1 Omnidirectional and omnifunctional connectivity

2 analyses with a diverse species pool

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Abstract 22

23 Connectivity among habitat patches in both natural and disturbed landscapes needs to be 24 accounted for in conservation planning for biodiversity maintenance. Yet methods to assess 25 connectivity are often limited, because simulating the dispersal of many species is 26 computationally prohibitive, and current simulations make simplifying assumptions about 27 movement that are potentially erroneous. Here we show how these limits can be circumvented 28 and propose a novel framework for the assessment of omnifunctional and omnidirectional 29 connectivity in a 28000 km2 area in the Laurentian region of Québec, Canada. Our approach 30 relies on (i) the use of Omniscape, an improved version of Circuitscape which allows 31 omnidirectional simulations that better emulate animal movement and (ii) the synthesis of large 32 volume of species-level dispersal simulations through a posteriori clustering of the current 33 intensity. Our analysis reveals that the movement of 93 species evaluated can be clustered into 34 three functional dispersal guilds, corresponding to mostly aquatic species, terrestrial species able 35 to use aquatic environments, and strictly terrestrial species. These functional guilds do not share 36 connectivity hotspots, suggesting that corridor planning would need to account for the 37 multiplicity of dispersal strategies. Although this approach requires a large volume of computing 38 resources, it provides richer information on which landscape features are critical to maintain or 39 need to be regenerated for broader biodiversity maintenance goals.

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Keywords : Circuitscape, Functional Dispersal Guilds, Landscape connectivity, Omniscape,

Introduction 41

42 Natural ecosystems are facing unprecedented threats as a function of both direct and indirect 43 anthropogenic disturbances, leading to a global and accelerating decline in biodiversity (Hooper 44 et al., 2012; Merino et al., 2019). Some of the main threats to biodiversity maintenance are the 45 joint effect of reduced area of natural habitat and connectivity loss among different habitat 46 patches across the landscape (Thompson et al., 2017). It reduces population size, gene flow, and 47 diversity, which in turn can lead to inbreeding and local extinction (Jackson and Fahrig, 2011). It 48 can also prevent species from reaching new suitable habitats, and therefore limits their chance of 49 both survival (Smith et al., 2013) and adaptation to climate change (Nuñez et al., 2013). A 50 possible solution is to establish ecological corridors between protected areas (Rayfield et al., 51 2011), or more broadly to facilitate movements across the landscape at large spatial scales 52 (McRae Brad H. et al., 2008). As ecosystems are home to multiple species with different needs 53 and behaviours, it is essential that these corridors be multifunctional, *i.e.* that they account for the 54 fact that the ability to move across a landscape is perceived differently by different species 55 (Albert et al., 2017). Corridors that are well planned and implemented have the potential to 56 promote survival, migration, and preserve small populations, for a large number of species 57 (Smith et al., 2013). Indeed, they are essential for successful biodiversity maintenance in the 58 long-term.

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In order to establish new ecological corridors, several methods to assess connectivity have been
developed in recent years. Belote et al. (2016) selected corridors with a least-cost path analysis
across the continental US, using Linkage-mapper (McRae et al., 2011). Cote et al. (2009) used

63 graph theory to assess structural connectivity of the Big Brook river drainage network (Terra 64 Nova National Park, Newfoundland, Canada): lakes were nodes linked by river reaches. Finally, 65 McRae et al. (2008), created Circuitscape, which used circuit theory to quantify the possibility of 66 crossing each territorial patch and tested this for Caspers Wilderness Park in California. Despite 67 a large variety of accessible techniques, most studies focused on the needs of terrestrial species 68 only (Appendix 1). Indeed, according to Correa Ayram et al. (2016), only 7% of connectivity 69 studies were conducted on fluvial habitats, while terrestrial ecosystems represent 88% of 70 research efforts on this topic between 2000 and 2013. However, without proper consideration of 71 connectivity to freshwater habitats (lakes and rivers), downstream health of river reaches could 72 degrade and critical riparian wetlands could dry up, resulting in both terrestrial and freshwater 73 biodiversity loss (Herbert et al., 2010; Smith et al., 2013). These ecosystems are naturally 74 integrated through their watersheds (Ballinger and Lake, 2006), therefore we argue that this is 75 the most ecologically relevant unit in which connectivity should be assessed.

