Appendix S1: Supplementary methods

Simulated networks

Following Thèbault & Fontaine (2010), we randomly and independently assigned each plant i and pollinator (animal) j the respective interaction probabilities of P_{Pi} and P_{Ai} drawn from a power law distribution of degree -2. This creates relatively few generalist species that interact with many other species and many specialist species that interact with few other species as is typically seen in empirical networks (Bascompte et al. 2003). Then, with a probability *pnest*, each species' interacting partners are sequentially chosen from all potential partners with a probability $\dfrac{P_{P_i}}{\sum\limits_{k=1}^{S^P} P_{P_k}}$ $\left(or \dfrac{P_{A_j}}{\sum\limits_{l=1}^{S^A} P_{A_l}}\right)$. With probability of 1-*pnest*, partners are chosen with a probability $1/S^P$ (or $1/S^A$), where S^P (or S^A) are the number of plant (or animal) species. When *pnest* is high, the algorithm generates more-nested matrices (Santamaria & Rodriguez-Girones 2007). We maintained, on average, the commonly observed ratio between number of pollinator and plant species of 2.5 among all simulated networks.

We measured nestedness based on overlap and decreasing fill (*NODF,* Almeida-Neto et al. 2008) by comparing its observed value (*NODF$_{obs}$*) against the mean expected value (*NODF$^{m}_{null}$*) generated by using the ANINHADO software (Guimarães & Guimarães 2006) to average *NODF* among 1000 iterations of ANINHADO's most conservative null model. This null model sets the probability of a link within its interaction matrix to be the mean fraction of links realized in the row and column of the same cell of the observed interaction matrix. We then calculate the standardized value (*NODF$_{st}$*) as (*NODF$_{obs}$* – *NODF$^{m}_{null}$*)/ *NODF$^{m}_{null}$*. We classify all networks that are significantly more nested than expected by chance (*p*-value ≤ 0.05) as nested while all other networks (*p*-value > 0.05) are classified as non-nested. The *NODFst* values of our generated networks vary from -0.33 to 2.3, which includes the values found for the empirical networks of Table S1 which vary from -0.37 to 1.3.

The dynamic model

A typical approach for modeling the dynamics of mutualistic networks exhibiting these architectures assumes that interactions between species are constant and either qualitatively or quantitatively positive or negative (Bascompte et al. 2006, Bastolla et al. 2009, Allesina & Tang 2012, James et al. 2012, Rohr et al. 2014). The simplicity of this approach has the advantage of analytical

tractability; for example Lyapunov or structural stability analyses can be computed directly from the resulting matrices. In contrast, our adaptive foraging model does not assume static interactions between mutualist partners. Instead, our model dynamically calculates these interactions by decomposing them into their underlying mechanisms, which include visitation, feeding, pollination and reproduction. While understanding such models require rigorous sensitivity analyses (see Appendix S2), they also generate parameters and predictions that are more easily measured and tested in the field.

We used Valdovinos et al.'s (2013) mechanistic consumer-resource model whose parameters are described below and in Table S2 along with their units. The model calculates the change of the density (p_i) of plant individuals, each with a single flower, of species i over time as;

$$\frac{dp_i}{dt} = \gamma_i \sum_{j \in A} e_{ij} \sigma_{ij} V_{ij} - \mu_i^P p_i \tag{S1}$$

where the first and second terms on the right represent population gains and losses, respectively. The realized fraction of seeds that recruit to adults is γ_i;

$$\gamma_i = g_i \left(1 - \sum_{l \neq i \in P} u_l p_l - w_i p_i \right) \tag{S2}$$

where g_i is the maximum fraction of seeds that can recruit to adulthood. We subject g_i to both inter-specific (u_l) and intra-specific (w_i) competition with $u_l < w_i$. e_{ij} in Eq. S1 is the constant expected number of seeds produced by a pollination event. We address the impacts of pollinator sharing on plant fitness (Ashman & Arceo-Gómez 2013, Briggs et al. 2015) by calculating σ_{ij}, the fraction of visits of animal j to plant i that successfully pollinate plant i;

$$\sigma_{ij} = \frac{\varepsilon_i V_{ij}}{\sum_{k \in P_j} \varepsilon_k V_{kj}} \tag{S3}$$

where ε_i is the pollen production of the plant i and V_{ij} is the frequency of visits by animal species j to plant species i;

$$V_{ij} = \alpha_i \tau_i \alpha_j p_i \tag{S4}$$

where $V_{ij}=0$ if plant i and animal j do not interact. The dimensionless function discussed further below, $0 \leq \alpha_{ij} \leq 1$, is the foraging preference of pollinator j on a plant i. τ_{ij} is the pollinator's visitation efficiency on plant i, which corrects for units and is fixed at 1 in this study. μ_i^P in Eq.S1 is the constant density-independent per capita mortality rate of plant i.

