

1 **A methodological roadmap to quantify animal-vectorized spatial ecosystem subsidies**

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3 Diego Ellis-Soto<sup>1,2+</sup>, Kristy M. Ferraro<sup>3+</sup>, Matteo Rizzuto<sup>4</sup>, Emily Briggs<sup>3,5</sup>, Julia D. Monk<sup>3</sup>, Oswald  
4 J. Schmitz<sup>3</sup>

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6 1 Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, USA

7 2 Center for Biodiversity and Global Change, Yale University, New Haven, CT, USA

8 3 School of the Environment, Yale University, 370 Prospect Street, New Haven, CT, USA

9 4 Department of Biology, Memorial University of Newfoundland St. John's, Canada

10 5 Department of Anthropology, Yale University, New Haven, CT, USA

11 Corresponding author: [diego.ellissoto@yale.edu](mailto:diego.ellissoto@yale.edu)

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13 + These authors contributed equally to this work

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17 stoichiometry, remote sensing

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19 **Abstract**

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Ecosystems are open systems connected through spatial flows of energy, matter, and nutrients. Predicting and managing ecosystem interdependence requires a rigorous quantitative understanding of the drivers and vectors that connect ecosystems across spatio-temporal scales. Animals act as such vectors when they transport nutrients across landscapes in the form of excreta, egesta, and their own bodies. Here, we introduce a methodological roadmap that combines movement, foraging, and ecosystem ecology to study the effects of animal-vectored nutrient transport on meta-ecosystems. The meta-ecosystem concept — the notion that ecosystems are connected in space and time by flows of energy, matter, and organisms across boundaries — provides a theoretical framework on which to base our understanding of animal-vectored nutrient transport. However, partly due to its high level of abstraction, there are few empirical tests of meta-ecosystem theory, and while we may label animals as important mediators of ecosystem services, we lack predictive inference of their relative roles and impacts on diverse ecosystems. Recently developed technologies and methods — tracking devices, mechanistic movement models, diet reconstruction techniques and remote sensing — have the potential to facilitate the quantification of animal-vectored nutrient flows and increase the predictive power of meta-ecosystem theory. Understanding the mechanisms by which animals shape ecosystem dynamics may be important for ongoing conservation, rewilding, and restoration initiatives around the world, and for more accurate models of ecosystem nutrient budgets. We provide conceptual examples that show how our proposed integration of methodologies could help investigate ecosystem impacts of animal movement. We conclude by describing practical applications to understanding cross-ecosystem contributions of animals on the move.

44 **Introduction**

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46 **Ecosystems and animal nutrient cycling**

47

48 Flows of energy, nutrients, matter, and organisms crisscross landscapes worldwide, connecting  
49 intrinsically open ecosystems over space and time. The advancement of meta-ecosystem  
50 theory (Loreau *et al.* 2003; Leroux & Loreau 2008; Massol *et al.* 2011; Marleau *et al.* 2014) has  
51 aided our understanding of the influence of these spatial exchanges in both donor and recipient  
52 ecosystem functioning (Gounand *et al.* 2018b). Classic ecosystem theory holds that the spatial  
53 flow of organic and inorganic matter from source to recipient locations is largely passive, coming  
54 for example from *in situ* weathering of parent geological material, release from riverine  
55 sediments, wind-born dust, or rain-driven and snowmelt-driven run-off (Chapin *et al.* 2012).  
56 Nevertheless, there is growing appreciation that ecosystems also receive subsidies via animal  
57 movement (Vanni, 2002; Atkinson, Capps, Rugenski, & Vanni, 2017; Schmitz *et al.*, 2018;  
58 McInturf, Pollack, Yang, & Spiegel, 2019). Such movement can result in an influx of new prey or  
59 predators to recipient locations, pulses of animal-transported nutrients in dung and urine, or the  
60 accumulation of organic matter via decomposition of carcasses deposited in recipient locations  
61 (henceforth, animal-vectored subsidies; Earl & Zollner 2017; McInturf *et al.* 2019). Whenever  
62 biotic—such as animal-vectored subsidies—or abiotic processes influence the structure and  
63 functioning of ecosystems, they are deemed ecosystem controls (Weathers *et al.* 2012). Theory  
64 predicts that animals can exert top-down control on ecosystems via subsidies, the magnitude of  
65 which could sometimes be equal to bottom-up (Leroux & Loreau, 2008; Allen & Wesner, 2016).

66

67 Increasingly, migratory populations of large bodied species are recognized for playing an  
68 especially important role as landscape-scale vectors of ecosystem subsidies (Bauer & Hoyer  
69 2014). Yet at the same time, across the globe, their populations are in decline (Wilcove &  
70 Wikelski 2008; Dirzo *et al.* 2014) and their movement is increasingly constrained by human  
71 activities (Tucker *et al.* 2018). The implications of such effects on top-down control over  
72 ecosystem functioning at broad spatial scales remain uncertain, but estimates suggest they can  
73 be substantial (Doughty *et al.* 2016). Hence, an important avenue of new research in ecosystem  
74 ecology is empirically resolving the relative importance of animal-vectored vs. passive subsidies  
75 on ecosystem functioning. We are at an opportune scientific and technical juncture to begin  
76 synthesizing advances made in disparate fields.

77

78 The empirical challenge in understanding and attributing how much control animals exert over  
79 ecosystem functioning is to quantify spatial flows of different kinds of animal-vectored subsidies  
80 (i.e. excretion, egestion, carcass deposition, reproductive material). While theory is in place to  
81 identify the different components that need measuring to obtain a coherent understanding of this  
82 phenomenon (Leroux & Loreau, 2008; Earl & Zollner, 2017; Gounand et al. 2018; Schmitz et al.,  
83 2018), it remains largely conceptual and offers few insights into how to operationalize empirical  
84 measurement. Here, we address this limitation by offering a methodological road map that  
85 discusses the various measurements that need to be integrated to develop a coherent picture of  
86 the quantitative effects of animals on nutrient dynamics across ecosystems. There is now  
87 unprecedented ability to characterize functional and structural properties of ecosystems  
88 including topography, vegetation community composition, and habitat structure across vast  
89 spaces (Bergen *et al.* 2009; Pettoirelli *et al.* 2018). Likewise, movements of a wide range of  
90 animal species can be monitored remotely (Kays, Crofoot, Jetz, & Wikelski, 2015; Wilmers et  
91 al., 2015a), which can facilitate quantification of the net effects of animals on nutrient and  
92 material transport. New DNA-based and isotopic analyses can resolve dietary nutrient sources.  
93 Additionally, these nutrient sources and fates can be mapped spatially using nutrient distribution  
94 modeling (West et al. 2010; Sitters *et al.* 2015; Leroux *et al.* 2017). While ripe for integration,  
95 these methods and technologies continue to be deployed separately in research that examines  
96 different components of animal movement and resource use within ecosystems. We show here  
97 how these different methods can be used jointly to give a coherent, theory-driven understanding  
98 of the ecosystem consequences of animal-vectored nutrient flows across landscapes.

99

## 100 **Materials and Methods**

101

### 102 **Meta-ecosystem models to understand animal-vectored subsidies**

103

104 The series of measurements we discuss are motivated by ecological theory on meta-ecosystem  
105 dynamics. A multitrophic version of such an ecosystem model can be used to consider how  
106 internal dynamics of ecosystems are connected by regional flows of materials and organisms  
107 between the ecosystems (Marleau *et al.* 2014). To identify the processes that need to be  
108 measured, we consider a model configured as a four trophic level food chain (Fig. 1), which  
109 describes the dynamics of a single abiotic nutrient or element (N), a plant (P), a herbivore (H),  
110 and a carnivore (C) within and between  $i$  local ecosystems that together create the meta-  
111 ecosystem. This structure is intended for simple illustrative purposes to show how to relate the

112 dynamical systems model to the salient ecosystem and spatial processes that need to be  
113 measured. The model can be made more complex by considering multiple nutrients to make it  
114 stoichiometrically explicit (Leroux *et al.* 2012; Cherif & Loreau 2013) as well as multiple species  
115 among trophic levels (McCann *et al.* 2005). Such granularity is beyond the scope of this paper.  
116 Instead, we use this theoretical framework specifically to identify salient processes (and inherent  
117 variables) that need to be measured to obtain a quantitative understanding the role of animals in  
118 connecting and shaping the structure and functioning of local ecosystems across spatial scales.  
119 The model reveals two salient processes that need to be considered: trophic interactions and  
120 nutrient translocation and deposition. These two processes can be subdivided into five more  
121 finely resolvable spatial components (Fig.1) that require detailed measurement. Hence, our  
122 roadmap focuses on measuring these five components.

