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Density-dependent network structuring within and across wild animal systems

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27 Abstract

28 High population density should drive individuals to more frequently share space and interact, 29 producing better-connected spatial and social networks. Despite this widely-held 30 assumption, it remains unconfirmed how local density generally drives individuals' positions 31 within wild animal networks. We analysed 34 datasets of simultaneous spatial and social 32 behaviour in >55,000 individual animals, spanning 28 species of fish, reptiles, birds, 33 mammals, and insects. >80% of systems exhibited strongly positive relationships between 34 local density and network centrality, providing broad empirical evidence that local density 35 increases connectedness at the individual level. However, >75% of density-connectedness 36 relationships were nonlinear, and density's importance declined at higher values in >70% of systems, signifying saturating effects. Density's effect was much stronger and less saturating 37 for spatial than social networks, suggesting population density drives individuals to become 38 39 disproportionately spatially connected rather than socially. These findings reveal 40 fundamental trends underlying societal structuring, with widespread behavioural, ecological, 41 and evolutionary implications.

42 Keywords: Behavioural ecology, Spatial ecology, Disease ecology, Epidemiology,
43 Population dynamics, Social network structure, Network analysis, Spatial analysis

44 Introduction

45 The number of individuals occupying a given space – i.e., population density – is a central 46 factor governing social systems. At higher densities, individuals are expected to more 47 frequently share space, associate, and interact, producing more-connected spatial and 48 social networks and thereby influencing downstream processes such as mating, learning, 49 and competition. In particular, density-driven increases in network connectedness should 50 provide more opportunities for parasites to spread between hosts [1-5]. Despite the 51 fundamental nature of such density-dependent processes, evidence is relatively limited that 52 individuals inhabiting higher-density areas have more spatial and social connections. 53 Furthermore, density's effects should differ for asynchronous space sharing (e.g. home 54 range overlap) versus social associations (e.g. den sharing or grouping) or interactions (e.g. 55 mating or fighting). While several studies have compared animal populations at different 56 densities to demonstrate variation in social association rates among populations (e.g., [6,7]) 57 or groups (e.g., [8-10]), attempts to identify such density effects within continuous 58 populations of individuals are rarer (but see [11–14]), and their findings have never been 59 synthesised or compared. We therefore have an incomplete understanding of how density, 60 as a fundamental ecological parameter, determines socio-spatial dynamics within and 61 across systems. This inhibits our ability to identify and predict how changes in density – e.g. 62 through culling, natural mortality, dispersal, or population booms - influence downstream 63 processes that depend on shared space and social interactions.

64 The rate at which an individual interacts with conspecifics depends on its spatial and social 65 behaviour within the context of the surrounding environment and population. Adding more 66 individuals into the same space should cause them to more frequently spatially overlap and 67 socially associate or interact (Figure 1). Often, individuals are modelled as randomly moving 68 and interacting molecules ("mass action" or "mean field"). In this conceptualisation, direct 69 contact between two molecules is analogous to a social interaction or association; rates of 70 such interactions are often assumed to increase with density ("density-dependent"; e.g., 71 [15]), and/or to be homogenous in space (e.g., [10]). In reality individuals are unlikely to 72 behave and interact randomly in space, and instead will be influenced by spatially varying 73 factors including local density [16]. Changes in density may cause individuals to alter their 74 foraging behaviour [17–19], dispersal [20,21], social preference or avoidance [13,22], mating 75 behaviour [23], or preferred group size [7]; in some cases, interaction rates may change to 76 remain constant in the face of changing densities [24]. These and related processes might 77 produce strong nonlinearities in density-interaction relationships, which can complicate the 78 predictions of density dependence models of pathogen transmission, for example [2,4,5]. 79 Nevertheless, these nonlinearities are poorly understood and rarely considered.

