A multi-scale problem arising in a model of avian flu virus in a seabird colony

C F Clancy, M J A O’Callaghan and T C Kelly

Department of Applied Mathematics, Aras na Laoi, University College Cork, Ireland
Department of Zoology, Ecology and Plant Science, Distillery Fields, North Mall, University College Cork, Ireland
*Corresponding author
E-mail: mja.ocallaghan@ucc.ie

Abstract. Understanding the dynamics of epidemics of novel pathogens such as the H5N1 strain of avian influenza is of crucial importance to public and veterinary health as well as wildlife ecology. We model the effect of a new virus on a seabird colony, where no pre-existing Herd Immunity exists. The seabirds in question are so-called K-strategists, i.e. they have a relatively long life expectancy and very low reproductive output. They live in isolated colonies which typically contain tens of thousands of birds. These densely populated colonies, with so many birds competing for nesting space, would seem to provide perfect conditions for the entry and spread of an infection. Yet there are relatively few reported cases of epidemics among these seabirds. We develop a SEIR model which incorporates some of the unusual features of seabird population biology and examine the effects of introducing a pathogen into the colony.

1. Introduction

Epidemics continue to be a major focus of modern science. Epidemic disease poses a threat to human kind, farm animals, crops and to wildlife and therefore to the stability of ecological systems and to the global economy (Millennium Ecosystems Synthesis Report 2005) [15]. Seabirds are an unusual element in the earth’s fauna. They are on average larger in size than land birds but there are many fewer species ($n = 300$ approximately — only 3% of the total). However, seabirds foregather and breed in very large inaccessible colonies which may number in excess of one million individuals (Croxall, 1987 [8]). It is therefore remarkable that there have been relatively few reported incidences of epidemics among marine birds at their densely populated colonies e.g. Newton (1998) [16].

Most directly transmitted infectious disease travels from host to host in a chain type reaction. Therefore the more densely packed the hosts the greater the opportunity for both the entry and spread of an infectious pathogen. In this paper we attempt to model the introduction and transmission dynamics of a novel avian pathogen, i.e. the bird flu H5N1, within the receiving population which is believed to have had no previous exposure to the virus and thus there is no Herd Immunity. More specifically we aim to model the epidemiology of a novel pathogen in a dense population of homeothermic vertebrates with exceptional life history strategies. Marine birds are so-called K-strategists. This means that they have a long life expectancy but in any one year have a very low — often minimal — reproductive output. Since the reproductive rate
is directly proportional to the number of susceptibles in the host population it is of interest to model the spread of a pathogen in this somewhat unusual potential disease focus.

Clearly it is vital to understand the dynamics of such an outbreak so that sufficient preventative measures can be taken. Mathematical modelling is a useful tool for this. Van der Goot et al [21], for instance, apply a model to identify the most effective vaccination strategy in chickens. The aim of this project is to analyze the spread of the H5N1 virus in a colony of seabirds. In particular, parameters such as transmission rates and lethality will be examined in order to assess their importance in the propagation and maintenance of the virus. It should be noted that the global stability properties of SEIR epidemic models with constant recruitment (Li and Wang 2000 [11]) have not been addressed here.

2. Basic Model

2.1. SEIR Approach

Many different methods are used to analyze virus transmission dynamics, including cellular automata (Keeling and Gilligan [13]) and forest-fire lattices (Rhodes et al [19]), and even field theory from physics (Adamek et al [1]).

In 1927, Kermack and McKendrick approached the problem by dividing the population under consideration into disjoint classes of those who are susceptible to an infection, those who are infected and those who have had the disease and are recovered. This is a very popular and much studied model (Anderson and May [3], James and Steele [12]). It has been used to describe the dynamics of numerous infectious diseases, including Bubonic plague (Keeling and Gilligan [13]), Severe Acute Respiratory Syndrome, SARS, (Anderson et al [2]) and West Nile virus (Wonham et al [23]).