123  
124 Trophic interactions within ecosystem  $i$  determine nutrient uptake and assimilation by  
125 herbivores and carnivores (Fig. 1) that may vary in size, and habitat structure within an  
126 ecosystem determines species spatial occurrences and the nature of their interactions (Schmitz  
127 *et al.* 2017). Thus, an accounting of animal spatial interactions will require analysis of: (1) the  
128 spatial extent and spatial grain size for analysis of the focal animal species and their  
129 interdependent predators or prey/resources (i.e., spatial trophic food chain structure) in relation  
130 to (2) the habitat structure within and between source and recipient local ecosystems. Moreover,  
131 animals can be selective in their choice of resources, necessitating further spatial analyses of  
132 (3) the resources selected by animals in source and recipient locations. Nutrient translocation  
133 and deposition in ecosystems will depend on (4) the movement rates and directional spatial  
134 flows of animal species and animal-vectored nutrients, and (5) the amounts and spatial  
135 deposition rate of animal transported nutrients or materials, which can include the animals' own  
136 body mass, waste products, reproductive material, and dispatched prey. Each of these  
137 components can be measured with its own set of technologies (Fig. 2). We next provide a brief  
138 review of these tools and of their potential use in the context of measuring animal-vectored  
139 subsidies.

140

#### 141 **(1) Spatial trophic structure**

142 The first step to understanding how animal movement shapes ecosystems is to describe the  
143 geographic domain over which focal animals roam and their trophic position within food chains,  
144 including the scope of interactions with predators and resources (Fig. 2). These factors will  
145 determine the geographic area and spatial grain of interest, the animals' habitat domain within

146 that area, and any ecosystem effects the animal could have within said domain through  
147 cascading impacts on associated food webs. The habitat domain is the spatial extent of habitat  
148 space used within a species' broader home range that is relevant to interspecific interactions,  
149 e.g., areas used for foraging or avoiding predation (Schmitz *et al.* 2017).

150  
151 Characterizing the spatial grains at which animals interact with other species and their  
152 environment is crucial to understanding their distributions. Animal movement can be described  
153 at fine spatial scales (e.g. responses to environmental resources such as foraging [see section  
154 3]) or at coarser scales, such as their broad home range (introduced in section 4) (Mertes *et al.*  
155 2020). Fine and coarse spatial grains have been termed “response grain” and “occupancy  
156 grains”, respectively (Mertes *et al.* 2020). To quantify an animal’s response grain, first passage  
157 time analysis can be employed. These are defined as the time it takes an animal to cross a  
158 circle with a defined radius -- and as such scale dependent -- and can quantify the time duration  
159 of an individual animal present within such a circle (Fauchald & Tveraa 2003). First passage  
160 time allows estimating the spatial scale at which an individual animal focuses its search efforts  
161 (i.e. by plotting variance in first passage time against the spatial scale, Fauchald & Tveraa 2003,  
162 Fig. 2 bottom left panel). As such, hierarchical scales of animal habitat selection (Johnson 1980;  
163 Mertes & Jetz 2017; Mertes *et al.* 2020) should drive the spatial resolution of remote sensing  
164 products selected for analysis, not the other way around. This is especially relevant for animal  
165 movement data, which are typically measured at finer spatio-temporal resolutions than data  
166 from remotely sensed imagery (Remelgado *et al.* 2017, 2019). The habitat domain can be  
167 measured using movement data by tracked individuals across a landscape, to calculate an  
168 animals utilization distribution and probabilities of spatial locations associated with foraging and  
169 migration behaviour across a landscape (Schmitz *et al.* 2017). A three-dimensional utilization  
170 distribution could be estimated if vertical movements are tracked, e.g. movement in forest  
171 canopies (McLean *et al.* 2016).

172  
173 Species interactions can alter animal movement behaviour, which can in turn impact ecosystem  
174 nutrient dynamics (Schmitz, Hawlena, & Trussell, 2010; Schmitz *et al.*, 2018). Hence  
175 consideration of the amount and spatial domain of animal vectored subsidies needs to consider  
176 species embeddedness within food chains. Moreover, such consideration will enhance the  
177 appreciation that animal vectored subsidies can trigger the rearrangement of food chains or  
178 initiate novel trophic interactions (Montagano *et al.* 2019). Generally in this context, primary  
179 producers have a trophic position of 1, primary consumers have a trophic position of 2,

180 secondary consumers have a trophic position of 3, and so on (Leroux & Loreau 2012). Yet there  
181 are many animals that occupy trophic positions between these discrete designations. For  
182 example, an omnivore may consume mostly primary consumers, but also some secondary  
183 consumers and therefore have a trophic position between 2 and 3 (Kelson et al 2020). We  
184 discuss how stable isotopes may be used to determine trophic position in section 3, which is  
185 important to resolve the nature and source of nutrients (e.g. largely plant-based vs. largely  
186 animal-based) that comprise subsidies (see section 3, Kelson et al. 2020).

187

## 188 **(2) Habitat structure within and between source and recipient locations**

189

190 Habitat structure and topographic features, within and between source and recipient locations,  
191 shape animal movement and nutrient transport within habitat domains (Leroux & Loreau, 2008;  
192 Gounand, Little, Harvey, & Altermatt, 2018; Schmitz et al., 2018). A spatially accurate  
193 characterization of these fundamental ecosystem attributes is key to understanding why, how,  
194 and where animals move over the landscape (Fig. 2). Earth observation via satellite, airborne,  
195 or drone imagery provides an important basis for developing such a characterization (Allan *et al.*  
196 2018; Pettorelli *et al.* 2018). Remotely sensed landcover maps (i.e. forest, grassland, urban) can  
197 be used to delineate ecosystem boundaries and assess how these change through time.  
198 Advances of LiDAR (Light Detection and Ranging) make it possible to characterize vertical  
199 habitat structure and above-ground vegetation biomass within and across ecosystem  
200 boundaries. Furthermore, ecosystem productivity can be remotely measured and represented  
201 as vegetation indices (de Araujo Barbosa *et al.* 2015; Pettorelli *et al.* 2018). Topographic  
202 products, such as slope and topographic ruggedness (Amatulli *et al.* 2018), can resolve passive  
203 abiotic flow pathways to pinpoint where nutrients may end up on the landscape (e.g., flow down  
204 concave and into convex surfaces; Lindeman, 1942; Leroux & Loreau, 2008). Finally, LiDAR  
205 estimates are becoming available from the Global Ecosystem Dynamics Investigation (GEDI)  
206 mounted on the International Space Station, which measures forest structure and above-ground  
207 biomass density across the globe (Hancock *et al.* 2019)

208

209 More finely resolved structure can be obtained within habitats using hyperspectral technologies  
210 to collect hundreds of bands across the electromagnetic spectrum which distinguish unique  
211 'fingerprints', referred to as spectral signatures for different kind of environmental features  
212 (Stuart *et al.* 2019). Such spectral signatures can be related to spatial patterns in plant  
213 functional diversity, vegetation elemental composition, and plant density (Knyazikhin *et al.* 2013;

214 Jetz *et al.* 2016; Schneider *et al.* 2017; Durán *et al.* 2019). Further, endmember extraction from  
215 multispectral imagery can be used to extract information on subpixel features, e.g., to identify  
216 signatures of water availability and abundance (Xie *et al.* 2016) .

217  
218 Remotely sensed environmental products have different pixel resolution, commonly referred to  
219 as 'grain size'. Accessing and utilizing a plethora of remote sensing products is facilitated  
220 through geoprocessing tools such as Google Earth Engine, the Movebank Env-Data system,  
221 and the getspatialdata package (Pettorelli *et al.* 2014; Clark *et al.* 2016; Wegmann 2017). We  
222 list a collection of remote sensing products available to study ecosystem features across source  
223 and recipient locations in Table 1. Regardless of the product used, coherent understanding  
224 requires a grain size that aligns with the grain size of measurement of animal movement.

