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1 Predator and scavenger movements among and within endangered seabird colonies:

2 opportunities for pathogen spread

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28 Abstract

The spatial structure of host communities is expected to constrain pathogen spread.
 However, predators and/or scavengers may connect distant host (sub)populations when
 foraging. Determining whether some individuals or populations play a prominent role in the
 spread of pathogens is critical to inform management measures.

We explored movements and epidemiological status of brown skuas (*Stercorarius antarcticus*), the only avian terrestrial consumer native of Amsterdam Island (Indian Ocean),
to assess whether and how they could be involved in the spread of the bacterium *Pasteurella multocida*, which recurrently causes avian cholera outbreaks in endangered albatross and
penguin species breeding on the island.

38 3. High proportions of seropositive and DNA-positive individuals for *P. multocida* indicated that 39 skuas are highly exposed to the pathogen and may be able to transmit it. Movement tracking 40 revealed that the foraging ranges of breeding skuas largely overlap among individuals and 41 expand all along the coasts where albatrosses and penguins nest, but not on the inland 42 plateau hosting the endemic Amsterdam albatross (*Diomedea amsterdamensis*).

43 4. Considering the epidemiological and movement data, skua movements may provide
44 opportunity for pathogen spread among and within seabird colonies.

5. *Synthesis and applications.* This work highlights the importance of considering the behaviour and epidemiological status of predators and scavengers in disease dynamics because the foraging movements of individuals of such species can potentially limit the efficiency of local management measures in spatially-structured host communities. Such species could thus represent priority vaccination targets to implement efficient management measures aiming at limiting pathogen spread and also be used as sentinels to monitor pathogen circulation and evaluate the effectiveness of management measures.

52 Résumé

1. La circulation d'agents infectieux dans les populations sauvages peut être fortement contrainte par la structuration spatiale de leurs communautés d'hôtes. Cependant, de par leurs comportements alimentaires, certains prédateurs et/ou charognards peuvent connecter des (sous-)populations spatialement éloignées. Identifier les individus ou populations susceptibles de jouer un rôle prépondérant dans la dissémination d'agents infectieux pathogènes est un élément clé pour la compréhension, et éventuellement le contrôle, des dynamiques épidémiologiques dans les populations sauvages.

2. Dans ce contexte, nous avons suivi les déplacements et statuts épidémiologiques de labbes
subantarctiques (*Stercorarius antarcticus*), uniques prédateurs et charognards terrestres
aviaires natifs de l'île Amsterdam (Océan Indien), afin d'évaluer leur implication dans la
dissémination de *Pasteurella multocida*, la bactérie responsable d'épizooties récurrentes de
choléra aviaire affectant les albatros et gorfous de l'île.

3. Les fortes proportions d'individus positifs à *P. multocida* par sérologie et PCR indiquent que les labbes sont très exposés à la bactérie et susceptibles de la transmettre. Par ailleurs le suivi des déplacements d'individus reproducteurs a révélé que les zones de recherche alimentaire individuelles des labbes se superposent et s'étendent tout le long de la partie de côte occupée par les albatros et les gorfous. Au contraire, le plateau central où se reproduit l'albatros d'Amsterdan (*Diomedea amsterdamensis*), espèce endémique de l'île, ne semble pas visité par les labbes en reproduction.

4. Compte tenu des données épidémiologiques et écologiques présentées les labbes sont
susceptibles de contribuer à dissémination d'agents infectieux au sein et entre des colonies
d'oiseaux marins menacés d'extinction.

5. Synthèse et applications. Cette étude met en évidence l'importance de prendre en
considération le comportement et le statut épidémiologique des prédateurs et charognards
lors de la mise en place de programmes de contrôle de dynamiques épidémiologiques. En

effet le comportement alimentaire de telles espèces peut limiter l'efficacité des mesures locales malgré l'apparente structuration spatiale des populations affectée. Prédateurs et charognards peuvent ainsi représenter des cibles prioritaires pour les programmes de vaccination visant à limiter la dissémination d'agents infectieux pathogènes mais également être utilisés comme sentinelles pour en suivre la circulation et évaluer l'efficacité des programmes de contrôle.

