Global spread of helminth parasites at the human – domestic animal – wildlife interface

Running head: Parasites at the human–animal interface

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Abstract

Changes in species distributions open novel parasite transmission routes at the human–wildlife interface, yet the strength of biotic and biogeographical factors that prevent or facilitate parasite host shifting are not well understood.

We investigated global patterns of helminth parasite (Nematoda, Cestoda, Trematoda) sharing between mammalian wildlife species and domestic mammal hosts (including humans) using > 24,000 unique country-level records of host-parasite associations. We used hierarchical modelling and species trait data to determine possible drivers of the level of parasite sharing between wildlife species and either humans or domestic animal hosts. We found the diet of wildlife species to be a strong predictor of levels of helminth parasite sharing with humans and domestic animals, followed by a moderate effect of zoogeographical region and minor effects of species' habitat and climatic niches. Combining model predictions with the distribution and ecological profile data of wildlife species, we projected global risk maps that uncovered strikingly similar patterns of wildlife parasite sharing across geographical areas for the different domestic host species (including humans). These similarities are largely explained by the fact that widespread parasites are commonly recorded infecting several domestic species.

If the dietary profile and position in the trophic chain of a wildlife species largely drives its level of helminth parasite sharing with humans/domestic animals, future range shifts of host species that result in novel trophic interactions may likely increase parasite host shifting and have important ramifications for human and animal health.

Introduction

The emergence of parasitic diseases is largely a consequence of the exploitation of novel host species by parasites capable of shifting hosts (Lloyd-Smith *et al.*, 2009). A central goal in disease ecology is thus to identify factors that enable parasite sharing, especially since determinants of parasite sharing can influence the spread of parasites to new habitats and biogeographic regions. For zoonotic diseases (i.e. infectious diseases of humans caused by parasites that have an animal reservoir) a key determinant of emergence is overlapping environmental conditions and biological traits that enable parasites to be shared by human and animal hosts. Along early human migration pathways, increased physical contact with endemic animal and plant species led to increased exposure to novel parasites (Pedersen & Davies, 2009; Pulliam, 2008), especially those acquired through ingestion of wild animal meat (Reinhard *et al.*, 2013). Anthropogenic land use, conversion of natural habitats into production landscapes, and intensification of international travel and wildlife trades continue to diminish or shift former geographical barriers between humans and wildlife, likely facilitating exposure to novel parasite pools (Murray *et al.*, 2015; Patz *et al.*, 2008). In contrast, decreasing wildlife populations and the isolation of populations through habitat fragmentation (through construction of roads or other barriers that prevent animal movement) may effectively decrease contact between humans and wildlife.

While direct human-wildlife parasite sharing is a topic of major importance, domestic animals that occur in close proximity to humans may also act as key hosts for wildlife parasites. Domestic animals (hereafter including domesticated animals, such as dogs, but also animals that live in close proximity to humans, such as commensal rats) have colonised almost all terrestrial environments (Hoberg & Brooks, 2008; Matisoo-Smith *et al.*, 1998). In turn, domestic animals commonly share subsets of their parasite fauna with humans. This

subset increases the longer a species has been domesticated (Morand *et al.*, 2014; Wolfe *et al.*, 2007). Parasite host shifting at the interface between humans, domestic animals and wildlife is a multifaceted and multidirectional problem, with potential effects for human and wildlife health (Daszak *et al.*, 2000). Yet, while previous studies found 60 % of human diseases to be of zoonotic origin (Taylor *et al.*, 2001; Woolhouse & Gowtage-Sequeria, 2005), global patterns in parasite sharing at the human–domestic animal–wildlife interface are poorly resolved.

Predicting zoonotic disease risk requires understanding wildlife characteristics that enable host shifting at local and global scales (Hoberg & Brooks, 2008). Host attributes, such as phylogenetic relatedness or overlap in habitat use, are useful for predicting whether hosts share the same parasite species through ecological fitting (Streicker *et al.*, 2010; Wells *et al.*, 2015) or how invasions into novel environments may result in novel host-parasite associations (Agosta & Klemens, 2008; Clark *et al.*, 2017). Conversely, knowledge of whether species attributes such as demography, body size or diet increase the likelihood of sharing parasites with humans, and whether zoonotic disease burdens in humans or domestic animals exhibit biogeographical structure, remains sparse (Han *et al.*, 2015; Just *et al.*, 2014; Stephens *et al.*, 2016).

A key gap in our understanding of zoonotic disease emergence is information on how patterns of wildlife parasite sharing differ among domestic host species or across biogeographical regions. Despite persisting in close spatial proximity, humans and domestic animals differ in habitat use, diet and other ecological traits. This may have consequences for determining subsets of parasites that humans and domestic animals share with wildlife. Humans and dogs, for example, each consume a large range of invertebrate and vertebrate species (many of which may be relevant reservoir hosts) and can access almost any type of terrestrial habitat. Other domestic species, such as cows, are confined to relatively few

habitats and food items (e.g. grassland vegetation). One may expect that different domestic animals will exhibit different patterns of wildlife parasite sharing and, consequently, different potential roles as carriers of zoonotic parasites. Globally, wildlife communities occur in distinct species assemblages according to biogeographical history, speciation events and habitat biomes (Holt *et al.*, 2013; Kraft *et al.*, 2007; Wallace, 1876). Such biogeographical structure may lead to spatial gradients in wildlife parasite sharing for humans and domestic animals.

Here, we investigate possible drivers of helminth parasite (Nematoda, Cestoda, Trematoda) sharing between wildlife and focal domestic host species (including humans) at a global scale. Using a large database of mammalian host-parasite associations, we addressed two key questions: 1) Which species traits make wildlife most prone to share helminth parasites with humans or domestic species? 2) Do patterns of wildlife parasite sharing exhibit biogeographical structure across the globe? Given that humans share parasites most intensively with domestic species, we expect to find similar patterns of wildlife parasite sharing among humans and domestic animals. We expect this to be especially true when comparing patterns for humans and dogs, as dogs have a long domestication history and share a broad range of habitats with humans. We also expect biogeographical structure in wildlife assemblages to drive global patterns in wildlife–human and wildlife–domestic animal parasite exchange, as different wildlife traits may facilitate or impede parasite transmission cycles and host shifting abilities.

Materials and Methods

Host-parasite database

We compiled a global database of mammalian host–parasite associations from the publicly available Natural History Museum (NHM), London's Host-Parasite Database (Gibson *et al.*,

2005). This database has been used as a backbone for the comprehensive Fauna Europaea biodiversity inventories of parasitic worms (Gibson & Bray, 1994; Gibson *et al.*, 2014) and is arguably the largest publicly available compilation of country-level records for helminth host associations to date. In humans, for example, previous estimates suggested > 300 helminth species infecting humans (Crompton, 1999), whereas our database reports a total of 397 helminth species (Nematoda, Cestoda, Trematoda) to be associated with humans. We downloaded all host-parasite data from the database using web-scraping tools implemented in the package *xml* in the software R (R Development Core Team, 2017). The data of interest for our study were country-specific combinations of parasite-mammal species associations, which included information from wild and domestic mammals as well as humans. We excluded all records from captive animals or experiments, and considered only records that included full binomial species names (scientific genus and species names). As the original database records were not specified in detail, records may include reports of molecular identification of parasite species and also dead-end hosts, from which parasites are not transmitted to other species. Mammal species synonyms were standardised using the taxonomy of Wilson & Reeder (2005) and the IUCN Red List. Parasite names were standardised using the WoRMS database (http://www.marinespecies.org), the tapeworm database at the University of Connecticut (http://tapewormdb.uconn.edu/) and GBIF (www.gbif.org/). Location names were standardised to country names of the current world geopolitical map and assigned to one of 11 global zoogeographical regions according to Holt *et al.* (2013). Since China covers different zoogeographical regions, and not all records from China could be assigned to any particular region, we classified these unspecified records into an extra category ("China unspecified").

