Oikos

OIK-07303

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Appendix 1–5

Appendix 1

Supplementary information about the data set

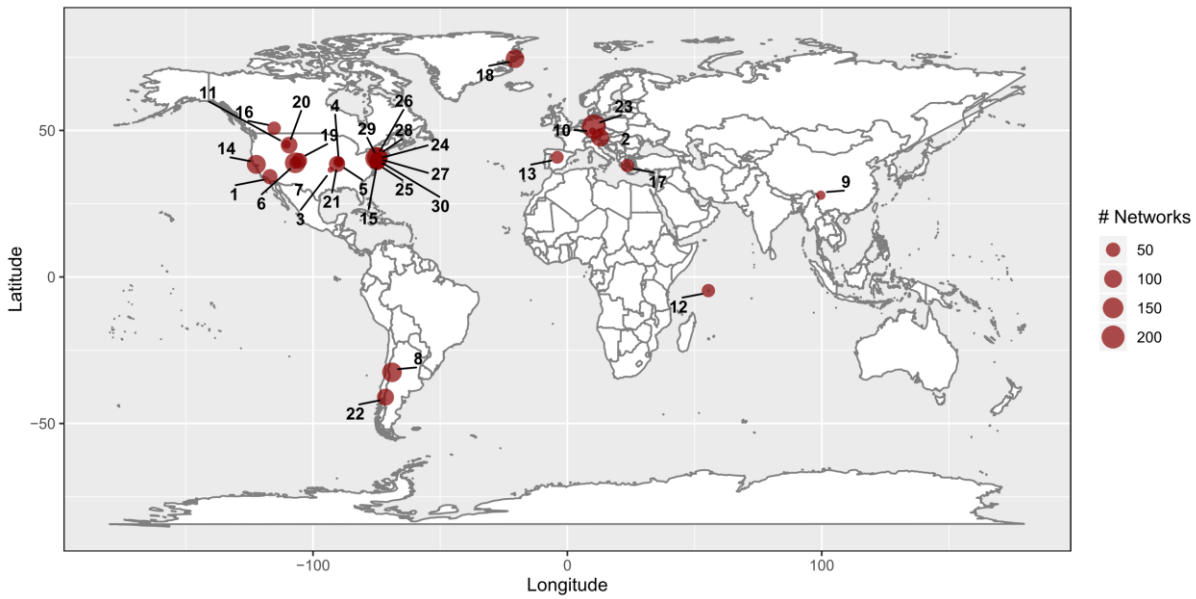

Figure A1. Map showing where studies (red dots labeled with numbers 1 to 30, see Table A1 for detailed information) were located. Size of dots represents the number of networks (sum across five temporal scales) that was used per study. Note that some studies were conducted at several sites, which mostly were located in the same region.

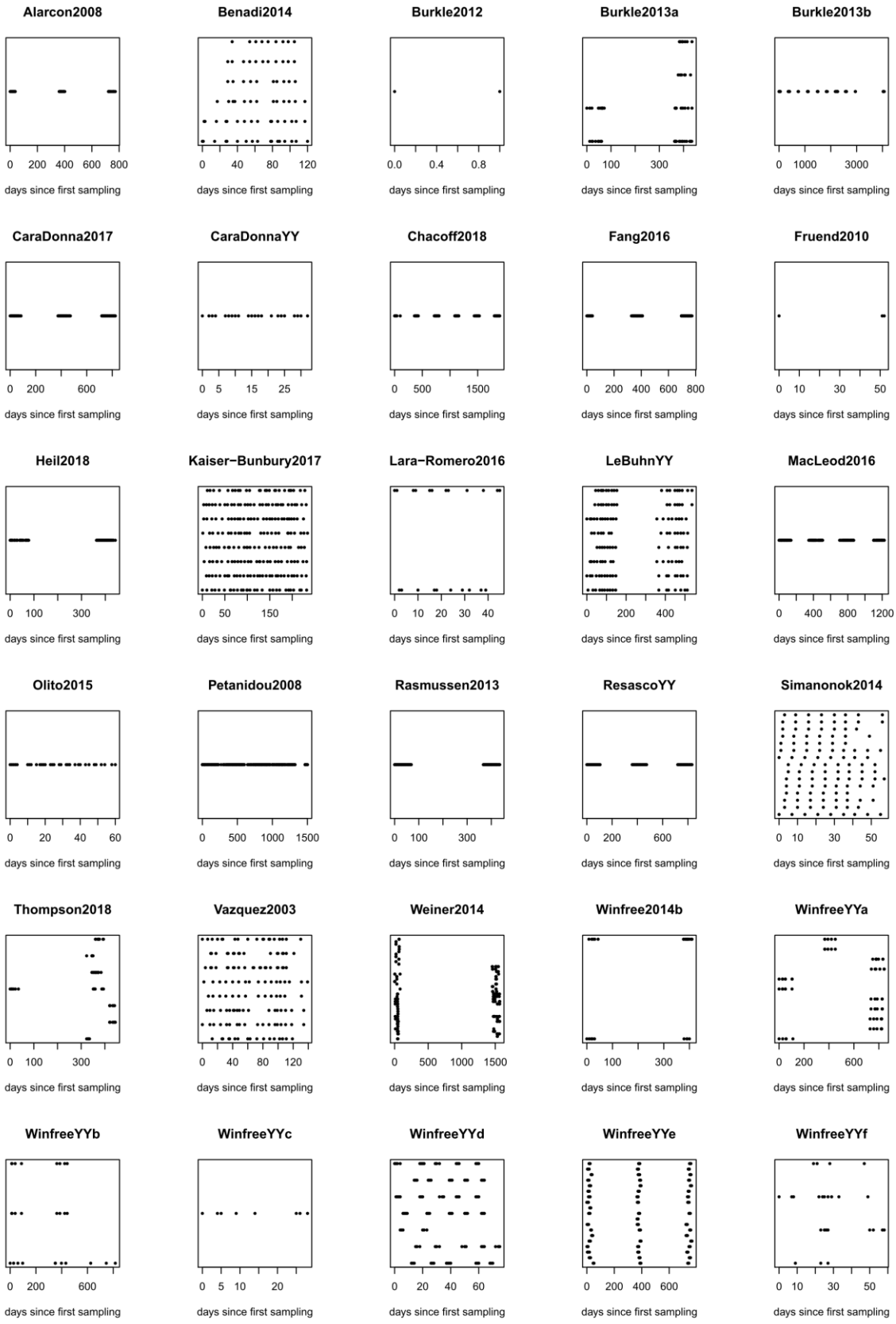

Figure A2. Sampling schemes per study and site that were used in our analyses. In each panel, different sites are indicated by different vertical positions (rows). Note that sites may not always represent the classification of sites in the original studies but an aggregation of those.

Table A1. List of data sets of plant-pollinator interaction networks that were used within this study. Numbers of sites and interactions may differ from the original studies as not all data fulfilled requirements to be used here. Asterisks (*) indicate that original sites were pooled. Daily or weekly networks were excluded from the analyses if sampling methods used in the respective studies were not appropriate to construct networks at these temporal scales.

No.	Study	References	Country	# sites	# interactions	# daily networks	# weekly networks	# monthly networks	# yearly networks	# multiple-year networks
1	Alarcon2008	Alarcon et al. 2008	USA	1	4032	41	15	4		1
2	Benadi2014	Benadi et al. 2014a, Benadi et al. 2014b	Germany	6	10504	76	9	11	6	
3	Burkle2012	Burkle & Knight 2012	USA	1	48	2	1			
4	Burkle2013a	Burkle et al. 2013	USA	4	506	excluded	10	6	3	2
5	Burkle2013b	Burkle et al. 2013	USA	1	865	excluded		6	1	1
6	CaraDonna2017	CaraDonna et al. 2017, CaraDonna 2020	USA	1*	5150	101	36	10	3	1
7	CaraDonnaYY	CaraDonna et al. unpublished data	USA	1*	3835	22	5	1		
8	Chacoff2018	Chacoff et al. 2012, Chacoff et al. 2018, Chacoff et al. 2021	Argentina	1*	7475	88	23	13	6	1
9	Fang2016	Fang & Huang 2016	China	1	5136	excluded	excluded	8	2	1
10	Fruend2010	Fründ et al. 2010, Fründ et al. 2011	Germany	1	146	3	1			
11	Heil2018	Heil & Burkle 2018	USA	1*	2130	excluded		6	2	1
12	Kaiser-Bunbury2017	Kaiser-Bunbury et al. 2017	Seychelles	8	12235	excluded	excluded	32	8	
13	Lara-Romero2016	Lara-Romero et al. 2016a, Lara-Romero et al. 2016b	Spain	2	5542	22	9	4		
14	LeBuhnYY	LeBuhn et al. unpublished data	USA	8	2505	100	1		11	6
15	MacLeod2016	MacLeod et al. 2016	USA	1*	8369	excluded	45	18	4	1
16	Olito2015	Olito & Fox 2015	Canada	1	902	29	9	2	1	

