Incidence functions and population thresholds

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The incidence rate

\[ f(S,I) = f(S,I) \]

Incidence term in models describes the rate that new infections arise.
\[ f(S,I) = \text{Force of infection} \times S \]

Force of infection, \( \lambda = c(N) p \frac{EN}{I} \)
\( c(N) = \text{contact rate (possibly density-dependent)} \)
\( p = \text{probability of transmission given contact} \)
\( EN = \text{prob. that randomly-chosen partner is infectious} \)

So
\[ f(S,I) = c(N)p \frac{SI}{N} \]

Density-dependent transmission

\[ f(S,I) = f(S,I) \]

If contact rate is linearly density-dependent:
\[ c(N) = kN \]
Then
\[ f(S,I) = kNp \frac{SI}{N} = \beta_{\text{MA}} SI \]
where \( \beta_{\text{MA}} = kp \)

\( \rightarrow \) "Mass action" transmission. Also known as density-dependent or, confusingly, "pseudo-mass action" (see McCallum et al, 2001)

Frequency-dependent transmission

\[ f(S,I) = f(S,I) \]

If contact rate is constant with respect to density:
\[ c(N) = c_0 \]
Then
\[ f(S,I) = c_0p \frac{SI}{N} = \beta_{\text{FD}} SI/N \]
where \( \beta_{\text{FD}} = c_0p \)

\( \rightarrow \) "Frequency-dependent" transmission. Also known as the standard incidence or, confusingly, "true mass action" (see McCallum et al, 2001)

Outline

- Incidence functions
- Density dependence
- Population thresholds
  - Invasion
  - Persistence
  - Thresholds and host extinction

Saturating transmission

Classically it was assumed that transmission rate increases with population size, because contacts increase with crowding. Mass action (\(\beta SI\)) was the dominant transmission term. Hethcote and others argued that rates of sexual contact are determined more by behaviour and social norms than by density, and favoured frequency-dependent transmission for STDs.

Since the 1990s, this has been a topic of active research using experimental epidemics, field systems, and epidemiological data.

Many choices – what to do?

How can we test for density dependence in transmission?

- Fit models with different transmission functions to epidemic time series.
- Look at indicators for transmission \(\propto N\) in epidemiological data:

  - With increased transmission rate, we expect:
    - \(\uparrow\) estimates of \(R_0\)
    - \(\uparrow\) exponential growth rate of epidemic, \(r\)
    - \(\downarrow\) proportion susceptible following epidemic, or at steady state
    - \(\downarrow\) mean age of infection in endemic setting

Detecting density dependence

Evidence for FD vs MA transmission

Measles in England and Wales

- \(R_0\) is \(\sim\) constant vs population size
  - \(\Rightarrow\) roughly FD transmission
  (recall that MA predicts that \(R_0 \propto N\))


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Evidence for FD vs MA transmission

Leptospirosis in California sea lions

Mean age of infection does not decrease with \(N\)
- \(\Rightarrow\) transmission not density-dependent.
Leptospirosis in California sea lions

Epidemic growth rate does not increase with $N$  
→ transmission not density-dependent.

Evidence for FD vs MA transmission

Model results: density-dependent transmission

Lepto data

Leptospirosis in California sea lions

Epidemic growth rate does not increase with $N$
→ transmission not density-dependent.

Evidence for FD vs MA transmission → neither?

Transmission of *Plodia interpunctella* granulosis virus does not conform to the mass action model

**PiGV in *Plodia* (Indian meal moth)**
Transmission rate is not FD or MA – need complex functional forms.
Interpret in terms of host heterogeneity and effects of density on behaviour.

So what should we do?

Despite its fundamental importance, the issue of how to formulate the transmission term in simple models is unresolved.

Some pointers:

- FD transmission is generally thought to be more appropriate than MA in large well-mixed populations.
- In quite small populations, transmission is generally thought to exhibit some density dependence and MA is acceptable.
- Think about population structure and mechanisms of mixing at the scales of space and time you're thinking about.
  Is a very simple model appropriate?  
  (more on this in the next lecture)

Population thresholds in epidemic dynamics

$R_0$ has been the central concept in epidemic dynamics since ~1980, thanks largely to the work of Anderson & May.