In order to model the effect of the H5N1 influenza virus on a seabird colony, we divide the total population $N(t)$, a function of time, into those birds which are susceptible $S(t)$; those which have been infected but are not yet infectious $E(t)$, i.e. cannot yet transmit the virus to others; those which are infectious, $I(t)$, and those which have recovered and are immune, $R(t)$. These subclasses are clearly disjoint so that at any time $t$, the total population is $N(t) = S(t) + E(t) + I(t) + R(t)$. This division is shown in Figure 1.

The following assumptions are made for the purpose of modelling:

Figure 1. Dividing the population into subclasses
• The colony is initially assumed to be isolated, so no birds arrive or leave.
• The population is assumed to be a function of time only. Spatial variation is not taken into account. This is reasonable due to the dense nature of seabird colonies.
• The birth rate, $\alpha$, is set to be constant. While this may seem unrealistic, there are seabird species in the tropics which breed continuously. Furthermore, it is assumed that only healthy birds, i.e. the susceptibles and recovered, will breed.
• A natural death rate of $\omega$ applies to all birds. This corresponds to an average life span of $1/\omega$ years. Infected birds in the $E$ class also die at a rate $\omega_E$ due to the lethality of the virus, while the lethality rate for the infectious class $I$ is $\omega_I$.
• The roles of the rates $\beta$, $\lambda$ and $\gamma$ are as shown in Figure 1. The latency period of the virus (the time between the point of infection and the point when the bird becomes infectious) is $1/\lambda$, while the recovery period is $1/\gamma$. Time is measured in years. The $\beta$ parameter, which measures the transmission rate, will be further discussed later on.

The system can thus be described with the following set of ordinary differential equations, which are simply derived from an examination of Figure 1:

$$
\dot{S} = \alpha(S + R) - \beta SI - \omega S,
\dot{E} = \beta SI - \lambda E - \omega E - \omega_E E,
\dot{I} = \lambda E - \gamma I - \omega I - \omega_I I,
\dot{R} = \gamma I - \omega R,
$$

where dot denotes the time derivative.

2.2. Initial Conditions
It is important to examine what happens when a new pathogen is introduced to a population which has no existing herd immunity, i.e. none of the population is immune. This can be a devastating event (Kelly [14]). In 1950, for example, myxomatosis was introduced to control the rabbit population in Australia. The rabbits were completely defenseless to this highly virulent disease and 99.8% of all those infected died (Shigesada and Kawasaki [20]).

In order to solve this system, we need one initial condition for each equation. In our model we denote the initial population $N(0)$ by $N_0$. There is just a single infectious bird and so $I(0) = 1$. All other birds are susceptible, so that $S(0) = N_0 - 1$. The other initial conditions must then be $E(0) = R(0) = 0$ so as to satisfy $N(0) = S(0) + E(0) + I(0) + R(0)$.

2.3. The $R_0$ Parameter
The basic reproductive rate, $R_0$, is one of the key concepts in epidemiological modelling. It is defined as the average number of further infections that a single virus can produce. Clearly, a virus can only establish itself and remain in a population if $R_0 > 1$.

There is no definite way of calculating $R_0$. Heffernan et al [10] describe a number of commonly used methods. Anderson and May [3] extensively use the formula

$$
R_0 = 1/s^*,
$$

where $s^*$ is the fraction of the population of susceptibles at equilibrium, that is, when the rates of change of the infected and infectious populations are zero. This will be the form of $R_0$ which we adopt here.
3. Modelling Adults and Chicks

3.1. The Seabird Colony

We now adapt the basic model described in the previous section to define the colony as accurately as possible.

Seabirds live in colonies on islands and cliff faces containing tens of thousands of birds. These colonies are very densely populated. As such, they would seem to provide ideal conditions for virus epidemics to occur. Yet, surprisingly, outbreaks are, in fact, quite rare.

The reproductive output of seabirds tends to be quite low. When a guillemot chick is born, it remains in the colony for about 22 days. It then leaves and does not return for 4–5 years (Crespin et al [7]).

