APPENDIX

Contribution of high risk groups' unmet needs may be underestimated in epidemic models without risk turnover: a mechanistic modelling analysis ☆

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A Turnover Framework

We introduce a system of parameters and constraints to describe risk group turnover in deterministic epidemic models with heterogeneity in risk.[1] We then describe how the system can be used in practical terms, based on different assumptions and data available for parameterizing turnover in risk. We conclude by framing previous approaches to this task using the proposed system.

A.1 Notation

Consider a population divided into G risk groups. We denote the number of individuals in risk group $i \in [1, \ldots, G]$ as x_i and the set of all risk groups as $\boldsymbol{x} = \{x_1, \ldots, x_G\}$. The total population size is $N = \sum_i x_i$, and the relative population size of each group is denoted as $\hat{x}_i = x_i/N$. Individuals enter the population at a rate ν per year, and exit at a rate μ per year. We model the distribution of risk groups among individuals entering into the population as $\hat{\boldsymbol{e}}$, which may be different from individuals already in the population $\hat{\boldsymbol{x}}$.[2] Thus, the total number of individuals entering into population $\boldsymbol{x}$ per year is given by νN, and the number of individuals entering into group i specifically is given by $\hat{e}_i \nu N$.

Turnover transitions may then occur between any two groups, in either direction. Therefore we denote the turnover rates as a $G \times G$ matrix ϕ. The element ϕ_{ij} corresponds to the proportion of individuals in group i who move from group i to group j each year. An example matrix is given in Eq. (A.1), where we write the diagonal elements as $*$ since they represent transitions from a group to itself.

$$\phi = \begin{bmatrix} * & x_1 \to x_2 & \cdots & x_1 \to x_G \\ x_2 \to x_1 & * & \cdots & x_2 \to x_G \\ \vdots & \vdots & \ddots & \vdots \\ x_G \to x_1 & x_G \to x_2 & \cdots & * \end{bmatrix} \tag{A.1}$$

Risk groups, transitions, and the associated rates are also shown for $G = 3$ in Figure A.1.

A.2 Parameterization

Next, we present methods to illustrate how epidemiologic data can be used to parametrize turnover in epidemic models. We construct a system like the one above which reflects the risk group dynamics observed in a specific context. We assume that the relative sizes of the risk groups in the model ($\hat{\boldsymbol{x}}$) are already known, and should remain constant over time. Thus, what remains is to estimate the values of the parameters: ν, μ, $\hat{\boldsymbol{e}}$, and ϕ, using commonly available sources of data.

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[1] A preliminary version of this framework was used by Knight et al. (2019).

[2] We could equivalently stratify the rate of entry ν by risk group; however, we find that the mathematics in subsequent sections are more straightforward using $\hat{\boldsymbol{e}}$.

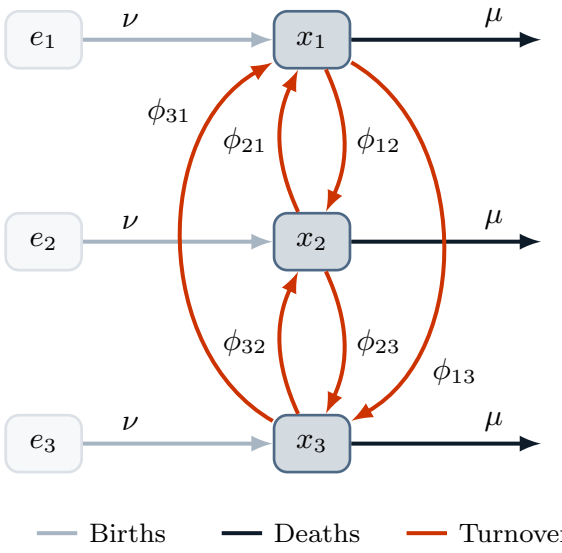


Figure A.1: System of $G = 3$ risk groups and turnover between them.
x_i: number of individuals in risk group i; e_i: number of individuals available to enter risk group i; ν: rate of population entry; μ: rate of population exit; ϕ_{ij}: rate of turnover from group i to group j.

A.2.1 Total Population Size

The total population size $N(t)$ is a function of the rates of population entry $\nu(t)$ and exit $\mu(t)$, given an initial size N_0. We allow the proportion entering the system to vary by risk group via $\hat{\boldsymbol{e}}$, while the exit rate has the same value for each group. We assume that there is no disease-attributable death. Because the values of ν and μ are the same for each risk group, they can be estimated independent of $\hat{\boldsymbol{x}}$, $\hat{\boldsymbol{e}}$, and ϕ.

The difference between entry and exit rates defines the rate of population growth:

$$\mathcal{G}(t) = \nu(t) - \mu(t) \tag{A.2}$$

The total population may then be defined using an initial population size N_0 as:

$$N(t) = N_0 \exp\left(\int_0^t \log\left(1 + \mathcal{G}(\tau)\right) d\tau\right) \tag{A.3}$$

which, for constant growth, simplifies to the familiar expression (Malthus, 1798):

$$N(t) = N_0(1 + \mathcal{G})^t \tag{A.4}$$

Census data, such as (DataBank, 2019), can be used to source the total population size in a given geographic setting over time $N(t)$, thus allowing Eqs. (A.3) and (A.4) to be used to estimate $\mathcal{G}(t)$.

If the population size is assumed to be constant, then $\mathcal{G}(t) = 0$ and $\nu(t) = \mu(t)$. If population growth occurs at a stable rate, then $\mathcal{G}$ is fixed at a constant value which can be estimated via Eq. (A.4) using any

two values of $N(t)$, separated by a time interval τ:

$$\mathcal{G}_\tau = \frac{N(t+\tau)^{\frac{1}{\tau}}}{N(t)} - 1 \tag{A.5}$$

If the rate of population growth $\mathcal{G}$ varies over time, then Eq. (A.5) can be reused for consecutive time intervals, and the complete function $\mathcal{G}(t)$ approximated piecewise by constant values. The piecewise approximation can be more feasible than exact solutions using Eq. (A.3), and can reproduce $N(t)$ accurately for small enough intervals τ, such as one year.

Now, given a value of $\mathcal{G}(t)$, either $\nu(t)$ must be chosen and $\mu(t)$ calculated using Eq. (A.2), or $\mu(t)$ must be chosen, and $\nu(t)$ calculated. Most modelled systems assume a constant duration of time that individuals spend in the model $\delta(t)$ (Anderson and May, 1991) which is related to the rate of exit μ by:

$$\delta(t) = \mu^{-1}(t) \tag{A.6}$$

In the context of sexually transmitted infections, the duration of time usually reflects the average sexual life-course of individuals from age 15 to 50 years, such that $\delta = 35$ years. The duration δ may also vary with time to reflect changes in life expectancy. The exit rate $\mu(t)$ can then be defined as $\delta^{-t}(t)$ following Eq. (A.6), and the entry rate $\nu(t)$ defined as $\mathcal{G}(t) - \mu(t)$ following Eq. (A.2).

A.2.2 Turnover

Next, we present methods for resolving the distribution of individuals entering the risk model $\hat{\boldsymbol{e}}(t)$ and the rates of turnover $\phi(t)$, assuming that entry and exit rates $\nu(t)$ and $\mu(t)$ are known. Similar to above, we first formulate the problem as a system of equations. Then, we explore the data and assumptions required to solve for the values of parameters in the system. The (t) notation is omitted throughout this section for clarity, though time-varying parameters can be estimated by repeating the necessary calculations for each t.

