2002)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Cleaveland et al (2002)	0	1	0	0	0	0	1	0	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Smith & Wilkinson (2002)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	1	0
Lyssavirus	Rabies virus	Smith et al (2002)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1
Lyssavirus	Rabies virus	Tuyl'ko & Kuzmin (2002)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Elrish and Twizell (2004)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lyssavirus	Rabies virus	Thulke et al (2004)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
Lyssavirus	Rabies virus	Eisinger et al (2005)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Knobel et al (2005)	0	1	0	0	0	0	1	0	0	0	1	0	0	0	1	0
Lyssavirus	Rabies virus	Russell et al (2005)	1	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1
Lyssavirus	Rabies virus	Smith et al (2005)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	1
Lyssavirus	Rabies virus	Haydon et al (2006)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
Lyssavirus	Rabies virus	Ou & Wu (2006)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Lyssavirus	Rabies virus	Vial et al (2006)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
Lyssavirus	Rabies virus	Dimitrov et al (2007)	1	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0
Lyssavirus	Rabies virus	Hampson et al (2007)	1	0	0	0	0	0	0	1	1	0	0	0	0	0	1	0

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
<i>Lyssavirus</i>	<i>Rabies virus</i>	Asano et al (2008)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Anderson & Trehwella (1985)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Barlow (1991a)	1	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Barlow (1991b)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Roberts (1992)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Barlow (1993)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Bentil & Murray (1993)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Smith et al (1995)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	White & Harris (1995a)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	White & Harris (1995b)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Roberts (1996)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Ruxton (1996)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Barlow et al (1997)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Smith et al (1997)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Swinton et al (1997)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	White et al (1997)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Barlow et al (1998)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	McCarty & Miller (1998)	1	0	0	0	0	0	1	0	1	1	0	0	0	0	0	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Wahlstrom et al (1998)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Kao & Roberts (1999)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Kean et al (1999)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Barlow (2000)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Smith et al (2001a)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Smith et al (2001b)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Caley & Hone (2002)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Fulford et al (2002)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Perez et al (2002a)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Perez et al (2002b)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Shirley et al (2003)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Cross et al (2004)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Wilkinson et al (2004)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Fischer et al (2005)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	van Asseldonk et al (2005)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Bar-David et al (2006)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Cross & Getz (2006)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Mathews et al (2006)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Smith et al (2007)	1	0	0	0	0	0	0	0	1	0	1	0	0	0	1	0