### 225 226 **(3) Resources available to and selected by animals in source and recipient locations**

227  
228 Characterization of species habitat domains and structure can next be used to determine why  
229 animals move where they do, and what resources they use in source and recipient locations  
230 (Fig. 2). This can be accomplished using resource selection functions (RSF; Boyce *et al.* 2002)  
231 and step selection functions (SSF; Fortin *et al.* 2005). Generally, these functions associate  
232 environmental variables with locations used by individual animals and compare these with  
233 randomly generated points representing locations available to, but not used by, them (Michelot  
234 *et al.* 2019). Both methods estimate the probability of animal presence as a function of  
235 environmental covariates. SSF can be used further to predict future movement paths of animals,  
236 while RSF predicts spatial patterns of species occurrences over spatio-temporal scales  
237 (Michelot *et al.* 2019). Parameters from SSF can highlight whether animals avoid or are  
238 attracted to certain landscape features or resources. For example, SSF analysis reveals that in  
239 Etosha National Park, Namibia, elephants avoided areas with high tree biomass and were  
240 attracted to water sources and grassland patches with long term patterns of productivity  
241 (Tsalyuk *et al.* 2019). This could indicate that waterholes and grasslands receive more animal-  
242 vectored subsidies from elephants when compared to steep areas or dense forests. Such  
243 behavioural information would improve mechanistic predictions of nutrient redistribution by  
244 these wide-ranging megafauna which are known to play a large effect on regional carbon  
245 budgets (Berzaghi *et al.* 2018).

246



247 Resource selection is a hierarchical process (Courbin et al. 2013). While RSF and SSF are  
248 broad-scale measures of animal movement and habitat use, more finely resolved measures are  
249 needed to understand which food items are used by animals and their nutritional values within  
250 different locations. This understanding of animal food consumption and eventual processing and  
251 deposition (in body material, or as urine and fecal matter) can provide an understanding of  
252 where and how nutrients removed from donor ecosystems end up in recipient ecosystems.  
253 Additionally, the identity of consumed resources directly impacts the quantity and quality of  
254 nutrients deposited by animals (Subalusky & Post 2018).

255  
256 Traditionally, dietary analyses have been performed based on physical dissection and  
257 microhistological analyses of stomach contents and fecal matter (Holechek et al., 1982, Joly,  
258 2018). These methods, however, often require either opportunistic sampling of carcasses or  
259 destructive harvesting of live animals. DNA-metabarcoding provides an alternative, as it allows  
260 for the identification of materials consumed using fecal matter alone (Kartzinel et al. 2015; see  
261 Deagle et al., 2019 for an overview of DNA-metabarcoding methods). DNA-metabarcoding can  
262 shed important insights into the trophic ecology of source and recipient sites, and how  
263 consumption, and thus acquisition and transport of nutrients, can change in time and space  
264 (Pansu et al. 2019). For example, Atkins et al. (2019) combined GPS tracking data of bushbuck  
265 (*Tragelaphus sylvaticus*) with DNA-metabarcoding of fecal samples to show that herbivores  
266 occupy new habitats and forage on novel food items after extirpation of their predators.  
267 Bushbuck presence further changed plant community composition (demonstrated by comparing  
268 plant composition in exclosure and control plots) (Atkins et al. 2019). A playback experiment of  
269 predator sounds was able to revert bushbuck behaviour as they perceived predation risk (Atkins  
270 et al. 2019).

271  
272 Stable isotopes, such as  $\delta^{15}\text{N}$ ,  $\delta^{13}\text{C}$ , and  $\delta^{18}\text{O}$ , are also powerful tools in elucidating the trophic  
273 position (Ben-David et al., 2012), diet, and foraging location of a focal species in a non-invasive  
274 manner (Newsome et al. 2010; Kristensen et al. 2011). In general animals are enriched by  $\sim 3\%$   
275 of nitrogen and  $\sim 1\%$  of carbon compared to what they eat, providing an estimate of trophic  
276 position (Post 2002). Therefore, trophic position can be discerned by using the isotopic  
277 signature (i.e.  $\delta^{15}\text{N}$ ) of the consumer, of the ecosystem's primary producers, and a  
278 discrimination factor for the change in  $\delta^{15}\text{N}$  enrichment between the ecosystem's trophic levels  
279 (Kelson et al. 2020). Using stable isotopes could also be a cost-effective way to identify the  
280 correct primers when conducting DNA-metabarcoding. For example, while white-tailed deer are

281 primarily herbivores, there is some evidence that they sometimes consume animal matter (Ellis-  
282 Felege *et al.* 2008). If stable isotopes revealed that deer have an omnivorous diet, DNA-  
283 metabarcoding could be used to discern exactly what animal material they consumed.

284

285 Stable isotopes can also be used to arrive at approximate estimates of diet. The isotopic  
286 signatures of food items (for example, C3 and C4 plants) often vary from one another.  
287 Therefore, examining the isotopic signature in bone, tooth, or feces has shown a successful  
288 method of coarsely understanding diet (Ben-David & Flaherty 2012). We recommend using  
289 stable isotopes to determine diet if DNA-metabarcoding is not financially possible, when using  
290 samples that have degraded and DNA-metabarcoding is no longer possible, or when a broad  
291 understanding of diet is sufficient for the question at hand For an extensive overview of using  
292 stable isotopes for ecological research, see Ben-David & Flaherty (2012), Hobson *et al.*, (2019),  
293 and West *et al.* (2010).

294

#### 295 **(4) The movement rates and directional patterns of animal species and subsequently** 296 **translocated nutrients**

297

298 Animals can transport nutrients along and against biophysical gradients (Earl & Zollner, 2017;  
299 Mcinturf *et al.*, 2019). Therefore, an understanding of animal movements will elucidate the  
300 nature and scale of consequent nutrient transfer (Fig. 2). Patterns of animal movement are  
301 directly related to the degree of connectivity ( $c_{ij}$ , Fig. 1) among local ecosystems as well as the  
302 movement rates of the animals ( $d_H$ ,  $d_C$ , Fig. 1), which depend on the topography of the  
303 biophysical gradient. Advances in animal tracking technologies – dubbed biologging – offer  
304 possibilities to study internal (e.g., physiology, metabolism, reproduction) and external (e.g.,  
305 social, environmental) drivers of animal movement (Nathan *et al.* 2008). Biologging enables  
306 quantification of the space-use and resource requirements of animals (Kays *et al.* 2015; Hays *et*  
307 *al.* 2019). The frequency with which animals visit certain areas (e.g., waterholes, fruit bearing  
308 tree, latrines) can be estimated via first passage times and recursive analysis (Mahoney &  
309 Young 2017; Bracis *et al.* 2018; Mertes *et al.* 2020).

310

311 Migrations are among the greatest examples of animal movement. Extensive research has  
312 explored their direction, length, and drivers (Dechmann *et al.* 2017; Somveille *et al.* 2018, 2019).  
313 Locations of an animal's track can be classified into specific movement strategies (i.e. disperser,  
314 migrator, nomad, central place forager) by segmentation methods (Bastille-Rousseau *et al.*

2016; Edelhoff *et al.* 2016), thus setting the stage for further analysis. Fine-scale animal behaviour (i.e. foraging, rest, travel) can be resolved in GPS data using behavioural change point analysis, expected-maximum binary clustering methods (Garriga *et al.* 2016), and state-space models (Patterson *et al.* 2008). A promising approach combining state-space and continuous time correlated random walk models (Michelot & Blackwell 2019) allows estimating behavioural states when using tracking data that are not sampled at regular time intervals, which is a common occurrence with biologging data.

