

Contribution of livestock movement network properties to R_0 for endemic chronic infections in the Scottish farm population

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Introduction

Animal movement is an important mode of spread for livestock infectious diseases (Fèvre *et al.* 2006). Livestock movements connect farms into networks; understanding how properties of these networks impact the potential for transmission of infections among the farms is crucial for designing efficient control. Here we consider the potential for transmission, expressed as the basic reproduction number, R_0 , for an infection affecting multiple livestock species (cattle, pigs, sheep and goats) in the population of Scottish farms. We examine how properties of the farm contact network affect the magnitude of R_0 . We consider one-year time span and do not attempt to capture the early dynamics of disease outbreaks, so our results are most directly relevant to endemic chronic infections, such as certain food-borne pathogens, e.g. *Campylobacter* spp. (Devane *et al.*, 2005; Jones *et al.*, 1984), *Yersinia enterocolitica* (McNally *et al.*, 2006; Milnes *et al.*, 2008) or *Cryptosporidium parvum* (O'Donoghue, 1995). Such infections are commonly asymptomatic and long-lasting in the livestock carriers, and are endemic. Different disease scenarios are explored by weighting the contact among the farms by the numbers of batches and total numbers of livestock moved.

Materials and Methods

Records of livestock movements for Scottish farms for the periods 01/07/2003-30/06/2004, 01/07/2004-30/06/2005, 01/07/2005-30/06/2006 and 01/07/2006-30/06/2007 were extracted from Scottish Animal Movement System and Cattle Tracing System of British Cattle Movement Service, and processed in Python programming environment and SAS@ 9.1.3 software for Windows (SAS Institute Inc.) as described in Volkova *et al.* (2008). Movements to slaughter, to shows, outside Scotland and with incomplete histories were excluded, leaving >1,000,000 records for analysis. The farm population was analyzed as a closed network considering all livestock movements between the farms: either direct or indirect via a Scottish livestock market. Between-farm transmission was assumed to occur through a movement of cattle, pigs, sheep or goats alike. The probability of within-farm transmission between livestock of different species was assumed to be absolute and equal among the species and among the farms. Therefore, the resulting magnitude of R_0 represented the upper bound for a multi-species, endemic, chronic infection spreading among Scottish farms. In each of the 4 years studied, the contribution to R_0 from the first order moments of the contact network (related to the mean number of contacts for a farm) and from the second order moments (related to the variances and covariances of movements on and off a farm) were calculated with SAS 9.1.3 software. The farm movement network can be represented by a contact matrix, A , where $a(i,j)$ (the element in i th row and j th column) is 0 if there was no movement from farm j to farm i but if movement took place $a(i,j)$ is either 1 (unweighted contact) or equal to the number of batches or animals moved as appropriate. R_0 is proportional to the dominant eigenvalue of the contact matrix (and incorporates the contribution of higher order moments of the contact network). The eigenvalues were calculated using ARPACK FORTRAN77 code libraries (Lehoucq *et al.*, 1997). The contribution of the network's higher order moments to R_0 was evaluated as the difference between the dominant eigenvalue of the year's contact matrix and the contribution of the first and second order moments of the network.

Results: Farm connectivity

The Scottish livestock movement network contained >20,000 farms in each of the 4 years. On average, a farm annually sent livestock to and received from 8.3-8.5 other Scottish farms; this resulted in 11.6-12.1 livestock batches and a total of 155-164 animals moved on and moved off. In each of the 4 years, 64-65% of the farms both brought livestock onto and sent off, 12% only brought on and 23-24% only sent off. The mean annual numbers of contacts for a farm were consistent over the 4 years. Contact patterns of individual farms were heterogeneous. Variability in annual numbers of in-contacts, batches moved on and animals moved on was greater than in numbers of out-movements on each of the three contact scales. The correlation between annual numbers of in-contacts and out-contacts for individual farms was positive and ranged over the 4 years from +0.15 to +0.17 for unweighted contact, from +0.07 to +0.17 for contacts weighted by number of batches, and from +0.18 to +0.37 for contacts weighted by total number of livestock moved.

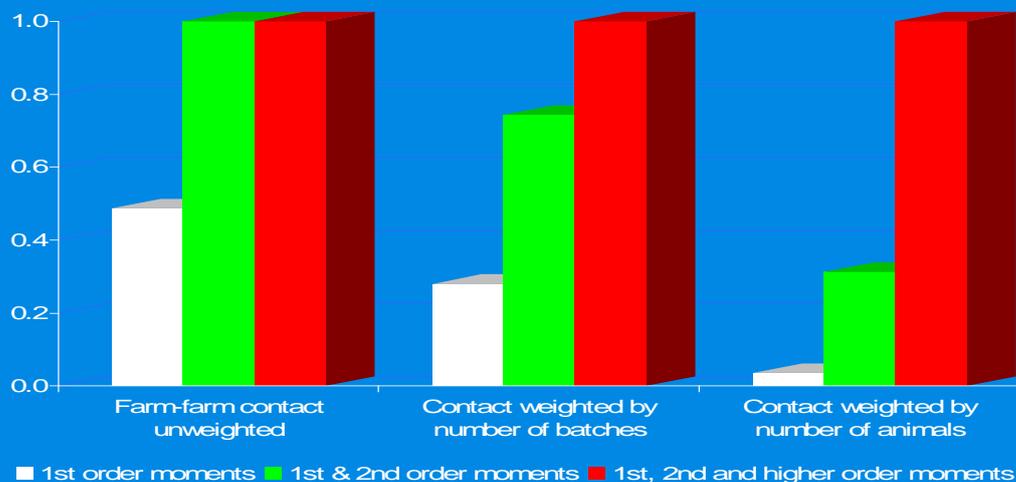
Results: Contribution of farm network properties to R_0

Evaluating the contribution of farm network properties to R_0 demonstrates that heterogeneities in farm contact patterns substantially influence the overall value of R_0 . Partitioning the impacts of the second and higher order moments shows that these influence R_0 differently on different contact scales. These relationships are less variable among the 4 years on a given contact scale. The figure (below) shows, for each of the three contact weightings, how the contribution of network properties to the magnitude of R_0 (scaled to 1) is partitioned between the first, second and higher order moments (averaged over the 4 years studied).

Conclusions

The key conclusions arising from this work are as follows. First, the higher order properties of a contact matrix (i.e. those not quantifiable from knowledge of the means, variances and covariances of contact rates) can have a very substantial impact on the relative magnitude of R_0 . Quantification of such effects requires knowledge of the complete network, which is rarely available for large populations. Second, the way in which contacts are weighted can make a substantial difference to quantification of R_0 and its components. The appropriate choice of weighting depends on the detailed epidemiology of the infection.

Endemic chronic infection R_0 : partitioning contribution of farm contact networks' properties



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