

SUPPORTING ONLINE MATERIAL

MATERIALS AND METHODS

Quantitative methods:

Probabilistic estimation of affiliate extinctions— The objective is to estimate the extinction of affiliate species as a function of the extinction of their host species, given an “affiliation matrix” that specifies which affiliates are dependent on which hosts. This problem is mathematically identical to the problem of estimating the expected number of species in a sub-sample of quadrats (or other sampling units) from presence/absence data, recently solved independently by Colwell et al. (S1) and Ugland et al. (S2). Our presentation for the affiliate-host problem follows the notation and approach of Colwell et al. (S1).

Suppose the affiliation matrix includes data for S affiliate species dependent on H host species. The S -by- H affiliation matrix consists of interaction indicators Z_{ij} , where

$$Z_{ij} = \begin{cases} 1 & \text{if the } i\text{th affiliate is dependent on the } j\text{th host} \\ 0 & \text{if the } i\text{th affiliate is not dependent on the } j\text{th host.} \end{cases}$$

Let s_j stand for the number of affiliate species each dependent on exactly j host species in the affiliation matrix. The s_j are called *counts* (frequencies of host-specificity categories).

Thus s_1 is the number of affiliate species that each depend on a single host species, s_2 is the number of affiliate species that each depend on exactly two host species, and so on.

The total number of affiliates in the matrix is therefore $n = \sum_{j=1}^H s_j$. The observed counts

$s_1, s_2 \dots s_H$ contain all the information necessary for estimating the number of affiliate extinctions as a function of host extinctions (S1).

Suppose E of the host species become extinct, at random, among the H host

species at risk. Then the number of surviving host species h is simply $h = H - E$, and the number of surviving affiliates τ as a function of the number of surviving hosts is $\tau(h)$.

Using the method of moments, Colwell et al. (SI) derived an unbiased estimator $\tilde{\tau}(h)$ for $\tau(h)$ that is based on the counts s_j , appropriately weighted by combinatorial coefficients:

$$\tilde{\tau}(h) = \sum_{j=1}^H (1 - \alpha_{jh}) s_j = n - \sum_{j=1}^H \alpha_{jh} s_j, h = 1, 2, \dots, H, \quad (1)$$

where the combinatorial coefficients α_{jh} are defined by

$$\alpha_{jh} = \begin{cases} \frac{(H-h)(H-j)!}{(H-h-j)!H!} & \text{for } (j+h \leq H) \\ 0 & \text{for } (j+h > H) \end{cases}.$$

(The estimator $\tilde{\tau}(h)$ is the best estimator of $\tau(h)$ in the sense that $\tilde{\tau}(h)/S$ achieves the minimum variance among all unbiased estimators for $\tau(h)/S$ (Ref. SI))

Equation (1) is implemented in the freeware application EstimateS (version 7) (S3). We used EstimateS to estimate $\tilde{\tau}(h)$ for $h = 1, 2, \dots, H$ from empirical affiliation matrices. The estimated number of affiliate species extinctions $\tilde{A}(E)$ when E host species become extinct (as shown in Figs. 1 and 3B), is then simply

$$\tilde{A}(E) = n - \tilde{\tau}(H - E). \quad (2)$$

To estimate the number of historical affiliate extinctions caused by recorded extinctions for a particular host taxon (Fig. 3A), one could use the affiliation matrix for extant hosts and affiliates for that taxon to extrapolate $\tilde{\tau}(h)$ to $h = H_{his} = H + E_{his}$, where H_{his} is the pre-extinction number of host species and E_{his} is the recorded number of historic host extinctions, then compute

$$\tilde{A}(E_{hist}) = \tilde{\tau}(H_{hist}) - n.$$

Colwell et al. (S1) outline likelihood-based methods for fitting a binomial mixture model by an expectation maximization algorithm guided by AIC. That method might be used, but it is quite complex. Instead, given the relatively small interval between $\tilde{\tau}(H - E_{hist})$ and $\tilde{\tau}(H + E_{hist})$, we approximated the number of historical affiliate extinctions by equation (2), assuming that $H = H_{hist}$ and $E = E_{hist}$. This approach assumes that $\tau(h)$ is approximately linear between $\tilde{\tau}(H - E_{hist})$ and $\tilde{\tau}(H + E_{hist})$.

