

The Parasite Extinction Assessment & Red List: an open-source, online biodiversity database for neglected symbionts

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Abstract Parasite conservation is a rapidly growing field at the intersection of ecology, epidemiology, parasitology, and public health. The overwhelming diversity of parasitic life on earth, and recent work showing that parasites and other symbionts face severe extinction risk, necessitates infrastructure for parasite conservation assessments. Here, we describe the release of the Parasite Extinction Assessment & Red List (PEARL) version 1.0, an open-access database of conservation assessments and distributional data for almost 500 macroparasitic invertebrates. The current approach to vulnerability assessment is based on range shifts and loss from climate change, and will be expanded as additional data (e.g., host-parasite associations and coextinction risk) is consolidated in PEARL. The web architecture is also open-source, scalable, and extensible, making PEARL a template for more efficient red listing for other high-diversity, data-deficient groups. Future iterations will also include new functionality, including a user-friendly open data repository and automated assessment and re-listing.

34 Introduction

35 Parasitism is one of the most common forms of life on Earth, if not, by species totals, the most
36 common (**Larsen et al., 2017; Dobson et al., 2008**). Even excluding microparasites—such as some
37 bacteria, viruses, and protozoans—the remaining diversity of macroparasites (e.g., helminths,
38 leeches, lice, ticks, fleas, and mites) is staggering and comparatively understudied in ecology. Basic
39 questions remain open at the intersection of parasitology with other fields like community ecology
40 (**Johnson et al., 2015**), evolutionary ecology (**Morand, 2015**), macroecology (**Stephens et al., 2016**),
41 and climate change biology (**Brooks and Hoberg, 2007; Altizer et al., 2013; Cizauskas et al., 2017**).
42 As the field of disease ecology has matured, a growing body of work has shown that parasites are a
43 critical part of ecosystems, acting as regulators of food webs and host populations, and serving
44 an important role in energy flow through trophic levels (**Dunne et al., 2013**). The increasingly-
45 apparent benefits of parasites make a case for their recognition as an important neglected target
46 for conservation (**Whiteman and Parker, 2005; Pizzi, 2009; Carlson et al., 2013; Gómez and Nichols,**
47 **2013; Dougherty et al., 2016; Rocha et al., 2016**), especially given that parasitic life cycles are already
48 known to be particularly extinction-prone due to cascading co-extinctions with hosts (**Durden and**
49 **Keirans, 1996; Dunn et al., 2009; Dallas and Cornelius, 2015; Farrell et al., 2015**). With recent work
50 showing that climate change and coextinction combined could threaten one in every three helminth
51 parasite species (**Carlson et al., 2017**), frameworks to assess and catalog parasite extinction risk are
52 urgently needed.

53 While institutions such as the IUCN have spent decades developing centralized frameworks
54 for prioritizing the conservation of free-living biodiversity, parasites are rarely included in main-
55 stream assessments; for example, only two animal macroparasites are listed on the IUCN Red
56 List (*Hematopinus oliveri*, the pygmy hog louse, and *Hirudo medicinalis*, the medicinal leech). The
57 under-representation of parasites speaks to broader deficiencies in IUCN invertebrate assess-
58 ments, but also to the comparative bias against parasites in conservation, which has conventionally
59 treated parasites and disease as synonymous (**Dougherty et al., 2016**). Mainstreaming parasites
60 into conservation requires researchers to address a number of additional factors: the independent
61 extinction risk of parasites as well as coextinction risk, the degree of host specificity, the modes and
62 efficiency of transmission, the possibility for unintended consequences to wildlife or human health,
63 the cost-effectiveness of parasite conservation as a compatible goal with host conservation, and
64 the feasibility of *ex situ* conservation (**Dougherty et al., 2016**).

65 At the most basic level, incorporating parasite conservation measures into existing free-living
66 species' conservation plans can prevent accidental or deliberate loss of affiliates (**Jørgensen, 2015**),
67 e.g. the extinction of the California condor's louse *Colpocephalum californianus*, or the black-footed
68 ferret louse *Neotrichodectes sp.* (**Stringer and Linklater, 2014**). Some key assessments have been
69 made for parasites of high-profile hosts like the black-footed ferret (**Gompper and Williams, 1998**)
70 or the Tasmanian devil (**Wait et al., 2017**), but more expansive assessments are rare. Recent work
71 has pushed to embrace a broader perspective on symbiosis within parasitology (**Jovani et al.,**
72 **2017**), and in the context of global change biology, we believe this is an important step towards
73 effective conservation. Symbionts as a broad group face a common set of challenges, and the
74 same conservation measures that make sense for parasites are part of a broader shift towards
75 symbiont-conscious conservation.