Keywords: conservation biology, disease ecology, dynamic space utilisation, individual
 heterogeneity, movement ecology, *Pasteurella multocida*, sentinel species, serology

86 Introduction

Infectious diseases threaten populations of many endangered wild species and are 87 now recognized as a main threat relevant to conservation biology (Young et al., 2017). The 88 structure of contact networks among hosts of infectious agents can strongly impact 89 epidemiological dynamics (Craft et al., 2008; Strona et al., 2018), hence extinction probabilities 90 91 (Cleaveland et al., 2002). Some individuals or populations may occupy key positions in contact networks and contribute more than others to spreading infectious agents through their 92 93 behaviour (Lloyd-Smith, Schreiber, et al., 2005; Paull et al., 2012; Dougherty et al., 2018), notably in multi-host systems (Craft et al., 2008). Such individuals or populations may thus 94 95 constitute particularly relevant targets for disease control protocols aiming at interrupting transmission chains (Rushmore et al., 2014; Pepin et al., 2016; Robinson et al., 2018). 96

97 Terrestrial predators and scavengers may effectively connect otherwise isolated 98 colonies or social groups when foraging, potentially contributing to pathogen spread with 99 conservation (Craft et al., 2008), public health (Navarro et al., 2019) or fundamental 100 implications (Boulinier et al., 2016). In wild communities subject to infectious disease 101 outbreaks, deciphering the contact structure and examining the hosts' respective contributions 102 in epidemiological dynamics is thus critical to develop control measures. The role of predator 103 and/or scavenger species as potential spreaders of infectious agents is poorly documented

because it requires targeted field efforts at the often unpredictable time of outbreaks (Daversa
et al., 2017). For instance, the role of scavengers has been suspected in avian cholera, caused
by the bacterium *Pasteurella multocida* (*Pm*), outbreaks (Wille et al., 2016), but their actual
contribution as spreaders still requires proper examination.

108 The recurrent outbreaks of avian cholera in seabirds on remote Amsterdam Island (Indian Ocean, 37°49'S, 77°33'E; Weimerskirch, 2004; Jaeger et al., 2018) provide a unique 109 opportunity to better understand the potential epidemiological role of a predator and scavenger 110 111 species within a relatively simple host community (Figure 1). Avian cholera is a widespread 112 disease severely threatening the viability of several avian populations (Samuel et al., 1999; Descamps et al., 2012). On Amsterdam Island, Indian yellow-nosed albatrosses 113 114 (Thalassarche carteri) have been recurrently hit by avian cholera outbreaks since the mideighties, potentially following the introduction of the pathogen through past human activities, 115 such as animal farming, or accidental rodent introduction from visiting ships (Micol & 116 117 Jouventin, 1995; Jaeger et al., 2018). Infection by Pm causes septicaemia in nestlings, leading to their rapid death (Bourret et al., 2018; Jaeger et al., 2018) with important consequences on 118 the breeding success of the local yellow-nosed albatross population. For instance, on Gough 119 Island (which is rodent infested but considered avian cholera free), the breeding success of 120 the Atlantic yellow-nosed albatross (Thalassarche chlororhynchos) is as high as 70% 121 (Cuthbert et al., 2003), while it has been below 10% most of the past twenty years on 122 Amsterdam Island for the Indian yellow-nosed albatross (Jaeger et al., 2018). This example 123 124 and others (e.g., Sebastiano et al., 2019), illustrate that infectious diseases can represent an 125 important, but often neglected, threat to seabird population viability. Avian cholera outbreaks on Amsterdam Island not only affect this globally-significant yellow-nosed albatross population 126 (Weimerskirch, 2004), but are also suspected to cause mortality in two other endangered 127 species: the sooty albatross (Phoebetria fusca) and the northern rockhopper penguin 128 129 (Eudyptes moseleyi; Jaeger et al., 2018).

130 Despite the strong impact of avian cholera outbreaks on the endangered seabirds of Amsterdam Island (Jaeger et al., 2018) and the availability of a vaccine proven to protect 131 albatross nestlings (Bourret et al., 2018), no control measure has been implemented besides 132 133 basic biosecurity measures. Indeed, relying on vaccination of nestlings to maintain the local 134 yellow-nosed albatross population to its current size (~22000 pairs; Heerah et al., 2019) would 135 require to vaccinate thousands of nestlings every year, and may thus not represent an efficient conservation strategy. In contrast, interrupting transmission chains by treating individuals 136 137 responsible for the among-colony circulation of the bacterium may help to protect some 138 colonies with minimal efforts. Since Pm transmission occurs primarily through an oro-faecal route (Samuel et al., 2003), it is unclear how Pm circulates locally. Indeed, seabirds on 139 Amsterdam Island breed in spatially structured, mostly mono-specific, colonies (Figure 140 S1.A.1) and albatrosses and penguins forage exclusively at sea (Heerah et al., 2019). Hence, 141 142 although contacts may be frequent within dense seabird colonies, contacts between individuals from different colonies may thus be rare besides potential limited prospecting 143 movements (Boulinier et al., 2016). 144

