

1 **Title:** Animal movement in pastoralist populations and implications for pathogen spread and
2 control

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12 **Abstract**

13 Infectious diseases are one of the most important constraints to livestock agriculture, and
14 hence food, nutritional and economic security in developing countries. In any livestock system,
15 the movement of animals is key to production and sustainability. This is especially true in
16 pastoralist systems where animal movement occurs for a myriad of social, ecological, economic
17 and management reasons. Understanding the dynamics of livestock movement within an
18 ecosystem is important for disease surveillance and control, yet there is limited data available on
19 the dynamics of animal movement in such populations. The aim of this study was to investigate
20 animal transfer networks in a pastoralist community in Kenya, and assess network-based strategies
21 for disease control. We used network analysis to characterize five types of animal transfer
22 networks and evaluated implications of these networks for disease control through quantifying
23 topological changes in the network because of targeted or random removal of nodes. To construct

24 these networks, data were collected using a standardized questionnaire (N=164 households) from
25 communities living within the Maasai Mara Ecosystem in southwestern Kenya. The median
26 livestock movement distance for agistment (dry season grazing) was 39.49 kilometers (22.03-
27 63.49 km), while that for gift, bride price, buying and selling were 13.97 km (0-40.30 km), 30.75
28 km (10.02-66.03 km), 31.14 km (17.56-59.08 km), and 33.21 km (17.78-58.49 km), respectively.
29 Our analyses show that the Maasai Mara National Reserve, a protected area, was critical for
30 maintaining connectivity in the agistment network. In addition, villages closer to the Maasai Mara
31 National Reserve were regularly used for dry season grazing. In terms of disease control, targeted
32 removal of highly connected village nodes was more effective at fragmenting each network than
33 random removal of nodes, indicating that network-based targeting of interventions such as
34 vaccination could potentially disrupt transmission pathways and reduce pathogen circulation in the
35 ecosystem. In conclusion, this work shows that animal movements have the potential to shape
36 patterns of disease transmission and control in this ecosystem. Further, we show that targeted
37 control is a more practical and efficient measure for disease control.

38 **Keywords:** Maasai Mara, Network analysis, Disease control, Animal transfer, Fragmentation
39 index, Pastoralist Mobility

40

41

42 **Introduction**

43 Rangeland ecosystems in Africa, defined as areas of natural or semi-natural vegetation in
44 arid or semi-arid climates, host large numbers of wildlife, livestock, and marginalized pastoralist
45 populations (Homewood, 2004; Le Houerou, 2012). Low rainfall and seasonally heterogeneous
46 resources characterize such areas, which necessitates human and livestock mobility to utilize

47 spatiotemporally distributed resources (Swallow, 1994; Butt, 2010; Goldman and Riosmena, 2013;
48 Turner and Schlecht, 2019). However, animal movements have been shown to impact disease
49 patterns (Fevre et al., 2006; Altizer et al., 2011), especially among pastoral communities (Rajeev
50 et al., 2017; Sintayehu et al., 2017; VanderWaal et al., 2017), where losses emanating from
51 livestock diseases affect livelihoods, and their control has the potential to enhance household
52 productivity and health outcomes (Marsh et al., 2016). Rangeland systems are especially at high
53 risk for pathogen introduction and spread because grazing livestock interact with both wildlife and
54 other livestock directly and indirectly through shared forage and water resources (Rajeev et al.,
55 2017). Thus, control of infectious diseases in livestock systems requires an understanding of
56 interaction not only between herds but also in different locations (Bastos et al., 2000; Fevre et al.,
57 2006; zu Dohna et al., 2014; Machado et al., 2019; Omondi et al., 2019).

58 Patterns of contact between livestock herds influences the spread of infectious pathogens
59 (Fevre et al., 2006) and thus can be used to characterize epidemiological dynamics (Kao et al.,
60 2006; VanderWaal et al., 2016; VanderWaal et al., 2017) and develop targeted surveillance and
61 control strategies (Bajardi et al., 2012; Frossling et al., 2014; Ribeiro-Lima et al., 2015). Herds
62 with high rates of between-herd contacts have a higher risk of acquiring infections (VanderWaal
63 et al., 2017). In addition, infections often propagate from a small number of actors (Woolhouse et
64 al., 1997; Volkova et al., 2010), with so-called “super-spreaders” disproportionately contributing
65 to transmission events (Lloyd-Smith et al., 2005). Thus, characterizing the underlying architecture
66 of contact patterns within a population can help elucidate important drivers and pathways for
67 disease transmission as well as critical points for surveillance and control (Bajardi et al., 2012;
68 VanderWaal et al., 2016).

69 Pastoralists have adopted a strategy of complex livestock movement to maximize the
70 utilization of seasonally available resources, leading to complex heterogeneous contact patterns
71 and variability in disease outcomes (Dejene et al., 2016; Rajeev et al., 2017; Sintayehu et al., 2017;
72 Turner and Schlecht, 2019). In such communities, livestock movement data is seldom available,
73 and thus contact is difficult to characterize. Several studies have attempted to model livestock
74 movement by analyzing sales records (Chaters et al., 2019), animal transaction records combined
75 with questionnaire surveys (Motta et al., 2017), census of migrating pastoralists (Pomeroy et al.,
76 2019), Global Positioning System data loggers (VanderWaal et al., 2017), and ego-based
77 approaches (Bronsvort et al., 2004). However, none of the methods above captures the diversity
78 of social drivers behind movements within pastoral cultural systems. For instance, in addition to
79 buying and selling, Maasai pastoralists move animals, with or without the transfer of ownership,
80 for instance for bride price payments, lending of animals between friends and families, gifts, and
81 for seasonal access to pasture and water (Perlov, 1987 in (Aktipis et al., 2016). In pastoralist
82 populations, moving or sharing animals is both a survival strategy, a relationship building exercise,
83 and often a method of risk pooling (Aktipis et al., 2011; Aktipis et al., 2016). Pastoralists
84 communities are known to use gifts of livestock as a means to build and enhance relationships (de
85 Vries et al., 2006). The role that such livestock movements play in disease dissemination is seldom
86 evaluated, but may be key to maximizing productivity of this management system (Sintayehu et
87 al., 2017).