The change of the density of pollinator individuals (a_j) of species j over time is;

$$\frac{da_j}{dt} = \sum_{i \in P} c_{ij} V_i b_{ij} \frac{R_i}{p_i} - \mu_j^A a_j \tag{S5}$$

where c_{ij} represents the constant per-capita conversion efficiency of pollinator j converting plant i's floral resources into j's births. b_{ij} is the constant efficiency of pollinator j extracting plant i's floral resources (R_i) whose change over time is;

$$\frac{dR_i}{dt} = \beta_i p_i - \phi_i R_i - \sum_{j \in A_i} V_{ij} b_{ij} \frac{R_i}{p_i} \tag{S6}$$

where β_i is plant i's per capita resource production rate and ϕ_i is a constant self-limitation parameter. μ_j^A in Eq. 5 is pollinator j's constant density-independent per capita mortality rates.

Adaptation of pollinator j's foraging preference on plant i (α_{ij} in Eq.S4) is:

$$\frac{d\alpha_{ij}}{dt} = G_j \alpha_{ij} \left(c_{ij} \tau_{ij} b_{ij} R_i - \sum_{k \in P_j} \alpha_{kj} c_{kj} \tau_{kj} b_{kj} R_k \right) \tag{S7}$$

where G_j is the basal adaptation rate of foraging preference and $\Sigma\alpha_{ij}=1$ for all plants that each pollinator j visits. Pollinator j allocates more foraging effort to plant i whenever such reallocation enhances j's food intake. While α_{ij} is called "foraging effort" in our model's original description (Valdovinos et al. 2013), we call α_{ij} "preference" here because foraging effort is better understood as an amount of an individual's activity as determined by its preference and abundance of plants that it pollinates (Eq. 5). Also, foraging effort, as used here, is what is most directly measured in the field which facilitates comparing model and field data. We ran the model for 3000 time steps.

Analysis of the model's results using Generalized Linear Mixed-Effects Models (GLMMs)

We analyzed the effects of AF, connectance, nestedness, and their interactions on species persistence (i.e. fraction of initial species that persisted through to the end of the simulations) using GLMMs on the *400 networks with S=200* (see above). Across all analyses, we assessed species' persistence using counts of extinct and persisting species bound together as a single binomial response variable. We assessed the effect of AF on persistence by analyzing the same networks with and without adaptive foraging. GLMMs allow us to account for the non-independence between these paired networks by using the network ID as a random effect (for more on GLMM approaches in ecology, see Bolker et al. 2009). We ran three separate types of statistical models, varying in fixed effects (i.e. explanatory variables), but all maintaining the same random effect of network ID. First, to analyze the effect of AF on species persistence alone, we ran models with AF (presence/absence) as the only fixed

effect. Second, to assess how AF affected networks with different values of connectance or nestedness, we analyzed models including AF and either connectance or nestedness as fixed effects as well as the statistical interaction between the two fixed effects. A statistically significant interaction term indicates that the impact of network architecture (connectance or nestedness) on persistence differs depending on whether or not AF was considered. We assessed the first and second model types for seven different datasets: all species combined (i.e., plants and animals), for plants and animals separately, and for specialist and generalist plants and animals separately (four datasets). Third, to explore additional interactions between all four explanatory variables, we ran GLMMs with AF, nestedness, and connectance, and all possible interactions between these variables for all plant and animal species combined. We used the "lme4" package (Bates et al. 2014) for the R Statistical Programming Language (R Core Team 2013) which effectively addresses effects of multiple comparisons on statistical significance. All GLMM results are shown in Table S3. For models in which 100% of species of a response group persisted across all models, we added a single extinction randomly to each contrast group (e.g., AF vs. no AF, or nested vs. non-nested), to allow binomial standard errors to be calculated. We corrected all models for overdispersion relative to a binomial distribution via inclusion of an individual-level random effect (Bolker et al. 2009). For consistency, we report the model results for models with individual-level random effects, even for the few models that were not overdispersed. We calculated binomial confidence intervals for presentation in the figures using the 'binom' package for R (Dorai-Raj 2014).

