

Modelling seasonal influenza in England: Approaches to capture immunity propagation Edward Hill¹

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The broader project

<u>MEMVIE: Mathematical and Economic Modelling for</u> <u>Vaccination and Immunisation Evaluation</u>

Provide a complementary second opinion on the work presented to the Joint Committee of Vaccination and Immunisation (JCVI).

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NIHR National Institute for Health Research

Pertussis (whooping cough)

Pneumococcal disease

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- Human papillomavirus (HPV)
- Seasonal influenza

Project webpage:

https://warwick.ac.uk/fac/cross_fac/zeeman_institute/zeeman_research/epidemiology/humans/memvie/



Seasonal influenza is a considerable burden on public health

Figure: Influenza confirmed hospital admissions in England, 2010 to 2017



Source: Reproduced from the Public Health England report "Surveillance of influenza and other respiratory viruses in the UK: Winter 2016 to 2017".

- Vaccination can offer some protection against infection.
 - Two influenza A subtypes: A(H1N1)pdm09, A(H3N2),
 - Two influenza B lineages: B/Victoria, B/Yamagata

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Use of modelling to inform policy



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RESEARCH ARTICLE

Assessing Optimal Target Populations for Influenza Vaccination Programmes: An Evidence Synthesis and Modelling Study

Marc Baguelin D, Stefan Flasche, Anton Camacho, Nikolaos Demiris, Elizabeth Miller, W. John Edmunds

Published: October 8, 2013 • https://doi.org/10.1371/journal.pmed.1001527

Prior models typically treat each influenza season and each strain circulating within that season independently.



4

Our study objectives

(1) Data amalgamation

• Gather relevant influenza vaccine and epidemiological data for England (post-2009 influenza pandemic).

(2) Mathematical model development

• SEIR-type seasonal influenza transmission model, incorporating multiple strains and immunity propagation.

(3) Parameter inference

- Calibrate model to data using Approximate Bayesian Computation.
- Quantify extent of immunity propagation.



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Data: Vaccine efficacy & uptake

Efficacy & uptake data from Public Health England

Figure: Vaccine uptake in 2016/17 influenza season 80 65+vrs 70 Vaccine uptake (%) 00 05 07 08 09 09 09 09 09 09 09 09 <65yrs at risk All pregnant women 2016/17 season indicated by bold lines, 2015/16 season indicated by fainter 10 dashed lines 0 41 43 45 39 47 49 51 1 3 5 7 9 Week number

Source: PHE Weekly National Influenza Report (25 May 2017)

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7



Data: Influenza attributed GP visits

GP consultation rate for strain m in season $y = \dots$





Data: GP visits for ILI

GP consultation rate for strain m in season $y = \text{GP ILI consultation rate} \times \dots$

Week	Age	Chronic Disease	Population	Num. of patients with ILI
01/2018	1	1	68,437	10
01/2018	1	0	578,907	13
01/2018	2	1	89,396	17
01/2018	2	0	743,470	28
01/2018	3	1	28,957	25
01/2018	3	0	956,278	13

Data source:

Royal College of General Practitioners (RCGP) Research and Surveillance Centre (RSC) network: www.rcgp.org.uk/rsc

Data: Virological positivity

GP consultation rate for strain m in season y = GP ILI consultation rate $\times \dots$ Proportion of ILI samples influenza positive $\times \dots$

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10



Data: Virological positivity

Figure: Number of influenza positive samples and % positive (2017/18 influenza season).



Data source:

Figure reproduced from Public Health England weekly national influenza reports.

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Data: Circulating strain composition

GP consultation rate for strain m in season y = GP ILI consultation rate $\times \ldots$ Proportion of ILI samples influenza positive $\times \ldots$ Proportion of influenza viruses in circulation of strain type m





Data: Circulating strain composition

Figure: Virologically sampled influenza cases attributed to each strain.



Data source:

WHO FluNet (https://www.who.int/influenza/gisrs_laboratory/flunet/en/)

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Data: Influenza attributed GP visits

Figure: Empirical, strain-stratified data for ILI GP consultations attributable to influenza per 100,000 population.



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14

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Full model schematic



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Vaccination model



Assumed a 'leaky' vaccine; reducing the overall susceptibility of the given group receiving vaccination.

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Immunity propagation model



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18

Immunity propagation model

Figure: Interaction between exposure history and susceptibility.

		Strain susceptibility			
		A(H1N1)pdm09	A(H3N2)	B/Victoria	B/Yamagata
Exposure history (h)	Naïve	1	1	1	1
	A(H1N1)pdm09	а	1	1	1
	A(H3N2)	1	а	1	1
	B/Yamagata	1	1	a	b
	B/Victoria	1	1	b	a
	Vacc. (V)	C _{A(H1N1)}	С _{А(НЗN2)}	C_{B/Victoria}	C_{B/Yamagata}
	A(H1N1)pdm09 & V	min(<i>a, c_{A(H1N1)})</i>	С _{А(НЗN2)}	C_{B/Victoria}	C_{B/Yamagata}
	A(H3N2) & V	с _{А(Н1N1)}	min(<i>a</i> , c _{A(H3N2)})	C_{B/Victoria}	C_{B/Yamagata}
	B/Victoria & V	C _{A(H1N1)}	С _{А(НЗN2)}	min(<i>a</i> , c _{B/Victoria})	min(b, c _{B/Yamagata})
	B/Yamagata & V	с_{А(Н1N1)}	C _{A(H3N2)}	min(b, c _{B/Victoria})	min(<i>a, c</i> _{B/Yamagata})

> Vaccine immunity carried over: $c_m^y = 1 - \xi \alpha_m^{y-1}; \quad \xi \in (0, 1)$

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19

Epidemiological model



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20

Epidemiological model

Figure: Vaccination and epidemiological model schematic.



