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

2

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).

3

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 (Bronsvoort 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 km^2 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 km^2 area with more than one million cattle, 2.3 million sheep and goats, and a

126   human population that is largely rural (KNBS, 2010).

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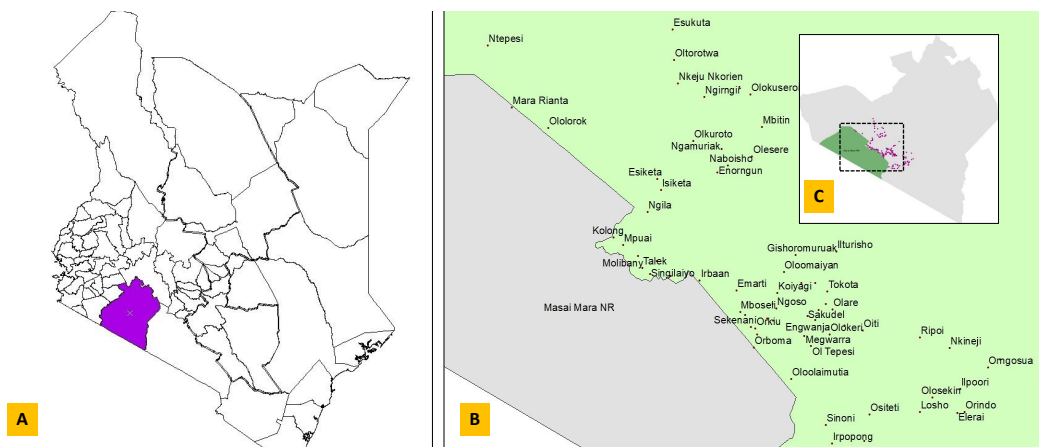
129   **Figure 1:** Map of the Maasai Mara Ecosystem. A. Map of Kenya with Narok County in red; B.
130   Unique villages sampled in this study; C. Map of Narok County with households sampled marked
131   in purple, dotted square represents an area equivalent to B.

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

185

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).

197

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).

219
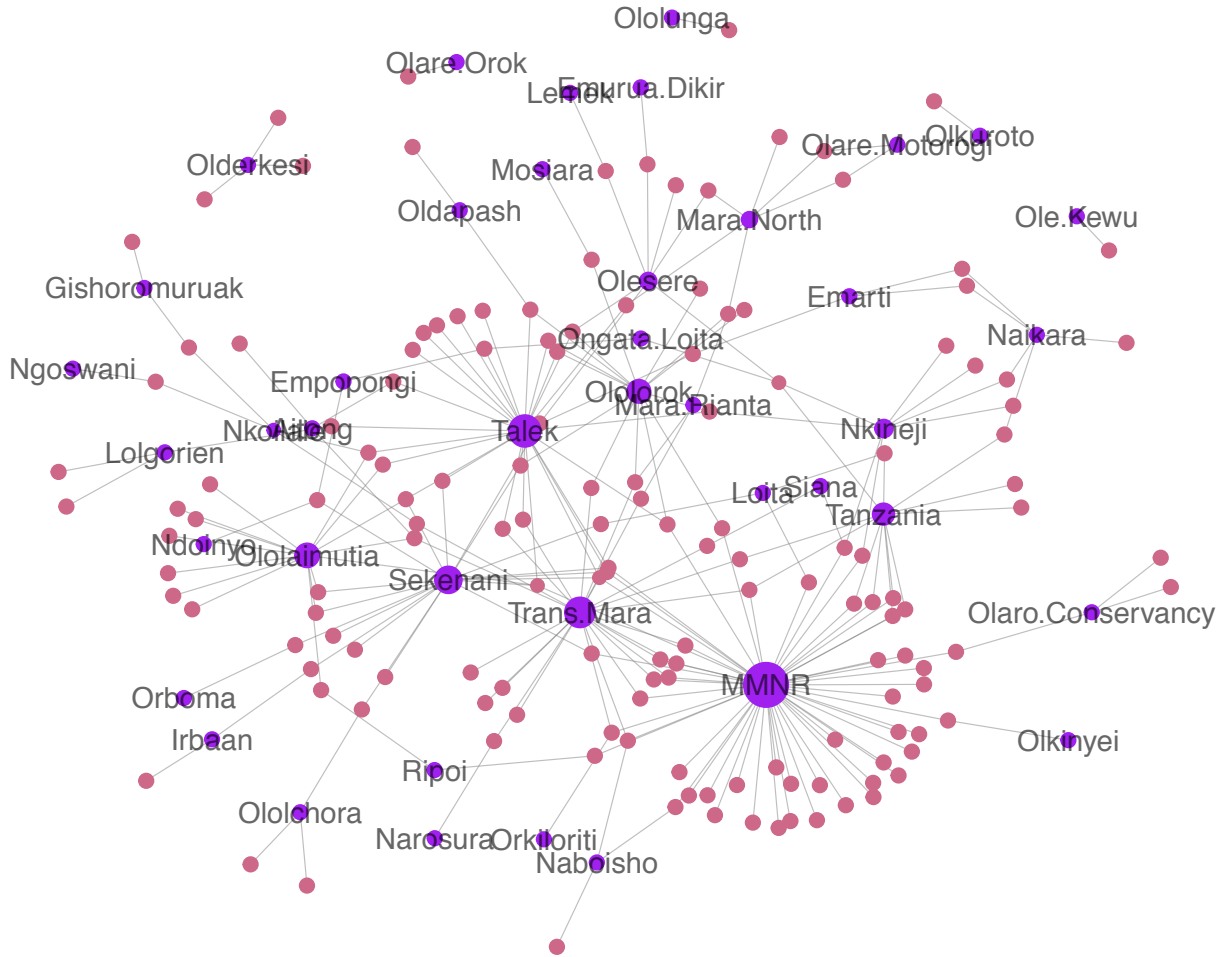
Figure 2: Agistment Network: Bipartite network of agistment locations within the Maasai Mara ecosystem, with node sizes scaled by degree. Purple nodes are villages, while pale violet nodes are households.

