1 Genetic relatedness cannot explain social bonds in black-and-white ruffed

- 2 lemurs (Varecia variegata).
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21 ABSTRACT

22 Several primates exhibit fission-fusion social dynamics, yet the factors 23 shaping variable associations among subgroup members have not been widely 24 addressed. Associations may occur simply because of shared habitat preferences; 25 however, social ties may also be influenced by genetic relatedness (kinship) or 26 social attraction. Here, we investigate the association patterns of wild black-and-27 white ruffed lemurs, Varecia variegata, in Ranomafana National Park, Madagascar 28 using behavioural, spatial (home range), and genetic data from twenty-four 29 individually identified animals. We collected 40,840 records of group composition 30 over a 17-month period and from this calculated pairwise association indices. We 31 also used ranging coordinates and genetic samples to estimate patterns of spatial 32 overlap and kinship, and then related these measures to patterns of affiliation using 33 Mantel tests and MRQAP. From these analyses, we found that dyadic ruffed lemur 34 social associations were generally sparse and weak; that home range overlap was 35 minimal; and that average relatedness within the community was low. We found 36 no evidence that kinship was related to patterns of either spatial overlap or social 37 association; instead, associations were primarily driven by space use. While home 38 range overlap explained most of the variation seen in social association, some 39 variation remains unaccounted for, suggesting that other social, ecological, and 40 biological factors such as shared resource defense or communal breeding might 41 also play a role in social attraction among members of this species.

42

43 *Keywords:* social network analysis, range use, spatial overlap, Association Index,

44 kinship, fission-fusion, microsatellites, primates

45

46 **INTRODUCTION**

47 Animal social systems reflect non-random relationships among 48 neighbouring conspecifics, the content, guality, and patterning of which define their 49 social structure (Hinde, 1976). In fact, there is growing evidence that taxa as 50 diverse as fishes, lizards, birds, cetaceans, and equids exhibit social associations 51 that are not only non-random, but highly structured (Augusto, Frasier, & 52 Whitehead, 2017; Croft et al., 2012, 2005; Firth et al., 2017; Spiegel, Sih, Leu, & 53 Bull, 2018; Stanley, Mettke-Hofmann, Hager, & Shultz, 2018). Individuals vary in 54 the numbers, strengths, and stabilities of their social ties (Croft et al., 2005; 55 McDonald, 2007; Silk, Alberts, & Altmann, 2006; Silk, Altmann, & Alberts, 2006; 56 Silk et al., 2010a; Stanley et al., 2018), as well as in their preferences for social 57 associates (e.g., Cords, 2002; Gero, Gordon, & Whitehead, 2015; Kohn, Meredith, 58 Magdaleno, King, & West, 2015; Mourier, Vercelloni, & Planes, 2012; Perry, 2012; 59 Schülke, Bhagavatula, Vigilant, & Ostner, 2010)-outcomes of which can be 60 evolutionarily significant (Seyfarth & Cheney, 2012; Silk, 2007). For example, the 61 extent and/or strength of females' social connections have been positively linked 62 to higher fertility (Macaca mulatta: Brent et al., 2013; humans: Balbo & Barban, 63 2014), longer lifespan (Papio cynocephalus: Alberts, 2019; Archie, Tung, Clark, 64 Altmann, & Alberts, 2014; Papio ursinus: Silk et al., 2010b), and greater offspring 65 survival (Equus caballus: Cameron, Setsaas, & Linklater, 2009; Papio

cynocephalus: Silk, Alberts, & Altmann, 2003; Papio ursinus: Cheney, Silk, & 66 67 Seyfarth, 2016; Silk et al., 2009; Physeter microcephalus: Whitehead, 1996). 68 Similarly, males that form strong social bonds have been shown to be more 69 successful at forming coalitions, achieving high rank, and siring more offspring 70 than males with weaker social bonds (e.g., *Chiroxiphia linearis*: McDonald, 2007; 71 Macaca assamensis: Schülke et al., 2010; Pan troglodytes: Gilby et al., 2013). 72 Nevertheless, while the long-term health and fitness outcomes of social bonds 73 have been the focus of much investigation, the proximate factors shaping social 74 preferences have received comparatively little attention.