Several wild animal studies have suggested saturating nonlinear relationships between density and social association rates [8–10,13]. Such relationships imply that association rates do not increase passively with density, and that behavioural or demographic processes likely change as density increases, with the ultimate consequence of slowing association rates. However, these nonlinearities are difficult to examine between populations or between species because they introduce a range of confounders and have few replicates along the

86 density axis [2]. Characterising gradients of density across individuals within a population 87 offers a workaround to this problem, and facilitates an appreciation of the fact that 88 interactions occur between individuals rather than at the population level. Examining 89 between-individual variation is one reason that social network analysis - which allows 90 characterisation and analysis of individual-level social traits, amongst other things - has 91 become so popular in animal ecology in recent years [25-29]. Additionally, recent years 92 have seen a substantial growth in understanding of socio-spatial behaviours, including 93 harmonising the concepts of spatial and social density [2,16,30]. Applying network analyses 94 coupled with this socio-spatial understanding of density could provide an individual-level 95 picture of density's effects on spatial and social connectedness, offering far higher resolution 96 and statistical power and greater ability to detect nonlinearities and between-system differences [2]. By providing new understanding of the correlates and emergent 97 98 consequences of variation in density, this expansion could help to identify general rules 99 underlying social structuring and network scaling in space.

100 Critically, different types of interactions or associations should show different relationships 101 with density: for example, the need to compete for food at higher densities could drive a 102 disproportionate increase in aggression [31], but this is unlikely to be true of mating 103 interactions. This rationale is well-understood in disease ecology, as differences in density-104 contact relationships are thought to drive differences in density dependence of infection -105 where "contact" is defined as an interaction or association that could spread a pathogen 106 (Figure 1). "Contacts" then form the basis of spatial and social networks used to investigate pathogen transmission dynamics, which should likewise diverge with density just as contacts 107 108 do. For example, density should drive greater transmission of respiratory pathogens but not 109 sexually transmitted pathogens [1,32]. Establishing these density-contact relationships is 110 integral to understanding disease dynamics and developing control measures [1,33], but we 111 still have a poor understanding of how different interactions (and therefore contact events for 112 different pathogens) are driven by density. This direct/indirect interaction dichotomy is most 113 fundamental to disease ecology [30], but given building interest in the spatial-social interface 114 and relationships between spatial and social networks in behavioural ecology [16], the 115 framework is readily related to other fields. Established density-interaction relationships are 116 diverse and include feral dog bites [11], ant antennations [34] and trophallaxis [24], ungulate 117 group memberships [12,17], rodent co-trapping [8,35], and agamid association patterns [13,14], but no study has yet synthesised how the rates of multiple interaction types relate to 118 119 density, within or across systems.

120 Identifying the general rules underlying density dependence requires quantifying density's 121 relationship with proxies of interaction rates at fine scales across a diversity of systems, then 122 identifying the factors determining their slope and shape. To this end, we collate a meta-123 dataset of over 55,000 individual animals across 34 wildlife systems globally to ask how 124 within-population variation in density determines between-individual interaction rates based 125 on connectedness in spatial and social networks. We fit multiple linear and nonlinear 126 relationships to identify the slope and shape of density effects within each system, and we 127 use meta-analyses to investigate general rules determining their slope and shape across 128 systems. In particular, we focus on comparing space sharing with social interactions and 129 associations as a cross-system case study. Ultimately, we present a de novo cross-system 130 analysis of individuals' social and spatial behaviour that traverses fields of behavioural,

- population, and disease ecology, which could help to inform general rules governing the
- 132 structure of social systems.



133

Figure 1: Schematic detailing the rationale underlying this study, outlining how population density drives the formation of spatial and social networks. This depiction uses the Wytham Wood great tits as an example. Ultimately, we aim to ask whether spatial or social connections generally show a stronger relationship with density, partly functioning as a proxy for indirect and direct contact events with the potential to transmit pathogens. This framework moves between concepts of network and contact formation traversing behavioural ecology, spatial and social network ecology, and disease ecology.

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144 Figure 2: The phylogenetic (A) and geographic (B) distribution of our 34 examined datasets of spatial 145 and social behaviour, with (C) schematic depicting the methodology for deriving local density values, 146 using the Isle of Rum red deer data as an example. The X and Y axes are bivariate spatial 147 coordinates. The panels within (C) show raw observations of individuals in space that we then 148 average at the individual level to make centroids; we use the centroids to generate annual density 149 distributions, which are then assigned to individuals in the form of local density measures. Animal 150 silhouettes are from phylopic.org; a list of attributions is in the supplement. NB the Potomac dolphins 151 are now defined as Tursiops erebennus; they are currently incorporated in Panel A as T. truncatus, 152 following the Open Tree of Life nomenclature.