Terrestrial predators and scavengers could however spread Pm across the island while 145 foraging among seabird colonies undergoing outbreaks. Notably, the small population of 146 brown skuas (Stercorarius antarcticus), the sole terrestrial vertebrate predators and 147 scavengers native to the island, could disseminate the bacterium when foraging through 148 shedding and/or by moving infected albatrosses and penguins (Pietz, 1987). Introduced brown 149 150 rats (Rattus norvegicus) and house mice (Mus musculus; Micol & Jouventin, 1995) could also 151 carry and shed the bacterium, notably as they prey and scavenge on seabird chicks (Figure S1.A.2; Thiebot et al., 2014), although the distribution of resources and geographical barriers 152 created by the island relief probably constrain the spatial scale of their contribution. In addition, 153 the endemic Amsterdam albatross (Diomedea amsterdamensis) could also be at risk of 154 155 exposure to Pm via foraging skuas because it nests a few kilometres inland from the yellow-

nosed albatross colonies, although nestling die-offs have seldom been recorded in thisspecies (Jaeger et al., 2018).

Considering the wide range of feeding habits of skuas and the potential heterogeneity 158 of foraging strategies among individuals (Furness, 1987), some individuals could play a 159 160 prominent role in the circulation of infectious agents. In the skua population of Amsterdam Island, we examined the extent to which the individuals (1) are exposed to Pm, (2) forage on 161 coastal versus inland areas, and (3) exploit exclusive feeding territories within the seabird 162 163 colonies. We expected the skuas to forage mostly on the coasts where prey species breed in 164 dense colonies (Figure 2a, scenarios 1 and 3), maximising feeding opportunities (Figure S1.A.2a), but also exposure risks to Pm. Further, we expected skuas to hold exclusive 165 individual feeding territories (Figure 2a, scenarios 1 and 2; Pietz, 1987; Trivelpiece et al., 1980; 166 Votier et al., 2004), with restricted movements of some individuals potentially inducing 167 heterogeneity in exposure to *Pm* and limited contacts among skuas (outside pairs, contacts 168 169 are expected to occur mostly on foraging sites and clubs, i.e., sites where individuals gather 170 outside breeding territories; Klomp & Furness, 1990). Testing these hypotheses should bring new insights on pathogen circulation in spatially structured host communities and help 171 managers to design and implement efficient disease control protocols. 172

173 Materials and Methods

174 Study population

Around 60 pairs of brown skuas breed at low density yearly on Amsterdam Island's "Plateau des Tourbières" (PDT; Figure 1). Breeders generally lay two eggs in October/November and nestlings hatch in late November/early December and fledge 40-50 days later. Skuas attend clubs notably in the north ("Mare aux Éléphants" [MAE]) and the south-west (bottom of "Entrecasteaux" cliffs). Amsterdam island holds important populations of Indian yellow-nosed albatrosses, sooty albatrosses (~400 pairs; Heerah et al., 2019) and northern rockhopper penguins (~12000 pairs), all breeding in mostly mono-specific colonies

182 on the south-west coastal cliffs between August and May (Figure 1). The 40-50 pairs of Amsterdam albatrosses nest biennially further inland, on the northern part of the PDT (Figure 183 184 1). A few small *Procellariiformes* are also present on the island in very low numbers (Micol & Jouventin, 1995). All around the island, subantarctic fur seals (Arctocephalus tropicalis) calve 185 186 on the beaches in December (Guinet, Jouventin, & Georges, 1994), also providing food 187 opportunities for skuas (placentas and dead pups). Introduced brown rats and house mice are often observed in seabird colonies (Figure S1.A.2). Feral cats (Felis catus) were also 188 189 introduced on the island (Micol & Jouventin, 1995), but are rarely observed in seabird colonies.

190 Field sampling

During three breeding seasons (2011-2012, 2015-2016, 2016-2017), blood samples 191 (1 mL from the metatarsal vein using heparinized syringes) and cloacal swabs (using sterile 192 cotton tips) were collected from 66 adults and 9 nestlings of brown skuas captured on their 193 nests in the southern part of PDT or in clubs at Entrecasteaux and MAE between November 194 195 and January (Table 1). Breeders handled in 2015-2016 and breeders and club attendants 196 handled in 2016-2017 were marked with leg rings for individual identification. Red blood cells and plasma were separated by centrifugation a few hours after collection. Swabs were stored 197 198 in 0.5 mL of a lysis buffer (RNA NOW[®], BIOGENTEX, USA, in 2011-2012; Longmire buffer 199 the following years; Longmire et al., 1988). Samples were kept at -20°C in the field, then stored 200 at -20°C (plasma) or -80°C (swabs) until analysis.