76 To evaluate landscape connectivity for entire communities, it has been suggested to analyse a 77 territory's features according to the needs of a diverse number of terrestrial and aquatic species 78 (Albert et al., 2017; Sahraoui et al., 2017). It should lead to a more robust and realistic output, as 79 a small number of focal species seldom encompass the whole range of dispersal behaviours (Liu 80 et al., 2018; Marrotte et al., 2017; Meurant et al., 2018). However, because multi-species 81 analyses are complex (Moilanen et al., 2005), most efforts have often relied on the movement of 82 a limited number of species (see Appendix 1). Moreover, according to Correa Ayram et al. 83 (2016), there is a great redundancy of the species selected for the connectivity analyzes.

84 Mammals alone would represent 41% of the analyzes, mammal carnivores more than 20%. One 85 of the issues with assessing connectivity across multiple types of habitats is that it requires to 86 merge the results of several species-level connectivity analyses, to account for the variety of 87 ways in which different species react to different types of landscape elements (Albert et al., 88 2017). When done with a large number of organisms, this imposes a double burden. One is to 89 reconcile the connectivity of possibly dozens of indicator species, not all of which may have 90 unbiased habitat use models (Olden et al., 2002). The other is having the computational capacity 91 to actually carry out this analysis. As the later is becoming less of a problem with increased 92 computational power and more diversified software offering to carry out connectivity 93 simulations, developing a general framework to include connectivity across ecosystem types, 94 with a diverse set of species, is an achievable and timely task.

95 A few studies have recently developed methods to aggregate multiple species-specific analyses 96 in a single result. For example, Albert et al. (2017) and Sahraoui et al. (2017) selected 14 and 16 97 eco-profiles respectively, each composed of one or more species, in order to represent a broader 98 range of dispersal behaviours and habitat requirements. These eco-profiles were designed 99 through dimensionality reduction based on species connectivity and habitat needs, either using 100 clustering or multivariate analysis. In another effort, Santini et al. (2016) selected all the 20 non-101 volant mammal species of Italy that had a dispersal ability of a median of 3 km to identifying 102 defragmentation priorities. The three studies have created composite maps by summing the 103 single-species results or by calculating the mean score for each patch of habitat. Santini et al 104 (2016) went even further by testing seven other ways to merge the species-specific maps, using

105 weighted means of different landscape features to assess link probabilities, and two different 106 summation types for nodes in the network. These studies have demonstrated that it is possible to 107 create connectivity analyses for a large number of species, which may be ecologically more 108 relevant. Indeed the results could be meaningful for decision-makers, helping them to target new 109 protection areas, restore others, and inform more sustainable strategies in city development 110 projects (Ersoy et al., 2019). Despite these successes, they remain limited by three key aspects. 111 First, even a pool of 20 species cannot represent the entire functional diversity of realistic 112 communities. Second, selected species pools continue to under value the contribution of semi-113 aquatic species and their habitats to landscape connectivity. Furthermore, freshwater biodiversity 114 is considered the most imperiled globally (Hendriks, 2016), suggesting that the need to include 115 aquatic and semi-aquatic species is urgent. Finally, because species clustering is done before the 116 simulations, this assumes that species connectivity depends on habitat requirements alone and 117 neglects differences that could emerge due to landscape configuration.

118 In this study we present a general framework for multi-species connectivity analysis, built 119 around the needs to (i) integrate terrestrial and aquatic ecosystems (Herbert et al., 2010), (ii) use 120 an ecologically relevant number of species to capture the diversity of ways in which species 121 interact with their landscape (Meurant et al., 2018), and (iii) provide measures of uncertainty 122 after different analyses have been merged. By contrast to previous studies relying on a priori 123 clustering of dispersal guilds (Lechner et al., 2017; Sahraoui et al., 2017) we propose an a 124 posteriori method for the creation of composite indicator species-guild. Our approach accounts 125 for the way species are predicted to move across the landscape by looking for similarities in their

- 126 dispersal simulations, rather than in the cost matrix of these species. We argue that this new way
- 127 of interpreting and post-processing connectivity simulations will result in a more integrative
- 128 view of landscape connectivity to favour biodiversity maintenance in the long-term.

