1 **Title:**

2 **A global picture of biological invasion threat on islands**

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20 **Words:**

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Introductory paragraph

Biological invasions are one of the main drivers of biodiversity losses. As threats from biological invasions increase, one of the most urgent tasks is to identify areas of high vulnerability. However, the lack of comprehensive information on the impacts of invasive alien species (IAS) is especially a problem on islands, where most recorded extinctions associated with IAS have occurred. Here we provide a global, network-oriented analysis of IAS on islands. Using network analysis, we structured 27,081 islands and 437 threatened vertebrates into 21 clusters, based on their profiles in term of invasiveness and shared vulnerabilities. These islands are mainly located in the southern hemisphere and many are in biodiversity hotspots. Some of them share similar characteristics regarding their connectivity that could be useful in understanding their response to invasive species. The major invaders found in these clusters of islands are feral cat, feral dog, pigs and rats. Our analyses reveal those IAS that systematically act alone or in combination, and the pattern of shared IAS among threatened species, providing new information to implement effective eradication strategies. Combined with further local, contextual information this can contribute to global strategies to deal with IAS.

Islands harbour a significant portion of the Earth's species and have an unusually high rate of endemism[1]. However, many species on islands are now recorded as threatened, and most recorded extinctions of vertebrate species have occurred on islands[2]. Invasive alien species (IAS) are considered the second most important driver of species extinctions on islands, and are associated with nearly 25% of birds and amphibians currently threatened worldwide[3]. Island ecosystems are particularly vulnerable to biological invasions[2]. To date, there have been over 700 attempted eradications of invasive alien mammals[4], which have benefited to 600 local populations, leading to larger populations or increased distributional areas[4]. Specifically, 236 species have benefited from those eradication programs, including 62 species that are at risk of extinction, and four species had their extinction risk reduced as a direct result of these eradications[4]. Despite these encouraging results, the threat posed by invasive alien species (IAS) remains significant and widespread for native species[3]. Thus, prioritization of research efforts and eradication strategies needs to be more effective[5] and there are many more opportunities to decrease extinction risk for island species by eradicating IAS.

Because funding allocated to conservation is limited, it is important that these interventions target islands where the conservation benefit will be highest. Efforts to prioritize research, management, and policy for IAS have traditionally relied on expert judgments, and have been limited to either single IAS[6] or subsets of islands[7,8]. In the absence of a systematic analysis of IAS impacts, it is difficult to see how an efficient and comprehensive strategy can be developed. While several recent papers have examined the threats posed by IAS globally[9] or for entire taxonomic groups (e.g., mammals[10]), all of these studies implicitly assume that the distribution of IAS reflects their impacts (e.g., in terms of the decline in native species populations they cause). However, there is much evidence that the impacts of IAS are context dependent[3,11,12], and spatially variable. Other large-scale studies have analyzed IAS impact on

89   specific archipelagoes[13] or on a particularly problematic subset of IAS[14]. But all these

90   approaches are piecemeal and cannot deliver the evidence needed to support an efficient

91   approach to focus IAS research and action at a global scale.

92   Here we use the comprehensive data compiled by the International Union for the

93   Conservation of Nature (IUCN) database, BirdLife International database and the Global

94   Invasive Species Database (GISD) to extract information about vertebrates threatened by IAS,

95   and the identity of the threatening IAS to address the three following questions: (i) How are

96   the impacts of IAS distributed among islands and threatened species? (ii) Are there

97   combinations of IAS for which targeted actions may have high conservation impacts? (iii)

98   Within the targeted areas what are the characteristics of the network between IAS and IAS-

99   threatened species that can improve strategies to deal with IAS?

100   Some species occur on multiple islands while others are endemic to a single island. Moreover,

101   some IAS are shared as threats by multiple species on the same or different groups of islands,

102   while others are very localized and specific. To gain insights into the structure of this complex

103   interconnected system we apply network approaches. Many systems can be represented as

104   networks of interconnected nodes. Networks are mathematical objects where a node is linked

105   (connected) to zero, one or several other nodes. The links highlight a relationship between

106   two nodes. For instance, each inhabitant of the world can be represented as a node in a

107   network graph and each email sent by those inhabitants to others can be represented as a link.

108   Of course with increasing node and link number, the complexity of network graphs grows

109   exponentially and limits our ability to identify structure. Network theory aims at extracting

110   significant patterns from networks.

111   In our study, we built two kinds of networks. In the first, the nodes are either species or

112   islands and the links represent the presence of a species on a given island. We clustered this

113   network to identify islands that are highly interconnected by the co-occurrence of many IAS-

114   threatened species, and selected the clusters with highest number and densities of IAS-

115   threatened species. The aim of this clustering approach is to identify group of islands that

116   share similar pattern of threatened species based on biogeographical knowledge. In the second

117   set of networks the IAS and their threatened species were linked, and related to the island

118   clusters identified in the first analysis (Methods and Materials for details). This allowed us to

119   determine the IAS that are mostly responsible of threats in those clusters of islands and we

120   used this to provide insights to deal with IAS threat.

121

122   **Results**

123   *How are the impacts of different IAS distributed among islands and threatened species?*

124   We analyzed more than 73,515 islands where the IUCN Red List recorded IAS-threatened

125   species. First, we selected islands for which we could expect high return in investment for

126   conservation program. Specifically, we selected islands that harbour more than 1% of the total

127   number of IAS-threatened species, and those with a high ratio of the number of threatened

128   species to area. We identified a total of 21 clusters (labeled in supplementary table 2) that

129   include a total of 437 IAS-threatened species on the 27,081 islands across the world that met

130   our criteria (figure 1, for the complete network see supplementary figure 1). These clusters

131   represent the groups of islands that are highly inter-connected by the co-occurrence of IAS-

132   threatened species (Figure 1) i.e., insular regions harbouring similar patterns of threatened

133   vertebrates by IAS. Most of these islands detected, vulnerable to invasions, are located in the

134   southern hemisphere and encompass most of the Caribbean and Pacific archipelagos

135   (including Hawaï), Madagascar and islands at southern of the coasts of Africa, Indonesia, the

136   coast of America, New Zealand and Australia (Figure 1a). The majority of the islands found

137   in the 21 clusters are included in the insular biodiversity hotspots[15].

138   Some clusters are fully isolated (i.e., disconnected to others in terms of IAS-threatened

139   species: e.g., Puerto Rico islands; Okinawa islands and Seychelles) because their IAS-

140   threatened species are found nowhere else. Two of the Caribbean clusters (including

141   Hispaniola and Jamaica islands), and Malaysia, Philippines, and South of east indies islands

142   are connected only to each other (Figure 1b). Overall, the clusters that share a high number of

143   threatened species with other clusters are Polynesia and Micronesia, North America Pacific

144   coast islands, as well as the South American, Antarctic, sub-Antarctic and Australian islands.

145   Our analysis revealed that most of the connections between clusters are due to bird species,

146   but amphibians, mammals and reptiles are also responsible for connections between the

147   southern part of New Zealand, Australia and southern-hemisphere islands, Caribbean clusters,

148   and African islands (supplementary figure 1). Some clusters are particularly noticeable due to

149   their high number of threaned species by IAS: New Caledonia, Hawaian islands and

150   Madagascar and African southeastern coast for reptiles, birds, and amphibians, respectively.

151   The 21 identified clusters vary in terms of number of threatened species (see size of the taxa

152   nodes of the outer circle Figure 1b), number of islands (size of the inner circle nodes, Figure

153   1b) and total area. Specifically, the number of threatened species ranges from 7 (the cut-off

154   point we selected that corresponds to at least 1% of the total number of insular threatened

155   vertebrates) to 61 species, while the number of islands ranges from 1 (i.e., Puerto Rico) to

156   7,460 (Table 1). Most of the threatened species found in these clusters are birds (51%),

157   followed by reptiles (18%), amphibians (17%) and mammals (14%), which is consistent with

158   the taxonomic groups that have been identified as threatened by IAS worldwide[3].