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Appendix S2: Sensitivity Analyses of the Dynamic Model

The results presented in the main text were obtained from model simulations run with parameter values drawn from uniform random distributions whose means and variances are shown in Table S2. To provide better context for those simulations, we conducted sensitivity analyses that evaluated the effects of systematically varying the mean and variance of parameters away from their baseline values shown in Table S2.

Our sensitivity analyses consisted of: i) evaluating the robustness of model output to different combinations of parameter values while varying all parameters simultaneously (global sensitivity analysis), and ii) determining the effect of varying only one parameter at a time (local sensitivity analysis). The results of the global analysis have been presented elsewhere (Valdovinos et al. 2013) and the local analysis results are presented here. We ran these analyses for models structured according to the empirical networks in Table S1 and found few differences among the results of the different networks (results not shown). Here, we show only the results for the realistically-connected Mauritian network (Kaiser-Bunbury et al. 2009), one of the most evenly and highly resolved empirical pollination networks to date. We explored the following six response variables: 1) the fraction of persistent plants, 2) the fraction of persistent animals, 3) the mean abundance of plant species, 4) the mean abundance of animal species, 5) the variance of plant abundances, and 6) the variance of animal abundances. Values of these response variables were obtained after 3000 time steps of the model. In addition, we conducted a sensitivity analysis of our main results.

a. Global sensitivity analysis

Closely following Thèbault & Fontaine (2010), we sampled wide areas of parameter space with relatively few simulations using a Latin hypercube technique to select different combinations of parameter values to run the dynamics of the realistically-connected Mauritian network. The parameter space ranged from one fourth to four times the baseline values discussed in the main text and summarized in Table S2. Each range was divided into 100 equal intervals. We generated each Latin hypercube sample by randomly sampling only one of the 100 intervals of each of 11 parameters. The 11 parameters subjected to sensitivity analyses were: 1. Conversion efficiency of floral resources to pollinator births (c_{ij}), 2. Expected number of seeds produced by a pollination event (e_{ij}), 3. Pollinator extraction efficiency of resource in each visit (b_{ij}), 4. Inter-specific competition coefficient of plants (u_i), 5. Intra-specific competition coefficient of plants (w_i), 6. Production rate of floral resources (β_i), 7.

Adaptation rate of foraging preferences of pollinators (G_j), 8. Maximum fraction of total seeds that recruit to plants (g_i), 9. Per capita mortality rate of pollinators (μ^A_j), 10. Per capita mortality rate of plants (μ_i), 11. Variances of animal parameters (var^A). We repeated this sampling 100 times to generate 100 different combinations of the 11 parameters for 100 sets of simulations. Each set was comprised by 2 simulations; one with and one without adaptive foraging. As seen in Fig. A1 in the Appendix of Valdovinos et al. (2013), this part of the sensitivity analysis demonstrated that AF usually increased species persistence of the studied network when parameter values were varied in the range of one quarter to four times the baseline values. All animal species persisted in about 65% of the simulations with AF pollinators among the sampled parameter combinations. All animal species went extinct in about 25% of these simulations while the remaining ~10% had at least one species persisting to the end of simulations. None of the simulations without AF exhibited 100% of animal persistence, whereas in 35% of those simulations all pollinators went extinct. Most of the remaining 75% exhibited in between 40% and 80% of animal persistence. The results for plant persistence were very similar between simulations with and without AF, with a slightly increase in simulations with AF. Through this global sensitivity analysis we demonstrated that for realistically-connected network the stabilizing effect of AF on our dynamic model is robust to parameter values ranging from one fourth to four times the values used in the present study.

b. Local sensitivity analysis

We explored the effects of individually varying each of the 11 parameters by running the model **with AF** 100 times each for parameter values 0.75, 1, and 1.25 times their previously described means (Table S2) and associated variances of the uniformly random distributions for a total of 3300 simulations. We linearly regressed the variation in the response variables against parameter variation (Fig. S2) and found that the persistence of adaptive pollinators of the realistically-connected Mauritian network was insensitive to changing any of the 11 model parameters ±25%. Plant persistence and animal abundance increased with 1) the efficiency (c_{ij}) of converting floral resources into pollinator reproduction and 2) the production rate of floral resources (β_i). Intra-specific competition of plant species decreased plant and animal abundance. Increasing per-capita mortality rate of pollinators decreased plant persistence and animal abundance (Fig. S2).