The number of risk groups G dictates the number of unknown elements in $\hat{\boldsymbol{e}}$ and ϕ: G and $G(G-1)$, respectively. We collect these unknowns in the vector $\boldsymbol{\theta} = [\hat{\boldsymbol{e}}, \boldsymbol{y}]$, where $\boldsymbol{y} = \text{vec}_{i \neq j}(\phi)$. For example, for $G = 3$, the vector $\boldsymbol{\theta}$ is defined as:

$$\boldsymbol{\theta} = \begin{bmatrix} \hat{e}_1 & \hat{e}_2 & \hat{e}_3 & \phi_{12} & \phi_{13} & \phi_{21} & \phi_{23} & \phi_{31} & \phi_{32} \end{bmatrix} \tag{A.7}$$

We then define a linear system of equations which uniquely determine the elements of $\boldsymbol{\theta}$:

$$\boldsymbol{b} = A\,\boldsymbol{\theta} \tag{A.8}$$

where A is a $M \times G^2$ matrix and $\boldsymbol{b}$ is a M-length vector. Specifically, each row in A and $\boldsymbol{b}$ defines a constraint: an assumed mathematical relationship involving one or more elements of $\hat{\boldsymbol{e}}$ and ϕ. For example, a simple constraint could be to assume the value $\hat{e}_2 = 0.20$. Each of the following four sections introduces a type of constraint, including: assuming a constant group size, specifying elements of $\boldsymbol{\theta}$ directly, assuming an average

duration in a group, and specifying a relationship between two individual rates of turnover. Constraints may be selected and combined together based on availability of data and plausibility of assumptions. However, a total of $M = G^2$ constraints must be defined in order to obtain a "unique solution": exactly one value of $\boldsymbol{\theta}$ which satisfies all constraints. The values of $\hat{\boldsymbol{e}}$ and ϕ can then be calculated algebraically by solving Eq. (A.8) with $\boldsymbol{\theta} = A^{-1}\boldsymbol{b}$, for which many algorithms exist (LAPACK, 1992).

1. Constant group size. One epidemiologic feature that epidemic models consider is whether or not the relative sizes of risk groups are constant over time (Henry and Koopman, 2015; Boily et al., 2015). Assuming constant group size implies a stable level of heterogeneity over time. To enforce this assumption, we define the "conservation of mass" equation for group i, wherein the rate of change of the group is defined as the sum of flows in / out of the group:

$$\frac{d}{dt}x_i = \nu N\hat{e}_i + \sum_j \phi_{ji}\, x_j - \mu\, x_i - \sum_j \phi_{ij}\, x_i \tag{A.9}$$

Eq. (A.9) is written in terms of absolute population sizes $\boldsymbol{x}$, but can be written as proportions $\hat{\boldsymbol{x}}$ by dividing all terms by N. If we assume that the proportion of each group $\hat{x}_i$ is constant over time, then the desired rate of change for risk group i will be equal to the rate of population growth of the risk group, $\mathcal{G}x_i$. Substituting $\frac{d}{dt}x_i = \mathcal{G}x_i$ into Eq. (A.9), and simplifying yields:

$$\nu\, x_i = \nu\, N\hat{e}_i + \sum_j \phi_{ji}\, x_j - \sum_j \phi_{ij}\, x_i \tag{A.10}$$

Factoring the left and right hand sides in terms of $\hat{\boldsymbol{e}}$ and ϕ, we obtain G unique constraints. For $G = 3$, this yields the following 3 rows as the basis of $\boldsymbol{b}$ and A:

$$\boldsymbol{b} = \begin{bmatrix} \nu x_1 \\ \nu x_2 \\ \nu x_3 \end{bmatrix}; \qquad A = \begin{bmatrix} \nu & \cdot & \cdot & -x_1 & -x_1 & x_2 & \cdot & x_3 & \cdot \\ \cdot & \nu & \cdot & x_1 & \cdot & -x_2 & -x_2 & \cdot & x_3 \\ \cdot & \cdot & \nu & \cdot & x_1 & \cdot & x_2 & -x_3 & -x_3 \end{bmatrix} \tag{A.11}$$

These G constraints ensure risk groups do not change size over time. However, a unique solution requires an additional $G(G-1)$ constraints. For $G = 3$, this corresponds to 6 additional constraints.

2. Specified elements. The simplest type of additional constraint is to directly specify the values of individual elements in $\hat{\boldsymbol{e}}$ or ϕ. Such constraints may be appended to $\boldsymbol{b}$ and A as an additional row k using indicator notation.[3] That is, with b_k as the specified value v, and A_k as the indicator vector, with 1 in the same position as the desired element in $\boldsymbol{\theta}$:

$$b_k = v; \qquad A_k = [0, \ldots, 1, \ldots, 0] \tag{A.12}$$

[3] Indicator notation, also known as "one-hot notation" is used to select one element from another vector, based on its position. An indicator vector is 1 in the same location as the element of interest, and 0 everywhere else.

For example, for $G = 3$, if it is known that 20% of individuals enter directly into risk group 2 upon entry into the model ($\hat{e}_2 = 0.20$), then $\boldsymbol{b}$ and A can be augmented with:

$$b_k = \begin{bmatrix} 0.20 \end{bmatrix}; \qquad A_k = \begin{bmatrix} \cdot & 1 & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \end{bmatrix} \tag{A.13}$$

since $\hat{e}_2$ is the second element in $\boldsymbol{\theta}$. If the data suggest zero turnover from group i to group j, then Eq. (A.13) can also be used to set $\phi_{ij} = 0$.

The elements of $\hat{\boldsymbol{e}}$ must sum to one. Therefore, specifying all elements in $\hat{\boldsymbol{e}}$ will only provide $G - 1$ constraints, as the last element will be either redundant or violate the sum-to-one rule. As shown in Appendix B.3, the sum-to-one rule is actually implicit in Eq. (A.11), so it is not necessary to supply a constraint like $1 = \sum_i \hat{e}_i$.

3. Group duration. Type 1 constraints assume that the relative population size of each group remains constant. Another epidemiologic feature that epidemic models considered is whether or not the duration of time spent within a given risk group remains constant. For example, in STI transmission models that include formal sex work, it can be assumed that the duration in formal sex work work remains stable over time, such as in (Mishra et al., 2014; Boily et al., 2015). The duration δ_i is defined as the inverse of all rates of exit from the group:

$$\delta_i = \left(\mu + \sum_j \phi_{ij} \right)^{-1} \tag{A.14}$$

Estimates of the duration in a given group can be sourced from cross-sectional survey data where participants are asked about how long they have engaged in a particular practice – such as sex in exchange for money (Watts et al., 2010). Data on duration may also be sourced from longitudinal data, where repeated measures of self-reported sexual behaviour, or proxy measures of sexual risk data, are collected (The DHS Program, 2019; ICAP, 2019). Data on duration in each risk group can then be used to define ϕ by rearranging Eq. (A.14) to yield: ${\delta_i}^{-1} - \mu = \sum_j \phi_{ij}$. For example, if for $G = 3$, the average duration in group 1 is known to be $\delta_1 = 5$ years, then $\boldsymbol{b}$ and A can be augmented with another row k:

$$b_k = \begin{bmatrix} 5^{-1} - \mu \end{bmatrix}; \qquad A_k = \begin{bmatrix} \cdot & \cdot & \cdot & 1 & 1 & \cdot & \cdot & \cdot & \cdot \end{bmatrix} \tag{A.15}$$