159   *Are there combinations of IAS for which targeted actions may have high conservation*

160   *impacts?*

161   In a second step, we analyzed the patterns of interactions between IAS and the vertebrate

162   species they threaten for the whole network and for the 21 identified clusters (Figure 2a, for

163   the complete network see supplementary figure 1). We built interaction networks with IAS

164   and IAS-threatened species as nodes. The links between nodes represent the vulnerability of a

165   given species to a known IAS (see supplementary figure 2 for each IAS-threatened species)

166   within a cluster (Figure 2a). The global interaction network revealed that most IAS are

167   threatening numerous species across different taxonomic groups. The top threatening IAS is

168   the feral cat (*Felis catus*), followed by other IAS such as rat (*Rattus spp*), feral dog (*Canis*

169   *familiaris*) and pig (*Sus scrofa*). Some IAS are more specialized, such as *Eucalyptus* spp. that

170   predominantly threatens vertebrates located in clusters of Madagascar and African

171   southeastern coast islands, the little fire ant (*Wasmannia auropunctata*) that affects reptiles in

172   the New Caledonia cluster (see also [16]) and the Chytrid Bd (*Batrachochytrium dendrobatidis)*

173   that mainly threatens amphibians in the Caribbean clusters.

174   The network approach can, in theory, help to identify the best strategies for combating IAS

175   that maximise the number of threatened species that will benefit from any eradications. For

176   example, the feral cat and feral dog eradicated alone would directly benefit to 10 and 6

177   species respectively, but targeted together could benefit up to 27 species (because 11 others

178   species are simultaneously threatened by those two IAS). Therefore, both need to be

179   controlled to achieve the highest overall conservation benefit. Note that other threatened

180   species will also benefit from such eradications because the IAS pressure on them will be

181   reduced even if other IAS are still threatening them. The control or eradication of the Chytrid

182   *Bd*, feral cats and feral dogs together could fully benefit at least 41 threatened island species

183   worldwide (Figure 2B), assuming that no other threats are significant for these species.

184   *Within the targeted areas what are the characteristics of the network between IAS and IAS-*

185   *threatened species that can improve strategies to deal with IAS?*

186   The characteristics of IAS and IAS-threatened species interaction networks within each

187   cluster can also be used to focus actions to deal with the IAS threat. In each cluster, we

188   identified the top-IAS that affect the most species (i.e., highest number of links with

189   threatened species), and the connectivity of IAS and threatened species. We also determined

190   which IAS or combinations of IAS should be targeted, in theory, to maximize the number of

191   threatened species that will fully benefit from IAS eradications per cluster. We found that the

192   top-IAS that threatens most of the native species is not necessarily the same as the IAS that

193   should in theory be eradicated to maximize the number of species that fully benefit (Table 1).

194   For most of the clusters, we found that a targeted combination of IAS will result in a better

195   outcome for threatened species than controlling only the most important invader. For instance,

196   the native species in the Polynesia and Micronesia cluster are highly threatened by feral cats.

197   Yet, targeting only feral cats would, in theory, lead to only one species fully benefiting,

198   because the other species threatened by cats are also threatened by others IAS. The combined

199   control of black rat (*R. rattus*), pacific rat (*R. exulans*) and feral cats could, in theory, fully

200   benefit to 13 species of IAS (Figure 3a). A specific example is Okinawa islands cluster. This

201   insular region might also offer good opportunities as the removal of IAS from the family

202   Herpestidae (e.g., *H. javanicus*) could directly benefit to at least 6 species and decrease

203   pressure for 6 additional species that are also threatened by other IAS (Figure 3a). The

204   number of links in the Okinawa cluster is quite low, so we can expect that the control of a low

205   number of IAS would result in a high benefit for native species. In addition, most of the

206   threatened species located in this cluster are found nowhere else (Figure 1b), so they have a

207   particularly high value for biodiversity. Note that neither the potential feasibility nor the cost-

208   effectiveness of such programs has been evaluated here and so our findings should be

209   complemented with local prioritization analyses at the island and IAS level.

210   We also identified some clusters where the networks share similar properties that could be

211   helpful in understanding their response to IAS. For example, two clusters (i.e., Papua New

212   Guinea cluster, and the South of east indies islands cluster) share both a high-density value (a

213   high ratio of the number of links per node to the number of possible links) and a relatively

214   low number of IAS in their clusters (Figure 3b). This means that the threatened species within

215   these two clusters are threatened by few IAS but these few IAS threaten most of the species in

216   this cluster. Hence, the control or eradication of this small number of IAS may offer great

217   opportunity for conservation, especially as the number of IAS-threatened species is important

218   (Figure 3a). Because these two clusters are highly disconnected from other clusters as well

219   (Figure 1b), protecting their species might be particularly significant globally. We observed

220   similar characteristics for Solomon, New Britain and New Ireland islands that may also offer

221   significant opportunities for conservation (Table 1). We also observed that the Hispaniola,

222   Jamaica and Puerto Rico clusters share similar characteristics in terms of the average number

223   of links, and density values. Some other interaction networks are particularly distinctive and

224   should be studied individually. For instance, Madagascar and Africa southeastern coast

225   clusters harbour a larger number of IAS-threatened species and New Caledonia cluster more

226   interconnections than any other clusters.

227

228   **Discussion**

229   We have identified 21 clusters of islands harbouring threatened vertebrates species that are

230   highly significant sites of IAS threat and where focusing resources, for both research and

231   conservation action should be most efficient. The spatial distribution of the 21 identified

232   clusters overlaps with the majority of global biodiversity hotspots (except some coastal

233   islands, see brown polygons represented in Figure 1a) that are priorities in terms of endemic

234   plants threatened by habitat loss[17]. Over $1 billion has been spent protecting the remaining

235   natural vegetation of these biodiversity hotspots[18]. We identified other areas important for

236   conservation, including many small islands and island groups that may offer high return on

237   investment. Specifically, we were able to identify clusters that harbour a unique part of

238   vertebrate species diversity threatened by IAS. These island clusters that include Caribbean,

239   Okinawa, Seychelles islands, and also Malaysia, Philippines, some of the Indonesian islands

240   and South of East Indies islands would qualify as priorities on their own while clusters that

241   are inter-connected (i.e., where IAS-threatened species are shared) will require also trans-

242   national efforts for conservation to be fully effective.

243   We also reaffirm here the role played by major invaders such as rats, cats, and the Chytrid *Bd*,

244   which are already known to cause widespread threats to species on islands[19–21, 22]. Feral cats

245   are well-known to drive numerous extinctions of endemic vertebrates (>175[6]). Yet, our

246   analysis quantifies their roles whether they are the only invader responsible of population

247   decline in islands or if they act in combination with other IAS on islands.

248   Most of the current eradication programs focus on single species, which may be ineffective

249   when multiple IAS are involved[23]. On the basis of our results, we suggest that targeting

250   multiple IAS simultaneously would be a more efficient strategy for species conservation[23] and

251   should be achievable as eradication programmes increase in coverage and complexity[24].

252   In our analyses we have identified the co-occurrences of IAS threat on islands and quantified

253   the potential number of species that, in theory, could benefit through the eradication of these

254   IAS. However, we do not account for predator release effect that could further threaten

255   species[25,26] or other unanticipated events (e.g., changes of vegetation or trophic webs that

256   could follow IAS eradication). In addition, we assume that all IAS have the same effect on

257   threatened species, which may not be a safe assumption but there is currently too little

258   information on which to improve this aspect of the analysis. Moreover, we did not assess the

259   potential for reintroductions or the feasibility of eradication events.

260   The eradication of the Chytrid *Bd* could, for example, be quite challenging. Indeed, we lack of

261   efficient methods to systematically eradicate the Chytrid *Bd*, although two recent advances

262   have greatly improved our understanding of amphibian-chytridiomycosis dynamics[27]. First,

263   the recognition that Bd is not one species but distinct lineages that vary in distribution and

264   virulence and, second, that species have been infected for much longer than initially thought

265   with some species co-evolving without any impact (see [27] for a review). Thus, preventing

266   measures to avoid further propagation of the Chytrid *Bd* in nearby clusters should be a

267   priority. In contrast, eradication attempts for vertebrates have been quite efficient for cats or

268   rats with failure rates of only 12%[28] as well as for invasive ants[29].