Our dataset consisted of 24,486 unique combinations of host–parasite–country records for selected helminth species (Nematoda, Cestoda, Trematoda), of which 1,737 involved humans

as a host, from a total of 4,507 selected parasite species. Of the 1,366 total mammalian host species in our dataset, we considered 21 species as 'domestic' (including humans and commensal murids) and all others as 'wildlife'. Domestic species were banteng (*Bos javanicus*), yak (*B. mutus*), cow (*B. taurus*), bactrian camel (*Camelus bactrianus*), dromedary (*C. dromedarius*), dog (*Canis familiaris*), goat (*Capra aegagrus*), guinea pig (*Cavia porcellus*), wild ass (*Equus africanus*), donkey (*E. asinus*), horse (*E. caballus*), cat (*Felis catus*), human (*Homo sapiens*), guanaco (*Lama guanicoe*), house mouse (*Mus musculus*), rabbit (*Oryctolagus cuniculus*), sheep (*Ovis aries*), brown rat (*Rattus norvegicus*), black rat (*R. rattus*), pig (*Sus scrofa*) and vicugna (*Vicugna vicugna*). From these domestic species, we selected parasite assemblages (Nematoda, Cestoda, Trematoda) from seven focal host species (hereafter termed focal species) to examine associations with wildlife: man, dog, cat, cow, pig, black rat and brown rat. Focal host species were selected because they are among the most cosmopolitan host species and are represented with enough records in the database to facilitate statistical inference of wildlife parasite sharing patterns.

We are aware that this dataset is incomplete in that it lacks recently described parasite species and recent records of host-parasite associations in different locations; while this limits inference about absolute species numbers, we believe this dataset provides meaningful insights into the relative strength of how wildlife species share parasites with domestic species in relation to ecological traits and projected global maps, which were the main interests of this study.

Host ecological traits

We selected nine ecological traits of terrestrial mammals, based on the PanTHERIA (Jones *et al.*, 2009) and EltonTraits 1.0 (Wilman *et al.*, 2014) databases, to include a broad range of attributes likely to distinguish hosts in terms of their suitability for a parasite's life and

transmission cycles. Selected traits included: body mass, which is a key feature of mammals in terms of their metabolism and adaptation to environments; average longevity, litter size and the average number of litters per year as demographic parameters that could be relevant for allowing parasites to complete parts of their life cycles in a host; diet breadth (calculated as a Shannon diversity index based on the proportional use of 10 diet categories as presented in EltonTraits) and diet class ('invertebrate predator', 'herbivore', 'omnivore' or 'carnivore') as trophic interactions traits; range area, which we expect to affect the exposure to other mammalian host species; average temperature within range as an indicator of climate niche; and habitat as multiple binary indicators of whether a species uses 1) forest, 2) open vegetation, and/or 3) artificial/anthropogenic habitats. Information about specific habitat utilisation was compiled from the International Union for the Conservation of Nature (IUCN) database (IUCN, 2014). We did not include a larger set of ecological traits in our analysis to avoid trait autocorrelation and colinearity issues in the modelling.

We accounted for phylogenetic distances between wildlife species and focal domestic species based on a correlation matrix (Paradis *et al.*, 2004) of phylogenetic branch lengths, which was built using a recent mammalian phylogenetic supertree (Bininda-Emonds *et al.*, 2007). We further considered the orders Carnivora, Rodentia and Primates as binary (categorical) indicator variables for the major taxonomic groups that are suspected to share parasites with the focal species; we used these as indicators to account for possible group-level taxonomic effects additional to the phylogenetic branching. To account for sampling bias among wildlife species, we queried the number of published references for each binomial wildlife species name from the Scopus literature database (accessed 25/02/2017); we used this measure as more refined searches, such as the number of references linked only to parasites, included large proportions of zeros and information on the true number of sampled individuals (which should determine the chance parasites are detected if prevalence is low) was not available.

Statistical analysis

The primary goal of this study was to identify drivers of parasite sharing between focal domestic species and wildlife. We addressed this aim using logistic hierarchical regressions to analyse the relative strength of covariates that could determine the probability of parasites from either humans or domestic species to be found in wildlife species (calibrated on host species from the NHM database). For each focal domestic host species *d*, we constructed presence-absence vectors $Y_d(w_r, p_d)$ that encompassed all combinations of mammalian wildlife species w_r (i.e. non-domestic species in the database) surveyed for parasites from any zoogeographical region *r* and all parasite species p_d from one of the selected parasite groups (Nematoda, Cestoda, Trematoda) recorded in the respective focal species. Here, we assume that any wildlife species recorded in our database has been potentially examined for all parasite species p_d known to occur in the respective region; the absence of such records are set to 0. These 'absence records' likely include false zeros due to missing observations and hence underestimate the link of parasite species from focal hosts to wildlife; however, we prefer this approach to presence-only modelling, as the true proportion of wildlife species infected remains unknown, and we thus expect techniques such as data imputation not to improve our analysis.

We assumed the resulting data vectors $Y_d(w_r, p_d)$ are random draws from the underlying association probability $\Psi_d(w_r, p_d)$ of a wildlife species sharing a parasite with a focal species according to a Bernoulli distribution, as commonly used in logistic regression. We modelled the probability $\Psi_d(w_r, p_d)$ further using a logit-link function such that

$$\text{logit}[\Psi_d(w_r, p_d)] = \mu_{Parasite}(p_d) + \mu_{Region}(r) + B\,ET_{wr}$$

where $\mu_{Parasite}(p_d)$ is the parasite-specific intercept, μ_{Region} are coefficient estimates that account for variation across zoogeographical regions *r*, and *B* is a vector of coefficient

estimates that accounts for variations in the association risk linked to the matrix of covariates ET_{wr} of the nine host ecological traits, the phylogenetic distance of wildlife to the focal host species and the number of publications, as specified above.

We used a hierarchical model with a common hyperprior η_μ for the intercept as

$$\mu(p_d) = N(\eta_\mu, \varepsilon_\mu).$$

where ε_μ is a random Gaussian variance term that allows species-specific intercepts to vary from the hyperprior (no group specific hyperprior was specified as we ran models separately for the three parasite groups). We fitted the model in a Bayesian framework with Markov Chain Monte Carlo (MCMC) sampling based on the Gibbs sampler in the freeware OpenBUGS (Lunn *et al.*, 2012). We used a Gibbs variable selection procedure (GVS) to only include variables in the model if sufficiently supported by the fit to data and joint sampling of the most likely coefficient values (selection frequencies were typically high for covariates with significant effects, except for the categorical effects of 'region'). We used normal priors with mean = 0 and variance $\sigma \sim Exp(1)$ for intercepts and all regression coefficients if selected as part of the GVS, and $\sigma \to 0$ otherwise. This prior gives close approximation to a logistic distribution and is appropriate for logit-scale estimates (Lunn *et al.*, 2012). Convergence of MCMC chains was assessed visually and with Gelman-Rubin diagnostics (all values < 1.2) after burn-ins > 50,000 MCMC samples. Parameter estimates were calculated as posterior modes and 95% highest posterior density credible intervals (CI) from 5,000 samples. Posterior predictive checks assessed whether model assumptions were reasonable approximations of the data generating process, with Bayesian *P*-values around 0.5 indicating a good fit. This model checking approach essentially compares whether the observed data resemble data simulated from the posterior distribution (Gelman *et al.*, 1996). All covariates were scaled (dividing centred values by one SD) and log-transformed if featuring overdispersion (body mass, range area, number of publications) to facilitate comparison of

effect sizes. Missing values of ecological trait covariates were imputed during MCMC updates, randomly drawing values from priors according to the mean and variance of all known trait values (considering all information in the trait databases) from species in the same orders. Specific trait data are currently not available for a considerable diversity of mammalian species; consequently, because of our ability to meaningfully impute missing data using a Bayesian sampling approach, account for uncertainty in parameter estimates, and make reasonably accurate parameter estimates, we preferred this approach over others, such as machine learning techniques, which are commonly used to more flexibly model nonlinear and interaction relationships (Elith *et al.*, 2008). Significance of model effects was determined by examining whether the 95% CI of regression coefficients did not overlap zero for continuous covariates or were clearly distinguished from each other for categorical covariates.