153 Methods

154 Data standardisation and behavioural pipeline

Data were manipulated and analysed using R version 4.2.3 [36], and all R code is available at https://github.com/gfalbery/DensityMetaAnalysis. Our 34 datasets each involved at least one continuous uninterrupted spatial distribution of observations in a single population; some datasets comprised multiple such populations. These datasets covered 28 different host species, including sharks, carnivores, cetaceans, ungulates, rodents, elephants, birds, reptiles, and one insect (Figure 2). In one case (The Firth of Tay and Moray Dolphins) we
used two distinct replicates despite being composed of overlapping groups of individuals,
because of their distinct spatial distributions, which made it difficult to fit a coherent density
distribution.

To standardise the timescale across studies, all systems were analysed as annual replicates - i.e., social and spatial networks were summarised within each year. Our analyses used 60 system-behaviour replicates, listed in Supplementary Table 1, and totalled 151,507 unique system-individual-year-behaviour data points.

168 All spatial coordinates were converted to the scale of kilometres or metres to allow 169 comparison across systems. To provide an approximation of local density, following prior 170 methodology [12,37], we took each individual's average location across the year (their 171 centroid) and created a spatial density kernel using the `adehabitathr` package [38], which 172 provides a probabilistic distribution of population density across each study system based on 173 the local frequencies of observed individuals. Each individual was assigned an annual 174 estimate of local density based on their centroid's location within this spatial density 175 distribution. We made these density distributions as comparable as possible between 176 systems by incorporating the density raster using metre squares; however, there were large 177 differences in density across populations that were difficult to resolve and put on the same scale (e.g. interactions per individual/km² unit of density). Consequently, we scaled and 178 179 centred density to have a mean of zero and a standard deviation of one within each 180 population, which allowed us to focus on differences in relative slope and shape across 181 systems.

182 To provide a measure of asynchronous space sharing, we constructed home range overlap 183 (HRO) networks based on proportional overlap of two individuals' minimum convex polygon 184 (MCP; i.e., the bounding polygon around all observations of each individual in a given year). 185 These HRO networks were restricted to only individuals with five or more observations in a 186 given year to allow us to create convex polygons effectively; 10/34 (29%) systems did not 187 have sufficient sampling for this analysis. We also repeated our analyses with a series of 188 higher sampling requirements for observation numbers to ensure that our findings were 189 robust to this assumption. The MCP approach is relatively low-resolution, and assumes 190 uniform space use across an individual's home range; however, this approach is less data 191 intensive – and less sensitive to assumptions – than density kernel-based approaches that 192 would estimate variation in space use across the home range, allowing us to apply the 193 models across more systems, more generalisably, and more conservatively.

194 To provide a measure of social connectedness, we built social networks using various 195 approaches as defined by the original studies: direct observations of dyadic interactions (e.g. 196 fighting or mating); gambit of the group (GoG; i.e. membership of the same group) [39]; co-197 trapping (i.e. trapped together or in adjacent traps within a given number of trapping 198 sessions); or direct contact measured by proximity sensors (defined by a certain distance-199 based detection threshold). Notably some analyses use indirect interactions – i.e., spatial 200 overlap - to approximate direct interactions, which requires spatiotemporal coincidence, 201 which we caution against particularly when modelling pathogen transmission [30,40]. While 202 the two do often correlate, here we are not using HRO to approximate direct interaction

rates, but rather as a measure of indirect interactions (e.g., indicative of transmission of environmental parasites).

For each social network, we scaled connection strength relative to the number of observations of each individual in a dyad (i.e., simple ratio index [41]). Our response variable therefore took the form of strength centrality, scaled to between 0-1 for each dyad, for each social and spatial network. We focus on comparing density effects on social interactions and associations with density's effects on space sharing.

210 Density-connectedness models: what forms do density effects 211 take?

We developed a novel workflow to allow us to derive and compare density's effects on connectedness – and their drivers – in a standardised way across our wild animal systems. These took three forms: linear models fitted to the whole dataset, nonlinear models fitted to the whole dataset, and linear models fitted separately to low- and high-density subsets of each dataset.

Linear models: For each system-behaviour replicate, we first fitted a linear model using the
 `Im` function in R, fitting scaled density as an explanatory variable to estimate linear density
 effect slopes.