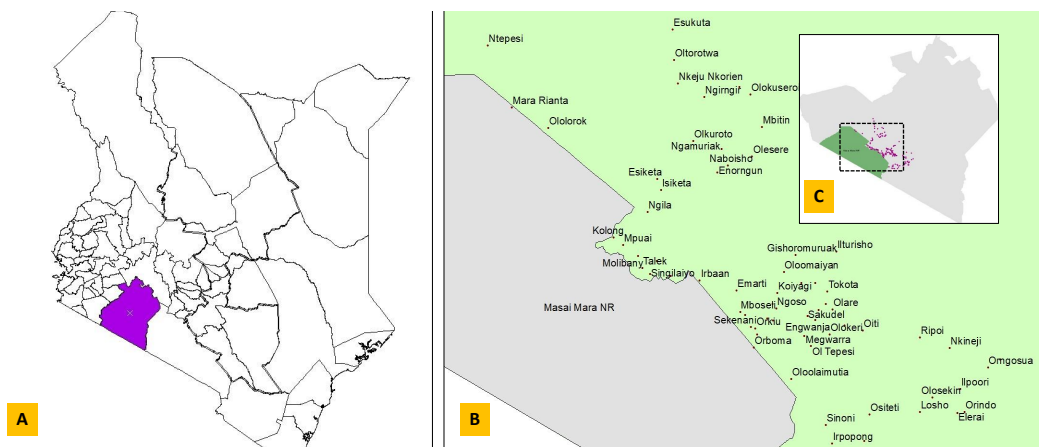
88 Designing control strategies is complex, and traditional epidemiological approaches often
89 fail to capture the dynamic, non-linear, and interconnected nature of pastoral systems (Benham-
90 Hutchins and Clancy, 2010). To further our understanding of cattle-associated movement
91 dynamics, graph theory can be used to quantify within- and- between village movements such that

92 household actions, for instance buying/selling, connect different villages. Such between-village
93 connections are expected to be important when developing disease surveillance and intervention
94 strategies (Watts, 1987; Woolhouse et al., 1997; Sintayehu et al., 2017; Ahmed et al., 2018; Russell
95 et al., 2018). In graph theory, networks are used to characterize interacting systems in which nodes
96 (here defined as households or villages) are inter-connected through edges (here defined as
97 movements (Craft and Caillaud, 2011; Danon et al., 2011; Silk et al., 2017; Sintayehu et al., 2017;
98 Balasubramaniam et al., 2018; Ogola et al., 2018). In our study, a network edge is a potential route
99 for transmission of pathogens between households through the movement of animals. Using
100 network analysis, we can calculate centrality metrics to evaluate the importance of a node in
101 connecting the network, investigate the propagation of a hypothetical disease, and assess the
102 potential for targeted surveillance or control if a node is removed - a measure equivalent to
103 vaccination or depopulation (Martinez-Lopez et al., 2009; Kinsley et al., 2019; Yang et al., 2019).
104 In this study, our objective was to use network analysis to characterize different types of animal
105 movement, and evaluate their potential role in disease transmission and control in a pastoralist
106 community in Kenya. We hypothesized that villages proximal to Maasai Mara National Reserve
107 will play an important role in the connectivity of the ecosystem, as measured by their centrality
108 metrics, and that targeted control measures aimed at villages with the most connections will be
109 more efficient at fragmenting the connectivity of the network than a non-targeted approach. This
110 study advances our understanding of the movement dynamics of livestock within a pastoralist
111 community characterized by variable animal transfer pathways and their role in network-based
112 interventions for livestock disease surveillance and control.

113 **Material and Methods**

114 **Study site:** This study examined the dynamics of livestock movement in pastoralist
115 communities living within the Maasai Mara Ecosystem (MME) (Figure 1). MME is located in
116 southwestern Kenya, and encompasses the 1,530 km² MMNR, within which livestock grazing is
117 banned and adjoining pastoral ranches where communal settlements, livestock grazing, and
118 tourism are permitted (Bhola et al., 2012). The livestock movement dynamics of the communities
119 in this ecosystem are driven by the Maasai Mara National Reserve (MMNR) due to the availability
120 of forage within this wildlife conservation area during the dry season (Reid et al., 2003; Butt et al.,
121 2009). Rainfall in this ecosystem is largely bimodal, varying from 500 mm in the southeast to 1300
122 mm in the northwest (Bartzke et al., 2018). These factors combine to create spatiotemporal
123 heterogeneity in water and forage distribution, which influences wild herbivores and domestic
124 stock movement within the ecosystem. This ecosystem is located within the larger Narok County,
125 which is a 17,953 km² area with more than one million cattle, 2.3 million sheep and goats, and a
126 human population that is largely rural (KNBS, 2010).

127



128

129 **Figure 1:** Map of the Maasai Mara Ecosystem. A. Map of Kenya with Narok County in red; B.
130 Unique villages sampled in this study; C. Map of Narok County with households sampled marked
131 in purple, dotted square represents an area equivalent to B.