(see the history of $R_0$ by Heesterbeek 2002, *Acta Biotheoretica*

Long before this, people studying epidemic dynamics have focused on population thresholds.

- Population threshold for invasion (Kermack & McKendrick 1927): host population size below which parasite cannot invade.
- Population threshold for persistence, or the critical community size (Bartlett 1957, Black 1966): host population size below which parasite cannot persist long-term.

**Population threshold for disease invasion**

Under **density-dependent transmission**, $R_0 = \beta ND$

or in fact $R_0 > 1$ any increasing function of $N$.
→ $R_0 > 1$ corresponds to a population threshold $N > N_T$.

**Population threshold for disease invasion**

Under **frequency-dependent transmission**, $R_0 = \beta D$.
→ No threshold $N$ for $R_0 > 1$. 

$R_0 > 1$

Disease can invade/persist

Host population size, $N$
Susceptibility threshold for disease invasion

Recall: under any form of transmission, \( R_{\text{effective}} = R_0 \times S/N \).

\( R_{\text{eff}} < 1 \)  
Disease dies out

\( R_{\text{eff}} > 1 \)  
Disease can invade/persist

\( 1/R_0 \)  
Proportion susceptible, \( S/N \)

This phenomenon is the basis for herd immunity.

Population thresholds for invasion: evidence

Despite its conceptual simplicity, real-world evidence for invasion thresholds is hard to find, for several reasons

- failed invasions are difficult to observe
- demographic stochasticity leads to variation in outbreak sizes
  - when \( R_0 < 1 \), limited chains of transmission can still occur
  - when \( R_0 > 1 \), epidemic can still die out by chance.

\( N=100 \)

\( R_0=0.9 \)

\( R_0=1.5 \)

Stochastic variation in outbreak size


Stochastic variation in outbreak size


Population thresholds for persistence

Even if parasite is able to invade \((R_0 > 1)\), this does not guarantee its persistence in the long term.

There are two broad mechanisms whereby a disease can fail to persist, or fade out:

- Endemic fadeout: random fluctuations around the endemic equilibrium can cause extinction of the parasite.
- Epidemic fadeout: following a major epidemic, the susceptible pool is depleted and the parasite runs out of individuals to infect.

Critical Community Size is population size above which a disease can persist long-term (yes, this definition is vague).

Persistence thresholds - another view

Broken chains of transmission can arise in two ways:

- Epidemic fadeout: parasite extinction occurring because susceptible numbers are so low immediately following an epidemic that small stochastic fluctuations can remove all parasites. (Susceptible bottleneck)
- Endemic fadeout: parasite extinction occurring because endemic numbers of infected individuals are so low that small stochastic fluctuations can remove all parasites. (Transmission bottleneck)

Branching process models allow analysis of outbreak size to make inference about the effective reproductive number.
Endemic fadeout
Stochastic SIR model with FD transmission and $R_0=4$.
10 simulations are shown. + signs show times when disease fades out.

Mean time to endemic fadeout for stochastic SIR model with $R_0=4$ and different rates of demographic turnover.
1. No sharp threshold in $N$; there’s a gradual trend of longer persistence.
2. Demographic rates are as important as $N$, if not more so.

Epidemic fadeout
Stochastic SIR model with FD transmission and $R_0=4$.
(exact same model as for endemic fadeout, but now started from $I=1$ instead of $I^*$.)
10 simulations are shown. + signs show times when disease fades out.

Probability that disease persists through the first post-epidemic trough
1. No sharp threshold in $N$; there’s a gradual trend of longer persistence.
2. Demographic rates are as important as $N$, if not more so.

The classic example of epidemic fadeout: measles
Note how measles is not endemic in Iceland, but instead has periodic outbreaks dependent on re-introduction of the virus.
The classic example of epidemic fadeout: measles

Measles in England and Wales

Extinction risk: can a disease drive its host extinct?

What if the host population itself has a threshold density below which it cannot persist?

Then the outcome depends on the relative values of the threshold population size for disease extinction vs host extinction.


Extinction risk: multiple host species and spillover

Spillover from reservoir can threaten endangered populations

1997 Mediterranean monk seal die-off in Mauritania.

>100 monk seals died (~1/3 of global population), probably due to dolphin morbillivirus (a relative of measles) that spilled over from another species.