c. Sensitivity analysis of our main results

The species persistence in networks without AF was very sensitive to the variability of parameters among animals (var^A in Table S2, data not shown) and to the intra-specific competition of plants (w_i, see Table S2). Species persistence in networks with AF, however, was very robust to parameter variability among species and among simulations. The mechanism of niche partitioning (see Figs. 1 & 2 in main text) is, in general, very robust to changes in the parameter values of the dynamic model in nested networks, whose S and C values were similar to those found in nature (Fig. S1a).

The only way we found to eliminate niche partitioning among animal species in networks with AF was to make the intra-specific competition coefficient of plants (w_i) negatively related to their degree (i.e. number of interactions). This causes generalist plants exhibit less self-inhibition which allows them to become more abundant than specialist plants. Note that without this reduced inhibition of generalists, all plant species have similar abundances (see Figs. 3 and 4 in Valdovinos et al. 2013). The reduced inhibition eliminates niche partitioning by increasing the total rewards that generalist plants over rewards of specialist plants. This stops generalist pollinators from preferring specialist plants providing that w_i decreases with increasing plant degree enough and the network is sufficiently large. We linearly decreased w_i with increasing degree setting $w_i = 1$ and $w_i = 0.3$ for the minimum and maximum degree plant, respectively. Niche partitioning was easier to eliminate in smaller networks because of the relatively small degree heterogeneity in small networks which reduces the difference in rewards between generalist and specialist plants. This causes generalist pollinators to insufficiently prefer specialist plants for niche partitioning to occur. Further research is needed to understand the conditions in which niche partitioning occurs.

Table S1. Description of the 49 empirical plant-pollinator networks used for Figure S1. Abbreviations: "#" = number of species; Main source:

	Dataset	Habitat type	Location	Data type	# plants	# pollin
42	Aizen *et al.* (2008) (8 webs)	South-Andean Temperate Forest	Argentina	Binary	4	17
43					7	28
44					12	34
45					17	51
46					11	29
47					17	52
48					14	36
49					16	37
1	Arroyo et al. (1982) (3 webs)	Andean scrub	Chile	Binary	87	98
2					43	62
3					41	28
4	Barrett and Helenurm (1987)	Boreal forest	Canada	individuals caught	12	102
5	Bartomeus et al. (2008) (3 webs)	Mediterranean shrublands	Catalonia, Spain	no. visits	31	77
6					31	79
7					29	75

8	Bezerra et al. (2009)	Caatinga (semi-arid vegetation)	Pernambuco State, Brazil	no. visits	13	13
9	Clements and Long (1923)	Montane forest and grassland	USA	Binary	96	276
10	Dupont et al. (2003)	High-altitude desert	Tenerife, Canary Islands	Binary	11	38
11	Elberling and Olesen (1999)	Alpine subarctic community	Sweden	no. visits	23	118
12	Hocking (1968)	Arctic community	Canada	Binary	29	86
17	Inouye and Pyke (1988)	Montane forest	Australia	individuals caught	42	91
13	Kaiser-Bunbury et al. (2009) (2 webs)	Heathland, invaded by alien plants	Mauritius	Rates	135	74
14		Heathland, alien plants removed	Mauritius	Rates	100	64
15	Kato et al. (1990)	Beech forest	Japan	individuals caught	93	679
16	Kevan (1970)	High Arctic	Lake Hazen, Canada	no. visits	32	115
18	McMullen (1993)	Multiple communities	Galápagos Islands	Binary	106	54
19	Medan et al. (2002)	Xeric scrub	Laguna Diamante, Mendoza, Argentina	Binary	21	45