Similar to specifying all elements of $\hat{\boldsymbol{e}}$, specifying δ_i may result in conflicts or redundancies with other constraints. A conflict means it will not be possible to resolve values of ϕ which simultaneously satisfy all constraints, while a redundancy means that adding one constraint does not help resolve a unique set of values $\boldsymbol{\theta}$. For example, for $G = 3$, if Type 2 constraints are used to specify $\phi_{12} = 0.1$ and $\phi_{13} = 0.1$, and $\mu = 0.05$, then by Eq. (A.14), we must have $\delta_1 = 4$. Specifying any other value for δ_1 will result in a conflict, while specifying $\delta_1 = 4$ is redundant, since it is already implied. There are innumerable situations in which this may occur, so we do not attempt to describe them all. Section A.2.2 describes how to identify conflicts and redundancies when they are not obvious.

4. Turnover rate ratios. In many cases, it may be difficult to obtain estimates of a given turnover rate ϕ_{ij} for use in Type 2 constraints. However, it may be possible to estimate relative relationships between rates of turnover, such as:

$$r\,\phi_{ij} = \phi_{i'j'} \tag{A.16}$$

where r is a ratio relating the values of ϕ_{ij} and $\phi_{i'j'}$. For example, for $G = 3$, let T_1 be the total number of individuals entering group 1 due to turnover. If we know that 70% of T_1 originates from group 2, while 30% of T_1 originates from group 3, then $0.7\,T_1 = \phi_{23}\,x_2$ and $0.3\,T_1 = \phi_{13}\,x_1$, and thus: $\phi_{23}\left(\frac{0.3\,x_2}{0.7\,x_1}\right) = \phi_{13}$. This constraint can then be appended as another row k in $\boldsymbol{b}$ and A like:

$$b_k = \begin{bmatrix} 0 \end{bmatrix}; \qquad A_k = \begin{bmatrix} \cdot & \cdot & \cdot & \cdot & \left(\frac{0.3\,x_2}{0.7\,x_1}\right) & \cdot & 1 & \cdot & \cdot \end{bmatrix} \tag{A.17}$$

The example in Eq. (A.17) is based on what proportions of individuals entering a risk group j came from which former risk group i, but similar constraints may be defined based on what proportions of individuals exiting a risk group i enter into which new risk group j. It can also be assumed that the absolute number of individuals moving between two risk groups is equal, in which case the relationship is: $\phi_{ij}\left(\frac{x_i}{x_j}\right) = \phi_{ji}$. All constraints of this type will have $b_k = 0$.

Solving the System. Table A.1 summarizes the four types of constraints described above. Given a set of sufficient constraints on $\boldsymbol{\theta}$ to ensure exactly one solution, the system of equations Eq. (A.8) can be solved using $\boldsymbol{\theta} = A^{-1}\boldsymbol{b}$. The resulting values of $\hat{\boldsymbol{e}}$ and ϕ can then be used in the epidemic model.

However, we may find that we have an insufficient number of constraints, implying that there are multiple values of the vector $\boldsymbol{\theta}$ which satisfy the constraints. An insufficient number of constraints may be identified by a "rank deficiency" warning in numerical solvers of Eq. (A.8) (LAPACK, 1992). Even if A has G^2 rows, the system may have an insufficient number of constraints because some constraints are redundant. In this situation, we can pose the problem as a minimization problem, namely:

$$\boldsymbol{\theta}^* = \arg\min f(\boldsymbol{\theta}), \quad \text{subject to: } \boldsymbol{b} = A\,\boldsymbol{\theta};\ \ \boldsymbol{\theta} \geq 0 \tag{A.18}$$

where f is a function which penalizes certain values of $\boldsymbol{\theta}$. For example, $f = ||\cdot||_2$ penalizes large values in $\boldsymbol{\theta}$, so that the smallest values of $\hat{\boldsymbol{e}}$ and ϕ which satisfy the constraints will be resolved.[4]

Similarly, we may find that no solution exists for the given constraints, since two or more constraints are in conflict. Conflicting constraints may be identified by a non-zero error in the solution to Eq. (A.8) (LAPACK, 1992). In this case, the conflict should be resolved by changing or removing one of the conflicting constraints.

[4] Numerical solutions to such problems are widely available, such as the Non-Negative Lease Squares solver (Lawson and Hanson, 1995), available in Python: `https://docs.scipy.org/doc/scipy/reference/generated/scipy.optimize.nnls.html`.

Table A.1: Summary of constraint types for defining risk group turnover

Name	Eq.	E.g.	Data requirements
1. Constant group size	(A.10)	(A.11)	all values of $\hat{x}_i$ and ν
2. Specified elements	(A.12)	(A.13)	any value of $\hat{e}_i$ or ϕ_{ij}
3. Group duration	(A.14)	(A.15)	any value of δ_i
4. Turnover rate ratios	(A.16)	(A.17)	any relationship between two turnover rates ϕ_{ij} and $\phi_{i'j'}$

ν: rate of population entry; ϕ_{ij}: rate of turnover from group i to group j; $\hat{x}_i$: proportion of individuals in risk group i; $\hat{e}_i$: proportion of individuals entering into risk group i; δ_i: average duration spent in risk group i.

A.3 Previous Approaches

Few epidemic models of sexually transmitted infections with heterogeneity in risk have simulated turnover among risk groups, and those models which have simulated turnover have done so in various ways. In this section, we review three prior implementations of turnover and their assumptions. We then highlight how the approach proposed in Section A.2 could be used to achieve the same objectives.

Stigum et al. (1994) simulated turnover among $G = 2$ risk groups in a population with no exogenous entry or exit ($\nu = \mu = 0$ and hence $\hat{\boldsymbol{e}}$ is not applicable). Turnover between the groups was balanced in order to maintain constant risk group sizes (Type 1 constraint),[5] while the rate of turnover from high to low was specified as κ (Type 2 constraint). Thus, the turnover system used by Stigum et al. (1994) can be written in the proposed framework as:

$$\begin{bmatrix} 0 \\ \kappa \end{bmatrix} = \begin{bmatrix} \hat{x}_1 & -\hat{x}_2 \\ 1 & \cdot \end{bmatrix} \begin{bmatrix} \phi_{12} \\ \phi_{21} \end{bmatrix}, \qquad \hat{e}_1 = \hat{e}_2 = 0 \tag{A.19}$$

Henry and Koopman (2015) also simulated turnover among $G = 2$ risk groups, but considered exogenous entry and exit, both at a rate μ. The authors used the notation f_i for our $\hat{x}_i$, and assumed that the population of individuals entering into the modelled population had the same distribution of risk groups as the modelled population itself: $\hat{e}_i = f_i$ (Type 2 constraint). The authors further maintained constant risk group sizes (Type 1 constraint) by analytically balancing turnover between the two groups using: $\phi_{12} = \omega\hat{x}_2$; $\phi_{21} = \omega\hat{x}_1$, where ω is a constant. However, it can be shown that this analytical approach is also the solution to the following combination of Type 1 and Type 2 constraints:

$$\begin{bmatrix} 0 \\ \omega f_2 \end{bmatrix} = \begin{bmatrix} f_1 & -f_2 \\ 1 & \cdot \end{bmatrix} \begin{bmatrix} \phi_{12} \\ \phi_{21} \end{bmatrix}, \qquad \hat{e}_i = f_i \tag{A.20}$$

[5] Due to its simplicity, this constraint is actually an example of both Type 1 and Type 4 constraints.