Each year then, there are many birds returning to find a nesting site. However, as previously mentioned, the colony is very densely inhabited and space is scarce. Thus, a ‘queue’ is formed, whereby there may considerable numbers of birds waiting nearby for an empty site to appear. A key assumption in analyzing the adult population, which seems to reasonably model the reality for seabird colonies, is that as a bird dies, thereby vacating a space in the colony, a bird from the queue fills the vacated space.

To consider these factors, we treat the adults and chicks as separate, albeit connected, populations, and apply the SEIR idea as before to each population. The extra assumptions for this separation are as follows:

- The adult susceptible population, \( S(t) \), is maintained by a ‘return’ rate which matches the total number of adults dying, both naturally and from the virus. This is done to model the queue for space that was mentioned. As soon as a bird dies, the site it vacates is immediately filled.
- Chicks are assumed to be born susceptible.
- All chicks leave at a rate \( \delta \). A value of \( 365/22 \) will be used for \( \delta \), i.e. they leave after 22 days.
- We consider the special case in which adults infect adults and chicks infect chicks. The more likely scenario of cross infection between both groups is not addressed at this time.
- All returning birds are assumed to return as susceptibles, that is, any immunity from earlier infection would be lost in the years in which it was away from the colony.
- The birth rate is still assumed constant.

The separation is as shown in Figure 2.

3.2. Equations

The following equations are readily established:

\[
\begin{align*}
\dot{S} &= \omega(S + E + I + R) + \omega_E E + \omega_I I - \beta SI - \omega S, \\
\dot{E} &= \beta SI - \lambda E - \omega E - \omega_E E, \\
\dot{I} &= \lambda E - \gamma I - \omega_I I, \\
\dot{R} &= \gamma I - \omega R, \\
\dot{S}_c &= \alpha(S + R) - \beta S_c I_c - \omega S_c - \delta S_c, \\
\dot{E}_c &= \beta S_c I_c - \lambda E_c - \omega E_c - \omega_E E_c - \delta E_c, \\
\dot{I}_c &= \lambda E_c - \gamma I_c - \omega I_c - \omega_I I_c - \delta I_c, \\
\dot{R}_c &= \gamma I_c - \omega R_c - \delta R_c.
\end{align*}
\]

The initial conditions, as discussed earlier, are given by:

\[
S(0) = N_0 - 1, \quad E(0) = 0, \quad I(0) = 1, \quad R(0) = 0, \quad S_c(0) = E_c(0) = I_c(0) = R_c(0) = 0.
\]
3.3. Scaling

We introduce the following scaling:

\[ S = N_0 A, \quad E = N_0 B, \quad I = N_0 C, \quad R = N_0 D, \]
\[ S_c = N_0 A_c, \quad E_c = N_0 B_c, \quad I_c = N_0 C_c, \quad R_c = N_0 D_c. \]

in which, now, each function is a fraction of the total initial population; for example, \( A(t) \) represents the fraction of \( N_0 \) who are adult susceptibles. On substituting these into the equations in (3), we obtain the following system:

\[
\begin{align*}
\dot{A} &= \omega (B + C + D) + \omega_E B + \omega_I C - \beta N_0 AC, \\
\dot{B} &= \beta N_0 AC - \lambda B - \omega B - \omega_E B, \\
\dot{C} &= \lambda B - \gamma C - \omega C - \omega_I C, \\
\dot{D} &= \gamma C - \omega D, \\
\dot{A}_c &= \alpha (A + D) - \beta N_0 A_c C_c - \omega A_c - \delta A_c, \\
\dot{B}_c &= \beta N_0 A_c C_c - \lambda B_c - \omega B_c - \omega_E B_c - \delta B_c, \\
\dot{C}_c &= \lambda B_c - \gamma C_c - \omega C_c - \omega_I C_c - \delta C_c, \\
\dot{D}_c &= \gamma C_c - \omega D_c - \delta D_c.
\end{align*}
\]  

The initial equations given in (4) now become

\[
\begin{align*}
A(0) &= 1 - N_0^{-1}, \quad B(0) = 0, \quad C(0) = N_0^{-1}, \quad D(0) = 0, \\
A_c(0) &= B_c(0) = C_c(0) = D_c(0) = 0.
\end{align*}
\]  