220 Generalised additive models (GAMs): We fitted GAMs in the `mgcv` package [42] to 221 identify whether each density effect was better described by a linear or nonlinear 222 relationship, and to identify the shape of these nonlinear relationships. For each model, we 223 fitted a default thin plate spline with k=4 knots. This knot number was selected to reduce 224 overfitting in our models, which formed several fits to the data that were difficult to reconcile 225 with functional formats. To assess whether nonlinear models fit better than linear models, we 226 used Akaike Information Criterion (AIC), with a contrast of $2\Delta AIC$ designated to distinguish 227 between models. See Supplementary Figure 1 for a schematic depicting our analytical 228 workflow.

229 **Saturation models:** To quantify whether density effects were generally saturating (i.e., that 230 density had steeper relationships with individuals' connectedness at lower density values), 231 we split the data into two portions: all values below the median density value, and all values 232 above the median. We then re-ran linear models examining the relationship between density 233 and strength in each portion. We attempted to investigate nonlinear patterns (especially 234 saturating effects) across all our systems using a range of other methods (e.g., comparing 235 specific functional relationships with nonlinear least squares), but found that they were 236 generally incapable of fitting well to the data in a standardised way across the many datasets 237 (i.e., non-convergence of nonlinear least squares using semi-automated starting estimates 238 across systems). As such, this approach represented a tradeoff between tractable, 239 generalisable model fitting, interpretability, and accurate representation of the relationship's 240 shape. All else being equal, we posit that investigating the relative slopes of two otherwise-241 identical portions of the data is a conservative and informative method of identifying 242 saturation, which was our main hypothesis for the expected shape of density effects.

243 Meta-analysis: what factors determine the slope of density-244 connectedness relationships?

245 To characterise the typical relative slope of density effects across systems and identify the 246 factors influencing their variation, we fitted hierarchical meta-analytical models using the 247 `metafor` package in R. The response variable was the standardised slope of the linear 248 density effect; because both individual network strength and density were scaled to have 249 mean of zero and standard deviation of one in the linear regression, this is equivalent to the 250 correlation coefficient (r) [43]. We converted all correlation coefficients into Fisher's $Z(Z_i)$ 251 and computed associated sampling variance. We then used an initial model that nested 252 observations within a system-level random effect to account for within- and between-system 253 heterogeneity [44], as 24/34 systems had more than one density effect. We used a random 254 effect for species to account for repeat observations per animal species.

We then added a separate random effect for animal phylogeny [45]. This used a phylogenetic correlation matrix of our 28 animal species derived from the Open Tree of Life via the `rotl` package [46], with the `ape` package used to resolve multichotomies and provide branch lengths [47]. We fitted the model using the `rma.mv()` function with restricted maximum likelihood (REML), weighted by inverse sampling variance, and used variance components to quantify l^2 , the contribution of true heterogeneity to the total variance in effect size.

262 We next fitted models with the same random effects structure that included explanatory 263 variables. To detect whether some animals were more likely to experience density effects, 264 we fitted Animal group as a factor with six categories, representing a combination of 265 species' taxonomy and general ecology: aquatic (fish and dolphins), birds, large herbivores 266 (elephants and ungulates), small mammals (rodents and hyraxes), carnivores, and 267 ectotherms (insects and reptiles). We also fitted several explanatory variables indicative of 268 greater statistical power that might increase the strength of density effects: Geographic 269 area (km², log₁₀-transformed), Number of years of study, and Number of individuals, all of 270 which we fitted as continuous covariates. Broadly, the animal group model was highly 271 uninformative and competed with the other effects, and we expected that the phylogeny 272 would be more informative, so we report the results of the model without the host group 273 effect fitted.

274 We ran several different versions of these meta-analyses: first, we fitted meta-analytical 275 models to the **overall linear models** of spatial and social interaction types separately, and 276 then together, to investigate differences between the spatial and social networks in terms of 277 their mean density slope. Next, we fitted duplicated versions of these models, but with the 278 saturation models. These models were identical, but each system replicate had two linear 279 estimates: one taken from the first 50% of the data (up to the median), and one to the latter 280 50%. By fitting a binary fixed effect of "data portion" to the meta-analytical models, this 281 model would tell us whether the slopes were generally higher in the first portion of the data 282 than the last (and therefore showed generally saturating shapes). We were unable to fit 283 meta-analytical models to our GAMMs, as methods capable of meta-analysing nonlinear 284 estimates are not yet well defined.