132

133 ***Data collection***

134 This research is part of a larger study aimed at understanding zoonotic disease occurrence
135 in the Maasai Mara Ecosystem, with all sampling conducted between November 2017 and June
136 2019. We defined households as persons living within an abode for a period of one month prior to
137 the sampling, and herds as groups of cattle, sheep and goats, and any other domestic stock owned
138 by the respondent. We purposively sampled one hundred and sixty four households, targeting those
139 within 20 kilometers of the Maasai Mara National Reserve. Pastoral cattle tend to move longer
140 daily distances than small stock, with an average of 2-9 kilometers being the norm for grazing
141 (Turner and Schlecht, 2019). For longer-term migration, or “travel mobility,” in pastoralist
142 systems, the average distance moved ranges from 47-170 kilometers (Turner and Schlecht, 2019),
143 with the wide variation indicative of an individual household’s cost-benefit valuation of the move.

144 For this study, we defined five animal transfer pathways identified from an initial scoping
145 survey in the ecosystem; agistment (defined as the temporary re-location of animals to access
146 forage and water in other locations during the dry season, usually lasting 2-3 months, while
147 maintaining a household in a single village), gift, bride price, buying, and selling. We interviewed
148 a household respondent using a structured questionnaire, in which the respondent was asked to
149 identify villages (by common name) from which they either sent or received animals through any
150 of the aforementioned pathways over the last five years. The respondents were requested to name
151 villages rather than specific household due to the logistical constraints of collecting locational data
152 on households named by respondents. For each household interviewed and village named,
153 locational data was recorded using a handheld Global Positioning System; a centroid was
154 calculated to represent the location of villages in which multiple household locations were
155 recorded. The University of Minnesota IRB (STUDY00000837), Kenya Wildlife Service

156 (KWS/BRM/5001), and the Narok County government (NCG/HEALTH/GEN/VOL.1/2)
157 authorized this study.

158

159 ***Data analysis***

160 *Network construction:* In graph theory, nodes can be partitioned into k independent sets or groups.
161 A network with $k \geq 3$ is a *multipartite* network, whereas those with one or two independent sets or
162 groups are *unipartite* and *bipartite* networks, respectively (Jacoby and Freeman, 2016). We
163 constructed a household-village bipartite network, where households are linked to villages to
164 which they received or moved animals. In this study, a separate bipartite network was constructed
165 for each type of contact. In a bipartite network $B = \{U, V, E\}$, where U and V are the disjoint set
166 of nodes representing households and villages, respectively, and E is the linkage between nodes,
167 such as $E = \{(u, v): u \in U, v \in V\}$. In this network, nodes in U can only connect to nodes in V , and
168 no connections among nodes of the same type exist (Banerjee et al., 2017). This representation of
169 contact is appropriate for the method by which data were collected for this project (households
170 were asked about movements of animals to different villages). These data can be represented by
171 an unweighted biadjacency matrix $B = \{U, V, E\}$, which is a $(0, 1)$ matrix of size $|U| \times |V|$; $B_{uv} = 1$ if
172 there is an edge between u and v , or $B_{uv} = 0$ when there is none. Thus, households are connected
173 to other households indirectly based on villages to which they had common connections. In this
174 sense, each set of nodes (villages and households) have independent properties that we can
175 estimate to evaluate the roles played by each set. These properties will be evaluated at two levels,
176 first, a household's role within the network, and secondly the villages' role in the network.

177

178 *Network metrics:* At the node-level, we calculated two centrality metrics: degree and betweenness.
179 We also summarized the density and fragmentation index of the network as a whole (Table 1), and
180 visualized network topology. All analysis were conducted using the *igraph* package (Csardi,
181 2013).

182

183

| Node-level Metrics | | Citation |
|-----------------------|---|-----------------------------|
| Degree | Total number of unique nodes that sent or received an animal to/from a particular node. | (Wasserman and Faust, 1994) |
| Betweenness | Number of times a node is located on the shortest path between any two pairs of nodes within the observed network | (Wasserman and Faust, 1994) |
| Network-level Metrics | | |
| Density | Number of observed contacts in the network relative to all possible contacts. | (Wasserman and Faust, 1994) |
| Fragmentation index | Proportion of pairs of nodes that are disconnected (no paths exist connecting them) in the network. | (Chen et al., 2007) |

184 **Table 1:** Definition of network metrics

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186

187 *Implications of node removal:* We used two approaches for node removal, random and targeted.
188 In random removal, we selected any 2, 5, or 10 nodes at random, calculated network-level metrics
189 before and after removal, and repeated this process for 1,000 iterations to generate an expected
190 distribution. For targeted removal, we selected top 2, 5, and 10 nodes based on degree, and
191 recalculated the network-level metrics before and after removal (Albert et al., 2000; Holme et al.,
192 2002; Chen et al., 2007). We quantified the topological impact of removing nodes using the
193 fragmentation index, F , which is the proportion of non-connected pairs of nodes in the network. F
194 = 0 would represent a fully-connected, non-fragmented network in which all pairs of nodes are

195 connected through paths in the network, and $F = 1$ would represent a fully fragmented network
196 where every node is isolated (Borgatti, 2006; Chen et al., 2007).