With this scaling the total population of adult birds remains constant, i.e.

\[ \dot{A} + \dot{B} + \dot{C} + \dot{D} = 0. \]

This satisfies the assumption that when a bird dies, another immediately fills place.
4. Analysis and Results

4.1. The basic reproductive rate $R_0$

We use equation (2) to derive an expression for $R_0$. For this we need the fraction of adult susceptibles at equilibrium. Thus we set $\dot{B} = \dot{C} = 0$ and solve for $A$ in the system of equations (5), thereby obtaining a value

$$s^* = A = (\lambda + \omega + \omega_E)(\gamma + \omega + \omega_I)/(\beta \lambda N_0)$$

and so, from $R_0 = 1/s^*$, we get

$$R_0 = \frac{\beta \lambda N_0}{(\lambda + \omega + \omega_E)(\gamma + \omega + \omega_I)}.$$  \hfill (7)

4.2. Numerical Analysis

Together with the initial conditions (6), the system (5) was solved numerically using the Runge–Kutta method, as outlined in Burden and Faires [5], implemented in a C program. The outputted results were then plotted in Mathematica.

4.3. Parameter Values

For the numerical simulations, values for each of the equation parameters were needed. These were taken to accurately model the birds and the H5N1 virus. As well as this, the parameters were varied to test how strongly the system depended on them.

Colonies of seabirds tend to be quite large. Crespin et al [7] record up to 20,000 breeding pairs of common guillemots $Uria aalge$ on the Isle of May in Scotland. With this information, the initial bird population $N_0$ was chosen, conservatively, to be 10,000. The birth rate, $\alpha$ was chosen to be 0.5. As previously mentioned, newly born chicks leave the colony after around 22 days, or $22/365$ years, so their rate of leaving $\delta$ was set at $365/22$.

Seabirds are known to have a long lifespan and high survival rates. Oesterblom et al [17] show that the annual survival rate of the guillemot in the Baltic seas is over 90%, while Wanless et al [22] give a similar rate for the gannet $Morus bassanus$. We thus take the death rate $\omega$ to be 0.1 in this analysis.

In their model of an influenza pandemic, Gani et al [9] take the latent period to be 2 days, with an infectious period of 4 days, that is, $\lambda = 365/2$ and $\gamma = 365/4$. Van der Goot et al [21] also quote a latent period of 2 days, while the infectious period is found experimentally to range from 1 to 7 days.

It is difficult to know exactly the rate of lethality induced by the H5N1 strain. Rajgopal [18] reports that when avian influenza was first discovered, the mortality was approaching 100%. The lethality parameters $\omega_E$ and $\omega_I$ will initially be taken to be 0.5 and 0.75 but will be varied to study their influence.

The final parameter needed to numerically solve the system is $\beta$, which controls the transmission of the virus. From equation (7) we have

$$\beta = (\lambda + \omega + \omega_E)(\gamma + \omega + \omega_I)R_0/(\lambda N_0).$$  \hfill (8)

So a value for $\beta$ can be found by inputting a value for $R_0$. The following table shows estimated $R_0$ values for various infections, taken from Heffernan et al [10], Chung [6], Brockman et al [4] and Anderson et al [2]:

| Infection                        | $R_0$         |
|---------------------------------|---------------|
| Pandemic Influenza              | 2–4           |
| Avian Influenza, Netherlands 2003 | up to 6.5    |
| SARS                            | 2–3           |
| BSE                             | 10–12         |
| Foot and Mouth Disease          | about 4.5     |
As mentioned earlier there is no one “correct” way to calculate $R_0$, so a precise value for the H5N1 strain of avian influenza isn’t known. Here we vary the $R_0$ value from 2 up to 10 to examine the resulting dynamics.

4.4. Results

In all of the simulations, the following parameter values were kept fixed, as described in the previous section, chosen to accurately reflect seabird profiles:

| Parameter | Value |
|-----------|-------|
| $N_0$     | 10,000|
| $\alpha$  | 0.5   |
| $\omega$  | 0.1   |
| $\delta$  | 16.59 |

Equation (8) gives a relationship between $R_0$ and $\beta$, and so the values of $\gamma$, $\lambda$, $\omega_E$, $\omega_I$ and $R_0$ were varied at each simulation.