285

286 Figure 3: Meta-analysis revealed drivers of variation in linear density effects on individual network 287 connectedness across systems. A) Our fitted linear model estimates of density effects on network 288 strength. Each point represents the mean estimate from a given system; the error bars denote 95% 289 confidence intervals. Opaque error bars were significant (i.e., do not overlap with 0); transparent ones 290 were not. The estimates are in units of standard deviations for both density and network strength. The 291 colour of the point denotes whether the network being examined was defined using spatial or social 292 connections. B) Meta-analyses revealed that centrality in spatial networks (i.e., home range overlap; 293 red points) had a significantly steeper relationship with density than social networks (blue points). C) 294 When linear models were fitted separately to two portions of the data (values below and above the 295 median), the slopes for the latter portion (pink points) were generally less positive than the former 296 portion (purple points), implying a general saturation shape. In panels B) and C), each coloured point 297 represents a study replicate fitted to the strength estimate; points are sized according to sample size, 298 and jittered slightly on the x axis to reduce overplotting. The large black points represent the mean 299 slope estimated from the meta-analysis, and the error bars represent 95% confidence intervals.

	Multimammate mice	Multimammate mice	Falkirk wood mice Trap proximity	Liverpool wood mice	Liverpool wood mice	Silwood wood mice	
	Silwood wood mice	Wytham wood mice Co-trapping	Mountain Lake mice	HRO	Kielder voles Trap provinity	Prairie dogs GOG	
	Rum deer Dominance	Rum deer GOG	Rum deer	Soay sheep GOG	Soay sheep HRO	Cornish cattle HRO	
	Comish cattle proximity collar	Reticulated giraffes GOG	Reticulated giraffes	Moray dolphins Census	HRO	Potomac dolphins GOG	
	Firth of Tay dolphins Census	Firth of Tay dolphins	Shark Bay dolphins Cegsus	Shark Bay dolphins	European boar HRO	European boar proximity collar	
	Woodchester badgers Co-trapping	Wytham badgers Co-trapping	African dogs	African dogs proximity collar	Katahari meerkats	Kalahari meerkats	
	Ein Gedi hyraxes GQG	Kenyan elephants GOG	Konyan elephants	Golden-crowned sparow GOG	Golden-crowned sparow HRO	Wytham fits GOG	
	Wytham tits HRO	Acom woodpeckers	Acom woodpeckers	Utiturine guinearowi	Vulturine guineafowl	Desert tortoises Den sharing	
	Desert tortoises	Water dragons Census proximity	HRO	Sleepy lizards GPS proximity	Steepy lizards	Chagos sharks GOG	
	Palmyra sharks GOG	Palmyra sharks HRO	Moorea sharks GOG	Fighting	Wild crickets HRO	Wild cnckets Maging	
	Density						

Animal group
 Aquatic
 Bird
 Carnivore
 Ectotherm
 Large herbivore
 Small mammal

300

Cton on the

301 Figure 4: Relationships between density and network connectedness varied substantially across 302 animal systems. Density in individuals per area is on the x axis; network connectedness (strength 303 centrality) is on the y axis. Both values have been standardised to have a mean of zero and a 304 standard deviation of 1 within each system; the axis ticks are in units of 1 standard deviation. Each 305 point represents an individual-year-behaviour replicate; the lines portray the model fit from our GAMs. 306 Red lengths of the smooth=significantly positive; grey=not significantly different from zero; 307 blue=significantly negative. Points are semi-transparent to enhance visibility. Panels are arranged 308 phylogenetically following the tree displayed in Figure 2A; GOG=gambit of the group; HRO=home 309 range overlap. Supplementary Figure 2 shows a version of this plot with variable smoothing 310 parameters to show variation in the possible shape of the curves. Animal silhouettes are from 311 phylopic.org; a set of links and attributions are in the Supplement.

312 Results and Discussion

We compiled an unprecedented comparative meta-dataset of over ten million observations of individual animals' spatial and social behaviour, across an expansive range of ecological systems. We then ran a standardised pipeline to align their spatial and social observations, identifying strong and predictable relationships between local density and network connectedness at the individual level.