<i>Mycobacterium</i>	<i>Mycobacterium bovis</i>	Green et al (2008)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Nairovirus</i>	<i>Crimean-Congo Hemorrhagic Fever</i>	Goldfarb et al (1980)	0	0	1	0	0	0	1	1	0	0	0	0	0	0	1	1
<i>Orthopoxvirus</i>	<i>Monkeypox virus</i>	Jezeq et al (1987)	0	0	0	0	1	0	1	0	0	1	0	0	0	0	1	1
<i>Orthopoxvirus</i>	<i>Monkeypox virus</i>	Fine et al (1988)	0	0	0	0	1	0	1	0	0	0	0	0	0	0	1	1

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
<i>Salmonella</i>	<i>Salmonella dublin</i>	Nielsen et al (2007)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0
<i>Salmonella</i>	<i>Salmonella dublin, typhimurium</i>	Van Schaik et al (2007)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i>	<i>Salmonella enteritidis</i>	Watier et al (1993)	0	0	1	0	0	0	1	1	0	1	0	0	0	0	0	1
<i>Salmonella</i>	<i>Salmonella enteritidis</i>	Prevost et al (2006)	1	0	0	0	0	0	1	1	1	0	0	0	1	0	1	1
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	Nauta et al (2000)	0	0	0	1	0	0	1	0	1	0	0	0	0	0	0	0
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	Ranta & Majjala (2002)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	Ivanek et al (2004)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	Krieter et al (2004)	1	0	0	1	0	0	0	1	0	0	0	0	0	0	1	1
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	van der Gaag et al (2004a)	1	1	0	1	0	0	1	0	1	0	0	0	0	0	1	0
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	van der Gaag et al (2004b)	1	1	0	1	0	0	1	0	1	0	1	0	0	0	1	0
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	Xiao et al (2005)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	Xiao et al (2006)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	1
<i>Salmonella</i>	<i>Salmonella typhimurium</i>	Xiao et al (2007)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	1	1
<i>Toxoplasma</i>	<i>Toxoplasma gondii</i>	Papoz (1986)	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	1
<i>Toxoplasma</i>	<i>Toxoplasma gondii</i>	Ades & Nokes (1993)	0	0	1	0	0	0	1	1	0	1	0	0	0	0	0	1
<i>Toxoplasma</i>	<i>Toxoplasma gondii</i>	Larsen & Lebech (1994)	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	1
<i>Toxoplasma</i>	<i>Toxoplasma gondii</i>	Mateus-Pinilla et al (2002)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1
<i>Toxoplasma</i>	<i>Toxoplasma gondii</i>	Naoi & Yano (2002)	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Toxoplasma</i>	<i>Toxoplasma gondii</i>	Welton & Ades (2005)	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	1
<i>Trypanosoma</i>	<i>Trypanosoma brucei rhodesiense</i>	Rogers (1988)	1	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0
<i>Trypanosoma</i>	<i>Trypanosoma brucei rhodesiense</i>	Baker et al (1990)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Trypanosoma</i>	<i>Trypanosoma brucei rhodesiense</i>	Baker (1992)	1	0	0	0	0	0	0	0	1	0	0	0	0	0	1	0
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	Rabinovich et al (1990)	0	0	1	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	Velasco-Hernandez (1991)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	Velasco-Hernandez (1994)	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1	0
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	Cohen and Gurtler (2001)	0	1	0	0	1	0	0	0	1	0	0	0	0	0	1	0
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	Paz-Bailey et al (2002)	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	Inaba & Sekine (2004)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Trypanosoma</i>	<i>Trypanosoma cruzi</i>	Das & Mukherjee (2006)	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>TSE</i>	<i>BSE</i>	Anderson et al (1996)	1	0	0	0	0	0	1	1	1	1	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	Ferguson et al (1997)	1	0	0	0	0	0	1	1	0	1	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	Ferguson et al (1998)	1	0	0	0	0	0	1	1	0	1	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	Ghani et al (1998)	0	0	1	0	0	0	1	1	0	1	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	Ferguson et al (1999)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	Ghani et al (2000)	0	0	1	0	0	0	1	1	0	1	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	Hagenaars et al (2000)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	d'Aignaux et al (2001)	0	0	1	0	0	0	1	0	0	1	0	0	0	0	0	1
