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Replicating disease spread in empirical cattle networks by adjusting the probability of infection in random networks.

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Abstract

Comparisons between mass-action or “random” network models and empirical networks have produced mixed results. Here we seek to discover whether a simulated disease spread through randomly constructed networks can be coerced to model the spread in empirical networks by altering a single disease parameter – the probability of infection. A stochastic model for disease spread through herds of cattle is utilised to model the passage of an SEIR (susceptible–latent–infected–resistant) through five networks. The first network is an empirical network of recorded contacts, from four datasets available, and the other four networks are constructed from randomly distributed contacts based on increasing amounts of information from the recorded network. A numerical study on adjusting the value of the probability of infection was conducted for the four random network models. We found that relative percentage reductions in the probability of infection, between 5.6% and 39.4% in the random network models, produced results that most closely mirrored the results from the empirical contact networks. In all cases tested, to reduce the differences between the two models, required a reduction in the probability of infection in the random network.

Keywords: Network; Mass-action; Disease; Recorded contacts; SEIR
simulation

1. Introduction

The assumption of random interactions, or mass-action mixing, is a method widely used in the modelling of disease (Anderson and May, 1991; Brauer et al., 2000; De Jong et al., 1995). With cheaper and easier methods of data capture now available to record contact networks (Craft and Caillaud, 2001) homogeneously mixed networks or “random networks” have been tested against the recorded contact networks with varying results (Duncan et al., 2012; Hamede et al., 2012; Kleinlützum et al., 2013; Salathé et al., 2010). In this publication we seek to discover whether a simple model of disease spread, based on the principles of homogeneous mixing, can approximate a recorded network if the probability of infection is suitably adjusted. If this is possible, we will also investigate: whether the simplicity of the model affects the closeness of fit to the recorded network; whether there is consistency in the adjustment of the probability of infection across a variety of random network models and whether there is a relationship between the network properties, through values of network metrics, and the adjustment to the probability of infection.

Results from comparisons of simulated disease spread on random and structured network, whether recorded, empirically derived (i.e. extrapolated from empirical data) or theoretically constructed, have been mixed. Some studies have found random networks to be a suitable substitute for structured network models (Bouma et al., 1995; Dobson and Meagher, 1996; Shirley and Rushton, 2005a) whilst others have found it inadequate (Barlow, 2000; D’ Amico et al., 1996; Hamede et al., 2012; Porphyre et al., 2008; Shirley and Rushton, 2005b). For

25 inter-herd contact networks, rather than the intra-herd networks discussed
26 herein, it has been shown that models should be at least based on any movement
27 data available (Vernon and Keeling, 2009). The modification of the transmission
28 rate of disease on a random network model has been shown to provide a good
29 representation of the results from theoretically constructed networks (Keeling,
30 2005). Simplified models of a complete contact network which take account of
31 rewiring or preferential mixing show closer agreement than a mean-field model
32 (random/mass-action mixing) when modelling Tasmanian devil facial tumour
33 disease (Hamede et al., 2012) and it was found that the networks had highly
34 connected animals, which would not be found in random networks. When
35 modelling spread of influenza in high school students (Salathé et al., 2010), it
36 was found that a small-world network (Watts and Strogatz, 1998) with a high
37 proportion of repeated contacts fitted the recorded data best, but a
38 homogeneous (random/mass-action) mixing model might be sufficient.

39

40 In our previous work (Duncan et al., 2012) we presented two stochastic models
41 of the passage of an SEIR (susceptible-latent-infected-resistant) disease
42 through herds of cattle. One model was based on a contact network constructed
43 via continuously recorded interaction data from two herds of cattle, the other, a
44 matching network constructed using the assumption of random mixing. Four
45 recorded contact datasets were produced by attaching proximity data loggers
46 (Drewe et al., 2012; Swain and Bishop-Hurley, 2007) to two separate herds of
47 cattle during two separate recording periods. For each dataset the network
48 constructed using the principles of random mixing had the same number of

49 contacts as the recorded network but these contacts were distributed randomly
50 amongst the animals. The differences shown between the two models were that
51 a lower proportion of simulations of the recorded network produced any disease
52 spread when compared to those simulations of the random network and, of
53 those that did, fewer infected animals were predicted. In this publication we
54 seek to estimate the optimal adjustment of the probability of infection of a
55 susceptible animal given a contact with an infectious animal so as to minimise
56 these differences.

57

58 We constructed four types of random networks, with increasing similarities to
59 the recorded contact network, and by adjusting the probability of infection
60 attempted to gain the best possible approximation for the recorded network.
61 Alongside the simulation of disease, we examined the network properties via six
62 network metrics: assortativity, average path length, closeness, clustering, degree
63 distribution and our own metric – the number of repeated contacts. It has been
64 shown that assortativity can be responsible for the lowering of the epidemic
65 threshold (Molina and Stone, 2012) and clustering to lower the reproductive
66 number R_0 and increase the threshold of disease (Miller, 2009). We have
67 already shown (Duncan et al., 2012) that the recorded networks had more
68 repeated contacts, lower closeness and clustering but higher average path
69 lengths. In this work we seek to relate any differences in these metrics to the
70 adjustment in the probability of infection. Networks can now be constructed
71 with algorithms, to have specific characteristics (Badham and Stocker, 2010a,b;
72 Bansal et al., 2009; Håkansson et al., 2010). Therefore, if it were the case that a

73 metric value was linked to the optimal adjustment in the probability of
74 infection, it would enable the use of specifically constructed theoretical networks
75 in place of recorded contact networks where recording was not feasible.