75 Several hypotheses have been proposed to explain social preference, the 76 most popular being kinship, whereby group members show preferential 77 associations with and, in the case of kin selection, are more likely to direct costly 78 altruistic behaviours toward close genetic relatives (Hamilton, 1964). For instance, many female mammals exhibit social preferences toward maternal kin (Smith, 79 80 2014), a pattern observed in primates in particular (reviewed in Langergraber, 81 2012), but also in spotted hyaenas (Wahaj et al., 2004), African elephants (Archie, 82 Moss, & Alberts, 2006), dolphins (Frère et al., 2010), and mountain goats (Godde, 83 Côté, & Réale, 2015), among others. Social preferences toward kin can be driven 84 by the benefits of associating with relatives, such as allomaternal care (reviewed 85 in Briga, Pen, & Wright, 2012; Pope, 2000; and in some cases even brood 86 parasitism, Andersson, 2017), reduced aggression and infanticide risk (reviewed 87 in Brown & Brown, 1996; Agrell, Wolff, & Ylonen, 1998), foraging advantages 88 (Griffiths & Armstrong, 2002; Nystrand, 2007), and shared social and ecological

89 knowledge (McComb, Moss, Durant, Baker, & Sayialel, 2001; Salpeteur et al., 90 2015). However, social integration has also been shown to have strong direct 91 fitness consequences between nonrelatives (Baden, Wright, Louis, & Bradley, 92 2013; Cameron et al., 2009; G. G. Carter & Wilkinson, 2015; Riehl, 2011), 93 suggesting that social bonds can evolve based on these direct benefits alone. 94 Moreover, evidence for kin-biased relationships in other species, particularly those 95 with higher fission-fusion dynamics, is weak (e.g., Best, Dwyer, Seddon, & 96 Goldizen, 2014; K. D. Carter, Seddon, Frère, Carter, & Goldizen, 2013; Hirsch, 97 Prange, Hauver, & Gehrt, 2013; Langergraber, Mitani, & Vigilant, 2007, 2009; 98 Moscovice et al., 2017; Wilkinson, Carter, Bohn, & Adams, 2016), raising 99 guestions as to the ubiguity of kinship in the formation and maintenance of social 100 ties.

101 One complicating factor in determining whether and how kinship shapes 102 social bonds is that it can be difficult to decouple social associations due to kinship 103 from associations due to other social and spatial contexts (reviewed in Doreian & 104 Conti, 2012; Wey, Blumstein, Shen, & Jordán, 2008). For example, in some 105 species it is difficult to differentiate whether strong associations are due to strong 106 genetic ties or to other factors, such as sex or age (Lusseau & Newman, 2004; 107 Mourier et al., 2012), habitat utilization (Wiszniewski, Allen, & Möller, 2009), or 108 foraging specializations (Daura-Jorge, Cantor, Ingram, Lusseau, & Simões-Lopes, 109 2012; Gilby & Wrangham, 2008; Griffiths & Armstrong, 2002; Mitani, Merriwether, 110 & Zhang, 2000). Indeed, patterns of social association have been found to 111 correlate with spatial overlap (i.e., overlapping home ranges) more strongly than,

112 or to the exclusion of, kinship in a number of species (Best et al., 2014; K. D. Carter 113 et al., 2013; Frère et al., 2010; Strickland, Gardiner, Schultz, & Frère, 2014). 114 Moreover, although individuals living in closer physical proximity are more prone 115 to interact (e.g., Clutton-Brock, 1989; Kossinets & Watts, 2006), conspecifics with 116 high levels of spatial overlap may also mediate their interactions by temporally 117 modifying range use, such that animals with highly overlapping ranges may 118 interact minimally, if at all (e.g., temporal avoidance) (Leu, Bashford, Kappeler, & 119 Bull, 2010; Ramos-Fernández, Boyer, Aureli, & Vick, 2009; Strickland et al., 2017). 120 While still rare, studies that consider the simultaneous effects of spatial overlap 121 and kinship on association patterns are thus important to understanding the role 122 of social preference in the evolution of social systems and sociality (e.g., Best et 123 al., 2014; K. D. Carter et al., 2013; Frère et al., 2010; Lusseau et al., 2006; Maher, 124 2009; Podgórski, Lusseau, Scandura, Sönnichsen, & Jędrzejewska, 2014; Strickland et al., 2014). 125

126 Ruffed lemurs (Genus Varecia) are moderately-sized frugivores (Baden, 127 Brenneman, & Louis Jr., 2008; Balko & Underwood, 2005) that live in groups 128 (hereafter "communities") comprising as many as 30 adult and subadult individuals 129 and their offspring (Baden, Webster, & Kamilar, 2016 and references therein). 130 From earlier work, we know that communities exhibit high fission-fusion dynamics, 131 with members varying in their degrees of home range overlap and number and 132 strength of social ties (Baden, 2011; Baden & Gerber, n.d.; Baden et al., 2016; 133 Vasey, 2006). Moreover, studies of microsatellite markers and mitochondrial DNA 134 have shown that while average pairwise relatedness within communities is low