130 Methods

131 Study area

We assessed our new connectivity approach using a 27 994 km² area located on the north shore 132 133 of the St. Lawrence River, near the city of Montréal, Québec, Canada (Fig. 1). Seven major 134 rivers are included in this region, and the area sits on two strikingly different geological 135 provinces, the Saint Lawrence lowlands, dominated by agriculture and urban areas, and the 136 Canadian Shield, covered largely by pristine temperate forests with a very high density of lakes 137 and rivers (19.8%). This high aquatic surface supports the need to account for more semi-138 aquatic species in our simulations. This region was chosen because it shows a strong gradient of 139 anthropogenic disturbance, with heavy urbanization and agricultural development to the south, 140 major highways on the north-south axis, many roads, large forested areas particularly on the 141 Shield where there is an active forestry industry, some major National Parks (Mont Tremblant, 142 Oka, la Mauricie), and several small cities that service a large cottage industry. Moreover, 143 biological surveys conducted by conservation agencies and different government bodies resulted 144 in the creation of a curated list of species, which we integrated in this analysis.

145 Selection of species

In order to select the species for this study, two lists of recorded species from the main National
Parks were used (SEPAQa, 2019; SEPAQb, 2019). We kept 45 mammals, all amphibians (16)
and 9 reptile species, plus 15 avian species with a conservation status. We added five more avian

- species, two amphibians and one reptile, which have been recorded in GBIF and Ebird databasesince 2000, for a final list containing 93 species (see Appendix 2).
- 151 Collecting species habitat preference data

From the list of focal species, we got information on habitat preference and the way they move across the landscape. Since these data are very heterogeneous, we gathered them from several sources. We used data from the IUCN Red list (IUCN, 2019.), identification guides of Quebec fauna (Desroches and Rodrigue, 2018 ; Prescott and Richard, 2014) and expert-curated websites for the herpetofauna ("aarq | EcoMuseum," 201.) and the avian fauna (Écopains d'abord, 2019.) The complete cost matrix for all species is given in **APPENDIX 2**.

158 Creating the resistance maps

159 **Resistance maps** are a mix between energetic landscape and habitat quality modelling. They 160 represent the energetic and ecological cost to cross a certain plot as a function of its configuration (topography, human structures) and composition (land cover) (Table I) (McRae 161 162 Brad H. et al., 2008). Matching preference data with the information on the land cover and 163 human structures present in the area allowed us to create a landscape resistance canvas for every 164 species, where 0 represents the absence of resistance and 100 the most important obstacle to 165 dispersal. Resistance maps are the sums of every spatial feature that could influence a species 166 dispersal.

167 According to the resistance canvas, we created the different layers composing the final resistance 168 map, using Qgis 3.4 (Qgis Development Team, 2019). We began with the land cover layer, 169 formed by thousands of polygons of 18 habitat types (agglomeration, crops, coniferous forest, 170 herbaceous wetland, etc.). To transform it into a resistance layer, we integrated the resistance 171 score of each species, to each type of land cover in the layer's data (Appendix 2). This is the 172 basic landscape features which influence species dispersal. In order to assess landscape 173 complexity to its fullest extent, we added the effect of slope, buildings presence, waterbodies, 174 roads, trails, and railways (Appendix 2) on species dispersal. For the roads, we have accounted 175 for their effect on a broader scale (150 m), with the resistance score decreasing according to the 176 distance from the road (Forman and Alexander, 1998). For the "slope" layer, we have considered 177 the degree of the slope as the degree of resistance (a slope of 50 degree equals a resistance of 178 50). Indeed, slope is known to have an impact on species displacement movement (Gaudry et al., 179 2015; Leblond et al., 2010).

In order to create a resistance map by summing the layers for each species, we converted vector resistance layers to raster layers. We first chose to use square cells at a resolution of 2 meters², which represents the smallest disturbance width considered in this study, hiking trails. Then, for each individual species, we summed the resistance layers corresponding to their canvas, which produced the 93 species-specific resistance maps. The resistance score of each cell represents the sum of all landscape features, according to the species dispersal behaviour canvas.