Modern biologging tags are comprised of GPS units, accelerometers, and additional on-board sensors. Accelerometers estimate change in velocity of body postures over time and can classify behavioural states of wild animals, including hunting, killing, resting (Brown *et al.* 2013; Williams *et al.* 2014), and even scent marking (Bidder *et al.* 2020). Accelerometers also allow quantifying energy expenditure of animals and of specific behaviours. Common methods for such energy expenditure are two closely linked metrics; Overall Dynamic Body acceleration (ODBA) and Vectorized sum of the Dynamic Body Acceleration (VeDBA) (Wilson *et al.* 2006, 2020). We refer to Joo, Boone, Clay, & Patrick, (2019) for a review on animal movement analysis.

Movement ecology increasingly studies fine scale behaviours such as foraging or sociality (Strandburg-Peshkin *et al.* 2015; Bennison *et al.* 2018) that can determine fine scale spatial heterogeneity in nutrient release, a process not yet considered in the current literature on animal-vectored subsidies (Gounand *et al.* 2018b). At the same time, movement ecology rarely quantifies the scale, scope, and magnitude of animal-mediated nutrient transfers.

##### **(5) The amounts and deposition rate of animal transported nutrients or material**

Remote sensing offers quantitative measures of ecosystem structure at broad geographic scales. Collecting environmental data in the field provides detailed information that is essential and complementary to remote sensing to understand how local microclimate influences ecosystem dynamics and the distribution of animals and the resources they consume (Zellweger *et al.* 2018) (Fig. 2, right panel). Local observations identify how trophic interactions and community structure vary across habitats and environmental gradients. For example, one could measure a site's microtopography (slope, elevation, roughness), surrounding vegetation type and cover. The development of methods to account for such micro-environmental variation

349 is necessary to facilitate realistic representations of environmental conditions experienced by  
350 organisms. Downscaled remote sensing products show promise in providing such fine spatial  
351 detail (Maclean *et al.* 2019; Maclean 2020) and, once overlaid with animal locations, enable  
352 identification of habitats that are source and recipient locations for animal-vectorized nutrient  
353 subsidies.

354  
355 Animal vectorized subsidies involve several processes, including consumption, excretion,  
356 egestion, and deposition of carcasses and parturition material (McSherry & Ritchie 2013;  
357 Subalusky & Post 2018; Wenger *et al.* 2019). For example in the Maasai Mara National Park  
358 Reserve, Kenya, every day Hippopotamus egest approximately 36 tons of wet biomass  
359 consumed in terrestrial ecosystems into the Mara river, approximately 15 % of the dissolved  
360 organic carbon loading from the upstream catchment (Subalusky *et al.* 2015). Also in the Mara,  
361 mass drowning of wildebeest contributes ~18% of the total dissolved organic carbon to the river  
362 ecosystem (Subalusky *et al.* 2017).

363  
364 Standard biogeochemical methods, which include analyses that quantify elemental composition  
365 of materials, can be used to characterize the stoichiometry and total nutritional composition of  
366 food items (Vanni *et al.*, 2002). Additionally, these methods can assess nutrient quality and  
367 quantity of animal-deposited material (e.g. egesta, excreta, carcasses) as well as the magnitude  
368 of nutrient influx into the surrounding environment through *in situ* measurement of various soil  
369 and plant properties (e.g., pH, soil texture, plant community composition, soil and plant nutrient  
370 content) at sites of animal activity (i.e. see Bump *et al.*, 2009, Risch *et al.* 2020). Finally, given  
371 that stable isotope that come from animal tissues and excreta are isotopically enriched  
372 compared to their diet, enriched plant and soil materials surrounding the deposition can indicate  
373 deposition and use of animal-vectorized subsidies (Bump *et al.* 2009a). Such enrichment may  
374 also help parse out passive from active subsidy input.

375  
376 The tracing and mapping of spatial nutrient flows and deposition can be aided by using  
377 stoichiometric distribution models (StDMs). Such models predict the geospatial distribution of  
378 nutrients in forage items (Leroux *et al.* 2017). Similar to a species distribution model and point  
379 Poisson process models, a resource – in this case a forage item's nutrient content, either  
380 absolute ( $\text{g}/\text{m}^2$ ; i.e. quantity) or relative (carbon:nitrogen ratio; i.e. quality) – can be defined as  
381 the abundance of a given nutrient (nitrogen, phosphorus or carbon) in location  $x_i$  which is  
382 predicted by a vector of environmental covariates  $z_{(x_i)}$ , their coefficients  $\beta_i$ , and an error term  $\mathcal{E}$ .

383 StDMs map the distribution of nutrients in ways that can be overlaid with animal spatial habitat  
384 domains, to reveal how animals respond to spatial variation in resource distribution across a  
385 landscape (Leroux *et al.* 2017) and may create microsites of heterogeneity where subsidies are  
386 transported against stoichiometric gradients in the broader landscape.

387

## 388 **From diverse data sources, to a coherent message - A road map for integrating methods**

389 The current technological and methodological juncture allows us to go beyond understanding  
390 the drivers of animal movement. We now have the tools to enhance our understanding of the  
391 ecosystem-wide consequences of animal movements, generating inference on the timing,  
392 directionality, and magnitude of animal mediated subsidies on both donor and recipient  
393 ecosystems. Our road map identifies five steps needed to develop such a coherent picture and  
394 is presented in Figure 2. We illustrate the value of this road map with two case studies, one of a  
395 herbivore and one of a top predator, discussing how methods from these five steps can be  
396 integrated to understand how animals on the move influence their ecosystems at fine scales.

397

### 398 **Case Studies**

#### 399 **Measuring nutrient loading by Galapagos tortoises during their seasonal migration**

400 Galapagos tortoises (*Chelonoidis porteri*) are ecosystem engineers due to their seed dispersal  
401 abilities, trampling of vegetation, and transport of nutrients (Gibbs *et al.* 2010; Blake *et al.* 2012;  
402 Ellis Soto 2020). Coupling tortoise tracking data with remotely sensed NDVI has identified that  
403 giant tortoises undergo seasonally recurring migrations in response to averages of long-term  
404 environmental conditions (Bastille-Rousseau *et al.* 2019). Behavioural observations revealed  
405 that tortoises preferentially feed on an agricultural crop (guava, *Psidium guajava*) when  
406 migrating from higher to lower elevation areas (Blake *et al.* 2015). By preferentially feeding on  
407 guava in agricultural areas, tortoises translocate guava seeds and nutrients into other habitats  
408 during their downslope migration, resulting in the spread of guava as an invasive species and  
409 posing a challenge to the maintenance of natural plant communities in Galapagos National Park  
410 (Ellis-Soto *et al.* 2017). The distribution of guava has been mapped through local vegetation  
411 sampling plots and drone and remote sensing imagery (Rivas-Torres *et al.* 2018; Laso *et al.*  
412 2019). Coupling tortoise movement patterns, resource selection, and habitat structure makes it  
413 possible to quantify giant tortoise vectored nutrient transfer in Santa Cruz Island, Galapagos.

414 Santa Cruz Island shows a distinct zonation of vegetation. Dry xerothermic plants dominate the  
415 low elevations of the national park, with rainfall and the presence of introduced species (e.g.,  
416 guava) increasing with elevation (Itow 2003). During their downslope migration, adult tortoises  
417 can migrate from agricultural areas at higher elevations into the lowlands of the Galapagos  
418 National Park (identified through net square displacement, Suppl. Material 1). Overlapping  
419 home ranges (Winner *et al.* 2018) of tagged tortoises located in the lowlands inside the national  
420 park can reveal core areas of tortoise utilization distributions, providing a picture of spatial  
421 trophic structure. Using this core area, a stratified sampling of surrounding vegetation, soil  
422 samples, and description of microtopography can help understand nutrient composition,  
423 microbial activity and abiotic properties of selected areas in an attempt to further characterize  
424 habitat structure. Such measurements could be compared with samples obtained in areas  
425 where tortoises are absent, serving as a control plot (i.e. via exclosures or randomly selecting  
426 points outside the tortoise core area) to further isolate animal impacts on biogeochemical cycles  
427 and ecosystem fluxes.