No.	Study	References	Country	# sites	# interactions	# daily networks	# weekly networks	# monthly networks	# yearly networks	# multiple-year networks
17	Petanidou2008	Petanidou 1991, Petanidou et al. 2008, Petanidou et al. 2014	Greece	1	6095	excluded	excluded	36	4	1
18	Rasmussen2013	Rasmussen et al. 2013, Cirtwill et al. 2018	Denmark (Greenland)	1	1566	82	21	6	2	1
19	ResascoYY	Resasco et al. unpublished data	USA	1	2810	48	4	10	3	1
20	Simanonok2014	Simanonok et al. 2014	USA	15	886	63	4	15		
21	Thompson2018	Thompson & Knight 2018	USA	7	1101	53	17	5		
22	Vazquez2003	Vasquez & Simberloff 2003	Argentina	8	1538	40	19	20	8	
23	Weiner2014	Weiner et al. 2014, Kühsel & Blüthgen 2015, Weiner et al. 2016, Blühtgen & Kühsel 2019	Germany	40	12821	169	51		3	
24	Winfree2014b	Winfree et al. 2014	USA	2	1242	25	5	1		1
25	WinfreeYYa	MacLeod et al. 2020a, MacLeod et al. 2020b	USA	11	2610	48	14		1	
26	WinfreeYYb	MacLeod et al. 2020a, MacLeod et al. 2020b	USA	3	814	20	3			
27	WinfreeYYc	Winfree et al. unpublished data	USA	1	734	7	2	1		
28	WinfreeYYd	Roswell et al. 2019a, Roswell et al. 2019b	USA	7	17620	100	33	13	3	
29	WinfreeYYe	Winfree et al. unpublished data	USA	19	4396	149	37			
30	WinfreeYYf	Smith et al. 2019a, Smith et al. 2019b	USA	4	1095	19	6	1		

Appendix 2

Figures and tables supporting the results presented in the main text

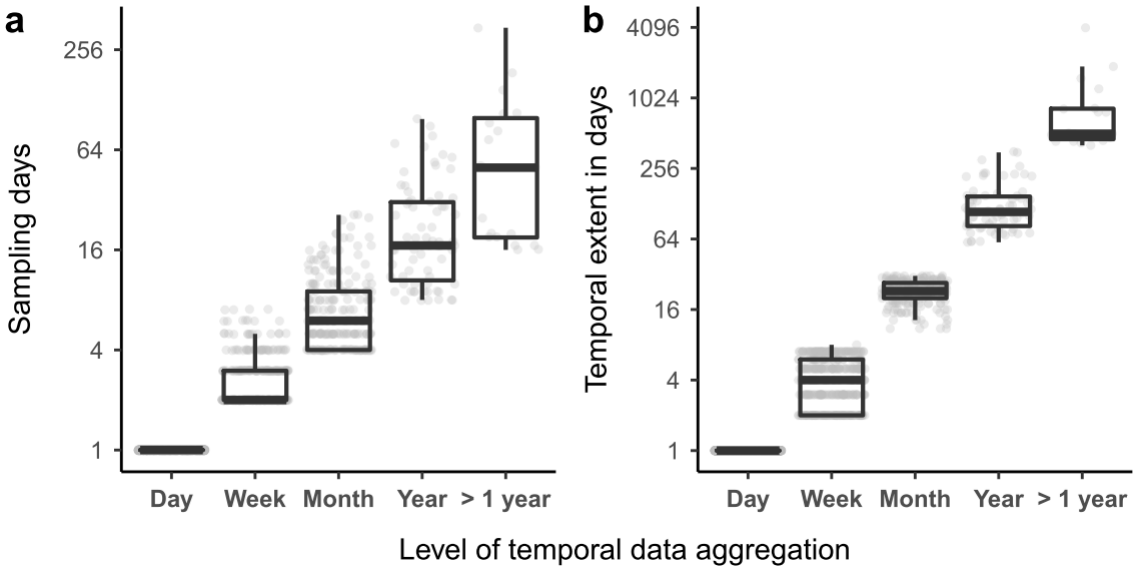

Figure A3. Effects of the temporal scale of data aggregation on sampling effort (the number of sampling days) and temporal extent (the time span over which interactions were observed). Note that data are plotted on a $\log_2$-scale.

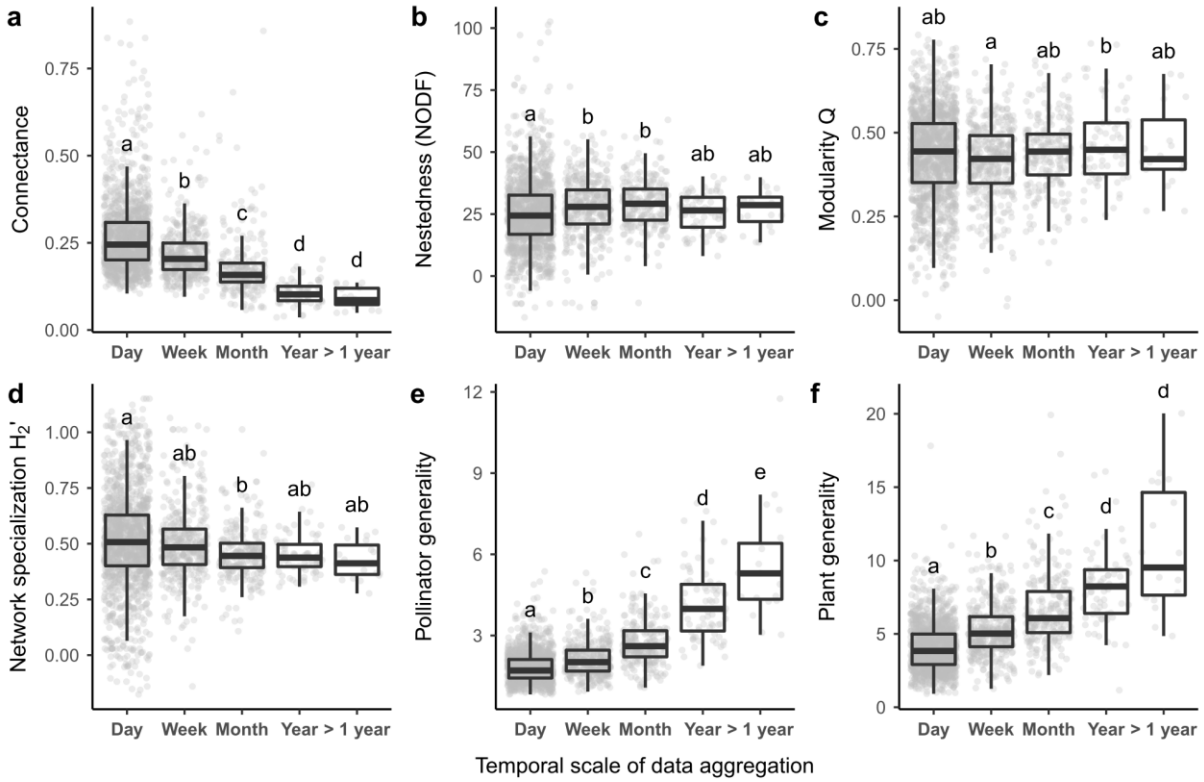

Figure A4. Effects of the temporal scale of data aggregation (categorical predictor) on (a) connectance, (b) nestedness (NODF), (c) modularity Q, (d) network specialization H_2', (e) pollinator generality, and (f) plant generality. Letters indicate statistically significant differences between temporal scales based on post-hoc Tukey HSD tests. Statistical fits for connectance, pollinator generality, and plant generality are based on log-transformed data, whereas figure axes represent the scale of the original data. These partial residual plots correct for baseline differences among studies and sites (specified as random effects in linear mixed models), which occasionally leads to data points lying outside the range of the variable.

