1	Title: Quantifying species contributions to ecosystem processes: a						
2	global assessment of functional trait and phylogenetic metrics across						
3	avian seed-dispersal networks						
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29 Quantifying the role of biodiversity in ecosystems not only requires understanding the 30 links between species and the ecological functions and services they provide, but also 31 how these factors relate to measurable indices such as functional traits and 32 phylogenetic diversity. However, these relationships remain poorly understood, 33 especially for heterotrophic organisms within complex ecological networks. Here we 34 assemble data on avian traits across a global sample of mutualistic plant-frugivore 35 networks to critically assess how the functional roles of frugivores are associated with 36 their intrinsic traits, as well as their evolutionary and functional distinctiveness. We 37 find strong evidence for niche complementarity, with phenotypically and 38 phylogenetically distinct birds interacting with more unique sets of plants. However, 39 interaction strengths — the number of plant species dependent on a frugivore — were 40 unrelated to evolutionary or functional distinctiveness, largely because distinct 41 frugivores tend to be locally rare, and thus have fewer connections across the 42 network. Instead, interaction strengths were better predicted by intrinsic traits, 43 including body size, gape width and dietary specialisation. Our analysis provides 44 general support for the utility of traits in quantifying species ecological functions, but 45 also highlights the need to go beyond simple metrics of functional or phylogenetic 46 diversity to consider the multiple pathways through which traits may determine 47 ecological processes.

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#### 51 Introduction

52 Anthropogenic activity is driving a worldwide decline in the abundance and diversity 53 of species [1], threatening the functional integrity of Earths ecosystems [2, 3]. 54 Reliably predicting and thus mitigating against the effects of biodiversity loss, is 55 contingent upon a robust understanding of the contributions of species to the 56 functioning, stability and resilience of ecosystems [4, 5]. However, direct 57 measurements of such contributions are rarely available, leading to the widespread 58 use of functional traits and phylogenetic history as surrogates for species ecological 59 roles [6-11].

60 The use of trait-based and phylogenetic tree-based proxies is largely based on 61 the idea of niche complementarity, whereby species with similar functional traits and 62 thus partially overlapping niches are expected to perform similar, and to a certain 63 degree redundant, ecological roles [12, 13]. This theory predicts that the functional 64 contributions of species increase with their functional trait distinctiveness (hereafter 65 FD) relative to other members of the community [14]. Because closely related species 66 are expected to share similar traits, ecological redundancy is also expected to decrease 67 with species evolutionary distinctiveness (ED), typically quantified using 68 phylogenetic branch lengths [15]. As a result, for a given richness, assemblages 69 containing a greater functional or phylogenetic diversity of species are expected to 70 provide a greater variety and efficiency of ecological functions [12, 15-17]. 71 Spurred by a growing availability of phenotypic and phylogenetic data, the 72 idea that species functional roles can be quantified on the basis of FD or ED has 73 rapidly been incorporated into conservation biology [6-11]. However, the extent to

which simple metrics of functional and phylogenetic diversity provide reliable

75 surrogates for the functional integrity of ecosystems remains unclear for at least two

76 key reasons [4, 18, 19]. First, most theory and evidence for the effects of functional 77 diversity is based on experimentally assembled plant communities structured 78 primarily by competition [20]. The extent to which this framework generalizes across 79 naturally assembled ecosystems, comprising complex ecological networks of species 80 linked by different kinds of interactions (e.g. predation, mutualism) has yet to be established [19, 21]. Second, in addition to FD, species functional contributions are 81 82 also expected to vary due to differences in abundance [22, 23] and the possession of 83 particular intrinsic traits, such as large body size, that may confer a disproportionate 84 impact on ecological processes [24, 25]. These effects of abundance and intrinsic 85 traits have the potential to amplify, counteract or even reverse the positive effects of 86 FD, but we know little about how these different factors co-vary across species and 87 thus combine to determine species functional roles [26-28]. This is especially the case 88 across large, heterotrophic organisms that are generally not amenable to experimental 89 manipulation and where species ecological roles are difficult to quantify. 90 Here we address this issue, using frugivorous birds as a model system for 91 examining the links between FD and species functional roles. Seed dispersal by 92 frugivorous birds is an essential process in plant recruitment, especially in tropical 93 forests where co-evolution between fruiting plants and their seed dispersal agents is 94 most pronounced [29, 30]. Furthermore, many studies have demonstrated that the 95 mutualistic interactions between plants and frugivorous birds are strongly structured 96 according to several clearly defined and easily measured functional traits [31-34]. For 97 instance, while foraging height determines which plants a bird is likely to encounter 98 [33], morphological traits such as beak shape and body size influence the rewards and 99 handling efficiency of feeding on different fruits [31, 34]. This tight association 100 between traits and resource use, leads to the prediction that frugivores with more

distinct traits will perform more unique functional roles [21, 35] and, all else being
equal, will thus support a greater number of plant species within the network than
those frugivores with less distinct traits [36-38].