135 (i.e., both sexes disperse: Baden et al., 2014), communities nevertheless contain 136 networks of closely related kin (e.g., Baden, 2011; Baden et al., 2013). Taken 137 together, these lines of evidence suggest that community members may be 138 actively choosing social associates, and that these associations may be shaped 139 by a number of ecological, social, and biological factors. Here, we investigate the 140 relative influences of space use and kinship on the strength of associations 141 amongst members of a black-and-white ruffed lemur (Varecia variegata) 142 community. Specifically, we quantify dyadic measures of association, home range 143 overlap, and genetic relatedness to address the overarching question: What 144 influences social association in ruffed lemurs?

145

146 **METHODS**

147 Study site and subjects

148 We collected data from one V. variegata community at Mangevo [21°220] 149 6000 S, 47°280 000 El, a mid-elevation (660-1,200 m) primary rainforest site located in the southeastern parcel of Ranomafana National Park, Madagascar 150 151 (Wright et al., 2012) during 16 months of study (August-December 2007; 152 February– December 2008). At the time of the study, the community included 24 153 adults and subadults (8 adult females, 11 adult males, 5 subadult males). All 154 individuals in this study were habituated and individually identified via radio-collars 155 or unique collar-tag combinations prior to behavioural observations (see Baden et 156 al., 2016 for specific details). Animals were collared under veterinary supervision 157 following a strict protocol (Glander, 1993). Nineteen infants were born in the 2008

birth season and were present from October to December 2008, when the study

159 ended. Sampling efforts resulted in a total of 4,044 focal observation hours.

160

161 Ethical note

Permission to conduct research was granted by Madagascar's National Parks (ANGAP/MNP, #084/07-041/08), and research protocols were in compliance with Stony Brook University IACUC #2005-20081449. All animal protocols followed the Guidelines for the treatment of animals for teaching and research recommended by ASAB/ABS (2019).

167

168

169 **Data collection**

170 Behavioural monitoring

171 We collected data during dawn to dusk follows of focal individuals. We 172 located focal subjects at the beginning of each observation period via radio-173 telemetry and selected new subjects daily. We never sampled focal subjects on 174 consecutive days and every effort was made to follow all subjects at least once per 175 month. If an individual with a collar-tag was located in association with a radio-176 collared focal individual prior to 10:00 h, this individual became the new focal 177 subject for that observation period. Observational periods ranged in duration 178 between 8 to 11 hours depending on seasonal differences in day length and time 179 needed to locate animals at dawn.

180 Upon initial contact with the focal individual, we recorded the number and 181 identities of all other individuals present within the subgroup. To do so, one 182 observer remained with the focal individual while the remaining three team 183 members spread out to locate and identify all other members of the subgroup. A 184 priori, individuals were considered members of a subgroup only if they were within 185 50 m of the group center and were seen associating, traveling with and maintaining 186 proximity to members of the subgroup being followed (see Baden et al., 2016 for 187 details). After initial contact, we monitored subsequent changes in subgroup size, 188 composition (age/sex class, individual identity), and cohesion (i.e., the greatest 189 distance between any two subgroup members), as well as activity state of the focal 190 subject using instantaneous scan sampling techniques collected at 5 min intervals 191 (Altmann, 1974). We recorded a total of 40,840 group scans.

We collected simultaneous GPS coordinates at 10-min intervals from as close to the focal individual as possible to document daily individual range use. We recorded spatial coordinates only if estimated positional error was less than 10 m.

196 Genetic sampling

In addition, we collected genetic samples from 38 black-and-white ruffed
lemurs from the Mangevo population, including all subjects in this study, during
five capture seasons spanning four consecutive years (2005-2008; see Baden,
200 2011 for details). Sample collection occurred under veterinary supervision and
followed a strict protocol outlined by Glander (1993). All capture procedures

202 occurred during non-reproductive seasons in the absence of infants and203 dependent offspring.

204 For each individual captured, one of us (ALB) collected approximately 1 205 ml/kg of whole blood (~4 cc) from the femoral vein and four 2mm tissue biopsies 206 from ear pinnae. All samples were stored in 5ml of lysis buffer solution (0.1 M Tris-207 HCI pH, 8.0, 0.1 M EDTA, 0.01 M NaCI, and 0.5% w/v SDS) at ambient 208 temperature in the field (7 to 21 days) (Longmire, Gee, Hardekopf, Graham, & 209 Mark, 1992). We then banked samples in a -80°C freezer at the Madagascar 210 Biodiversity Partnership headquarters in Antananarivo, Madagascar and 211 subsequently at the Yale Molecular Anthropology Lab in New Haven, CT until 212 analysis.