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187 Table 1 – Compilation of the data use, their type, resolution, the possible scores attributed to and their source

| | Vector or | Scale / | | |
|-----------------|-----------|------------|----------------------|-------------------|
| Variable | Raster | Resolution | Possible scores | Source |
| Hydrological | | | | NTDB + National |
| network | Vector | 1:50 000 | 0, 25, 50, 75 or 100 | Hydro Network |
| Dames | Vector | 1:50 000 | 100 | NTDB |
| Slope | Raster | 1:50 000 | 0 to 59 | NTDB |
| Road Network | Vector | 1:50 000 | 0, 25, 50, 75 or 100 | NTDB |
| Railway network | Vector | 1:50 000 | 0, 25, 50, 75 or 100 | NTDB |
| | | | | Land Cover, circa |
| Land cover | Vector | 1 : 50 000 | 0, 25, 50, 75 or 100 | 2000-Vector |

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189 Analyzing landscape connectivity using Omniscape

190 We analysed species-specific resistance maps in OmniScape 0.1.2 (McRae et al., 2016), 191 implemented with julia 1.2.0 (Bezanson et al., 2015). OmniScape uses a round sliding windows 192 approach to connectivity simulations, which amounts to assuming that the species is aware of its 193 immediate surroundings, but not of the entire landscape. Indeed, species use the landscape 194 without knowing it entirely, which is assumed by the least-cost analysis (McRae Brad H. et al., 195 2008). We used three different radiuses (30, 60 or 120 blocks, each block being a square parcel of 180m²), and averaged the quantiles of the cumulative current map for all. This resulted in 196 197 connectivity scores ranging from close to 0 (specifically the inverse of the number of simulated 198 pixels) to 1. The choice to examine quantiles as opposed to raw cumulative current values was

199 driven by the fact that although different species will disperse at different rates (and therefore 200 will have different total cumulative currents), quantiles provide information as to their relative use of the landscape. This would therefore facilitate the search for functional dispersal guilds. 201 202 Note that for some applications, analyzing the normalized current (*i.e.* the cumulative current 203 divided by the potential flow, as in *e.g.* McRae (2008), which is to say measuring how *surprising* 204 the observed current is compared to a null expectation) is preferable, notably for corridor 205 mapping or the identification of dispersal bottlenecks. In this analysis, we focus on how 206 organisms could disperse in the landscape, and therefore use the cumulative maps.

All simulations were performed on the beluga supercomputer, operated by Calcul Québec; the project required an estimated total of 3 core-years to complete, being roughly equivalent to 3 years of time on a single-core machine.

210 A posteriori functional dispersal guilds

211 After all the simulations were complete, we aggregated the maps using fuzzy C-means (C. 212 Bezdek, 1981; Dunn, 1973). This approach allows to have species contribute to more than a 213 single cluster (for example, species that are terrestrial but have an affinity for water will have 214 landscape use that borrows from strictly aquatic and strictly terrestrial species), as captured by 215 the fuzziness parameter. Following community-established best practices, we set this parameter 216 to 2. Specifically, we applied fuzzy C-means by transforming all the connectivity scores into a s 217 by p matrix, with s the number of species and p the number of pixels with non-null connectivity 218 values, then by calculating the s by s Euclidean distance matrix between all pairs of species. We extracted the centers of every cluster, and the species with the highest weight was the most representative species for the dispersal guild. It may therefore be used as an indicator species in the future. In addition, the weight of each species for each cluster can be used to measure species specificity; we used PDI (Poisot et al., 2012) as a specificity estimator, which has the desirable property of returning values that are lower than 0.5 for generalist species, and values above 0.5 for specialist species.

Fuzzy C-means lacks an established way to optimize the number of clusters[12]. As our goal is to identify functional dispersal guilds that move across the landscape in different ways, we relied on a simple heuristic to identify the optimal grouping. Fuzzy C-means results in a c by s matrix, where c is the number of clusters; every column in this matrix is therefore the contribution of all species to a cluster. Based on this information, we computed a c by c correlation matrix between clusters, and retained the solution in which no pair of clusters had a positive significant correlation.