269   In general we argue that network approaches should complement local prioritization schemes

270   including eradication feasibility information to target regions and IAS for which actions

271   should be undertaken[8,30]. For example, a recent study analyzed conservation opportunities for

272   sea-bird populations in most of the 800 small, uninhabited, and high-middle-income countries

273   islands[31]. Our analyses also revealed that in some clusters it might be quite challenging to

274   protect native species from extinctions, because of the high number of IAS combinations that

275   threaten native species as shown by their high values of connectivity. Yet, local removals of

276   IAS could prevent local extirpations of native populations and therefore benefit biodiversity.

277   This is particularly the case of the Polynesia and Micronesia cluster.

278   There are some limitations of our approach that are discussed in the following. First, we

279   considered the impacts of IAS as a reduction in population size or distribution range

280   determined by the IUCN Red list of threatened species, but other type of impacts on

281   functional or genetic diversity through hybridization or ecosystem services might also be

282   important. Our network-based analyses only accounted for the existence of an impact between

283   IAS and IAS-threatened species, but not the types of impact (predation, competition, habitat

284   modification) nor the population abundance of IAS-threatened species. Moreover, we focused

285   on IAS threat, but many IAS threatened species are also affected by habitat loss or

286   overexploitation, and these threats might prevent full recovery of populations even if IAS are

287   controlled or eradicated[32]. Our work considered only IAS-threatened vertebrate species, for

288   which data are most comprehensively available, but invertebrate species are also known to be

289   particularly affected by IAS. In addition, IUCN and BirdLife provide comprehensive data for

290   some regions and taxa, but are far from being comprehensive in some regions (e.g., Africa).

291   Regarding these limitations, the analyses here should be considered as a first step to inform

292   about the combination of IAS that, in theory, might offer high return for species conservation.

293   In spite of these limitations, our results have the potential to help mitigate the impacts of

294   invasive species in insular habitats known for their remarkably rich biodiversity.

295   *Concluding remarks*

296   Our network-oriented analysis of threats posed by IAS on islands allowed us (i) to structure

297   27,081 islands and 437 threatened vertebrates into 21 clusters that could be used to define

298   priorities for conservation research and actions to address threats from biological invasion,

299   and (ii) to identify the major invaders that threaten a large number of vertebrate species. We

300   suggest that an approach based on networks that take into account islands, IAS and their

301   impacts has been largely missing from biological invasion studies, despite its potential to

302   guide effective responses. The clusters of islands with similar profiles in terms of IAS impacts

303   represents an efficient and innovative way to determine priorities for both areas and species

304   and then to better understand and mitigate the IAS threat. Continuous investment to

305   understand, eradicate, control or prevent new invasions in islands could benefit a high number

306   of endemic species that are predicted to be extirpated (e.g., [10]), and the high phylogenetic and

307   functional richness located on those islands offering an unique opportunity to mitigate the loss

308   of biodiversity and contribute to achieve international conservation commitments such as the

309   Aichi Targets 9.

310

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316

317 **Author Contributions**

318 CB and JFR conceived the study designed with the contribution of GM M. JFR and CB did

319 the analyses, BL provided initial version of computing code. CB and JFR wrote the first draft

320 of the manuscript and all authors significantly contributed to interpreting and writing the

321 manuscript.

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323 **Competing Financial Interests statement**

324 The authors declare no competing financial interests.

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327 **Material & Method**

328 **Data**

329 Information about vertebrate species threatened by invasive species was extracted from the

330 International Union for the Conservation of Nature (IUCN Red List[33]), and the BirdLife

331 International database[34]. We used the Global Invasive Species Database (GISD[35]) for

332 information on the identity of invasive alien species responsible for the threat and the Global

333 islands database from IUCN[33] website to obtain spatial data on islands worldwide

334

335 *Vertebrates threatened by IAS*

336 The species assessments of the IUCN Red List classify the risk of species extinction into one

337 of the following categories: extinct (EX), extinct in the wild (EW), critically endangered

338 (CR), endangered (EN), vulnerable (VU), near threatened (NT), least concern (LC) and data

339   deficient (DD). These categories are based on quantitative criteria that indicate the extinction

340   risk including the rate of population decline (criterion A), the size and decline of the

341   geographical range (criterion B), the population size, its fragmentation and decline rate

342   (criteria C and D) or quantitative analyses (criterion E)[36]. Prior to 2001, Red List assessments

343   were based on expert opinion but now all assessments use the standard quantitative Red List

344   Categories and Criteria, so they are objective, transparent, and repeatable. As part of the

345   species assessment process, factors associated with decline are collated for each species[37].

346   Specifically, the IUCN and BirdLife International have classified these factors into 11 main

347   threat categories (i.e. the IUCN threat classification scheme v. 3.0). These threats are: (1)

348   residential and commercial development; (2) agriculture and aquaculture; (3) energy

349   production and mining; (4) transportation and service corridors; (5) biological resource use;

350   (6) human intrusion and disturbance; (7) natural system modifications; (8) invasive and other

351   problematic species, genes and diseases; (9) pollution; (10) geological events; and (11)

352   climate change and severe weather[37]. We extracted information for terrestrial vertebrates (i.e.,

353   mammals, reptiles, amphibians and birds) that classified under (8) and identified those

354   threatened by IAS to be included our analysis.

355   We selected vertebrates that were classified into one of the threatened categories (i.e., CR, EN

356   and VU; N= 1,324) and extracted their spatial distributions (spatial polygons) from IUCN

357   spatial data for mammals, amphibians and reptiles, and from the BirdLife database[34] for birds

358   (resulted in a total N= 1,291). Spatial data were missing for 4 mammals and 29 reptiles. Note

359   that in our analyses any IAS-threat associated with a species is a binary response - either an

360   invasive alien species does impact a species or it does not; we do not consider different

361   intensities of invasive species impact (but see supplementary figure 3-4). In this way we were

362   able to identify which vertebrates are threatened by any IAS among islands.

363   *Information about invasive alien species*

364   We used the Global Invasive Species Database (GISD) which interlinks the IUCN Red List

365   with IAS information[35]. The information in the GISD has been compiled from many sources

366   including scientific papers and regional databases that have been reviewed by international

367   expert contributors. Specifically, for vertebrate species identified as threatened by IAS, we

368   collected information about the identity of IAS responsible.

369

370   *Island data*

371   We used the Global islands database from IUCN website

372   (http://www.iucnredlist.org/technical-documents/red-list-training/iucnspatialresources), a

373   spatial dataset of more than 180,488 islands [33]. We overlaid the spatial polygon of islands and

374   the polygon of vertebrate species distributions to derive a set of 73,515 islands where

375   vertebrate species are threatened by IAS (see supplementary methods for more details). When

376   an overlap between an island and the polygon of species distribution was indistinct, we

377   visually checked the species distribution. In order to restrict the analysis to insular vertebrates

378   (persisting only on islands), we excluded species that were both on continental coastal areas

379   and islands. The resulting dataset includes 97 amphibians threatened by IAS on 903 islands,

380   120 reptiles on 2,340 islands, 336 birds on 72,433 islands and 110 mammals on 9,709 islands.

381

382   **Bipartite networks**

383   We first built an island and IAS-threatened species network that we clustered into groups of

384   islands on the basis of shared IAS-threatened species. Then, for each of the clusters, we

385   conducted analyses of IAS and IAS-threatened species interaction networks.

386   *Analyses of the island - IAS-threatened species network*

387   Recently, geographical relationships between species and localities has been abstracted as a

388   bipartite association network, where links are the occurrences of species within geographical

389   locations[38]. Similarly, the occurrence of species on islands worldwide can be represented as a

390   network for which nodes are either species or islands. When a species is present on a given

391   island, a connection between this species and the island is established in the network. As

392   species never connect to species, and islands never connect to islands (i.e., links only connect

393   species to island in the network), such a network is called a bipartite network. This network

394   provides information on co-occurrences of species on islands, the number of times species co-

395   occur, and the number of species shared by particular groups of islands. In this study, we built

396   the network with all vertebrate species threatened by IAS on islands. We chose a

397   biogeographical approach to represent connections between islands, IAS-threatened species

398   and invasive without any *a priori* knowledge of political jurisdiction or geographical

399   proximity. Indeed, native and invasive species do not respect political boundaries, but mostly

400   environmental boundaries. Thus, it makes more biological sense to use biogeography of

401   species (spatial distribution of species) to delimit the impact of invasive species across islands

402   as it will better reflect the processes of dispersion among islands than other types of

403   boundaries.