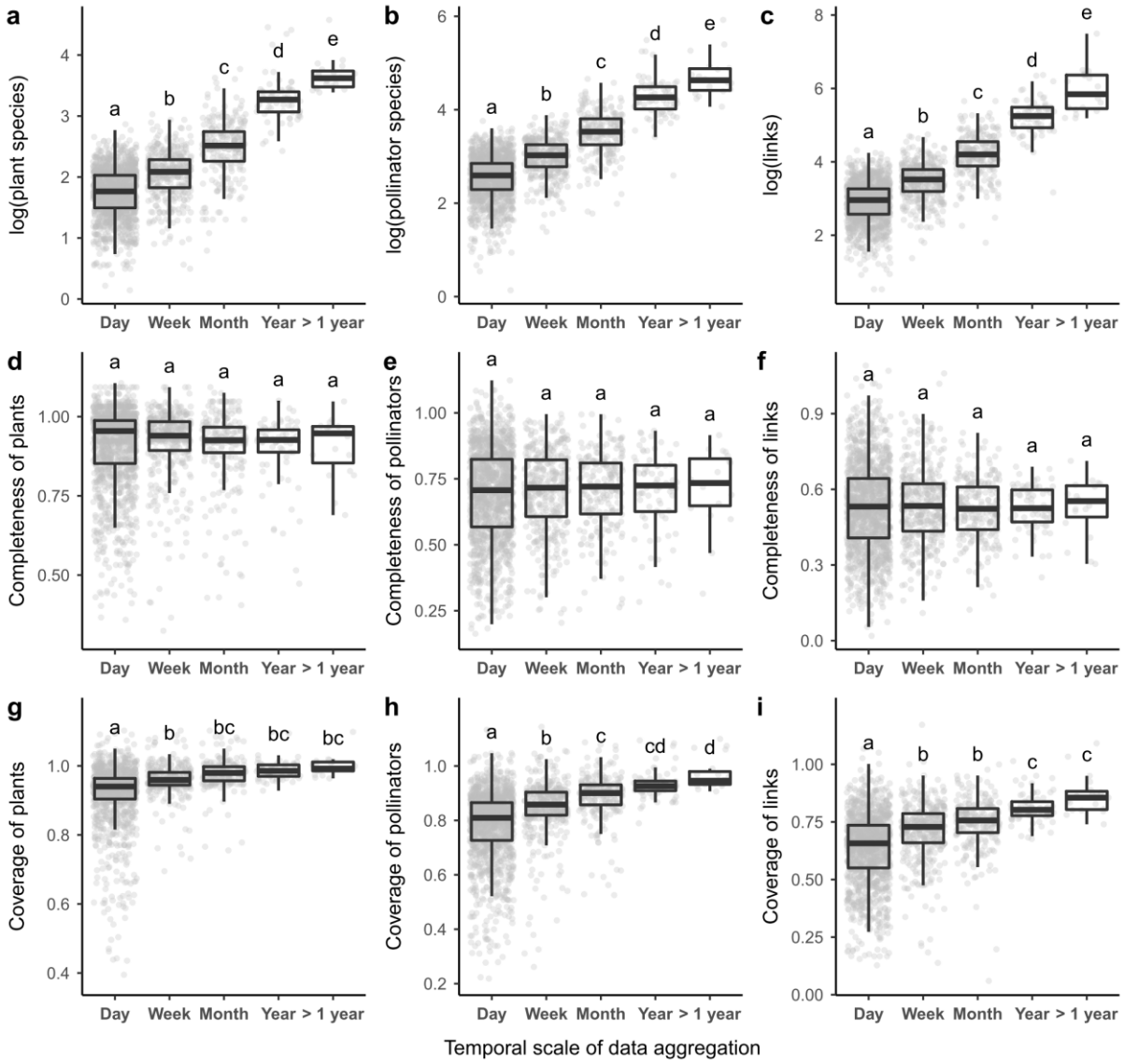

Figure A5. Effects of the temporal scale of data aggregation (categorical predictor) on network size, sampling completeness, and sampling coverage. The nine panels show effects on the log-transformed numbers of (a) plant species, (b) pollinator species, and (c) links, effects on sampling completeness of (d) plant species, (e) pollinator species, and (f) links, as well as effects on sampling coverage at the level of (g) plants, (h) pollinators, and (i) links. Letters indicate statistically significant differences between temporal scales based on post-hoc Tukey HSD tests. Sampling completeness was quantified as the proportion of observed species or link numbers of the species and link numbers estimated by the Chao1 richness estimator. Sampling coverage is an estimation of the proportion of all individuals or interactions that belong to the observed species or links. These partial residual plots correct for baseline differences among studies and sites (specified as random effects in linear mixed models), which occasionally leads to data points lying outside the range of the variable.

Table A2. Effects of the temporal scale of data aggregation (categorical predictor) on six commonly used network indices, network size (species and link richness), sampling completeness, and sampling coverage. Significant effects ($p < 0.05$) are reported in bold.

Response	Sum Sq	Mean Sq	Num. d.f.	Den. d.f.	F value	Pr(>F)
Network indices						
log(Connectance)	76.38	19.09	4	1860.98	152.63	**<0.001**
Nestedness (NODF)	2924.30	731.07	4	1866.31	3.93	**0.004**
Modularity Q	0.18	0.05	4	1862.94	2.67	**0.031**
Network specialization H_2'	0.65	0.16	4	1814.44	3.75	**0.005**
log(Pollinator generality)	67.07	16.77	4	1869.67	183.65	**<0.001**
log(Plant generality)	71.19	17.80	4	1857.46	111.22	**<0.001**
Network size						
log(Plant richness)	224.45	56.11	4	1855.29	315.18	**<0.001**
log(Pollinator richness)	311.67	77.92	4	1870.88	351.75	**<0.001**
log(Link richness)	569.84	142.46	4	1870.27	467.58	**<0.001**
Sampling completeness						
Plant completeness	0.06	0.02	4	1842.86	0.97	0.422
Pollinator completeness	0.07	0.02	4	1867.24	0.61	0.654
Link completeness	0.03	0.01	4	1880.49	0.27	0.900
Sampling coverage						
Plant coverage	0.85	0.21	4	1656.30	34.71	**<0.001**
Pollinator coverage	3.17	0.79	4	1868.80	52.81	**<0.001**
Link coverage	4.08	1.02	4	1814.03	49.40	**<0.001**