Nomographic estimation of affiliate extinctions— The objective is to estimate affiliate extinction probability as a function of two empirical variables: mean host specificity and host extinctions (historical or projected, based on endangered species lists). From the probabilistic model, we generated co-extinction curves to estimate expected affiliate extinctions (\bar{A}) as a function of host extinctions (\bar{E}) for 20 well-studied affiliate-host systems that vary in mean host specificity (\bar{s}) (see Fig. 2 in text). For increasing levels of host extinction \bar{E} (10%, 25%, 50%, 75% and 90%), we regressed $\frac{\bar{A}}{\bar{E}}$ on $\ln(\bar{s})$ (Fig. S1) to fit the equation

$$\frac{\bar{A}}{\bar{E}} = k_{\bar{E}} \ln(\bar{s}) + b, \quad (3)$$

Note that the intercept b (at $\bar{s} = 1$, for affiliates with a single host) must equal unity. The slope $k_{\bar{E}}$ of this function varies with \bar{E} (Fig. S1). To get an expression for $k_{\bar{E}}$, we regressed $k_{\bar{E}}$ on \bar{E} , yielding $k_{\bar{E}} = 0.35\bar{E} - 0.43$. Substituting this expression into equation (3) and setting $b = 1$, we arrive at the nomographic model,

$$\bar{A} = (0.35\bar{E} - 0.43)\bar{E} \ln(\bar{s}) + \bar{E}.$$

Complexities and assumptions:

Data constraints — All ambiguous records in the datasets (i.e., those without species names of either affiliates or hosts) were excluded from our analyses. Our projections of affiliate extinctions were based on the best affiliation matrices available or the best estimates of mean host specificity, affiliate species richness, host species richness, and the number of endangered and extinct hosts (Table S1). However, given the preliminary nature of nearly all datasets on these variables, particularly for invertebrates, errors and biases in our data sources are bound to exist. First, errors in estimates of affiliate host specificity may result from the incomplete sampling of cryptic affiliate species, such as fig-wasps and their host figs (*S4*). Second, we have likely underestimated the species richness of affiliates due to the paucity of research on many affiliate species. Third, we have excluded from our analyses all affiliate-host associations that have yet to be studied or enumerated. Therefore, our projections of affiliate extinctions were, of necessity, based on the assumption that the studied host species are a statistically representative subset of all host species. Fourth, although our estimates of historical species co-extinctions were based on best available data of extinct species from the IUCN (*21*), the number of historically extinct species and therefore the number of affiliate co-extinctions will always be debatable. As such, we have also shown the proportion of affiliate species expected to go extinct for the given proportion of host species recorded as extinct (Fig. 3 in text). As better data on historical extinctions become available, the estimates of affiliate co-extinctions will improve correspondingly.

Patterns of affiliate-host associations — We assumed that affiliates are distributed randomly with respect to the endangerment level of their hosts. That is, an endangered host has the same probability of being associated with affiliate species as does a less endangered host. Although a recent study showed that endangered primate species may have fewer parasites than less endangered primate species (*S5*), we suspect this is likely due to the recent extinctions of parasites from endangered primates. To the extent that endangered species have fewer affiliates than less endangered species in general, we will have overestimated the levels of affiliate co-extinctions. Nevertheless, the generality and implications of the pattern of distribution of affiliates with respect to the endangerment level of their hosts deserve further investigation. Further, the extinction level of affiliate species due to co-extinction for any given level of host specificity is almost entirely a function of the affiliate's host specificity distribution (see Fig. S2). To our knowledge no theoretical basis exists for expecting a particular shape for host specificity distributions. Although Jaenike (*S6*) suggests that such distributions may be lognormal for insect herbivores, he did not test for log-normality statistically. In fact, we find that host specificity distributions of all the datasets we considered were consistently right log-skewed (Fig. S2). This consistency in host specificity distribution across different affiliate-host systems is the reason for the ubiquitous log-linear relationship between mean host specificities and affiliate extinction levels in our study (Figs. S1), which allowed us to use mean host specificity as a proxy for host specificity distributions in our predictive nomographic model. Nevertheless, we need to characterize a much broader array of host specificity distributions than are currently available, not only to assess the