404   Since such an interconnected network has a high degree of complexity (663 species, 73,515

405   islands), numerous techniques have been developed to synthesize information by clustering

406   nodes (e.g., the map equation minimization approach[39] and the modularity maximization

407   approach[40]). Among these techniques, the map equation algorithm[39] has been proven

408   particularly well suited for cluster networks in comparative studies[41,42,38]. This technique

409   allows us to extract meaningful ecological structure composed of islands and species that are

410   similar. Specifically, this technique will allow us to cluster our bipartite network based on

411   biogeographical knowledge (species distribution) and detect common patterns of threatened

412   species among islands.

413   The map equation algorithm is iterative: first it chooses a random node, and then randomly

414   selects a second node that is connected to the first one. This process is repeated a random

415   number of times. Then another node is chosen randomly and the same process repeated. If

416   some nodes are strongly interconnected, this process tends to frequently select the same

417   nodes, which are then attached to a cluster. In groups of islands with marked structure (high

418   connectivity), the algorithm will focus mostly within clusters, crossing only when a cross-

419   cluster species is selected. Once the algorithm go through all the nodes of the system, it will

420   provide the list of clusters where it spent more time[38]. This technique allows us to extract

421   meaningful ecological structure composed of islands and species that are connected.

422   We expected a hierarchical structure in the dataset – due to the nested nature of species

423   distribution - as species may be located on specific islands, which are encompass in

424   archipelagos, and on larger regions. Consequently, we applied the multiple-level

425   implementation of the map equation, which produces hierarchically nested groups of clusters.

426   Thus, the algorithm hierarchically partition the groups of nodes into clusters [43,44].

427   In this study, a three-step approach was used to identify clusters of islands and species that are

428   of high interest for conservation.

429   (1) We applied the map equation algorithm to define clusters of island based on IAS-

430   threatened species co-occurrences, and attributed hierarchical levels into clusters that

431   correspond to a subset of the original network in which species and islands are strongly inter-

432   connected to each other, but weakly linked to species and islands outside the group[45].

433   (2) We selected clusters with high conservation interest defined as those that harbour at least

434   1% of all IAS-threatened species (>6 IAS-threatened species, see supplementary figure 6 for

435   sensitivity analyses of this parameter).

436   (3) We then selected, for each branch in the hierarchy, clusters that maximize the ratio of the

437   number of IAS threatened species to the total area. In this way we identify islands with a high

438   density of threatened species. Specifically, we chose to maximize the ratio between number of

439   threatened species and total area for a given unit area (km2 here), so the eradication events

440   could benefit to a high number of species. Indeed, eradications outcome are more likely to

441   succeed on a small area[46] than large ones. We made the assumptions here that all species have

442   the same value and interest for conservation, without any distinctions of their originality or

443   role for the community or ecosystem Therefore, we attempted with this criterion to consider

444   the opportunity for eradication to protect many species as possible.

445   The application of those criteria results in the exclusion of 226 species (24 amphibians, 111

446   birds, 50 mammals, and 41 reptiles) (black nodes in Figure 1b) as they did not meet the

447   criteria detailed below. Note that 14 of the excluded IAS-threatened species could offer

448   particular opportunities for research and eradication programs as 4 birds, 5 reptiles and 5

449   amphibians are both located on single islands and are threatened by only one identified IAS

450   (see list in the supplementary table 1).

451   From these three steps we obtained 21 clusters that correspond to groups of strongly inter-

452   connected species and islands with a high density of IAS-threatened species (see

453   supplementary figure 5 for illustration of the 3-step approach). For each cluster we document

454   the number of IAS-threatened species, number of islands, total area (km^2), and identities of

455   IAS-threatened species (Table 1).

456

457   *IAS - IAS-threatened species interaction network*

458   Thereafter, for each of the 21 clusters, we constructed an interaction network between IAS-

459   threatened species and their associated IAS. This relationship is based on the IUCN GISD

460   information that identified which IAS threatens which species. The majority of IAS-

461   threatened species are threatened by several invasive alien species. Using a network to

462   describe the relationships between IAS-threatened species and IAS provides the means to list

463   all species threatened by a given IAS and how they are linked to other IAS.

464   For each of the 21 interaction networks we identified the (i) top-IAS per cluster (*i.e.,* IAS with

465   the highest number of links to threatened species), (ii) number of nodes (total number of IAS

466   and threatened vertebrates included in the cluster), (iii) number of links (total number of

467   interactions between IAS and threatened vertebrates), (iv) the connectivity of IAS and their

468   threatened species nodes (i.e., the average number of links (interactions) per IAS and their

469   threatened species) and (v) graph density: a ratio of the number of links per node to the

470   number of possible links. Knowing a network's property regarding connectivity is important

471   here for two reasons. First, it will help us to identify if control of certain IAS in the network

472   will have positive effects on a number of threatened species. Conversely, knowing the number

473   of connections of IAS-threatened species will help determine which IAS should primarily be

474   controlled or eradicated. Indeed, the connectivity of IAS and their threatened species nodes

475   will help us to identify how IAS and threatened species are connected. It can be used to

476   identify which IAS threaten a large number of species and if those threatened species share

477   the same IAS or not. This can indicate how eradication of any IAS will benefit different

478   threatened species. We also measured whether the network is close to saturation (density

479   value close to 1, indicating that all the possible interactions have been achieved). In a

480   saturated network where the threatened species are threatened by many IAS it will be very

481   difficult to release significant pressure on threatened species, as most IAS would have to be

482   removed to release significant pressure on threatened species. Yet, in a saturated network,

483   where the threatened species are threatened by a low number of IAS, it will be highly

484   beneficial to conduct eradication campaings, especially if the number of threatened species is

485   high.

486

487   *Maximising the number of IAS-threatened species that may benefit from IAS eradication*

488   Finally we calculated, for the whole network (n=21 clusters), the combination of IAS for

489   which control or eradication programs could theoretically benefit the largest number of

490   threatened species. Specifically, for each potential combination of invasive species (from 1 to

491   5 IAS), we calculated the number of species that would be invasive free after eradication of

492   that combination of IAS. We found the best strategy by testing every possible eradication

493   scenario (see Fig. 2b). Any IAS-threatened species could benefit from the eradication of one

494   or several of its associated IAS, but the highest conservation benefit would require all of its

495   known IAS (according to the IUCN-GISD data) to be eradicated. For this analysis, we assume

496   that a threatened species only benefits from the eradication, if all invasive species that affect it

497   are eradicated. Obviously, this assumption does not necessarily reflect of real ecological

498   situations because other native species might also benefit from such eradications. But, it is not

499   possible to predict the effect of eradication for partially benefited species (such data do not

500   exist at the global scale). In addition it is worth noting that many other factors, such as Allee

501   effects or the existence of other threats may limit recovery, even if all invasive species are

502   eradicated. Consequently, for the purposes of the analyses, we define conservation success as

503   the eradication all of the known IAS threatening a given species. Note that eradicating any

504   IAS may also benefit others species by releasing pressure on them, even if other IAS are still

505   threatening them. For example if a $species_A$ is threatened only by a IAS_B the eradication of

506   this IAS_B in the cluster will theoretically allow $species_A$ to recover. But, if $species_A$ is

507   threatened by IAS_B, IAS_C, IAS_D, the removal of IAS_B will not be sufficient to permit the full

508   recovery of the $species_A$, it will only release some pressure. We report the top 5 IAS whose

509   eradication would most benefit IAS-threatened species across the whole network.

510   We conducted the same analysis for each cluster. We kept the identity of the IAS or the

511   combination of IAS that maximize the ratio of the number of invasive-free species to the

512   number of necessary eradicated IAS per cluster.