201 Immunological assays

202 *Pm*-specific antibody levels in plasma samples of skuas were measured using two 203 immunoassays in order to ascertain past exposure to *Pm*: an enzyme-linked immunosorbent 204 assay (ELISA; ID Screen[®] *Pasteurella multocida* Chicken and Turkey Indirect, IDvet, France; 205 with the positivity threshold determined following Garnier et al., 2017) and a microagglutination 206 test (MAT; SEROPAST[®], Ceva-Biovac, France). Technical details are given in Appendix S1.B.

207 Molecular detection of *Pm*

Total nucleic acids were extracted following the RNA NOW[®] isolation and purification protocol for skua cloacal swabs preserved in RNA NOW[®], and with the QIAamp cador Pathogen Mini[®] kit (QIAGEN, USA) for skua cloacal swabs preserved in Longmire lysis buffer. *Pm* DNA was detected with a real-time polymerase chain reaction (RT-PCR) targeting the strain previously detected in a dead sooty albatross on Amsterdam Island (Jaeger et al., 2019). Technical details are given in Appendix S1.B.

214 Movement tracking

In 2015-2016 and 2016-2017, 18 breeding skuas captured on the southern PDT were 215 also equipped with solar-powered GPS-UHF devices with a remote data download link (GPS-216 UHF Harrier-L[®], Ecotone, Poland). The GPS acquisition frequency was set at 2 to 5 min and 217 altitude above sea level was also recorded in 2015-2016 (see Appendix S1.C for more details). 218 Loggers were deployed during the early chick-rearing period (late November/early December), 219 when skuas' energetic needs are at their highest (Furness, 1987) and avian cholera outbreaks 220 221 occur in albatross colonies (Weimerskirch, 2004; Bourret et al., 2018). Sufficient data for spatial analysis (> 24h) were collected from 13 individuals, with data spanning 12-102 days 222 (median [25 and 75% quartiles] = 54 [47;85]; Table S1.C.1), covering most of the chick-rearing 223 period for the majority of the tracked individuals. A bootstrap analysis estimated this sample 224 225 to adequately represent space use of the skua population breeding on southern PDT during 226 this period (Lascelles et al., 2016; see Appendix S1.C and Figure S1.C .1).

Using the GPS data, the intensity (spatial distribution of the mean residence time per visit of each area, *i.e.*, areas where an individual tends to spend more time) and recursion (spatial distribution of the number of visits in each area, *i.e.*, areas that an individual tends to repeatedly visit) distributions were computed to get a dynamic picture of space utilisation (Benhamou & Riotte-Lambert, 2012). The overlap of the patches recursively used by different individuals was visually examined to inform on the existence of exclusive feeding territories in

233 this population. To estimate the intensity and recursion distributions, non-overlapping virtual circles of 50m in radius (referred to as "areas") were delimited. A new visit to an area occurred 234 235 each time the tracked individual re-entered it after a time lag spent outside the area longer 236 than 10 min and remained in that area for at least 15 min (to exclude cases in which birds 237 went through an area without using it) using the BRB|MKDE program (for Biased Random 238 Bridges for Movement-based Kernel Density Estimation; Benhamou, 2011). All data were analysed and represented after exclusion of locations recorded within the nesting area of the 239 240 tracked individuals unless indicated otherwise. Resulting distributions were visualized in QGIS 241 2.18.21.

242 Monitoring of yellow-nosed albatrosses

In order to assess whether skuas were present in coastal seabird colonies during avian cholera epizootics, the proportions of yellow-nosed albatross nestlings surviving and excreting *Pm* DNA in a subcolony of Entrecasteaux were used as a proxy for the progress of the epizootics. *Pm* DNA excretion was assessed using the same design used in brown skuas. Details and sample sizes are given in Appendix S1.D.

248 Statistical analyses

All statistical analyses were run using R 3.6.1 and the script available in Appendix S3. Seroprevalences were calculated as the proportion of seropositive individuals among tested individuals each year. Differences in antibody levels among locations within a year or among years in a location were investigated using Wilcoxon tests with a Bonferroni correction and a 5% significance level.

254 **Results**

255 **Detection of** *Pm* and anti-*Pm* antibodies

256 Specific antibodies were detected in all but two plasma samples from adult brown skuas by both MAT and ELISA, resulting in seroprevalence varying between 80% and 100% 257 depending on the site and year (Table 1). In 2016-2017, based on the ELISA results, antibody 258 259 levels were significantly lower in MAE than in Entrecasteaux and PDT (both p<0.01; Table 260 S1.B.1). All other pairwise comparisons were not statistically different (Figure 3). The same results were obtained from the MAT data. Pm DNA was detected in cloacal swabs of adults 261 from PDT and Entrecasteaux, but not from MAE (Table 1). The proportion of Pm positive 262 263 samples was generally low (\leq 33%), except for PDT in 2016-2017 with 8/10 positive individuals. 264 Regarding nestlings, neither specific antibodies nor Pm DNA were detected in samples from 2011-2012. In 2016-2017, Pm DNA was detected in three seronegative nestlings; one other 265 266 nestling was seropositive but not excreting Pm DNA (Table 1; Figure S1.E.1).