318 We observed strong positive relationships between individuals' local population density and 319 their connectedness in spatial and social networks across a wide range of wild animals: of 320 our 60 replicates, 48 (80%) were significantly positive when analysed using linear models 321 (Figure 3A; Supplementary Table 1). Meta-analyses identified a highly significant positive 322 mean correlation between density and connectedness, both for social networks (Estimate 323 0.22; 95% CI 0.16, 0.27) and spatial networks (0.45; 0.36, 0.53; Figure 3B). Our study 324 therefore provides fundamental evidence that high local population density broadly drives 325 greater connectedness within ecological systems, at the individual level. Slopes were highly 326 variable across systems for both spatial and social networks (Figure 3A; Q-test of 327 heterogeneity across systems: $Q_{35} = 5744.83$ and $Q_{23} = 1559.08$, both P<0.0001), indicating 328 that quantifying these slopes within and between multiple systems and comparing them is 329 important for understanding animal socio-spatial structure. That is, relationships between 330 density and individual connectedness differ substantially between populations, and the 331 biological mechanisms underlying these divergent trends are likely important. As well as 332 adding resolution and allowing comparisons of density effects across systems, our 333 methodology facilitated fitting of nonlinear relationships. This approach has only rarely been 334 applied before, and then at much coarser resolution (see [8,9,11]). As such, this study fills an 335 important empirical gap by providing insights into the slope and shape of density-336 connectedness relationships for a variety of animal groups and their social and spatial 337 behaviours (Figure 4). Nevertheless, we were able to identify several further general trends 338 in our data.

339 Remarkably, density's effect more than doubled in size for spatial compared to social 340 networks (Figure 3B; r=0.45 versus 0.22); there was a difference of 0.28 (CI 0.17, 0.38, 341 P<0.0001) for this effect when we meta-analysed the two contact types together. This finding 342 indicates that as density increases, wild animals are more likely to share space with each 343 other, but that social connections increase at a much slower rate. Similarly, we discovered 344 that saturating shapes were extremely common: as density increased, its effect on 345 connectedness decreased, such that 44/60 systems (73%) had a steeper slope at low 346 density values than at high ones. This effect was strong for social networks (effect on r= -347 0.11; CI -0.20, -0.03; P=0.01) and similar in size but marginally insignificant for spatial 348 networks (-0.14; -0.29, 0.01; P=0.058); due to the greater overall effect for space sharing, 349 the latter half of the density-spatial connections effect was still higher than the first half of the 350 density-social connections effect (Figure 3C). In fact, the second half of the social effect 351 overlapped with zero (Figure 3C; lower CI=-0.0119): that is, considering only the upper half 352 of density values would not have uncovered a significant effect of density on individuals' 353 connectedness in social networks. Together, these observations suggest that density-354 dependent processes act to limit the increase in social connectedness with density, but 355 without limiting spatial overlaps to the same extent. Consequently, higher-density areas are 356 characterised disproportionately by individuals asynchronously sharing space rather than

socially associating, while in lower-density areas individuals are disproportionately moresocially connected proportional to their shared space.

359 There are many possible social reasons for saturating nonlinearity in density-dependent 360 network structuring: for example, individuals in higher density areas may begin to avoid each 361 other, seeking to avoid competition or aggression [31] or exposure to infectious disease [48]. 362 Eastern water dragons (Intellagama lesueurii) show greater avoidance at higher densities 363 [13], supporting this mechanism. Alternatively, in species with high social cognition or stable 364 bonds, saturation could reflect lower social effort or ability to keep track of social affiliates at 365 higher densities [49]. In general, individuals likely have a preferred social interaction rate or 366 group size – a preference that they may increasingly exert at higher densities [7]. It remains 367 to be seen how this preference varies among individuals, and whether individuals vary in 368 their preferred social network position given a certain density. Given that individuals vary in 369 their movement and spatial phenotypes [50–52], and social phenotypes [52–54] in ways that 370 should manifest for density-dependent behaviours specifically [16], it seems likely that these 371 slopes could vary between individuals as they do between populations. Future analyses 372 might fit variable density-connectedness slopes between individuals to identify socio-spatial 373 syndromes across systems, as has been done previously in single systems including caribou 374 (Rangifer tarandus) [55] and red squirrels (Tamiasciurus hudsonicus) [56].