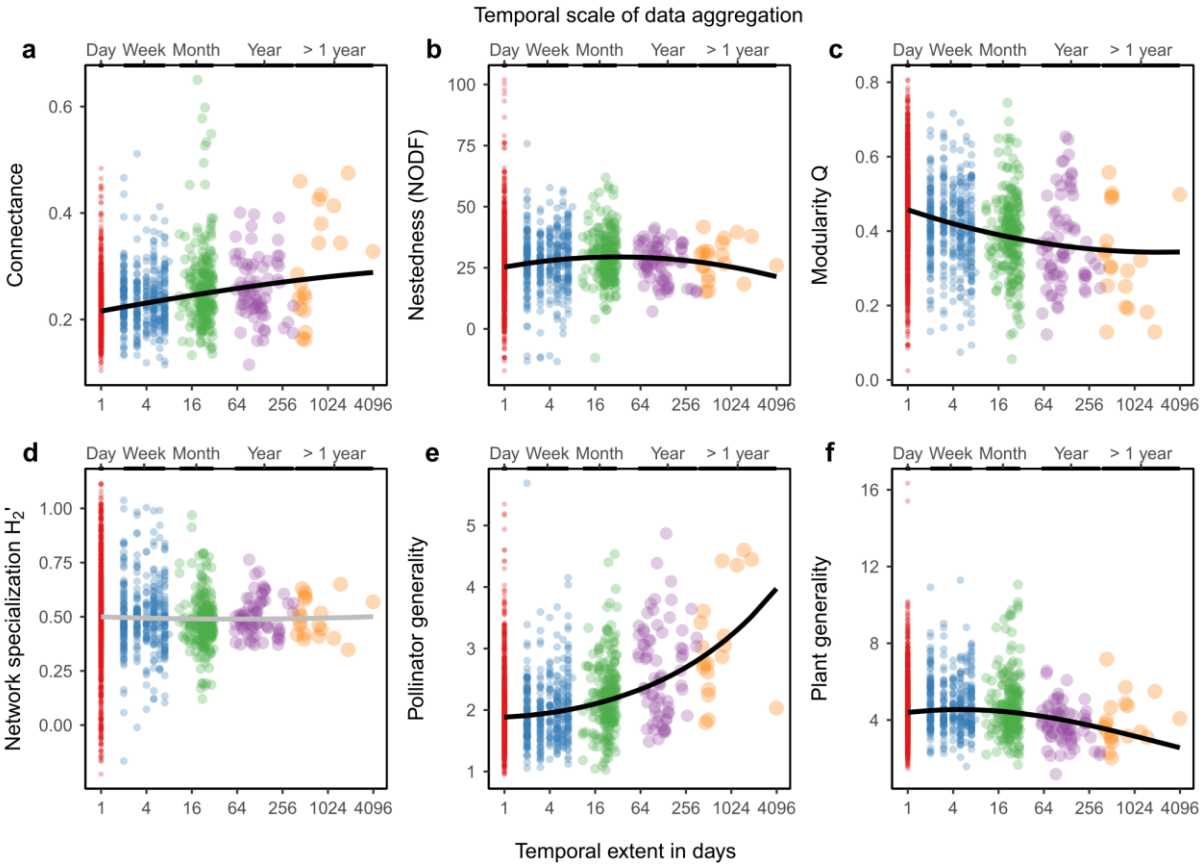

Figure A6. Effects of the temporal scale of data aggregation on network structure when controlling for species richness. Trendlines are based on predictions of linear mixed models testing the effect of temporal extent as single and quadratic term. Statistical fits for connectance, pollinator generality, and plant generality are based on log-transformed data, whereas figure axes represent the scale of the original data. These partial residual plots correct for baseline differences among studies and sites (specified as random effects in linear mixed models) as well as for species richness differences (specified as fixed effect in linear mixed models), which occasionally leads to data points lying outside the range of the variable. Note that lower x-axes are on a $\log_2$-scale.

Table A3. Effects of temporal extent (as single and quadratic term) and species richness on six commonly used network indices. Significant effects ($p < 0.05$) are reported in bold.

Response	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
log(Connectance)						
log(Temporal extent)	1.24	1.24	1	1869.19	23.48	**<0.001**
log(Temporal extent)^2	0.05	0.05	1	1844.57	0.92	0.337
log(Species richness)	142.63	142.63	1	1825.32	2698.30	**<0.001**
Nestedness (NODF)						
log(Temporal extent)	2679.71	2679.71	1	1877.14	14.39	**<0.001**
log(Temporal extent)^2	1403.72	1403.72	1	1874.69	7.54	**0.006**
log(Species richness)	312.25	312.25	1	1413.95	1.68	0.196
Modularity Q						
log(Temporal extent)	0.41	0.41	1	1878.34	25.51	**<0.001**
log(Temporal extent)^2	0.04	0.04	1	1853.22	2.70	0.101
log(Species richness)	1.95	1.95	1	1538.99	122.19	**<0.001**
Network specialization H_2'						
log(Temporal extent)	0.01	0.01	1	1825.33	0.28	0.595
log(Temporal extent)^2	0.00	0.00	1	1860.98	0.11	0.745
log(Species richness)	0.57	0.57	1	1004.31	13.33	**<0.001**
log(Pollinator generality)						
log(Temporal extent)	0.09	0.09	1	1891.57	1.20	0.273
log(Temporal extent)^2	0.99	0.99	1	1861.85	13.49	**<0.001**
log(Species richness)	34.15	34.15	1	1948.60	466.17	**<0.001**
log(Plant generality)						
log(Temporal extent)	0.77	0.77	1	1882.59	7.03	0.008
log(Temporal extent)^2	1.93	1.93	1	1848.80	17.54	**<0.001**
log(Species richness)	100.52	100.52	1	1884.17	914.86	**<0.001**

Table A4. Results of simplified structural equation models referred to in the main text. Presented are correlations between variables accounted for in the models. These correlations were the same across the six models for the different network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	Predictor	Estimate	S.E.	Df	Crit. Value	P	Std. Estim.	
~~Temporal extent	~~Sampling effort	0.88	-	482	41.09	<0.001	0.88	***
~~Link rewiring	~~Species turnover	0.20	-	484	4.44	<0.001	0.20	***
~~Link rewiring	~~Species richness	0.34	-	484	8.01	<0.001	0.34	***

Table A5. Results of simplified structural equation models referred to in the main text. Presented are effects of sampling effort and temporal extent on species richness, link rewiring, and species turnover. These effects were the same across the six models for the different network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	Predictor	Estimate	S.E.	Df	Crit. Value	P	Std. Estim.	
Species turnover	Temporal extent	0.53	0.04	349	12.40	<0.001	0.49	***
Link rewiring	Sampling effort	0.17	0.05	349	3.80	<0.001	0.15	***
Species richness	Sampling effort	0.51	0.02	349	25.01	<0.001	0.60	***

Table A6. Results of simplified structural equation models referred to in the main text. Presented are direct effects of sampling effort, temporal extent, species richness, link rewiring, and species turnover on six network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	Predictor	Estimate	S.E.	Df	Crit. Value	P	Std. Estim.	
Connectance	Sampling effort	0.23	0.03	346	8.63	<0.001	0.27	***
	Species turnover	-0.21	0.02	346	-11.06	<0.001	-0.27	***
	Link rewiring	0.07	0.02	346	3.88	<0.001	0.09	***
	Species richness	-0.92	0.04	346	-24.16	<0.001	-0.93	***
Nestedness	Sampling effort	0.30	0.05	346	5.81	<0.001	0.31	***
	Species turnover	-0.44	0.04	346	-11.84	<0.001	-0.50	***
	Link rewiring	0.21	0.03	346	6.10	<0.001	0.25	***
	Species richness	-0.23	0.07	346	-3.13	0.002	-0.20	**
Modularity	Sampling effort	-0.52	0.05	346	-9.98	<0.001	-0.54	***
	Species turnover	0.56	0.04	346	15.15	<0.001	0.64	***
	Link rewiring	-0.10	0.04	346	-2.84	0.005	-0.12	**
	Species richness	0.57	0.07	346	7.91	<0.001	0.51	***
Network specialization H_2'	Temporal extent	-0.22	0.04	347	-5.46	<0.001	-0.25	***
	Species turnover	0.29	0.04	347	7.70	<0.001	0.37	***
	Link rewiring	-0.33	0.03	347	-10.25	<0.001	-0.43	***
Pollinator generality	Sampling effort	0.29	0.05	346	6.11	<0.001	0.29	***
	Species turnover	-0.09	0.03	346	-2.65	0.008	-0.10	**
	Link rewiring	0.21	0.03	346	6.72	<0.001	0.24	***
	Species richness	0.50	0.07	346	7.44	<0.001	0.42	***
Plant generality	Species turnover	-0.14	0.02	348	-5.74	<0.001	-0.19	***
	Species richness	0.70	0.03	348	20.16	<0.001	0.76	***

Appendix 3

Effect of the temporal scale of data aggregation on a normalized nestedness index (NODFc)

Here, we compare the temporal scale-dependence between the NODF nestedness index we have used in our analyses and an alternative nestedness index, which was proposed to facilitate network comparisons. In a recent study, maximum values of NODF nestedness were found to be curtailed by the number of species and links in the network (Song et al. 2017). NODF nestedness therefore is correlated with connectance and network size, which could limit its application for network comparisons. Thus, a normalized nestedness index that accounts for connectance, network size and the maximum nestedness of a network was proposed by Song et al. (2017). To evaluate whether this normalized nestedness index (NODFc) shows a different pattern of temporal scale-dependence than NODF nestedness, we tested the effect of the temporal scale of data aggregation on both indices. We used the *maxnodf* package in R to calculate maximum values of NODF (Hoeppke and Simmons 2020) and calculated a normalized nestedness index (NODFc) following Song et al. (2017). We found that the temporal extent of the network significantly affected maxNODF as quadratic term ($F=11.51$, $P<0.001$) but not as single term ($F=0.15$, $P=0.696$), while temporal extent significantly affected NODFc as single term ($F=25.61$, $P<0.001$) as well as quadratic term ($F=11.86$, $P<0.001$). Importantly, the normalized nestedness index NODFc responded to temporal extent in a very similar way as the raw NODF index (Figure A7). Considering this similarity in temporal scale-dependence, we present in the main text only the results for NODF nestedness, which is more frequently used in other studies.

