Transmissibility of H5N1 avian influenza in Nigeria: The 2006 epidemic

Emmanuel J. Morales-Butler

Mathematical and Computational Modeling Sciences Center,
School of Human Evolution and Social Change,
Arizona State University

January 13, 2011

Outline:

Introduction

Introduction

- **Global health concerns:**

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths
    - Case fatality of $\approx$ 2-6 percent

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths
    - Case fatality of $\approx$ 2-6 percent
- **Basic facts about HPAI H5N1:**

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths
    - Case fatality of $\approx$ 2-6 percent
- **Basic facts about HPAI H5N1:**
  - Virus isolation: 1996 in Guangdong Province, China

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths
    - Case fatality of $\approx$ 2-6 percent
- **Basic facts about HPAI H5N1:**
  - Virus isolation: 1996 in Guangdong Province, China
  - **To date:**

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths
    - Case fatality of $\approx$ 2-6 percent
- **Basic facts about HPAI H5N1:**
  - Virus isolation: 1996 in Guangdong Province, China
  - **To date:**
    - 505 cumulative human cases (known)

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths
    - Case fatality of $\approx$ 2-6 percent
- **Basic facts about HPAI H5N1:**
  - Virus isolation: 1996 in Guangdong Province, China
  - **To date:**
    - 505 cumulative human cases (known)
    - 300 cumulative fatal cases

Introduction

- **Global health concerns:**
  - Highly pathogenic avian influenza virus subtype H5N1 (HPAI H5N1) as a **human treat**
  - **Adaptation** of HPAI H5N1 for human-to-human transmission
    - **Consequences:** pandemic with high morbidity and mortality
    - **Economic impact** in a human pandemic from the HPAI H5N1: several billion to several trillion dollars
- **An example**
  - 1918-1919 influenza pandemic (Spanish flu)
    - Most devastating in recent history
    - From $\approx$ 20 to 100 million deaths
    - Case fatality of $\approx$ 2-6 percent
- **Basic facts about HPAI H5N1:**
  - Virus isolation: 1996 in Guangdong Province, China
  - **To date:**
    - 505 cumulative human cases (known)
    - 300 cumulative fatal cases
    - **Case fatality rate**: 59.4 percent

Introduction

Introduction

- **Factors that might facilitate the spreading:**

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks
  - Corruption

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks
  - Corruption
  - Hesitation by farmers to report outbreaks

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks
  - Corruption
  - Hesitation by farmers to report outbreaks

- **Factors that increase public understanding:**

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks
  - Corruption
  - Hesitation by farmers to report outbreaks

- **Factors that increase public understanding:**
  - News media

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks
  - Corruption
  - Hesitation by farmers to report outbreaks

- **Factors that increase public understanding:**
  - News media
  - Government delayed public health messages

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks
  - Corruption
  - Hesitation by farmers to report outbreaks

- **Factors that increase public understanding:**
  - News media
  - Government delayed public health messages
  - Veterinarians

Introduction

- **Factors that might facilitate the spreading:**
  - Poverty
  - Inadequate primary health care facilities
  - Inadequate knowledge of food safety protocols on poultry farms
  - Inability to differentiate risk factors associated with HPAI and other poultry diseases

- **Constrains containing the HPAI H5N1:**
  - Delayed official decisions
  - Lack of prompt intervention planning
  - Poor preparedness for potential disease outbreaks
  - Corruption
  - Hesitation by farmers to report outbreaks

- **Factors that increase public understanding:**
  - News media
  - Government delayed public health messages
  - Veterinarians
  - Internet

In this study:

In this study:

- A preliminary assessment of the basic reproduction number ($\mathcal{R}_0$) of the HPAI H5N1 between poultry farms

In this study:

- A preliminary assessment of the basic reproduction number ($\mathcal{R}_0$) of the HPAI H5N1 between poultry farms
- Evaluation of the effectiveness of the intervention strategies

Data

Data

- **Source:** National Veterinary Research Institute of Nigeria

Data

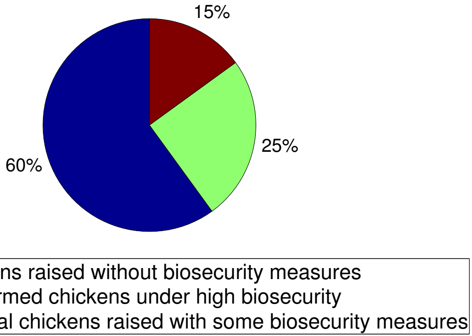
- **Source:** National Veterinary Research Institute of Nigeria
- **Description:**

Data

- **Source:** National Veterinary Research Institute of Nigeria
- **Description:**
  - Weekly number of newly infected farms (by state), that were infected with HPAI H5N1 between January and June of 2006

Data

- **Source:** National Veterinary Research Institute of Nigeria
- **Description:**
  - Weekly number of newly infected farms (by state), that were infected with HPAI H5N1 between January and June of 2006



Deterministic epidemic model

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**
  - Constant **rates** throughout time

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**
    - Constant **rates** throughout time
    - Incubation and infectious **periods** are gamma-distributed with parameters $(n_E, n_E\kappa)$ and $(n_I, n_I\gamma)$, respectively

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**
  - Constant **rates** throughout time
  - Incubation and infectious **periods** are gamma-distributed with parameters $(n_E, n_E\kappa)$ and $(n_I, n_I\gamma)$, respectively
    - Means $1/\kappa$ and $1/\gamma$, respectively

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**
  - Constant **rates** throughout time
  - Incubation and infectious **periods** are gamma-distributed with parameters $(n_E, n_E\kappa)$ and $(n_I, n_I\gamma)$, respectively
    - Means $1/\kappa$ and $1/\gamma$, respectively
    - Variances $1/(n_E\kappa^2)$ and $1/(n_I\gamma^2)$, respectively

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**
  - Constant **rates** throughout time
  - Incubation and infectious **periods** are gamma-distributed with parameters $(n_E, n_E\kappa)$ and $(n_I, n_I\gamma)$, respectively
    - Means $1/\kappa$ and $1/\gamma$, respectively
    - Variances $1/(n_E\kappa^2)$ and $1/(n_I\gamma^2)$, respectively
  - **Contact process** is assumed to be driven by homogeneous mixing

Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**
  - Constant **rates** throughout time
  - Incubation and infectious **periods** are gamma-distributed with parameters $(n_E, n_E\kappa)$ and $(n_I, n_I\gamma)$, respectively
    - Means $1/\kappa$ and $1/\gamma$, respectively
    - Variances $1/(n_E\kappa^2)$ and $1/(n_I\gamma^2)$, respectively
  - **Contact process** is assumed to be driven by homogeneous mixing
    - Infected poultry farms have the same transmission potential

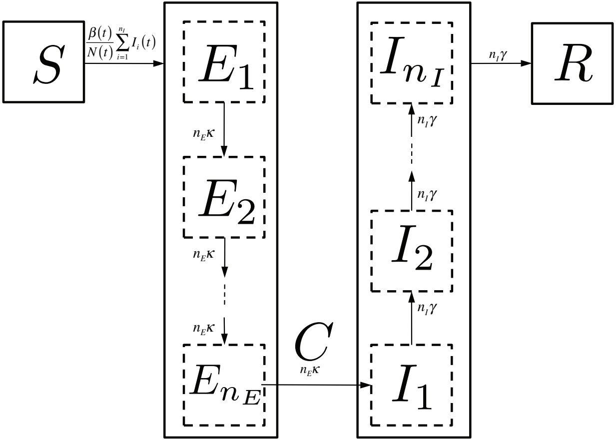
Deterministic epidemic model

- **Type of model**: a temporal, non-spatial multi-stage compartmental epidemic model with classes of poultry farms
- **Model assumptions:**
  - Constant **rates** throughout time
  - Incubation and infectious **periods** are gamma-distributed with parameters $(n_E, n_E\kappa)$ and $(n_I, n_I\gamma)$, respectively
    - Means $1/\kappa$ and $1/\gamma$, respectively
    - Variances $1/(n_E\kappa^2)$ and $1/(n_I\gamma^2)$, respectively
  - **Contact process** is assumed to be driven by homogeneous mixing
    - Infected poultry farms have the same transmission potential
    - The network of poultry farms is completely connected

Deterministic epidemic model

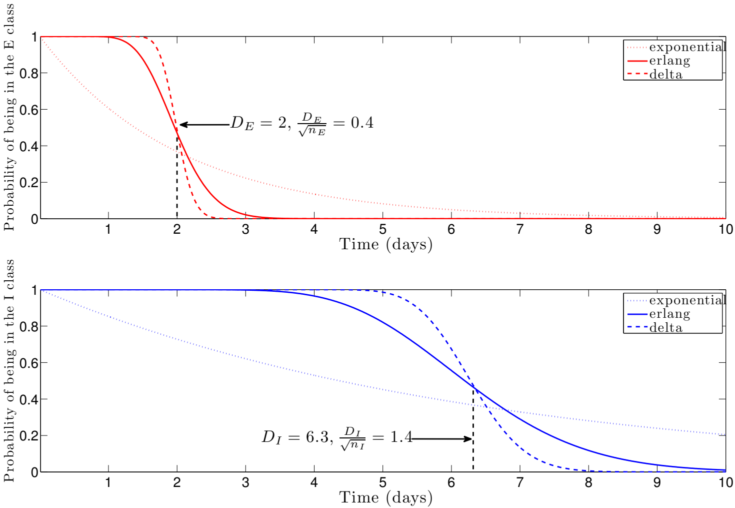
Deterministic epidemic model

- Schematic diagram



Survivor functions

Survivor functions



The impact of interventions on the HPAI H5N1 transmission rate

The impact of interventions on the HPAI H5N1 transmission rate

- The **intervention strategies** to control the spread of HPAI H5N1 include:

Type of intervention	Implementation date
Culling (depopulation of infected premises or decontamination)	Feb. 7^{th}, 2006
Movement restrictions	Feb. 20^{th}, 2006
Payment of compensation	late 2006 until early 2007
Improved biosecurity	—

The impact of interventions on the HPAI H5N1 transmission rate

- The **intervention strategies** to control the spread of HPAI H5N1 include:

Type of intervention	Implementation date
Culling (depopulation of infected premises or decontamination)	Feb. 7^{th}, 2006
Movement restrictions	Feb. 20^{th}, 2006
Payment of compensation	late 2006 until early 2007
Improved biosecurity	—

- **Assumption:** the net effect of these interventions have an instantaneous impact on the transmission rate $\beta(t)$

$$\beta(t) = \begin{cases} \beta_0 & \text{for } t < \tau, \\ \beta_1 & \text{for } t \geq \tau, \end{cases}$$

where $\beta_0 > \beta_1$, and τ is the time at which interventions begin

Parameter estimation

Parameter estimation

- **Vector of parameters:** $\vec{\theta} = (\beta_0, \beta_1)^T \in \mathbb{R}_+^2$

Parameter estimation

- **Vector of parameters:** $\vec{\theta} = (\beta_0, \beta_1)^T \in \mathbb{R}^2_+$
- **Mathematical model:**

$$f(t_i, \vec{\theta}) = \begin{cases} C(t_1) & \text{if } i = 1 \\ C(t_i) - C(t_{i-1}) & \text{if } 2 \leq i \leq n \end{cases}$$

Parameter estimation

- **Vector of parameters:** $\vec{\theta} = (\beta_0, \beta_1)^T \in \mathbb{R}^2_+$
- **Mathematical model:**

$$f(t_i, \vec{\theta}) = \begin{cases} C(t_1) & \text{if } i = 1 \\ C(t_i) - C(t_{i-1}) & \text{if } 2 \leq i \leq n \end{cases}$$

- **Statistical model:** (ordinary least square)

Parameter estimation

- **Vector of parameters:** $\vec{\theta} = (\beta_0, \beta_1)^T \in \mathbb{R}_+^2$
- **Mathematical model:**

$$f(t_i, \vec{\theta}) = \begin{cases} C(t_1) & \text{if } i = 1 \\ C(t_i) - C(t_{i-1}) & \text{if } 2 \leq i \leq n \end{cases}$$

- **Statistical model:** (ordinary least square)
  - Random variable: $Y_i = f(t_i; \vec{\theta}_0) + \varepsilon_i, \quad \text{for } i = 1, \ldots, n$

Parameter estimation

- **Vector of parameters:** $\vec{\theta} = (\beta_0, \beta_1)^T \in \mathbb{R}^2_+$
- **Mathematical model:**

$$f(t_i, \vec{\theta}) = \begin{cases} C(t_1) & \text{if } i = 1 \\ C(t_i) - C(t_{i-1}) & \text{if } 2 \leq i \leq n \end{cases}$$