76 **2. Materials and Methods**

77 *2.1. Disease*

78 The SEIR disease that is modelled through all of the network models can be
79 described by the system of ordinary differential equations (ODEs) (Anderson
80 and May, 1991),

$$\begin{aligned}\frac{dS}{dt} &= -\alpha\beta\frac{SI}{N}, \\ \frac{dE}{dt} &= \alpha\beta\frac{SI}{N} - \sigma E, \\ \frac{dI}{dt} &= \sigma E - \gamma I\end{aligned}\tag{1}$$

and

$$\frac{dR}{dt} = \gamma I,$$

81 with $S + E + I + R = N$, where N is the total (constant) population size. Each
82 susceptible animal moves from the susceptible state (S) to the latent state (E)
83 with rate $\alpha\beta$ following a contact with an infectious animal, where α is the
84 probability of infection from a single contact with an infectious animal and β is
85 the average number of daily contacts per animal. The parameter σ is the rate at
86 which those in the latent class move to the infectious class and γ the rate at
87 which animals move from the infectious class to the resistant class.

88 *2.2. Datasets*

89 Four datasets were available to us. These were recorded using two herds of
90 cattle during two recording periods. The datasets are labelled 1A, 1B, 2A and

91 2B with the number denoting the recording period, first or second, and the
92 letter representing the herd. Datasets 1A and 1B were recorded during July
93 2009, both producing 30 complete days of usable data with both of the herds
94 returning complete data for 29 animals. The final two datasets recorded 28
95 complete days of data across August and September 2009 with 2A recording
96 data for 21 animals whilst 2B returned data for 17 animals.

97 *2.3. Network Construction*

98 In order to answer the question about how close the approximation to our
99 recorded network needed to be, we constructed four types of random network.
100 Each type of network was constructed using increasing amounts of information
101 taken from the recorded data. Details of how all the networks were constructed
102 follows, including details on the construction of the recorded and
103 matched-on-day network used in our previous publication (Duncan et al.,
104 2012). The matched-on-day network was previously referred to as a
105 mass-action or random network but for the purposes of this paper we are using
106 the description “matched-on-day” to demonstrate its relationship to the other
107 types of random network we present. The information required from the
108 recorded network and the mathematical construction for each type of random
109 network can be seen in table 1.

110 *2.3.1. Recorded and Matched-On-Day Networks*

111 For each of the four datasets a contact network was established, with the nodes
112 representing the animals, and the edges, the contacts. A contact was defined to
113 be any recorded interaction that lasted longer than 4 minutes. Although the

114 term contact has been used, only close proximity of the animals can be assumed
115 rather than actual physical contact. These networks were split into consecutive
116 12 hour time steps to give a manageable number of edges for each step in the
117 later disease simulation. An identical number of random networks were
118 constructed by taking the total number of interactions recorded in the
119 particular 12 hour period for a particular dataset, creating the same number of
120 random contacts and randomly allocating each of these contacts to pairs of
121 animals in the respective herd. For each dataset and 12 hour period this gave us
122 two networks, a recorded contact network and a random (“matched-on-day”)
123 network, with the same number of nodes and edges but with different edge
124 distributions for each 12 hour period for each of the four datasets.

125 *2.3.2. Additional Random Networks*

126 For each dataset, in addition to the matched-on-day network, we constructed
127 three other random networks: “constant-on-animal”, “constant-on-day” and
128 “matched-on-animal”. For the constant-on-animal network all animals had the
129 same number of contacts as one another for every 12 hour period. The contacts
130 were randomly assigned amongst the animals whilst ensuring that each animal
131 had the required number of contacts. The number of contacts per animal was
132 calculated by averaging all the recorded contacts over the number of animals
133 and the number of 12 hour time periods per dataset. Due to rounding, this
134 meant that the total number of contacts for each of these networks was different
135 from the total number of contacts in the recorded dataset they were derived
136 from.

138 For the constant-on-day network, the same total number of contacts per 12
139 hour time period as with the constant-on-animal network was used but the
140 contacts were allocated randomly amongst all the animals. There were no other
141 constraints on the number of contacts an individual animal could have. The
142 structure of this network was seen as lying between that of the
143 constant-on-animal network and the matched-on-day network. Very little
144 information (see table 1) from the recorded network was used in the construction
145 of either the constant-on-animal network or the constant-on-day networks.

146

147 In the matched-on-animal network each animal had exactly the same number
148 of contacts as in the recorded network, for each 12 hour period, but those
149 contacts were randomly distributed amongst the other animals subject to this
150 condition i.e. that the number of contacts each animal had was the same as the
151 recorded network. As with the other random network, matched-on-animal
152 networks were constructed for all four datasets.

