Dynamic pair formation models
Application to sexual networks and STI

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Models for sexually transmitted infections
Which frameworks?

- HIV/AIDS: SI framework
- chlamydia and gonorrhoea: SIS framework
- hepatitis B: SIR framework
What do we have to consider?

Behaviour and disease specific parameters

Contact patterns:
- heterogeneity in number of contacts (core group)
- mixing
- partnership duration
- partnership overlap

Disease specific characteristics:
- Variable infectivity
- symptomatic/asymptomatic infections
- long/short time scales
- immunity
- reinfection
most people have few partners

some have many (core group)

men and women report different numbers of partners
some partnerships dissolve very quickly, others have exponentially distributed duration
ongoing partnerships censored
model with instantaneous contacts cannot capture this feature
Partnership duration
Nelson et al. 2010

- age dependence
- 25% partnerships casual
- what is impact of partnership duration on transmission dynamics?
Historical remarks

Pair formation models used in mathematical demography (marriage models).

First introduced to epidemiology by Dietz & Hadeler (1988).

They study age dependent pair formation models in a deterministic framework.
Model formulation
Partnership formation and dissolution

\[
\frac{dX}{dt} = B - \mu X - \rho X + 2\sigma P + 2\mu P \\
\frac{dP}{dt} = \frac{1}{2} \rho X - \sigma P - 2\mu P
\]

Assume pair formation process is at equilibrium.
**Model formulation**

Equilibrium

The model formulation for the pair formation model is given by the equations:

\[
X^* = \frac{B(\sigma + 2\mu)}{\mu(\rho + \sigma + 2\mu)}
\]

\[
P^* = \frac{B\rho}{2\mu(\rho + \sigma + 2\mu)}
\]

So \( N = X + 2P = B/\mu \). This means that a fraction \( x^* = \frac{\sigma + 2\mu}{\rho + \sigma + 2\mu} \) is single.

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Dynamic pair formation models
Model formulation
pair formation and SIS infection

Assumptions:
- no distinction between men/women
- individuals are born susceptible
- infection does not increase mortality
- transmission only in pairs of infected and susceptible
We can simplify this model by assuming that the pair formation process is at equilibrium. Then $X_0 = X^* - X_1$ and $P_{00} = P^* - P_{01} - P_{11}$.
Model formulation
reduction to 3 equations

\[
\begin{align*}
\frac{dX_1}{dt} &= -(\mu + \rho + \gamma)X_1 + (\sigma + \mu)(2P_{11} + P_{01}) \\
\frac{dP_{01}}{dt} &= \rho X_1 \left(1 - \frac{X_1}{X^*}\right) - (\sigma + 2\mu + \beta + \gamma)P_{01} + 2\gamma P_{11} \\
\frac{dP_{11}}{dt} &= \frac{\rho X_1^2}{2X^*} - (\sigma + 2\mu + 2\gamma)P_{11} + \beta P_{01}
\end{align*}
\]

We can write the prevalence as \( I = X_1 + P_{01} + 2P_{11} \).
The basic reproduction number can be computed as the product of:

- the probability of moving into the single state after being infected
- the number of partners in the remaining life time $M$
- the probability of infecting a susceptible partner $b$

Let us first assume that there is no recovery, i.e. $\gamma = 0$. Then

$$R_0 = \frac{\beta \rho (\sigma + \mu)}{\mu (\rho + \sigma + 2\mu)(\sigma + 2\mu + \beta)}$$
If there is recovery, we also have to take reinfection into account. An individual's partner can recover and get reinsfected, so that the index case moves back and forth between $P_{11}$ and $P_{01}$ before the pair separates.

The probability of moving from $P_{11}$ to $X_1$ either directly or via recovery of the partner, but without reinfecting the partner is

$$q_0 = \frac{\sigma + \mu}{\sigma + 2\mu + 2\gamma} \left( 1 + \frac{\gamma}{\sigma + 2\mu + \beta + \gamma} \right)$$

The probability of reinfecting the partner $i > 0$ times before separation is

$$p^i = \left( \frac{\gamma}{\sigma + 2\mu + 2\gamma} \frac{\beta}{\sigma + 2\mu + \beta + \gamma} \right)^i$$

We have to sum the $p^i$ over all $i = 1, 2, ...$ to get the probability that any number of reinfections occur before separation. Because $p < 1$ the sum over all $p^i$ converges to

$$\sum_{i=0}^{\infty} p^i = \frac{1}{1-p} = \frac{(\sigma + 2\mu + 2\gamma)(\sigma + 2\mu + \beta + \gamma)}{\sigma + 2\mu(\sigma + 2\mu + \beta + 2\gamma + \gamma \beta)}$$
Partner can also reinfect the original index case. In effect reinfection is a prolongation of the infectious period.