- **Statistical model:** (ordinary least square)
  - Random variable: $Y_i = f(t_i; \vec{\theta}_0) + \varepsilon_i, \quad \text{for } i = 1, \ldots, n$
  - A realization: $y_i = f(t_i; \vec{\theta}_0) + \epsilon_i, \quad \text{for } i = 1, \ldots, n$

Parameter estimation

- **Vector of parameters:** $\vec{\theta} = (\beta_0, \beta_1)^T \in \mathbb{R}^2_+$
- **Mathematical model:**

$$f(t_i, \vec{\theta}) = \begin{cases} C(t_1) & \text{if } i = 1 \\ C(t_i) - C(t_{i-1}) & \text{if } 2 \leq i \leq n \end{cases}$$

- **Statistical model:** (ordinary least square)
  - Random variable: $Y_i = f(t_i; \vec{\theta}_0) + \varepsilon_i, \quad \text{for } i = 1, \ldots, n$
  - A realization: $y_i = f(t_i; \vec{\theta}_0) + \epsilon_i, \quad \text{for } i = 1, \ldots, n$
- **Cost functional:**

$$J_n(\vec{\theta}) = \sum_{i=1}^{n} |y_i - \mathrm{f}(t_i; \vec{\theta})|^2$$

Parameter estimation

- **Vector of parameters:** $\vec{\theta} = (\beta_0, \beta_1)^T \in \mathbb{R}^2_+$
- **Mathematical model:**

$$f(t_i, \vec{\theta}) = \begin{cases} C(t_1) & \text{if } i = 1 \\ C(t_i) - C(t_{i-1}) & \text{if } 2 \le i \le n \end{cases}$$

- **Statistical model:** (ordinary least square)
  - Random variable: $Y_i = f(t_i; \vec{\theta}_0) + \varepsilon_i, \quad \text{for } i = 1, \ldots, n$
  - A realization: $y_i = f(t_i; \vec{\theta}_0) + \epsilon_i, \quad \text{for } i = 1, \ldots, n$
- **Cost functional:**

$$J_n(\vec{\theta}) = \sum_{i=1}^{n} |y_i - \mathrm{f}(t_i; \vec{\theta})|^2$$

- **Estimation of $\hat{\theta}$:** (*fminsearch*, *lsqnonlin* and *lsqcurvefit*: MATLAB 7.9.0 (R2009b, The MathWorks))

$$\vec{\theta}^{(k+1)} = \arg\min_{\vec{\theta} \in \mathbb{R}^2_+} J_n(\vec{\theta}^{(k)})$$

Parameter estimation: implementation

Parameter estimation: implementation

Input:

symbol	description
N_{iter}	maximum number of iterations
q	resolution desired for convergence ($TOL = 10^{-q}$)
k	set the number of iterations to zero ($k = 0$)
$\vec{\theta}^{(0)}$	initial guess values

Parameter estimation: implementation

Input:

symbol	description
N_{iter}	maximum number of iterations
q	resolution desired for convergence ($TOL = 10^{-q}$)
k	set the number of iterations to zero ($k = 0$)
$\vec{\theta}^{(0)}$	initial guess values

step 1 Do { step 2 to step 3 }
While$((k \leq N_{iter}) \& (||\vec{\theta}^{(k-1)} - \vec{\theta}^{(k)}||_2 \geq \text{TOL}))$

Parameter estimation: implementation

Input:

symbol	description
N_{iter}	maximum number of iterations
q	resolution desired for convergence ($TOL = 10^{-q}$)
k	set the number of iterations to zero ($k = 0$)
$\vec{\theta}^{(0)}$	initial guess values

step 1 Do { step 2 to step 3 }

While$((k \leq N_{iter})\&(||\vec{\theta}^{(k-1)} - \vec{\theta}^{(k)}||_2 \geq \text{TOL}))$

step 2 Compute the $k+1$ estimate $\vec{\theta}^{(k+1)}$ for the estimator $\vec{\theta}_{LS}$ by solving

$$\vec{\theta}^{(k+1)} = \arg\min_{\vec{\theta} \in \mathbb{R}^2_+} J_n(\vec{\theta}^{(k)})$$

Parameter estimation: implementation

Input:

symbol	description
N_{iter}	maximum number of iterations
q	resolution desired for convergence ($TOL = 10^{-q}$)
k	set the number of iterations to zero ($k = 0$)
$\vec{\theta}^{(0)}$	initial guess values

step 1 Do { step 2 to step 3 }
While$((k \leq N_{iter})\&(||\vec{\theta}^{(k-1)} - \vec{\theta}^{(k)}||_2 \geq \text{TOL}))$

step 2 Compute the $k+1$ estimate $\vec{\theta}^{(k+1)}$ for the estimator $\vec{\theta}_{LS}$ by solving

$$\vec{\theta}^{(k+1)} = \arg\min_{\vec{\theta}\in\mathbb{R}^2_+} J_n(\vec{\theta}^{(k)})$$

step 3 Increment the number of iteration by one $k = k + 1$

Parameter estimation: implementation

Input:

symbol	description
N_{iter}	maximum number of iterations
q	resolution desired for convergence ($TOL = 10^{-q}$)
k	set the number of iterations to zero ($k = 0$)
$\vec{\theta}^{(0)}$	initial guess values

step 1 Do { step 2 to step 3 }
While$((k \leq N_{iter})\&(||\vec{\theta}^{(k-1)} - \vec{\theta}^{(k)}||_2 \geq \text{TOL}))$

step 2 Compute the $k+1$ estimate $\vec{\theta}^{(k+1)}$ for the estimator $\vec{\theta}_{LS}$ by solving

$$\vec{\theta}^{(k+1)} = \arg\min_{\vec{\theta}\in\mathbb{R}^2_+} J_n(\vec{\theta}^{(k)})$$

step 3 Increment the number of iteration by one $k = k + 1$

Output: Set the estimator $\hat{\theta}_{LS} = \vec{\theta}^{(k)}$, where $\vec{\theta}^{(k)}$ is a realization of the random variable $\hat{\theta}_{LS}$

Empirical distributions

Empirical distributions

Definitions:

Empirical distributions

Definitions:

1) The **peak epidemic size** is defined as the maximum number of new infected farms throughout the entire course of an epidemic ($max\{f\}$)

Empirical distributions

Definitions:

1) The **peak epidemic size** is defined as the maximum number of new infected farms throughout the entire course of an epidemic ($max\{f\}$)
2) The **epidemic size** at week ten is defined as the cumulative number of new infected poultry farms at week ten ($C(t = 10)$)