232 Uncertainty analysis

To produce the final connectivity map, we averaged the scores for the centroids of the clusters identified in the previous step, measured the standard deviation within each pixel, and finally measured the coefficient of variation and Pielou's evenness within each pixel. The average connectivity gives an idea of dispersal potential, and the coefficient of variation and evenness informs about the areas in which the guilds differ markedly in their landscape use. In addition, in keeping with the Aichi objectives (SCBD, 2011), we mapped the best 17% of pixels (*i.e.* with the

- highest connectivity scores), using the average connectivity map as well as the map for every
- dispersal guild.

242 **Results**

243 Guild clustering

244 From the 93 connectivity maps created, the fuzzy C-means identified an optimal fuzzy 245 partitioning into three functional dispersal guilds (FDG henceforth), whose most representative 246 species are the Horned grebe (Podiceps auratus, Linnaeus, 1758) (FDG1; fig. 3a), (FDG2; fig. 247 3b), the American black bear (Ursus americanus, Linnaeus, 1758) and Northern Two-lined 248 Salamander (Eurycea bislineata, Green, 1818) (FDG3; fig. 3c). All of these guilds share a very 249 poor connectivity score in the lowlands (although FDG3 can use some of the wooded areas for 250 east-west traversal), and differ in how they use the rest of the study area. In particular, FDG3 251 tends to have almost unrestricted movement outside of the lowlands, while FDG2 is predicted to 252 be more canalized in some places. Interestingly, while the two guilds for the more terrestrial 253 species were not correlated (rho = 0.054), they were both correlated negatively to the cluster with 254 more aquatic species (rho approx. -0.7 in both cases). This reveals not only that the needs of 255 aquatic and semi-aquatic species are different, but that favoring terrestrial species only in 256 connectivity planning will impede the movement of semi-aquatic species. The complete 257 clustering result, including specificity analysis, is given in Appendix 3. Applying PDI on the 258 clustering weight identified 15 generalist species, including notably the Canada Lynx (Lynx 259 canadensis, Kerr, 1792) (PDI = 0.45), moose (Alces Alces, Linnaeus, 1758), (PDI = 0.44), Red-260 headed woodpecker (*Melanerpes erythrocephalus*, Linnaeus, 1758) (PDI = 0.27), and Hoary bat 261 (Aeorestes cinereus, Beauvois, 1796) (PDI = 0.42). Whereas specialist species, or species with

high affinity for a specific FDG can be good indicator species, generalist species can provide an
overall view of landscape connectivity.

Average connectivity and variation

265 As expected, the St-Lawrence lowlands performed uniformly worse in terms of connectivity, 266 with nevertheless some areas running parallel to the shore that can work as dispersal avenues (fig 267 3a), though these are mostly used by FDG3. Even in the more forested areas it is strikingly easy 268 to identify more developed regions or axes, corresponding to highways connecting the island of 269 Montréal to smaller clusters of anthropogenic activity. With the exception of these areas, the 270 region is remarkably well connected overall. The coefficient of variation and Pielou's evenness 271 for connectivity reveals areas in which the needs of species that favour either aquatic or 272 terrestrial habitats are more difficult to reconcile (fig 4b, 4c). This includes, trivially, the St 273 Lawrence river itself, but also areas surrounding large water bodies such as the Lac Taureau to 274 the North. It should be noted that although both the coefficient of variation and Pielou's evenness 275 provide a similar information (namely, the homogeneity in the use of every pixel by the three 276 FDGs), the later is a more appropriate measure. Although widely used, the coefficient of 277 variation performs better on ratio scales, whereas the quantiles of dispersal, being bounded, are 278 expressed on an interval scale.