\[ R_0 = b \sum_{i=1}^{\infty} (dq)^i = b \frac{dq}{1-dq} \]

- **b**: Probability that the woman transmits her infection to her susceptible partner
- **q**: Probability of a woman getting out of a partnership and still being infected after \( n \) number of re-infections (this is mainly dependent on the infection process)
- **d**: Probability of an infected woman getting into a partnership before death or recovery (this is mainly dependent on the pair formation process)
The basic reproduction number depends on the average duration of partnerships. For very short or very long partnership durations the infection cannot establish itself in the population. Contribution of reinfection to Chlamydia transmission and effects of screening and partner notification

joint work with Janneke Heijne, Sereina Herzog, and Nicola Low (University of Bern).
Different types of partnerships
Steady and casual

Model can reproduce observed distributions of partnership durations.
Variable infectivity
Two stages of infection

Question: how do partnership duration and variable infectivity interact?
Pair formation model with instantaneous contacts added (casual partnerships).
Xiridou et al AIDS 2003; AIDS 2004
Conclusions:

- **Primary HIV infection**: important in transmission from casual partners, but not in transmission from steady partners.
- **Advanced epidemic**: contribution of PHI to HIV incidence is small, if steady partners are the major source of infection.
Other issues ...
other models?

- age dependence, age mixing
- differences men - women
- heterosexual and homosexual populations
- heterogeneity in partner change rates
- overlap in partnerships, concurrent partnerships

→ Networks

One option: use individual based simulations to model overlapping partnerships.
Is concurrency driving the HIV epidemic in Sub Saharan Africa?

Halperin & Epstein Lancet 2004

Reniers & Watkins AIDS 2010
Modelling polygyny

Project KaYin Leung, joint work with Odo Diekmann.
Equations for pair formation process

\[ x : = \text{the fraction of single women}, \]
\[ p_j : = \text{the fraction of men with } j \text{ partners, } j \geq 0. \]

The set of ODEs describing the partnership dynamics is:

\[
\frac{dx}{dt} = \frac{\mu}{2} - \frac{2B\rho}{\mu} x \sum_{k=0}^{\infty} p_k + (\sigma + \mu) \sum_{k=1}^{\infty} kp_k - \mu x, \\
\frac{dp_0}{dt} = \frac{\mu}{2} - \frac{2B\rho}{\mu} xp_0 + (\sigma + \mu)p_1 - \mu p_0, \\
\frac{dp_j}{dt} = \frac{2B\rho}{\mu} xp_{j-1} - \left( \frac{2B\rho}{\mu} x + (\sigma + \mu)j \right) p_j + (\sigma + \mu)(j + 1)p_{j+1} - \mu p_j, \tag{1} \\
\text{for } j \geq 1.
\]
Equations for infection dynamics:

- $x_0$, $x_1$, denote the fractions of susceptible and infected women
- $p_{n,k}$, and $q_{n,k}$ denote the fractions of men with $n$ partners of which $k$ are infected

We assume that the pair formation process is at equilibrium, then the susceptible fractions can be eliminated from the system.

The fraction of infected men is given by

$$i_m = \sum_{n=0}^{\infty} \sum_{k=0}^{n} q_{n,k},$$

and the fraction of infected women by

$$i_f = x_1 + \sum_{n=1}^{\infty} \sum_{k=1}^{n} k(p_{n,k} + q_{n,k}).$$
First results

$R_0$ can be computed from $R_f$ (number of infected men by one infected woman) and $R_m$ (number of infected women by one infected man) as

$$R_0 = \sqrt{R_f R_m}. \quad (2)$$

Comparison of $R_0$ for monogamous (orange) and polygamous (purple) populations.

$$R_0 = \sqrt{R_m R_f} > R_f = R_0^M,$$

i.e. the basic reproduction number is always larger in the polygynous population than in the monogamous population.
Ongoing work

Polygyny model (with KaYin Leung and Odo Diekmann):
- can we compute endemic equilibrium explicitly?
- Relaxing the assumptions: dependency between partners
- Adding instantaneous contacts between men and women
- Dependence of $R_0$ on parameters in more complex situations
- Relationship with data

Reinfection in partnerships (with Janneke Heijne, Sereina Herzog, Nicola Low):
- take short term immunity into account
- effectiveness of screening and partner notification
- distinguish risk levels (core group)
- Estimate contribution of reinfections in partnerships to prevalence

Open question:
Are other analytically tractable variants of the pair formation framework possible?
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