Stochastic epidemic model

Stochastic epidemic model

- Markov jump process: $X_t = \{(S_t, E_{1,t}, \ldots, E_{n_E,t}, I_{1,t}, \ldots, I_{n_I,t}, R_t) : t \in \mathbb{R}_+\}$

Stochastic epidemic model

- Markov jump process: $X_t = \{(S_t, E_{1,t}, \ldots, E_{n_E,t}, I_{1,t}, \ldots, I_{n_I,t}, R_t) : t \in \mathbb{R}_+\}$
- State space: $\mathbb{Z}_+^{n_E+n_I+2}$

Stochastic epidemic model

- Markov jump process: $X_t = \{(S_t, E_{1,t}, \ldots, E_{n_E,t}, I_{1,t}, \ldots, I_{n_I,t}, R_t) : t \in \mathbb{R}_+\}$
- State space: $\mathbb{Z}_+^{n_E+n_I+2}$
- The notation $X + (e_{i+1} - e_i)^T = [X_1, \ldots, X_i - 1, X_{i+1} + 1, \ldots, X_{n_E+n_I+2}]$ indicates the current state of the process X after the occurrence of an event or "jump"

Stochastic epidemic model

- Markov jump process: $X_t = \{(S_t, E_{1,t}, \ldots, E_{n_E,t}, I_{1,t}, \ldots, I_{n_I,t}, R_t) : t \in \mathbb{R}_+\}$
- State space: $\mathbb{Z}_+^{n_E+n_I+2}$
- The notation $X + (e_{i+1} - e_i)^T = [X_1, \ldots, X_i - 1, X_{i+1} + 1, \ldots, X_{n_E+n_I+2}]$ indicates the current state of the process X after the occurrence of an event or “jump”

Event	From	To	Rate
Exposure of poultry farms	X	$X + (e_2 - e_1)^T$	$\beta SI/N$
Progression from the latent stage E_i to E_{i+1} for $i = 1, \ldots, n_E - 1$	X	$X + (e_{i+2} - e_{i+1})^T$	$n_E \kappa E_i$
Infection	X	$X + (e_{n_E+2} - e_{n_E+1})^T$	$n_E \kappa E_{n_E}$
Progression from the infectious stage I_i to I_{i+1} for $i = 1, \ldots, n_I - 1$	X	$X + (e_{i+n_E+2} - e_{i+n_E+1})^T$	$n_I \gamma I_i$
Removal	X	$X + (e_{n_E+n_I+2} - e_{n_E+n_I+1})^T$	$n_I \gamma I_{n_I}$

Stochastic epidemic model

Stochastic epidemic model

The corresponding transition probabilities of the events are given by:

$$
\begin{aligned}
P(X_{t+\Delta t} - X_t = (e_2 - e_1)^T) &= \frac{\beta_t}{N_t} S_t \sum_{j=1}^{n_I} I_t \Delta t + o(\Delta t) \\
P(X_{t+\Delta t} - X_t = (e_{i+2} - e_{i+1})^T) &= n_E \kappa E_{i,t} \Delta t + o(\Delta t) \\
&\quad \text{for } i = 1, \ldots, n_E - 1 \\
P(X_{t+\Delta t} - X_t = (e_{n_E+2} - e_{n_E+1})^T) &= n_E \kappa E_{n_E,t} \Delta t + o(\Delta t) \\
P(X_{t+\Delta t} - X_t = (e_{i+n_E+2} - e_{i+n_E+1})^T) &= n_I \gamma I_{i,t} \Delta t + o(\Delta t) \\
&\quad \text{for } i = 1, \ldots, n_I - 1 \\
P(X_{t+\Delta t} - X_t = (e_{n_E+n_I+2} - e_{n_E+n_I+1})^T) &= n_I \gamma I_{n_I,t} \Delta t + o(\Delta t)
\end{aligned}
$$

Stochastic epidemic model

Stochastic epidemic model

Assumptions:

Stochastic epidemic model

Assumptions:

- **Waiting times** $(0 < W_1 < W_2 < \ldots)$ with exponentially distributed increments $(\{T_i\})$

$$P(T_i = W_i - W_{i-1} > t | W_j, j \leq i-1) = e^{-t\mu(W_{i-1})}$$

Stochastic epidemic model

Assumptions:

- **Waiting times** $(0 < W_1 < W_2 < \ldots)$ with exponentially distributed increments $(\{T_i\})$

$$P(T_i = W_i - W_{i-1} > t | W_j, j \leq i - 1) = e^{-t\mu(W_{i-1})}$$

- Parameter μ

$$\mu(W_{i-1}) = \left(\frac{\beta(W_{i-1})}{N(W_{i-1})} S(W_{i-1}) \sum_{j=1}^{n_I} I_j(W_{i-1}) + n_E \kappa \sum_{j=1}^{n_E} E_j(W_{i-1}) + n_I \gamma \sum_{j=1}^{n_I} I_j(W_{i-1}) \right)^{-1}$$

Stochastic epidemic model

Assumptions:

- **Waiting times** $(0 < W_1 < W_2 < \ldots)$ with exponentially distributed increments $(\{T_i\})$

$$P(T_i = W_i - W_{i-1} > t | W_j, j \leq i-1) = e^{-t\mu(W_{i-1})}$$

- Parameter μ

$$\mu(W_{i-1}) = \left(\frac{\beta(W_{i-1})}{N(W_{i-1})} S(W_{i-1}) \sum_{j=1}^{n_I} I_j(W_{i-1}) + n_E \kappa \sum_{j=1}^{n_E} E_j(W_{i-1}) + n_I \gamma \sum_{j=1}^{n_I} I_j(W_{i-1}) \right)^{-1}$$

Implementation:

Stochastic epidemic model

Assumptions:

- **Waiting times** ($0 < W_1 < W_2 < \ldots$) with exponentially distributed increments ($\{T_i\}$)

$$P(T_i = W_i - W_{i-1} > t | W_j, j \leq i-1) = e^{-t\mu(W_{i-1})}$$

- Parameter μ

$$\mu(W_{i-1}) = \left(\frac{\beta(W_{i-1})}{N(W_{i-1})} S(W_{i-1}) \sum_{j=1}^{n_I} I_j(W_{i-1}) + n_E \kappa \sum_{j=1}^{n_E} E_j(W_{i-1}) + n_I \gamma \sum_{j=1}^{n_I} I_j(W_{i-1}) \right)^{-1}$$