It was found that, regardless of changing these values, the chicks tended to make up only around 3% of the total population, and so had negligible impact on the general dynamics of the infection. Instead, we focused on the adult populations.

An $R_0$ value of 10, representing a highly infectious disease, resulted in the general behaviour, similar for all other parameter values, which is shown in Figure 4.

The fraction of susceptibles begins close to 1. Over the first two to three months or so, (similar to that seen in Figure 3, even though the latter is for the case for $R_0 = 2$) there is a devastating outbreak, affecting almost all of the birds. After this, the number of susceptibles grows slowly, due to the low birthrate. Despite further small tremors, the majority of birds are recovered and thus immune. It is unlikely that another catastrophic epidemic involving this particular virus will occur.

For $R_0$ equal to 2, we obtain the pseudo-periodic behaviour portrayed in Figure 5.

Again, there is an initial population crash as in Figure 3. This time, however, it is less severe and the population of susceptibles has a greater chance of recovery. Subsequent outbreaks occur, represented by the jumps in the graph. We varied the values of the lethality parameters $\omega_E$ and $\omega_I$ from the probable values assumed above to unreasonably high values such as 80 and 100 respectively. It was found that these lethality parameters govern the length of time between the outbreaks — the higher the values, the closer the occurrences. We further investigated the results of changing the recovery rate $\gamma$ and the latency period $1/\lambda$ from the estimated values.

Figure 3. Fraction of susceptibles and recovered over the first year for $R_0 = 2$
Figure 4. Fraction of adult susceptibles and recovered for $R_0 = 10$; time in years (note that the initial population crash follows the trajectory shown in Figure 3, which refers to a time interval of one year)

Figure 5. Pseudo-periodic behaviour in the system

as above to values as low as 20 and 50 respectively. The steepness of the jumps, that is, the duration of the epidemics, seems to be controlled by the rate of recovery and the latent period of the virus.

5. Discussion and Conclusion

5.1. Dynamics

When a novel pathogen, such as the H5N1 strain of avian influenza, is introduced into a seabird colony, the resulting dynamics depend largely on the virus’s basic reproductive rate $R_0$. For a high $R_0$ value of 10, a devastating epidemic occurs very soon after the infected bird is introduced. Almost all of the adult birds become sick. Once the epidemic has passed however, the colony consists almost entirely of recovered birds which are immune to the virus and the low birth rate of the birds means that this situation remains largely unchanged. Therefore, while small outbreaks may frequently occur, the virus does not have enough susceptible hosts to begin another significant epidemic.

The dynamics of the virus are quite different for a lower $R_0$ value of 2.

The initial epidemic is not as severe in this case and fewer birds are affected. There remains a significant population of susceptible birds and this facilitates more future outbreaks. The general system behaviour looks like that in Figure 4, with the jumps corresponding to outbreaks.

The lethality of the virus governs the length scales involved in these ‘cycles’. The higher the
value of the lethality, the closer together the outbreaks will occur. The severity of the population changes are governed by the latent period and recovery period of the virus. For longer periods the changes are less sudden.

It is interesting that, regardless of how devastating the virus, the overall population size, in the long term, remains largely unaffected which appears to be the case for seabird colonies in general. This may be explained by the combination of a low reproductive rate and a long life span of seabirds. The proportion of adults in the population is so high that the colony dynamics are undisturbed by the chicks. The colony tends to be largely inhabited by adult birds who have been sick at some point but who have recovered and gained immunity. This makes it difficult for the virus to continually establish itself.

Acknowledgments
The authors wish to gratefully acknowledge Prof. Vladimir Sobolev, Samara State University, Russia, and Prof. Alexei Pokrovskii, University College Cork for helpful discussions and advice. The helpful assistance in rewriting the paper in \LaTeX{} by Dr. Dmitrii Rachinskii of University College Cork is also gratefully acknowledged.