213

214 Data analysis

215 Association strength

216 Sampling was biased toward radio-collared females; we therefore 217 subsampled our data prior to association analyses. Details are presented in Baden 218 et al. (2016), but briefly, we divided our dataset into monthly periods and according 219 to the sex of the focal individual. Using only scans for which all individuals were 220 known, we randomized point scans and selected X scans to include in the dataset 221 for each sex, where X is 90% of the point scans for the sex with the fewest scans 222 in a given month. This procedure resulted in the inclusion of a total of 11,784 point 223 scans, with equal numbers of scans targeting male and female focal subjects in 224 each month (Baden et al., 2016).

225 We used SOCPROG 2.9 (Whitehead, 2009) to calculate association indices 226 between all pairs of individuals using the "simple ratio" index, which quantifies the 227 proportion of time that two individuals are observed together relative to their total 228 observation time overall. This index is appropriate when individuals are equally 229 likely to be correctly identified (Cairns & Schwager, 1987; Ginsberg & Young, 1992; 230 Whitehead, 2008), which is the case for this population. Given that subgroup composition in this community changes approximately every 90 minutes (Baden 231 232 et al., 2016), we used a 6-hour sampling interval to reduce autocorrelation among 233 periods. We also removed any subject observed in fewer than 10 sampling 234 periods. Our final dataset included 8 adult females and 9 adult males observed in 235 over 11,171 point scans.

236 To examine seasonal variation in associations, we organized the subsetted 237 data from 2008 into three seasons according to female reproductive state as 238 defined by Baden et al. (2013). Using the protocols described above, our final 239 datasets included: 8 females and 9 males over 5,051 scans during the 240 nonbreeding season (January through June); 7 females and 8 males over 3,267 241 scans during the mating/gestation season (July through September); and 8 242 females and 6 males over 2,664 scans during the birth/lactation season (October 243 through December).

244

245 Spatial overlap

246 We calculated home range overlap between all pairs of individuals using a 247 utilization distribution overlap index (UDOI; Fieberg & Kochanny, 2005)

248 implemented in the R package adehabitat (Calenge, 2011), as described in Baden 249 & Gerber (n.d.). The UDOI is an index of space-use sharing between two utilization 250 distributions (UDs). UDOI values can range from 0 to 1, with a UDOI of 0 indicating 251 no home range overlap and a UDOI of 1 indicating that home ranges are uniformly 252 distributed and have 100% overlap. Values can also be >1 if both UDs are 253 nonuniformly distributed and also have a high degree of overlap. Values <1 254 indicate less overlap relative to uniform space, whereas values >1 indicate higher 255 than normal overlap relative to uniform space. We calculated four UDOIs for all 256 pairs of individuals: one annual UDOI, and three seasonal UDOIs according to 257 female reproductive state, as for association analyses described above.

258

259 Relatedness

We genotyped individuals at a suite of 15 polymorphic microsatellite loci (see Baden, 2011 and Baden et al., 2014 for details). We extracted total genomic DNA from blood and/or tissue samples using standard nucleic acid extraction kits (QIAamp DNA Mini Kit; Qiagen) automated on a QiaCube (Qiagen). Extraction procedures followed the manufacturer's protocols, with the following modification to the tissue extraction procedures: samples were allowed to lyse initially in ASL buffer for 24-48 hours rather than 10 minutes.

We carried out PCR amplifications in a total reaction volume of 25 μ l consisting of 2 μ l template, 12.5 μ l Qiagen HotStar Taq Master Mix, and 10 μ M of each primer. Amplification conditions were as follows: initial denaturation at 95 °C for 15 min; 35 cycles of 30 s at 94 °C, 40 s at 54 to 60 °C (see Louis et al., 2005),