Eaton and Hallett (2014) simulated turnover among $G = 3$ risk groups, considering a distribution of risk among individuals entering into the modelled population $\hat{\boldsymbol{e}}$ which was different from $\hat{\boldsymbol{x}}$. Turnover was considered from high-to-medium, high-to-low, and medium-to-low risk, all with an equal rate ψ; the reverse transition rates were set to zero (six total Type 2 constraints). Given the unidirectional turnover, risk group sizes were maintained using the values of $\hat{e}_i$, computed using Type 1 constraints as follows:

$$\begin{bmatrix} \nu x_1 + 2x_1\psi \\ \nu x_2 - x_1\psi + x_2\psi \\ \nu x_3 - x_1\psi - x_2\psi \end{bmatrix} = \begin{bmatrix} \nu & \cdot & \cdot \\ \cdot & \nu & \cdot \\ \cdot & \cdot & \nu \end{bmatrix} \begin{bmatrix} e_1 \\ e_2 \\ e_3 \end{bmatrix}, \qquad \begin{aligned} \phi_{12} = \phi_{13} = \phi_{23} = \psi \\ \phi_{21} = \phi_{31} = \phi_{32} = 0 \end{aligned} \tag{A.21}$$

In sum, the framework for modelling turnover presented in this section aims to generalize all previous implementations. In so doing, we hope to clarify the requisite assumptions, dependencies on epidemiologic data, and relationships between previous approaches.

B Supplemental Equations

Table B.1: Notation

Symbol	Definition
i	risk group index
j	risk group index for "other" group in turnover
k	risk group index for "other" group in incidence
t	time
$\mathcal{S}_i$	number of susceptible individuals in risk group i
$\mathcal{I}_i$	number of infectious individuals in risk group i
$\mathcal{T}_i$	number of treated individuals in risk group i
N	total population size
ν	rate of population entry
μ	rate of population exit
ϕ_{ij}	rate of turnover from group i to group j
λ_i	force of infection among susceptibles in risk group i
τ	rate of treatment initiation among infected
$\hat{x}_i$	proportion of individuals in risk group i
$\hat{e}_i$	proportion of individuals entering into risk group i
δ_i	average duration spent in risk group i
C_i	number of partners per year among individuals in risk group i
β	probability of transmission per partnership
ρ_{ik}	probability of partnership formation between risk groups i and k

B.1 Model Equations

$$\frac{d}{dt}\mathcal{S}_i(t) = +\sum_j \phi_{ji}\mathcal{S}_j(t) - \sum_j \phi_{ij}\mathcal{S}_i(t) - \mu\mathcal{S}_i(t) + \nu\hat{e}_i N(t) - \lambda_i(t)\mathcal{S}_i(t) \tag{B.1a}$$

$$\frac{d}{dt}\mathcal{I}_i(t) = +\sum_j \phi_{ji}\mathcal{I}_j(t) - \sum_j \phi_{ij}\mathcal{I}_i(t) - \mu\mathcal{I}_i(t) + \lambda_i(t)\mathcal{S}_i(t) - \tau\mathcal{I}_i(t) \tag{B.1b}$$

$$\frac{d}{dt}\mathcal{T}_i(t) = +\sum_j \phi_{ji}\mathcal{T}_j(t) - \sum_j \phi_{ij}\mathcal{T}_i(t) - \mu\mathcal{T}_i(t) + \tau\mathcal{I}_i(t) \tag{B.1c}$$

$$\underbrace{+\sum_j \phi_{ji}\mathcal{T}_j(t)}_{\text{turnover into}} \underbrace{- \sum_j \phi_{ij}\mathcal{T}_i(t)}_{\text{turnover from}} \underbrace{- \mu\mathcal{T}_i(t)}_{\text{death}} \underbrace{+ \nu\hat{e}_i N(t)}_{\text{birth}} \underbrace{+ \lambda_i(t)\mathcal{S}_i(t)}_{\text{incidence}} \underbrace{- \tau\mathcal{I}_i(t)}_{\text{treatment}}$$

B.2 Complete Example Turnover System

$$
\begin{array}{r}
\text{constant group size} \\ \\ \\
\text{specified } e \\ \\ \\
\text{group duration} \\ \\ \\
\text{turnover rate ratios} \\ \\ \\
\end{array}
\left\{
\begin{array}{c}
\left[\begin{array}{c}
\nu x_1 \\ \nu x_2 \\ \nu x_3 \\ e_1^* \\ e_2^* \\ e_3^* \\ {\delta_1}^{-1} - \mu \\ {\delta_2}^{-1} - \mu \\ {\delta_3}^{-1} - \mu \\ 0 \\ 0 \\ 0
\end{array}\right]
\end{array}
\right.
=
\left[\begin{array}{ccccccccc}
\nu & \cdot & \cdot & -x_1 & -x_1 & x_2 & \cdot & x_3 & \cdot \\
\cdot & \nu & \cdot & x_1 & \cdot & -x_2 & -x_2 & \cdot & x_3 \\
\cdot & \cdot & \nu & \cdot & x_1 & \cdot & x_2 & -x_3 & -x_3 \\
1 & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\
\cdot & 1 & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\
\cdot & \cdot & 1 & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\
\cdot & \cdot & \cdot & 1 & 1 & \cdot & \cdot & \cdot & \cdot \\
\cdot & \cdot & \cdot & \cdot & \cdot & 1 & 1 & \cdot & \cdot \\
\cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & 1 & 1 \\
\cdot & \cdot & \cdot & x_1 & \cdot & -x_2 & \cdot & \cdot & \cdot \\
\cdot & \cdot & \cdot & \cdot & x_1 & \cdot & \cdot & -x_3 & \cdot \\
\cdot & \cdot & \cdot & \cdot & \cdot & \cdot & x_2 & \cdot & -x_3
\end{array}\right]
\left[\begin{array}{c}
e_1 \\ e_2 \\ e_3 \\ \phi_{12} \\ \phi_{13} \\ \phi_{21} \\ \phi_{23} \\ \phi_{31} \\ \phi_{32}
\end{array}\right]
\tag{B.2}
$$

B.3 Redundancy in specifying all elements of $\hat{e}$

Whenever it is assumed that risk groups do not change size, G rows of the form shown in Eq. (A.11) are added to $\boldsymbol{b}$ and A:

$$
\boldsymbol{b} = \left[\begin{array}{c} \nu x_1 \\ \nu x_2 \\ \nu x_3 \end{array}\right]; \qquad A = \left[\begin{array}{ccccccccc}
\nu & \cdot & \cdot & -x_1 & -x_1 & x_2 & \cdot & x_3 & \cdot \\
\cdot & \nu & \cdot & x_1 & \cdot & -x_2 & -x_2 & \cdot & x_3 \\
\cdot & \cdot & \nu & \cdot & x_1 & \cdot & x_2 & -x_3 & -x_3
\end{array}\right] \tag{A.11}
$$