Implementation:

- Gillespie's direct algorithm [D. T. Gillespie, 1976]

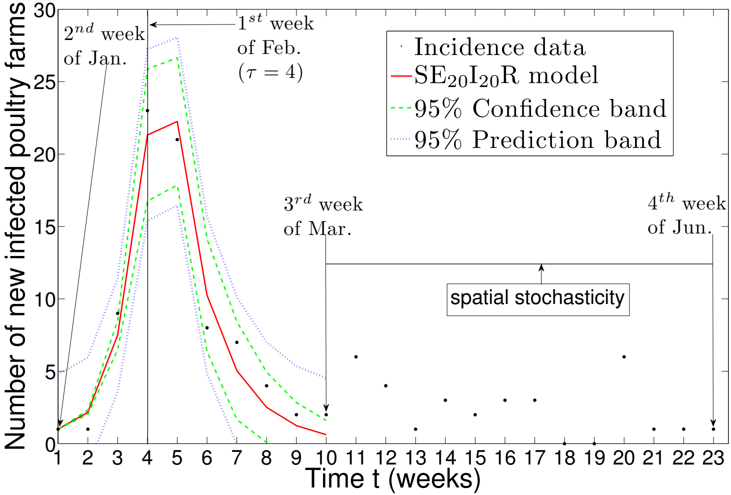
Table 1: Model parameters

Table 1: Model parameters

Symbol	Description	Source	Value
β_0	Pre-intervention transmission rate	Estimated	2.33 weeks^{-1} (95% CI: 2.26, 2.41)
β_1	Post-intervention transmission rate	Estimated	0.63 weeks^{-1} (95% CI: 0.54, 0.73)
$1/\kappa$	Mean incubation period	[J. A. Van der Goot, *et. at.*, PNAS 2005]	2 days
$1/\gamma$	Mean infectious period	[J. A. Van der Goot, *et. at.*, PNAS 2005]	6.3 days
$I_1(t_1)$	Initial number of infected poultry farms	From data	1
$N(t_1)$	Initial total number of poultry farms	[Federal Department of Livestock]	$7,000$
n_E	Number of sub-compartment for the exposed class	[J. A. Van der Goot, *et. at.*, PNAS 2005, M. E. Bos, *et. at.*, Vet. Research 2007]	20
n_I	Number of subcompartment for the infectious class	[J. A. Van der Goot, *et. at.*, PNAS 2005, M. E. Bos, *et. at.*, Vet. Research 2007]	20
τ	Time at which interventions begin	[F. O. Fasina, *et. at.*, Epid. Inf. 2009]	4^{th} week (Feb. 7^{th}, 2006)

Data and fit

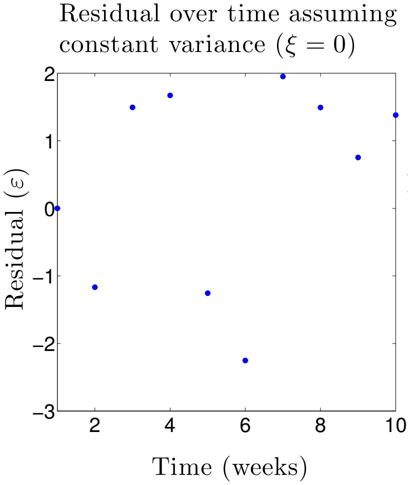
Data and fit



Number of new infected poultry farms
Time t (weeks)
Incidence data
SE$_{20}$I$_{20}$R model
95% Confidence band
95% Prediction band
2^{nd} week of Jan.
1^{st} week of Feb. ($\tau = 4$)
3^{rd} week of Mar.
4^{th} week of Jun.
spatial stochasticity

Residual plots

Residual plots



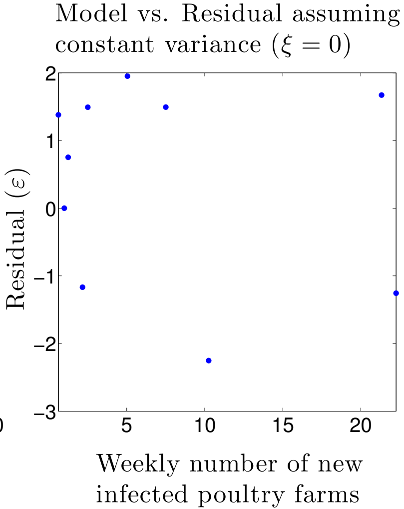


Table 2: Basic reproduction number estimates

Table 2: Basic reproduction number estimates

Number of compartments n_E	n_I	Basic reproduction number formula $(\mathcal{R}_0(\lambda = 1.156, n_E, n_I))$	Estimate $(\hat{\mathcal{R}}_0)$	$SE(\hat{\mathcal{R}}_0)$	95% CI
–	–	$\mathcal{R}_0 = \beta_0 D_I$	2.10	0.03	(2.04, 2.17)
–	–	$\mathcal{R}_p = \beta_1 D_I$	0.57	0.04	(0.48, 0.67)
1	1	$(\lambda D_I + 1)(\lambda D_E + 1)$	2.72	0.04	(2.59, 2.84)
1	$n_I = 20$	$\frac{\lambda D_I(\lambda D_E+1)}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.17	0.03	(2.08, 2.26)
1	$n_I \to \infty$	$\frac{\lambda D_I(\lambda D_E+1)}{1-e^{-\lambda D_I}}$	2.14	0.03	(2.05, 2.23)
$n_E = 20$	1	$(\lambda D_I + 1)(\lambda D_E/n_E + 1)^{n_E}$	2.83	0.04	(2.69, 2.98)
$n_E = 20$	$n_I = 20$	$\frac{\lambda D_I(\lambda D_E/n_E+1)^{n_E}}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.27	0.03	(2.16, 2.37)
$n_E = 20$	$n_I \to \infty$	$\frac{\lambda D_I(\lambda D_E/n_E+1)^{n_E}}{1-e^{-\lambda D_I}}$	2.23	0.03	(2.13, 2.34)
$n_E \to \infty$	1	$(\lambda D_I + 1)e^{\lambda D_E}$	2.84	0.05	(2.7, 2.98)
$n_E \to \infty$	$n_I = 20$	$\frac{\lambda D_I e^{\lambda D_E}}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.27	0.03	(2.17, 2.38)
$n_E \to \infty$	$n_I \to \infty$	$\frac{\lambda D_I e^{\lambda D_E}}{1-e^{-\lambda D_I}}$	2.24	0.03	(2.14, 2.34)