428 Given their different photosynthetic pathways (C3 and CAM, respectively) guava likely contains  
429 a different isotopic signature (Sage & Zhu 2011) than the tortoises' most-consumed xerothermic  
430 plant at lower elevations of the National Park, the *Opuntia echios* cacti. Thus, stable isotope  
431 analysis of fecal matter containing guava could disentangle contributions by tortoises during  
432 their migrations from a donor ecosystem (agricultural areas) to a recipient ecosystem (lowlands  
433 of the Galapagos National Park) and make spatially explicit predictions of this animal-vectored  
434 nutrient flux. Finally, all of these measures can be combined to develop a nutrient budget for the  
435 lowland ecosystem of the Galapagos National Park and include the downslope migration of *C.*  
436 *porteri* as the mechanism for vectored subsidy (Fig. 3, Fig. 4). Such nutrient ecosystem budgets  
437 often attempt to quantify the flows of nutrients through different pools providing an  
438 understanding of how these flows may impact ecosystem functioning (Loreau & Holt 2004).  
439 Coupling an assessment of nutrient loading with past and present tortoise population numbers  
440 could provide a baseline for ongoing conservation initiatives aimed at restoring degraded island  
441 habitats by reintroducing giant tortoises to act as ecosystem engineers (Gibbs *et al.* 2010;  
442 Hunter *et al.* 2020). We provide the necessary code to replicate steps detailed in this conceptual  
443 tortoise example (Suppl. Material 1).

444 **Quantifying how *Canis lupus* creates landscape heterogeneity through prey hunting and**  
445 **killing**  
446

447 Predators can have profound cascading impacts on ecosystem nutrient dynamics mediated by  
448 their effects on prey mortality and space use (Fig. 5). For example, the hunting behaviour of  
449 wolves (*Canis lupus*) and the subsequent deposition of prey carcasses may create nutrient  
450 hotspots across a landscape, creating heterogeneity in nutrient distribution as carcasses  
451 decompose at sites with high rates of predation (Bump *et al.* 2009a; Joseph *et al.* 2009). To  
452 explore this, a recursive analysis (Bracis *et al.* 2018) based on how often animals return to  
453 specific landscape areas defined by a determined circular radii — which could be chosen based  
454 on grain sizes identified from First Passage Times (Mertes *et al.* 2020) — display where and  
455 how collared wolves revisit areas in their range. Coupling accelerometer and animal location  
456 data can identify hunting, eating, and killing by predators in the wild through behavioural  
457 classification and ground-truthing GPS clusters at presumed kill sites (Williams *et al.* 2014;  
458 Wang *et al.* 2015). These methodologies can pinpoint the exact coordinates and time of hunting  
459 and killing events and therefore quantify the movement of the nutrients through these  
460 processes. Once a carcass's presence is identified, camera traps can provide insight into how  
461 the predation behaviours of top predators may have cascading impacts on subsidizing  
462 scavengers and invertebrates (Perrig *et al.* 2017; Cunningham *et al.* 2018).

463  
464 Using a stratified sampling scheme of plant and soil characteristics, it is also possible to quantify  
465 the nutrients deposited by the carcasses, explore the spatial diffusion of those nutrients, and  
466 estimate how long those nutrients stay in the local system before leaching away or being  
467 scavenged. These sites can be compared to measurements collected in randomly selected  
468 points, which may serve as a control treatment. Assessing the plant community composition and  
469 cover will help identify whether killing behaviour of predators leads to changes in plant  
470 composition, while soil samples collected below carcasses can be used to compare microbial  
471 activity and nutrient availability between carcass and control sites (Metcalf *et al.* 2016; Risch *et al.*  
472 *et al.* 2020). Both total soil and plant nutrient concentration as well as enriched  $\delta^{15}\text{N}$  in plant and  
473 soil samples can be used to identify and quantify the impact of this animal vectorized subsidy  
474 (Bump *et al.* 2009b; Holtgrieve *et al.* 2009; Barton *et al.* 2016). This conceptual study design  
475 highlights how predators could concentrate nutrients at kill sites, contributing to landscape  
476 heterogeneity with potential knock-on effects on scavenger and plant community distribution.  
477 Such knowledge is key for understanding the ecosystem consequences of predator loss (Ripple  
478 *et al.* 2014).

479

480 **Moving forward: Future Directions**

481  
482 We have illustrated how individual studies may productively integrate disparate fields and tools  
483 to address specific questions about animal-vectorized nutrient subsidies within a study system.  
484 These disciplines and methodologies can be united to address larger questions about animals  
485 and nutrient transport in diverse systems and at multiple scales. Below, we identify the next  
486 frontiers in ecological research, which can be resolved through synergistic research linking  
487 animal movement and nutrient transport.

488

### 489 **Improve tracing and mapping of animal vectorized subsidies**

490

491 We see opportunities to improve predictions of animal vectored subsidies based on advances of  
492 Species Distribution Modeling (SDM) such as incorporating a priori expert knowledge (Merow *et*  
493 *al.* 2016) and joint species distribution modeling (jSDM) (Pollock *et al.* 2014). Such expert  
494 knowledge can represent species geographic ranges or species specific elevational ranges as  
495 known from field guides. Expert knowledge could enter StDM's in the form of a statistical offset  
496 which has been shown to improve model predictions from SDM's (Ellis-Soto *et al.* n.d.; Merow  
497 *et al.* 2016). Such offset is independent of the predictor variable (nutrient quantity or quality) and  
498 would provide *a priori* expectations of how resources are distributed across a study region  
499 rather than assuming an equal likelihood for each cell in a landscape. StDMs could also  
500 incorporate soil nutrient maps derived from coarse scale remote sensing (soilgrids database) as  
501 an offset reflecting the a priori expectation of a nutrient concentration in a cell. We refer to  
502 Merow, Wilson, & Jetz, (2017) for specifics about deploying offsets in logistic regression, but the  
503 motivation is that expert information can provide estimates that are complementary to point  
504 estimates that could predict nutrient quantity ( $\text{g/m}^2$ ) or nutrient ratios (C:N).

505

506 jSDMs predict spatial occurrences of entire communities of species, rather than distributions of  
507 single species, as in SDM (Pollock *et al.* 2014). StDMs could be similarly extended to consider  
508 the distribution of multiple individual nutrients (not just their ratios). Particularly, we see potential  
509 in adapting jSDM developments from Generalized joint attribute modelling (Clark *et al.* 2017),  
510 Bayesian Ordination and Regression Analysis of Multivariate Abundance Data (Hui 2016), and  
511 Spatial factor analysis (Thorson *et al.* 2015) to develop joint StDM. Such jStDM could be  
512 overlapped with autocorrelated kernel density estimators (Fleming *et al.* 2015) to investigate  
513 how animal space use relates to spatial stoichiometry.

514



515 We see potential in building upon mechanistic models of animal movement and seed and  
516 nutrient dispersal to map the distribution and magnitude of animal vectored subsidies (Bampoh  
517 *et al.* 2019; Kleyheeg *et al.* 2019; van Toor *et al.* 2019). These models couple animal movement  
518 and gut retention with remotely sensed land cover information to create spatially explicit maps of  
519 nutrient dispersal. Such models have provided insights about how extinct and extant animals  
520 have influenced nutrient translocations at coarse spatial scales across the globe (Doughty *et al.*  
521 2016; Doughty 2017). These estimates could be refined by incorporating movement models  
522 such as allometric random walks (Hirt *et al.* 2018) and individual based movement models  
523 (Bampoh *et al.* 2019), rather than coarser lateral diffusion movement models which have  
524 hitherto been used.

525

### 526 **Estimating animal-mediated nutrient translocation within a home range**

527

528 Core areas where individuals within groups or populations might have strongest animal-  
529 vectorized subsidies effects can be identified using home range overlap indices between  
530 individuals. Such overlap indices may be simple convex hulls around individual home ranges to  
531 describe population ranges or more sophisticated utilization distributions based on bias-  
532 corrected Bhattacharyya coefficient as shown by Winner *et al.*, (2018). RSFs of individuals with  
533 overlapping home ranges could reflect how these animals utilize resources across long-term  
534 timescales.