After multiplying by $\boldsymbol{\theta}$, these G rows can be row-reduced by summing to obtain:

$$
\begin{aligned}
[\nu x_1 + \nu x_2 + \nu x_3] &= [\nu e_1 + \nu e_2 + \nu e_3 + 0\,\phi_{12} + 0\,\phi_{13} + 0\,\phi_{21} + 0\,\phi_{23} + 0\,\phi_{31} + 0\,\phi_{32}] \\
\nu\,[x_1 + x_2 + x_3] &= \nu\,[e_1 + e_2 + e_3]
\end{aligned} \tag{B.3}
$$

which therefore implies that $\sum_i x_i = \sum_i e_i$, or equivalently $\sum_i \hat{x}_i = \sum_i \hat{e}_i = 1$. Thus, it is redundant to specify all G elements of $\hat{e}$, as the final element will be dictated by constant group size constraints.

B.4 Factors of Incidence

Substituting the proportional mixing definition of ρ_{ik} into the incidence equation, Eq. (3), we have:

$$
\begin{aligned}
\lambda_i &= C_i \sum_k \rho_{ik} \beta \frac{\mathcal{I}_k}{\mathcal{X}_k} \\
&= C_i \beta \sum_k \frac{C_k \mathcal{X}_k}{\sum_{\mathrm{k}} C_{\mathrm{k}} \mathcal{X}_{\mathrm{k}}} \frac{\mathcal{I}_k}{\mathcal{X}_k} \\
&= C_i \beta \underbrace{\frac{\sum_k C_k \mathcal{I}_k}{\sum_{\mathrm{k}} C_{\mathrm{k}} \mathcal{X}_{\mathrm{k}}}}_{f}
\end{aligned} \tag{B.4}
$$

We can factor the term f as:

$$\begin{aligned} f &= \frac{\sum_k C_k \mathcal{I}_k}{\sum_{\mathrm{k}} C_{\mathrm{k}} \mathcal{X}_{\mathrm{k}}} \\ &= \frac{\sum_k C_k \mathcal{I}_k}{\sum_k \mathcal{I}_k} \cdot \frac{\sum_k \mathcal{I}_k}{\sum_k \mathcal{X}_k} \cdot \frac{\sum_k \mathcal{X}_k}{\sum_k C_k \mathcal{X}_k} \end{aligned} \tag{B.5}$$

which we recognize as the following terms:

$$= \hat{C}_{\mathcal{I}} \cdot \hat{\mathcal{I}} \cdot \hat{C}^{-1} \tag{B.6}$$

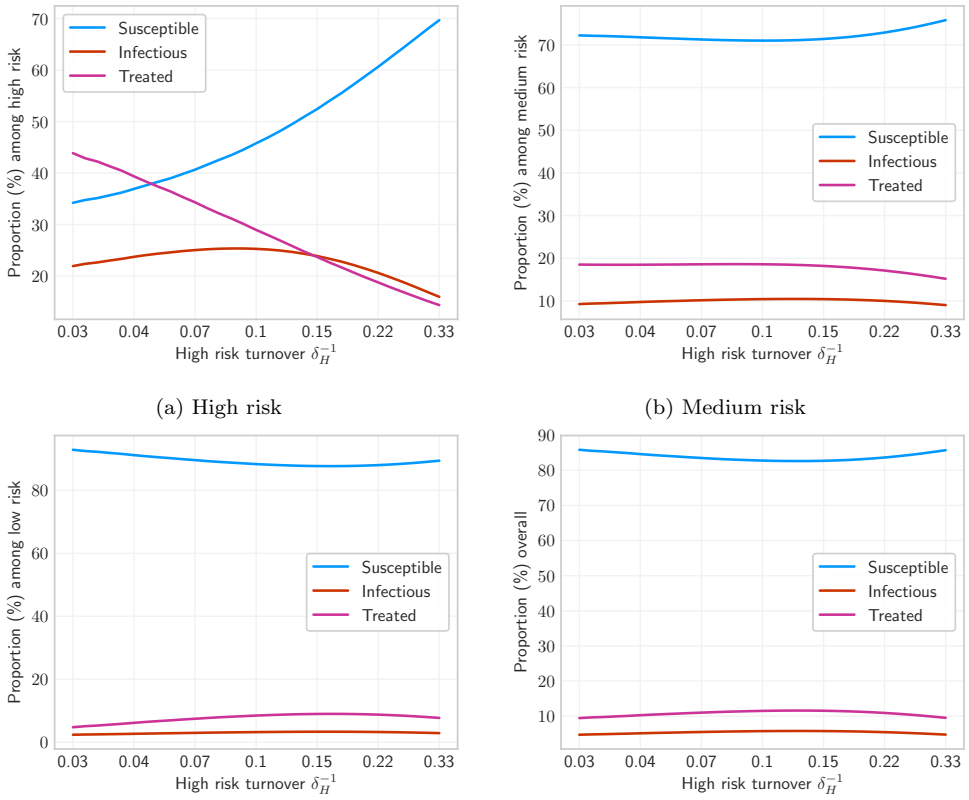
Namely,

1. $\hat{C}_{\mathcal{I}}$ is the average number of partners among infectious individuals
2. $\hat{\mathcal{I}}$ is the proportion of the population who are infectious (overall prevalence)
3. $\hat{C}$ is the average number of partners among all individuals (constant)

Therefore, only two non-constant factors control incidence per susceptible: 1) the average number of partners among infectious individuals $\hat{C}_{\mathcal{I}}$, and 2) overall prevalence $\hat{\mathcal{I}}$. The product of these factors $\hat{C}_{\mathcal{I}} \hat{\mathcal{I}}$, scaled by $\beta C_i / \hat{C}$, then gives λ_i. In fact, the incidence in each group individually is proportional to incidence overall, as C_i is only factor depending on i.