generality of the nomographic model, but also to better understand the evolution of host specialization and the magnitude and dynamics of species co-extinctions.

Causes of affiliate extinction — We assumed that affiliates go extinct only when their hosts go extinct. However, affiliate extinctions may occur simply when host populations are reduced or when their breeding, migratory patterns, or phenology are altered. To the extent that reductions or other changes in host population lead to the loss of affiliate species, we may have underestimated the extinction levels of affiliates. Further, affiliates may go extinct from other drivers of extinction, such as habitat destruction, overkill and introduced species (*S7*), which often act in concert. For example, where deforestation is the cause of plant extinctions, butterflies may go extinct either from the loss of their larval hostplants or from the loss of the nectar (and in some cases pollen) sources that many adults rely on. For this study, we have assumed the simplest scenario, with co-extinction being the single causal factor in affiliate extinctions. Disentangling co-extinction from other causes of extinction has important conservation implications and should be the focus of future research.

Figure S1. Scaling for the nomographic model. Symbols represent data generated from the probabilistic model (Fig. 2 in text). Lines and adjacent equations indicate regression of $\frac{\bar{A}}{\bar{E}}$ on $\ln(\bar{s})$ for increasing levels of host extinction, \bar{E} , scaled by percentage extinction of hosts (10%, 25%, 50%, 75% and 90%).