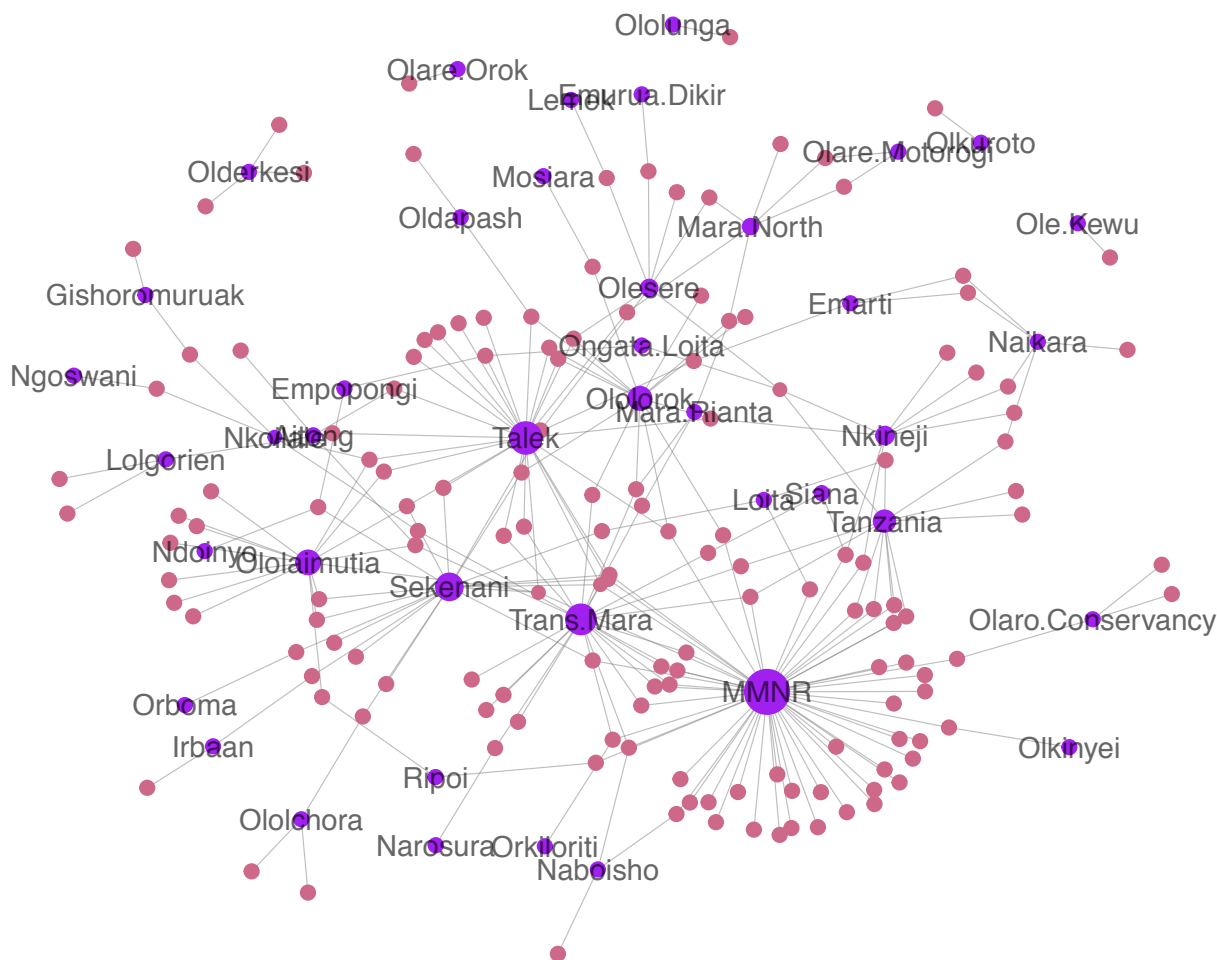
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198 **Results**

199 We sampled 164 households in 67 unique villages (Figure 1 B) across the Maasai Mara Ecosystem,
200 with 30% of the respondents being female (50/164), 70% male (114/164), and the median length
201 of time they had lived in the area being 8 years (4 -100 years). Of the respondents interviewed,
202 99% identified as pastoralists, though 12% also reported formal employment, and 4% were
203 merchants involved in various trades.