104 To test the extent to which FD can provide a surrogate for frugivore functional 105 roles we assembled a comprehensive database of avian functional traits across a 106 global compilation of plant-frugivore interaction networks (see table S1 for references 107 of the original studies). These networks collectively describe >58000 unique 108 interaction events across 546 species of birds and allow us to address the following 109 key aims. First, we examine how trait and phylogenetic similarity relates to the 110 dietary overlap between frugivores, and thus test the importance of niche 111 complementarity, a key assumption underlying the relationship between functional 112 diversity and function. Second, we conduct analyses examining how the functional 113 roles of frugivores within networks are related to their FD (and ED) as well as a 114 number of intrinsic traits for which an effect on function is expected. We quantified 115 species functional roles according to three quantitative network metrics relevant to 116 understanding the effects of FD, including the frequency of interactions [39], 117 interaction specialisation [40] and interaction strength — a measure of the number of 118 plant species dependent on each frugivore [41]. Finally, because direct estimates of 119 species abundance are not available for the networks we study, we examine the link 120 between species FD and abundance across a global database of avian communities 121 [42] using ED as a proxy for FD. Through this approach, we aim to provide a critical 122 and broad-scale assessment of the utility of functional traits as surrogates for the 123 ecological functions supported by frugivorous birds.

124

125 Methods

#### 126 (a) Avian seed-dispersal networks

127 We compiled from the literature a database of mutualistic networks describing the 128 visitation and feeding events between birds and fruiting plants. In total, we obtained 129 34 networks from 25 studies distributed across all the world's continents (except 130 Antarctica) (table S1). Of these networks, 23 are 'quantitative', recording not only the 131 presence or absence of interactions but also the number of individuals visiting each 132 plant species (i.e. visitation rate). Although interaction events are not synonymous 133 with seed-dispersal events [43], they are the best available proxy at this scale in the 134 absence of more detailed information on disperser effectiveness [26, 39]. To ensure 135 that we focused on species most likely functioning as seed dispersal agents, we 136 excluded known seed predators (species in the family Psittacidae, n = 23 species). The 137 functional traits included in this study are specific to birds, and thus we also removed 138 the small number of observations for non-avian frugivores (n = 43 species). Our final 139 database included a total of 58401 unique interaction events between 546 species of 140 birds and 1141 species of plants (table S1, database S1). 141

### 142 (b) Avian local abundance

143 Published seed-dispersal networks rarely contain information on species local

144 abundance. To assess how functional distinctiveness may be related to abundance, we

therefore downloaded count data for a global compilation of avian assemblages from

the online 'Ecological Register' repository (<u>http://ecoregister.org/</u>) [42]. This dataset

147 contains 166 avian assemblages, comprising 6976 count estimates from across 2344

148 species.

149 (c) Avian functional traits and phylogenetic relationships

150 For each avian species, we collected ten morphometric measurements, including 151 published estimates of mean species body mass (g) [44] and nine traits measured from 152 field collections and preserved museum skins (database S1). The nine traits measured 153 here (to the nearest 0.01 mm) were: beak length (two separate measures), beak width, 154 beak depth, gape width, tarsus length, tail length, wing length, and Kipp's distance, 155 the distance between the tip of the longest primary and the first secondary (see table 156 S2 for further details). Previous results indicate that these traits are robust proxies for 157 resource use, foraging manoeuvre and substrate [45]. Where possible, we obtained 158 measurements from at least two individuals from each sex for each species (n = 2665159 specimens, mean = 5 per species). Throughout, we used the LN-transformed mean 160 species values to calculate trait distances between frugivores.

Phylogenetic relationships among avian species were extracted from the Jetz et al [46] time-calibrated phylogeny assuming the Hackett backbone topology. To account for phylogenetic uncertainty, we conducted our analysis across 100 trees drawn at random from the posterior distribution.