271 1 min at 72 °C, and a final extension of 7 min at 72 °C. The 5' end of the forward 272 primer was fluorescently labeled, and amplification products were separated and 273 visualized using capillary electrophoresis (ABI 3730xl Genetic Analyzer). We 274 assessed allele sizes relative to an internal size standard (ROX-500) using Gene 275 Mapper software (Applied Biosystems), and scored final genotypes based on 276 multiple independent reactions (Taberlet, 1996). Panels yielded Plsjb (Queller & Goodnight, 1989) values of 2.7×10^{-5} , demonstrating the very low probability that 277 278 two individuals would share the same multilocus genotype by chance. We further 279 tested the robusticity of this suite of loci for estimating relatedness with a 280 rarefaction analysis as in Altmann & Alberts (1996) and de Ruiter & Geffen (1998) 281 using the program RE-RAT (http://people.musc.edu/~schwaclh/). We estimated 282 pairwise relatedness among individuals (r) following Queller & Goodnight (1989) using 283 the program GenAIEx 6.5 (Peakall & Smouse, 2012). Relatedness was based on allele 284 frequencies derived from a larger population of 38 adult multilocus genotypes (Baden, 285 2011). Fine scale dyadic relatedness assessments (e.g., distinguishing between 286 full and half-sibs) are not possible in most microsatellite studies, and in fact, the 287 ability to differentiate relatedness disjunctions on such a scale would probably 288 require 30 to 60 microsatellite loci (Stone & Björklund, 2001). We therefore 289 consider "related dyads" to be those with r-values ≥ 0.25 ; we made no attempt to 290 further distinguish categories or degrees of relatedness.

291

292 Correlations among association strengths, spatial overlap, and relatedness

293 We used Mantel tests to examine whether association indices were related 294 to either spatial overlap or relatedness, as well as test for a correlation between 295 spatial overlap and relatedness (Mantel, 1967). We further used a multiple 296 regression guadratic assignment procedure (MRQAP; Dekker, Krackhardt, & 297 Snijders, 2007) to determine relationships between the response variable-298 association index—and predictor variables—sex, spatial overlap, and relatedness. 299 For sex, we used a matrix of sex similarity, which used values of 1 (same sex) and 300 0 (different sex). MRQAP tests each pairwise combination of response and 301 predictor matrices while holding the remaining predictor matrices constant. We 302 performed both Mantel tests and MRQAP for the overall dataset as well as in each 303 of the three seasons using SOCPROG 2.9 (Whitehead, 2009).

304

305 Quantifying relatedness among dyads with "preferred" association strengths or
 306 spatial overlap

307 In addition to the correlations described above, we further investigated 308 patterns of kinship among individuals identified as "preferred" associates (Als) and 309 those with "preferred" spatial overlap (UDOIs) following methods described in 310 Frère et al. (2010) and Carter et al. (2013). We first divided relationships into 311 "preferred" (>95th percentile of association indices or UDOIs) and "non-preferred" 312 (<=95th percentile). Note that the descriptor "preferred" is clear for associates 313 (dyads observed together more often than others), but dyads with high spatial 314 overlap were not necessarily utilizing shared ranges in coordinated ways. Unlike 315 Frère et al. (2010) and Carter et al. (2013), we did not include an 'avoided' category

316 because the number of dyads that did not associate and/or overlap spatially 317 exceed the 5th percentile, which was used as a threshold in previous studies. We 318 then calculated mean observed relatedness for each of the two categories 319 ("preferred" and "non-preferred") for both AI and UDOI datasets. Next, we 320 randomly resampled relatedness values with replacement for each of the two 321 datasets, using the sample sizes for each category in the empirical data (i.e., sample sizes for "preferred" and "nonpreferred" were held constant). We repeated 322 323 this procedure 10,000 times to generate a distribution, and then calculated 324 significance as the fraction of replicates (out of 10,000) in which relatedness of 325 "preferred" AI or UDOI was greater than the observed, empirical value. The script 326 in which we implemented this procedure is available at 327 https://github.com/thw17/Varecia social preferences.

328

329 **RESULTS**

330 Association strength and spatial overlap

331 The average overall association index (AI) was 0.05 ± 0.03 (Baden et al., 332 2016). We observed similar mean Als in each of the three reproductive seasons 333 (nonbreeding = 0.04 ± 0.02 ; mating/gestation = 0.06 ± 0.03 ; birth/lactation = 0.07334 \pm 0.03). Within seasons, however, individuals varied substantially in their Als. 335 Average individual AIs varied from 0.01 to 0.11 (nonbreeding = 0.01-0.08; 336 mating/gestation = 0.01-0.11; birth/lactation = 0.01-0.10), while maximum 337 individual AIs ranged from 0.07 to 0.82 (nonbreeding = 0.08-0.82; mating/gestation 338 = 0.07-0.79; birth/lactation = 0.08-0.82).