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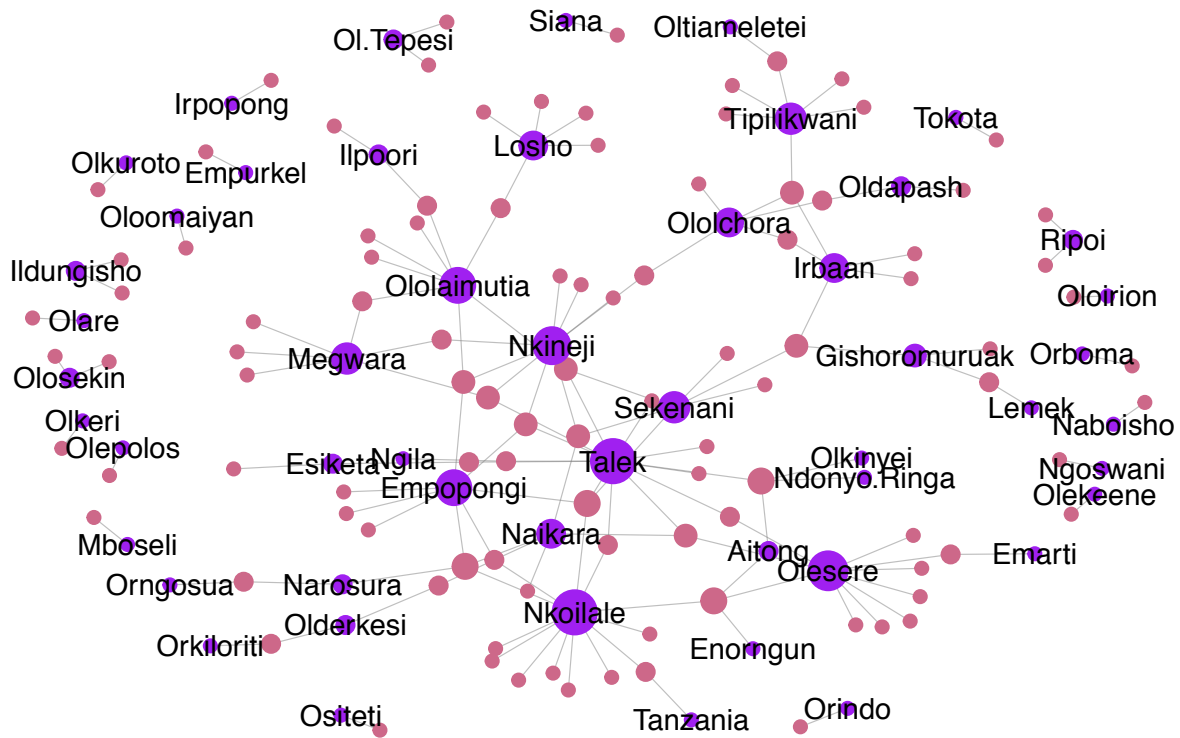
Figure 3: Gift Network: Bipartite network of gift locations within the Maasai Mara ecosystem, with node sizes scaled by degree. Purple nodes are villages, while pale violet nodes are households.