153 *2.4. Network Metrics*

154 To investigate the differences between the five networks (constant-on-animal;
155 constant-on-day; matched-on-day; matched-on-animal and recorded) six
156 different network metrics were calculated. The first was our own metric, the
157 number of repeated edges, chosen to quantify the observed difference in
158 repeated contacts. The second was closeness, the inverse of the average length
159 of the shortest paths to/from all the other vertices in the network (Csardi,

160 2013), and the third metric chosen was the clustering coefficient, a measure of
161 the degree to which nodes in a network tend to cluster together (Newman,
162 2003). The fourth metric that we used, average path length (Strogatz, 2001), is
163 the average number of steps along the shortest path for all possible pairs of
164 nodes. We also calculated the average degree distribution and finally the
165 assortativity coefficient to establish whether assortative mixing, connections
166 between nodes that are similar, was taking place (Molina and Stone, 2012).
167 Each of these metrics were calculated for each network and for each dataset.

168 *2.5. Modelling Disease Spread*

169 All the models, using recorded or any of the four random network types, were
170 implemented as stochastic due to the small numbers of animals in each of the
171 datasets, and hence the increased influence of individual stochastic events on
172 the overall disease transmission process (Brauer et al., 2000). Infection was
173 always introduced by randomly infecting a single animal at the start of each
174 model simulation, thus this animal began the simulation in the latent state.
175 The periods of time each animal spends in the latent and infectious states were
176 sampled from exponential distributions with means $1/\sigma$ and $1/\gamma$. For simplicity,
177 and because the largest dataset only contained 30 days of continuously recorded
178 interactions, each infected animal had its length of resistance set to greater than
179 30 days. Both models were simulated many times and it was found that the
180 probability densities of the number of animals in each disease state at each time
181 point, appeared to stabilise by 5000 simulations. All results presented were
182 produced from 5000 simulations, where each simulation was run for the number

183 of days contained in the respective dataset with an initially infected animal
184 randomly chosen for each simulation.

185

186 The value of β , the mean contact rate, used in the simulations was dependent
187 on the dataset used, as each of the four datasets had a different average contact
188 rate. Thus we had four values for β corresponding to our four datasets.

189

190 The disease spread through each model was a hypothetical disease with
191 parameter values that allowed the peak of infection of an epidemic to occur
192 within the 28 days of data available from the shortest dataset. Latent and
193 infectious periods of six days were chosen. Using average values of $\beta = 7.987$
194 from our data and $R_0 = 5$ (considered reasonable), a rounded value of $\alpha = 0.1$
195 was calculated from

$$R_0 = \frac{\alpha\beta}{\gamma}. \quad (2)$$

196 As each dataset has a different value of β , the contact rate, they will also have a
197 different value of R_0 but the characteristics specific to the disease ($\alpha = 0.1$,
198 $1/\sigma = 6$ days and $1/\gamma = 6$ days) remain fixed across all datasets for the recorded
199 network. For all random networks only the value of α was altered. It was
200 assumed that when an animal became infected its behaviour did not change
201 such that its contacts continued as normal. This is not necessarily the case
202 (Rush et al., 2008; Wilesmith, 1998) but until there exists actual contact data
203 for a herd with spreading disease, it is parsimonious to use the actual data that
204 we do have.

205 *2.6. Measuring the Differences in Disease Spread*

206 The results of our previous paper (Duncan et al., 2012) were divided into two
207 parts: the proportion of 5000 simulations that produced no infection and
208 percentiles of the number of infected animals predicted by those simulations
209 that did produce infection. For all values of the disease parameters, the
210 recorded network model had a higher proportion of simulations showing no
211 infection and of those simulations that did show infection, fewer animals were
212 modelled as infected. In an attempt to minimise the differences between the
213 recorded and random network models the value of α was altered in each type of
214 random network model. The value of α was chosen because the value of β was
215 defined by the datasets and needed to be constant to maintain the continuity in
216 number of contacts between the networks and γ has a basis in other diseases
217 and was dependent on the amount of data available to us, a maximum of 30
218 days. Additionally the large uncertainty in the estimates of the probability of
219 infection for real diseases makes α an attractive candidate for adjustment in
220 random network models.

221

222 The standard value of $\alpha = 0.1$ from our previous paper (Duncan et al., 2012)
223 was used again for the recorded network model and a numerical study
224 conducted on the value of α for the various random network models. For each of
225 the 40 equally spaced values of α in the range $0.025 \leq \alpha \leq 0.4$, all random
226 network models were run with 5000 simulations. The mean absolute difference
227 in both the number of infected animals $\text{M.A.D.}_{\text{No. Inf.}}$ and in the proportion of the
228 5000 simulations showing no infection $\text{M.A.D.}_{\text{Probn. Zero Sims.}}$ were calculated as shown in

229 equations (3) and (4). In these equations P_{rec} and P_{rand} represent the proportion
 230 of the 5000 simulations that produced no infection for the recorded and random
 231 network models respectively with \bar{I}_{rec} and \bar{I}_{rand} the mean number of infected
 232 animals for each model from those simulations that did produce infection. The
 233 *rand* refers to any of the four types of random network: constant-on-animal,
 234 constant-on-day, matched-on-day and matched-on-animal. Each individual
 235 time period is represented by t and T is the total number of time periods.