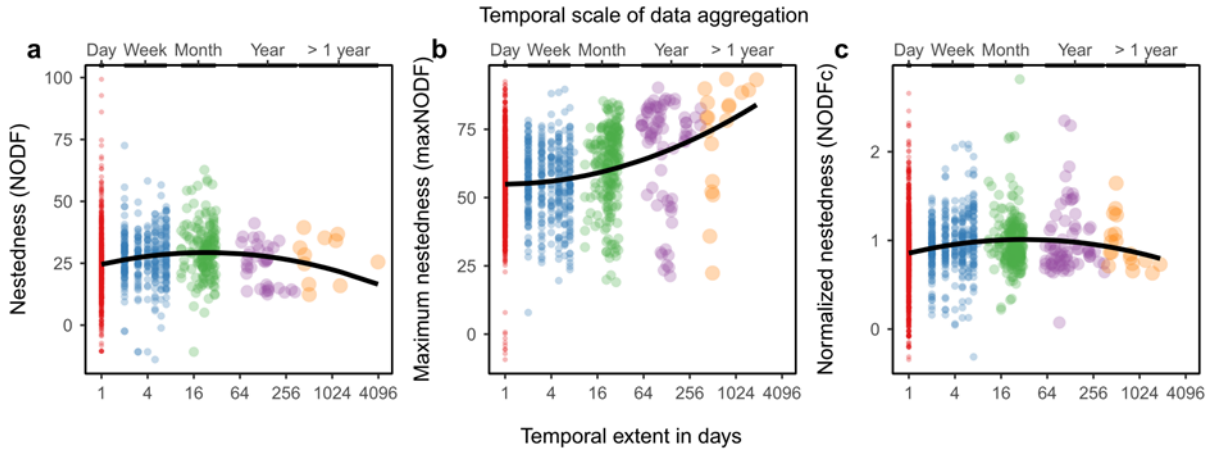

Figure A7. Effects of the temporal scale of data aggregation on (a) raw nestedness (NODF), (b) maximum nestedness (maxNODF), and (c) normalized nestedness (NODFc). Trendlines are based on predictions of linear mixed models testing the effect of temporal extent as single and quadratic term. These partial residual plots correct for baseline differences among studies and sites (specified as random effects in linear mixed models), which occasionally leads to data points lying outside the range of the variable. Due to limitations in the calculation of maxNODF, panels (b) and (c) show slightly fewer data points than panel (a). Note that lower x-axes are on a $\log_2$-scale.

Appendix 4

Roles of sampling completeness and sampling coverage in the temporal scale-dependence of network structure

To better understand how sampling completeness and sampling coverage are affected by the temporal scale of data aggregation and how they in turn contribute to the temporal scale-dependence of network structure, we included link completeness and link coverage as co-variables in the structural equation models. We found that link completeness increased with sampling effort and decreased with species richness and species turnover (Table A11), and that link coverage increased with sampling effort and decreased with species turnover and link rewiring (Table A13). In turn, link completeness had positive but weak effects on connectance, nestedness, network specialization H_2', and plant generality (Table A12), while link coverage had positive effects on connectance, nestedness, network specialization H_2', and a negative effect on modularity (Table A14).

As expected, sampling completeness as well as sampling coverage were positively affected by sampling effort. However, our findings also suggest that with increasing temporal scale high species turnover is counterbalancing the positive effects of sampling effort. Thus, considering the constant turnover of species and their links, temporal data aggregation seems to be of limited suitability to increase overall sampling completeness. Interestingly, network indices were only weakly affected by sampling completeness, while at least nestedness, modularity, and network specialization H_2' were more strongly affected by sampling coverage. Strong effects of sampling completeness on network structure reported by other studies are not in contradiction to our findings as these studies did not test the effect of sampling completeness based on the Chao1 estimator but used other measures of sampling completeness more directly related to sampling effort (Rivera-Hutinel et al. 2012, Fründ et al. 2016). Thus, network indices may depend more strongly on sampling effort, species richness, and species turnover rather than on sampling completeness. However, the weak effects of sampling completeness on network indices may also be because sampling completeness based on the Chao1 estimator can be a biased estimate (Fründ et al. 2016).

The effects of sampling coverage on nestedness, modularity, and network specialization H_2' means that these indices depend on how well the most frequent links are represented by the network. However, sampling coverage may not just be a function of effective sampling effort, but could also be affected by network structure itself—it may be easier to achieve high sampling coverage for certain network structures that concentrate a high proportion of interactions (visits, weights) in a few links. Conceptually, differences between sampling coverage and sampling effort are difficult to interpret. Further investigation on the mechanistic links between sampling completeness, sampling coverage, and network structure might be needed.

Notwithstanding, it is important to note that including link completeness or link coverage as co-variables had only minor influence on how the predictor variables in the SEMs referred to in the main text affected the six tested network indices. Thus, our findings on the direct and indirect effects of temporal extent, sampling effort, species richness, species turnover, and link rewiring on the six network indices reported in the main text appear to be robust.

Table A7. Results of simplified structural equation models including link completeness as co-variable. Presented are effects of sampling effort and temporal extent on species richness, link rewiring, species turnover, and link completeness as well as effects of species richness and species turnover on link completeness. These effects were the same across the six models for the different network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	Predictor	Estimate	S.E.	Df	Crit. Value	P	Std. Estim.	
Species turnover	Temporal extent	0.53	0.04	349	12.40	<0.001	0.49	***
Link rewiring	Sampling effort	0.17	0.05	349	3.80	<0.001	0.15	***
Species richness	Sampling effort	0.51	0.02	349	25.01	<0.001	0.60	***
Link completeness	Sampling effort	0.38	0.06	347	6.33	<0.001	0.40	***
	Species turnover	-0.25	0.04	347	-6.11	<0.001	-0.30	***
	Species richness	-0.47	0.08	347	-5.99	<0.001	-0.43	***

Table A8. Results of simplified structural equation models including link completeness as co-variable. Presented are direct effects of sampling effort, temporal extent, species richness, link rewiring, species turnover, and link completeness on six network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001. Effects of link completeness are reported in bold.

Response	**Predictor**	**Estimate**	**S.E.**	**Df**	**Crit. Value**	**P**	**Std. Estim.**	
Connectance	Sampling effort	0.20	0.03	345	7.37	<0.001	0.23	***
	Species turnover	-0.19	0.02	345	-9.97	<0.001	-0.25	***
	Link rewiring	0.07	0.02	345	4.14	<0.001	0.10	***
	Species richness	-0.88	0.04	345	-23.11	<0.001	-0.89	***
	Link completeness	0.08	0.02	345	4.17	<0.001	0.09	***
Nestedness	Sampling effort	0.26	0.05	345	4.90	<0.001	0.27	***
	Species turnover	-0.41	0.04	345	-10.86	<0.001	-0.47	***
	Link rewiring	0.22	0.03	345	6.42	<0.001	0.26	***
	Species richness	-0.18	0.07	345	-2.48	0.014	-0.16	*
	Link completeness	0.13	0.04	345	3.30	0.001	0.12	**
Modularity	Sampling effort	-0.52	0.05	346	-9.98	<0.001	-0.54	***
	Species turnover	0.56	0.04	346	15.15	<0.001	0.64	***
	Link rewiring	-0.10	0.04	346	-2.84	0.005	-0.12	**
	Species richness	0.57	0.07	346	7.91	<0.001	0.51	***
Network specialization H_2'	Temporal extent	-0.23	0.04	346	-5.72	<0.001	-0.26	***
	Species turnover	0.31	0.04	346	7.96	<0.001	0.39	***
	Link rewiring	-0.32	0.03	346	-9.75	<0.001	-0.42	***
	Link completeness	0.08	0.04	346	2.00	0.046	0.08	*
Pollinator generality	Sampling effort	0.29	0.05	346	6.11	<0.001	0.29	***
	Species turnover	-0.09	0.03	346	-2.65	0.008	-0.10	**
	Link rewiring	0.21	0.03	346	6.72	<0.001	0.24	***
	Species richness	0.50	0.07	346	7.44	<0.001	0.42	***
Plant generality	Species turnover	-0.13	0.02	346	-5.43	<0.001	-0.18	***
	Link rewiring	0.05	0.02	346	2.00	0.046	0.07	*
	Species richness	0.68	0.04	346	18.92	<0.001	0.75	***
	Link completeness	0.09	0.03	346	3.29	0.001	0.11	**

Table A9. Results of simplified structural equation models including link coverage as co-variable. Presented are effects of sampling effort and temporal extent on species richness, link rewiring, species turnover, and link completeness as well as effects of species richness and species turnover on link coverage. These effects were the same across the six models for the different network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	Predictor	Estimate	S.E.	Df	Crit. Value	P	Std. Estim.	
Species turnover	Temporal extent	0.53	0.04	349	12.40	<0.001	0.49	***
Link rewiring	Sampling effort	0.17	0.05	349	3.80	<0.001	0.15	***
Species richness	Sampling effort	0.51	0.02	349	25.01	<0.001	0.60	***
Link coverage	Sampling effort	0.45	0.03	347	13.48	<0.001	0.51	***
	Species turnover	-0.40	0.03	347	-12.02	<0.001	-0.50	***
	Link rewiring	-0.06	0.03	347	-2.07	0.039	-0.08	*

Table A10. Results of simplified structural equation models including link coverage as co-variable. Presented are direct effects of sampling effort, temporal extent, species richness, link rewiring, species turnover, and link coverage on six network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001. Effects of link coverage are reported in bold.