20		Woody riverine vegetation and xeric scrub	Río Blanco, Mendoza, Argentina	Binary	23	72
21	Memmott (1999)	Meadow	Bristol, U.K.	frequency of visits	25	79
22	Mosquin and Martin (1967)	Arctic community	Canada	individuals caught	11	18
23	Motten (1982)	Deciduous forest	USA	no. visits	13	44
24	Olesen et al. (2002)	Coastal forest	Mauritius Island	no. visits	14	13
25	(2 webs)	Rocky cliff and open herb community	Azores Islands	no. visits	10	12
26	Ollerton et al. (2003)	Upland grassland	KwaZulu-Natal region, South Africa	individuals caught	9	56
27	Ramírez and Brito (1992)	Palm swamp community	Venezuela	Binary	33	53
28	Robertson (1929)	Agricultural area dominated by crops, with some natural forest and pasture	USA	Binary	456	1429
29	Santos et al. (2010)	Caatinga (semi-arid vegetation)	Bahia State, Brazil	Binary	51	25
30	Schemske et al. (1978)	Maple-oak woodland	USA	no. visits	7	32
31	Small (1976)	Peat bog	Canada	individuals	13	34

				caught		
40	Smith *et al.* (2005)	Temperate rain forest	Chiloe island, Chile	Binary	26	128
41	Valdovinos *et al.* (2009)	Andean scrub	Chile	Binary	77	110
32	Vázquez and Simberloff (2002) (8 webs)	Evergreen montane forest	Argentina	no. visits	10	29
33					9	33
34					9	27
35					10	29
36					8	35
37					8	26
38					7	24
39					8	27

Table S2. Model parameters and state-variables: short definition, units and mean values of parameters and initial conditions used in the simulations. Values were drawn from a uniform random distribution with the specified mean, and variances of var^P=10% and var^A=0.01% of means for plants' and animals' parameters, respectively. Asterisks indicate initial conditions and k_{aj} is the number of interactions of animal j. *Comb* indicates where a function identified in the first column of the table is a function of parameters that were varied (see main text) which causes the function's mean value to be a combination of other parameter values and is therefore not listed. We run two sets of simulations, one with high mortality rates of animals and low mortality rates of plants (μ_j^A=0.01, μ_i^P=0.002) used to calculate species persistence of animals, and the other with low mortality rates of animals and high mortality rates of plants (μ_j^A=0.001, μ_i^P=0.02) used to calculate species persistence of plants.

Definition	*Symbol*	Dimension	Mean value
Density of plant population i	p_i	individuals /area	0.5*
Density of animal population j	a_j	individuals /area	0.5*
Total density of floral resources of plant population i	R_i	mass/ area	0.5*
Foraging preference	α_{ij}	None	$1 /k_{aj}$*
Frequency of visits of animal *j* to plant *i*	V_{ij}	visits /(area*time)	*comb*
Pollination success	σ_{ij}	None	*comb*
Realized fraction of seeds that recruit to adults	γ_i	None	*comb*
Visitation efficiency	τ_{ij}	(visits *area) / (time*individuals*individuals)	1
Expected number of seeds produced by a pollination event	e_{ij}	Individuals / visits	0.8

Per capita mortality rate of plants	μ_i^P	1 / time	0.0020 .02
Conversion efficiency of floral resources to pollinator births	c_{ij}	individuals/ mass	0.2
Per capita mortality rate of pollinators	μ_j^A	1 / time	0.001 0.01
Pollinator extraction efficiency of resource in each visit	b_{ij}	individuals / visits	0.4
Maximum fraction of total seeds that recruit to plants	g_i	None	0.4
Inter-specific competition coefficient of plants	u_i	area / individuals	0.002
Intra-specific competition coefficient of plants	w_i	area / individuals	1.2
Production rate of floral resources	βi	mass / (individuals * time)	0.2
Self-limitation parameter of resource production	ϕ_{ij}	1 / time	0.04
Adaptation rate of foraging preferences of pollinators	G_j	None	2

Table S3. Results of Generalized Linear Mixed-Effects Models (GLMMs). Results correspond to the *400 networks with S=200* shown in Fig. 3. 'AF Only' refers to the GLMM estimate with adaptive foraging (AF) as the only fixed factor, which estimates the effect of AF on species persistence. 'AF x N' and 'AF x C' refer to the interaction terms of GLMMs that consider AF and either Nestedness (N) or connectance (C) as fixed factors. The positive interaction terms indicate that AF decreases the destabilizing effects of nestedness on the networks. The negative interaction terms indicate that AF decreases the stabilizing effects or increases the destabilizing effects of connectance on the networks. Results are reported for each taxonomic group. Asterisks depict significance of fixed effects, ***: P <0.001; **: P <0.01; *: P<0.05. Full results shown in Table S4.