$$\text{M.A.D.}_{\text{No. Inf.}} = \frac{\sum_t |\bar{I}_{rec} - \bar{I}_{rand}|}{T}. \quad (3)$$

$$\text{M.A.D.}_{\text{Propn. Zero Sims.}} = \frac{\sum_t |P_{rec} - P_{rand}|}{T}, \quad (4)$$

236 This examination of α gave an initial estimate of where the minima occurred for
 237 each type of random network and dataset. To improve these estimates an
 238 interval of length 0.05, including this first estimate, was examined in increments
 239 of length 0.00125 for each type of network and each dataset. To get a single
 240 value for the minima, splines were fitted to these data points for the mean
 241 absolute difference in both number of infected animals and proportion of
 242 simulations showing no infection, using the `smooth.spline` function of CRAN R
 243 (CRAN-R, 2013) with a smoothing parameter of 0.7 which gave the closest
 244 agreement with the visual minimum of the data points. This left two values of α
 245 for each random network and dataset: one value minimising $\text{M.A.D.}_{\text{No. Inf.}}$ and a
 246 second minimising $\text{M.A.D.}_{\text{Propn. Zero Sims.}}$. The arithmetic mean of these two values was
 247 calculated to leave one value α_m to minimise the differences between the
 248 recorded and random network models for each of the four random networks and

249 the four datasets. We conducted similar examinations to find α_m for the
250 matched-on-day network model when we set $\alpha = 0.05$ and $\alpha = 0.2$ in the
251 recorded network model. This sensitivity analysis was carried out to establish
252 whether the value of α used in the recorded network model had any effect on
253 the adjustment to find α_m .

254 **3. Results**

255 *3.1. Network Metrics*

256 The 5000 simulations of the random contact networks, outlined above, were
257 stored to calculate average values for the six metrics. For each dataset the
258 contact networks were split into 12 hour periods and the metrics calculated on
259 each of the 5000 simulations. The results were averaged across the simulations
260 and then over the 12 hour periods. These were then compared to the equivalent
261 metrics calculated for the recorded network which was split into 12 hour periods
262 after the disease simulations.

263

264 Figure 1 shows the results of the metrics in six separate plots. Each plot shows
265 results for all networks split by the four datasets. There is no clear result from
266 the metrics as to which of the random networks provides the closest
267 approximation to our recorded network. The recorded network had more
268 repeated edges and lower closeness than any of the random networks and this
269 was consistent across all the datasets. In all but one dataset the recorded
270 network also had higher average path length than the random networks. The
271 more information from the recorded network used to construct the random

272 network – the greater the number of repeated edges in the random networks
273 and hence closer to that of the recorded network.

274

275 Each network shows disassortativity across all datasets. For three of the
276 datasets the recorded network was more disassortative than all four random
277 networks and, as with the repeated edges, the more information from the
278 recorded network used by the random network, in general, the more
279 disassortative they became. Generally speaking in, three metrics (average path
280 length, average closeness and average repeated edges) increasing similarity with
281 the recorded network was associated with the random model utilising increased
282 information from the recorded network.

283 *3.2. Disease Spread*

284 A sample of the results for the mean absolute differences in both the number of
285 infected animals and the proportion of 5000 simulations showing no infection
286 $\left(\begin{matrix} \text{M.A.D.} & \text{M.A.D.} \\ \text{No. Inf.} & \text{Propn. Zero Sims.} \end{matrix} \right)$ can be seen in figure 2. These are the results for
287 the matched-on-day network for all four datasets. The results for the other
288 random networks can be seen in the supplementary information. The results for
289 $\begin{matrix} \text{M.A.D.} \\ \text{No. Inf.} \end{matrix}$ are shown in the solid lines using the left hand axes with the results of
290 $\begin{matrix} \text{M.A.D.} \\ \text{Propn. Zero Sims.} \end{matrix}$ plotted as dashed lines using the right hand axes.

291

292 For each of the datasets and across all the random networks the results were
293 very similar with four points to note. First there is a single minimum value of
294 α_m and the differences in $\begin{matrix} \text{M.A.D.} \\ \text{No. Inf.} \end{matrix}$ and $\begin{matrix} \text{M.A.D.} \\ \text{Propn. Zero Sims.} \end{matrix}$ at this value of α_m are very

295 small. Secondly the value of α_m is always less than the value of $\alpha = 0.1$ used in
 296 the recorded network. It is also consistent, across all networks and datasets,
 297 that the value of α that results in minimising the differences in the proportion
 298 of the 5000 simulations showing no infection is larger than the respective value
 299 of α for the difference in the number of infected animals. Finally, there are clear
 300 but not very large differences in the value of α_m for each type of network across
 301 the four datasets.

