The network of patient movements between Norwegian hospitals and its potential to contribute to the spread of hospital infections

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One year of detailed patient data from "half" of Norway, can follow each individual in the hospital system (at the individual ward level) + covariates

- Analyse the data and describe the network

Elementary nodes = wards
Movements = patient in or out of ward (to the "exterior") or between wards

- the wards have several aggregation "levels":
therapeutic: wards belong to specific "therapeutic units",
administrative: ward < hospital < local health organization,
geographical: ward<hospital<municipality<county.

- individuals have "single registrations" in the register, involving a given ward, event and time period,

- these events have different "intensity" of contact=policlinic, day-patient, inpatient

- individuals have connected "episodes" in time (may contain several events and movements),

- individuals have "histories" during the year

=> rather complicated description of "duration of stay"/individual.

- Add a model for spread of infectious agent
Important difference between "carriage" and "serious infection"

Infection may be brought in from the "exterior", may spread within the ward during stay or between wards because of movement => choice of spread mechanism (may depend on agent, type of ward, hypotheses about interpatient, environmental, personnel mediated spread...)

- Data and inference

Data (on infections) is complicated by the (probable) sampling scheme: not random sample of prevalence, but event driven (one serious case of infection generates search in "neighbourhood" and subsequent treatment of cases...) + some screening activity...

- What kind of inference is desired?

Essentially, from the point of view of parameters, various infection probabilities (between patients in same ward , in different wards sme hospital, from environment in hospital, from "outside") and the potential of being "discovered" = becoming data...

From the point of view of prediction, if we represent the whole system by a stochastic system "in equilibrium" (a simulation model...), the conditional distribution of prevalence in other nodes given that infection is observed in one node...

Please, wish us good luck… ☺