513   All analyses were carried out with R version 3.2.4 using ggplot2[47] maptools[48], igraph[49],

514   infomap version 0.18.2[41] and dplyr[50] packages, and gephi software[51] under Debian-Linux

515   operating system.

516

Data availability:

518 The dataset of the co-occurrence of species on islands is available in Zenodo data repository
519 (http://doi.org/10.5281/zenodo.884886). The code to create the network is available on
520 request.

521

522 **References**

523

524 1. Kier, G. *et al.* Global patterns of plant diversity and floristic knowledge. *Journal of*
525   *Biogeography* **32,** 1107–1116 (2005).

526 2. Bellard, C., Cassey, P. & Blackburn, T. M. Alien species as a driver of recent
527   extinctions. *Biology Letters* **12,** 20150623 (2016).

528 3. Bellard, C., Genovesi, P. & Jeschke, J. M. Global patterns in threats to vertebrates by
529   biological invasions. *Proceedings of the Royal Society B: Biological Sciences* **283,**
530   20152454 (2016).

531 4. Jones, H. P. *et al.* Invasive mammal eradication on islands results in substantial
532   conservation gains. *Proceedings of the National Academy of Sciences* 1–6 (2016).
533   doi:10.1073/pnas.1521179113

534 5. Nogales, M. *et al.* Feral Cats and Biodiversity Conservation. *BioScience* **63,** 804–810
535   (2013).

536 6. Helmstedt, K. J. *et al.* Prioritizing eradication actions on islands: it's not all or nothing.
537   *Journal of Applied Ecology* **53,** 733–741 (2016).

538 7. Dawson, J. *et al.* Prioritizing islands for the eradication of invasive vertebrates in the
539   United Kingdom overseas territories. *Conservation Biology* **29,** 143–153 (2015).

540 8. Early, R. *et al.* Global threats from invasive alien species in the twenty-first century
541   and national response capacities. *Nature Communications* **7,** 12485 (2016).

542   9.   McCreless, E. E. *et al.* Past and estimated future impact of invasive alien mammals on

543   insular threatened vertebrate populations. *Nature Communications* **7,** 12488 (2016).

544   10.   Gallardo, B., Clavero, M., Sanchez, M. I. & Vila, M. Global ecological impacts of

545   invasive species in aquatic ecosystems. *Global Change Biology* 151–163 (2015).

546   doi:10.1111/gcb.13004

547   11.   Kumschick, S. *et al.* Ecological Impacts of Alien Species: Quantification, Scope,

548   Caveats, and Recommendations. *BioScience* **65,** 55–63 (2015).

549   12.   Carrion, V., Donlan, C. J., Campbell, K. J., Lavoie, C. & Cruz, F. Archipelago-wide

550   island restoration in the Galápagos Islands: reducing costs of invasive mammal

551   eradication programs and reinvasion risk. *PloS one* **6,** e18835 (2011).

552   13.   Courchamp, F., Chapuis, J.-L. & Pascal, M. Mammal invaders on islands: impact,

553   control and control impact. *Biological Reviews* **78,** 347–83 (2003).

554   14.   Berman, M. *et al.* Overview of the Distribution, Habitat Association and Impact of

555   Exotic Ants on Native Ant Communities in New Caledonia. *PLoS ONE* **8,** e67245

556   (2013).

557   15.   Myers, N., Mittermeier, R. A., Mittermeier, C. G., Da Fonseca, G. A. & Kent, J.

558   Biodiversity hotspots for conservation priorities. *Nature* **403,** 853–858 (2000).

559   16.   Sloan, S., Jenkins, C. N., Joppa, L. N., Gaveau, D. L. A. & Laurance, W. F.

560   Remaining natural vegetation in the global biodiversity hotspots. *Biological*

561   *Conservation* **177,** 12–24 (2014).

562   17.   Doherty, T. S., Glen, A. S., Nimmo, D. G., Ritchie, E. G. & Dickman, C. R. Invasive

563   predators and global biodiversity loss. *Proceedings of the National Academy of*

564   *Sciences* **113**, 11261-11265 (2016).

565   18.   Bonnaud, E. *et al.* The diet of feral cats on islands : a review and a call for more

566   studies. *Biological Invasions* **13**, 581–603 (2011).

567 19. Medina, L. I. X. M., Bonnaud, E., Vidal, E. & Tershy, B. R. A global review of the

568   impacts of invasive cats on island endangered vertebrates. *Global Change Biology* **17,**

569   3503–3510 (2011).

570 20. Jones, H. P. *et al.* Severity of the Effects of Invasive Rats on Seabirds: A Global

571   Review. *Conservation Biology* **22,** 16–26 (2008).

572 21. Glen, A. S. *et al.* Eradicating multiple invasive species on inhabited islands: the next

573   big step in island restoration? *Biological Invasions* **15,** 2589–2603 (2013).

574 22. Keitt, B. *et al.* Best practice guidelines for rat eradication on tropical islands.

575   *Biological Conservation* **185,** 17–26 (2015).

576 23. Bergstrom, D. M. *et al.* Indirect effects of invasive species removal devastate World

577   Heritage Island. *Journal of Applied Ecology* **46,** 73–81 (2009).

578 24. Rayner, M. J., Hauber, M. E., Imber, M. J., Stamp, R. K. & Clout, M. N. Spatial

579   heterogeneity of mesopredator release within an oceanic island system. *Proceedings of*

580   *the National Academy of Sciences of the United States of America* **104,** 20862–5

581   (2007).

582 25. Lips, K. R. Overview of chytrid emergence and impacts on amphibians. *Philosophical*

583   *Transactions of the Royal Society of London B: Biological Sciences* **371,** (2016).

584 26. B. Keitt *et al.* in *Island invasives: eradication and management* (ed. Veitch, C. R.;

585   Clout, M. N. and Towns, D. R. (eds. .) 74–77 (2011).

586 27. Hoffmann, B. D., Luque, G. M., Bellard, C., Holmes, N. D. & Donlan, J. Improving

587   invasive ant eradication as a conservation tool: A review. *Biological Conservation*

588   **198**, 37-49 (2016)

589 28. Helmstedt, K. J. *et al.* Prioritizing eradication actions on islands: it's not all or nothing.

590   *Journal of Applied Ecology* **53,** 733–741 (2016).

591   29. Spatz, D. R. *et al.* The biogeography of globally threatened seabirds and island

592   conservation opportunities. *Conservation Biology* **28,** 1282–1290 (2014).

593   30. Doherty, T. S., Dickman, C. R., Nimmo, D. G. & Ritchie, E. G. Multiple threats, or

594   multiplying the threats? Interactions between invasive predators and other ecological

595   disturbances. *Biological Conservation* **190,** 60–68 (2015).

596   31. IUCN. (2015). International union for Conservation of Nature

597   http://www.iucnredlist.org/

598   32. BirdLife International and NatureServe (2014) Bird species distribution maps of the

599   world. Version 4.0. BirdLife International, Cambridge, UK and NatureServe,

600   Arlington, USA. [Available for download

601   at: http://www.birdlife.org/datazone/info/spcdownload]

602   33. ISSG. Global Invasive Species Database. *Invasive Species Specialist Group (ISSG) of*

603   *the IUCN Species Survival Commission* (2016). at http://www.issg.org/database

604   34. Mace, G. M. *et al.* Quantification of extinction risk: IUCN's system for classifying

605   threatened species. *Conservation biology : the journal of the Society for Conservation*

606   *Biology* **22,** 1424–42 (2008).

607   35. Salafsky, N. et al. A standard lexicon for biodiversity conservation: unified

608   classifications of threats and actions. Conservation Biology 22, 897–911 (2008).

609   36. Vilhena, D. a & Antonelli, A. Beyond similarity : A network approach for identifying

610   and delimiting biomes. Nature Communications **6**, 1–9 (2014).

611   37. Rosvall, M. & Bergstrom, C. T. Multilevel compression of random walks on networks

612   reveals hierarchical organization in large integrated systems. PLoS ONE 6, (2011).

613   38. Graham, J. I. M. et al. Vision of a Cyberinfrastructure for Nonnative , Invasive Species

614   Management. BioScience **58**, 263–268 (2008).

615   39. Lancichinetti, A. & Fortunato, S. Community detection algorithms: A comparative

616   analysis. Physical review E 80, 1–11 (2009).