302

303 The results from the proportion of simulations with no infected animals and the
 304 values of the 25th, 50th and 75th percentiles of the number of infected animals
 305 from those simulations showing infection are plotted for both the recorded
 306 network model ($\alpha = 0.1$; black, solid lines) and the matched-on-day network
 307 model ($\alpha_m = 0.0696$; red, dashed lines) are plotted in figure 3 for dataset 1A.
 308 Similar plots for the other random networks are shown in the supplementary
 309 information. In all cases it is clear that by adjusting α the results of simulated
 310 disease spread through the random networks are extremely close to the results
 311 from the recorded network. Using the single value of α_m provides very close
 312 agreement and it is not necessary to use both the value of α that resulted in

313 $\frac{\text{M.A.D.}}{\text{No. Inf.}}$, and the one that gives $\frac{\text{M.A.D.}}{\text{Propn. Zero Sims.}}$.

314

315 To compare the differences between the results for each of the four types of
 316 random networks the minimum values of $\frac{\text{M.A.D.}}{\text{No. Inf.}}$ and $\frac{\text{M.A.D.}}{\text{Propn. Zero Sims.}}$ are shown
 317 in figure 4. These were plotted for each dataset along with the relative
 318 percentage decrease in α needed to achieve α_m . Figure 4 also shows the

319 differences α_m for each type of network across the four datasets. It is clear from
320 the plot that the mean differences in number of infected animals are much less
321 than a single animal for each of the networks. The value is dependent on the
322 network being used in the simulation as can be seen by the consistent order of
323 results (constant-on-day, constant-on-animal, matched-on-day and
324 matched-on-animal). It is worth noting that the network using the least
325 information from the recorded network, constant-on-animal, is not the poorest
326 performing. The relative percentage decrease needed to achieve α_m is
327 somewhere between 5.6% and 39.4% but this varies depending on the dataset
328 and the random network used.

329

330 It is clear from the left-hand plot in figure 4 that the values of $\frac{\text{M.A.D.}}{\text{No. Inf.}}$ are
331 dependent on the simplicity of the model. The model using the most
332 information, the matched-on-animal network, is closest to the recorded
333 network. However the simplest network (constant-on-animal) was numerically
334 closer to the recorded network than the second simplest network
335 (constant-on-day). This was also the case for $\frac{\text{M.A.D.}}{\text{Propn. Zero Sims.}}$ for all but dataset
336 1B. The loss of representativeness that arises from choosing the simplest
337 random network is not large.

338

339 The right-hand plot of figure 4 shows the relative percentage decrease of α
340 needed to achieve α_m for each the random networks and for each dataset. The
341 patterns in the adjustment are not completely consistent either with regard to
342 the datasets or networks. There appears by eye to be a dataset effect in the

343 right-hand plot of figure 4. General linear regression, included in the
344 supplementary information, suggests there is evidence of both a dataset effect
345 and random network effect. Each factor was fairly strongly significant after the
346 addition of the other factor, $p = 0.0007$ and $p = 0.042$ for dataset and network
347 respectively. The mean reduction in α was 26.8% and the median reduction was
348 30.0%.

349

350 The exact values of α_m are shown in table 2. For three of the datasets the
351 highest value of α_m occurred in the matched-on-animal network, the network
352 using the most information from the recorded network. Nevertheless for dataset
353 2A, the matched-on-animal had the second highest value of α_m . For the first
354 recording period (datasets 1A and 1B) the value of α_m increases as the networks
355 use more information from the recorded network and this trend is less clear for
356 the second recording period.

357

358 Also included in the supplementary information are plots of the differences in
359 the proportion of 5000 simulations that produced no infection and the median
360 number of infected animals from those simulations that did produce infection.

361 4. Discussion

362 It is clear from the simulations of disease spread that a simple homogeneous
363 mixing model can approximate, very closely, a recorded network if the
364 probability of infection, α , is optimally adjusted. Each of our four types of
365 random network can approximate the recorded network and can do so for each

366 of the four datasets. The adjustment was consistently a reduction in α . The size
367 of the adjustment was dependent on the dataset and random network used for
368 the simulations. The relative percentage reduction in α ranged from 5.6% to
369 39.4%. The results of the sensitivity analysis shown in the supplementary
370 information would suggest that the value of α_m as a proportion of α is
371 negatively associated with the value of α used in the recorded network, at least
372 for the values of α that we tested.

373

374 It has previously been shown that higher clustering tends to produce shorter
375 path lengths within theoretical networks (Shirley and Rushton, 2005a), that
376 clustering and assortativity can reduce epidemic size (Miller, 2009) and that
377 increased clustering or increased assortativity can increase the likelihood of
378 simulated disease spread occurring (Badham and Stocker, 2010a). There is
379 however disagreement over whether clustering influences epidemics on
380 undirected networks with regular (many repeated contacts) or random
381 construction (Eames, 2008; Moslonka-Lefebvre et al., 2009).

382

383 Theoretical networks constructed with many repeated contacts show slower
384 disease spread than random networks (Eames, 2008). This is also shown by
385 both our earlier work (Duncan et al., 2012) and further demonstrated by
386 random networks constructed here. In general, our random networks with lower
387 repeated contacts, i.e. the simpler networks (contact-on-animal and
388 contact-on-day) required smaller values of α_m suggesting that disease spreads
389 quicker through them.

390

391 As all the random networks are derived from the recorded network and the
392 average degree distributions are either extremely close to one another or
393 identical, we can gain little insight from degree distribution. However, degree
394 distribution alone has been shown to not provide enough information for
395 prediction of disease spread (Ames et al., 2011; Boily et al., 2007).