Taxa/Model	AF Only	AF x N	AF x C
all species	1.0***	3.9***	-5.0***
all animals	6.2	8.6*	-4.9
gen animals	5.5	7.5***	-7.4***
spec animals	6.3	8.2*	-4.5
all plants	0.2*	2.8***	-3.0***
gen plants	-3.9***	0.7	-5.2***
spec plants	1.7***	2.8***	-1.6***

Table S4. All GLMM results: Effects of AF and network structure on species persistence, assessed with Generalized Linear Mixed-Effects Models with binomial errors (see Supplementary Methods). We assessed three types of models: Adaptive Foraging (AF) Only, AFxNestedness, AFxConnectance, each for seven different taxonomic categories (plants vs. animals, all vs. generalist vs. specialist, as well as all plant and animal species combined). To assess the effects of Adaptive Foraging (AF) on Nestedness and Connectance, we used the interaction term between the two. The positive interaction terms indicate that AF decreases the destabilizing effects of nestedness on the networks. The negative interaction terms indicate that AF decreases the stabilizing effects or increases the destabilizing effects of connectance on the networks. Asterisks depict significance of fixed effects, ***: P < 0.001; **: P < 0.01; *: P < 0.05.

Model	Taxa	Factor	Est.	Std.E	z val	Pr(>|z|)	Pr(>|z|)	
AF Only	all species	AF	1.0	0.2	6.6	0.0	0.0	***
	all animals		6.2	6.5	1.0	0.3	0.3	
	gen animals		5.5	6.5	0.9	0.4	0.4	
	spec animals		6.3	5.8	1.1	0.3	0.3	
	all plants		0.2	0.1	2.1	0.0	0.0	*
	gen plants		-3.9	0.3	-13.3	0.0	< 2E-16	***
	spec plants		1.7	0.1	16.2	0.0	< 2E-16	***
AF & Nestedness	all species	AF	-1.3	0.2	-7.4	0.0	0.0	***
		Nestedness	-4.1	0.2	-19.0	0.0	< 2E-16	***
		AF * Nestedness	3.9	0.2	16.4	0.0	< 2E-16	***
	all animals	AF	1.1	2.8	0.4	0.7	0.7	
		Nestedness	-8.6	1.4	-5.9	0.0	0.0	***
		AF * Nestedness	8.6	3.6	2.4	0.0	0.0	*
	gen animals	AF	0.0	1.8	0.0	1.0	1.0	
		Nestedness	-7.5	2.2	-3.4	0.0	0.0	***
		AF * Nestedness	7.5	2.0	3.7	0.0	0.0	***
	spec animals	AF	1.1	2.5	0.4	0.7	0.7	
		Nestedness	-8.1	1.3	-6.1	0.0	0.0	***
		AF * Nestedness	8.2	3.4	2.4	0.0	0.0	*
	all plants	AF	-1.6	0.1	-15.5	0.0	< 2E-16	***
		Nestedness	-3.0	0.2	-15.3	0.0	< 2E-16	***
		AF * Nestedness	2.8	0.1	21.6	0.0	< 2E-16	***
	gen plants	AF	-4.1	0.4	-11.5	0.0	< 2E-16	***
		Nestedness	0.2	0.6	0.4	0.7	0.7	
		AF * Nestedness	0.7	0.6	1.2	0.2	0.2	
	spec plants	AF	0.0	0.1	-0.3	0.8	0.8	
		Nestedness	-2.9	0.2	-16.5	0.0	< 2E-16	***
		AF * Nestedness	2.8	0.1	21.5	0.0	< 2E-16	***
AF & Connectance	all species	AF	4.3	0.2	28.4	0.0	< 2E-16	***