375 We considered spatial behaviours might explain these trends: for example, density could 376 create greater competition over resources and therefore reduce energy to roam (and contact 377 others). Individuals may partition their niches [57], or reduce their territory or home range 378 sizes [56,58,59], potentially driven by years of plentiful resources supporting higher densities 379 alongside smaller home ranges which could drive lower association rates. However, our 380 findings do not seem to support explanations related to small home ranges, because such 381 explanations should produce an equivalent or stronger reduction in (relative) spatial 382 connectedness. In contrast, we observed that density drove individuals to become spatially 383 connected faster than socially, such that the underlying mechanisms likely involve 384 behaviours and demographic processes that specifically affect social collocation in space 385 and time. Testing the precise underlying mechanism might require finer-scale behavioural 386 observations, as described below. Regardless of mechanism, these saturating density-387 connectedness relationships strongly support the idea that examining density effects at the 388 individual level – rather than between populations – is highly informative. For many systems, 389 "mean field" expectations of homogenous interactions under increasing density likely 390 produce an inaccurate (i.e., inflated) picture of density's effects.

391 The fact that spatial networks show stronger and more linear density dependence than 392 social networks is likely to have important implications for the ecology of wild animal 393 systems. For example, indirectly transmitted (i.e., environmentally latent) parasites may 394 exhibit greater density dependence than directly transmitted ones, given that individuals 395 likely experience disproportionately more indirect contact at higher densities. This 396 observation contrasts with orthodoxy that contagious parasites are most likely to be density 397 dependent [60], and supports the value of investigating nonlinear changes in socio-spatial 398 behaviour and grouping patterns in response to density when considering density 399 dependence. Saturating density-connectedness functions further have implications for 400 disease modelling and control. Rather than assuming constant behavioural mixing at higher 401 densities, epidemiological models could benefit from incorporating density-dependent shifts

402 in behaviours and demography that influence direct and indirect interaction frequencies, as 403 previously suggested empirically and by epidemiological theory [15]. These relationships 404 could influence our targets for culling or vaccination coverage [61]. Given that animals at 405 high density seem likely to have a relatively shallow relationship between density and 406 contact rates, reducing population density – for example via culling – might not be effective 407 at reducing pathogen transmission initially, particularly when considering socially transmitted 408 pathogens, where contact rates are particularly likely to have saturated (Figure 3C). Similar 409 problems with culling have already been acknowledged in specific systems - e.g. in canine 410 rabies [33,62,63] - but our study implies that shallow nonlinear density-contact trends could 411 be more general than previously thought and could be driven by flexible density-dependent 412 changes in behaviour and demographic processes.

413 Operationally, the common nature of saturating density effects will impact researchers' ability 414 to detect density dependence: that is, density dependence could be harder to observe in 415 higher-density areas given the shallower slopes we observed. Most of the systems in this 416 study are relatively long-term studies of known individuals; these populations tend to be in 417 carefully selected, high-density areas that make it convenient to study the focal animal with 418 relatively low operational costs. For example, it has previously been noted that the badgers 419 of Wytham Wood, the red deer of the Isle of Rum, and the Soay sheep of St Kilda are all at 420 high densities for their respective species [64-66]. As such, we may be inherently 421 investigating the upper end of density-connectedness relationships in the wild, and it could 422 be difficult and costly to investigate the effects of low density so widely.

423 Beyond these general trends, our GAMs revealed that 46/60 density effects on network 424 connectedness (77%) were significantly nonlinear ($\Delta AIC>2$); these relationships took a wide 425 variety of shapes, representing a range of nonlinear functions that are hard to generalise 426 (Figure 4; Supplementary Table 2). Notably, while many GAM smooths were eventually 427 significantly negative (Figure 4), the vast majority of linear models fitted to the second half of 428 the data were positive (Figure 3C); this result is likely an artefact of restricted model fitting, 429 rather than true downturns in connectedness with density. Nonlinearity did not cluster 430 according to connection type definitions, or according to host group. These observations 431 were largely corroborated by our meta-analytical models, which found no factors influencing 432 the slope and shape of density effects (P>0.05). This observation speaks to the complexity 433 of these relationships within and across systems, while accentuating that simple functional 434 relationships are often likely to be complicated by contravening ecological factors like habitat 435 selection [67,68], parasite avoidance [69], and demographic structuring [70]. While we were 436 unable to identify specific between-system predictors of nonlinearity of density-437 connectedness relationships, the finding that most such relationships are strongly nonlinear 438 is an important consideration for future work.