396

397 We found no clear relationship between the values of the metrics and the values
398 of α_m and formal inferential statistics are not possible given the sample size.
399 Any inferential statistical relationship will, however, depend on a large number
400 of herds being assessed in the same manner.

401

402 One of the largest differences between the recorded network and the random
403 networks is the number of repeated edges. One possible reason for the high
404 number of repeated edges in the recorded network was that the herds were
405 constructed of cows with calves at foot. Of the repeated edges recorded, 15% to
406 30%, depending on dataset, were between a cow and her calf. These repeated
407 edges could also be a reason for the increased disassortativity found in the
408 recorded network. Assortative mixing would normally entail cows contacting
409 cows and calves contacting calves. With young calves present in the herd, the
410 disassortative mixing, resulting from cow contacting calf, would seem probable.
411 Assortativity has been shown to decrease epidemic size (Miller, 2009) and we
412 have found that $\alpha_m < 0.1$ for all networks and datasets, showing that the
413 recorded network produces slower disease spread than the random networks.

414 The age of the calves may also explain why in the first recording period
415 (datasets 1A and 1B) the value of α_m increases as the random networks
416 approach the recorded network. In the second recording period, where the
417 calves were a little older, there is not such a clear pattern.

418

419 It has recently been shown that indirect, environmental or faecal, contact may
420 aid the spread of disease in herds of cattle (Kleinlützum et al., 2013). These
421 factors cannot be taken into account with the data available to us. Likewise we
422 only have proximity data with which to construct our contact networks. We do
423 not know the extent of the contacts and how likely each one is to spread disease.
424 However, the only way to gather such data would be to film the animals at all
425 times and to monitor real life spread of infection. Even those studies which
426 attempt to take such things into account by observing animals and categorising
427 the contacts by strength (Norton et al., 2012) are still summarising the contact
428 networks as they extrapolate their networks from the observed data.

429 **5. Conclusion**

430 We have shown that it is possible to closely model disease spread through a
431 network of recorded contacts with a network of randomly allocated contacts by
432 adjusting the probability of infection. The adjustment in probability of infection
433 is consistently a reduction and there appears to be a dataset effect in the value
434 of the reduction. The exact values in adjustment varies between 5.6% and
435 39.4% and as yet, with only four datasets, we have no clear relationship between
436 the network properties and the adjustment in the probability of infection.

437 Recommended reductions in α should not be made until further intra-herd
438 contact data becomes available. Importantly, the simplest network, requiring
439 least information to construct, performed reasonably well by giving a close
440 match to disease spread in the recorded network. This is important because it
441 suggests that in the absence of real contact data a good approximation to
442 disease spread could be made if the correct adjustment in the probability were
443 known.

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Table 1: Descriptions of how the four random networks relate to the recorded network and how much information from the recorded network was necessary to create them.

Information needed to construct random network	Random Network	Mathematical Comparison
Total number of contacts, number of animals, total number of time periods	constant-on-animal	$\sum_j x_{i,j,t} = k \quad \forall i, t$
Total number of contacts, number of animals, total number of time periods	constant-on-day	$\sum_{i,j;i>j} x_{i,j,t} = kN \quad \forall t$
Total number of contacts per time period, number of animals	matched-on-day	$\sum_{i,j;i>j} x_{i,j,t} = \sum_{i,j;i>j} r_{i,j,t} \forall t$
Total number of contacts per animal per time period, number of animals	matched-on-animal	$\sum_j x_{i,j,t} = \sum_j r_{i,j,t} \forall i, t$

where:

$x_{i,j,t}$ = a simulated contact between animals i and j during time period t with $i \neq j$

$r_{i,j,t}$ = a recorded contact between animals i and j during time period t with $i \neq j$

$$k = \text{round} \left(\frac{\sum_{i,j,t;i>j} r_{i,j,t}}{NT} \right)$$

N = Total population size (Number of animals)

T = Total number of timeperiods

Table 2: Values of α_m , the value of the probability of infection α , used to minimise the differences between the recorded and random network models for each of the four types of random networks - for each of the four datasets. A value of $\alpha = 0.1$ was used for the recorded model across all simulations.

Network	α_m per dataset			
	1A	1B	2A	2B
constant-on-animal	0.0645	0.0684	0.0705	0.0944
constant-on-day	0.0649	0.0770	0.0606	0.0757
matched-on-day	0.0695	0.0830	0.0664	0.0844
matched-on-animal	0.0799	0.0915	0.0765	0.0886

