Pathogen dissemination in the intensive care unit

This study demonstrates the simplest general approach we use for the stochastic spatial analysis of pathogen dissemination and also illustrates the effects of overlapping caregiver contact networks on the dynamics of pathogen dissemination. Accordingly, we will describe the associated model in some detail.

The model is based on the explicit assignment of each class of caregiver to a specific subpopulation of patients. During a caregivers' shift (8 hours for nurses, 12 hours for physicians), the caregiver makes a specified minimum number of visits to each patient in his or her specified population. Three classes of caregivers are included: nurses, primary physicians, and consultant physicians. There are three shifts of nurses each day, and one "shift" for physicians. Each caregiver and patient is explicitly tracked throughout the entire simulation. Staffing levels and patient assignments are set by the user, and remain constant throughout the simulation. Only patient: caregiver interactions are modeled. The model can be configured to reflect ICUs of arbitrary sizes, staffing levels, caregiver allocation practices, and flow patterns. The configured model can be parameterized with arbitrary pathogen transmissibilities for each interclass interaction, and variable durations of caregiver and/or patient contamination. In the simulations presented, we configured the model as two "adjacent" 12 bed ICUs that share user-specified staff members:

10	12	22	24
9	11	21	23
6	8	18	20
5	7	17	19
2	4	14	16
1	3	13	15

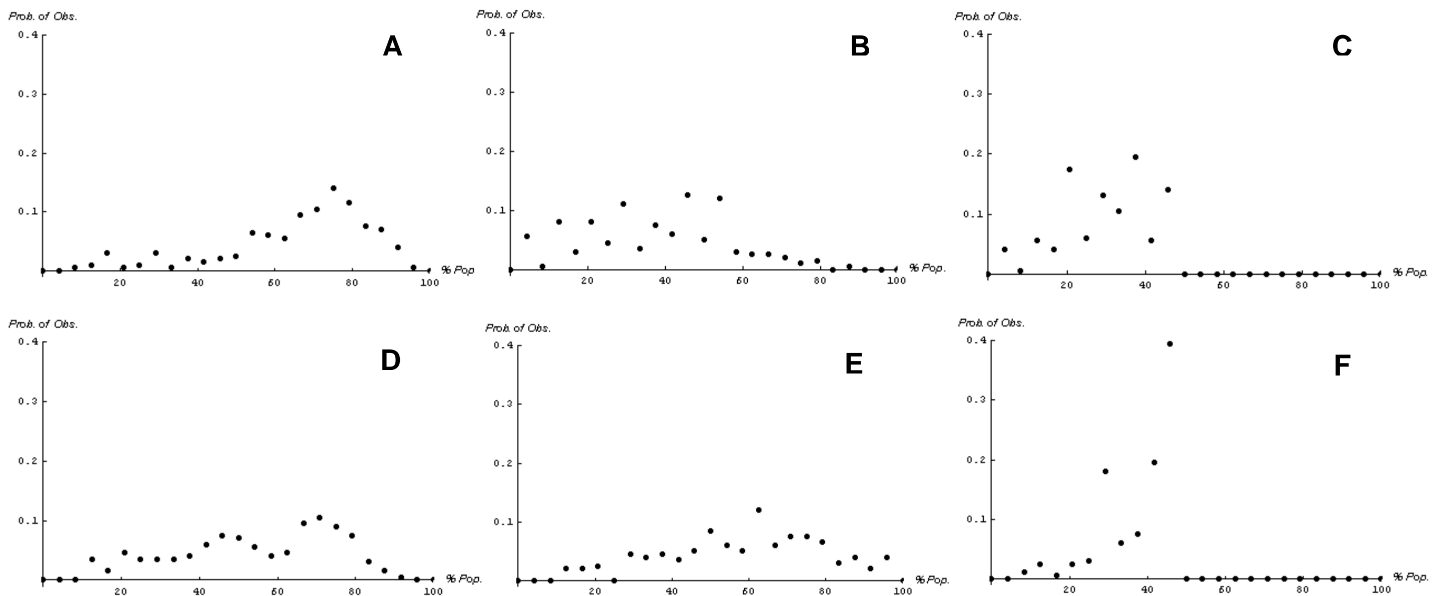
The initial number of positive patients and caregivers, their locations, the number of nurses, consultants, and primary physicians, the patient assignments for each caregiver, the minimum number of visits (per shift) by each class of caregiver, and the maximum number of additional "random patient contacts" are specified. Caregiver domains are allowed to overlap; the user specifies the degree of overlap. During the simulation, every caregiver is moved along a pseudorandom path within his or her specified domain; in these simulations the model moved caregivers every fifteen minutes. In the results presented, the model was run through 672 fifteen-minute cycles, corresponding to one week, for each panel presented.

