Mathematical models used to inform study design or surveillance systems in infectious diseases: a systematic review

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Additional File 2
Additional tables

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eTable S1. Supplementary characteristics of publications – Observational and surveillance studies (N=12)

First author, year	Model reporting					Infection in model		Study design – details	Remarks [b]
	Equations/ Figure/ Program	Parameters listed/ source [a]	Population characteristics at baseline	Model previously published/ specifically built	Sensitivity analyses	Course of infection	Static or Dynamic		
Graat, 2001	Yes/No/No	Yes/Mixture	Yes	No/Yes	Yes	SI	Dynamic	Surveillance system	–
Michael, 2006	No/No/No	No/–	–	Yes/No	Yes	–	–	Large-scale community-based intervention programmes; monitoring strategies compared	Model not fully described in the article
Savill, 2008	Yes/No/No	Yes/Mixture	No	Yes/No	Yes	Latent, asymptomatic, and symptomatic	Dynamic	Surveillance system	–
Arnold, 2013	NA/No/No	Yes/Mixture	Yes	No/Yes	Yes	Within premises: SEIR Between premises: spatial transmission	Dynamic	Nine different surveillance strategies compared	–
Smieszek, 2013	NA/No/Yes	Partly/ Mixture	Yes	Yes/No	Yes	SEIR	Dynamic	Sentinel surveillance system	–
Ciccolini, 2014	Yes/No/No	Partly/ Mixture	Yes	No/Yes	Yes	SI	Dynamic	Sentinel surveillance system	–
Gonzales, 2014	No/No/No	Yes/ Estimated from other data	Yes	Yes/Yes	No	SIR	Dynamic	Surveillance system	–
Leslie, 2014	NA/No/Yes	Yes/ Estimated from other data	Yes	Yes/No	No	Susceptible, latent, infectious, immune, dead	Dynamic	Different surveillance strategies compared	–
Mizumoto, 2014	Yes/Yes/Yes	Yes/Mixture	Yes	No/Yes	Yes	SIR with W: protected state due to a short-lasting cross-protective immunity.	Dynamic	Prospective cohort study	Equations combined the states of the 2 serotypes
Pinsent, 2014	Yes/Yes/Yes	Yes/Mixture	Yes	No/Yes	Yes	SEIR with C (seroconversion state); E,I,C classes divided into 5, 5, 10 compartments	Dynamic	Surveillance system	–
van Bunnik, 2015	Yes/No/No	Yes/Mixture	Yes	Yes/Yes	Yes	SI	Dynamic	Sentinel surveillance system (comparison current system vs. 2 other schemes)	Model validated
Vinh, 2015	Yes/Yes/Yes	Yes/Mixture	No	Yes/Yes	Yes	Exposed (E), infected (I), recovered individuals who have not yet mounted a full antibody	Dynamic	Serial sero-epidemiological study design	–

First author, year	Model reporting					Infection in model		Study design – details	Remarks [b]
	Equations/ Figure/ Program	Parameters listed/ source [a]	Population characteristics at baseline	Model previously published/ specifically built	Sensitivity analyses	Course of infection	Static or Dynamic		
						response (P), recovered individuals whose specific antibody levels would give a result i in an immunological assay (Ri) [used 10 R compartments]			

NA: not applicable; S: susceptible individuals; E: exposed individuals; I: infected individuals; R: recovered individuals.

[a] parameter source: mixture – mixture of calibration, assumed by authors, and estimated from other data

[b] explicitly mentioned in remarks: if model validation was done; if source code for model is available

eTable S2. Supplementary characteristics of publications – Clinical trials (N=11)