Table 2: Basic reproduction number estimates

Number of compartments n_E	n_I	Basic reproduction number formula $(\mathcal{R}_0(\lambda = 1.156, n_E, n_I))$	Estimate $(\hat{\mathcal{R}}_0)$	$SE(\hat{\mathcal{R}}_0)$	95% CI
–	–	$\mathcal{R}_0 = \beta_0 D_I$	2.10	0.03	(2.04, 2.17)
–	–	$\mathcal{R}_p = \beta_1 D_I$	0.57	0.04	(0.48, 0.67)
1	1	$(\lambda D_I + 1)(\lambda D_E + 1)$	2.72	0.04	(2.59, 2.84)
1	$n_I = 20$	$\frac{\lambda D_I(\lambda D_E+1)}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.17	0.03	(2.08, 2.26)
1	$n_I \to \infty$	$\frac{\lambda D_I(\lambda D_E+1)}{1-e^{-\lambda D_I}}$	2.14	0.03	(2.05, 2.23)
$n_E = 20$	1	$(\lambda D_I + 1)(\lambda D_E/n_E + 1)^{n_E}$	2.83	0.04	(2.69, 2.98)
$n_E = 20$	$n_I = 20$	$\frac{\lambda D_I(\lambda D_E/n_E+1)^{n_E}}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.27	0.03	(2.16, 2.37)
$n_E = 20$	$n_I \to \infty$	$\frac{\lambda D_I(\lambda D_E/n_E+1)^{n_E}}{1-e^{-\lambda D_I}}$	2.23	0.03	(2.13, 2.34)
$n_E \to \infty$	1	$(\lambda D_I + 1)e^{\lambda D_E}$	2.84	0.05	(2.7, 2.98)
$n_E \to \infty$	$n_I = 20$	$\frac{\lambda D_I e^{\lambda D_E}}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.27	0.03	(2.17, 2.38)
$n_E \to \infty$	$n_I \to \infty$	$\frac{\lambda D_I e^{\lambda D_E}}{1-e^{-\lambda D_I}}$	2.24	0.03	(2.14, 2.34)

[H. J. Wearing *et. at.*, PLoS Medicine 2005]

Table 2: Basic reproduction number estimates

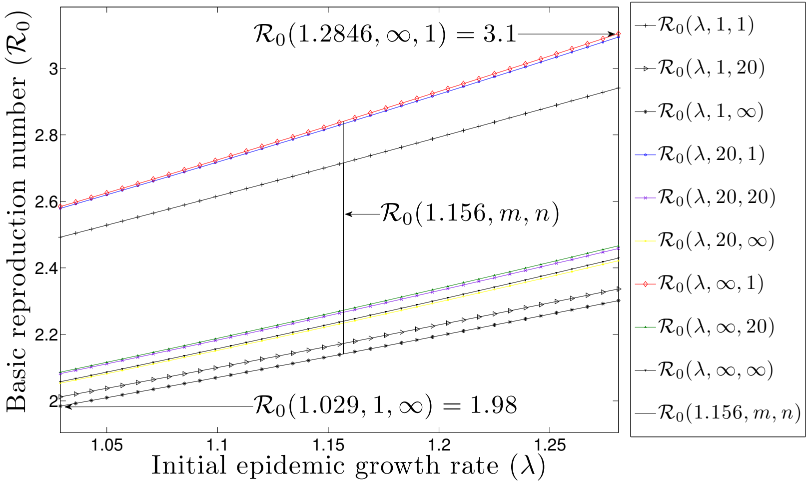
Number of compartments n_E	n_I	Basic reproduction number formula ($\mathcal{R}_0(\lambda = 1.156, n_E, n_I)$)	Estimate ($\hat{\mathcal{R}}_0$)	$SE(\hat{\mathcal{R}}_0)$	95% CI
–	–	$\mathcal{R}_0 = \beta_0 D_I$	2.10	0.03	(2.04, 2.17)
–	–	$\mathcal{R}_p = \beta_1 D_I$	0.57	0.04	(0.48, 0.67)
1	1	$(\lambda D_I + 1)(\lambda D_E + 1)$	2.72	0.04	(2.59, 2.84)
1	$n_I = 20$	$\frac{\lambda D_I(\lambda D_E+1)}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.17	0.03	(2.08, 2.26)
1	$n_I \to \infty$	$\frac{\lambda D_I(\lambda D_E+1)}{1-e^{-\lambda D_I}}$	2.14	0.03	(2.05, 2.23)
$n_E = 20$	1	$(\lambda D_I + 1)(\lambda D_E/n_E + 1)^{n_E}$	2.83	0.04	(2.69, 2.98)
$n_E = 20$	$n_I = 20$	$\frac{\lambda D_I(\lambda D_E/n_E+1)^{n_E}}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.27	0.03	(2.16, 2.37)
$n_E = 20$	$n_I \to \infty$	$\frac{\lambda D_I(\lambda D_E/n_E+1)^{n_E}}{1-e^{-\lambda D_I}}$	2.23	0.03	(2.13, 2.34)
$n_E \to \infty$	1	$(\lambda D_I + 1)e^{\lambda D_E}$	2.84	0.05	(2.7, 2.98)
$n_E \to \infty$	$n_I = 20$	$\frac{\lambda D_I e^{\lambda D_E}}{1-(\lambda D_I/n_I+1)^{-n_I}}$	2.27	0.03	(2.17, 2.38)
$n_E \to \infty$	$n_I \to \infty$	$\frac{\lambda D_I e^{\lambda D_E}}{1-e^{-\lambda D_I}}$	2.24	0.03	(2.14, 2.34)

[H. J. Wearing *et. at.*, PLoS Medicine 2005]

[A.L. Lloyd, 2009]