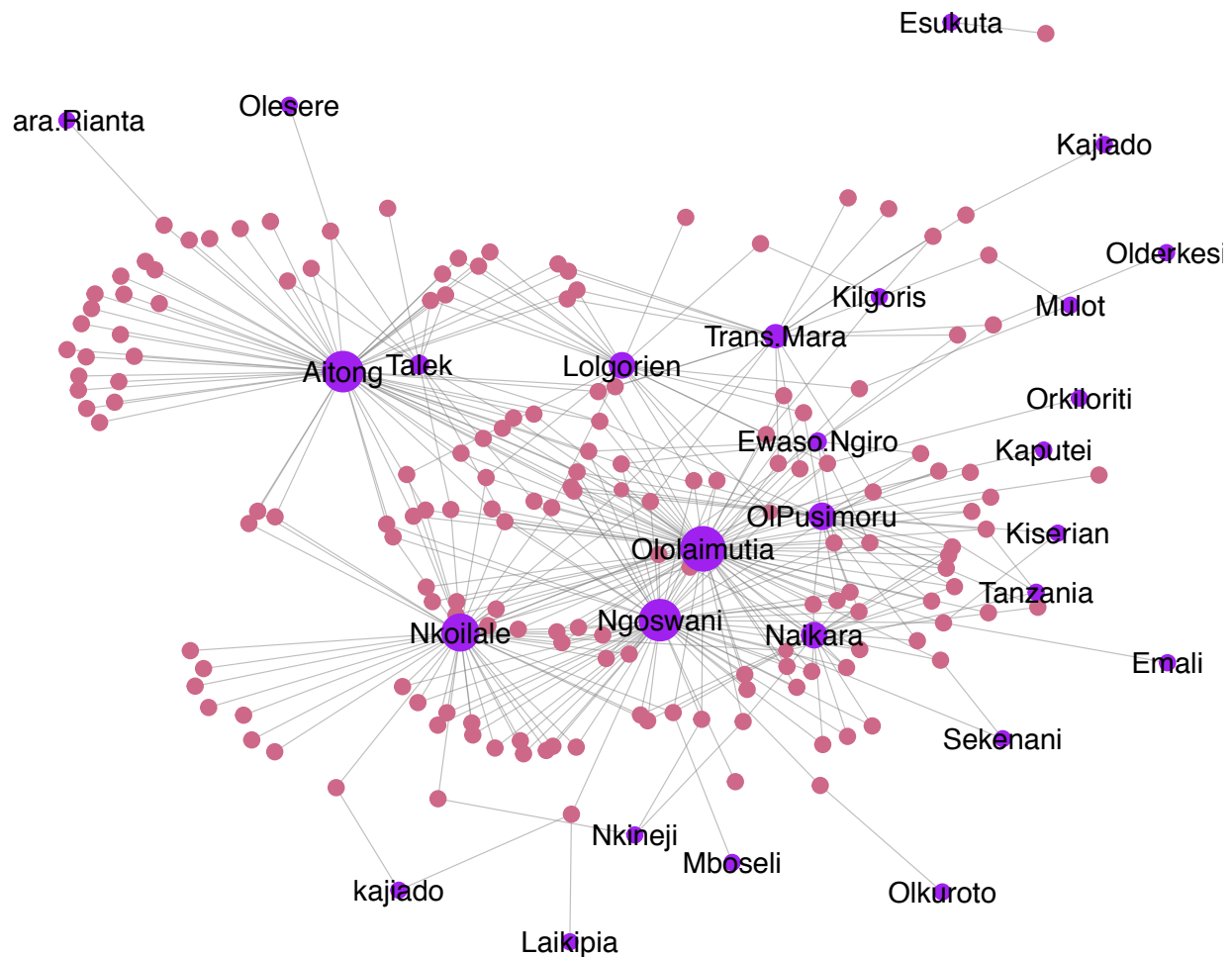
Figure 4: Buying Network: Bipartite network of major buying locations within the Maasai Mara ecosystem, with node sizes scaled by degree. Purple nodes are villages, while pale violet nodes are households.