Values of six metrics calculated for all networks – random and recorded

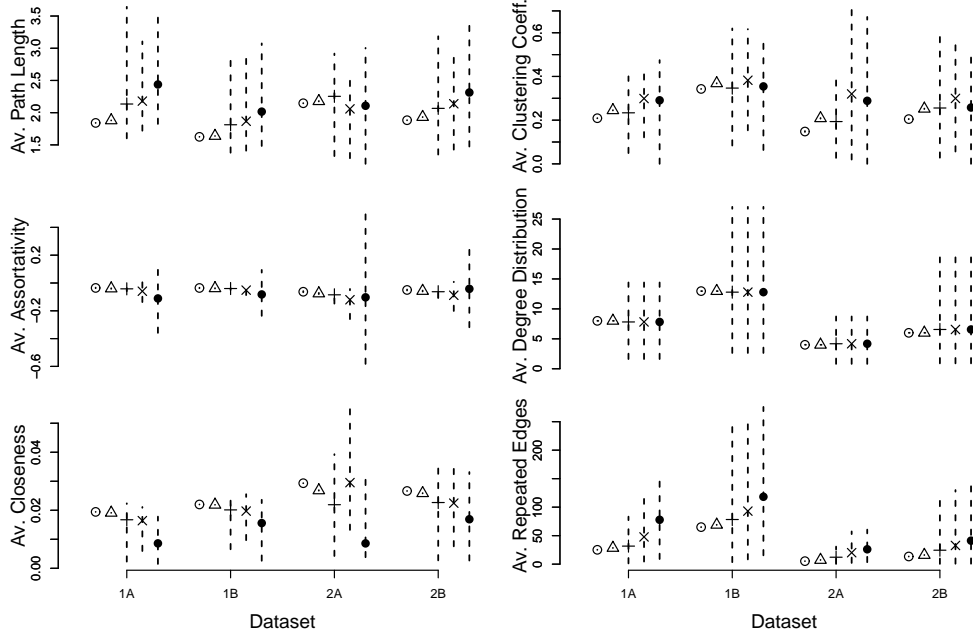


Figure 1: The average values of all six metrics calculated for each of the five networks. The symbols \circ , \triangle , $+$, \times and \bullet denoting results from the constant-on-animal, constant-on-day, matched-on-day, matched-on-animal and recorded networks respectively. The vertical dashed lines represent the 95% percentiles for each metric.

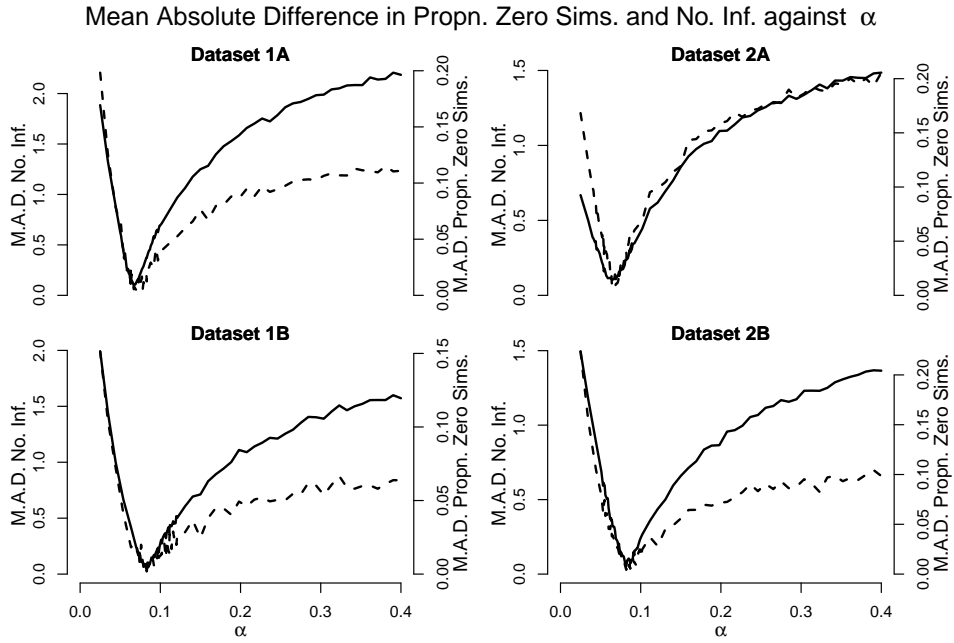


Figure 2: Plots of the mean absolute difference in the number of infected animals $\left(\begin{matrix} \text{M.A.D.} \\ \text{No. Inf.} \end{matrix} \right)$ (left-hand axis, solid line) and mean absolute difference in the proportion of the 5000 simulations showing no infection $\left(\begin{matrix} \text{M.A.D.} \\ \text{Propn. Zero Sims.} \end{matrix} \right)$ (right-hand axis, dashed line) against α for all four datasets. $\alpha = 0.1$ was used in the recorded network model.

Plots of Proportion Zero Simulations and Percentiles of Infected Animals from Dataset 1A