We computed the relative risk that a wildlife species will share parasites with each of the focal host species for all 5,289 terrestrial mammal species in the IUCN database by entering species' ecological traits into equations from the fitted models above (using posterior modes of parameter estimates). We hereafter refer to this relative risk as the association risk, which is appropriate in this case since the analysed data vectors included all combinations of parasites from a focal host and wildlife species. Thus, the association risk would be '1' if a wildlife species is likely to share all parasite species known from a particular focal species. We set the respective parameter values to zero if trait variables were missing (i.e. assuming an 'average' effect of the respective covariate for computing the respective species-level association risk).

The second aim of this study was to examine whether patterns of wildlife parasite sharing among domestic hosts exhibit biogeographical structure, which could be informative for understanding the future spread of zoonotic parasites. We addressed this goal by

exploring global patterns in observed parasite associations for focal host species and forecasted associations of wildlife infestation with parasites shared with the focal host species. First, for each focal host species, we used our model outputs to generate a series of maps (10km^2 raster cell sizes) to forecast global patterns in both wildlife parasite association risks and parasite assemblage structure. Using IUCN geographical range maps for wildlife species, we projected the respective parasite association risks on a global raster and, for each cell, computed average species-level and cumulative community-level geographical association risks for local wildlife assemblages. We were not able to account for possible regional variation in realized host-parasite interactions (which could arise due to variation in local conditions that enable host-parasite interactions) within the given wildlife range maps and, for simplicity, assumed homogenous association risks throughout species' given ranges.

Next, to explore variation in parasite assemblage structure across zoogeographical regions, we computed for each cell the hypothetical presence of focal host parasites in local wildlife by assuming that a parasite species occurred throughout the range of its associated wildlife host species. We then aggregated the presence-absence of these parasites at the zoogeographical region level and calculated parasite species turnover across regions using the *βsim* index, a basic turnover index that is based on the number of shared and unique species and is relatively unbiased by species richness (Lennon *et al.*, 2001). As an index of parasite assemblage distinctiveness in each region, we calculated the mean of all region-specific pairwise *βsim* indices. We explored geographical sampling bias by computing the number of wildlife species examined for helminths (including species not found in domestic host species) and wildlife species richness for each cell.

Spearman rank correlation tests were used to compare biogeographical patterns. First, we assessed whether infestation of a greater number of focal host species leads to broader biogeographical spread by testing the correlation strength between the Shannon index of

biogeographical spread and the total number of associated focal host species. We then explored whether wildlife species show similar biogeographical patterns in the risk for sharing parasites with different focal host species by testing all pairwise correlations between the geographical association risks for parasites from the different focal host species.

We quantified the biogeographical spread of parasites (Nematoda, Cestoda, Trematoda) found in any focal species. We did this by calculating a Shannon index H_p for each parasite species p to account for both 'richness', according to the number of zoogeographical regions where a species was recorded, and 'evenness', according to the proportion $\varphi_p(r)$ of wildlife species infected with the respective parasite species in each zoogeographical region r (Magurran, 2004). We calculated the index as

$$H_p = \sum_{r=1}^{R} \varphi_p(r) \ln[\varphi_p(r)].$$

Larger values indicate higher proportions of wildlife species infected and a more even spread by the parasite across zoogeographical regions.

All statistical analyses and distributional map constructions were conducted separately for the three groups of Nematoda, Cestoda and Trematoda using R (R Development Core Team, 2017) for data preparation and summary statistics.

Results

Of the 1,345 mammalian wildlife species in our host-parasite database, 41 % (n = 553 spp.) were infected with helminth parasite species (Nematoda, Cestoda and Trematoda) also found in humans. For humans, in turn, 49 % (195 of 397 spp.) of all helminth parasite species were also found in wildlife and 45 % (182 spp.) in at least one other domestic host species. The wildlife species associated with the highest numbers of zoonotic parasites were *Vulpes vulpes* (red fox, 51 spp.), *Canis lupus* (grey wolf, 33 spp.) and *Nyctereutes procyonoides* (raccoon dog, 29 spp.). For the other focal domestic host species, proportions of examined wildlife

326 species that shared parasites ranged from 21 – 31 % (**Table S1, Supplementary**
327 **Information**).
328 Diet class was the strongest predictor of sharing parasites with focal host species for all
329 combinations of parasites (Nematoda, Cestoda, Trematoda) and focal host species, explaining
330 25 – 78 % of variation in wildlife infestation risk (all 95 % credible intervals, CIs = 13 – 96
331 %) (**Fig. 1**). Wild insectivorous and omnivorous mammals were at significantly lower risk of
332 sharing parasites with humans than were herbivores and carnivores, a pattern that was also
333 true for other domestic host species (with a few exceptions; **Fig. S1**). Risks of wildlife
334 species sharing parasites with the focal species also differed across zoogeographical regions.
335 Overall, risks were relatively high in the Palaearctic region (**Fig. S2**), though some
336 combinations of parasite and domestic host species exhibited other informative
337 zoogeographical patterns. Wildlife had increased risk of sharing trematodes with cows and
338 black rats in the Neotropical region and increased risk of sharing nematodes with humans,
339 dogs and cats in the Nearctic region. In contrast, the risk for wildlife sharing cestodes with
340 focal host species was generally low in the Neotropical region (**Fig. S2**). Nevertheless, the
341 overall effect of zoogeographical region was weaker than the effect of diet class (**Fig. 1**).
342 Coefficient estimates for all other covariates are presented in **Table S2**; notably, various
343 coefficient estimates were significantly different from zero, though they explained much less
344 variance than diet and zoogeographical region. Bayesian *p* values ranged from 0.43 to 0.79
345 for the various models.
346