617   40.   Aldecoa, R. et al. Exploring the limits of community detection strategies in complex

618   networks. Scientific Reports **3**, 75–174 (2013).

619   41.   Rosvall, M., Axelsson, D. & Bergstrom C.T. The map equation. Eur. Phys. J. Special

620   Topics **178**, 13–23 (2009).

621   42.   Rosvall, M. & Bergstrom, C. T. Maps of random walks on complex networks reveal

622   community structure. Proceedings of the National Academy of Sciences of the United

623   States of America **105**, 1118–23 (2008).

624   43.   Tylianakis, J. M., Laliberte, E., Nielsen, A. & Bascompte, J. Conservation of species

625   interaction networks. Biological Conservation **143**, 2270–2279 (2010).

626   44.   Wickham, H. ggplot2: Elegant Graphics for Data Analysis. (2009). at

627   <http://ggplot2.org>

628   45.   Bivand, R. & Lewin-Koh, N. maptools: Tools for Reading and Handling Spatial

629   Objects. (2016). at https://cran.r-project.org/package=maptools

630   46.   Pluess T, Cannon R, Jarošík V, et al When are eradication campaigns successful? A

631   test of common assumptions. Biological Invasions **14**,1365–1378 (2012)

632   47.   G, C. & Nepusz T. The igraph software package for complex network research.

633   (2006). at <http//igraph.org>

634   48.   Wickham, H. & Francois, R. dplyr: A Grammar of Data Manipulation. (2015). at

635   <https://cran.r-project.org/package=dplyr>

636   49.   Bastian, M. & Heymann, S. Gephi: an open source software for exploring and

637   manipulating networks. (2009). at

638   <http://www.aaai.org/ocs/index.php/ICWSM/09/paper/view/154>

639   50.   Mittermeier, R. A. A. et al. Hotspots Revisited : Earth's biologically richest and most

640   endangered ecoregions. Sierra (Mexico : CEMEX, 2004). at

641   <http://www.worldcat.org/isbn/9686397779>

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Figure legends

Figure 1: Bipartite IAS-threatened species/islands network. A - The map represents the location of the 27,081 islands included in the 21 clusters coded using ID number and colour (see legend). Brown areas show the location of biodiversity hotspots originally defined by Myers and then updated to 35 hotspots[17,52]. B- Graphical summary of the 21 clusters; each cluster is defined by islands and IAS-threatened species, and distinguished using the same colour as in (a). with the ID numbers shown (see the legend for the labels). The size of the nodes in the inner circle is log-proportional to the number of islands in the cluster, and the size of the nodes in the outer circle is log-proportional to the number of species of each taxon in a cluster. Shapes representing the higher taxa are shown in the circle when possible. The width of the grey links is log-proportional to the number of species that are located in two given clusters. Nodes (islands and IAS-threatened species) represented in black on the right-hand side of the figure show the species and islands that were not included the analysis (see Materials and Methods)

Figure 2: A- Global interaction network between IAS in black (n=169) and individual threatened species (n=397; green = mammals, red = birds, purple = amphibians, blue = reptiles). Node size of the IAS is proportional to the number of species that it is reported to threaten, while the node size for higher taxa is log-proportional to the number of species threatened by IAS. Some IAS shapes are represented: rats (including R. exulans, R. norvegicus, R. rattus, and R. unspecified), pig *(Sus scrofa),* ant *(Wasmannia auropunctata),* feral dogs *(Canis familiaris), Chytrid Bd, and* feral cat *(Felis catus)* **B**- *Barplot of the theoretical number of vertebrate species that would fully benefit from the removal of the top (Chytrid Bd) to top 5 IAS in the network.*

Figure 3: A-Representation of two networks between IAS (in black) and IAS-threatened species (in color, green = mammals, red = birds, purple = amphibians, blue = reptiles) for ID 1 and ID 18. Some IAS shapes are represented: ant, pig, rats and feral cat for ID1, Herpestidae family and cat for ID 18. Note that Herpestes sp. appears twice because one node represens the whole Herpestidae family and the other represents species identified as H. javanicus B- Radarplot showing the network characteristics for Caribbean clusters (ID 13, 14, 15), and the Indonesian region clusters (ID 17, 20). All the variables (number of

threatened species, total number of nodes, total number of links, density, average number of
700 *links per threatened species, average number of links per IAS, and number of islands) have*
701 *been normalized for comparison.*
702
703 **Table 1:** *Characteristics of the 21 clusters based on the two types of networks: the network of*
704 *IAS-threatened species and islands, and the interaction network between IAS and their*
705 *threatened species. The table reports the cluster ID, the number of IAS-threatened species, the*
706 *number of islands, the total area in km2, the top invaders, the percentage of IAS included in*
707 *the network, the average number of links per IAS-threatened species and per IAS, the density*
708 *of the network, the combination of IAS that in theory could benefit to the highest number of*
709 *vertebrate species, and the number of vertebrate species free of IAS. The latter quantity is*
710 *defined as the number of threatened species for which all known IAS in the cluster are*
711 *eradicated based on the stated combination of IAS. Note that when the ratio between the*
712 *number of targeted IAS and the number of vertebrates free of IAS is less than 1, we did not*
713 *include it in the table.*
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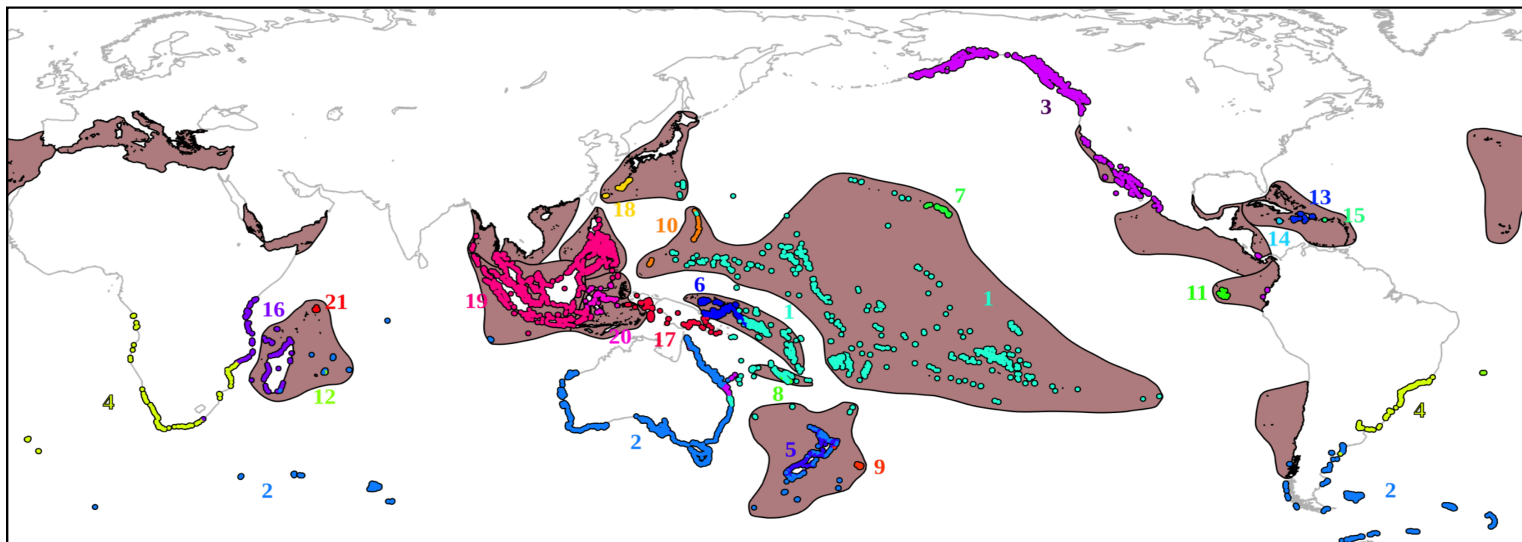715
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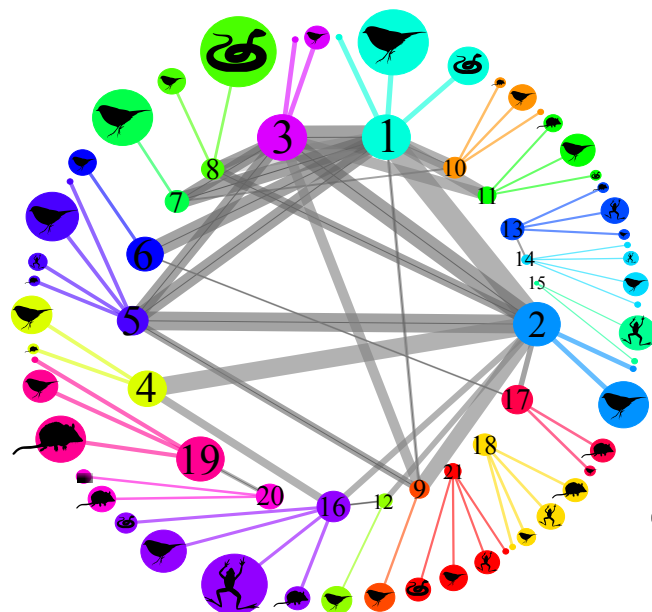723
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733 **Table 1:**