First author, year	Model reporting					Infection in model		Study design – details	Remarks [b]
	Equations/ Figure/ Program	Parameters listed/ source [a]	Population characteristics at baseline	Model previously published/ specifically built	Sensitivity analyses	Course of infection	Static or Dynamic		
Atlas, 1993	Yes/No/No	Yes/Assumed by authors	Yes	Yes/Unclear	Yes	Not modelled	–	Experimental study (supplementary analysis for a research protocol)	–
Lipsitch, 2001	Yes/Yes/No	Yes/Assumed by author	Yes	Yes/Yes	No	Not colonized, colonized with penicillin-susceptible *S. pneumoniae*, colonized with penicillin-resistant *S. pneumoniae*	Static	Authors suggest this approach can be used for other study types	–
Wu, 2002,Wu, 2005	Yes/No/No	Yes/Mixture	No	Yes/Yes	Yes	Productively infected cells; long-lived/latently infected cells	Dynamic	HIV dynamics study	–
Clermont, 2004	Yes/No/Yes	Yes/Mixture	Yes	No/Yes	No	Not modelled	–	Modelling of components of the human inflammatory response (within-host)	–
Hallett, 2008	Yes/No/No	Yes/Mixture	Yes	Yes/Yes	Yes	HIV negative, HIV acute infection, latent infection, AIDS	Dynamic	Cluster RCT	–
Dimitrov, 2013	Yes/Yes/No	Yes/Mixture	Yes	Yes/Yes	Yes	Susceptible, infected with wild-type or drug-resistant HIV, AIDS	Dynamic	Individual RCTs (two interventions modelled separately).	–
Nishiura, 2013	Yes/No/No	No/Calibrated	No	Yes/No	No	SI	Dynamic	One-to-one animal transmission experiments	–
Cori, 2014 Hayes, 2014	Yes/Yes/No	Yes/Mixture	Yes	No/Yes	Yes	SI extended (with circumcision, antiretroviral therapy, …)	Dynamic	Three-arm cluster RCT	–
Cuadros, 2014	NA/Yes/Yes	Yes/Mixture	Yes	Yes/Yes	Yes	SI	Dynamic	Two completed trials discussed: Treatment with (val)acyclovir; Male circumcision	Model source code given in supplemental material
Scott, 2014	Yes/Yes/No	Yes/Mixture	Yes	No/Yes	Yes	SIS	Dynamic	Cross-sectional observation in the RCT	Model validated
Herzog, 2015	Yes/Yes/Yes	Yes/Mixture	Yes	Yes/Yes	Yes	$S\text{-}I_1\text{-}I_2\text{-}S$	Static	Re-analysing a RCT	Model source code available by request

NA: not applicable; S: susceptible individuals; E: exposed individuals; I: infected individuals; R: recovered individuals; RCT: randomized controlled (clinical) trials

[a] parameter source: mixture – mixture of calibration, assumed by authors, and estimated from other data

[b] explicitly mentioned in remarks: if model validation was done; if source code for model is available

eTable S3. Characteristics of publications – Clinical trials with Markov model (N=5)

First author, year	Infection		Population	Model		Main outcome	Design outcome(s)	Remarks
	Epidemiological category	Name		Type [a]	Structured / Network [b]			
Chen, 1999	Human, respiratory	Epstein-Barr virus	Hypothetical Hong Kong males 40-69y	Markov - deterministic	No/No	Death or surrogate endpoint	- Frequency - Sample size - Power	–
Longini, 1999	Human, STI	HIV	Uninfected primary participants and their uninfected steady sexual partnership	Markov - stochastic	Yes/No	Vaccine efficacy: susceptibility and infectiousness	- Frequency	–
Hoad, 2009	Human, respiratory	*Mycobacterium tuberculosis*	Adult, data from Asembo and Gem (Western Kenya)	Markov - stochastic	Yes/No	Tuberculosis prevalence	- Sample size	Spatial model
Tuite, 2011	Human, STI	Hypothetical STI	Serodiscordant couples	Markov - stochastic	No/No	STI incidence	- Sample size - Power	–
Auranen, 2014	Human, respiratory	*Streptococcus pneumoniae*	Infants, children	Markov - stochastic[c]	No/No	Vaccine efficacy	- Timing of sampling - Sample size - Power	–

[a] model type: IBM – individual based model; [b] structured: a population structure is reflected in model, network: a network of contacts between individuals is explicitly modelled; [c] model type obtained from the original article

eTable S4. Supplementary characteristics of publications – Clinical trials with Markov model (N=5)

First author, year	Model reporting					Infection in model		Study design – details	Remarks [b]
	Equations/ Figure/ Program	Parameters listed/ source [a]	Population characteristics at baseline	Model previously published/ specifically built	Sensitivity analyses	Course of infection	Static or Dynamic		
Chen, 1999	Yes/No/No	Yes/ Calibrated	Yes	No/No	Yes	0- No disease; 1- Epstein-Barr Virus infection; 2- Pre-clinical screen-detectable phase; 3- Clinical phase	Static	Hypothetical RCT with a screening vs. no screening regime. Four screening regimes compared.	Infection not the main purpose of the article
Longini, 1999	Yes/Yes/No	Yes/ Assumed by author	Yes	No/Yes	Yes	SI	Static	Augmented RCT	
Hoad, 2009	Yes/No/No	Yes/ Mixture	Yes	No/No	Yes	SIS	Dynamic	Group or community randomised trial	
Tuite, 2011	No/Yes/Yes	Yes/ Mixture	Yes	No/No	No	SI	Static	(Sero-)discordant couple studies	–
Auranen, 2014	No/No/No	No/–	No	Yes/Yes	No	–	–	Cross-sectional observation in vaccine trials	Model not fully described in the article

NA: not applicable; S: susceptible individuals; E: exposed individuals; I: infected individuals; R: recovered individuals; RCT: randomized controlled (clinical) trials
[a] parameter source: mixture – mixture of calibration, assumed by authors, and estimated from other data
[b] explicitly mentioned in remarks: if model validation was done; if source code for model is available

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