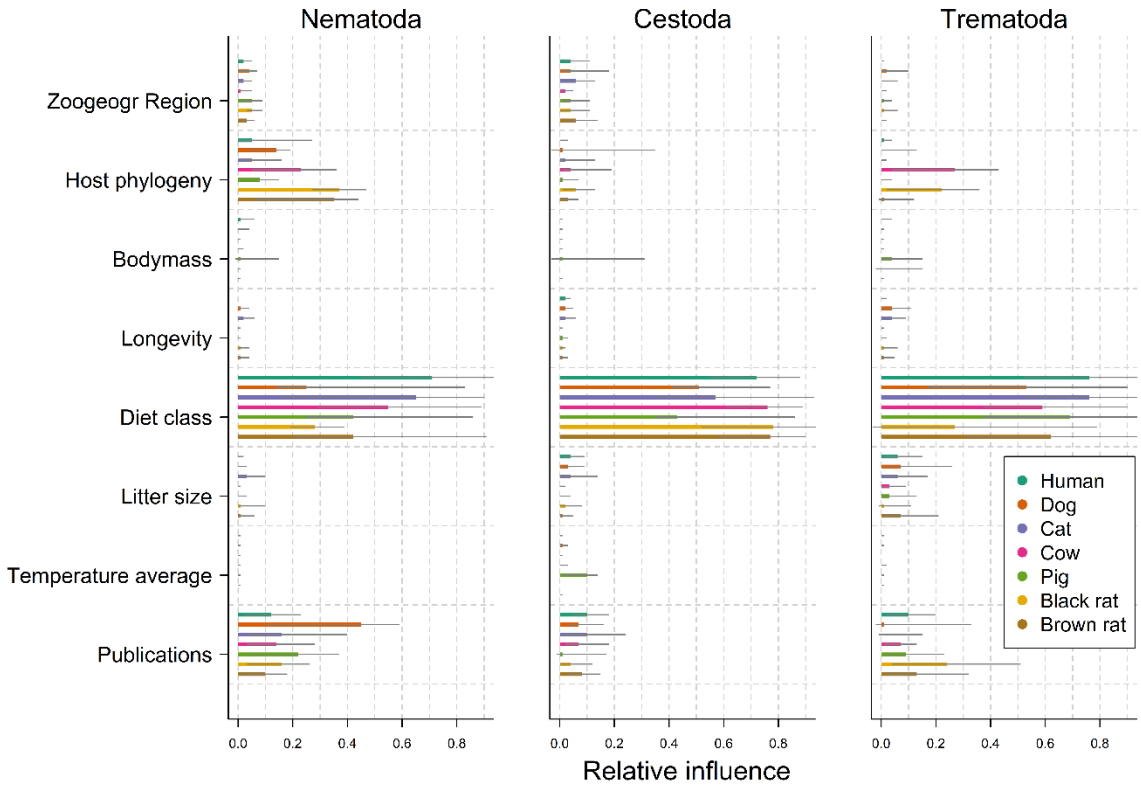
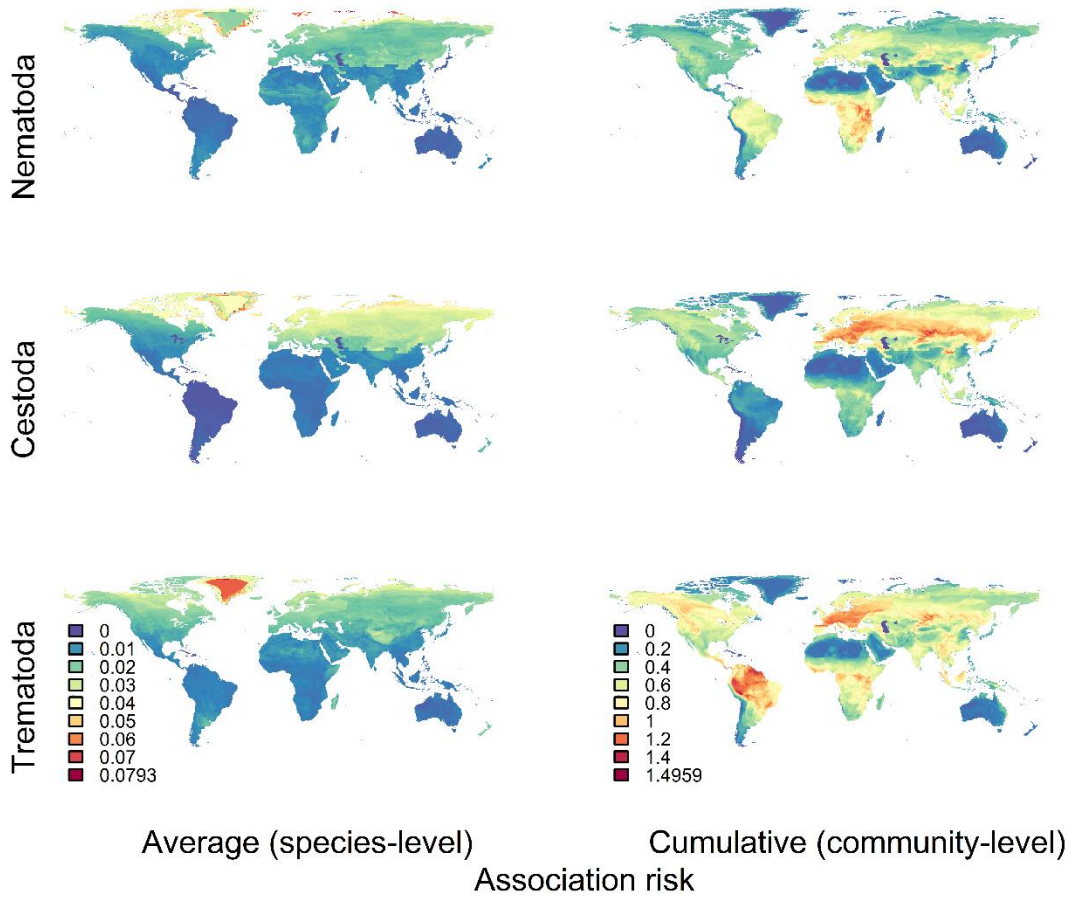


Figure 1. Relative influence (% variance explained) of wildlife host ecological traits, zoogeographical region and number of publications (a surrogate of sampling effort) on the probability that wildlife species shared helminth parasite species with humans or selected domestic species. Coloured bars represent posterior modes, grey bars show 95 % credible intervals based on the statistical sampling approach. The trait variables habitat, range area, diet breadth and litters per years were excluded from the plot because of their negligible effects.

Model-based predictions of association risk revealed two prominent patterns: first, bat species (Chiroptera) are predicted to show a low risk of sharing parasites with focal hosts (**Fig. S3**). Second, wildlife association risks were often strongly correlated across different focal hosts. The strongest of these correlations were between the risk of wildlife species sharing human cestodes and dog cestodes, human trematodes and dog trematodes, and human cestodes and dog trematodes (Spearman's r = 0.97, 0.98, and 0.96, respectively) (**Fig. S4**).

Wild mammals occurring in the Nearctic and Palaearctic regions were predicted to show high association risk for sharing parasites with humans, a pattern that held across all three parasite groups (**Fig. 2**). In contrast, this predicted risk was remarkably low when considering human-associated cestodes in the Neotropical region and human-associated parasites from all three parasite groups in the Australian region (**Fig. 2**). Cumulative community-level association risks (summed over all wildlife species in local species pools) resulted in some different patterns. The risk of sharing human parasites was high for wildlife communities occurring in the Nearctic region (particularly for cestodes and trematodes) and in mammalian diversity hotspots such as the Panamanian and Neotropical (especially for trematodes) and Afrotropical (nematodes and trematodes) regions (**Fig. 2**). Note that relationships between observed proportions of shared parasites and the trait-based prediction of association risks exhibited some uncertainty (**Fig. S5**). Nevertheless, correlations in community-level association risks were even stronger than were species-level correlations, suggesting broad-scale patterns in parasite sharing are predictable (**Fig. S6**). We did not identify any major global patterns in parasite assemblage distinctiveness (mean turnover in shared parasite species across zoogeographical regions), though this metric appeared to be relatively higher in trematodes than in cestodes, and relatively moderate in nematodes (**Fig. S7**).