165

## 166 (d) Testing for niche complementarity between frugivores

167 For each pair of species in each network we quantified an inverse measure of

168 interaction similarity using the Horn-Morisita distance (d<sub>HM</sub>). For each network we

169 then calculated the Spearman rank correlation ( $\rho$ ) between d<sub>HM</sub>, species phylogenetic

170 patristic distance and Euclidian trait distance. We compared the observed correlation

- to that expected under a null model of random network structure (1000 replicate
- 172 simulations) in which interactions between birds and plants were randomly re-

assigned while maintaining the exact species degree (i.e. number of partners) of each

174 node, using the 'permatfull' function in the R package Vegan [47]. We calculated the

175 standardised effect size of observed ρ values (i.e. the z-score) and quantified the

176 number of networks exhibiting a significant positive or negative z-score. We assessed

177 the overall significance of a departure from null model expectations using a t-test (p =

178 0.05, two-tailed test). To ensure that our results are robust to the quality of network

data and null model assumptions, we repeated our analysis using only quantitative

180 networks (n = 23 networks, database S2). In this case, the null model maintained the

181 observed frequency of interactions for each node [48].

182

183 (e) Quantifying species functional roles

184 We quantified the roles of frugivores within the network using three complementarity

185 metrics, focusing on quantitative networks (n = 485 observations from 320 species),

186 which provide the most robust information on species interactions [49].

i) Visitation rate: the number of interactions performed by a species represents
a major quantitative constraint on species functional impact [26]. Although this metric
ignores any potential differences in the 'quality' of dispersal agents, these effects may
generally be outweighed by the large observed variation in visitation rates [39].

191 ii) Specialisation (d'): we quantified the degree of specialisation of each 192 frugivore using the standardised Kullback-Leibler distance [40]. This metric of 193 specialisation varies from 0 (generalist) to 1 (specialist), and accounts for differences 194 in visitation rates both across frugivores and plants. Specifically, frugivores that 195 deviate from a random sampling of available interaction partners by preferentially 196 interacting with otherwise rarely visited plants are deemed more specialised. 197 iii) Species weighted interaction strength: The strength of the interaction 198 between frugivore species *i* and plant species *j* is calculated as the number of visits by

frugivore *i* to plant *j*, divided by the total number of visits to plant *j* [41]. A higher

interaction strength indicates a greater dependency of plant *j* on frugivore *i*, and the
sum of these values for each frugivore thus provides an integrated measure of its
quantitative impact on the plant community.

203

204 (f) Identifying the predictors of species functional roles

205 We examined a number of potential predictors of visitation rates, specialisation d' and 206 interaction strength. We quantified species functional trait distinctiveness (FD) 207 relative to other members of the network using three standard metrics: i) the mean 208 trait distance (MTD), ii) the mean nearest neighbor distance (MNTD), and iii) the 209 distance to the centroid of trait space (CenD). These metrics quantify different aspects 210 of distinctiveness that are expected to influence network roles in different ways. In 211 particular, while MTD and CenD quantify the departure from the average trait value 212 of a community, MNTD is more sensitive to the effects of niche partitioning between 213 the most ecologically similar species [50]. Based on phylogenetic data, we quantified 214 the evolutionary distinctiveness (ED) of species both globally (between all bird 215 species) and locally (between members of the network) using the equal splits (EDES) 216 and fair proportions (EDFP) measures [51]. We account for phylogenetic uncertainty 217 using the mean species ED value from across 100 phylogenetic trees drawn at random 218 from the Bayesian posterior distribution.

We compared the effects of FD and ED to a number of intrinsic traits proposed to influence frugivore functional roles, including the degree of obligate frugivory, average foraging height, body mass and gape width. We extracted gape width measurements (mm) and body mass (g) from our dataset of morphological traits. The degree of obligate frugivory (%) was obtained from an independent dataset containing the percentage contribution of fruit, as well as six other food types

225 (invertebrates, vertebrates, carrion, seeds, nectar and 'other plant material'), to 226 species' diets [44]. We also used this dataset to calculate species foraging height as 227 the weighted mean across five ordinal levels (1 [ground], 2 [understorey], 3 228 [midstorey-lower], 4 [midstorey-upper] and 5 [canopy]). Finally, previous evidence 229 suggests that geographically rare species may be more functionally distinct [7], and so 230 we also included geographic range size, calculated by overlaying species breeding 231 extent of occurrence maps on an equal area grid (cell resolution of 110 km  $\approx$  1° at the 232 equator) [52]. Terms exhibiting a positive skew were LN-transformed and all 233 predictors were normalised to enable a direct comparison of effect sizes. 234 Species within networks are not independent and networks from the same 235 region may share similar characteristics. We therefore modeled species functional 236 roles using linear mixed-effects models, fitted in the R package lme4, including 237 'region' (typically corresponding to countries), 'network' and 'species' as random 238 effects. We also included 'avian family' as a random effect to ensure that any 239 significant relationships are not driven by individual clades. Finally, we accounted for 240 over-dispersion in the residuals of our model predicting visitation rates by including 241 an additional observation level random effect [53].