76 Rising interest in parasite conservation comes at a time when open data in parasitology is rapidly
77 expanding; while host-parasite association data have historically been available from scientific
78 collections or online databases (**Strona and Lafferty, 2012; Dallas, 2016**), only in the last few years
79 have major sources such as the U.S. National Parasite Collection (**Lichtenfels et al., 1992; Carlson**
80 **et al., 2017**) or Global Mammal Parasite Database (**Stephens et al., 2017**) been updated to include
81 the detailed spatial data that are critical for conservation assessments. Expanding existing reposi-
82 tories, and improving access to collections data, is already a key part of ongoing work bridging the
83 gap between parasitology and other fields like epidemiology, disease ecology, and conservation

84 (*DiEuliis et al., 2016*). For parasite conservation to be operational and actionable in the shortest
85 term, researchers currently need a detailed and dedicated bioinformatic repository for the explicit
86 purpose of centralizing data on population trends, extinction risk, distributions, and conservation
87 efforts. Here, we present the Parasite Extinction Assessment & Red List (PEARL: pearl.berkeley.edu),
88 the first standalone global parasite conservation assessment, database, and web interface.

89 **PEARL version 1.0**

90 The Parasite Extinction Assessment & Red List compiles the preliminary work of the Parasite
91 Extinction Research Project (2013-2016). The core study (*Carlson et al., 2017*) accomplished three
92 tasks:

- 93 1. The georeferencing of the U.S. National Parasite Collection (USNPC), and the compilation of
94 the most detailed occurrence dataset for macroparasites currently available.
- 95 2. The estimation of global parasite extinction risk: an estimated 5-10% of species face direct
96 extinction risk from climate change, while up to 30% of helminths face a combined threat
97 from coextinction and climate change.
- 98 3. The preliminary release of PEARL version 0.1, a prototype with a static interface, PDF maps,
99 and no search functionality.

100 Building on PEARL v0.1, the full PEARL v1.0 was released on August 11, 2017 and features an open-
101 source web architecture, which allows a more flexible interface and tool to access the underlying
102 open-access database. Here we formalize the documentation for PEARL v1.0, explaining the
103 updated mechanics of PEARL as a new, standalone form of red listing for parasites and other
104 symbionts; and to outline the use of the framework in the inclusion of parasites in conservation
105 research, and more generally for invertebrate conservation.

106 **The Assessment**

107 As a scientific resource, PEARL serves two main purposes: an *extinction assessment*, which compiles
108 the extinction risk of enough species that global parasite extinction rates from climate change can
109 be measured; and a *red list*, analogous to the IUCN Red List but focused specifically on measuring
110 the vulnerability of macroparasitic species. The species currently included in the assessment fall
111 into eight major groups: helminth endoparasites (acanthocephalans, cestodes, nematodes, and
112 trematodes) and arthropod ectoparasites (fleas, lice, mites, and ticks). The term parasites is used
113 broadly both here and in the underlying premise of PEARL. While the focus of the assessment is
114 parasitic species, in the overarching goal of mainstreaming parasites into conservation (*Dougherty
115 et al., 2016*), several species and groups are included that are not strictly parasitic. For example,
116 vane-dwelling feather mites (Acariformes: Analgoidea, Pterolichoidea), like many other symbionts,
117 may contextually change roles between parasitism and commensalism or mutualism (*Galván et al.,
118 2012*); within other significant groups in our study, parasitism has secondarily evolved multiple
119 times (*Dorris et al., 1999; Bochkov and Mironov, 2013*).