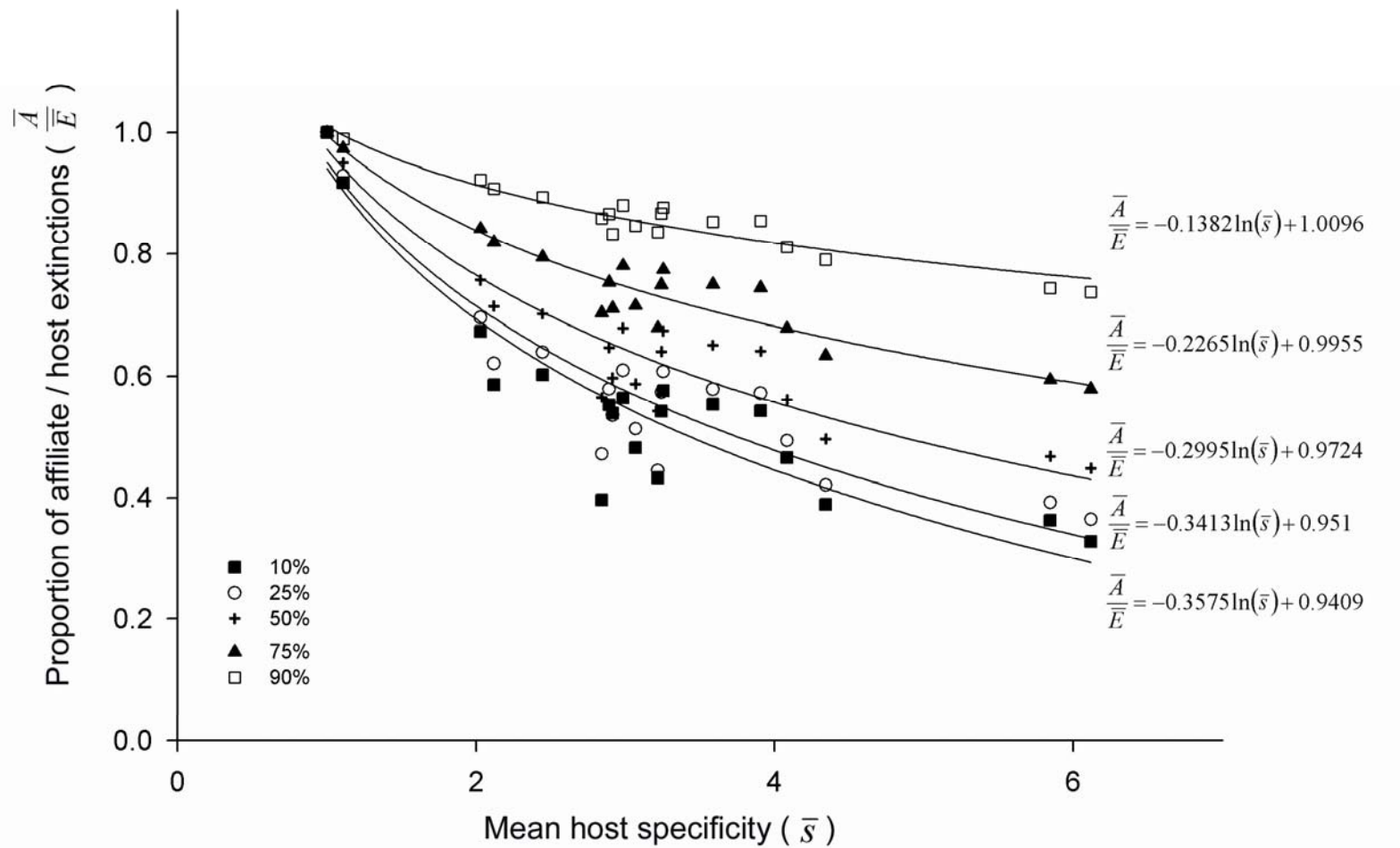


Figure S2. Log-transformed host specificity distributions of eight relatively well-studied affiliate-host systems: pollinating Agaonidae *Ficus* wasps and *Ficus* (S8), primate *Pneumocystis* fungi and primates (S9), primate nematodes and primates (S10-S12), primate lice and primates (S13, S14), seabird lice and seabirds (S14), bird mites (represented by Avenzoariidae) and birds* (S15), butterflies (represented by Papilionidae) and larval hostplants (S16, S17), and ant butterflies (Lycaenidae) and the ants on which their larvae depend (S18). Lines represent smoothed normal curves, and \bar{s} represents the mean host specificity of the respective affiliate-host systems. *Data on relationships between bird mites and their host birds were collected by H.C.P. from published literature from the 1800s to 2004 (e.g., ref. S15).