242 We tested the predictors of interaction strength and specialisation following 243 LN and angular transformation respectively. For visitation rate, we used a generalised 244 linear mixed model, assuming a Poisson error structure. When predicting visitation 245 rates we accounted for difference in overall sampling intensity across networks by 246 including the total number of observed interaction events as an offset term. Because 247 interaction strengths will also vary due to sampling intensity and species richness, we 248 standardised species scores relative to the maximum value observed in each network. 249 Predictor terms were assessed both in isolation and in combination using multi-model

250	averaging [54]. Specifically, we calculated the AIC of models including every
251	combination of predictors and then used model AIC weights to calculate average
252	effect sizes, significance and relative variable importance. Metrics of FD and ED
253	provide alternative measures of distinctiveness and so we fit five different model sets,
254	one for each metric. Finally, because gape width and body mass (Pearson correlation $r$
255	> 0.8) are strongly correlated we fit separate models for each of these variables.
256	
257	(g) Quantifying the relationship between distinctiveness and abundance
258	We tested the relationship between the local abundance of species in each assemblage
259	and local ED (LN-transformed) using a generalised linear mixed effects model,
260	assuming a Poisson error structure and including 'assemblage', 'species', 'avian
261	family' and observation level random effects. We also calculated the correlation
262	coefficient between ED and local abundance within each avian assemblage to
263	examine how this relationship varies as a function of species richness and across
264	geographic space.
265	
266	Results
267	
268	(a) Functional trait-based complementarity of frugivore niches
269	We found that dietary distance $(d_{HM})$ between avian frugivores was positively
270	correlated with trait dissimilarity (figure 1, table S3). Of the 34 networks, 27 exhibited
271	a positive standardised effect that was significant in 14 cases $[p < 0.05]$ , strongly
272	rejecting a null model of random network structure (t-test: $t = 4.87$ , $p < 0.001$ ).
273	Phylogenetic distance was positively associated with trait distance (33 of 34 networks
274	exhibited a positive slope, mean correlation = $0.42$ ; table S3) and accordingly, we also

275 detected a significant positive relationship between d<sub>HM</sub> and phylogenetic distance (t-276 test: t = 3.77, p < 0.001; table S3). These results were largely robust to the type of 277 network and null model used. When we focused exclusively on quantitative networks, 278  $d_{HM}$  remained positively correlated with both trait (t-test: t = 3.06, p = 0.006) and 279 phylogenetic distance (t-test: t = 1.82, p = 0.08), although the latter relationship was 280 marginally non-significant (table S4). 281 (b) The relationship between functional traits, visitation rates and 282 abundance 283 284 The strongest predictor of visitation rates was the degree of obligate frugivory, with 285 specialist frugivores undertaking more visits than dietary generalists (figure 2, table 286 S5). Although visitation rates increased significantly with foraging height when 287 assessed in isolation, this term was not significant in a multi-predictor model. In a 288 single-predictor model, visitation rates decreased significantly with FD according to 289 the MTD metric. However, when we accounted for the degree of obligate frugivory in 290 a multi-predictor model, all FD (except CenD) and local ED metrics were strongly 291 negatively associated with visitation rates. In contrast to local distinctiveness metrics, 292 Global ED was unrelated to visitation rates (figure 2, table S5). 293 In accordance with the patterns of visitation rates, species abundance in avian 294 assemblages was negatively associated with local ED (slope = -0.36, P < 0.001, n =295 6976 records). This negative relationship was globally consistent and evident across 296 88% of assemblages (figure S1). 297

298 (c) The relationship between functional traits and specialisation

Specialisation (d') increased with FD, an effect that was strongest when quantified
using the MTD metric (figure 2, table S5). d' also increased significantly with body
mass. This latter effect appears to arise because of the covariation between body mass
and MTD, because when including both terms in a multi-predictor model only MTD
retained its significant effect. All other intrinsic traits had low variable importance
scores and were not significant predictors of d' (figure 2, table S5).