120 The vulnerability of species is measured based on projected range loss in the face of climate
121 change, which was forecasted through the use of ecological niche modeling (*Carlson et al., 2017*).
122 Eighteen climate change scenarios are included in that assessment for 457 non-marine macropara-
123 sitic species, and extinction risk is estimated based on those projected rates of habitat loss. These
124 are translated into “red listing categories” based on estimated percent range loss in the next 50
125 years (i.e., by 2070):

- 126 • **Critically endangered (CR):** projected decline by $\geq 80\%$ in 50 years
- 127 • **Endangered (EN):** projected 50–79% decline in 50 years
- 128 • **Vulnerable (VU):** projected 25-49% decline in 50 years
- 129 • **Least Concern (LC):** < 25% decline in 50 years

130 The assessment is designed to be fully transparent about accuracy and bias; accuracy metrics for
131 niche modeling (the true skill statistic and the area under the receiver-operator curve), as well as
132 categorical measures of data quality, are presented alongside distribution models. We developed
133 two data quality metrics based on percentiles within our dataset. Data *coverage* is based on sample
134 size:

| Coverage | Percentile | Occurrence Points |
|-------------|------------|-------------------|
| "Poor" | 0-25 | 0-28 |
| "Fair" | 25-50 | 29-42 |
| "Good" | 50-75 | 43-80 |
| "Excellent" | 75-100 | 81-3289 |

136 Data *uncertainty* is based on the mean uncertainty radius of every point from manual georefer-
137 encing; some species only had GPS-identified data, which were classified as zero uncertainty from
138 georeferencing:

| Uncertainty | Percent | Distance (km) |
|-------------|---------|---------------|
| "Perfect" | - | 0 |
| "Excellent" | 0-25 | 0-5.1 |
| "Good" | 25-50 | 5.1-6.5 |
| "Fair" | 50-75 | 6.5-7.9 |
| "Weak" | 75-100 | 7.9-21.3 |

140 By presenting quality as a mainstreamed part of the assessment, we improve transparency, better
141 inform practitioners relying on these data for any applied research, and clearly identify species for
142 which improved data collection is needed (i.e., more precise locality data).

143 The Web Interface

144 PEARL is an open-source web app that builds on several frontend and backend APIs and novel
145 software libraries in both the *Python* and *JavaScript* programming languages. In the backend, PEARL
146 builds upon a **Python 3.5** based web framework developed by Z. Miao and O. Muellerklein called
147 Extensible Web App Interactive Mapping, **EWAIM on Github**¹. EWAIM incorporates continuous
148 unit testing, a basic yet extensible library for server-side (i.e. *backend*) data analysis, and native
149 integration with spatial data structures through **PostGIS / PostgreSQL** or **SQLite**. PEARL's use of
150 the underlying EWAIM server-side web framework allows near endless GIS functionality to be used
151 on spatial or time series data.

152 In the frontend, PEARL uses standard *GET / POST* events to process user events to and from the
153 server-side application, allowing interactivity with the backend database via species maps and other
154 functionality in the various web pages / interfaces. Building upon EWAIM, PEARL handles user events
155 to and from web pages through *Flask* protocol, a Python based extensible web microframework.
156 Within the frontend components of PEARL a range of mapping APIs are called. Frontend libraries
157 and API used in PEARL include:

- 158 • **D3.js - Data Driven Documents**²: an open-source JavaScript library for dynamic, interactive
159 data visualizations
- 160 • **Leaflet API**³: an open-source JavaScript library that allows interactive mapping of PEARL
161 tilemaps and provides a mobile-friendly design