References
[1] Adamek J, Keller M, Senftleben A and Hinrichsen H 2005 Epidemic spreading with long-range infections and incubation times J. of Stat. Mech. P09002
[2] Anderson R M, Fraser C, Ghani A C, Donnelly C A, Riley S, Ferguson N M, Leung G M, Lam T H and Hedley A J 2005 Epidemiology, transmission dynamics, and control of SARS: the 2002–2003 epidemic SARS: A Case Study In Emerging Infections ed A R McLean, R M May, J Pattison and R A Weiss (Oxford: Oxford University Press)
[3] Anderson R M and May R M 1992 Infectious Diseases of Humans: Dynamics and Control (Oxford: Oxford University Press)
[4] Brockmann D, Hufnagel L and Geisel T 2005 Dynamics of modern epidemics SARS: A Case Study In Emerging Infections ed A R McLean, R M May, J Pattison and R A Weiss (Oxford: Oxford University Press)
[5] Burden R L and Faires J D 1997 Numerical Analysis (California: Brooks/Cole Publishing)
[6] Chung P H A 2005 Preparing for the worst-case scenario Science 310 1117
[7] Crespin L, Harris M P, Lebreton J D, Frederiksen M and Wanless S 2006 Recruitment to a seabird population depends on environmental factors and on population size J. of Animal Ecology 75 228–38
[8] Croxall J P (ed) 1987 Seabirds: Feeding Ecology and Role in Marine Ecosystems (Cambridge University Press)
[9] Gani R, Hughes H, Fleming D, Grin T, Medlock J and Leach S 2005 Potential impact of antiviral drug use during influenza pandemic Emerging Infectious Diseases www.cdc.gov/eid 11 no 9
[10] Heffernan J M, Smith R J and Wahl L M 2005 Perspectives on the basic reproductive ratio J. R. Soc. Interface 2 281–93
[11] Li M Y and Wang L 2000 Global stability in some SEIR models Preprint http://mat.ualberta.ca
[12] James G and Steele N 1990 Epidemics and the spread of diseases Mathematical Modelling: a Source Book of Case Studies ed I D Huntley and D J G James (Oxford: Oxford University Press)
[13] Keeling M J and Gilligan C A 2000 Bubonic plague: a metapopulation model of a zoonosis Proc. R. Soc. Lond. B 267 2219–30
[14] Kelly T 2004 Globetrotting Germs — and the transport of their carriers The Effects of Human Transport on Ecosystems: Cars and Trains ed J Davenport and L J Davenport (Royal Irish Academy) 227–43
[15] Millennium Ecosystems Synthesis Report 2005 (Washington DC: Island Press)
http://www.millenniumassessment.org/en/Products.Synthesis.aspx
[16] Newton Ian 1998 Population Limitation In Birds (London and New York: Academic Press)
[17] Oesterblom H, Van Der Jeugd H P and Olsson O 2004 Adult survival and avian cholera in common guillemots Uria aalge in the Baltic Sea (Ibis, British Ornithologists’ Union) 146
[18] Raigopal T 2005 Coping with pandemic avian influenza Indian J. of Occup. Environ. Med. 9 99–102
[19] Rhodes C J, Jensen H J and Anderson R M 1997 On the critical behaviour of simple epidemics Proc. R. Soc. Lond. B 264 1639–46
[20] Shigesada N and Kawasaki K 1997 Biological Invasions: Theory and Practice (Tokyo: Oxford University Press)

[21] Van der Goot J A, Koch G, de Jong M C M and van Boven M 2005 Quantification of the effect of vaccination on transmission of avian influenza (H7N7) in chickens Proc. Natl. Acad. Sci. USA 102 no 50, 18141–6

[22] Wanless S, Frederiksen M, Harris M P and Freeman S N 2006 Survival of Gannets Morus bassanus in Britain and Ireland, 1959–2002 Bird Study 53 79–85

[23] Wonham M J, de-Camino-Beck T and Lewis M A 2004 An epidemiological model for West Nile virus: invasion analysis and control applications Proc. R. Soc. Lond. B 271 501–7