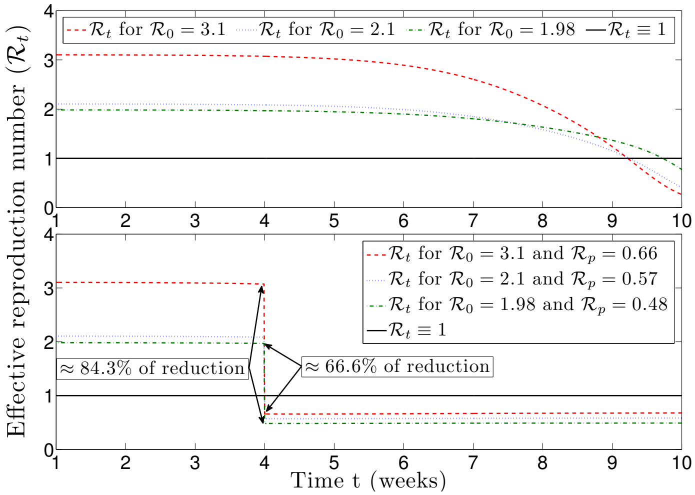
Basic reproduction number

Basic reproduction number



Effective reproduction number

Effective reproduction number



$$66.6\% = \left(1 - \frac{0.66}{1.98}\right)100\% \leq \left(1 - \frac{\mathcal{R}_p}{\mathcal{R}_0}\right)100\% \leq \left(1 - \frac{0.48}{3.1}\right)100\% = 84.3\%$$

Histograms

Histograms

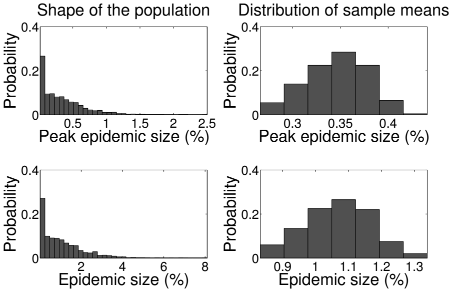


Figure: With interventions

Histograms

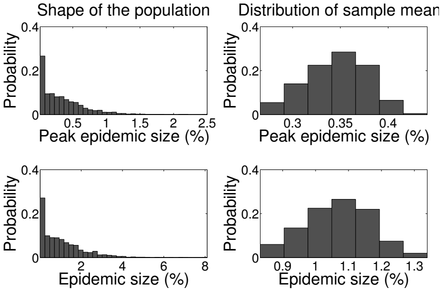


Figure: With interventions

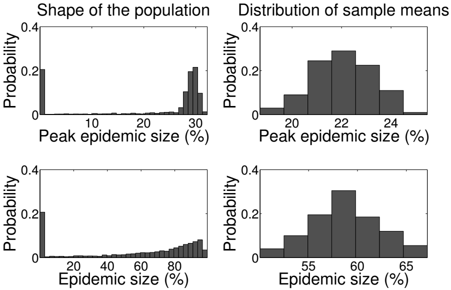


Figure: Without interventions

Table 3: Peak and epidemic size estimates

Table 3: Peak and epidemic size estimates

		Random variables	
		Peak epidemic size	Epidemic size at the 10^{th} week
With interventions	No.	29.8 (95% CI: 29.06, 30.7)	92.4 (95% CI: 89.7, 95.1)
	% of the $N(t_1)$	0.42% (95% CI: 0.41%, 0.43%)	1.32% (95% CI: 1.28%, 1.35%)
Without interventions	No.	1906.5 (95% CI: 1891, 1921)	5071.6 (95% CI: 5003, 5140)
	% of the $N(t_1)$	27.2% (95% CI: 27.02%, 27.45%)	72.4% (95% CI: 71.4%, 73.4%)
Reduction	No.	1,876.7	4,979.2
	%	98.4%	98.2%

Table 4: Comparison of basic reproduction number estimates

Table 4: Comparison of basic reproduction number estimates

Country	**Time period**	**A. I. virus subtype**	**Serial interval (days)**	$\mathcal{R}_0$	Reference
Nigeria	Jan 2006-Jun 2006	H5N1	12	1.98-3.1	This study
*Thailand	Jul 2004-Nov 2004	H5N1	1-4	2.26-2.64	[T. Tiensin *et. al.*, J. Infect. Dis. 2004]
Romania	May 2006-Jun 2006	H5N1	7	1.95-2.68	[M. P. Ward, *et. al.*,, Epid. Infect. 2008]
The Netherlands	Feb 2003-May 2003	H7N7	12	3.1-6.5	[A. Stegeman, *et. al.*, J. Infect. Dis. 2004]
The Netherlands	Feb 2003-May 2003	H7N7	12	4.0-6.9	[A. Le Menach, *et. al.*, Proc Biol. Sci. 2006]
The Netherlands	Feb 2003-May 2003	H7N7	1.9-3.4	1.1-1.9	[T. Garske, *et. al.*, PLoS ONE 2007]
Italy	Mar 1999-Apr 2000	H7N7	5	1.9	[T. Garske, *et. al.*, PLoS ONE 2007]
Canada (British Columbia)	Feb 2004 May 2004	H7N3	8.4	2.4	[T. Garske, *et. al.*, PLoS ONE 2007]

*With the exception of the Thai study (where $\mathcal{R}_0$ was estimated at the within-flock level, Tiensin *et al.*, 2007), all of these studies estimated $\mathcal{R}_0$ between flocks

Discussion

Discussion

- **Summary:**

Discussion

- **Summary:**
  - From the deterministic and statistical approaches: $\hat{\beta}_0, \hat{\beta}_1, \hat{\lambda} \rightarrow \hat{\mathcal{R}}_0, \hat{\mathcal{R}}_p, \hat{\mathcal{R}}_t \rightarrow$ % of reduction in $\hat{\mathcal{R}}_t$

Discussion

- **Summary:**
  - From the deterministic and statistical approaches:
    $\hat{\beta}_0, \hat{\beta}_1, \hat{\lambda} \rightarrow \hat{\mathcal{R}}_0, \hat{\mathcal{R}}_p, \hat{\mathcal{R}}_t \rightarrow$ % of reduction in $\hat{\mathcal{R}}_t$
  - From the stochastic approach:
    Empirical distributions $\rightarrow$ expectations $\rightarrow$ % of reduction

Discussion

- **Summary:**
  - From the deterministic and statistical approaches: $\hat{\beta}_0, \hat{\beta}_1, \hat{\lambda} \rightarrow \hat{\mathcal{R}}_0, \hat{\mathcal{R}}_p, \hat{\mathcal{R}}_t \rightarrow$ % of reduction in $\hat{\mathcal{R}}_t$
  - From the stochastic approach: Empirical distributions $\rightarrow$ expectations $\rightarrow$ % of reduction
- **Main weakness our approaches:** non-spatial consideration

Discussion

- **Summary:**
  - From the deterministic and statistical approaches: $\hat{\beta}_0, \hat{\beta}_1, \hat{\lambda} \rightarrow \hat{\mathcal{R}}_0, \hat{\mathcal{R}}_p, \hat{\mathcal{R}}_t \rightarrow$ % of reduction in $\hat{\mathcal{R}}_t$
  - From the stochastic approach: Empirical distributions $\rightarrow$ expectations $\rightarrow$ % of reduction
- **Main weakness our approaches:** non-spatial consideration
- **Future considerations:**