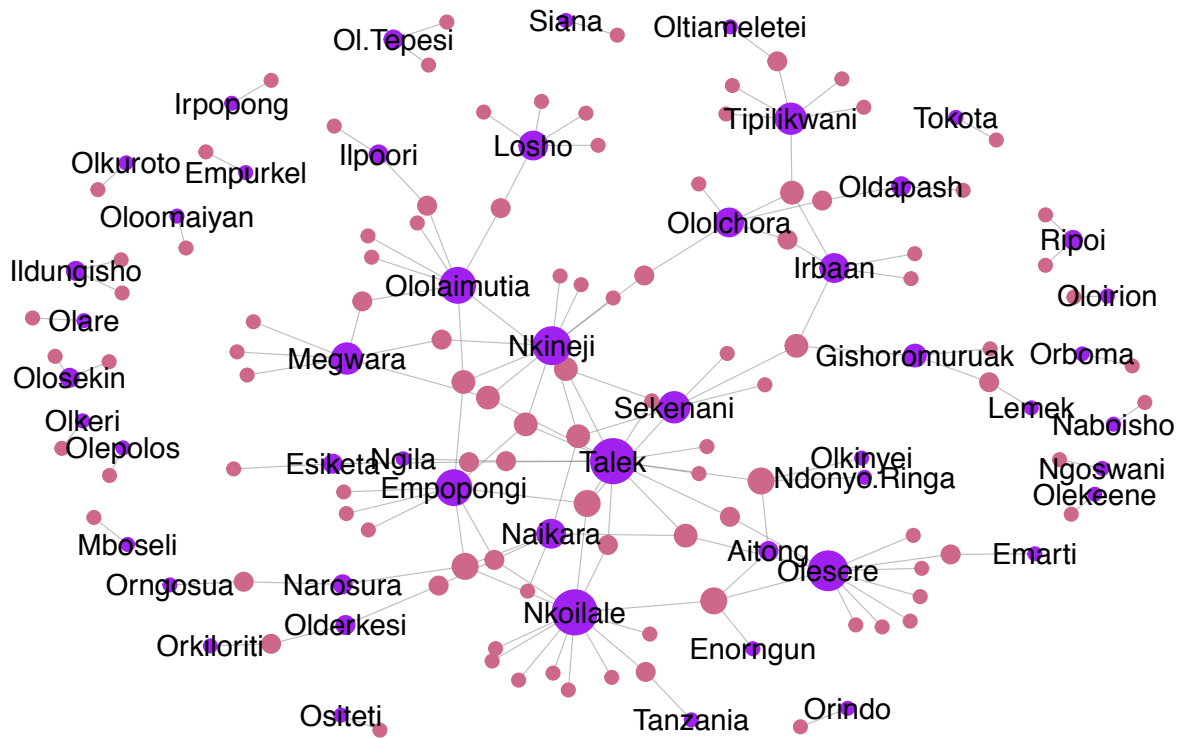
204 *Network metrics and visualization:* Five animal movement ‘reasons’ were examined; agistment,
205 bride price, gift, buying, selling. The median livestock movement distance for agistment was 39.49
206 kilometers (22.03-63.49 km), while that for gift, bride price, buying, and selling were 13.97 km
207 (0-40.30 km), 30.75 km (10.02-66.03 km), 31.14 km (17.56-59.08 km), and 33.21 km (17.78-
208 58.49 km), respectively. For agistment, gift, bride price, buying and selling networks, network
209 densities were 0.0038, 0.0023, 0.0022, 0.0082, and 0.0056, respectively. In addition, we
210 summarized the degree of the villages and the households in our networks separately. The median
211 household degrees in agistment, gift, bride price, buying and selling network node degrees were 2
212 (interquartile range: 1-2), 1 (0-1), 1 (1-2), 2 (1-3), and 2 (1-3), respectively. We report the median
213 degree for households only, as the interpretation of degree for villages is less straight forward
214 because some villages were identified by a respondent but not sampled during questionnaire
215 interviews. With that caveat, seven villages were shown to be important across all networks. These
216 included Sekenani, Talek, Ololaimutia, Nkineji, Olesere, Nkoilale and Naikara (Table 2). Of the

217 villages evaluated, Maasai Mara National Reserve (though technically not a village) had the
218 highest degree and betweenness for agistment (Table 2).



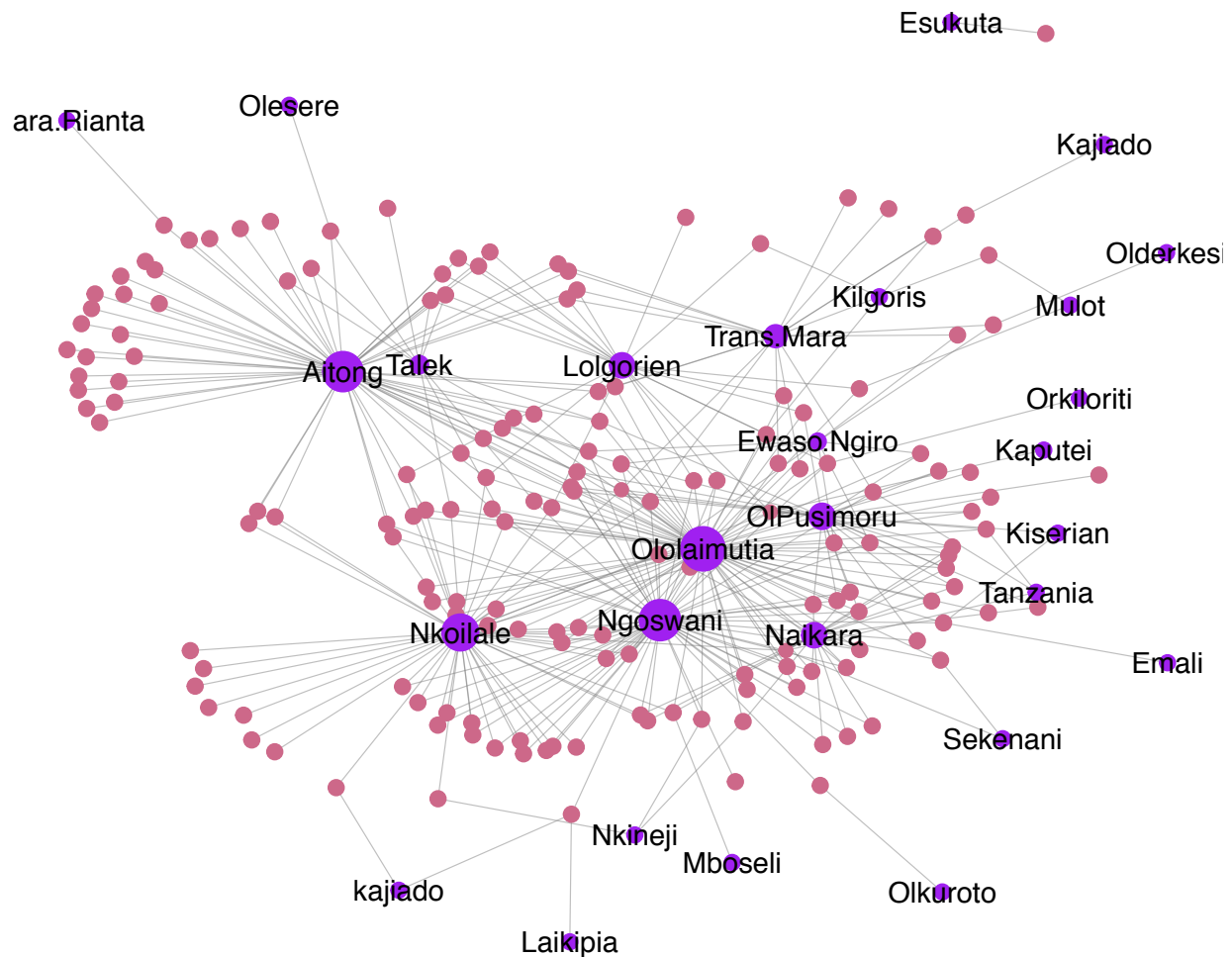
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220 **Figure 2:** Agistment Network: Bipartite network of agistment locations within the Maasai Mara
221 ecosystem, with node sizes scaled by degree. Purple nodes are villages, while pale violet nodes are
222 households.