279 Best-connected pixels

In fig. 5a, we represent the 17% of pixels with the highest *average* connectivity, which can be thought of as forming the basis for a dispersal network across the region, independent of guilds.

| 282 | This information should be contrasted to fig. 4b, in which we show the spatial distribution of the |
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| 283 | best 17% of pixels for each of the different FDGs and superimposed them. Because the guilds |
| 284 | are optimized to maximize the differences between them, their most connected areas rarely |
| 285 | overlap. As a result, protecting the top 17% of pixels for all guilds combined would cover up to |
| 286 | three times more surface than the best 17% pixels on average. Furthermore, note that very few |
| 287 | aquatic habitats would be protected using the average classification as a target. |
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291 **Discussion**

292 We have simulated the dispersal of 93 species across a 220 by 230 km area in the Laurentian 293 region of Ouébec. We then classified the multi-model average of connectivity maps using Fuzzy 294 C-means, to provide a regional average (Fig. 4a). Based on this result, we identified areas of 295 higher uncertainty (Fig. 4b, 4c) as well as candidate indicator species for each of the three 296 Functional Dispersal Guilds (FDGs). We found that connectivity is lower in the St Lawrence 297 Lowlands, which is more impacted by anthropogenic activities, and generally better in the 298 forested areas of the Canadian Shield. Although this result was expected, our approach was the 299 first to assess connectivity across such a large heterogeneous landscape, by accounting for the 300 full taxonomic diversity of both terrestrial and semi-aquatic species. Furthermore, these species 301 belong to different guilds representing three emergent dispersal landscapes that coexist within 302 the study region. Conservation actions that may neglect the protection of a specific guild due to 303 poor representativity of indicator species could have overall negative consequences on the 304 biodiversity maintenance of the entire region. Indeed, semi-aquatic, which form a guild on their 305 own, are often neglected.

We have used fuzzy C-means to cluster the species into FDGs, as it represents a more objective approach in which species are able to contribute relatively among dispersal guilds. Indeed, we identified about 16% of species classified as generalists that contribute in similar proportions to all FDGs. Under a non-fuzzy scheme, this information would be lost as species would be forced into one guild only. This being said, as we show in fig 6, the results of the fuzzy C-means

311 algorithm are directly comparable with a hierarchical clustering using Ward's agglomeration on 312 the pre-squared distance matrix. Although simple hierarchical clustering would have led to the 313 same dispersal guilds, the rich information of the movement of generalists species among guilds 314 could only be achieved using the fuzzy C-means approach.

315 Clustering returns groups of species based on predicted dispersal, and therefore represents a 316 process to select indicator species within each guild. By contrast, the *a priori* selection of 317 indicator species risks either underrepresenting or over representing different dispersal modes. 318 This is a particularly concerning issue, since as we illustrate in fig 4, the identification of the 319 most connected pixels varies greatly depending on whether the FDGs, or the average 320 connectivity, are used. Knowing the importance of the choice of representative species, the more 321 ecologically relevant *a posteriori* clustering should be favored, especially given that this amount 322 of simulations is computationally feasible. Indeed, among the 93 species used in this study, several that would be considered "terrestrial" only, were found to benefit from freshwater 323 324 habitats for travel and therefore clustered differently. For example, this was notably the case for 325 the clustering of moose (Alces alces, Linnaeus 1758) with the common garter snake 326 (Thamnophis sirtalis, Linnaeus 1758) and many avian species, among others. This 327 counterintuitive association demonstrates that with regards to landscape connectivity, our 328 preconceived ideas of species groupings do not apply.

329 Despite the large diversity of species and their habitat preferences, fuzzy C-means identified an 330 optimal grouping of three functional dispersal guilds only. Surprisingly this is a lower number of 331 classes than most multi-species simulations have been using, and so it calls into question whether

332 using more species would have led to pseudo-replication, or to over-representing the needs of 333 some groups of organisms. Previous methods to suggest surrogate species for connectivity 334 modeling also resulted in a larger number of species (e.g. between 5 to 7 for Meurant et al. 335 2018). We argue that the number of species guilds should not be determined *a priori*, since these 336 classifications would rely only on between-species differences in habitat preferences, and would 337 not be able to account for how these differences interact with the spatial configuration and 338 habitat diversity in the landscape. Therefore we suggest our approach be used with the largest 339 number of species available, particularly in biophysically complex and species rich landscapes.