381

382 **Figure 2**. Predicted average (species-level) and cumulative (community-level) geographical
383 association risks for local wildlife assemblages sharing helminth parasites (Nematoda,
384 Cestoda, Trematoda) with humans. The risk of wildlife species sharing parasites with humans
385 were computed using data on host-parasite associations and ecological profiles for 1,345
386 wildlife species. Projections of model-based predictions on a global map are based on
387 computed wildlife species-level association risks for all extant mammals, rasterised at 10 km^2
388 resolution and respective IUCN range maps.

389

390 At the parasite species level, Shannon indices describing the biogeographical spread
391 of the 1,103 recorded helminth species followed an exponential distribution (**Fig. 3**). The
392 most globally widespread parasite species were *Calodium hepaticum* (Nematoda),

393 *Echinococcus granulosus* (Cestoda), *E. multilocularis* (Cestoda), *Hydatigera taeniaeformis*
394 (Cestoda) and *Hymenolepis diminuta* (Cestoda), all of which infected 50 – 73 wildlife species
395 and were recorded in at least three of the focal host species (**Fig. 4**). The correlation between
396 the index of parasite biogeographical spread and the total number of associated focal host
397 species, however, was only moderate (Spearman's r = 0.5, p < 0.01).
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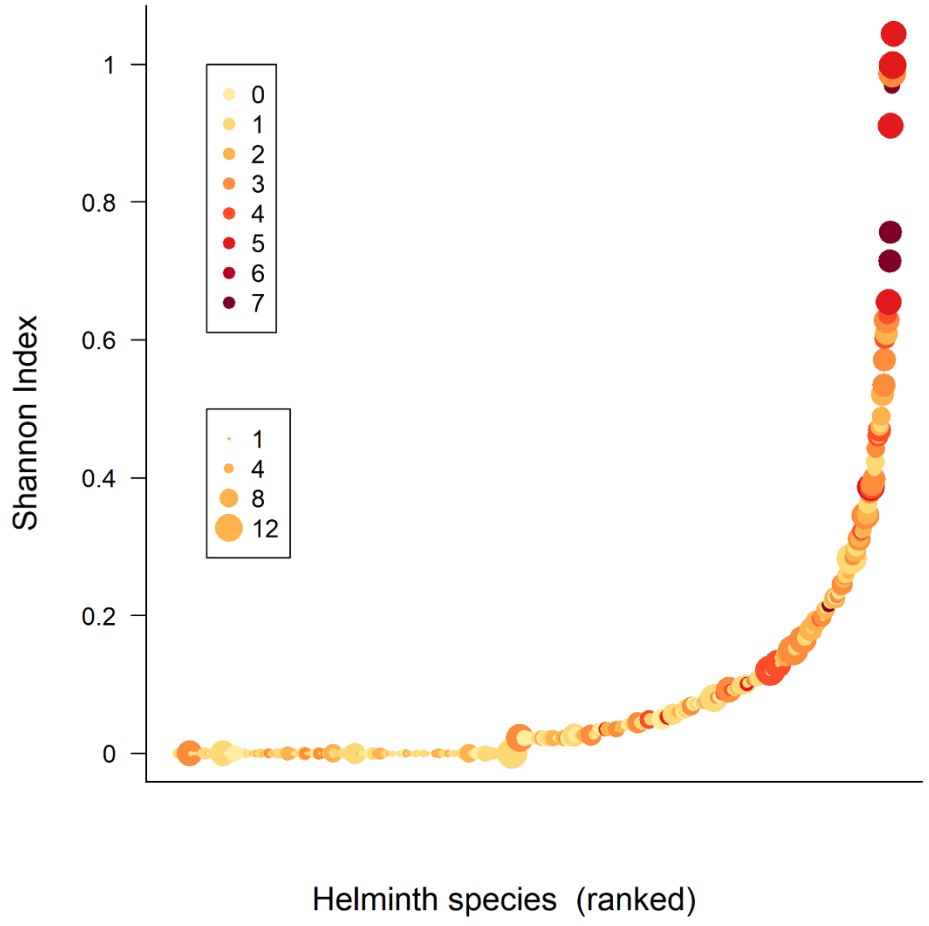

400

401 **Figure 3**. Rank distribution plot of Shannon indices for 1,103 helminth parasite species
402 (Nematoda, Cestoda and Trematoda) recorded in domestic host species, indicating the
403 relative global spread and linkage to wildlife for each parasite species (Shannon indices are
404 based on the proportion of wildlife species associated with the parasites in different

zoogeographical regions). Colours represent the number of focal domestic host species (human, dog, cat, cow, pig, black rat, brown rat) also associated with that parasite species. The size of points reflects the number of zoogeographical realms in which the respective helminth species have been recorded (1 – 12, including one class of unspecified records from China).

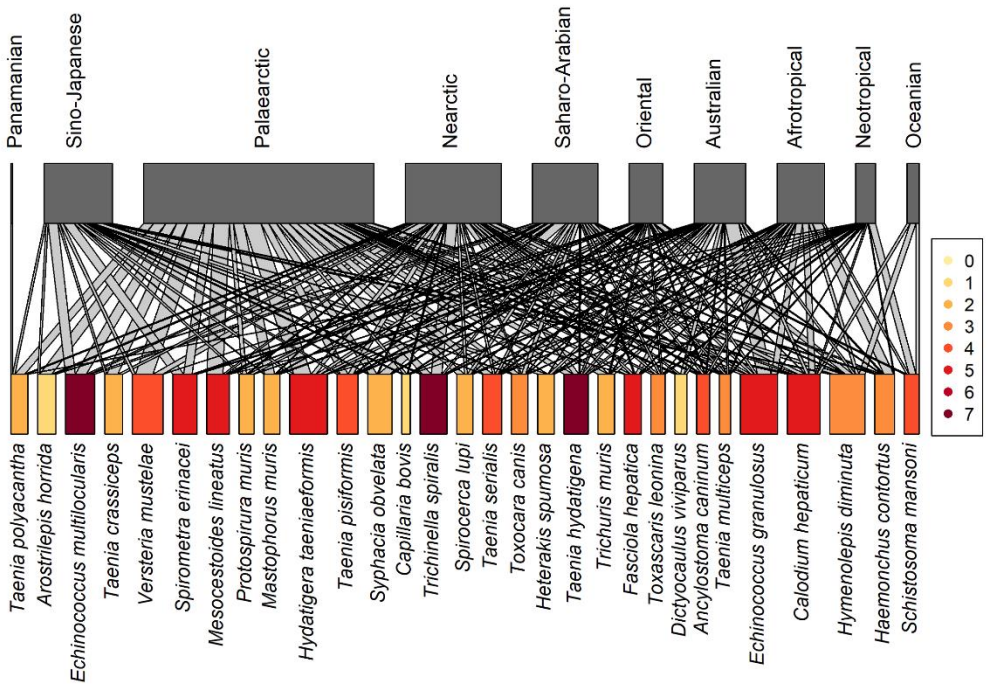

Figure 4. Bipartite network plot of the most globally widespread helminth parasite species associations with wildlife species pools in different zoogeographical regions. Upper nodes represent zoogeographical regions and lower nodes parasite species. The widths of links represent the relative proportion of wildlife species from the regional species pool associated with the respective parasites. Colours of lower nodes (parasites) represent the number of focal domestic host species (humans, dog, cat, cow, pig, black rat, brown rat) also associated with that parasite species, illustrating that the majority of globally spread parasites are linked to

multiple domestic host species. Widespread parasites species (n = 31) were identified as those with the highest Shannon index scores, accounting for the associated proportions of sampled wildlife species in different zoogeographical realms. Note the Madagascan region is not shown, as no wildlife species were associated with the displayed parasites.