267 Individual movement tracking

Both years, breeding skuas moved along the western coast (south to north-east) of the island, where fur seals, albatrosses and penguins breed (Figure 4). Some individuals visited the whole western coast within 24 hours (Figure S1.C.3, Appendix S2). Breeding skuas visited the surroundings of Entrecasteaux and MAE clubs. When travelling along the cliffs, skuas exploited a large altitudinal gradient, suggesting that they potentially visited fur seals, penguins and albatross colonies (Figures S1.C.2, S1.C.3). However, none of the tracked individuals visited the Amsterdam albatross breeding area.

275 Recursively exploited areas largely overlapped among the tracked individuals (Figures 276 5, S1.C.4). Entrecasteaux cliffs were intensively and recursively exploited by all the tracked 277 individuals (Figures 5, S1.C.4, S1.C.5, Table S1.C.2), notably during avian cholera outbreaks 278 (Figure S1.D.1), and represented the only recursively visited site for four of them. Other sites 279 recursively visited included the northern part of the south-west cliff, harbouring large seabird 280 and fur seal colonies, the north coast, hosting another large fur seal colony, and the south 281 plain where seabirds and fur seals are rare, but rodent populations may be present. Note that

all the tracked individuals were seropositive and *Pm* DNA was detected in 8/13 birds (Table
S1.C.2) at the time of logger deployment.

284 **Discussion**

285 Here, we explored different scenarios of foraging strategies of a predator and 286 scavenger, the brown skua, in relation to the circulation of a pathogen within a spatiallystructured community of endangered seabirds. Movement data suggest that skuas may inter-287 connect several seabird colonies during avian cholera epizootics, potentially contributing to 288 pathogen spread. Our study allowed to characterise biological processes relevant to pathogen 289 290 circulation, such as the fact that skuas do not hold foraging territories, a necessary first step 291 to build mechanistic models of eco-epidemiological dynamics and explore potential control 292 measures (Daversa et al., 2017; Dougherty et al., 2018).

293 Skua exposure and infection by *Pm* and implications for epidemiological surveillance

294 We report the first detection of anti-Pm antibodies in skuas and show that the 295 population of brown skuas from Amsterdam Island is highly exposed to this bacterium. The 296 proximity of Entrecasteaux cliffs, where skuas may be exposed to Pm through feeding on 297 infected albatrosses and penguins (Figure S1.A.2a), may intensify exposure and explain the 298 high specific antibody levels measured in individuals sampled at the Entrecasteaux club or 299 breeding on PDT (Pepin et al., 2017). Because detailed antibody kinetics are not available, it is not possible to estimate the timing of infection from serological data. Nevertheless, the 300 detection of PCR-positive birds at Entrecasteaux club or breeding on PDT reveals ongoing 301 302 infection at the time of sampling. In contrast, skuas attending the MAE club may forage preferentially on nearby fur seal colonies, potentially minimising their exposure to Pm, which 303 would explain their lower antibody levels and the absence of PCR-positive birds at this site. 304 More generally, the important proportion of seropositive but PCR-negative adult skuas 305 306 suggests that specific antibodies may persist past the infection period, as commonly observed 307 in acute infections (Pepin et al., 2017).

308 Jaeger et al. (2018) reported the circulation of a unique Pm strain among sooty and yellow-nosed albatrosses, but technical constraints for field microbiology (e.g. low availability 309 of fresh carcasses, difficulty to obtain bacterial isolates from non-invasive approaches) limited 310 311 the sample sizes. While it is not possible to confirm that the epizootic Pm strain killing 312 albatrosses is circulating in skuas, our current understanding of the system supports the 313 circulation of a common Pm strain circulating in the different species of the island. Future works should aim at sequencing more Pm isolates from different species of the island to 314 315 confirm this hypothesis.