535

536 Behavioural pattern identification could characterize a suite of animal behaviours within home  
537 ranges (e.g., forage, rest, fight, prey capture; Kie *et al.* 2010) to identify how animals transport  
538 nutrients at shorter timescales (Fig. 3). Revisitation and accelerometer analysis hold promise to  
539 identify feeding sites, scent marking sites or latrines (Bracis *et al.* 2018; Bidder *et al.* 2020). High  
540 urine concentration at latrines could influence plant communities, soil nutrient loads, and  
541 microbial communities, constituting a nutrient hotspot. Other methods estimate nest locations  
542 and reproductive output from telemetry data (Picardi *et al.* 2019; Bidder *et al.* 2020). Such  
543 behavioural identification can identify where animals assimilate or excrete resources and under  
544 which conditions animals act as nutrient sources (bring more nutrients in than they consume,  
545 i.e. high urine concentration at latrines or high offspring mortality at nests) or sinks (have a  
546 negative net effect on nutrient concentrations at the site). Calculating integrated step selection  
547 functions (Avgar *et al.* 2016) using exclusively animal locations that were associated with  
548 foraging behaviour (Nathan *et al.* 2012) could identify such nutrient sources. Habitat selection

549 could be explored at fine detail by using drones to create study-site specific landcover maps  
550 (Strandburg-Peshkin *et al.* 2017).

551

## 552 **Animal-vectored subsidies in the Anthropocene**

553

554 In human-modified landscapes, animals find themselves crossing a matrix of fragmented  
555 habitats and human pressures (i.e. population density, infrastructure and agricultural areas) that  
556 vary in permeability. Human modification of landscapes, such as urban development of roads or  
557 C4 plant monocultures for agriculture, can alter diet and nutrient transfer by animals (Magioli *et*  
558 *al.* 2019). For example, Roe deer (*Capreolus capreolus*) in central France routinely act as  
559 vectors for large quantities of artificially-introduced nitrogen, which they obtain by foraging in  
560 agricultural areas, which are deposited near resting sites in forested areas (Abbas *et al.* 2012).  
561 In New Mexico, USA, snow geese (*Chen caerulescens*) perform daily foraging trips from wildlife  
562 refuges to agricultural areas to feed on corn and alfalfa. This nutrient translocation was shown  
563 to increase phosphorous nutrient loadings up to 75% in wetland ponds (Kitchell *et al.* 1999).  
564 Thus, animals can link natural areas with human modified landscapes and modify the nutrient  
565 budgets of ecosystems.

566 Mechanistic models of animal vectored subsidies (Bampoh *et al.* 2019) could predict  
567 how nutrient budgets of ecosystems are altered by the removal of species, such as large bodied  
568 animals (Bello *et al.* 2015; Sobral *et al.* 2017), or specific individuals (i.e. elephant bulls in  
569 Kruger National Park (Davies & Asner 2019)), or animal introductions (goat introduction in the  
570 Galapagos (Bastille-Rousseau *et al.* 2017)). These models could identify causal links between  
571 ecosystem functioning and animal mediated subsidies. Such knowledge would provide evidence  
572 to rewilding initiatives aiming to restore lost ecosystem services through animal reintroductions  
573 (Falcon Wilfredo & Hansen 2018; Lundgren *et al.* 2018).

574

## 575 **Conclusion**

576

577 Understanding how animals move through both natural and human dominated landscapes to  
578 influence ecosystem properties and functions is in need of concerted analysis. To this end, we  
579 have provided a methodological road map that draws together methods of analysis across  
580 disciplinary fields. We show how, when combined, these can lead to integrative, coherent  
581 understanding of how animal vectored subsidies drive spatial ecosystem structure and  
582 functioning. It is through the integration and collaboration of disciplines that we can address and

583 understand the importance of this type of nutrient transport in a spatially explicit manner. We  
584 hope that the introduced methodological roadmap will facilitate empirical studies that quantify  
585 how much the fluxes of nutrients from one pool to another across landscapes can be attributed  
586 to animal-vectored subsidies.

587  
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598 K.M.F. led the writing of the manuscript. D.E.S. and O.J.S. created the figures of the  
599 manuscript. All authors contributed to this work and provided final approval for publication.

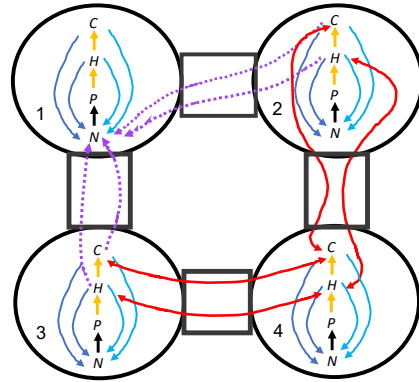
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603

$$\begin{aligned} \frac{dN_i}{dt} &= I - EN_i - U(N_i, P_i) + \epsilon M(P_i) \\ &\quad + \chi_H L_H(H_i) + \chi_C L_C(C_i) + \gamma_H W(P_i, H_i) + \gamma_C W(H_i, C_i) \\ &\quad + d_H \sum_{j=1}^n c_{ij} \gamma_H W(P_j, H_j) + d_C \sum_{j=1}^n c_{ij} \gamma_C W(H_j, C_j) \\ \frac{dP_i}{dt} &= U(N_i, P_i) - M(P_i) - W(P_i, H_i) \\ \frac{dH_i}{dt} &= (1 - \gamma_H) W_H(P_i, H_i) - L_H(H_i) + d_H \sum_{j=1}^n c_{ij} H_j - W_C(H_i, C_i) \\ \frac{dC_i}{dt} &= (1 - \gamma_C) W_C(H_i, C_i) - L_C(C_i) + d_C \sum_{j=1}^n c_{ij} C_j \end{aligned}$$

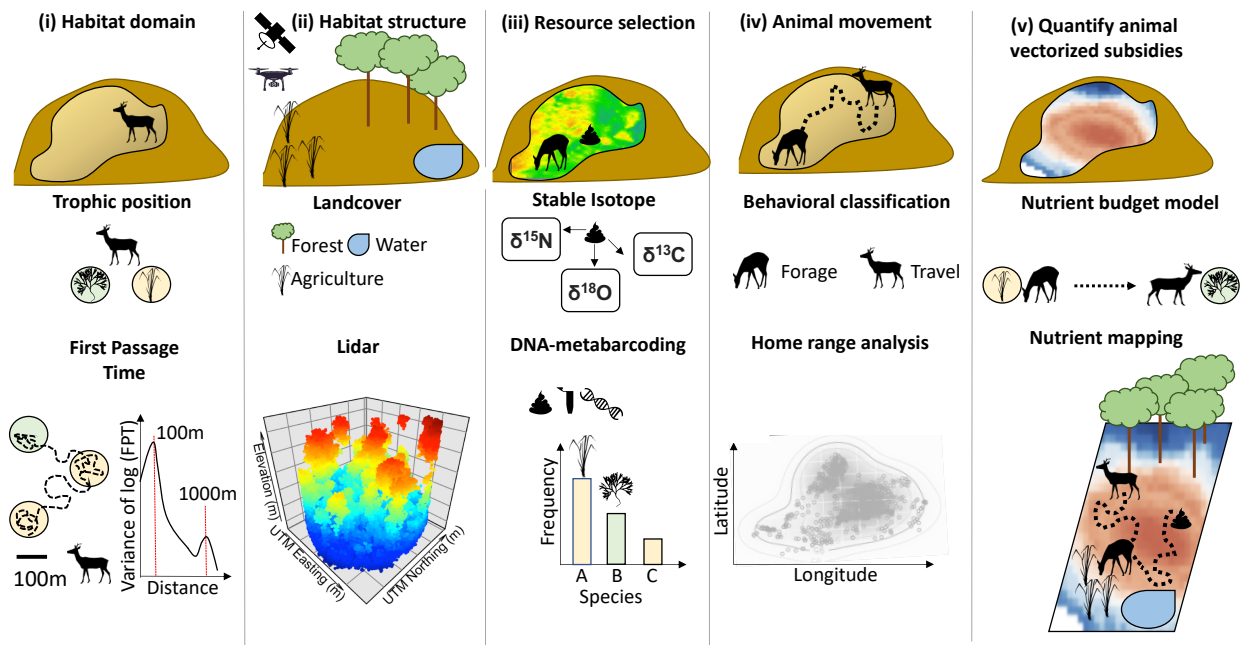


Ecosystem model component	Spatial measurements needed (sections)
Trophic interactions within and between local ecosystems	(i) The spatial extent and spatial grain size of animal movement (ii) Habitat structure shaping where animals move (iii) Available and selected resources
Nutrient translocation and deposition due to within-ecosystem carcass and nutrient deposition and between ecosystem nutrient deposition	(iv) Movement rates directional spatial flow of animals and nutrients (v) Amount of animal carcass and nutrients deposited spatially