Discussion

Global biodiversity change will affect human and animal health in many ways, but potential shifts in disease burden at the human–animal interface are largely unexplored (Myers *et al.*, 2013), particularly at the macro-ecological scale (Stephens *et al.*, 2016). We show that diet is a key driver of the risk that wild mammal species share helminth parasites with humans. Carnivores and herbivores, in particular, are at high risk of sharing parasites with humans, while insectivores are generally at low risk. Relatively weaker effects of a wildlife species' climatic and habitat niches indicate that zoonotic parasite spread will not be contained if contacts between wildlife and humans continue to increase. Crucially, these same patterns hold when assessing the risk of wildlife sharing helminths with important domestic animals. While parasite sharing is a multifaceted one-health issue, we show that decomposing risk of parasite sharing based on species' ecological and climatic niches is an important first step towards predicting future parasite emergence.

Diet as a key driver of helminth parasite sharing

Our study focuses on terrestrial mammalian species, of which many interact in predator–prey relationships. The completion of life cycles for some of the most globally widespread helminths, such as *Echinococcus* spp. and *Fasciola* spp., which are also of significant health concern (Garcia *et al.*, 2007), depend on such trophic interactions among mammalian hosts. Unlike microparasites (viruses, bacteria, protozoa, fungi), the majority of parasitic helminth

444 species do not replicate in the definitive vertebrate host, with many species requiring
445 transmission through a diversity of invertebrates to complete their life cycles. For wildlife
446 insectivores, the low risks of carrying domestic animal helminths found by our study suggest
447 there is a transmission disruption that prevents host shifting (e.g. if humans consume
448 insectivorous species such as bats or shrews, but these species do not in turn ingest
449 contaminated material from humans or other infected species). Alternatively, domestic
450 animals and insectivorous wildlife species may not adequately share resources, such as
451 invertebrate food items or particular habitats, which would enable parasite transmission.
452 The majority of parasitic nematode species undergo free-living life-history stages in the
453 environment; some are transmitted by direct skin penetration into the definite host, whereas
454 others are transmitted through trophic interactions that may involve the ingestion of
455 intermediate invertebrate hosts (Anderson, 2000). This environmental transmission may play
456 an important role in governing nematode host sharing. Wild and domestic ungulate species,
457 for example, may share considerable proportions of their nematode fauna through grazing on
458 common grounds (Walker & Morgan, 2014). Importantly, although one might expect host-
459 shifting of parasites with free-living stages to be susceptible to environmental conditions, our
460 results suggest host sharing is more strongly linked to the diet strategy of the host species.
461 Focusing just on helminth parasites, we found notable differences compared to previous
462 studies examining zoonotic disease risk and reservoir potential for wildlife species. A recent
463 study on the zoonotic reservoir potential of rodents for both helminths and microparasites
464 (viruses, bacteria, protozoa, fungi), for example, predicted that the rather fast-paced life
465 history strategies of rodents should be linked to a higher reservoir potential for zoonotic
466 diseases (Han *et al.*, 2015). Furthermore, Luis *et al.* (2013) reported both bats and rodents to
467 be major natural reservoirs for viral zoonoses. In contrast, we predicted the majority of bat
468 species are less likely to share parasites with humans and domestic species (see **Fig. S4**).

Different mechanisms may apply in relation to how helminths and microparasites are spread through multi-species systems at the human–domestic animal–wildlife interface, warranting future research.

Roles of domestic animal hosts at the human – wildlife interface

Consistent with our expectations, we found strong correlations between the risk that wildlife will share cestodes with human and the risk that wildlife will share cestodes with dogs. Previous work has suggested that dogs and humans share a considerable number of parasites (Morand *et al.*, 2014). We extend these findings to show that, concomitant with man's long association with dogs and the collective exploitation of environments, both humans and dogs share a considerable number of their helminth parasites with wildlife. However, this pattern is not restricted to dogs, but can be also seen in patterns of parasite sharing for various domestic species at a global scale. We found generally strong correlations in the spatially projected wildlife associations risks – both at the species-level and the community-level – across domestic host species (**Fig. S6**, **S7**). This emphasises, that for helminth parasites, the human–wildlife interface is not independent of domestic species.

Our findings support previous calls for multi-species and community-level approaches to understand parasite and disease spread (Fenton *et al.*, 2015; Johnson *et al.*, 2015; Viana *et al.*, 2014). Notably, we provide a starting point for explaining how overlapping distributions and contact patterns between humans, domestic animals and wildlife may impact zoonotic helminth spread at a global scale. Based on our results, future geographical spread of helminth parasites will likely be facilitated through infection of multiple domestic hosts (and possibly also invasive mammal species) that show similar trophic relationships.

We demonstrate clear zoogeographical structure in predicted risks that wildlife will

494 share parasites with humans and domestic host species. The highest risk is consistently found
495 in the Palaearctic and Nearctic regions. Similar global patterns have been reported for rodent-
496 borne zoonotic diseases, for example by Han *et al.* (2015). In previous work, we found the
497 two commensal rat species included in our study generally share helminth parasites with
498 wildlife species of least conservation concern (Wells *et al.*, 2015), which are likely those
499 species well adapted to anthropogenically modified landscapes. Possibly, strong adaptation to
500 anthropogenically modified landscapes by many wildlife species in the Palaearctic and
501 Nearctic regions, in combination with relevant ecological profiles, could contribute to the
502 strong geographical gradients in risks of parasite sharing.

503 Unfortunately, it is very difficult to discern historical host shifts by parasites, and thus
504 any possible spill-over and spill-back events, unless adequate molecular data for ancestral
505 state reconstruction are available (Hoberg *et al.*, 2001; Terefe *et al.*, 2014). Our analysis does
506 not determine whether wildlife hosts have acquired parasites from humans and domestic
507 animals, or vice versa. This is especially challenging for humans and domestic species, which
508 hardly exist in isolation from each other.

509

510 **Future parasite spread through mechanisms of parasite sharing**

511 Our finding that trophic interactions are important for interspecific helminth sharing
512 indicates the need for quantitative approaches that predict whether potential host species may
513 interact locally in predator-prey relationships. Our predictions can foster a better
514 understanding of how future domestic animal and wildlife assemblages might impact
515 potential parasite host shifting through ecological fitting and changed biotic interactions (e.g.
516 predator-prey relationships). Zoonotic disease risk caused by helminths, for example, could
517 then be refined to sophisticated measures that take multi-species networks of trophic
518 interactions into account, rather than only considering the number of wildlife species in local

519 assemblages (Karesh *et al.*, 2005). Given the variable sensitivities among wildlife species to
520 climate change, such work could also account for shifting trophic interactions among
521 potential parasite hosts through regionally altered community assemblages (Lurgi *et al.*,
522 2012).

523 The wildlife and domestic animal trade, together with species invasions and shifting
524 species ranges, will continue to mix formerly disjunctive host species assemblages and cause
525 biotic homogenisation (Hobbs *et al.*, 2009). However, future climate-induced range shifts,
526 decreasing population sizes or newly arising barriers that prevent wildlife movement can also
527 decrease contact intensity between humans and some wildlife species. This may serve to
528 inhibit the sharing of parasites. We nevertheless believe that very few wildlife species will be
529 sufficiently 'left alone' by humans to prevent parasite exchange unless such wildlife species
530 are extremely rare.