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224

225 **Figure 3:** Gift Network: Bipartite network of gift locations within the Maasai Mara ecosystem,
226 with node sizes scaled by degree. Purple nodes are villages, while pale violet nodes are
227 households.



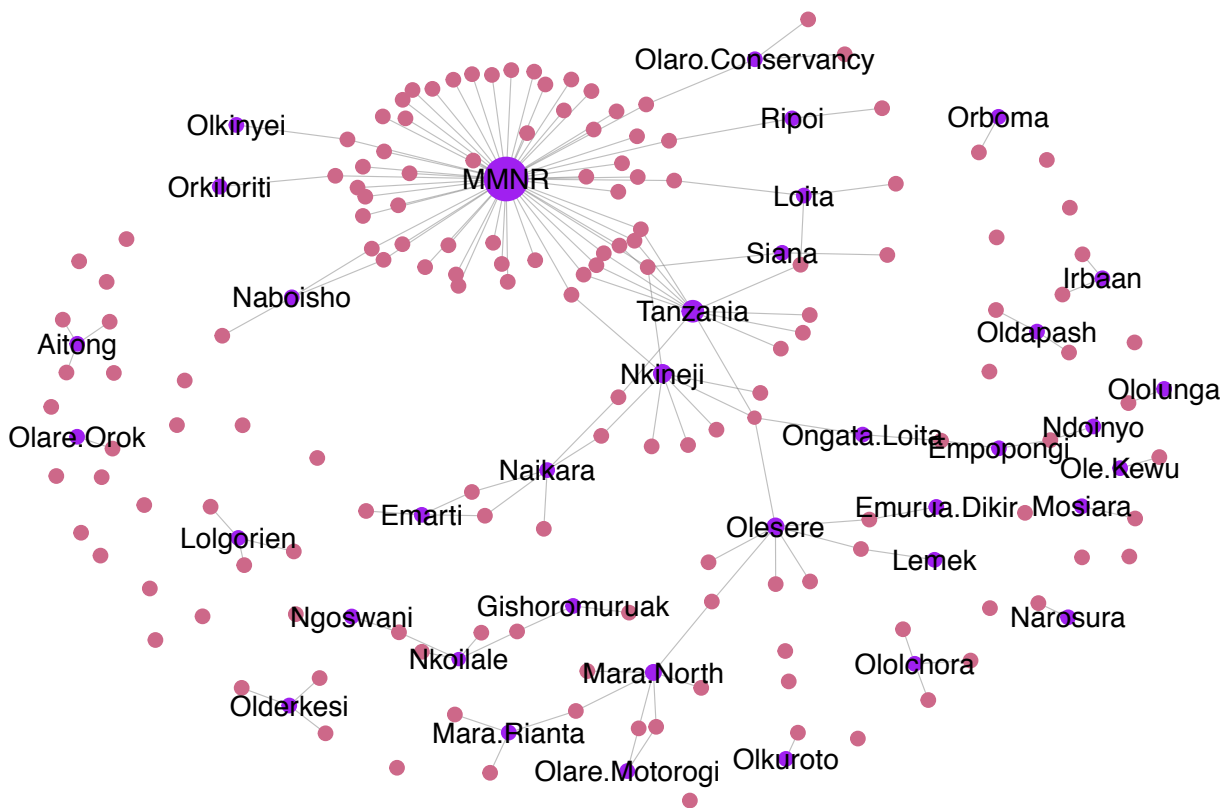
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229 **Figure 4:** Buying Network: Bipartite network of major buying locations within the Maasai Mara
230 ecosystem, with node sizes scaled by degree. Purple nodes are villages, while pale violet nodes are
231 households.

232

233 *Implications of node removal:* We used the fragmentation index to examine changes in network
234 topology following the targeted and random removal of nodes in the five networks. Consistent
235 with our hypothesis, targeted removal outperformed random removal of nodes in terms of
236 increasing network fragmentation. The fragmentation indices of the full networks were 0.51, 0.83,
237 0.93, 0.45 and 0.47 for agistment, gift, bride price, buying and selling, respectively. Across all
238 network types, targeted removal of nodes based on their degree resulted in substantially higher

239 fragmentation than random removal of nodes; the fragmentation indices for the targeted removals
240 always exceeded the upper bounds of the 95% interval that was achieved through random
241 removals. This result was consistent regardless of whether the top 2, 5, or 10 nodes with highest
242 degree were removed (Table 2). The biggest change in fragmentation was realized when five nodes
243 were targeted for removal, with only a modest additional benefit in removing 10 nodes as opposed
244 to five (complete list of figures are included in the supplementary materials).