<i>TSE</i>	<i>BSE</i>	de Koeijer et al (2002)	1	0	0	0	0	0	1	1	0	0	0	0	0	0	1	1
<i>TSE</i>	<i>BSE</i>	Donnelly (2002)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>TSE</i>	<i>BSE</i>	Donnelly et al (2002)	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1
<i>TSE</i>	<i>BSE</i>	Ferguson et al (2002)	1	1	0	0	0	0	1	0	1	1	0	0	0	0	1	1

Pathogen		Study	Zoonotic phases					Topics addressed							Data use			
Pathogen genus	Pathogen species	Citation	Reservoir dynamics	Spillover: explicit	Spillover: implicit	Spillover: food-borne	Stuttering chains	Outbreaks in humans	Parameter estimation	Explain patterns	Control measures	Prediction	Economic aspects	Pathogen evolution	Within-host dynamics	Pathogen interactions	Data used: Individual level	Data used: Population level
TSE	BSE	Habtemariam et al (2002)	1	1	0	0	0	1	0	0	0	1	0	0	0	0	1	1
TSE	BSE	Kao et al (2002)	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
TSE	BSE	Arnold & Wilesmith (2003)	1	0	0	0	0	0	1	1	1	1	0	0	0	0	0	1
TSE	BSE	Boelle et al (2003)	0	0	1	0	0	0	1	1	0	1	0	0	0	0	0	1
TSE	BSE	d'Aignaux et al (2003)	1	1	0	0	0	0	1	0	0	1	0	0	0	0	0	1
TSE	BSE	Ferguson & Donnelly (2003)	1	1	0	0	0	0	1	0	1	1	0	0	0	0	1	1
TSE	BSE	Ghani et al (2003a)	0	0	1	0	0	0	1	1	0	1	0	0	0	0	1	1
TSE	BSE	Ghani et al (2003b)	0	0	1	0	0	0	1	1	0	1	0	0	0	0	1	1
TSE	BSE	Morley et al (2003)	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1
TSE	BSE	Arnold & Wilesmith (2004)	1	0	0	0	0	0	1	0	0	1	0	0	0	0	0	1
TSE	BSE	de Koeijer et al (2004)	1	0	0	0	0	0	1	0	1	0	0	0	1	0	1	1
TSE	BSE	Chadeau-Hyam & Alperovitch (2005)	0	0	1	0	0	1	1	0	0	1	0	0	0	0	1	1
TSE	BSE	Clarke & Gani (2005)	1	1	0	0	0	0	1	1	0	1	0	0	0	0	0	1
TSE	BSE	Garske et al (2006)	0	0	0	0	1	0	1	0	1	0	0	0	0	0	1	1
TSE	BSE	Clarke et al (2007)	0	0	0	0	1	0	1	0	1	0	0	0	0	0	0	1
TSE	BSE	Dietz et al (2007)	1	1	0	0	1	0	1	0	1	0	0	0	0	0	1	1
TSE	BSE	Fryer et al (2007)	1	1	0	0	0	0	1	0	1	0	0	0	0	0	1	1
TSE	BSE	Jacob & Magal (2007)	1	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1
TSE	BSE	Sugiura & Murray (2007)	1	0	0	0	0	0	1	0	1	0	1	0	0	0	0	1
TSE	BSE	Sugiura et al (2008)	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1
TSE	BSE	Yamamoto et al (2008)	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Yersinia</i>	<i>Yersinia enterocolitica</i>	Jones et al (1994)	1	0	0	1	0	0	1	1	0	0	0	0	0	0	0	1
<i>Yersinia</i>	<i>Yersinia pestis</i>	Noble (1974)	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0
<i>Yersinia</i>	<i>Yersinia pestis</i>	Keeling & Gilligan (2000a)	1	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0
<i>Yersinia</i>	<i>Yersinia pestis</i>	Keeling & Gilligan (2000b)	1	1	0	0	0	1	0	1	0	0	0	0	0	0	1	0
<i>Yersinia</i>	<i>Yersinia pestis</i>	Davis et al (2004)	1	0	0	0	0	0	0	1	0	0	1	0	0	0	0	1
<i>Yersinia</i>	<i>Yersinia pestis</i>	Gani & Leach (2004)	0	0	0	0	0	1	1	0	1	1	0	0	0	0	0	1
<i>Yersinia</i>	<i>Yersinia pestis</i>	Nishiura et al (2006)	0	0	0	0	0	1	1	0	1	0	0	0	0	0	0	1
<i>Yersinia</i>	<i>Yersinia pestis</i>	Webb et al (2006)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Yersinia</i>	<i>Yersinia pestis</i>	Davis et al (2007a)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Yersinia</i>	<i>Yersinia pestis</i>	Davis et al (2007b)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Yersinia</i>	<i>Yersinia pestis</i>	Foley et al (2007)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Yersinia</i>	<i>Yersinia pestis</i>	Kausrud et al (2007)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1
<i>Yersinia</i>	<i>Yersinia pestis</i>	Snall et al (2008)	1	0	0	0	0	0	0	1	0	1	0	0	0	0	1	0
<i>Yersinia</i>	<i>Yersinia pestis</i>	Buzby et al (2008)	1	1	0	0	0	0	0	1	0	0	0	0	0	0	1	0
<i>Yersinia</i>	<i>Yersinia pestis</i>	Davis et al (2008)	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1

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