531

532 **Host-parasite interactions and sampling bias**

533 Based on records of presence-only host-parasite associations, we consider the results of our
534 study to be indicative for unravelling general patterns, rather than for providing precise
535 predictions. Several challenges are associated with studying species interactions and macro-
536 ecological patterns from presence-only data. First, it is well known from sampling and
537 probability theory that parasites are likely overlooked in host species sampled with relatively
538 low intensity (Little, 2004). This will be especially true when low parasite prevalence
539 prevents detection in a limited number of examined host individuals. Helminth species
540 richness in freshwater fish, for example, was found to be highly correlated with the number
541 of individuals examined per host species (Walther *et al.*, 1995). An obstacle to accounting for
542 this sampling bias is that the true sampling effort, that is the number individuals per host
543 species examined, was not available for our study; this would have enabled us to better

correct for sampling bias when making inferences about host-parasite associations (Wells *et al.*, 2013). Moreover, spatial bias, both in the species sampled and in species–species interactions, is generally known to strongly bias inference of macro-ecological patterns (Boakes *et al.*, 2010; Meyer *et al.*, 2015). Bias may be also linked to parasite size, if large species are more likely to be detected. Our trait-based approach may leverage (to some extent) poorly sampled species and we used the number of publications for each host species as a simplified proxy of sampling bias. Limitations in the currently available data on host-parasite associations and infectious disease prevent concise mapping of the majority of parasites and diseases (Hay *et al.*, 2013). Considering further sampling bias – as far as relevant data are available – could be of especial interest for inferring large-scale global patterns. The proportion of wildlife species examined for parasites, for example, exhibits considerable gradients across zoogeographical regions (**Fig. S8**). This warrants future research and a critical revision of whether the particularly strong linkage of human parasites to wildlife in temperate Europe and North America, as found in this study and others (Han *et al.*, 2015; Murray *et al.*, 2015), is a true biological phenomenon or a consequence of uneven survey efforts. Moreover, improving the spatial resolution to understand whether host-parasite interactions and disease emergence are constrained to only those parts of a species range where enabling conditions are met would improve predictions and our understanding of how natural barriers may prevent disease emergence. This is of particular importance as, ultimately, ecological and epidemiological dynamics are driving the interaction between hosts and parasites and possible parasite spill-over among hosts (Plowright *et al.*, 2017).

Anticipating and mitigating future changes in parasite host shifting at the human–wildlife interface may require quantitative approaches that consider novel transmission pathways. These shifting pathways could be caused by the ongoing decline and/or extinction

of native species (Schipper *et al.*, 2008), the introduction of invasive species (Clavero & García-Berthou, 2005) and/or the increasing density of domestic livestock species (Jones *et al.*, 2013). Novel trophic interactions at the human–wildlife interface may also be largely driven by human behaviour, such as expanding the menu of consumed animal species, or the exposure of domestic species to potentially contaminated food waste (Macpherson, 2005). Disentangling the roles of trophic and other biotic interactions versus environmental conditions in driving parasite host sharing will improve public and wildlife health measures.

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REFERENCES

Agosta SJ, Klemens JA (2008) Ecological fitting by phenotypically flexible genotypes: implications for species associations, community assembly and evolution. *Ecology Letters*, **11**, 1123-1134.

Anderson RC (2000) *Nematode parasites of vertebrates: their development and transmission*, Wallingford, Oxon, U.K., CABI Publishing.

Bininda-Emonds ORP, Cardillo M, Jones KE *et al.* (2007) The delayed rise of present-day mammals. *Nature*, **446**, 507-512.

Boakes EH, Mcgowan PJK, Fuller RA, Chang-Qing D, Clark NE, O'Connor K, Mace GM (2010) Distorted views of biodiversity: spatial and temporal bias in species occurrence data. *Plos Biology*, **8**, e1000385.

Clark NJ, Clegg SM, Sam K, Goulding W, Koane B, Wells K (2017) Climate, host

phylogeny and the connectivity of host communities govern regional parasite assembly. *Diversity and Distributions,* doi: 10.1111/ddi.12661.

Clavero M, García-Berthou E (2005) Invasive species are a leading cause of animal extinctions. *Trends in Ecology and Evolution,* **20**, 110.

Crompton DWT (1999) How much human helminthiasis is there in the world? *Journal of Parasitology,* **85**, 397-403.

Daszak P, Cunningham AA, Hyatt AD (2000) Emerging infectious diseases of wildlife - threats to biodiversity and human health. *Science,* **287**, 443-449.

Elith J, Leathwick JR, Hastie T (2008) A working guide to boosted regression trees. *Journal of Animal Ecology,* **77**, 802-813.

Fenton A, Streicker DG, Petchey OL, Pedersen AB (2015) Are all hosts created equal? Partitioning host species contributions to parasite persistence in multihost communities. *The American Naturalist,* **186**, 610-622.

Garcia HH, Moro PL, Schantz PM (2007) Zoonotic helminth infections of humans: echinococcosis, cysticercosis and fascioliasis. *Current Opinion in Infectious Diseases,* **20**, 489-494.

Gelman A, Meng XL, Stern H (1996) Posterior predictive assessment of model fitness via realized discrepancies. *Statistica Sinica,* **6**, 733-760.

Gibson DI, Bray RA (1994) The evolutionary expansion and host-parasite relationships of the Digenea. *International Journal for Parasitology,* **24**, 1213-1226.

Gibson DI, Bray RA, Harris EA (2005) Host-parasite database of the Natural History Museum, London. pp Page, Natural History Museum.

Gibson DI, Bray RA, Hunt D *et al.* (2014) Fauna Europaea: helminths (animal parasitic). *Biodiversity Data Journal,* **2**, e1060.

Han BA, Schmidt JP, Bowden SE, Drake JM (2015) Rodent reservoirs of future zoonotic

619 diseases. *Proceedings of the National Academy of Sciences,* **112**, 7039-7044.
620 Hay SI, Battle KE, Pigott DM *et al.* (2013) Global mapping of infectious disease.
621 *Philosophical Transactions of the Royal Society B-Biological Sciences,* **368**, 0120250.
622 Hobbs RJ, Higgs E, Harris JA (2009) Novel ecosystems: implications for conservation and
623 restoration. *Trends in Ecology and Evolution,* **24**, 599-605.
624 Hoberg EP, Alkire NL, Queiroz AD, Jones A (2001) Out of Africa: origins of the *Taenia*
625 tapeworms in humans. *Proceedings of the Royal Society of London B: Biological*
626 *Sciences,* **268**, 781-787.
627 Hoberg EP, Brooks DR (2008) A macroevolutionary mosaic: episodic host-switching,
628 geographical colonization and diversification in complex host–parasite systems.
629 *Journal of Biogeography,* **35**, 1533-1550.
630 Holt BG, Lessard J-P, Borregaard MK *et al.* (2013) An update of Wallace's zoogeographic
631 regions of the world. *Science,* **339**, 74-78.
632 Johnson PTJ, Ostfeld RS, Keesing F (2015) Frontiers in research on biodiversity and disease.
633 *Ecology Letters,* **18**, 1119-1133.
634 Jones BA, Grace D, Kock R *et al.* (2013) Zoonosis emergence linked to agricultural
635 intensification and environmental change. *Proceedings of the National Academy of*
636 *Sciences,* **110**, 8399-8404.
637 Jones KE, Bielby J, Cardillo M *et al.* (2009) PanTHERIA: a species-level database of life
638 history, ecology, and geography of extant and recently extinct mammals. *Ecology,* **90**,
639 2648-2648.
640 Just MG, Norton JF, Traud AL *et al.* (2014) Global biogeographic regions in a human-
641 dominated world: the case of human diseases. *Ecosphere,* **5**, 1-21.
642 Karesh WB, Cook RA, Bennett EL, Newcomb J (2005) Wildlife trade and global disease
643 emergence. *Emerging Infectious Diseases,* **11**, 1000-1002.