Discussion

- **Summary:**
  - From the deterministic and statistical approaches:
    $\hat{\beta}_0, \hat{\beta}_1, \hat{\lambda} \rightarrow \hat{\mathcal{R}}_0, \hat{\mathcal{R}}_p, \hat{\mathcal{R}}_t \rightarrow$ % of reduction in $\hat{\mathcal{R}}_t$
  - From the stochastic approach:
    Empirical distributions $\rightarrow$ expectations $\rightarrow$ % of reduction
- **Main weakness our approaches:** non-spatial consideration
- **Future considerations:**
  - [G. Chowell *et. al.*, Preventive Veterinary Medicine 2006]

Discussion

- **Summary:**
  - From the deterministic and statistical approaches:
    $\hat{\beta}_0, \hat{\beta}_1, \hat{\lambda} \to \hat{\mathcal{R}}_0, \hat{\mathcal{R}}_p, \hat{\mathcal{R}}_t \to$ % of reduction in $\hat{\mathcal{R}}_t$
  - From the stochastic approach:
    Empirical distributions $\to$ expectations $\to$ % of reduction
- **Main weakness our approaches:** non-spatial consideration
- **Future considerations:**
  - [G. Chowell *et. al*., Preventive Veterinary Medicine 2006]
  - 1) the estimated total number of chickens, where each chicken is treated as an individual epidemiological unit, 2) the spatial coordinates for every poultry farm, 3) the inter-centroid for every county, and 4) the actual number or average number of farms per county, we could potentially analyze the epidemic at both the local and national level

Conclusion

Conclusion

- This study shows that it is possible to adjust the incidence data with a non-spatial mathematical model and still obtain reasonable estimates of the basic reproduction number of HPAI H5N1 between poultry farms at a national level

Conclusion

- This study shows that it is possible to adjust the incidence data with a non-spatial mathematical model and still obtain reasonable estimates of the basic reproduction number of HPAI H5N1 between poultry farms at a national level
- However, given the mechanisms of propagation of avian influenza between or within poultry farms, incorporating explicit spatial features into the mathematical model may be essential for understanding the dynamics of the Nigerian epidemic

Conclusion

- This study shows that it is possible to adjust the incidence data with a non-spatial mathematical model and still obtain reasonable estimates of the basic reproduction number of HPAI H5N1 between poultry farms at a national level
- However, given the mechanisms of propagation of avian influenza between or within poultry farms, incorporating explicit spatial features into the mathematical model may be essential for understanding the dynamics of the Nigerian epidemic
- Our results confirmed the effectiveness of the intervention strategies

Conclusion

- This study shows that it is possible to adjust the incidence data with a non-spatial mathematical model and still obtain reasonable estimates of the basic reproduction number of HPAI H5N1 between poultry farms at a national level
- However, given the mechanisms of propagation of avian influenza between or within poultry farms, incorporating explicit spatial features into the mathematical model may be essential for understanding the dynamics of the Nigerian epidemic
- Our results confirmed the effectiveness of the intervention strategies
- Overall, estimates for $\mathcal{R}_0$ are in line with those estimates for the HPAI H5N1 outbreaks in Romania and an outbreak of H7N3 in British Columbia, Canada

Conclusion

- This study shows that it is possible to adjust the incidence data with a non-spatial mathematical model and still obtain reasonable estimates of the basic reproduction number of HPAI H5N1 between poultry farms at a national level
- However, given the mechanisms of propagation of avian influenza between or within poultry farms, incorporating explicit spatial features into the mathematical model may be essential for understanding the dynamics of the Nigerian epidemic
- Our results confirmed the effectiveness of the intervention strategies
- Overall, estimates for $\mathcal{R}_0$ are in line with those estimates for the HPAI H5N1 outbreaks in Romania and an outbreak of H7N3 in British Columbia, Canada
- If spatial data related to the distribution of future outbreaks of HPAI H5N1 in Nigeria were to become available through improved surveillance, it could be incorporated into mathematical models to more accurately estimate key epidemiological parameters at both the local and national level, thus improving our ability to assess intervention strategies, and to predict and prevent future outbreaks

Acknowledgements

Acknowledgements

Dr. Michael Golinski

Mathematical and Computational Modeling Sciences Center,
School of Human Evolution and Social Change,
Arizona State University, PO Box 872402, Tempe, AZ 85287-2402, USA

Acknowledgements

Dr. Michael Golinski

Mathematical and Computational Modeling Sciences Center,
School of Human Evolution and Social Change,
Arizona State University, PO Box 872402, Tempe, AZ 85287-2402, USA

Dr. Ariel L. Rivas

Population Health and Pathobiology,
North Carolina State University, Raleigh, NC 27606, USA

Acknowledgements

Dr. Michael Golinski

Mathematical and Computational Modeling Sciences Center,
School of Human Evolution and Social Change,
Arizona State University, PO Box 872402, Tempe, AZ 85287-2402, USA

Dr. Ariel L. Rivas

Population Health and Pathobiology,
North Carolina State University, Raleigh, NC 27606, USA

Dr. Folorunso O. Fasina

National Veterinary Research Institute,
PMB 01, Vom, Plateau, Nigeria and
Department of Farm Animal Health, Faculty of Veterinary Medicine,
Utrecht University, Yalenaan, the Netherlands

Acknowledgements

Dr. Michael Golinski

Mathematical and Computational Modeling Sciences Center,
School of Human Evolution and Social Change,
Arizona State University, PO Box 872402, Tempe, AZ 85287-2402, USA

Dr. Ariel L. Rivas

Population Health and Pathobiology,
North Carolina State University, Raleigh, NC 27606, USA

Dr. Folorunso O. Fasina

National Veterinary Research Institute,
PMB 01, Vom, Plateau, Nigeria and
Department of Farm Animal Health, Faculty of Veterinary Medicine,
Utrecht University, Yalenaan, the Netherlands

Dr. Gerardo Chowell

Mathematical and Computational Modeling Sciences Center,
School of Human Evolution and Social Change,
Arizona State University, PO Box 872402, Tempe, AZ 85287-2402, USA and
Division of Epidemiology and Population Studies, Fogarty International Center
National Institutes of Health, Bethesda, MD, USA