316 Interestingly, detection of specific antibodies in the majority of PCR-negative adults also suggests that a large proportion may survive *Pm* exposure, contrasting with the high 317 mortality rate reported during previous outbreaks in Antarctica (Parmelee, Maxson, & 318 Bernstein, 1979; Leotta et al., 2006). This heterogeneity is not surprising given the known 319 320 variability of *Pm* virulence in different hosts (Christensen & Bisgaard, 2000). Moreover, the 321 low mortality rate of adult skuas on Amsterdam Island is similar to that of adult yellow-nosed albatrosses on that island (Rolland et al., 2009; Gamble, Ganier et al., 2019), but the higher 322 seroprevalence in skuas suggests different rates of exposure and/or persistence of antibody 323 levels. If skuas are highly exposed but resistant or tolerant to infection by Pm, they could also 324 be involved in the maintenance of the pathogen on the island. This result also shows that 325 skuas are potentially good sentinels to detect the circulation of *Pm*, especially using serology 326 (Halliday et al., 2007). Hence, implementing long-term serosurveys targeting such species can 327 be especially useful for the acquisition of baseline data on (pathogenic and non-pathogenic) 328 329 infectious agent circulation and for the early detection of pathogen circulation. Indeed, in longlived species such as seabirds, monitoring protocols based only on breeding pair counts can 330 take several years before capturing juvenile mortality events because of late recruitment. 331

332 Movements and disease transmission in structured communities

333 Apex predator movements have been well studied in relation to foraging during the breeding season, but their implications for infectious agent circulation have only recently been 334 considered (Boulinier et al., 2016; de Souza Petersen et al., 2017). As observed elsewhere 335 (Carneiro et al., 2014; Pietz, 1987), skuas breeding on Amsterdam Island foraged almost 336 337 exclusively onshore, mostly along the coastal cliffs harbouring dense seabird colonies with 338 high feeding opportunities. This population may thus regularly be in contact with yellow-nosed 339 and sooty albatrosses, rockhopper penguins and subantarctic fur seals during avian cholera 340 outbreaks. Interestingly, several individuals recursively used different patches along the 341 western coasts, corresponding to different seabird and fur seal colonies: this may reflect particular opportunities for the dissemination of infectious agents. In addition, as opposed to 342 343 other populations (Trivelpiece et al., 1980; Pietz, 1987; Votier et al., 2004; but see Carneiro et al., 2014), breeding skuas on Amsterdam Island did not seem to hold individual-exclusive 344 345 feeding territories, as supported by the large space utilisation overlap among individuals. The high food availability in large breeding colonies of vertebrates may explain the absence of 346 such territories on Amsterdam Island. Accordingly, the absence of individual-exclusive feeding 347 territories associated with high seroprevalences suggests that, if breeding individuals 348 349 contribute to *Pm* circulation on the island, their role could be rather homogeneous (Figure 2), contrary to other systems (Marchand et al., 2017; Dougherty et al., 2018). However, other 350 possible sources of heterogeneity among individuals remains to be explored, such as 351 variations in the duration or intensity of shedding. 352

We did not observe breeding skuas foraging in the small and low-density breeding population of the Amsterdam albatross, suggesting that they may not connect this population to others (Figure 2b). This is consistent with the high breeding success of this albatross population over the last decades (Jaeger et al., 2018). Although a few skua pairs nest among Amsterdam albatrosses (Figure 1), contacts between the two species may be rare if skuas forage only on the coast, as movements around the nests are usually limited. However, considering the flexibility of skuas' foraging behaviour and potential behavioural differences between breeders and non-breeders, some individuals may occasionally visit this colony, especially if environmental conditions and food availability change (Carneiro et al., 2015). Such changes, modifying the host space-utilisation, can have important consequences on the dynamics of infectious agents (Merkle et al., 2017; Giles et al., 2018). Long-term monitoring of these dynamics is essential to better understand pathogen circulation, and design robust management options.

366 Maintenance and circulation of infectious agent

The population of brown skuas may play a key role in the circulation of *Pm* on 367 Amsterdam Island, but the complete maintenance community (*i.e.*, the set of connected host 368 populations that together can maintain the pathogen over the long term, notably in winter when 369 most seabirds are absent of the island; Viana et al., 2014) remains to be functionally 370 characterized. Rodents may be good candidates as local maintenance hosts of Pm, but little 371 data are yet available to examine this hypothesis. Rodents can reach high densities and are 372 373 present year-round; they may feed on dead seabird nestlings and are preved upon by skuas (Figure S1.A.2b, d). In addition, as observed in poultry (Curtis, 1983), rodents may directly 374 transmit *Pm* through movements within colonies and biting of live nestlings (Thiebot et al., 375 376 2014; Figure S1.A.2c). Hence, spatio-temporal aspects of rodent exposure to Pm and 377 subsequent shedding need to be explored from an eco-epidemiological standpoint (Lloyd-Smith, Cross, et al., 2005; Guzzetta et al., 2017). Because the home range radius of rodents 378 is likely much smaller than that of skuas, rodents could be important in the within-colony 379 spreading of *Pm*, while skuas may play a key role at a larger spatial scale. These elements 380 suggest potentially complex epidemiological networks involving several bridge hosts (Caron 381 382 et al., 2015) linking cliff-nesting seabirds to Amsterdam albatrosses. Skuas could move Pm from the costal cliffs to PDT, where a few breed in proximity to Amsterdam albatrosses. 383 Foraging rodents could then move the bacterium from those skuas to the Amsterdam 384 albatrosses. More generally, this stresses the importance of considering processes occurring 385 at nested spatial scales, and epidemiological networks in their entirety when exploring chains 386