ID	Nb. of IAS-threatened sp.	Nb. of Islands	Area (km²)	Top-1st IAS	% of IAS	Mean nb. of link per IAS-threatened sp.	Mean nb. of link per IAS	Density	Combination of IAS to target	Nb. of full benefit
1	54	6011	52488	F. catus	42,3	3,3	4,5	0,1	R. rattus+F. catus+R. exulans	13
2	20	4836	106070	F. catus	67,2	3,9	1,9	0,1	F. catus+R. norvegicus	3
3	7	7460	124150	F. catus	60	2,8	1,9	0,31	R. rattus	1
4	15	1034	3004	Rattus spp.	46,1	2	2,3	0,17	F. catus	2
5	28	263	266420	M. erminea	62,2	5,3	3,2	0,12	Chytrid Bd	1
6	7	741	48737	F. catus	36,4	1,9	3,2	0,46	C. familiaris+F. catus+Rattus spp.	6
7	28	70	16891	P. relictum	63,2	8,1	4,7	0,17	-	-
8	55	56	16700	Family rodentia	24,7	3,7	11,4	0,21	-	-
9	8	31	983	F. catus	61,9	4	2,5	0,31	-	-
10	10	56	1523	B. irregularis	64	3,8	2,1	0,24	B. irregularis	1
11	16	24	8081	R. rattus	62,5	4,7	2,8	0,19	M. musculus+R. Rattus	4
12	8	13	1894	L. robustum	74,2	6,25	2,2	0,27	-	-
13	11	63	74555	Chytrid Bd	41,2	1,6	2,3	0,23	Chytrid Bd	6
14	11	5	11028	Rattus spp. + others	54,2	1,7	1,5	0,13	-	-
15	12	1	8761	Chytrid Bd	36,9	1,6	2,7	0,23	Chytrid Bd	7
16	61	387	598629	Eucalyptus spp.	30,9	2,1	4,7	0,08	-	-
17	8	256	823053	R. rattus + others	40	1,2	1,7	0,29	C. familiaris	2
18	18	64	3091	F. catus	54,2	1,9	3,6	0,21	family herpestidae	6
19	30	5566	1656400	F. catus	40	1,6	2,4	0,10	Rattus spp.	4
20	10	126	196869	C. familiaris	36,4	1,7	3	0,43	C. familiaris + F. catus	5
21	20	18	250	F. catus	53,9	2,9	2,5	0,21	T. ecaudatus	2

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a
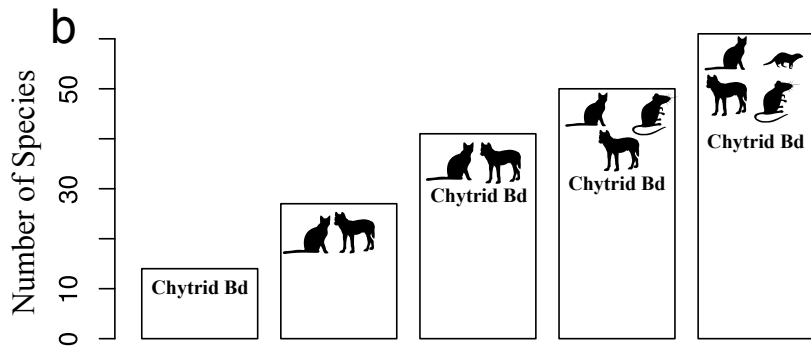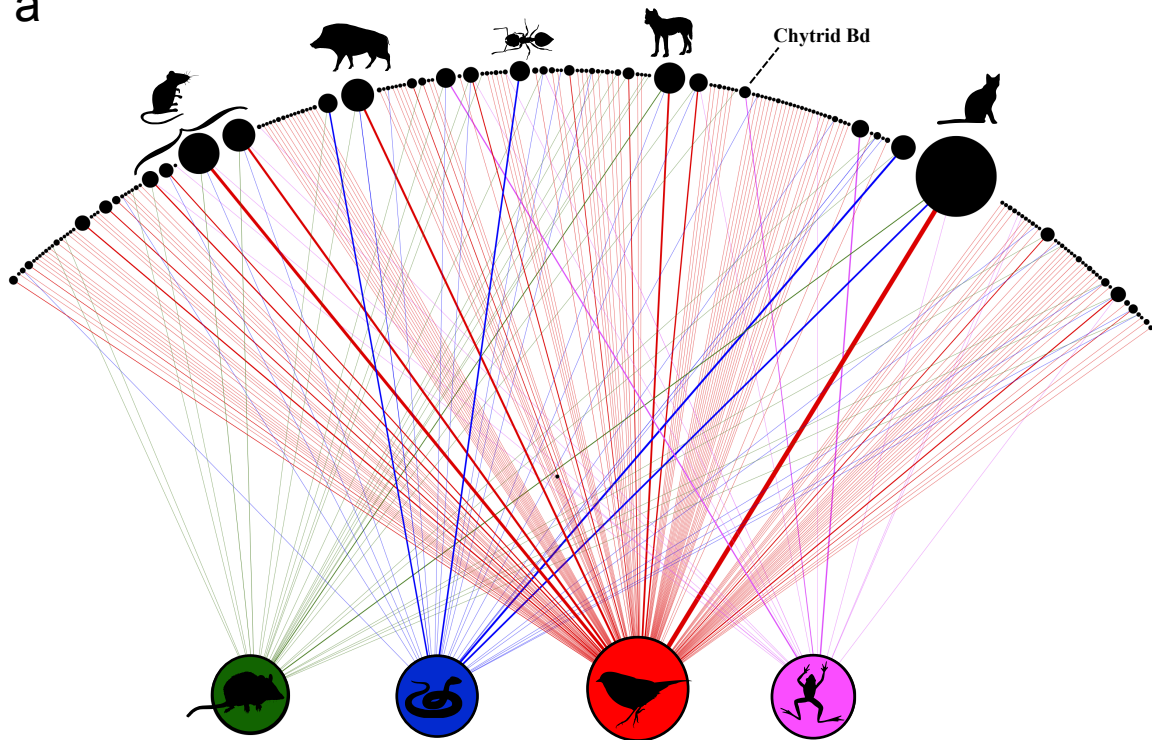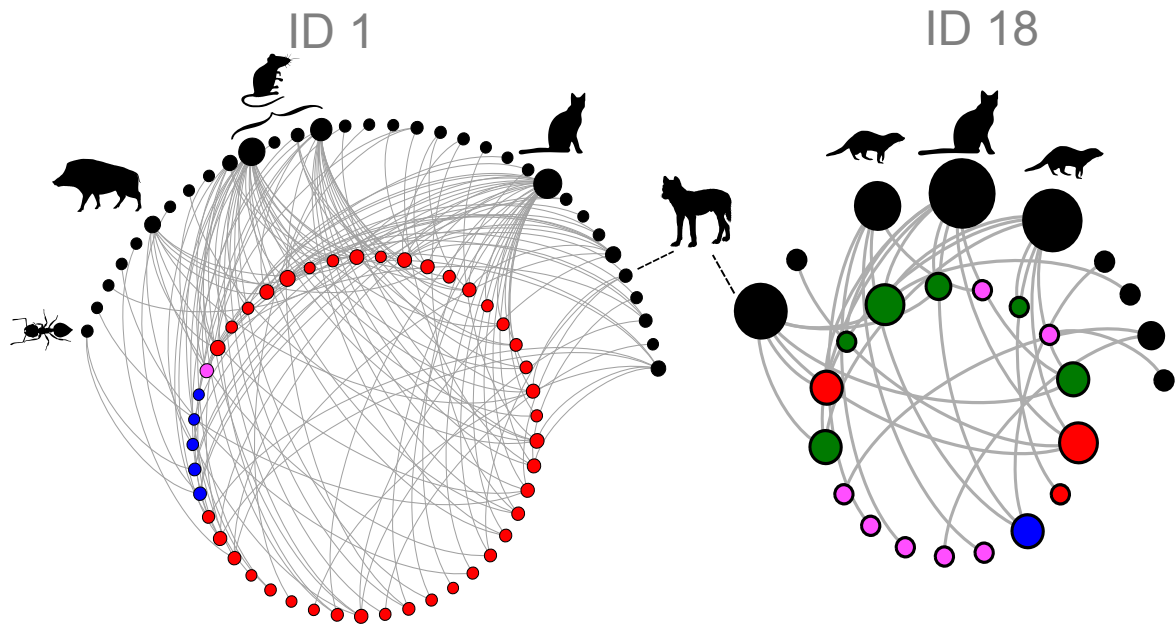
b