Average home range overlap (UDOI) was 0.211 ± 0.357 . Some dyads did not overlap at all (UDOI = 0), while the maximum UDOI observed was 1.895 (Figure 1). As with Als, we observed similar mean UDOIs in each of the three reproductive seasons (nonbreeding = 0.17 ± 0.27 ; mating/gestation = 0.15 ± 0.29 ; birth/lactation = 0.20 ± 0.43 ; Table 1)

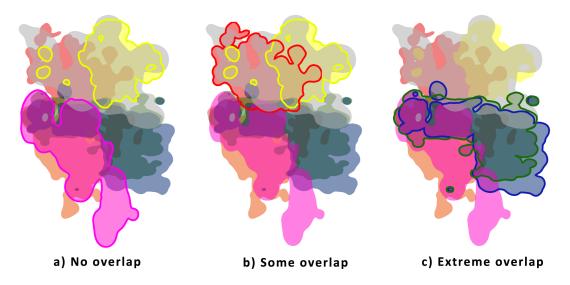


Figure 1. Examples of home range overlap among pairs of individuals within the Mangevo ruffed lemur
 community: a) Females Pink-Yellow and Radio-Yellow have no spatial overlap among home ranges (i.e.,
 UDOI = 0.00), whereas b) females Radio-Yellow and Radio-Red and c) females Radio-Blue and Radio-Green
 share some (UDOI = 0.106) to nearly complete home range overlap (UDOI = 0.951), respectively.

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344

351 Table 1. Summary of association indices, utilization distribution overlap indices

Association Indices	n	Mean	SD	Min	Max
Overall	136	0.05	0.03	0.00	0.80
Nonreproductive	136	0.04	0.12	0.00	0.82
Mating/Gestation	105	0.06	0.13	0.00	0.79
Birth/Lactation	91	0.07	0.15	0.00	0.82
UDOIs	n	Mean	SD	Min	Max
Overall	136	0.21	0.36	0.00	1.90
Nonreproductive	136	0.17	0.27	0.00	1.97
Mating/Gestation	120	0.15	0.29	0.00	1.74
Birth/Lactation	78	0.20	0.43	0.00	2.13
Relatedness	n	Mean	SD	Min	Max
Overall	171	-0.06	0.02	-0.72	0.65
Female-female	45	-0.13	0.04	-0.60	0.52
Female-male	90	-0.15	0.02	-0.72	0.28
Male-male	36	-0.13	0.04	-0.54	0.60

352 (UDOIs), and relatedness overall and by reproductive season.

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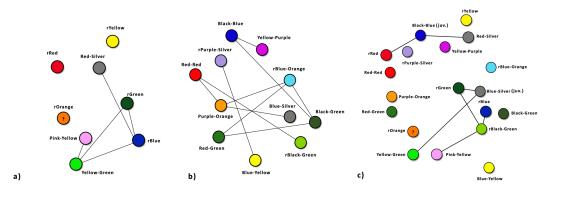
355

356 Relatedness

357 Genotypes were 93% complete; all subjects (n = 38) were scored for at least 358 12 loci (average = 14, range = 12 to 15). Allelic richness was 4.33 and average 359 observed heterozygosity was 0.400. There were no significant deviations from 360 Hardy-Weinberg Equilibrium for any of the loci examined, nor was there evidence 361 of null alleles.

Results of the rarefaction curve (y = 0.7991, $r^2 = 0.9992$) showed average 362 363 relatedness values stabilizing after 5 loci, with the difference between mean 364 relatedness using 5 and 6 loci changing by only 0.95% (0.023), and the difference 365 between using 6 and 7 loci changing by only 0.56% (0.016). Thus, subsequent

366 dyadic r-value calculations included all possible dyads (n = 703 dyads), as all 367 individuals could be compared at 5 or more loci. Average pairwise relatedness 368 among adults within the community was -0.06 ± 0.02 and ranged from -0.72 to 369 0.65 (Table 1; Figure 2).



370

Figure 2. Pairwise genetic relatedness (r >= 0.25) among a) female-female dyads, b) male-male dyads, and
c) female-male dyads within the Mangevo social community. "?" indicates individuals for which genotype data
are unavailable. Nodes are organized according to individual home range centroids.

374

375 Relationships between association strength, spatial overlap, and relatedness

376 Using the full dataset, Mantel tests revealed that kinship was unrelated to 377 either home range overlap (UDOI; n = 25, r = 0.047 p = 0.724) or association 378 indices (AI; n = 14, r = 0.120, p = 0.294), whereas UDOI and AI were significantly 379 correlated (n = 17, r = 0.789, p << 0.001; Figure 3). This pattern held across all 380 three reproductive seasons (Table 2). It is worth noting, however, that the 381 correlation coefficient between UDOI and AI in the nonbreeding season was much 382 lower, albeit still significantly positive, than the mating/gestation and birth/lactation 383 seasons, which were very similar (Table 2). Similarly, when we used MRQAPs to 384 jointly analyze the effects of UDOI, kinship, and sex on AI, in every time period we 385 analyzed, the partial correlations between UDOI and AI were always significantly