of transmission (Boulinier et al., 2016; Daversa et al., 2017). In the case of Amsterdam Island,
future work should examine the role of introduced rodents in the maintenance and small-scale
circulation of avian pathogens.

390 Implications for conservation

391 Our study revealed that the movements of potential bridge hosts (here, skuas and potentially rodents) may reduce the efficiency of local actions aiming at controlling multi-host 392 393 infectious agents. For instance, locally intensive vaccination programs targeting albatrosses (e.g., Bourret et al., 2018; Gamble, Garnier et al., 2019) combined to rodent population control 394 395 would seem feasible in accessible seabird colonies. However, such attempts would likely fail to control the pathogen because, although the system appears highly spatially structured, 396 skuas could re-introduce the pathogen from inaccessible, hence non-treated, seabird 397 colonies. In such a system, efficient disease control measures would likely need to interrupt 398 the transmission network by targeting bridge hosts by, for instance, vaccinating native 399 400 terrestrial predators (here skuas) with a vaccine blocking transmission and eradicating introduced rodents. However, we do not recommend culling native terrestrial predators as 401 402 there are growing evidences that scavenging contribute in disease controls (e.g., Sage et al., 403 2019) and the culling of a native species would raise strong ethical issues. In the case of avian 404 cholera on Amsterdam island, an autogenous vaccine has proven efficient to protect yellow-405 nosed albatross nestlings (Bourret et al., 2018), but whether it blocks transmission remains to 406 be investigated. The direct negative impact of introduced rodents on seabird populations is 407 well documented and their eradication is seen as a priority for seabird conservation (see Duron, Shiels & Vidal, 2017 for a review). In contrast, their role in epidemiological dynamics 408 409 has rarely been explored, but its potential is highlighted by our results. Implementing the eradication of introduced rodent populations on Amsterdam Island in parallel to the 410 epidemiological monitoring of seabird populations, would provide a unique opportunity to 411 semi-experimentally assess their role in the eco-epidemiological dynamics while representing 412 413 a significant management action in itself.

414 When deciding what management measure to implement in a situation such as the one on Amsterdam Island, modelling approaches can enable the stakeholder to clearly outline 415 the management objectives, the available means to reach them, and the level of uncertainty 416 in the parameters underlying the dynamics of the system. Indeed, comparing the potential 417 418 benefits of different management strategies is not as straightforward as it may seem and we encourage stakeholders to work hand in hand with disease ecologists and modellers, even in 419 an apparently simple situation such as that on Amsterdam Island. For instance, 420 421 compartmented epidemiological models represent attractive options to assess the necessary level of rodent population control (Mariën et al., 2019) or vaccination coverage and protocols 422 423 (Haydon et al., 2006; Baker et al., 2019) to efficiently benefit endangered species while 424 accounting for their particular life-history traits (Garnier et al., 2012). Network models based on (direct or indirect) contact networks at the inter-specific (Craft et al., 2008; Woodroffe & 425 426 Donnelly, 2011) and intra-specific levels (Rushmore et al., 2014; Pepin et al., 2016; Robinson et al., 2018) could be used to explore the benefits of targeting potential super-spreading 427 428 individuals or group of individuals for vaccination or population control. Models also allow to explore sources of heterogeneity in pathogen maintenance and transmission (Marchand et 429 430 al., 2017; Dougherty et al., 2018; Robinson et al., 2018). Finally, management should ideally be conducted in an adaptive dynamic framework (Keith et al., 2011), requiring a design 431 allowing to track eco-epidemiological variables, notably through the monitoring of sentinel 432 species (Halliday et al., 2007), before and after interventions (Viana et al., 2014). The present 433 paper provide key elements to fuel such modelling approaches. 434

Authors' contributions. TB conceived the idea of this work; TB, JT, HW, KD and CB designed the study; JT, AG and J-BT collected the data; HG and ET developed the MAT; AG, AJ, CL, PT and EL performed the serology and molecular analyses; AG analysed the epidemiological data; AG, RB and J-BT analysed the tracking data; AG and TB led the writing of the manuscript. All authors contributed substantially to the drafts and gave final approval for publication.