644 Kraft Nathan jB, Cornwell William k, Webb Campbell o, Ackerly David d (2007) Trait
645 evolution, community assembly, and the phylogenetic structure of ecological
646 communities. *The American Naturalist,* **170**, 271-283.
647 Lennon JJ, Koleff P, Greenwood JJD, Gaston KJ (2001) The geographical structure of British
648 bird distributions: diversity, spatial turnover and scale. *Journal of Animal Ecology,*
649 **70**, 966-979.
650 Little RJ (2004) To model or not to model? Competing modes of inference for finite
651 population sampling. *Journal of the American Statistical Association,* **99**, 546-556.
652 Lloyd-Smith JO, George D, Pepin KM *et al.* (2009) Epidemic dynamics at the human-animal
653 interface. *Science,* **326**, 1362-1367.
654 Lunn D, Jackson C, Best N, Thomas A, Spiegelhalter D (2012) *The BUGS Book - A practical*
655 *introduction to Bayesian analysis,* London, CRC Press / Chapman and Hall.
656 Lurgi M, López BC, Montoya JM (2012) Novel communities from climate change.
657 *Philosophical Transactions of the Royal Society B-Biological Sciences,* **367**, 2913-
658 2922.
659 Macpherson CNL (2005) Human behaviour and the epidemiology of parasitic zoonoses.
660 *International Journal for Parasitology,* **35**, 1319-1331.
661 Magurran AE (ed) (2004) *Measuring biological diversity,* Oxford, Blackwell.
662 Matisoo-Smith, E. , Roberts, R. M., Irwin, G. J. , Allen, J. S., Penny, D. , Lambert, D. M.
663 (1998) Patterns of prehistoric human mobility in Polynesia indicated by mtDNA from
664 the Pacific rat. *Proceedings of the National Academy of Sciences,* **95**, 15145-15150.
665 Meyer C, Kreft H, Guralnick R, Jetz W (2015) Global priorities for an effective information
666 basis of biodiversity distributions. *Nature Communications,* **6**, 8221.
667 Morand S, Mcintyre KM, Baylis M (2014) Domesticated animals and human infectious
668 diseases of zoonotic origins: domestication time matters. *Infection, Genetics and*

669 *Evolution,* **24**, 76-81.
670 Murray KA, Preston N, Allen T, Zambrana-Torrelio C, Hosseini PR, Daszak P (2015) Global
671 biogeography of human infectious diseases. *Proceedings of the National Academy of*
672 *Sciences,* **112**, 12746-12751.
673 Myers SS, Gaffikin L, Golden CD *et al.* (2013) Human health impacts of ecosystem
674 alteration. *Proceedings of the National Academy of Sciences,* **110**, 18753-18760.
675 Paradis E, Claude J, Strimmer K (2004) APE: Analyses of phylogenetics and evolution in R
676 language. *Bioinformatics,* **20**, 289-290.
677 Patz JA, Olson SH, Uejio CK, Gibbs HK (2008) Disease emergence from global climate and
678 land use change. *Medical Clinics of North America,* **92**, 1473–1491.
679 Pedersen AB, Davies TJ (2009) Cross-species pathogen transmission and disease emergence
680 in primates. *Ecohealth,* **6**, 496-508.
681 Plowright RK, Parrish CR, McCallum H, Hudson PJ, Ko AI, Graham AL, Lloyd-Smith JO
682 (2017) Pathways to zoonotic spillover. *Nature Review Microbiology*, doi:
683 10.1038/nrmicro.2017.45.
684 Pulliam JRC (2008) Viral host jumps: moving toward a predictive framework. *Ecohealth,* **5**,
685 80-91.
686 R Development Core Team (2017) R: A language and environment for statistical computing,
687 Vienna, Austria, R Foundation for Statistical Computing.
688 Reinhard KJ, Ferreira LF, Bouchet F *et al.* (2013) Food, parasites, and epidemiological
689 transitions: a broad perspective. *International Journal of Paleopathology,* **3**, 150-157.
690 Schipper J, Chanson JS, Chiozza F *et al.* (2008) The status of the world's land and marine
691 mammals: diversity, threat, and knowledge. *Science,* **322**, 225-230.
692 Stephens PR, Altizer S, Smith KF *et al.* (2016) The macroecology of infectious diseases: a
693 new perspective on global-scale drivers of pathogen distributions and impacts.

694 *Ecology Letters*, **19**, 1159–1171.
695 Streicker DG, Turmelle AS, Vonhof MJ, Kuzmin IV, Mccracken GF, Rupprecht CE (2010)
696 Host phylogeny constrains cross-species emergence and establishment of rabies virus
697 in bats. *Science,* **329**, 676-679.
698 Taylor LH, Latham SM, Woolhouse MEJ (2001) Risk factors for human disease emergence.
699 *Philosophical Transactions of the Royal Society of London B Biological Sciences,*
700 **356**, 983-989.
701 Terefe Y, Hailemariam Z, Menkir S *et al.* (2014) Phylogenetic characterisation of *Taenia*
702 tapeworms in spotted hyenas and reconsideration of the "Out of Africa" hypothesis of
703 Taenia in humans. *International Journal for Parasitology,* **44**, 533-541.
704 Viana M, Mancy R, Biek R, Cleaveland S, Cross PC, Lloyd-Smith JO, Haydon DT (2014)
705 Assembling evidence for identifying reservoirs of infection. *Trends in Ecology &*
706 *Evolution,* **29**, 270-279.
707 Walker JG, Morgan ER (2014) Generalists at the interface: nematode transmission between
708 wild and domestic ungulates. *International Journal for Parasitology: Parasites and*
709 *Wildlife*, **3**, 242-250.
710 Wallace AR (1876) *The geographical distributions of animals, with a study of the relations of*
711 *living and extinct faunas as elucidating the past changes of the Earth's surface,*
712 London, Macmillan.
713 Walther BA, Cotgreave P, Price RD, Gregory RD, Clayton DH (1995) Sampling effort and
714 parasite species richness. *Parasitology Today,* **11**, 306-310.
715 Wells K, O'Hara RB, Morand S, Lessard J-P, Ribas A (2015) The importance of parasite
716 geography and spillover effects for global patterns of host–parasite associations in
717 two invasive species. *Diversity and Distributions,* **21**, 477-486.
718 Wells K, O'Hara RB, Pfeiffer M, Lakim MB, Petney TN, Durden LA (2013) Inferring host

719 specificity and network formation through agent-based models: tick–mammal
720 interactions in Borneo. *Oecologia*, **172**, 307-316.
721 Wilman H, Belmaker J, Simpson J, De La Rosa C, Rivadeneira MM, Jetz W (2014)
722 EltonTraits 1.0: species-level foraging attributes of the world's birds and mammals.
723 *Ecology*, **95**, 2027-2027.
724 Wolfe ND, Dunavan CP, Diamond J (2007) Origins of major human infectious diseases.
725 *Nature*, **447**, 279-283.
726 Woolhouse MEJ, Gowtage-Sequeria S (2005) Host range and emerging and reemerging
727 pathogens. *Emerging Infectious Diseases*, **11**, 1842-1847.