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

13

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).
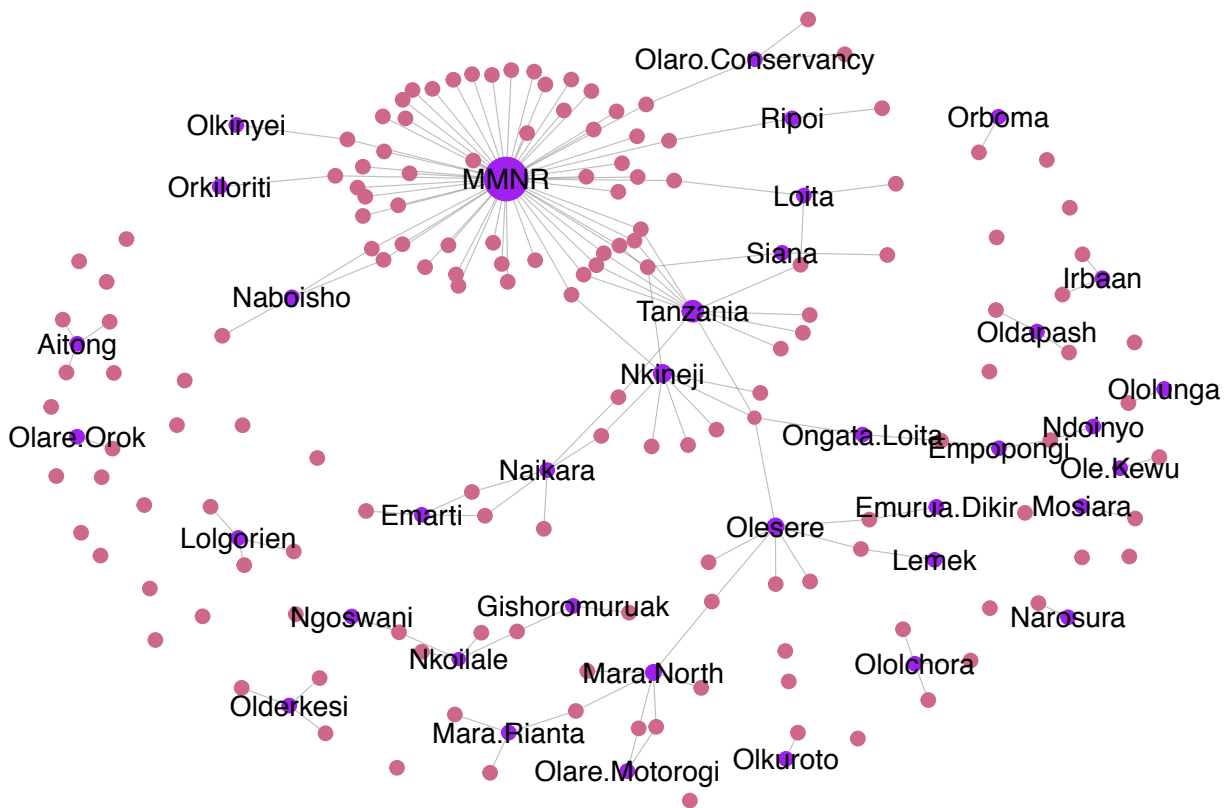
245

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												

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

		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)	

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.

Discussion

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

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

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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.,

18

316   2007). We demonstrated that the removal of the top five nodes with the highest degree was effective

317   at fragmenting all the networks. The agistment network, however, was more robust to node removal

318   in that the removal of top 5 or 10 villages resulted in fragmentation indices of 81% and 90%, whereas

319   this value was close to 100% for the other networks in this study. This might be due to the fact that,

320   we cannot remove MMNR from the network or that household decisions to move to a particular

321   location is highly influenced by an individual household's cost-benefit analysis of the move

322   independent of other household decisions (Turner and Schlecht, 2019). This is unlike buying and

323   selling, which follow the law of supply and demand, and sometimes are dictated by intermediaries

324   (Alemayehu, 2011; Alarcon et al., 2017; Chaters et al., 2019).

325   Agistment, buying, and selling networks occur much more frequently with potentially greater

326   implications for pathogen dissemination than gifting and bride price (Macpherson, 1995; Bett et al.,

327   2009). Anecdotally, we may conclude that the fragmentation of the selling network may serve to

328   protect markets outside the Mara Ecosystem, such as Dagoretti, Ngong and Ongata Rongai. On the

329   contrary, the fragmentation of the buying network leaves the markets in the neighboring counties

330   connected to those in the Maasai Mara Ecosystem (Supplementary material) and may need to be

331   considered when designing a comprehensive disease control strategy.

332   Our study has several limitations. First, data were collected at a single time point, and

333   temporal changes in a network's topology is a common phenomenon, especially in pastoralist

334   production systems (VanderWaal et al., 2017; Pomeroy et al., 2019). Secondly, respondents were

335   asked about movements made during the last five years, which limits the temporal resolution of when

336   movements occurred and introduces potential recall bias. Third, because data were collected in a

337   defined geographical area, the results may not be readily generalizable to other areas. Finally, our

338   network structure did not account for common areas of daily contact, such as congregation during

339   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

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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