Response	Predictor	Estimate	S.E.	DF	Crit. Value	P	Std. Estim.	
Connectance	Sampling effort	0.18	0.03	345	6.46	<0.001	0.22	***
	Species turnover	-0.17	0.02	345	-8.05	<0.001	-0.22	***
	Link rewiring	0.07	0.02	345	4.20	<0.001	0.10	***
	Species richness	-0.92	0.04	345	-24.57	<0.001	-0.93	***
	Link coverage	0.10	0.03	345	4.12	<0.001	0.11	***
Nestedness	Temporal extent	0.17	0.05	345	3.17	0.002	0.18	**
	Species turnover	-0.32	0.04	345	-7.83	<0.001	-0.36	***
	Link rewiring	0.24	0.03	345	7.11	<0.001	0.28	***
	Species richness	-0.23	0.07	345	-3.42	0.001	-0.20	***
	Link coverage	0.33	0.05	345	6.99	<0.001	0.30	***
Modularity	Sampling effort	-0.38	0.05	345	-6.97	<0.001	-0.39	***
	Species turnover	0.44	0.04	345	10.73	<0.001	0.50	***
	Link rewiring	-0.12	0.03	345	-3.54	0.001	-0.14	***
	Species richness	0.58	0.07	345	8.45	<0.001	0.52	***
	Link coverage	-0.32	0.05	345	-6.67	<0.001	-0.29	***
Network specialization H_2'	Sampling effort	-0.30	0.04	346	-6.93	<0.001	-0.34	***
	Species turnover	0.37	0.04	346	8.83	<0.001	0.46	***
	Link rewiring	-0.31	0.03	346	-9.74	<0.001	-0.40	***
	Link coverage	0.23	0.05	346	4.56	<0.001	0.23	***
Pollinator generality	Sampling effort	0.29	0.05	346	6.11	<0.001	0.29	***
	Species turnover	-0.09	0.03	346	-2.65	0.008	-0.10	**
	Link rewiring	0.21	0.03	346	6.72	<0.001	0.24	***
	Species richness	0.50	0.07	346	7.44	<0.001	0.42	***
Plant generality	Species turnover	-0.14	0.02	348	-5.74	<0.001	-0.19	***
	Species richness	0.70	0.03	348	20.16	<0.001	0.76	***

Appendix 5

Analyses of a reduced data set

To test the robustness of our results, we re-run all analyses discussed in the main text using a reduced data set assuring that at the site-level exactly the same data were used across all temporal scales. That means, for example, we excluded sampling days that could not be combined with other sampling days to aggregate weekly networks, although they could have been used to construct monthly networks. In contrast, in the main text we refer to the results found for the complete data set, which, for example, allows that all sampling days within a month were aggregated to a monthly network although not all of these sampling days were used to aggregate weekly networks. Assuring that results for each temporal scale are based on exactly the same data avoids uneven influence of certain interactions on different temporal scales, but also involves the risk to reduce information content. Thus, in the main text we present the results for the complete data set, which allows to aggregate networks that are more complete for their respective temporal scale and thus likely better capture the underlying temporal dynamics.

Temporal scale of data aggregation and network structure

For both the complete and the reduced data set we found the same overall patterns of temporal scale-dependence for all six network indices (Figure A8, Table A4). There were only two minor differences between both data sets. Temporal extent significantly affected modularity only as quadratic term for the complete data set, while both single and quadratic terms were significant for the reduced data set (Figure A8, Table A4). In addition, we found no quadratic effect of temporal extent on plant generality for the complete data set but for the reduced data set (Figure A8, Table A4). These differences between data sets could simply arise because of the difference in the number of data points (n=2006 vs. n=1328). As we found for both data sets almost identical patterns, our results and conclusions shown in the main text appear to be robust.

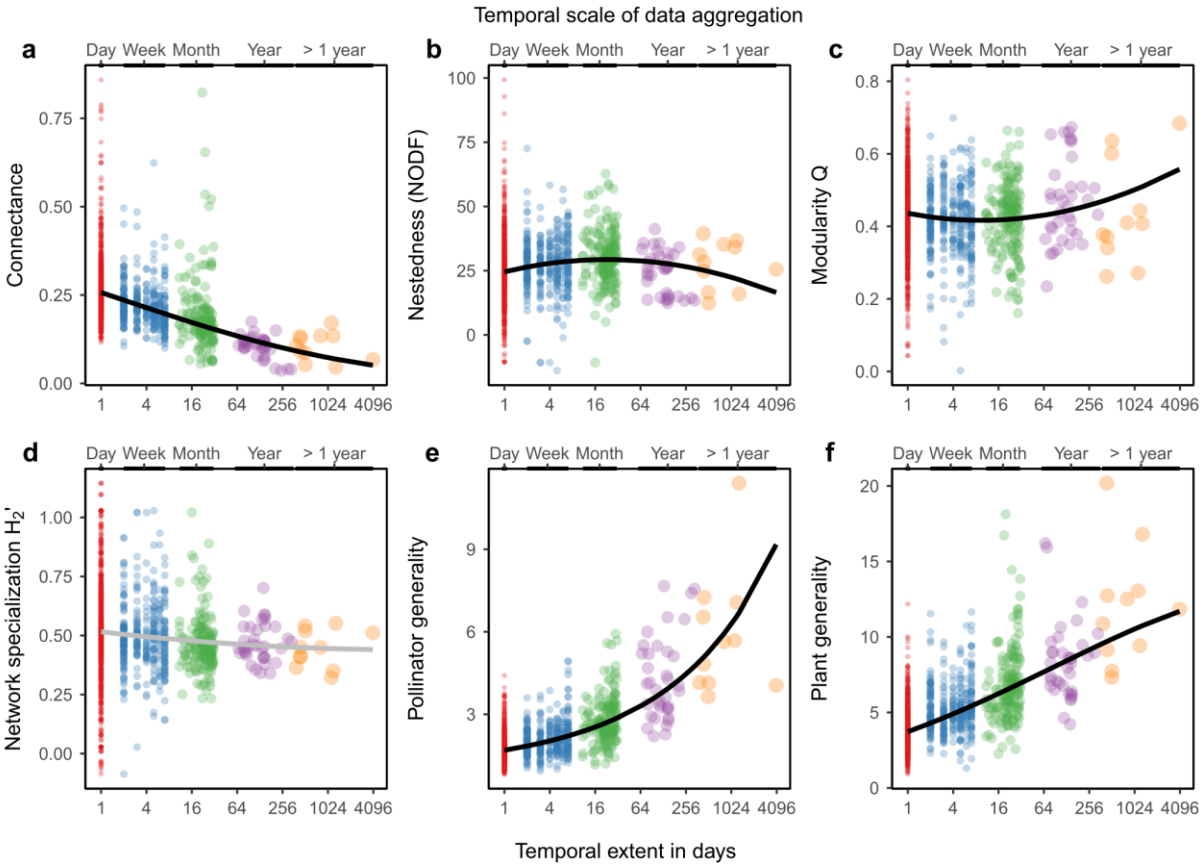

Figure A8. Effects of the temporal scale of data aggregation on network structure found for a reduced data set assuring that at the site-level each temporal scale is represented by exactly the same interaction data. Trendlines are based on predictions of linear mixed models testing the effect of temporal extent as single and quadratic term. Statistical fits for connectance, pollinator generality, and plant generality are based on log-transformed data, whereas figure axes represent the scale of the original data. These partial residual plots correct for baseline differences among studies and sites (specified as random effects in linear mixed models), which occasionally leads to data points lying outside the range of the variable. Note that lower x-axes are on a $\log_2$-scale.