C Supplemental Results

C.1 Equilibrium health states and rates of transition



(a) High risk

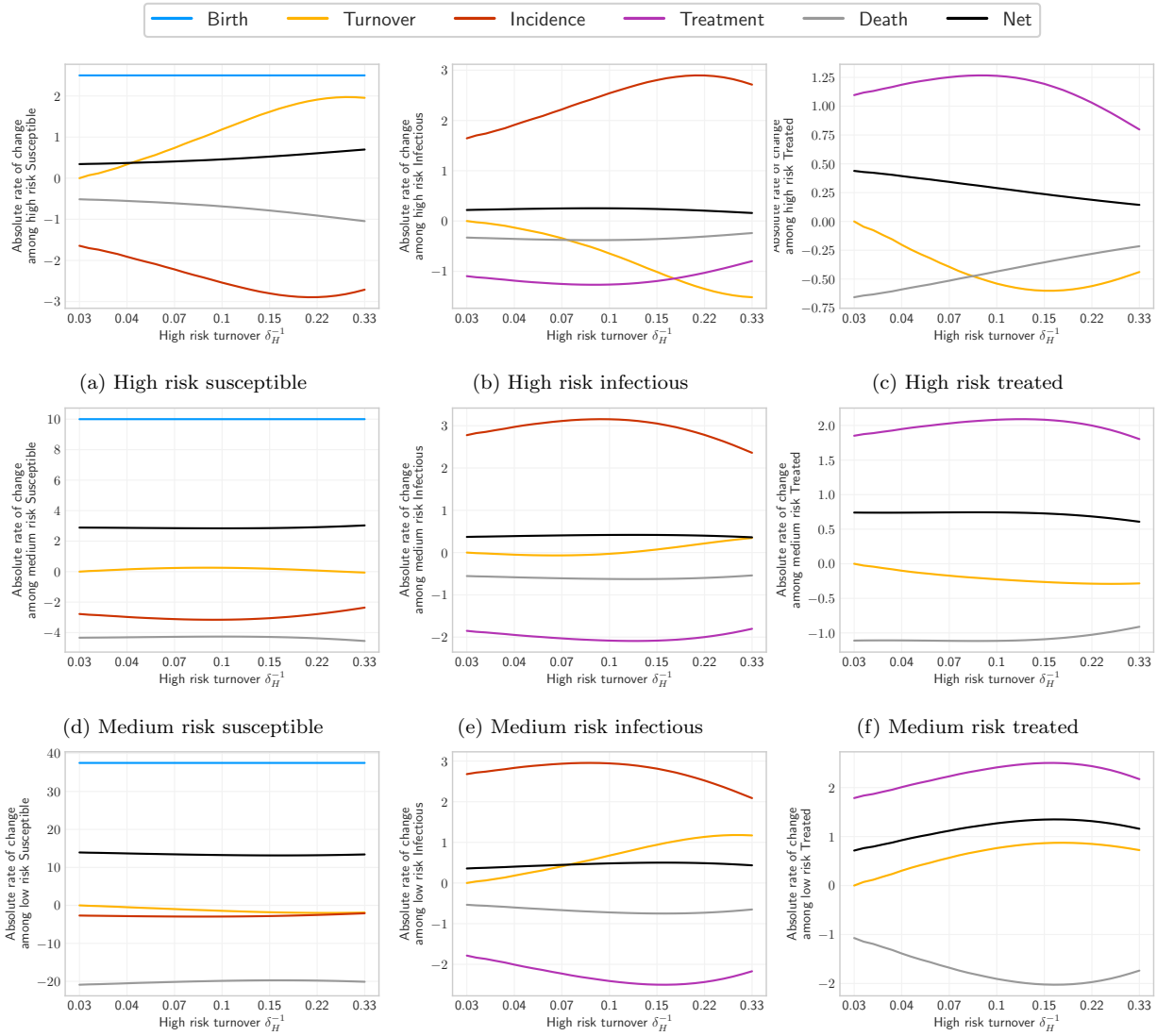
(b) Medium risk

(c) Low risk

(d) Overall

Figure C.1: Equilibrium health state proportions under different rates of turnover.

Turnover rate (log scale) is a function of the duration of time spent in the high risk group δ_H, where shorter time spent in the high risk group yields faster turnover. No turnover is indicated by $\delta_H^{-1} = 0.03$, due to population exit rate $\mu = 0.03$.



(a) High risk susceptible (b) High risk infectious (c) High risk treated

(d) Medium risk susceptible (e) Medium risk infectious (f) Medium risk treated

(g) Low risk susceptible (h) Low risk infectious (i) Low risk treated

Figure C.2: Absolute rates of change at equilibrium (number of individuals gained/lost per year) among individuals in each health state and risk group, broken down by type of change: gain via births, loss/gain via incident infections, loss/gain via treatment, loss/gain via turnover, loss via death, and net change. Based on Eq. (B.1).

Turnover rate (log scale) is a function of the duration of time spent in the high risk group δ_H, where shorter time spent in the high risk group yields faster turnover. No turnover is indicated by $\delta_H^{-1} = 0.03$, due to population exit rate $\mu = 0.03$. Rates of change do not sum to zero due to population growth.

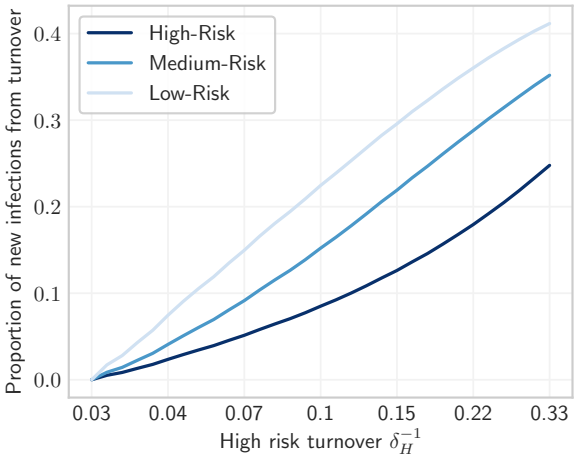
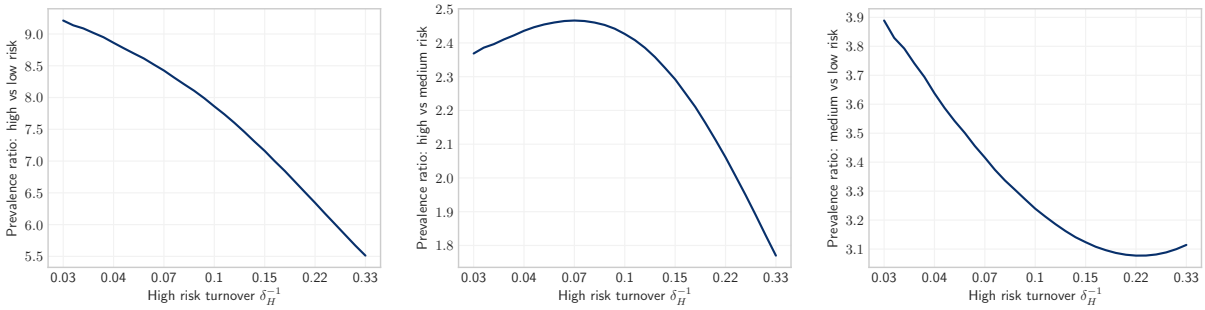


Figure C.3: Proportion of new infectious individuals in each risk group which are from turnover of infectious individuals, as opposed to incident infection of susceptible individuals in the risk group.

C.2 Equilibrium Prevalence Ratios

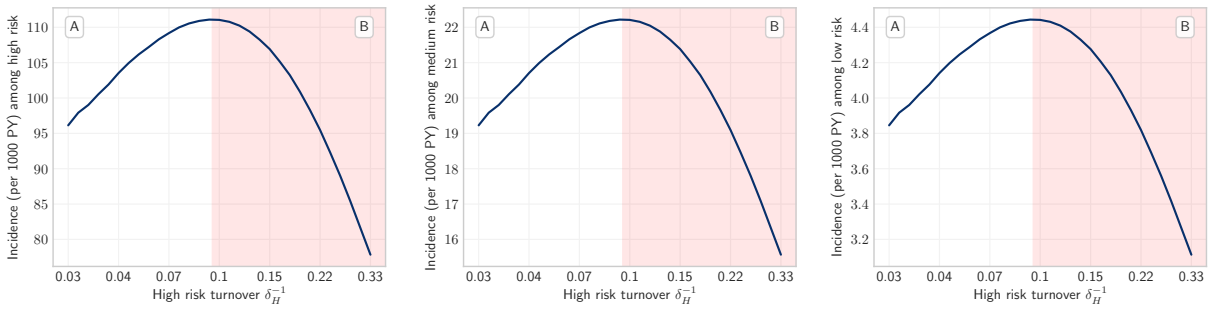


(a) High vs Low risk (b) High vs Medium Risk (c) Medium vs Low Risk

Figure C.4: Equilibrium prevalence ratios between risk groups under different rates of turnover.