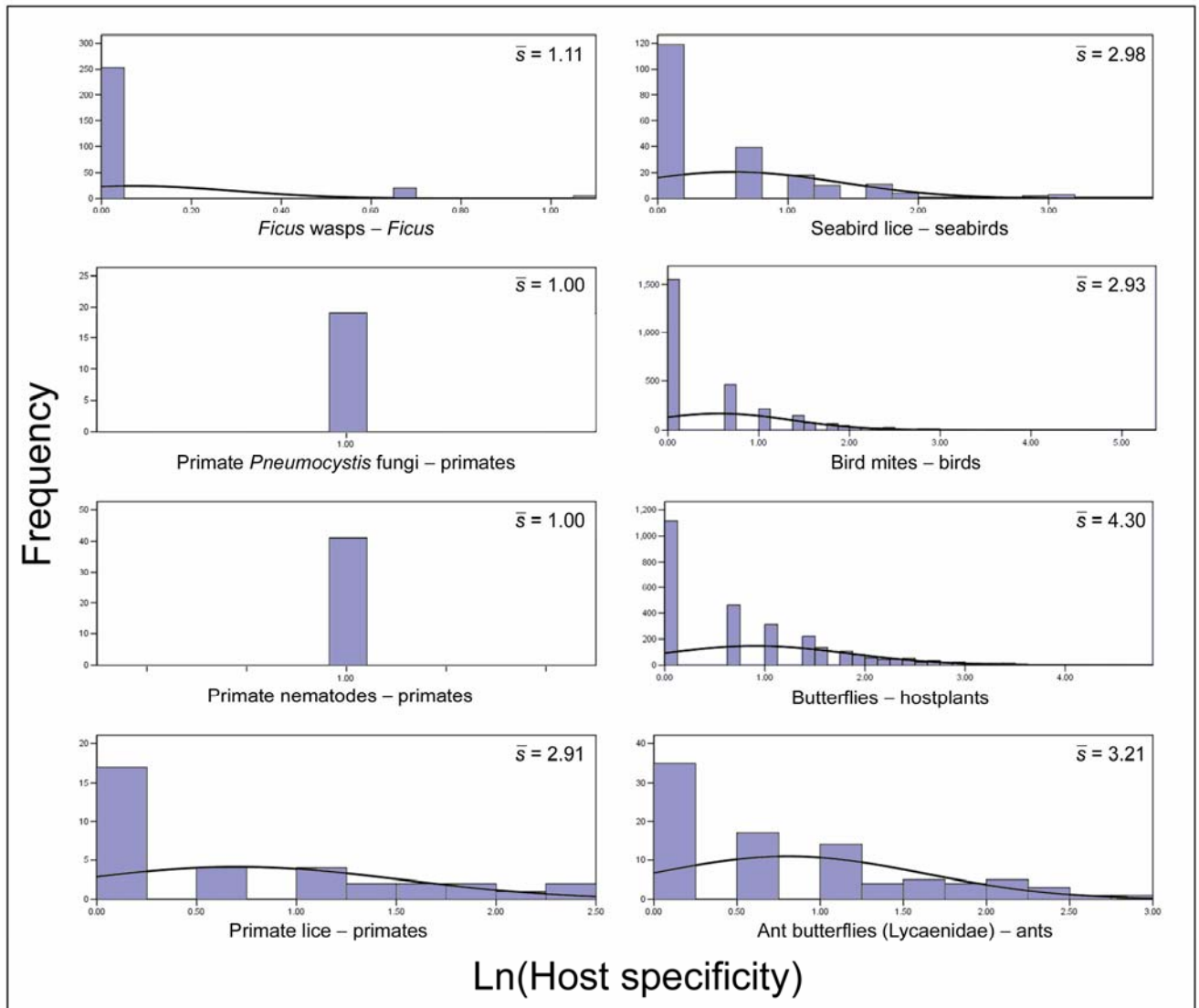


Table S1. Datasets used for calculating the number of historical and projected affiliate extinctions. Source references appear in parentheses. *Data on relationships between bird mites and their host birds were collected by H.C.P. from published literature from the 1800s to 2004 (e.g., ref. *S15*).