If the caregiver encounters a patient, the class of interaction (P+C+,P-C-,P+C-,P-C+) is determined, hwere "P+" or "C+" designates a contaminated caregiver, and "P-" or "C-" denote a noncontaminated patient or caregiver. For interactions of class P+C- and P-C+, the uncontaminated member of the pair may become contaminated with a probability PEAP ("Per Encounter Acquisition Probability"). Caregivers may or may not clear their contamination during their "off shift" time. In the data presented the probability of transmission in either direction and between classes of agents were set equal, simplifications that are easily relaxed. At the conclusion of the simulation (672 cycles), the number of patients becoming positive during the simulation is counted and expressed as a percentage of the total patient population. The model is then re-set to the initial conditions and the simulation repeated. In these examples, each of the panels presents a probability distribution obtained by setting the simulation to repeat 200 times. The probability of observing a given percentage of the patient population becoming positive over the examined time period was determined by dividing the number of simulations resulting in that level of dissemination by 200.

Results are presented as the probability (y-axis, Prob. of obs) of observing a given fraction of the patient population (x-axis, % Pop.) becoming positive over the selected period of observation (one week). Thus, the model generates the probability distribution for a given fraction of the population becoming contaminated under specified spatial, initial prevalence, and dynamic conditions; data points in the upper right-hand quadrant of each panel reflect a higher probability of more extensive pathogen dissemination. In the data presented, the

model was configured to emulate a hospital with two separate 12-bed critical care units, 4 physicians and either 36 or 18 nurses (three nursing shifts with a patient: nurse ratio of either 2:1 or 4:1). A nurse visits each patient at least once per hour. The minimum number of physician visits to each patient is 4 per day, reflecting either a single daily visit by each of 4 physicians, or 2 daily visits by each of 2 physicians. In each simulation, there is initially a single patient capable of transmitting the pathogen of interest.

The data presented illustrate interactions between the degree to which caregiver domains overlap and pathogen dissemination. Upper panels (A to C) present data from the 36-nurse model; lower panels (D to F) present data from the 18-nurse model. In panels A and D the model was configured to reflect homogeneous mixing of patients, physicians, and nurses- each patient is seen by every caregiver- the assumptions underlying most current models of pathogen dissemination in "well-mixed" populations. In panels B and E, each nurse sees either 2 (B) or 4 (E) patients, and each patient is visited twice a day by each of two physicians; all physicians see patients in both intensive care units. This corresponds to a pair of "open" ICUs. In panels C and D, two physicians see all of the patients in one ICU, and the other two physicians see all of the patients in the other ICU. This corresponds to a pair of "closed" ICUs.



Limiting the overlap of caregiver domains attenuates pathogen dissemination, an effect that would be difficult to capture using traditional models predicated on well-mixed populations. Progressive restriction of provider contact networks from well-mixed, albeit stochastic (A and D), to regional (C and F) significantly reduces the predicted level of dissemination, despite an equal number of caregiver: patient contacts between panels A, B and C and between panels D, E, and F. Lower patient: nurse ratios result in smaller nurse domains and reduced dissemination, except in the homogeneously mixed scenario (where the lower number of interacting individuals in the 18 nurse configuration becomes the dominant factor). More detailed analyses, including effects of caretaker contamination duration, patient cohorting, and active surveillance, are covered in the original paper.

Implications

Social network-based measures could significantly attenuate pathogen transmission in the intensive care unit. In addition, many current approaches to estimating pathogen transmissibility may significantly underestimate the "per contact" risk of pathogen transmission. Our data suggest that the social contact network itself can serve as a barrier to transmission. Accordingly, approaches to estimating transmissibility that are based on overall pathogen prevalence but that do not account for temporal and spatial aspects of the contact network may significantly underestimate the "per-encounter" transmission risk faced by caregivers or patients. A very transmissible pathogen might appear much less transmissible if the effects of the social network on limiting dissemination are erroneously attributed to the pathogen's transmissibility.