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455 Supporting Information. Appendices S1: text and figures; S2: tracking data animation; S3:
456 R notebook.

457 Data availability statement. Data are available on the OSU-OREME Repository
458 <u>https://doi.oreme.org/b4b4a2e1-3d00-45b7-b3b2-2ca05d054346</u> (Gamble, Bazire et al.,
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Table 1. Proportions of brown skuas from Amsterdam Island positive for anti-*Pm* antibodies according to MAT and ELISA and for *Pm* DNA according to PCR or RT-PCR from cloacal swabs. Clopper-Pearson 95% confidence intervals are indicated between brackets and numbers of positive/tested individuals between parentheses.

Cite	Stage	2011-2012			2015-2016			2016-2017		
Site		MAT	ELISA	PCR	MAT	ELISA	RT-PCR	MAT	ELISA	RT-PCR
Plateau des	Breeding adults	1.00 [0.79;1.00] (16/16)	1.00 [0.79;1.00] (16/16)	0.06 [0.00;0.30] (1/16)	1.00 [0.69;1.00] (10/10)	1.00 [0.69;1.00] (10/10)	0.10 [0.00,0.45] (1/10)	1.00 [0.69;1.00] (10/10)	1.00 [0.69;1.00] (10/10)	0.80 [0.44;0.97] (8/10)
Tourbières	Nestlings	0.00 [0.00;0.71] (0/3)	0.00 [0.04;0.78] (0/3)	0.00 [0.00;0.31] (0/10)	-	-	-	0.17 [0.00;0.64] (1/6)	0.17 [0.00;0.64] (1/6)	0.50 [0.12;0.88] (3/6)
Entrecasteaux	Club attendants	-	-	-	1.00 [0.69;1.00] (10/10)	1.00 [0.69;1.00] (10/10)	0.33 [0.07;0.65] (3/10)	1.00 [0.69;1.00] (10/10)	1.00 [0.69;1.00] (10/10)	0.20 [0.03;0.56] (2/10)
Mare aux Éléphants	Club attendants	-	-	-	-	-	-	0.80 [0.44;0.97] (8/10)	0.75 [0.35;0.97] (6/8)	0.00 [0.00;0.31] (0/10)



Figure 1. Breeding sites of colonial vertebrates on Amsterdam Island (37°49'S, 77°33'E). Amsterdam albatrosses (a) nest on the northern part of the inland plateau; brown skuas (b) mostly nest on the southern part on the inland plateau; subantarctic fur seals (c) breed all around the island; Indian yellow-nosed albatrosses (d1), northern rockhopper penguins (d2) and sooty albatrosses (d3) nest in the high cliffs laying south-west of the island. The red star denotes the monitored yellow-nosed albatross subcolony. Photos: Romain Bazire, IPEV. Map background: Réserve Naturelle Nationale des Terres Australes Françaises.



660

661 Figure 2. Hypothetical (a) and observed (b) epidemiological networks linking seabirds on Amsterdam Island based on breeding brown skua movements. Each orange node represents 662 an individual skua. The hatched and white nodes represent grouped subpopulations of cliff 663 nesting birds (*i.e.*, yellow-nosed albatrosses, rockhopper penguins and sooty albatrosses) and 664 665 Amsterdam albatrosses respectively. Edge widths between skuas and other species represent 666 the relative time spent in each potential foraging area. Panel b was built based on data collected on skuas breeding in the Southern part of PDT and presented in Figure 4. Edge 667 widths between two skuas represent the probability of two individuals being present in the 668 669 same potential foraging area at the same time (see Appendix S1.F for calculation details).



670

Figure 3. Evidence of high exposure of brown skuas to *Pasteurella multocida*: anti-Pm antibody levels for skuas measured by ELISA (a) and MAT (b) over three years on Plateau des Tourbières (the main skua breeding ground on Amsterdam Island), and two clubs (Entrecasteaux and Mare aux Éléphants). Mean ± standard deviation are shown in grey. The dashed lines represent the seropositivity thresholds. For ease of visualisation, data points were horizontally jittered.



Figure 4. Space utilisation by breeding brown skuas. Left: distribution of space utilisation outside of their breeding area by all individuals equipped with GPS-UHF loggers during the chick rearing period on Amsterdam Island in 2016-2017 and 2015-2016. Right: corresponding unfiltered raw locations; each colour represents an individual.



682

Figure 5. Recursive space utilisation by breeding brown skuas equipped with GPS-UHF loggers during the chick rearing period on Amsterdam Island. The contours correspond to the individual 50% recursion distribution isopleths; each colour represents an individual with dashed and solid lines for individuals tracked in 2015-2016 and 2016-2017 respectively. See Figure S1.C.4 for individual data.