386 positive, while kinship and sex were never significantly correlated with AI (Table



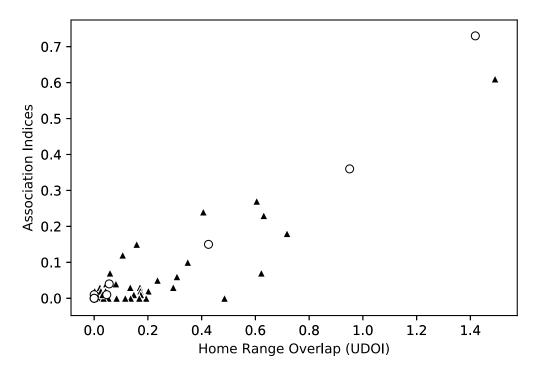


Figure 3. Scatterplot illustrating the relationship between social association (AI) and home range overlap (UDOI). Als range from 0 (no association) to 1 (100% association). Similarly, UDOIs range from 0 (no overlap) to 1 (complete overlap); values of >1 are possible if both UDs are nonuniformly distributed and also have a high degree of overlap. Values <1 indicate less overlap relative to uniform space, whereas values >1 indicate higher than normal overlap relative to uniform space. White circles indicate kin (r>=0.25); black triangles indicate non-kin (r<0.25).

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388

- 397 Table 2. Results from Mantel tests correlating Association Indices with utilization
- 398 distribution overlap indices (UDOIs), and relatedness overall and by reproductive
- 399 season.
- 400

Season	Variable	Records	N	Correlation	<i>p</i> -value
Overall	UDOI	11,171	17	0.789	<<0.001
Overall	Relatedness	11,171	14	0.120	0.294
Mating	UDOI	3,267	13	0.891	<<0.001
Mating	Relatedness	3,267	13	0.099	0.392
Nonbreeding	UDOI	5,051	14	0.566	<<0.001
Nonbreeding	Relatedness	5,051	14	0.149	0.184
Birth/gestation	UDOI	2,664	11	0.892	<<0.001
Birth/gestation	Relatedness	2,664	11	0.159	0.254

401 Note: Overall includes 2007-2008, whereas seasonal measures are from 2008
402 only. N indicates the number of individuals included in each analysis; individuals
403 had to be represented in both datasets in order to be included in the analyses for
404 a given season.

- 405
- 406

- 408 Table 3. Results from a multiple regression quadratic assignment procedure (MRQAP) investigating the partial relationships
- 409 of association (AI) with utilization distribution overlap indices (UDOI), relatedness, and sex.

		UDOI		Relatedness		Sex	
Season	Ν	Partial corr	<i>p</i> -value	Partial corr	<i>p</i> -value	Partial corr	<i>p</i> -value
Overall	14	0.920	<<0.001	0.035	0.754	0.056	0.617
Nonbreeding	11	0.655	<<0.001	0.123	0.356	-0.113	0.460
Mating/gestation	10	0.873	<<0.001	-0.049	0.742	0.281	0.720
Birth/lactation	8	0.941	<<0.001	0.296	0.144	0.102	0.530

411

412 Relatedness among dyads with "preferred" association strengths or spatial overlap 413 Average relatedness among "preferred" dyads, defined as falling in the 414 >95th percentile of AIs (5 of 91 dyads), was significantly higher than among dyads 415 classified as "not preferred" (mean R_{xAI preferred} = 0.109 versus mean R_{xAI non-preferred} 416 = -0.095; p = 0.049). In contrast, average relatedness of dyads with the greatest home range overlap, defined as falling in the >95th percentile of UDOI (10 of 190 417 418 dyads), was not statistically different from other dyads (mean $R_{xUDOI preferred} = -$ 419 0.015326 versus mean $R_{xUDOI \text{ non-preferred}} = -0.03464$, p = 0.3978).

420

421 Discussion

422 Results from this study illustrate complex relationships among social 423 association, space use, and kinship in wild black-and-white ruffed lemurs, patterns 424 that-while unusual for primates-are well aligned with much of the broader 425 mammalian literature. We found that ruffed lemur social associations varied 426 immensely, ranging from no association between some individuals to dyads 427 observed together more than 75% of the time. From a community perspective, the 428 social network was sparse, with weak associations (Als) being common. Similarly, 429 home range overlap was minimal and average relatedness among community 430 members was low. These patterns were consistent throughout the year and across 431 reproductive seasons. Together, these and earlier lines of evidence (e.g., Baden, 432 2011; Baden et al., 2016) can be used to characterize ruffed lemurs as having a 433 spatiotemporally dispersed fission-fusion social organization with weak social and434 kinship ties.