¹EWAIM on Github: <https://github.com/Thru-Echoes/ewaim-webapp>

²D3.js homepage: <https://d3js.org/>

³Leaflet API homepage: <http://leafletjs.com/>

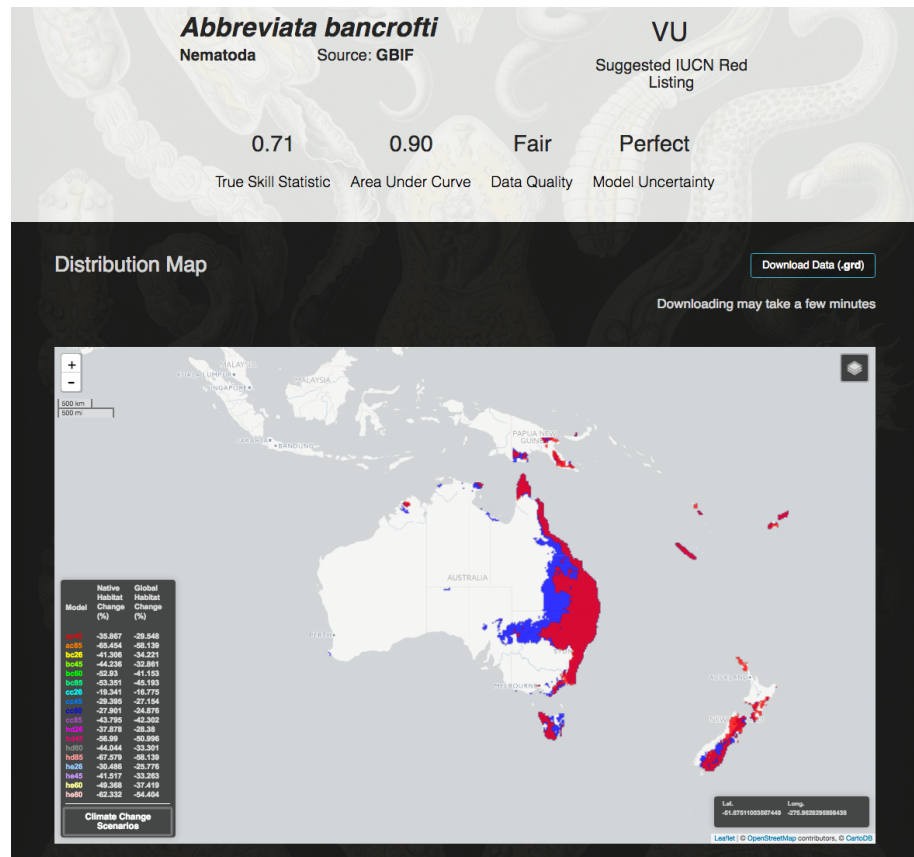


Figure 1. The online interface to PEARL v1.0, illustrated for *Abbreviata bancrofti* (Physalopteridae; Irwin-Smith, 1922), a nematode parasite of the Australian leaf-tailed gecko, *Phyllurus platurus* (Reptilia: Gekkonidae). Results include the current distribution of the nematode (blue) and 18 future climate scenarios. Above, information about the entry is available, including data sources, and model accuracy metrics.

- **CARTO Maps API:**⁴ an open-source engine that is scalable and extensible, powers a range of basemaps, and interacts with Leaflet, Google Earth Engine, and CARTO SQL data structures

PEARL, as a web app and open-source software, is fully documented and available publicly as a Github repository⁵ with version releases and community-based issues tracked accordingly. The underlying raster files can be downloaded in grid file (.grd) format directly from species pages, and R- and Python-based APIs are currently in development that will allow users to pull data from multiple species at once. Future iterations of PEARL development include, but are not limited to, a more robust mobile-friendly structure; public data uploads and downloads through user login and associated profiles; and the incorporation of a novel dynamic, real-time algorithm that would automate generating and rendering distribution models and associated data analysis based on user data contributions (see Dynamic Updating section below).

Extending the Framework

The purpose of PEARL is to create a stable platform for parasite conservation that allows continuous improvements by existing teams, and that can incorporate future collaborations from other researchers both in PEARL development and database-building. The full expanded platform makes the interface, and underlying database, extensible in a number of important ways that will be useful both for the future of PEARL, and as a template for the broader problem of invertebrate

⁴CARTO homepage: <https://carto.com/>

⁵PEARL Github repository: <https://github.com/Thru-Echoes/PEARL1.0>

179 conservation assessments. After the release of version 1.0, a number of scheduled advances are
180 planned for PEARL over the coming years. We detail five here:

181 Assessment II

182 A major goal for PEARL is the expansion of assessments beyond the 457 species in the pilot study
183 by *Carlson et al. (2017)*, to include some of the other increasingly-available open data sources
184 in parasitology. The goal of fully georeferencing the U.S. National Parasite Collection—including
185 species with insufficient unique locality points for the main extinction study—by 2018 gives a clear
186 rationale for an expanded assessment, especially in conjunction with the recent release of the
187 Global Mammal Parasite Database v2.0 with spatial data (*Stephens et al., 2017*). Also critical is
188 including smaller, regional datasets from biodiversity hotspots like the Amazon, or the Cape Floristic
189 Region of South Africa. Given that distribution modeling requires a minimum of at least 20-50
190 occurrences, it would be useful to include species that are currently impossible to map in future
191 iterations by presenting raw occurrence data, rather than niche models. Providing these data may
192 help guide targeted field collection programs that address these data deficiencies.