305

306 (d) The relationship between functional traits and interaction strength

307 Obligate frugivory and body mass were the strongest predictors of species interaction

308 strengths, indicating that large-bodied specialist frugivores have the highest

309 quantitative impact in the network (figure 2, table S5). Although interaction strength

310 increased significantly with gape width when assessed in isolation, this term was no

311 longer significant when accounting for other covariates. Importantly, across both

312 single and multi-predictor models, interaction strength was not significantly related to

313 either FD or ED. In fact, most distinctiveness metrics exhibited a weak negative

association with interaction strength that was marginally non-significant in the case of

315 MTD (figure 2, table S5).

316

### 317 Discussion

Our analysis of the functional and phylogenetic structure of avian frugivore networks provides support for trait-based niche complementary between species, a key pattern thought to underpin the positive relationship between functional trait diversity and ecological function. In particular, we found that closely related frugivores with similar functional traits consistently interact with more similar sets of plants, while distantly related birds with distinct traits exhibit relatively little overlap in resource use. In

accordance with this, our analysis showed that frugivores with distinct traits also tend
to be more functionally specialised, interacting with plants that are less frequently
visited by other members of the community. The importance of functional trait
matching in structuring interactions within plant-frugivore networks is well
established [31-34, 55] [56], and our analysis across multiple networks, regions and
ecosystems, further highlight the utility of functional traits as general predictors of the
overlap and specialisation of these mutualistic interactions.

331 The pattern of niche complementarity that we report here is expected to lead to 332 a positive relationship between FD and species functional contributions, because 333 species with distinct traits should be less ecologically redundant [21]. We found that 334 functionally distinct birds do tend to feed on less frequently visited plants, suggesting 335 that species per capita impacts may indeed increase with FD. However, our analysis 336 also shows that this does not translate into stronger interaction strengths and thus 337 higher quantitative impact at the species level because functionally distinct species 338 tend to undertake fewer interactions overall (i.e. have lower visitation rates). As a 339 result, on average, plants were no more dependent on interactions with functionally 340 distinct frugivores than they were on species with seemingly more redundant traits. 341 This lack of relationship between FD and species interaction strength was true 342 regardless of the metric used to calculate FD or whether we employed ED as a proxy 343 for trait distinctiveness.

One possible explanation for the decline in visitation rates with FD is the occasional inclusion in the networks of distinct and distantly related species from other trophic guilds that rarely feed on fruit. However, this is unlikely to explain our results, because we found that the negative effects of FD on visitation rates actually became stronger when we statistically accounted for the degree of obligate frugivory

349 and other intrinsic species traits. Visitation rates are expected to strongly reflect 350 underlying differences in species abundance [39] and thus an alternative explanation 351 is that the decline in visitation rates with FD is driven by a lower abundance of 352 distinct species within local assemblages. Here, using phylogenetic relatedness as a 353 proxy for trait similarity, we reveal this trend in birds at a global scale by showing 354 that locally evolutionary distinct species consistently occur at lower densities than 355 those species coexisting with many close relatives. Thus, our results suggest that the 356 quantitative impacts of frugivores are independent of FD, because the positive effects 357 of reduced ecological redundancy are nullified by a corresponding decrease in 358 abundance.

359 A lower abundance of species with distinct functional traits has been 360 demonstrated in assemblages of plants and reef fish [7, 57] and a similar trend of 361 declining visitation rates with FD has also recently been reported for insect pollinators 362 in New Zealand [50]. The processes driving these trends are unclear, but trait-363 dependent environmental selection provides a likely candidate [58]. In particular, we 364 speculate that if certain trait combinations are unfavorable in the local environment, 365 then these trait values will be represented by both few individuals and species. While 366 this negative relationship between abundance and trait distinctiveness is not included 367 in traditional biodiversity-ecosystem function theory [12], our results suggest that it 368 may be sufficient to decouple FD from the functional impacts of frugivores within 369 seed-dispersal networks.

Although species interaction strengths were generally unrelated to metrics of
functional diversity, we detected a significant effect of intrinsic functional traits,
notably obligate frugivory, body size and gape width. Previous studies have suggested
that obligate frugivores play an important role as 'network connectors' because of

374 their nutritional requirement to feed on multiple different fruits [59]. In contrast, our 375 analysis shows that frugivory is unrelated to interaction specialisation, and that the 376 stronger interaction strengths of obligate frugivores is instead likely due to their 377 higher feeding rates. The positive contributions of body size and gape width to 378 interaction strength also make sense. While plants producing small fruits can be 379 dispersed by a wide variety of birds, only large-bodied frugivores with wide gapes are 380 able to disperse the fruits of large-seeded plants [31]. The primary importance of 381 large-gaped frugivores for seed-dispersal has previously been shown [60] and our 382 analysis extends this finding across different avian assemblages, highlighting the 383 status of large-gaped species as what might be termed 'network keystones'. 384 Furthermore, large-bodied specialist frugivores also appear highly sensitive to human 385 pressures, being the first to disappear following habitat degradation [25], suggesting 386 that even the loss of only a few frugivore species may have a disproportionate impact 387 on the maintenance of seed-dispersal services.