606  
 607 **Figure 1:** Meta-ecosystem model characterizing the trophic structure and dynamics of nutrients  
 608 (N), plants (P), herbivores (H) and carnivores (C) within and between four local ecosystems. In  
 609 the model carnivore abundance changes as a function of assimilated intake of  
 610 herbivore biomass within ecosystem  $i$   $(1 - \gamma_C)W_C(H_i, C_i)$ , where  $\gamma_C$  is the degree of inefficiency in  
 611 assimilation, loss due to natural mortality at rate  $L_C(C_i)$ , and gain due to  
 612 migration from another local ecosystem  $d_C \sum_{j=1}^n c_{ij} C_j$ , where  $d_C$  is the movement rate of a  
 613 carnivore and  $c_{ij}$  is the spatial connectivity between two local ecosystems (where high values  
 614 reflect high connectivity and hence high ease of flow). Herbivore abundance changes as a  
 615 function of assimilated intake of plant biomass  $(1 - \gamma_H)W_H(P_i, H_i)$ , loss due to natural mortality at  
 616 rate  $L_H(H_i)$ , loss due to predation at rate  $W_C(H_i, C_i)$  and gain due to migration from another local  
 617 ecosystem  $d_H \sum_{j=1}^n c_{ij} H_j$ . Plant biomass changes as a function of nutrient uptake at rate  $U(N_i, P_i)$ ,  
 618 loss due to senescence at rate  $M(P_i)$  and herbivory at rate  $W_H(P_i, H_i)$ . Finally nutrient  
 619 abundance changes due to global inputs  $I$  from weathering of parent geological material,  
 620 release from riverine sediments, wind-born dust, or rain-driven and snowmelt-driven run-  
 621 off, loss due to leaching out of the ecosystem  $EN_i$  and plant uptake at rate  $U(N_i, P_i)$ , and

622 additions due to recycling of plant material  $\epsilon M(P_i)$ , herbivore and carnivore carcasses at  
 623 rates  $\chi_H L_H(H_i) + \chi_C L_C(C_i)$ , and release of unassimilated consumption by herbivores and  
 624 carnivores (e.g. egesta) at rates  $\gamma HW(P_i, H_i) + \gamma CW(H_i, C_i)$ . Local ecosystem nutrient budgets  
 625 are also subsidized by unassimilated nutrient release as herbivores and carnivores migrate  
 626 among local ecosystems  $d_H \sum_{(j=1)} c_{ij} \gamma_H W P_j, H_j) + d_C \sum_{(j=1)} c_{ij} \gamma_C W(H_j, C_j)$ . These components  
 627 describing nutrient dynamics can ultimately be grouped according to two broad spatial  
 628 processes: spatial trophic interactions and spatial nutrient translocation and deposition. These  
 629 spatial processes can be further decomposed into five subprocesses that require different  
 630 methodologies to measure. A coherent picture of spatial nutrient dynamics can be developed  
 631 when data from the five subprocess measurements are combined into a dynamic map that  
 632 portrays spatial animal movement and nutrient flow in relation to the biophysical features within  
 633 and between local ecosystems across a landscape. Model and illustration adapted from  
 634 Marleau et al. (2014).

635

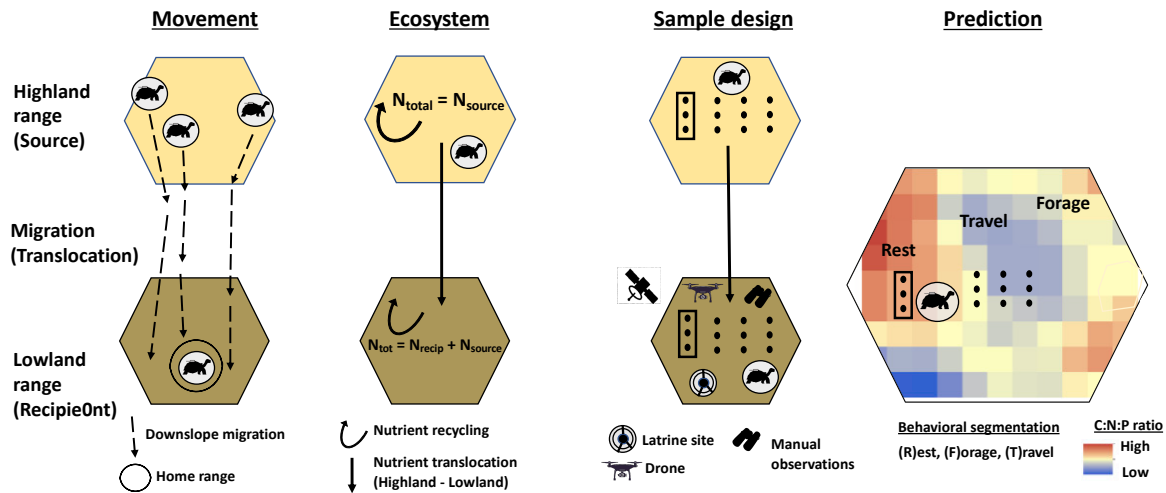


636

637 **Figure 2:** Conceptual demonstration of integrating different disciplines (sections 1,-4) for  
 638 quantifying animal vectorized subsidies across a landscape (section 5). (i) The habitat domain  
 639 helps understand the trophic position. In our hypothetical example, a roe deer (*Capreolus*  
 640 *capreolus*) travels across yellow patches containing agricultural areas and a green patch with  
 641 forested area. A first passage time analysis would reveal the scale of roe deer selection to be