	Connectance	0.2	0.2	0.7	0.5	0.5	
	AF * Connectance	-5.0	0.2	-27.6	0.0	< 2E-16	***
all animals	AF	9.1	3.2	2.9	0.0	0.0	**
	Connectance	4.9	0.6	8.6	0.0	< 2E-16	***
	AF * Connectance	-4.9	4.5	-1.1	0.3	0.3	
gen animals	AF	7.5	1.0	7.4	0.0	0.0	***
	Connectance	7.6	2.3	3.4	0.0	0.0	***
	AF * Connectance	-7.4	2.0	-3.6	0.0	0.0	***
spec animals	AF	8.7	2.9	3.0	0.0	0.0	**
	Connectance	4.5	0.5	8.6	0.0	< 2E-16	***
	AF * Connectance	-4.5	4.1	-1.1	0.3	0.3	
all plants	AF	2.2	0.1	16.8	0.0	< 2E-16	***
	Connectance	-0.9	0.2	-5.9	0.0	0.0	***
	AF * Connectance	-3.0	0.2	-19.1	0.0	< 2E-16	***
gen plants	AF	1.3	0.6	2.2	0.0	0.0	*
	Connectance	-0.9	0.4	-2.5	0.0	0.0	*
	AF * Connectance	-5.2	0.6	-8.5	0.0	< 2E-16	***
spec plants	AF	2.8	0.2	15.8	0.0	< 2E-16	***
	Connectance	-1.2	0.2	-6.2	0.0	0.0	***
	AF * Connectance	-1.6	0.2	-7.8	0.0	0.0	***

Figure Legends

Fig. S1. Connectance and species richness combinations for networks found in nature and the 1,200 simulated networks. a: Prediction (blue) and confidence intervals (red) for the regression of the logarithm of connectance to the logarithm of richness of 49 empirical networks (blue filled circles) listed in Table S1. b: The 1200 simulated networks (black filled circles). Prediction (blue) and regression line (red) are kept from a.

Fig. S2. Ecological effects of an animal species shifting from non-adaptive to adaptive foraging. Each panel show the time series of a simulated generalist pollinator species that non-adaptively forages from time steps 1 to 5999 and adaptively forages from time steps 6000 to 12000 (nested network, S = 42, C = 0.23). (a) Abundance of the pollinator species. (b) The per-capita oral resource consumption rate of the pollinator species. (c) The population growth rate of the pollinator species, calculated as [a(t=i+1)-a(t=i)] / [t(i+1)- t(i)], where a(t=i) is the abundance of the pollinator species at time step i. (d) The change per time step in per-capita consumption rate of - oral resource by the pollinator species, calculated as [Rcons(t=i+1)-Rcons(t=i)] / [t(i+1)- t(i)], where Rcons(t=i) is the per-capita R consumption at time step i (see Eqs. 5 and 6). Note the mismatch of the scales on the y-axes between a and c, and between b and d. Given this mismatch large variations in the latter are invisible in the former. The shift to adaptive foraging (AF) increases near-term resource uptake (b) and population growth (c), but results in lower population sizes (a) over the long-term. The generalist pollinator increases its per-capita R consumption and population growth rates at time step 6000 but by time step 6002, its per-capita consumption rate decreases, consequently reducing its abundance.