193 Reconsidered Criteria

194 Red listing parasites—or, in fact, any dependent species—poses a more severe methodological
195 problem than already-challenging work on free-living species. In particular, well-designed criteria
196 must accommodate the tremendous diversity of symbiotic groups, and rescale important metrics
197 of viability to an appropriate level; but effective criteria must also (presumably) include information
198 about the vulnerability of hosts. The criteria underlying assessment version 1.0 only indirectly
199 addressed the first of these two challenges, by presenting a radically simplified version of the
200 *Thomas et al. (2004)* criteria, which were already reduced from the IUCN Red List criteria.

201 For comparison, the criteria used in *Thomas et al. (2004)* are designed to correspond directly to
202 projected extinction risk:

- 203 • **Extinct (EX):** species with a projected future area of zero (100% of species assumed to be
204 committed to eventual extinction)
- 205 • **Critically endangered (CR):** projected future distribution area < 10 km², or decline by ≥ 80%
206 in 50 years (species assigned a 75% chance of extinction)
- 207 • **Endangered (EN):** projected area 10–500 km², or 50–79% decline in 50 years (species assigned
208 a 35% chance of extinction)
- 209 • **Vulnerable (VU):** projected area 501–2,000 km², or > 50% decline in 100 years on the basis of
210 linear extrapolation of 50-year projection (species assigned a 15% chance of extinction)
- 211 • **Not Threatened (NT):** 0% extinction risk, no area loss

212 In the *Carlson et al. (2017)* study and PEARL v0.1 (and v1.0), these criteria are reduced to percentage-
213 based criteria only:

- 214 • **Critically endangered (CR):** projected decline by ≥ 80% in 50 years
- 215 • **Endangered (EN):** projected 50–79% decline in 50 years
- 216 • **Vulnerable (VU):** projected 25-49% decline in 50 years
- 217 • **Least Concern (LC):** < 25% decline in 50 years

218 The inadequacy of these criteria is a key point articulated by *Carlson et al. (2017)*, and we return to
219 it here to note that it offers only the coarsest level of possible resolution for categorizing extinction
220 risk. More detailed criteria are needed that incorporate risk factors like small ranges (with minimal
221 projected declines), but parasite conservation has yet to develop meaningful benchmarks for these
222 criteria; what is a “small range” for a parasitic species? Is a small range for a trophically-transmitted
223 nematode the same size as a small range for a tick with a single common host? The role of
224 microclimate and heterogeneity within ranges, or of habitat selection and dispersal patterns of
225 hosts, further complicates this problem. Similarly, *Dougherty et al. (2016)* highlighted the need for

226 advances in population viability analysis for parasites, such that concepts like “minimum viable
227 population” can be readily applied, and included in these criteria.

228 Better Host & Parasite Bioinformatics

229 Host and symbiont extinction risk are fundamentally linked, and conservation of parasites and
230 other symbionts cannot exist in the absence of detailed host information. For ticks and feather
231 mites, underlying data from the *Carlson et al. (2017)* study contains host association data that can
232 be mainstreamed into future versions. Moreover, access to portals like the helminthR package in R
233 (*Dallas, 2016*) will make it possible to compile detailed information on host-parasite associations for
234 helminths, but these data lack information about the life stage at which different hosts are relevant.
235 Adding life stage-structured data to host-parasite associations will be a key part of PEARL expansion,
236 especially given that host-range disjunctions might be a substantial pressure on parasites in a
237 changing climate (*Pickles et al., 2013; Cizauskas et al., 2017*). A new database published this year
238 makes significant strides towards aggregating life cycle data for acanthocephalans, nematodes,
239 and cestodes (*Benesh et al., 2017*); compiling that data for every species in our study will still likely
240 require the concerted effort of researchers contributing to the expansion of the PEARL database.