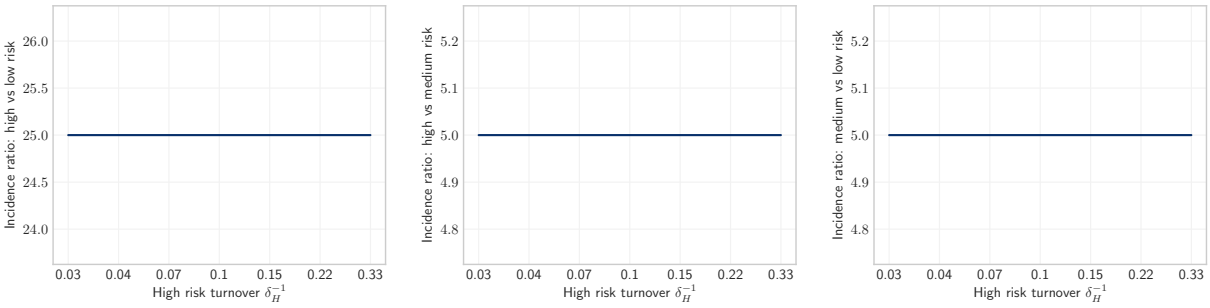
Turnover rate (log scale) is a function of the duration of time spent in the high risk group δ_H, where shorter time spent in the high risk group yields faster turnover. No turnover is indicated by $\delta_H^{-1} = 0.03$, due to population exit rate $\mu = 0.03$.

C.3 Equilibrium Incidence



(a) High risk (b) Medium risk (c) Low risk

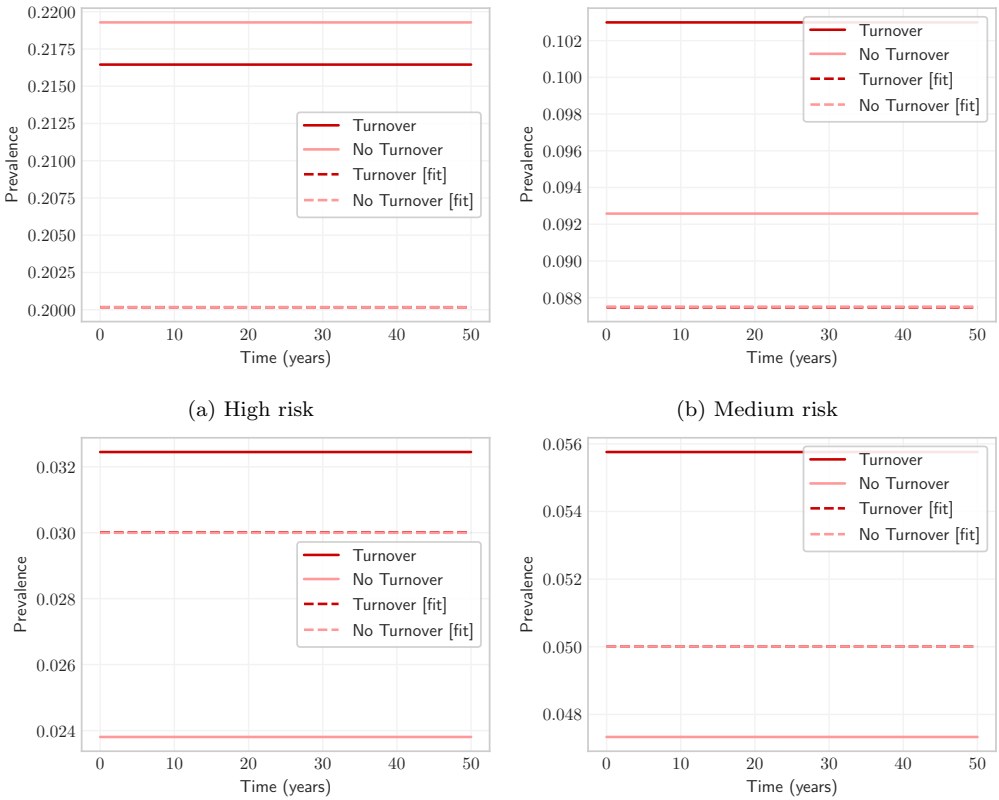
Figure C.5: Equilibrium incidence among high, medium, and low risk groups under different rates of turnover. Turnover rate (log scale) is a function of the duration of time spent in the high risk group δ_H, where shorter time spent in the high risk group yields faster turnover. No turnover is indicated by $\delta_H^{-1} = 0.03$, due to population exit rate $\mu = 0.03$. Incidence in each risk group is proportional to overall incidence with C_i as a scale factor.



(a) High vs low risk (b) High vs medium risk (c) Medium vs low risk

Figure C.6: Equilibrium incidence ratios between risk groups under different rates of turnover. Incidence ratios do not depend on turnover.
Turnover rate (log scale) is a function of the duration of time spent in the high risk group δ_H, where shorter time spent in the high risk group yields faster turnover. No turnover is indicated by $\delta_H^{-1} = 0.03$, due to population exit rate $\mu = 0.03$.