Fig. S3. Interactive effects of nestedness and AF on species' persistence and abundance. Simulated influence of nestedness on the effect of AF on persistence of specialist animals (a), abundance per species of generalist animals (b), and persistence of specialist plants (c). Each full circle represents the species persistence of one of the 1200 networks (see Methods).
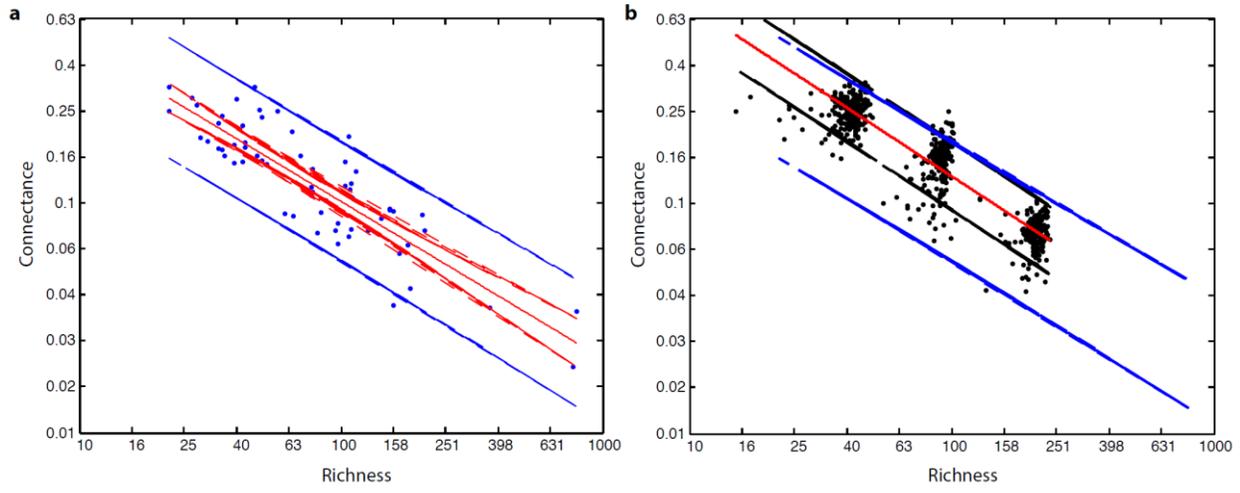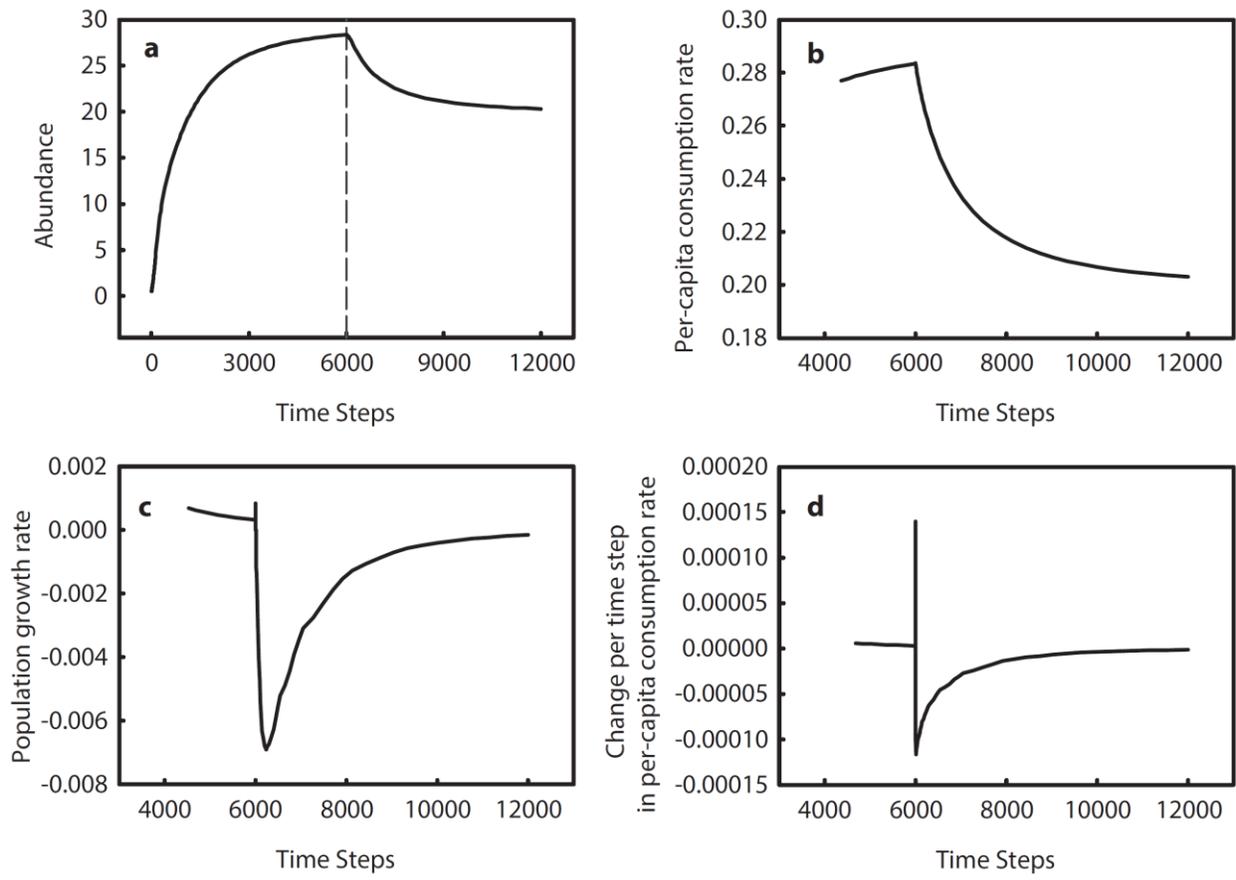
Fig. S1

Fig. S2

Fig. S3