241 The integration of host-parasite association data is an especially sensitive matter in the design of
242 actual parasite conservation schemes. The potential for conflict between parasite conservation and
243 the broader goals of wildlife and human health has already been noted by *Dougherty et al. (2016)*,
244 and a fundamental tenet of effective parasite conservation is attention to potential unanticipated
245 consequences for conservation or public health. Parasites with zoonotic potential or that act
246 as vectors of zoonoses are an especially difficult case, as they may be the target of eradication
247 campaigns simultaneous to conservation efforts for closely related parasites. Developing an
248 aggregated bioinformatic infrastructure that serves both purposes will support parasite research in
249 diverse realms, and facilitate the work of public health practitioners and conservation managers
250 alike. Consequently, future assessments should not only include wildlife (and domestic) host
251 associations, but also detailed information on the known zoonotic potential of every species.

252 Integrating Genomic Data

253 The increasing availability of genomic data associated with the continuous improvements in se-
254 quencing and bioinformatics (*Stephens et al., 2015*), and with global initiatives such as the Earth
255 BioGenome project (EBP; *Pennisi (2017)*), is becoming a huge source of data for conservation
256 assessments (*Pauls et al., 2013; Ikeda et al., 2017; Razgour et al., 2017*). Genomic data can be
257 programmatically gathered from massive databases, such as the NCBI Genome database⁶ and the
258 European Nucleotide Archive (ENA⁷). Notwithstanding, given the bias against symbiont genomes
259 (*Del Campo et al., 2014*), PEARL may need dedicated projects to generate genomic data for the
260 species already included. Doing so open the doors to a number of important new analyses, such
261 as genetically informed ecological niche models (ENMs; *Marcer et al. (2016); Ikeda et al. (2017)*)
262 following integrative frameworks (*Razgour et al., 2017*). In this way, assessments can include mea-
263 sures based on neutral and adaptive genomic information to assess the sensitivity of species to
264 environmental variables associated with global change. For these computationally challenging
265 purposes, PEARL will likely require of an increase in computational resources (*Hayden, 2015*).

266 Dynamic Updating

267 One strength of PEARL's dynamic interface is the potential for continuously-updating red listing,
268 which updates existing species assessments and adds new ones in real-time as new data are
269 contributed by researchers around the world. In an upcoming release, we hope to include an
270 automated tool for continuous integration of new data and assessments, in which submitted spatial
271 data automatically augments the existing global database. This workflow will pave the way for future

⁶<http://www.ncbi.nlm.nih.gov/genome/>

⁷<http://www.ebi.ac.uk/ena>

272 conservation approaches by allowing dynamically updated red listing, via continuous integration of
273 data into self-updating niche models and respective quality metrics. PEARL can serve as a launching
274 point for an alternative red listing protocol that incorporates machine learning methods to evaluate
275 conservation status at the community or global level (e.g. see recent work by *Darrah et al. (2017)*),
276 rather than on a manual species-to-species basis (like most current efforts operate), something
277 that will likely be helpful in red listing the 300,000 estimated species of helminths alone.

278 **Application to Other Conservation Efforts**

279 PEARL is designed to be a template for more successful rapid assessment of conservation risk and
280 status for invertebrates and other difficult-to-profile groups, especially other types of symbionts
281 and coextinction-prone affiliate species. All code for PEARL is publicly available, allowing the rapid
282 and easy development of parallel tools for non-parasitic groups, and encouraging a broader culture
283 of open, reproducible science in conservation. The Github repository contains a detailed user-guide
284 to installing local and server-side instances of PEARL and its underlying web architecture across a
285 number of operating systems, making it easily adaptable for a diverse range of ecological projects.
286 Developing better, broader frameworks for invertebrate conservation could be substantially accel-
287 erated with readily available, open-source frameworks for red listing that allow more decentralized
288 data collection and assessment. Data deficiencies for invertebrates are overwhelming (*Clausnitzer*
289 *et al., 2009; Régnier et al., 2015*), and despite the priority put on red listing insects, there is concern
290 that hyper-diverse groups like the insects will never be described thoroughly enough that conser-
291 vation assessments can keep pace with extinction rates (*Warren et al., 2007*). Decentralizing the
292 red listing process, and enabling smaller assessments as data are collected, is an important step to
293 protecting not just parasites, but all symbionts and other neglected or understudied groups.

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