

Evidence for history-dependence of influenza pandemic emergence

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Influenza pandemic definition

"World-wide epidemic, caused by an emergent influenza A strain that transmits among humans, was not previously circulating among humans and to which most people do not have immunity"



Impact of influenza pandemics

1918 flu pandemic: Infected 500 million, killed 20-40 million.





Why are influenza A viruses capable of causing global pandemics?

There are several Influenza A virus strains, categorised into subtypes.



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- > Virus is notable for following dynamics:
 - antigenic drift
 - antigenic shift

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Antigenic shift



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Influenza A inhabits many hosts



<u>Source</u>: R. Jennings & R.C. Read, *Influenza: Human and Avian.* Royal Society of Medicine Press (2006).

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Objectives

(1) Historic pandemic influenza data

 Produce timelines listing possible pandemics from 1700 to the present

(2) Model Selection

• Are influenza pandemic waiting times plausibly generated by a memoryless or history-dependent process?

(3) Predictions

• What is the probability of a given number of influenza pandemics in the next 100 years?

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"World-wide epidemic, caused by an emergent influenza A strain that transmits among humans, was not previously circulating among humans and to which most people do not have immunity "

Only during the virological era can we recognise a pandemic with certainty.

> Which pre-1900 epidemics were actually pandemics?



The data

Three distinct data sets (referred to as timelines) were constructed based on:

- The century the pandemic occurred
- The number of supporting sources for the epidemic being a pandemic.

References:

- 1. KD Patterson (1986) Pandemic Influenza 1700-1900. Rowman and Littlefield, New Jersey.
- 2. W Beveridge (1991) The chronicle of influenza epidemics. *History and philosophy of the life sciences* **13**: 223-234.
- 3. CW Potter (2001) A history of influenza. *Journal of applied microbiology* **91**: 572-579.

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Date	Popular Name	Timeline A	Timeline B	Timeline C
1729				
1732		—		
1761				
1781		52 yrs		
1788				
1800				
1830		49 yrs		
1847		—		
1857		_		
1889	Russian Flu	59 yrs		
1918	Spanish Flu	29 yrs		
1957	Asian Flu	39 yrs		
1968	Hong Kong Flu	11 yrs		
1977	Russian Flu	_		
2009	Swine Flu	41 yrs		

Date	Popular Name	Timeline A	Timeline B	Timeline C
1729				
1732		—	_	
1761			32 yrs	
1781		52 yrs	20 yrs	
1788		_	7 yrs	
1800			12 yrs	
1830		49 yrs	30 yrs	
1847		_	17 yrs	
1857			10 yrs	
1889	Russian Flu	59 yrs	59 yrs	
1918	Spanish Flu	29 yrs	29 yrs	
1957	Asian Flu	39 yrs	39 yrs	
1968	Hong Kong Flu	11 yrs	11 yrs	
1977	Russian Flu		_	
2009	Swine Flu	41 yrs	41 yrs	

Date	Popular Name	Timeline A	Timeline B	Timeline C
1729				
1732		—	_	3 yrs
1761			32 yrs	29 yrs
1781		52 yrs	20 yrs	20 yrs
1788		_	7 yrs	7 yrs
1800			12 yrs	12 yrs
1830		49 yrs	30 yrs	30 yrs
1847		—	17 yrs	17 yrs
1857		_	10 yrs	10 yrs
1889	Russian Flu	59 yrs	59 yrs	59 yrs
1918	Spanish Flu	29 yrs	29 yrs	29 yrs
1957	Asian Flu	39 yrs	39 yrs	39 yrs
1968	Hong Kong Flu	11 yrs	11 yrs	11 yrs
1977	Russian Flu	_	—	9 yrs
2009	Swine Flu	41 yrs	41 yrs	32 yrs

^{||}Widely believed to have occurred due to human factors

Date	Popular Name	Timeline A	Timeline B	Timeline C
1729				
1732		_	—	3 yrs
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1781		52 yrs	20 yrs	20 yrs
1788		_	7 yrs	7 yrs
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➢ Model 1 − Exponential; Model 2 − Gamma.

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Model comparison method: Reversible-jump MCMC

Allows simulation of posterior distribution on spaces of varying dimensions.

 $\pi(m, \theta_m | D) \propto L(D|m, \theta_m) p(\theta_m | m) p(m)$

Gives posterior model probabilities, as well as parameter posterior distributions.



Reversible-jump MCMC priors

Rate parameters: Uniform

Gamma distribution shape parameter:



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Exponential model posterior distributions

Rate parameter:



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Gamma model posterior distributions – Not clockwork assumption

Rate parameter:

Shape parameter:



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Gamma model posterior distributions – Weakly mechanistic assumption

Rate parameter:

Shape parameter:

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Gamma model posterior distributions – Strongly mechanistic assumption

Rate parameter:

Shape parameter:



Model selection results

Table: Posterior probabilities given to the history-dependent hypothesis.

		Kappa prior			
	Not Clockwork	Weakly mechanistic	Strongly mechanistic		
Timeline A	0.70	0.82	0.86		
Timeline B	0.77	0.89	0.92		
Timeline C	0.45	0.73	0.77		

Gamma distributed model preferred for eight out of nine sets of modelling assumptions.

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Goodness-of-fit verification

Figure: Predicted posterior influenza pandemic inter-event time survival functions versus the empirical survival function. (left) history-dependent model; (right) memoryless model



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Predicted pandemic event number distributions

Carried out forward simulations using Gillespie algorithm:

- 1) Posterior model probabilities used to choose the model used for each forward simulation.
- 2) For the selected model, pick sample parameters generated from RJMCMC.

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Figure: Proportion of simulations predicting the specified number of pandemics between 2010-2110.



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One Health approach?



The One Health concept recognizes the interrelationship between animal, human and environmental health.

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Limitations & future work

> Data uncertainty and small nature of the dataset

Including pre-1700 outbreaks avenue for further study

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- > Alternative distributions for history-dependent model
 - Weibull distribution
- Alternative priors for shape parameter



Summary of findings

(1) Historic pandemic influenza data

Constructed three alternative timelines of presumptive influenza pandemics since 1700.

(2) Model Selection

Spillover of strains with pandemic potential is a history-dependent process.

(3) Predictions

Shown a high level of variability in the predicted number of pandemics.

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