ID	Main location		
1	Polynesia and Micronesia	12	Mauritius and Trindade
2	South America, Antarctic, sub-Antarctic and Australian islands	13	Hispaniola
3	North America Pacific Coast	14	Jamaica
4	Southeastern Brazil and South Africa	15	Puerto Rico
5	New Zealand	16	Madagascar and Africa southeastern coast
6	Solomon, New Britain and New Ireland islands	17	Papua New Guinea
7	Hawaiian islands	18	Okinawa Islands
8	New Caledonia islands	19	Malaysia, Philippines and Indonesian islands
9	New Zealand and Chatham islands	20	South of east indies islands
10	Mariana Islands	21	Seychelles
11	Galápagos Islands		
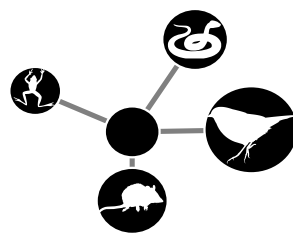
Islands and species outside of the 21 clusters

a

Chytrid Bd

b

Number of Species

Chytrid Bd

Chytrid Bd

Chytrid Bd

Chytrid Bd

Chytrid Bd

a

ID 1   ID 18
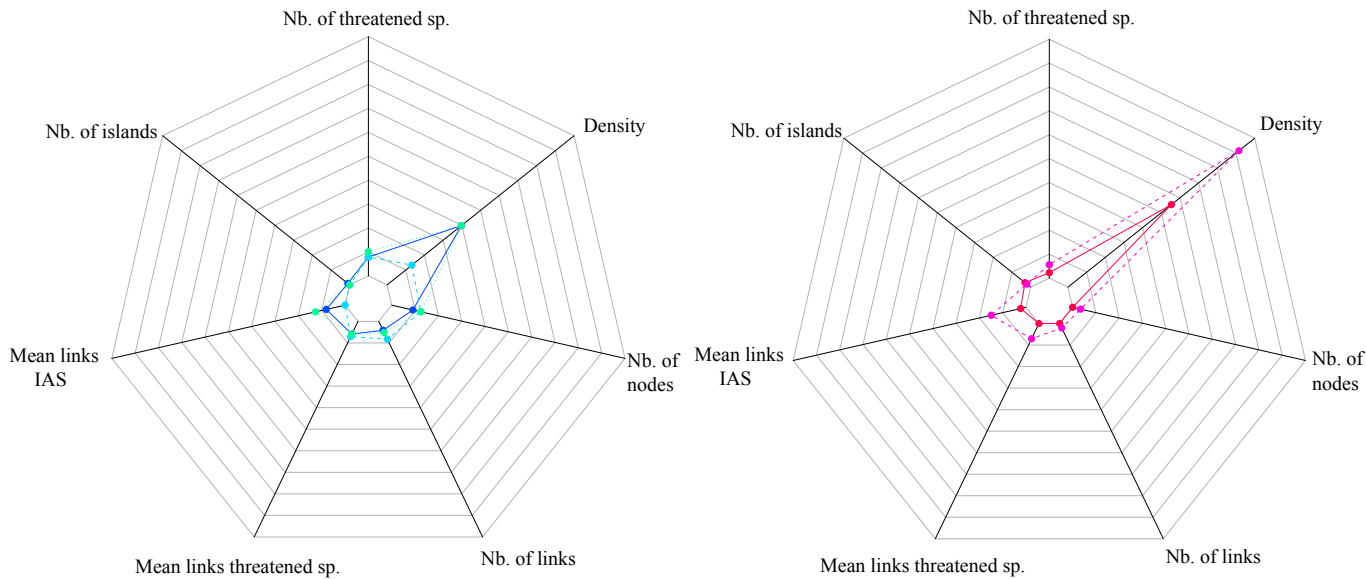
b

ID 13 14 15 (Hispaniola, Jamaica, Puerto rico)

ID 17 20 (Papua New Guinea, South of east indies islands)

Nb. of threatened sp.

Density

Nb. of islands

Nb. of nodes

Mean links IAS

Mean links threatened sp.

Nb. of links

Nb. of threatened sp.

Density

Nb. of islands

Nb. of nodes

Mean links IAS

Mean links threatened sp.

Nb. of links

Table 1:

ID	Nb. of IAS-threatened sp.	Nb. of Islands	Area (km²)	Top-1st IAS	% of IAS	Mean nb. of link per IAS-threatened sp.	Mean nb. of link per IAS	Density	Combination of IAS to target	Nb. of full benefit
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3	7	7460	124150	*F. catus*	60	2,8	1,9	0,31	*R. rattus*	1
4	15	1034	3004	Rattus spp.	46,1	2	2,3	0,17	*F. catus*	2
5	28	263	266420	*M. erminea*	62,2	5,3	3,2	0,12	Chytrid Bd	1
6	7	741	48737	*F. catus*	36,4	1,9	3,2	0,46	*C. familiaris+F. catus+Rattus spp.*	6
7	28	70	16891	*P. relictum*	63,2	8,1	4,7	0,17	-	-
8	55	56	16700	Family rodentia	24,7	3,7	11,4	0,21	-	-
9	8	31	983	*F. catus*	61,9	4	2,5	0,31	-	-
10	10	56	1523	*B. irregularis*	64	3,8	2,1	0,24	*B. irregularis*	1
11	16	24	8081	*R. rattus*	62,5	4,7	2,8	0,19	*M. musculus+R. Rattus*	4
12	8	13	1894	*L. robustum*	74,2	6,25	2,2	0,27	-	-
13	11	63	74555	Chytrid Bd	41,2	1,6	2,3	0,23	Chytrid Bd	6
14	11	5	11028	Rattus spp. + others	54,2	1,7	1,5	0,13	-	-
15	12	1	8761	Chytrid Bd	36,9	1,6	2,7	0,23	Chytrid Bd	7
16	61	387	598629	Eucalyptus spp.	30,9	2,1	4,7	0,08	-	-
17	8	256	823053	*R. rattus + others*	40	1,2	1,7	0,29	*C. familiaris*	2
18	18	64	3091	*F. catus*	54,2	1,9	3,6	0,21	*family herpestidae*	6
19	30	5566	1656400	*F. catus*	40	1,6	2,4	0,10	*Rattus spp.*	4
20	10	126	196869	*C. familiaris*	36,4	1,7	3	0,43	*C. familiaris + F. catus*	5
21	20	18	250	*F. catus*	53,9	2,9	2,5	0,21	*T. ecaudatus*	2

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