C.4 Equilibrium prevalence and number of partners before and after model fitting



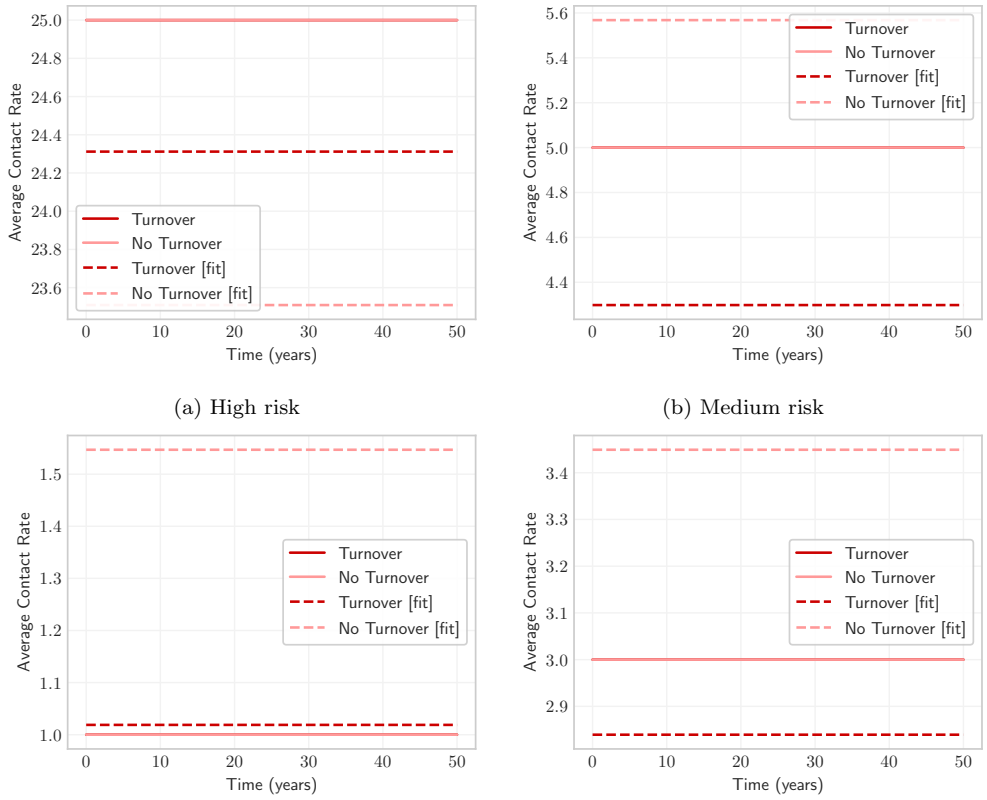
(a) High risk

(b) Medium risk

(c) Low risk

(d) Overall

Figure C.7: Equilibrium STI prevalence among high, medium, and low risk groups as well as overall, with and without turnover, and with and without fitted C_i to group-specific prevalence.



(a) High risk

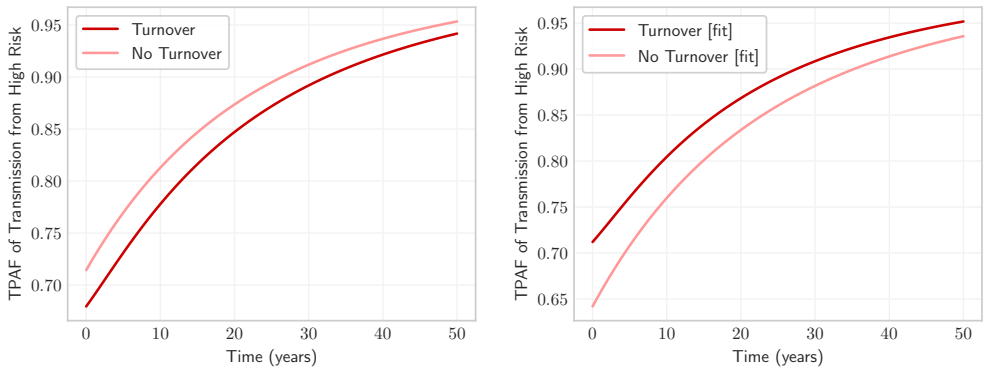
(b) Medium risk

(c) Low risk

(d) Overall

Figure C.8: Numbers of partners C_i among high, medium, and low risk groups as well as overall, with and without turnover, and with and without model fitting to group-specific prevalence.

C.5 Influence of turnover on tPAF of the high risk group before and after model fitting



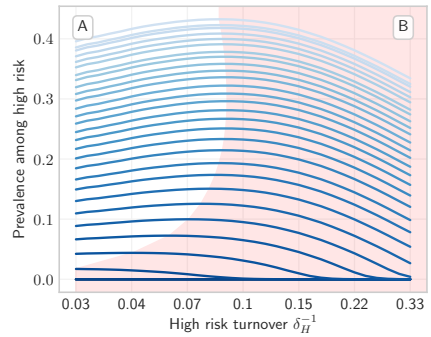
(a) High risk, before fitting

(b) High risk, after fitting

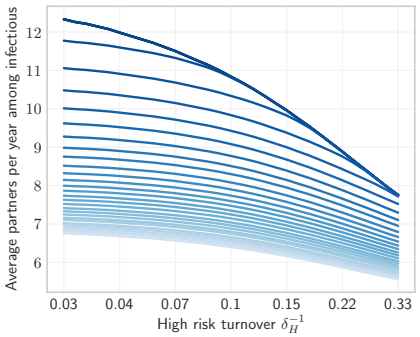
Figure C.9: Transmission population attributable fraction (tPAF) of the high risk group in models with and without turnover, before and after model fitting.

C.6 Effect of treatment rate on the influence of turnover on equilibrium prevalence

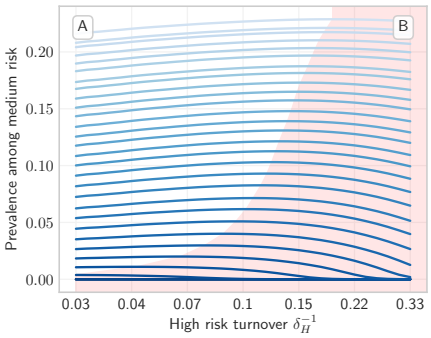
In order to examine the effect of treatment rate τ on the results of Experiment 1 – the influence of turnover on equilibrium prevalence – we recreated Figures 4 and 7 for a range of treatment rates $\tau \in [0.05, 1.0]$. The results are shown in Figure C.10.



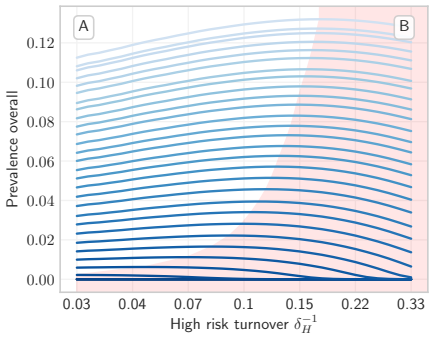
(a) Prevalence among high risk



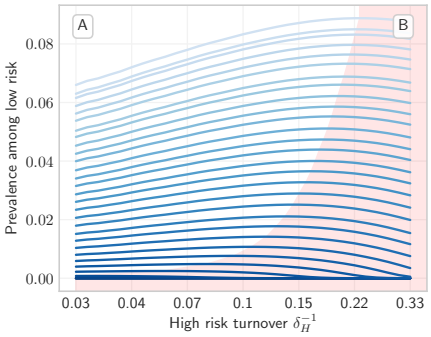
(d) Average C among infectious individuals $\hat{C}_{\mathcal{I}}$



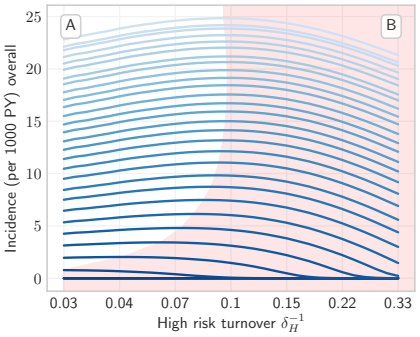
(b) Prevalence among medium risk



(e) Prevalence overall



(c) Prevalence among low risk



(f) Incidence overall λ

Figure C.10: Relationship between turnover rate and equilibrium STI prevalence in high, medium, and low risk groups, as well as overall STI prevalence and incidence, and average C among infectious individuals, for a range of treatment rates τ. Darker blue indicates higher treatment rate. The threshold turnover rate separating regions A and B decreases with treatment rate, meaning that increasing turnover becomes more likely to decrease equilibrium prevalence as treatment rate increases. Turnover rate (log scale) is a function of the duration of time spent in the high risk group δ_H, where shorter time spent in the high risk group yields faster turnover. No turnover is indicated by $\delta_H^{-1} = 0.03$, due to population exit rate $\mu = 0.03$.

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