Track incidence rate (per 100,000) of new strain m influenza infections in season y:

$$Z_m(y) = \left(\int_{y-1}^{y} \gamma_{1,m} (E_m^N + E_m^V) \, \mathrm{dt} \right) \times 100,000.$$

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21

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Observation model



Estimated ascertainable influenza cases:

 $Z_m^+(y) = \epsilon_y Z_m(y).$

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22



Table: Overview of parameters in the model.

Description	Notation	Value
Fixed parameters		
Mortality rate (day ⁻¹)	B,D	$\frac{1}{81 \times 365}$
Rate of latency loss, influenza A subtypes (day^{-1})	$\gamma_{1,A}$	$\frac{1}{1.4}$
Rate of latency loss, influenza B lineages (day^{-1})	$\gamma_{1,B}$	$\frac{1}{0.6}$
Recovery rate (day^{-1})	γ_2	$\frac{1}{3.8}$
Time-varying parameters		
Vaccination rate at time t	u(t)	
Vaccine efficacy, season y strain m	$lpha_m^y$	
Inferred parameter description	Notation	Prior
Influenza virus transmissibility, strain m	β_m	$\mathcal{U}(0.2632, 0.7896)$
Modified susceptibility given natural infection in prior season	a	$\mathcal{U}(0,1)$
Modified susceptibility due to type B influenza cross-reactivity	b	$\mathcal{U}(0,1)$
Proportion of prior season vaccine efficacy carried over	ξ	$\mathcal{U}(0,1)$
Ascertainment probability in season y	ϵ_y	$\mathcal{U}(0,0.05)$

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Quantify extent of immunity propagation.



Parameter set summary statistics



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 $M_{m,y}$ the model estimate for strain *m* in season *y*.

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Data: Influenza attributed GP visits

Figure: Empirical, strain-stratified data for ILI GP consultations attributable to influenza per 100,000 population (influenza seasons 2012/13-2017/18.



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26

Parameter fits: Transmissibility

Figure A: Inferred posterior distributions for the transmissibility associated parameters.



Similar estimates for the two influenza A subtypes.

Exceed corresponding estimates for the two type B lineages.

27

Parameter fits: Ascertainment



28

Parameter fits: Immunity propagation

Figure C: Inferred posterior distributions for the immunity propagation associated parameters.



Observe modulation of susceptibility due to propagation of immunity arising from natural infection.

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29

Parameter fits: Immunity propagation

Figure C: Inferred posterior distributions for the immunity propagation associated parameters.



> Minimal propagation of influenza B cross-reactive immunity.



30

Parameter fits: Immunity propagation



- Very little carry over of prior season vaccine efficacy.
- Corroborates reports vaccine-mediated immunity wanes rapidly.

Reference: Kissling E, Rondy M, study team IMM. Early 2016/17 vaccine effectiveness estimates against influenza A(H3N2): I-MOVE multicentre case control studies at primary care and hospital levels in Europe. *Eurosurveillance*. 2017;**22**(7):30464.

Goodness-of-fit verification

- Perform 1,000 independent simulations using parameter sets drawn from the ABC inference procedure.
- Generate variability in epidemic composition due to the posterior distribution for the underlying parameters.
- Compare projected flu attributed GP consultations (per 100,000) to the data.



Goodness-of-fit verification

Figure: Posterior predictive distributions for influenza positive GP consultations per 100,000 population.



33

Limitations & future work

- Include age structure
 - Age-specific vaccine uptake and efficacy
 - Heterogeneous social contact patterns



Figure: Representations in logarithmic scale of contact matrices by one-year age brackets for the United Kingdom.

Source: Reproduced from L. Fumanelli *et al.* Inferring the Structure of Social Contacts from Demographic Data in the Analysis of Infectious Diseases Spread. *PLOS Computational Biology* **8**(9): e1002673 (2012).

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34



Limitations & future work

- Include age structure
 - Age-specific vaccine uptake and efficacy
 - Heterogeneous social contact patterns
- Propagation of immunity limited to a single season
- Appraise cost-effectiveness of prospective vaccination programmes



Summary of advances

(1) Data amalgamation

Compiled influenza vaccine and epidemiological data subsequent to the 2009 influenza pandemic for England.

(2) Mathematical model development

Constructed a dynamic multi-strain SEIR-type transmission model for seasonal influenza, with immunity propagation mechanisms between seasons.

(3) Parameter inference

Propagation of seasonal influenza immunity from one season to the next is weaker if vaccine derived, compared to natural immunity from infection.

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