340 Once initial clustering is made, the entire species list may no longer be required for subsequent 341 simulations carried out for the same region. In a context such as a predicting the effect of land-342 use or climate change on connectivity, which would involve many thousands of simulations, one 343 strategy would be to identify the most representative species for the optimal number of FDGs, 344 and then use these indicator species in the simulations. While this results in the loss of some 345 information, this offers a reasonable compromise between the effort to identify relevant species 346 in initial computationally intensive analysis, and the effort to perform projections of future 347 connectivity maps. Additional schemes to pick a subset of species to work on should be 348 evaluated on a case by case basis and can involve picking a mix of specialist and generalist 349 species.

Here we provide, to our knowledge, the most robust and fully integrated terrestrial and aquatic multi-dispersal connectivity assessment at a regional scale. We used a broad suite of diverse taxa in a heterogeneous landscape structured by a number of different anthropogenic disturbances

353 across two major geological provinces. The integration of the multiple dispersal pathways 354 provides a robust connectivity conservation plan and our approach offers a road map for future 355 connectivity assessments. Given the ongoing biodiversity crisis, identifying and implementing corridors to maintain habitat connectivity for conservation for as many species as possible is 356 357 increasingly urgent. Yet, current conservation strategies often neglect the diversity of ways in 358 which species actually use the landscape, since they focus largely on terrestrial species. For 359 example, as a worst case scenario, habitat patches crucial to the dispersal of a specific functional 360 group would not be adequately protected; this connectivity loss for an entire subgroup of species 361 could have a cascading effect with the potential to destabilize the entire ecosystem.

362 **Data availability:** Data will be deposited on DataDryad upon acceptance.

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- 374 DLT and TP performed the analyses, all authors contributed to study design and writing.

375 Figure legends

Figure 1 - Study area, on the North Shore of the Saint Lawrence river, province of Québec,
Canada. A. Oka National Park B. Mont-Tremblant National Park C. La Mauricie National Park
D. Lac Taureau. The study area is astride two geological provinces, the Saint Lawrence
Lowlands (yellow) and the Canadian Shield (green).

380 Figure 2. - Representation of the overall method flow. For each species (93), landscape layers 381 features got scored between 0 and 100 for their resistance (1). Then, the layers were converted in 382 a raster format to be summed, which created one resistance map by species (2). Following this 383 step, the maps were analysed using Omniscape, which created connectivity maps (3). We 384 assigned to each pixel its quantile in the observed map of the cumulative current for the species 385 (4) and conducted a clustering fuzzy C-means analysis on the unfolded 93 connectivity map to 386 get the *a posteriori* dispersal guilds (5). After the clustering, we extracted the weighted centroids 387 of each cluster (6) and measured the additional indices (evenness, variation, location of the most 388 connected pixels) (7).

Figure 3 – Connectivity scores for the three different guilds. Higher values indicate more potential for movement. St. Lawrence Lowlands have areas with medium connectivity potential for FDG1 and FDG2 but are globally lowly connected and do not have real potential to facilitate the movement of species from FDG3. The Canadian shield, however, show high connectivity potential for the three guilds, especially FDG2. A. FDG1 – Species of open and undisturbed habitats B. FDG2 – Species of forested habitats C. FDG3 – Species of freshwater habitats

395 Figure 4 – Representation of the Average connectivity score (A), Coefficient of variation (B) and 396 Pielou's evenness (C) A. Average connectivity across the three functional guilds. The St. 397 Lawrence Lowlands have a lower connectivity overall, though some more intact habitats running 398 parallel to the shore allow for traversal. B. Coefficient of Variation across the three FDGs (n=3), 399 corrected for small sample size by a coefficient of (1+1/4n). Values on the map have been 400 capped at 1, as values larger than unity are generally regarded as noise. C. Pielou's evenness 401 across FDGs. Note that the color scale has been inverted, to reflect the fact that high values 402 correspond to more similar connectivity across FDGS.

403 Figure 5 – Spatial distribution of the best 17% of pixels with the highest average connectivity
404 (A) and the best 17% of pixel for all guilds combined (B). The pixels in panel B cover
405 approximately 40% of the entire territory, suggesting that the three functional guilds have very
406 high complementarity.

Figure 6 – Comparison between Ward's clustering (A) and the Fuzzy C-Means (B) results. Both
methods identify three distinctives groups of dispersal behaviour (guilds), but only Fuzzy Cmeans allows to uncover the fact that some species are actually generalists.

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