245

246 **Figure 5:** Bipartite network of agistment locations following targeted removal of top five villages.
247 Purple nodes are villages, while pale violet nodes are households.

| Agistment | | | Gift | | | Bride Price | | | Buying | | | Selling | | |
|--------------------------|-----|-------|--------------------------|-----|-------|-----------------------|-----|-------|--------------------------|-----|-------|--------------------------|-----|-------|
| VILL | DGR | BETWN | VILL | DGR | BETWN | VILL | DGR | BETWN | VILL | DGR | BETWN | VILL | DGR | BETWN |
| MMNR * | 54 | 10348 | Talek ^ψ | 13 | 2006 | Nkoilale ^ψ | 7 | 836 | Ololaimutia ^ψ | 72 | 6311 | Ngoswani | 91 | 7791 |
| Sekenani ^ψ | 19 | 7534 | Sekenani ^ψ | 6 | 1645 | Ololchora | 7 | 677 | Aitong | 59 | 6293 | Aitong | 71 | 7538 |
| Talek ^ψ | 27 | 4646 | Ololaimutia ^ψ | 8 | 1265 | Olesere ^ψ | 6 | 580 | Ngoswani | 62 | 4899 | Ololaimutia ^ψ | 47 | 3139 |
| Trans Mara | 24 | 2718 | Nkoilale ^ψ | 13 | 1225 | Tanzania | 5 | 471 | Nkoilale ^ψ | 49 | 3496 | Ewaso Ngiro | 47 | 2062 |
| Ololaimutia ^ψ | 15 | 1905 | Irbaan | 5 | 1016 | Sekenani ^ψ | 6 | 454 | Trans Mara | 18 | 1673 | Nkoilale ^ψ | 36 | 1627 |
| Ololorok | 14 | 1822 | Nkineji ^ψ | 9 | 993 | Empopongi | 4 | 451 | Lolgorien | 22 | 1138 | Dagoretti | 32 | 994 |
| Nkineji ^ψ | 8 | 1400 | Olesere ^ψ | 10 | 858 | Tipilikwani | 5 | 444 | Ol Pusimoru | 24 | 754 | Naikara ^ψ | 17 | 250 |
| Olesere ^ψ | 7 | 1047 | Empopongi | 8 | 709 | Nkineji ^ψ | 3 | 314 | Naikara ^ψ | 22 | 451 | Lolgorien | 4 | 26 |
| Nkoilale ^ψ | 4 | 914 | Naikara ^ψ | 5 | 689 | Megwara | 4 | 313 | Talek ^ψ | 11 | 370 | Ol Pusimoru | 3 | 8 |
| Mara North | 6 | 707 | Tipilikwani | 6 | 614 | Talek ^ψ | 4 | 224 | Ewaso Ngiro | 9 | 285 | Sekenani ^ψ | 2 | 6 |
| Naikara ^ψ | 5 | 521 | | | | | | | | | | | | |
| Tanzania * | 12 | 483 | | | | | | | | | | | | |

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252 **Table 2:** Network metrics; degree and betweenness of the top 10 villages in the five networks evaluated in this study. * Not a village
 253 within the ecosystem but serves as an important hub in the network – this was only in the agistment network. ^ψ Villages that are common
 254 across all evaluated networks. VILL = Village; DGR = degree; BETWN = betweenness.

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| Fragmentation of the network following targeted versus random node removal | | | | | | | |
|--|--------------|-----------------------|------------------|-----------------------|------------------|------------------------|------------------|
| Reason | Full Network | Removal of 2 villages | | Removal of 5 villages | | Removal of 10 villages | |
| | Targeted | Random | Targeted | Random | Targeted | Random | Targeted |
| Buying | 0.45 | 0.54 | 0.48 (0.45-0.59) | 0.86 | 0.53 (0.47-0.67) | 1.00 | 0.64 (0.51-0.82) |
| Selling | 0.47 | 0.71 | 0.49 (0.47-0.66) | 0.94 | 0.56 (0.49-0.73) | 1.00 | 0.75 (0.52-0.89) |
| Agistment | 0.51 | 0.61 | 0.54 (0.52-0.59) | 0.81 | 0.58 (0.53-0.65) | 0.90 | 0.64 (0.57-0.74) |
| Gift | 0.83 | 0.89 | 0.84 (0.83-0.87) | 0.96 | 0.86 (0.83-0.91) | 0.99 | 0.89 (0.85-0.94) |
| Bride Price | 0.93 | 0.97 | 0.94 (0.93-0.96) | 0.99 | 0.95 (0.94-0.98) | 1.00 | 0.97 (0.95-0.99) |

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Table 3: Network metrics; fragmentation index of the five networks evaluated in this study following the removal of 2, 5 and 10 nodes, with nodes removed either selected randomly or targeted based on degree. For random removals, the median (95% confidence interval) fragmentation is reported, summarized across 1,000 iterations.

268 **Discussion**

269 In this study, our goal was to characterize animal transfer networks in pastoralist communities
270 in Kenya, and evaluate their potential role in disease control and management. As described in Table
271 1, degree, betweenness, density, and fragmentation index are important measures of a network's
272 topology and for assessing potential impact of perturbing this topology for disease control
273 (Wasserman and Faust, 1994; Chen et al., 2007). We showed that animals were moved the longest
274 distances (median = 39.49 km) for agistment (movement of animals to forage and water during the
275 dry season), followed by bride price, buying and selling, which were approximately similar (ranging
276 between 30-33 km). Finally, movement due to gifting was more localized (with the lowest median
277 distance at 13.97 km). Thus this study shows that buying, selling and agistment driven movements
278 potentially play a bigger role than gift and bride price in disease propagation risk (with respect to
279 both higher network densities and longer distance of movement). The protected area, Maasai Mara
280 National Reserve, played an important role in connecting the ecosystem in that it was highly used for
281 dry season grazing, as shown by its highest degree and betweenness. In addition, our results support
282 the hypothesis that villages proximal to Maasai Mara National Reserve (Sekenani, Talek, and
283 Ololaimutia) were more connected in the ecosystem (highest centrality metrics). In all networks,
284 targeted removal of villages served to better fragment the network than randomly removing nodes,
285 highlighting the potential benefits of targeted disease control strategies. Thus, targeted removal, such
286 as vaccination, may provide an efficient approach for disease control in the ecosystem.