Table A11. Effects of temporal extent (as single and quadratic term) on six commonly used network indices found for a reduced data set assuring that at the site-level each temporal scale is represented by exactly the same interaction data. Significant effects ($p < 0.05$) are reported in bold.

Response	**Sum Sq**	**Mean Sq**	**NumDF**	**DenDF**	**F value**	**Pr(>F)**
log(Connectance)						
log(Temporal extent)	5.15	5.15	1	1177.67	46.32	**<0.001**
log(Temporal extent)^2	0.67	0.67	1	1169.37	6.05	**0.014**
Nestedness (NODF)						
log(Temporal extent)	3357.86	3357.86	1	1206.46	20.63	**<0.001**
log(Temporal extent)^2	1918.61	1918.61	1	1187.41	11.79	**0.001**
Modularity Q						
log(Temporal extent)	0.11	0.11	1	1186.59	7.97	**0.005**
log(Temporal extent)^2	0.12	0.12	1	1169.66	8.94	**0.003**
Network specialization H_2'						
log(Temporal extent)	0.10	0.10	1	1199.55	2.50	0.114
log(Temporal extent)^2	0.01	0.01	1	1178.48	0.15	0.694
log(Pollinator generality)						
log(Temporal extent)	4.97	4.97	1	1184.80	59.99	**<0.001**
log(Temporal extent)^2	0.90	0.90	1	1175.49	10.88	**0.001**
log(Plant generality)						
log(Temporal extent)	16.18	16.18	1	1178.05	115.46	**<0.001**
log(Temporal extent)^2	0.64	0.64	1	1167.75	4.58	**0.032**

Temporal scale of data aggregation, network size, sampling completeness, and sampling overage

Effects of the temporal scale of data aggregation on network size, sampling completeness, and sampling coverage were very similar between the complete and the reduced data set. There were only two minor differences between both data sets. For the complete data set we found that temporal extent significantly affected pollinator richness as single and quadratic term, while for the reduced data set only the single term was significant (Figure A9, Table A5). In addition, the non-significant effect of the quadratic term of temporal extent on link coverage found for the complete data set became significant for the reduced data set (Figure A9, Table A5). These slight differences could be related to the lower number of data points as well as to the lower variation of the number of sampling days per network in the reduced data set.

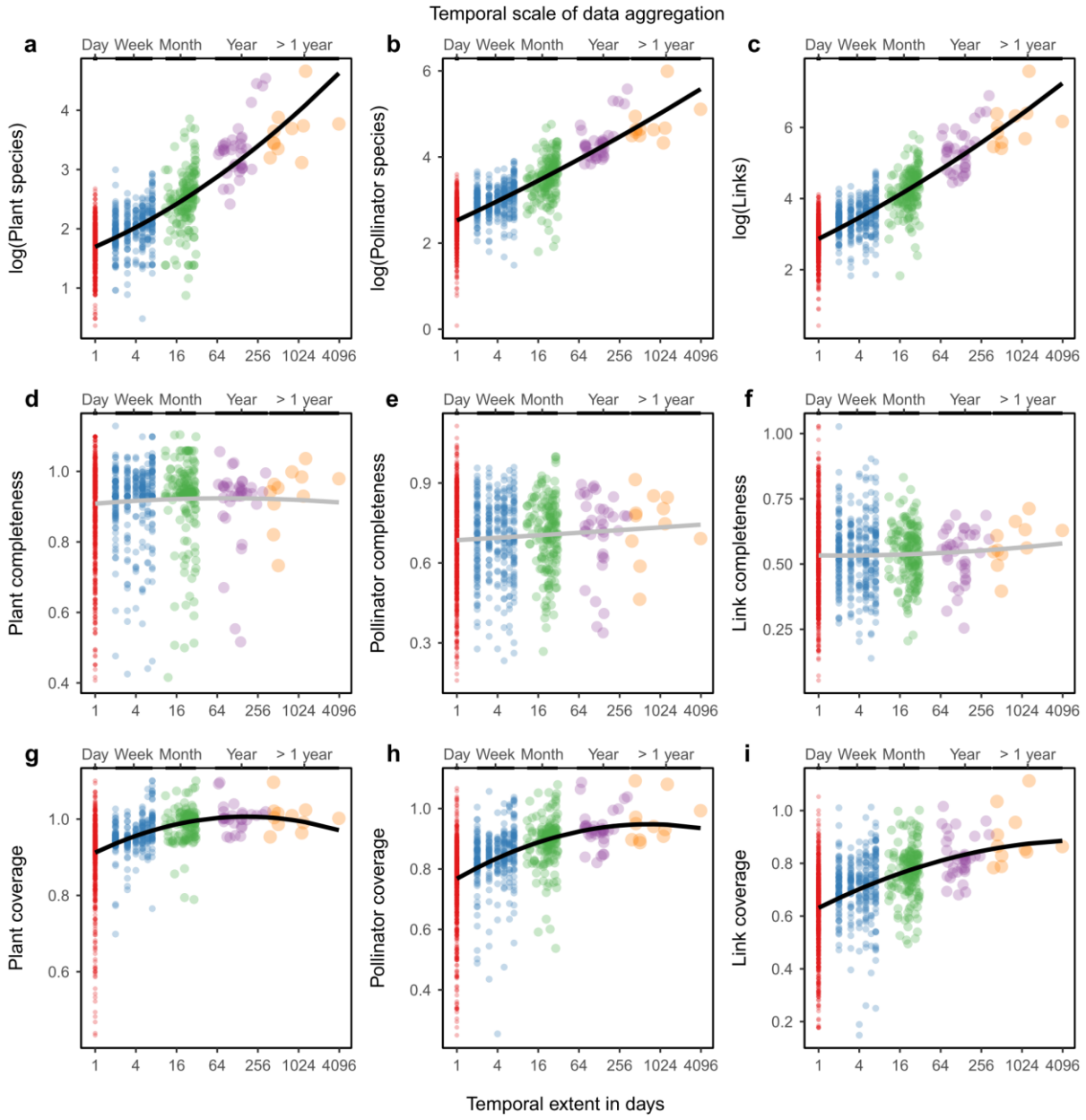

Figure A9. Effects of the scale of temporal data aggregation on network size, sampling completeness, and sampling coverage found for a reduced data set assuring that at the site-level each temporal scale is represented by exactly the same interaction data. The nine panels show effects on the log-transformed numbers of (a) plant species, (b) pollinator species, and (c) links, effects on sampling completeness of (d) plant species, (e) pollinator species, and (f) links as well as effects on sampling coverage at the level of (g) plants, (h) pollinators, and (i) links. Trendlines are based on predictions of linear mixed models testing the effect of temporal extent as single and quadratic term. Overall, effects were very similar to the effects found for the complete data set. Sampling completeness was quantified as the proportion of observed species or link numbers of the species and link numbers estimated by the Chao1 richness estimator. Sampling coverage is an estimation of the proportion of all individuals or interactions that belong to the observed species or links. These partial residual plots correct for baseline differences among studies and sites (specified as random effects in linear mixed models), which occasionally leads to data points lying outside the range of the variable. Note that lower x-axes are on a $\log_2$-scale.

Table A12. Effects of temporal extent (as single and quadratic term) on network size (species and link richness), sampling completeness, and sampling coverage found for a reduced data set assuring that at the site-level each temporal scale is represented by exactly the same interaction data. Significant effects ($p < 0.05$) are reported in bold.