435 Kin selection theory (Hamilton, 1964) has long been invoked to explain the 436 social preferences observed among mammals (e.g., Archie et al., 2006; Frère et 437 al., 2010; Godde et al., 2015; Smith, 2014; Wahaj et al., 2004), particularly in 438 primates (reviewed in Langergraber, 2012; Silk, 2002). In this study, however, we 439 found no evidence that kinship structured either spatial overlap or social 440 association overall in the community. There were exceptions, however, as some, 441 but not all, of the very closest social relationships were between closely related 442 individuals. The closest social ties in the community appear to occur primarily 443 between females and their preferred (often unrelated male) social partners, 444 followed by mothers and their pre-dispersal-aged subadult and adult offspring. 445 Nevertheless, although fewer than ten percent (8.8%) of adults within the 446 community were genetic relatives, nearly three-quarters of adult females (71%) 447 and all of adult males (100%) were closely related to at least one, and up to as 448 many as three other same-sex relative(s) within the community. Thus, while overall 449 patterns of dyadic relatedness suggest that ruffed lemur communities are 450 composed of both kin and non-kin, and that preferred associates are sometimes 451 close relatives, related dyads are not forming spatial networks of kin within the 452 larger communal range. These patterns contrast with the spatially structured 453 matrilines described in *Microcebus murinus* (Eberle & Kappeler, 2006; Radespiel, 454 Lutermann, Schmelting, Bruford, & Zimmermann, 2003), another communally 455 breeding strepsirrhine. Some authors have used this model to hypothesize that, at

least in part, kin networks have facilitated the evolution of cooperative infant care
(Eberle & Kappeler, 2006). That kin networks don't exist in ruffed lemurs, who also
engage in cooperative infant care (Baden et al., 2013), further highlights the
uniqueness of their communal breeding strategies.

460 These results build on growing evidence that spatial overlap is more 461 strongly associated with social association than kinship in many taxa characterized 462 by high fission-fusion dynamics (Best et al., 2014; K. D. Carter et al., 2013; Frère 463 et al., 2010; Strickland et al., 2014). Importantly, not all dyads with a high degree 464 of home range overlap were close social associates. Indeed, many dyads with 465 nonzero spatial overlap were never observed together. Similar patterns have been 466 observed in dolphins, giraffes, and water dragons, wherein subjects did not 467 associate, despite sharing complete or near complete home range overlap (i.e., 468 'social avoidance' in dolphins: Frère et al., 2010; giraffes: K. D. Carter et al., 2013; 469 water dragons: Strickland et al., 2014). Thus, spatial overlap does not necessitate 470 social association. Instead, these results raise important questions related to 471 causation. What motivates social association? Are individuals that bias their time 472 toward overlapping areas simply more likely to associate? Or, in cases where 473 patterns of spatial overlap and social association do not align, is there some 474 additional force shaping these spatial and social decisions? Evaluating these 475 alternatives requires further investigation.

476 Moreover, while home range overlap explained most of the variation seen
477 in social association in ruffed lemurs, some variation remains unaccounted for,
478 suggesting that other social, ecological, and biological factors must also be at play.

479 One possibility is that even weak or infrequent social associations may facilitate 480 cooperative resource defense against other frugivorous competitors. For instance, 481 ruffed lemurs actively defend fruit-bearing trees against larger brown lemur (Genus 482 *Eulemur*) groups for days or even weeks during the resource scarce austral winter 483 (Baden, personal observation). Perhaps social association during these times 484 better equips otherwise solitary individuals to defend valuable fruit resources 485 against interspecific competitors. If this was the case, one might expect higher Als 486 during resource scarce seasons, periods that correspond primarily with 487 mating/gestation, but also birth/lactation seasons. Als were lowest in the 488 nonbreeding, resource abundant periods, though not significantly so, lending 489 minimal support for this hypothesis. In addition, communal breeding plays an 490 important role in female reproductive success in this species (Baden et al., 2013) 491 and might also be important in driving social preferences. For instance, recent work 492 suggests social networks in guppies may be structured by the propensity for non-493 kin to cooperate (Croft et al., 2009), which could lead to the maintenance of 494 cooperation in the absence of kin assortment (Fletcher & Doebeli, 2009). These 495 lines of research offer exciting opportunities to better understand the myriad factors 496 shaping social preferences in fission-fusion species.

497

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