287 The fact that villages closer to MMNR were used regularly for dry season grazing is not a
288 surprise given that, although grazing in the reserve is banned, it has been reported previously in the
289 literature (Ogutu et al., 2009). In this study, respondents consistently identified the Maasai Mara
290 National Reserve as a reservoir for forage during the dry season, even in the face of animal
291 confiscation and fines levied by the County government (personal communication). The MMNR has

292 become especially attractive following increased fencing of the ecosystem that has disrupted
293 traditional animal foraging routes and grazing lands (Løvschal et al., 2017). Further, though buying
294 and selling median distances were identical, a closer look at the network topology reveals more
295 context. First, buying commonly includes transactions with villages outside Narok County (the study
296 area). For instance, the respondents indicated that they bought their cattle from Tanzania, Kajiado,
297 Kiserian, Emali, and Laikipia, all of which fall outside the county boundaries. This could be a strategy
298 to acquire different or “better” livestock genetics (Ilatsia et al., 2012). On the contrary, selling of
299 livestock mostly occurred in local markets. These included major markets such as Aitong, Nkoilale,
300 Ololaimutia, Ewaso Ngiro, and Ol Pusimoru. In addition, a few farmers sold livestock in larger, peri-
301 urban markets (e.g. Dagoretti, Ngong and Ongata Rongai) serving the capital city of Nairobi, possibly
302 as a means of getting higher returns (Alarcon et al., 2017).

303 Network-based disease control relies on identifying a population’s contact structure and
304 evaluating the role of the different nodes (e.g. villages, households, or farms) that could influence
305 connectivity thus fragmenting the transmission network (Kiss et al., 2005; Tanaka et al., 2014). To
306 evaluate the efficiency of network-based control strategies, we compared the effect of random versus
307 targeted removal of nodes on the networks’ topological structure using the fragmentation index.
308 Random removal of nodes requires no prior information on the network structure, but has been shown
309 to be an inefficient approach (Albert et al., 2000). In our study, targeted removal of village nodes
310 outperformed random removal, demonstrating the utility of network analysis in identifying highly
311 connected villages that could be used for more strategic disease control or surveillance. Here, node
312 removal mimics vaccination or depopulation, depending on the disease and context of infectious
313 disease control (Keeling and Eames, 2005; Bansal et al., 2010). Ideally, an efficient fragmentation
314 strategy should be one that removes minimal number of nodes as it represents, for instance, the
315 minimum number of villages to be vaccinated to prevent further spread of an infection (Chen et al.,

2007). We demonstrated that the removal of the top five nodes with the highest degree was effective at fragmenting all the networks. The agistment network, however, was more robust to node removal in that the removal of top 5 or 10 villages resulted in fragmentation indices of 81% and 90%, whereas this value was close to 100% for the other networks in this study. This might be due to the fact that, we cannot remove MMNR from the network or that household decisions to move to a particular location is highly influenced by an individual household's cost-benefit analysis of the move independent of other household decisions (Turner and Schlecht, 2019). This is unlike buying and selling, which follow the law of supply and demand, and sometimes are dictated by intermediaries (Alemayehu, 2011; Alarcon et al., 2017; Chaters et al., 2019).

Agistment, buying, and selling networks occur much more frequently with potentially greater implications for pathogen dissemination than gifting and bride price (Macpherson, 1995; Bett et al., 2009). Anecdotally, we may conclude that the fragmentation of the selling network may serve to protect markets outside the Mara Ecosystem, such as Dagoretti, Ngong and Ongata Rongai. On the contrary, the fragmentation of the buying network leaves the markets in the neighboring counties connected to those in the Maasai Mara Ecosystem (Supplementary material) and may need to be considered when designing a comprehensive disease control strategy.

Our study has several limitations. First, data were collected at a single time point, and temporal changes in a network's topology is a common phenomenon, especially in pastoralist production systems (VanderWaal et al., 2017; Pomeroy et al., 2019). Secondly, respondents were asked about movements made during the last five years, which limits the temporal resolution of when movements occurred and introduces potential recall bias. Third, because data were collected in a defined geographical area, the results may not be readily generalizable to other areas. Finally, our network structure did not account for common areas of daily contact, such as congregation during daily herding and at water resources, which may be important for localized disease transmission.

340 Thus, our networks may under-represent connectivity amongst villages, particularly at local scales.
341 However, our networks do represent longer distance movements in the ecosystem, with
342 corresponding implications for longer distance pathogen spread.

343

344 **Conclusions**

345 We have shown that the identification of highly connected villages could be beneficial in designing
346 disease control programs that fragment potential transmission pathways in the livestock population.
347 This fragmentation can be achieved through immunization of a node (node removal). Our findings
348 demonstrate that even at a restricted spatial scale, network centrality measures may provide sufficient
349 information to fragment networks, thus showing their utility not only for disease control but also in
350 developing targeted risk-based surveillance approaches. Our approach of identifying villages rather
351 than households has multiple advantages including cost implications and protection of privacy.
352 However, the use of bipartite networks also allows for the identification of household nodes that may
353 be relevant in the connecting the ecosystem. There is need however, to incorporate disease data from
354 households in the ecosystem and evaluate the network topologies with respect to real-world
355 transmission dynamics. In addition, it may be useful to consider economic costs of the information
356 gathering and integrate risk analysis as a way to enhance the utility and robustness of the realized
357 networks as presented here.

358

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