388 Metrics used as surrogates for ecosystem function in conservation biology 389 generally only consider the functional and phylogenetic diversity of species and rarely 390 account for species abundance or intrinsic functional traits (e.g. [8-11]). This is 391 because, at such broad spatial and taxonomic scales, information on abundance is 392 generally unavailable while the relationships between intrinsic traits and ecosystem 393 functions are generally unclear. However, abundance and intrinsic traits are known to 394 exert major constraints on species functional effects [22, 27, 28], and our results 395 suggest that standard functional and phylogenetic diversity metrics ignoring these 396 aspects of assemblage structure may misrepresent the diversity of interactions 397 supported by avian frugivores [61], and within ecological networks more generally 398 [50].

399 These conclusions are subject to a number of caveats. First, we have focused 400 on how functional traits relate to the present day quantitative impacts of species 401 within networks. In contrast, the functional resilience of networks is likely to also 402 depend on network topological plasticity and the ability of species interactions to be 403 're-wired' following extinction [62]. It seems likely that species with distinct traits are 404 generally less functionally substitutable than those with more redundant phenotypes, 405 although this remains conjecture until further empirical evidence has been compiled 406 from 're-wiring' events. Second, birds mediate a number of critical ecological 407 processes beyond seed dispersal, including pollination, predation and nutrient 408 recycling [63]. Our results therefore do not preclude the possibility that a positive 409 effect of functional distinctiveness on function may emerge when considering 410 multiple ecological processes (i.e. multi-functionality) [17]. Finally, our meta-analysis 411 examining the quantitative component of seed-dispersal networks assumed that higher 412 interaction strengths translate into larger functional impacts [26, 39], which may not 413 always be the case given the potential for interspecific variation in the effectiveness of 414 avian dispersal agents [43].

415 Broad-scale comparative analyses of how functional traits and phylogenetic 416 metrics relate to the functional roles of species provide an important perspective in 417 helping to translate the results of detailed experimental studies to reliably predict, and 418 thus mitigate, the consequences of species loss in natural ecosystems. However, these 419 efforts remain preliminary and the robustness of any conclusions drawn at this scale 420 will depend on the quality and relevance of the ecological data used to quantify 421 species functional roles. Our analysis using data on frugivore-plant interaction 422 intensities confirms a general pattern of trait-based niche complementarity across 423 networks, but nonetheless suggests that functional trait diversity may provide a

- 424 relatively weak surrogate for frugivore functional roles. A more detailed examination
- 425 of the links between functional diversity, abundance, and ecological processes is a key
- 426 priority for future research.
- 427
- 428

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430

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- 437

### 438 Data accessibility statement

- The data used in this study has been deposited in Data Dryad database S1
- 440

#### 441 Author contributions

- 442 AP devised the research, TB, CS, BD compiled data, AP performed the analyses, AP,
- 443 RE and JAT wrote the paper.

444

#### 445 **Competing Interests**

446 There are no competing interests.

447

# 448 Ethics Statement

449 NA

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Figure 1. Functional trait-dependent structure of mutualistic seed-dispersal networks. Observed correlations between dietary  $d_{HM}$  and functional trait dissimilarity (circles) across the 34 empirical networks compared to the expectations under the null model (horizontal bars indicate 95% confidence interval). Filled circles indicate correlations that are stronger than expected under the null model.



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657 Figure 2. Functional trait and phylogenetic predictors of species network roles 658 quantified on the basis of visitation rates, interaction specialization d' and interaction 659 strength (n = 485). Results are shown for both univariate (U) and multivariate (M) 660 models. M1-M4 denote models of interaction strength including various combinations 661 of visitation rate and d' as predictors. Circle colour denotes positive (magenta) or 662 negative (green) trends and statistical significance (dark: p < 0.05; light: p > 0.05). 663 Circle size is proportional to the absolute effects size scaled relative to other 664 predictors in each model. 665 666