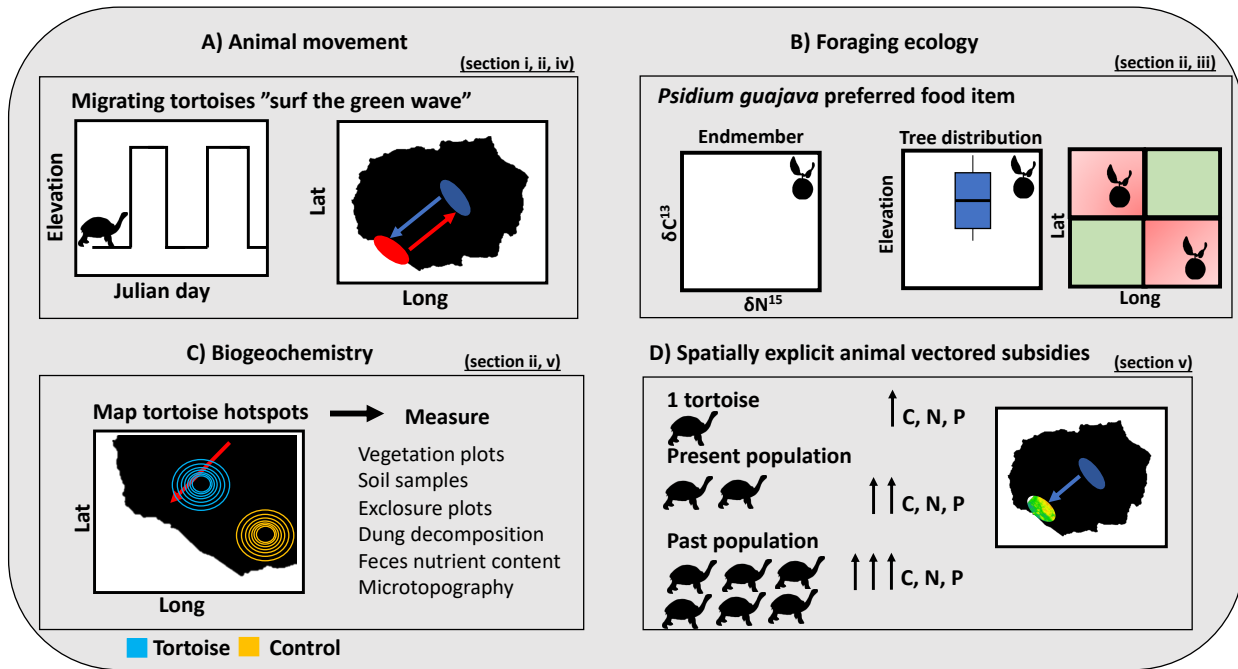
642 strongest at approximately 100m. With this knowledge we can proceed on estimating the trophic  
643 positions and interactions at that scale, choosing subsequent remote sensing products at the  
644 same spatial scale. If we were to select a scale of 1000m – where extensive remote sensing  
645 products are available (Table 1), we would see a weaker response of animals selecting their  
646 environment. (ii) The habitat structure of our study region can be identified through remotely  
647 sensed products, such as landcover maps. In this example, agriculture and water would be  
648 convex ecosystems and likely receive abiotic inputs from forest leaves (concave ecosystem)  
649 due to runoff. Convex and concave can be defined with elevation products or with Lidar to  
650 obtain a 3D matrix of the environment across which animals navigate (i.e. against elevation  
651 gradients during animal upslope movement). Lidar imagery was created using the rLidar and  
652 rGedi packages. Habitat and environmental information (ii) can then be used as response  
653 variables to understand how animals select and avoid resources and associated habitat  
654 structures, using resource selection. Such resource use map is displayed in (iii) with green  
655 colors indicating hotspots of habitat selection by our animal. Further, DNA-metabarcoding (iii) of  
656 animal fecal matter in the study region can reveal the trophic position and the resources  
657 consumed and deposited at great taxonomic detail. Understanding the stoichiometry of  
658 resources consumed through stable isotopes (iii) provides insights into the composition and type  
659 of nutrients that are moved by animals. (iv) Detailed information of roe deer movement obtained  
660 through GPS collars reveals detailed space use of individuals (i.e. their home range) which can  
661 be overlaid with the habitat structure of the landscape. Behavioural change point analysis (iv)  
662 based on movement data could classify animal behaviour into foraging and travel. Coupling  
663 behavioural classification and animal movement with faecal sampling for DNA-metabarcoding  
664 and stable isotope can reveal sources (foraging locations) and sinks (excretion locations) of roe  
665 deer-vectorized subsidies. (v) Integrating the different methodologies described, allows  
666 quantifying animal-vectorized subsidies through spatial modelling such as Stoichiometric  
667 Distribution Models (section v; Leroux et al. 2017). Importantly, coupling such models with  
668 abiotic nutrient deposition rates (e. g. leaching), allows us to contextualize the magnitude and  
669 direction of biotic nutrient deposition rates. We could thus begin including animal vectorized  
670 subsidies into ecosystem nutrient budget models (in our hypothetical case the roe deer brings  
671 nutrients from the agricultural matrix into the forest ecosystem). Integrating these steps (i-v)  
672 allows us to paint a picture of the landscape in which the ecological consequences of moving  
673 animals are incorporated into cross-ecosystem models. Silhouettes were obtained from the  
674 PhyloPic website ([phylopic.org](http://phylopic.org)).

675



676  
 677 **Figure 3:** Integration of diverse disciplines and methodologies to characterize animal-vectorated  
 678 subsidies; in this case nitrogen recycling and translocation by Galapagos tortoises (*Chelonoidis*  
 679 *porteri*) in time and space. (a) Movement determines the timing and direction of animal arrival  
 680 and departure of ecosystems. (b) Ecosystem nutrient budgets incorporate inputs from outside  
 681 ecosystem boundaries, such as animal-vectorated subsidies. (c) Careful sample design helps  
 682 elucidating drivers and predict consequences of nutrient transport by animals. Coupling large  
 683 extent (remote sensing, drones) with local field measurements (manual, drones) and animal  
 684 population estimates, allows (d) quantifying magnitude and flow of animal-vectorated subsidies  
 685 in a spatially explicit manner and estimate what proportion of total nutrients are being mobilized  
 686 by animals on the move. Tortoise silhouettes were obtained from the PhyloPic website  
 687 (phylopic.org).  
 688

Galapagos tortoise (*Chelonoidis porteri*)

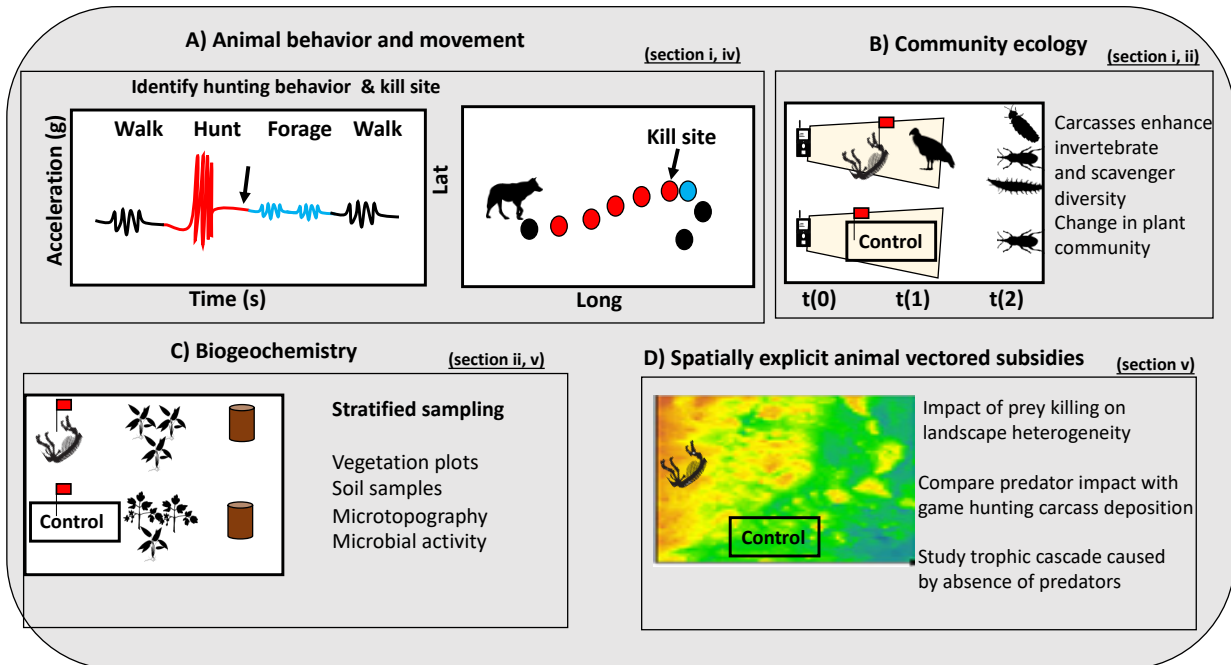


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**Figure 4:** Conceptual example of studying nutrient transport of giant tortoises (*Chelonoidis porteri*) in Santa Cruz Island. Integrating known movement patterns and foraging behaviour of this species with the distribution and nutritional composition of food items, it is possible to design an experiment to estimate the influence of tortoises transporting nutrients to the Galapagos National Park boundaries during their downslope migration. Silhouettes were obtained from the PhyloPic website (phylopic.org).



## Wolf (*Canis lupus*)



697  
 698 **Figure 5:** Conceptual example to identify killing sites of Wolves (*Canis lupus*) with biologging  
 699 technologies and quantify how predators drive landscape heterogeneity. Identifying kill sites  
 700 allows studying how carcass presence affects local biogeochemistry and community  
 701 composition when compared to control locations. Silhouettes were obtained from the PhyloPic  
 702 website (phylopic.org).

703  
 704 **Table 1:** Collection of applicable remote sensing products for animal mediated subsidies. We  
 705 elucidate the spatio-temporal resolution and grain size of these products.

706  
 707 **Appendix – Supplementary Material**  
 708

709 **Supplementary Material 1: Necessary code to perform movement ecology and remote**  
 710 **sensing analysis of the Galapagos tortoise example**

711  
 712 **References**  
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