Heterogeneity in animal contact networks: its measurement, modelling and consequences

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Contact networks between animals or groups of animals are typically modelled using a static structure. They are either modelled using simple summaries of the data, such as proportion of time spent in contact or numbers of animals sold or they are modelled using the details of a single observation of the network, possibly made over a period of time. Such approaches suffer because they neither consider the dynamic nature of the network, nor the randomness inherent in contacts. Furthermore they are specific to the data observed, and therefore may give erroneous inferences if used to predict future events. Although the static approach does allow comparison of networks, it only allows us to say whether the declared networks are the same or different: in the absence of an error structure, we can not quantify the statistical significance of differences relative to random variability. We have developed a stochastic framework to examine contact networks, fitting probability distributions independently to different random variables defining the network. For example, inter-contact times and contact durations between individuals within a group can each be described using gamma distributions. Fitting these distributions using two generalised linear models also allows us to incorporate covariates into the models. This approach results in a complete description of the network that can be used both to make robust predictions and to compare networks in a statistically meaningful manner. We have used this approach to demonstrate the effect of heterogeneity in contacts on the spread of disease. The model predicts that an assumption of homogeneity of contacts across all pairs of animals will lead to inaccuracies in the estimation of the basic reproductive ratio R0. We have also demonstrated statistically significant differences in the contact network of a group of animals before and after the introduction of an unfamiliar animal.