It's simple: increasing complexity of models does not necessarily increase their accuracy

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Mathematical modeling of infectious diseases is an important tool in the understanding and prediction of epidemics. Knowledge of social interactions is used to understand how infectious diseases spread through populations and how to control epidemics. New research published in *BMC Medicine* shows that a model, which included dynamic information about the heterogeneity of contact length and rate of making new contacts, was as effective as a more complex model which included the order of contacts.

Data was collected over a two-day period, within the Socio Patterns project, which brings together researchers from Turin (Italy), Marseilles and Lyon (France). 405 people attending the 2009 Annual French Conference on Nosocomial Infections volunteered to wear radiofrequency identification device ([RFID](#)) which recorded face to face contacts (within a distance of 1-2m). Each day researchers recorded the number and duration of meetings between participants. Nearly 30,000 social contacts were recorded over the two days of the conference allowing dynamic networks to be constructed.

Three aggregations of this data set were used in a SEIR (Susceptible, Exposed, Infectious, Recovered) model of infection. The first (DYN) utilized dynamic and time-order specific data, the second (HET) retained [heterogeneity](#) of contacts but not the order of interactions, and the third (HOM) assumed that all interactions were random, homogeneous, and of the same length.

While it might be assumed that knowing the precise order of social contacts may help refine the model, the results from the first two scenarios, DYN and HET, were very similar producing a comparable number of infected individuals and taking the same time to reach peak infection. However, without enough data, the simplest scenario, HOM, estimated a larger number of infected people and therefore a more severe epidemic.

Dr Juliette Stehlé from Université de Marseilles concluded, "Adding real life data about the movement of people within social situations is important in refining computational models of how disease is spread. Our results have important implications for understanding the level of detail required needed to produce functional models and better models lead in turn to better anticipation, prevention, and management of emerging infection and epidemics."

More information: Simulation of an SEIR infectious disease model on the dynamic contact network of conference attendees, Juliette Stehle, Nicolas Voirin, Alain Barrat, Ciro Cattuto, Vittoria Colizza, Lorenzo Isella, Corinne Régis, Jean-Francois Pinton, Nagham Khanafer, Wouter Van den Broeck and Philippe Vanhems, *BMC Medicine* (in press)

Commentary: The importance of including dynamic social networks when modeling epidemics of airborne infections: does increasing complexity increase accuracy? Sally Blower and Myong-Hyun Go, *BMC Medicine* (in press)

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