439 We acknowledge several limitations of our study, which we nevertheless believe could be 440 remedied in the future. First, many of our social networks were formed of general 441 spatiotemporal associations, and relatively few from specific social interactions – particularly 442 those involving direct physical contact. Our current dataset could therefore benefit from 443 supplementation with a broader range of direct interactions, particularly involving antagonism 444 or bonding. For example, datasets concerning aggression or dominance interactions (e.g. 445 [71]) or grooming alongside spatial behaviour could inform how density dependence affects 446 the transmission of certain parasites such as mycobacteria [72] or tattoo skin disease [73].

447 The meta-dataset was also unevenly distributed across animal taxa (Figure 1): there were 448 no primates or bony fishes and only one invertebrate, while rodents and ungulates were 449 over-represented. These biases likely emerge through differences in data collection 450 approaches: for example, although primate social behaviour is often studied with 451 observations of direct interactions that could augment our data as described above (e.g. 452 [74]), the spatial data required to build density distributions are rarely collected in these 453 systems. This is linked to their social structures: our workflow was best suited to studies of 454 fission-fusion societies or relatively asocial animals, rather than those with wide-ranging 455 fixed social groups that are more common in primate systems. Finally, given that our data 456 were observational, we could not account for (or estimate) bidirectional causality between 457 density and social relationships (point 4 in Figure 1): that is, as well as encountering more 458 conspecifics in areas of high density, individuals may be drawn to conspecifics, creating 459 areas of high density [16]. To do so might require creating in-depth, high-resolution models 460 of animal movement and group formation (e.g. [75]), potentially making use of telemetry 461 approaches and drawing from large-scale open movement repositories like Movebank [76].

462 Aside from incorporating more specific interaction types, there exist a range of potential 463 extensions to our analysis. For example, density dependence often varies between age or 464 sex classes (e.g. [77,78]), and age effects on infection are common and ecologically 465 important [79,80], as are sex differences [81]. We chose not to analyse how individual 466 animals' traits alter the shape or slope of density's effects for brevity and simplicity; however, 467 given that many of the systems nevertheless include these data, future analyses could make 468 use of this meta-dataset to investigate how density affects connectedness of different 469 classes of hosts. Further, researchers could investigate other behavioural questions such as 470 the role of observation biases; the factors influencing the correlation between spatial and 471 social networks; and the role of environmental drivers and spatial autocorrelation in driving 472 observed patterns of connectivity [12,16]. Finally, as our analysis approximated density-473 contact relationships and not host-parasite interactions specifically, important future work 474 could investigate whether contact rates (as approximated by network connectedness) 475 ultimately translate to greater infection risk or parasite burden. Although some previous 476 investigations have linked density-related metrics to aspects of infection [82,83], density 477 covaries with a range of other factors including nutrition, cooperation, and competition, all of 478 which could complicate density-driven increases in exposure [2]. For example, in the case of 479 ectoparasite transmission, although contact rates in general would likely increase with 480 density, so too might grooming behaviours that remove parasites; in cases such as these, 481 density's overall effect on ectoparasite infection may be neutral. In the future, verifying that 482 within- and between-population variation in density-contact relationships translate to 483 variation in infection – and whether these trends might be influenced by flexible avoidance 484 behaviours [37] – will be a vital part of understanding and predicting density-dependent 485 disease dynamics.

486 Density is a universal factor underlying the dynamics of animal populations, and its linear 487 and nonlinear effects on spatial and social network structure are likely to impact myriad 488 processes in behaviour, ecology, and evolution. Similar to other studies that have reported 489 general scaling patterns in network analysis [84] and in food web ecology [85], the patterns 490 we report strongly suggest that animal systems generally become better connected spatially 491 than socially under increasing density. These might extrapolate to human networks, given 492 that other scaling patterns in animal networks do [84]. As these patterns seemingly manifest

regardless of animal group and interaction type, they may reflect a generalisable rule
governing the socio-spatial structure of ecological systems. Further refining and
implementing these models could facilitate prediction of network structure in novel systems.

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503 Code availability

504 All R code is available at https://github.com/gfalbery/DensityMetaAnalysis.

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