Affiliate	Host	Mean host specificity	Affiliate species richness	Host species richness	Number of endangered hosts	Number of extinct hosts
	Canadian					
Fish metazoan parasites	fish	7.53 (<i>S19</i>)	188 (<i>S19</i>)	191 (<i>S20</i>)	22 (<i>S21</i>)	-
Ant butterflies (<i>Lycaenidae</i>)	Ants	3.21 (<i>S18</i>)	665 (<i>S22</i>)	10000 (<i>S23</i>)	142 (<i>S21</i>)	-
Pollinating <i>Ficus</i> wasps	<i>Ficus</i>	1.11 (<i>S8</i>)	300 (<i>S24</i>)	750 (<i>S25</i>)	23 (<i>S21</i>)	-
Primate <i>Pneumocystis</i> fungi	Primates	1.00 (<i>S9</i>)	19 (<i>S9</i>)	233 (<i>S26</i>)	114 (<i>S21</i>)	-
Primate lice	Primates	2.91 (<i>S13, S14</i>)	34 (<i>S13, S14</i>)	233 (<i>S26</i>)	114 (<i>S21</i>)	-
Primate nematodes	Primates	1.00 (<i>S10-S12</i>)	41 (<i>S10-S12</i>)	233 (<i>S26</i>)	114 (<i>S21</i>)	-
Mammal lice	Mammals	2.53 (<i>S13, S14</i>)	554 (<i>S13, S14</i>)	4627 (<i>S26</i>)	1130 (<i>S21</i>)	78 (<i>S21</i>)
Butterflies (all families)	Hostplants	4.30 (<i>S16, S17</i>)	17500 (<i>S27</i>)	310000 (<i>S28</i>)	6279 (<i>S21</i>)	99 (<i>S21</i>)
Bird mites (all families)	Birds	2.93* (<i>S15</i>)	2734* (<i>S15</i>)	9881 (<i>S29</i>)	1194 (<i>S21</i>)	132 (<i>S21</i>)
Bird lice	Birds	2.04 (<i>S14</i>)	3910 (<i>S14</i>)	9881 (<i>S29</i>)	1194 (<i>S21</i>)	132 (<i>S21</i>)
Fish monogenean parasites	Fish	1.25 (<i>S30</i>)	25000 (<i>S30</i>)	28500 (<i>S31</i>)	746 (<i>S21</i>)	90 (<i>S21</i>)
Beetles	Hostplants	6.48 (<i>S32</i>)	1,100,000 (<i>S33</i>)	310,000 (<i>S28</i>)	6279 (<i>S21</i>)	99 (<i>S21</i>)

Table S2. Selected probable examples of species co-extinction.

Example	Reference
1. Six species of bird lice went extinct with the extinction of their host birds. None of the extinct lice is listed on the IUCN red list.	(S34)
2. The parasitic bird louse (<i>Columbicola extinctus</i>) was thought to have gone extinct with the extinction of the passenger pigeon (<i>Ectopistes migratorius</i>), but was later discovered on extant birds.	(S35, S36)
3. Three species of chestnut moths are presumed extinct with the local extinction of their hostplant, the American chestnut (<i>Castanea dentate</i>).	(S37)
4. A species of ferret louse may have gone extinct with its host, the black-footed ferret (<i>Mustela nigripes</i>), either when ferret populations were reduced, or when the ferrets were deloused during captive breeding. Not listed on the IUCN red list.	(S38)
5. The large blue butterfly (<i>Maculinea arion</i>) went locally extinct with the extinction of its host ant (<i>Myrmica sabuleti</i>).	(S39)
6. Fifty-six butterfly species went extinct with the extinction of their specific hostplants.	(S40)
7. California condor louse, <i>Colpocephalum californici</i> , and potentially other parasites. Not listed on the IUCN red list.	(S41)
8. Carolina parakeet, <i>Conuropsis carolinensis</i> , mites (6 species). Not listed on the IUCN red list.	(S42)
9. Mite, <i>Pterotrogus</i> sp., from the ivory-billed woodpecker, <i>Campephilus principalis</i> . Not listed on the IUCN red list.	(S42)
10. Mite, <i>Compressalges nipponiae</i> , from the Japanese crested ibis, <i>Nipponia nippon</i> , .Not listed on the IUCN red list.	(S43)
11. Mite, <i>Diplaegidia gladiator</i> , from the passenger pigeon, <i>Ectopistes migratorius</i> . Not listed on the IUCN red list.	(S44)
12. The parasitic brush cuckoo (<i>Cacomantis variolosus</i>) went locally extinct with the extirpation of their hosts the pied fantail (<i>Rhipidura javanica</i>) and the hill blue-flycatcher (<i>Cyornis banyumas</i>).	(S45)

References and Notes

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