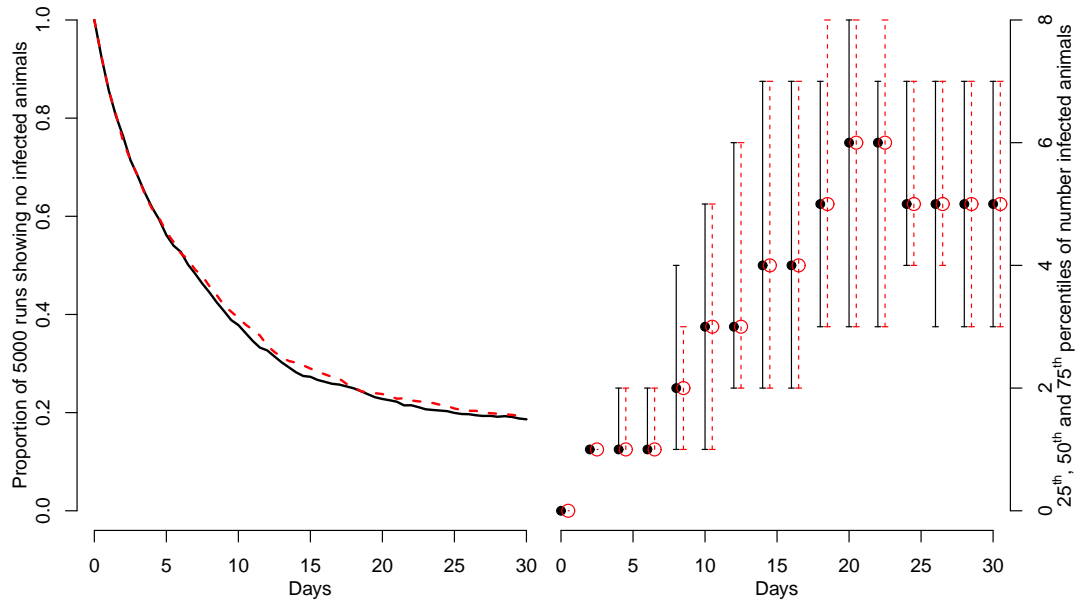


Figure 3: Left-hand plot: Proportion of 5000 simulations that produced no infection for the recorded network model with $\alpha = 0.1$ (black, solid line) and the adjusted random network model with $\alpha = \alpha_m$ (red, dashed line). Right-hand plot: The 25th, 50th and 75th percentiles of the number of infected animals from those simulations that did produce infection for the recorded network model with $\alpha = 0.1$ (black, solid line) and the adjusted random network model with $\alpha = \alpha_m$ (red, dashed line). Dataset 1A was used for both models.

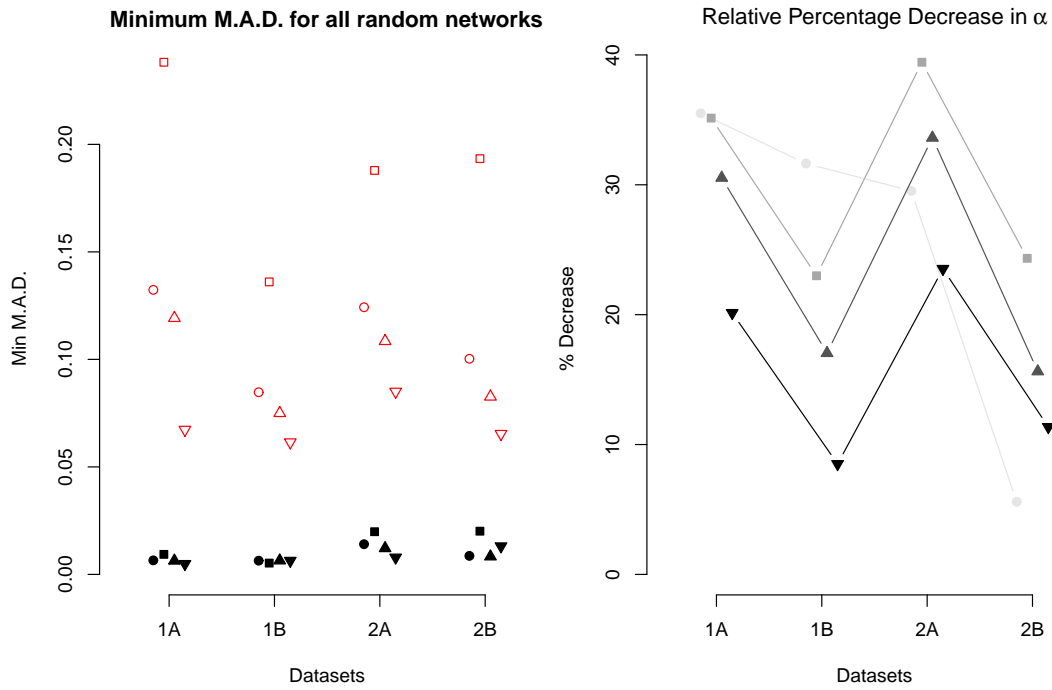


Figure 4: Left-hand plot: The values of the mean absolute difference in the number of infection animals $\left(\begin{matrix} \text{M.A.D.} \\ \text{No. Inf.} \end{matrix} \right)$ (unfilled, red symbols) and the mean absolute difference in the proportion of 5000 simulations showing no infection $\left(\begin{matrix} \text{M.A.D.} \\ \text{Probn. Zero Sims.} \end{matrix} \right)$ (filled, black symbols) for α_m plotted for each of the four random networks. Right-hand plot: The relative percentage decrease in α to achieve α_m from the value of $\alpha = 0.1$ used in the recorded network. The shading denotes the amount of information from the recorded needed to construct the random network, lightest representing the least information and the darkest representing the most information. In both plots the symbols \circ , \square , \triangle and ∇ represent the constant-on-animal, constant-on-day, matched-on-day and matched-on-animal networks.