Response	Sum Sq	Mean Sq	NumDF	DenDF	F value	Pr(>F)
log(Plant richness)						
log(Temporal extent)	16.77	16.77	1	1174.04	107.91	**<0.001**
log(Temporal extent)^2	2.28	2.28	1	1167.26	14.65	**<0.001**
log(Pollinator richness)						
log(Temporal extent)	36.43	36.43	1	1176.12	186.24	**<0.001**
log(Temporal extent)^2	0.31	0.31	1	1167.14	1.58	0.209
log(Link richness)						
log(Temporal extent)	61.59	61.59	1	1175.54	226.90	**<0.001**
log(Temporal extent)^2	1.58	1.58	1	1167.14	5.82	**0.016**
Plant completeness						
log(Temporal extent)	0.02	0.02	1	1186.36	1.15	0.283
log(Temporal extent)^2	0.00	0.00	1	1181.18	0.33	0.568
Pollinator completeness						
log(Temporal extent)	0.02	0.02	1	1213.02	0.58	0.447
log(Temporal extent)^2	0.00	0.00	1	1185.58	0.00	0.968
Link completeness						
log(Temporal extent)	0.00	0.00	1	1180.42	0.02	0.902
log(Temporal extent)^2	0.01	0.01	1	1163.19	0.22	0.642
Plant coverage						
log(Temporal extent)	0.45	0.45	1	1028.83	71.29	**<0.001**
log(Temporal extent)^2	0.10	0.10	1	1008.54	15.12	**<0.001**
Pollinator coverage						
log(Temporal extent)	1.10	1.10	1	1160.93	80.49	**<0.001**
log(Temporal extent)^2	0.14	0.14	1	1146.79	10.64	**0.001**
Link coverage						
log(Temporal extent)	1.09	1.09	1	1131.04	59.27	**<0.001**
log(Temporal extent)^2	0.07	0.07	1	1120.09	3.94	**0.047**

Effects of species richness, species turnover, and link rewiring

The structural equation models also yielded similar results for the complete and the reduced data set. When analyzing the reduced instead of the complete data set, the weak positive effect of link rewiring on connectance, the weak negative effect of link rewiring on modularity, and the negative effect of temporal extent on H_2' diminished while there was a new negative effect of sampling effort on H_2' (Figure A10, Table A17). The fact that H_2' was affected by either temporal extent or sampling effort likely is related to species that establish different links on different days. This decrease in specialization is not captured by link rewiring if only one of the partners is shared, but could be captured by either temporal extent or the number of sampling days. For nestedness, pollinator generality, and plant generality the structural equation models for the complete and the reduced data set resulted in the same significant pathways (Figure A10, Table A17). All in all, our conclusions that the temporal scale-dependence of network structure is largely driven by species richness, which increases with sampling effort, and species turnover, which increases with temporal extent, are the same for both the complete and the reduced data set.

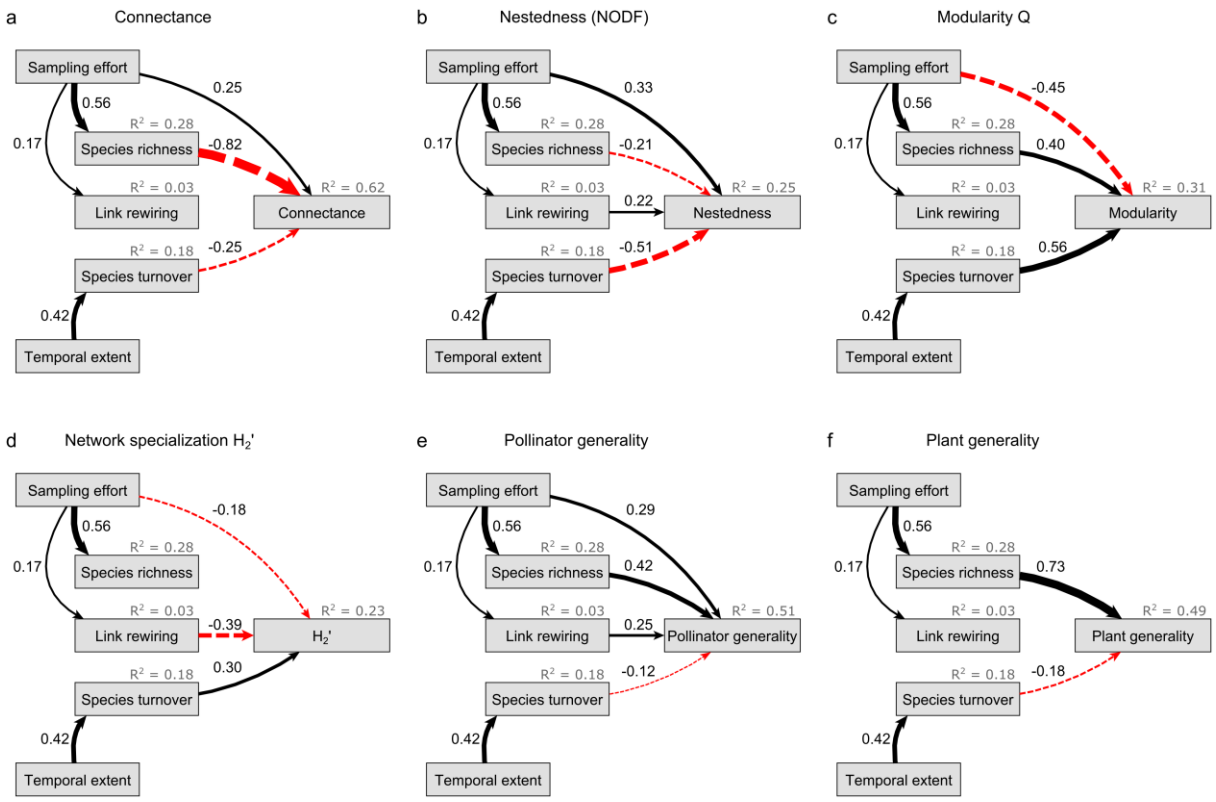

Figure A10. Structural equation models of the effects of potential drivers of the influence of temporal data aggregation on (a) connectance, (b) nestedness (NODF), (c) modularity Q, (d) network specialization H2', (e) pollinator generality, and (f) plant generality. Models were run using a reduced data set, which assured that at the site-level each temporal scale is represented by exactly the same interaction data. Standardized coefficients are presented as numbers on or below arrows. To indicate relative effect strengths, arrow widths are scaled to standardized coefficients. Red and black arrow colors indicate negative and positive effects, respectively. Marginal R^2 values indicate the proportion of variance in the response variables explained by the fixed effects. See Supplementary Information for model fits. During model simplification only statistically significant pathways have been retained ($P < 0.05$). Correlations among variables are not shown. Note that the six models only differ in the network index used, explaining identical effects of sampling effort and temporal extent on species richness, link rewiring, and species turnover in each model.

Table A13. Results of simplified structural equation models based on a reduced data set. Presented are correlations between variables accounted for in the models. These correlations were the same across the six models for the different network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	Predictor	Estimate	S.E.	Df	Crit.Value	P	Std. Estim.	
~~Temporal extent	~~Sampling effort	0.85	-	363	30.90	<0.001	0.85	***
~~Link rewiring	~~Species turnover	0.18	-	365	3.43	<0.001	0.18	***
~~Link rewiring	~~Species richness	0.30	-	365	5.98	<0.001	0.30	***

Table A14. Results of simplified structural equation models based on a reduced data set. Presented are effects of sampling effort and temporal extent on species richness, link rewiring, and species turnover. These effects were the same across the six models for the different network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	Predictor	Estimate	S.E.	Df	Crit.Value	P	Std. Estim.	
Species turnover	Temporal extent	0.49	0.06	231	8.94	<0.001	0.42	***
Link rewiring	Sampling effort	0.21	0.06	231	3.44	0.001	0.17	***
Species richness	Sampling effort	0.52	0.03	231	18.17	<0.001	0.56	***

Table A15. Results of simplified structural equation models based on a reduced data set. Presented are direct effects of sampling effort, temporal extent, species richness, link rewiring, and species turnover on six network indices. Given are unstandardized path coefficients (estimate), standard error of regression weights (S.E.), standardized path coefficients (Std. Estim.), degrees of freedom (Df), critical values (Crit. Value), and level of significance (P). *: P<0.05, **: P<0.01, ***: P<0.001.

Response	**Predictor**	**Estimate**	**S.E.**	**Df**	**Crit.Value**	**P**	**Std. Estim.**	
Connectance	Sampling effort	0.23	0.03	229	7.15	<0.001	0.25	***
	Species turnover	-0.20	0.02	229	-9.12	<0.001	-0.25	***
	Species richness	-0.83	0.04	229	-20.20	<0.001	-0.82	***
Nestedness	Sampling effort	0.36	0.06	228	5.53	<0.001	0.33	***
	Species turnover	-0.46	0.04	228	-10.69	<0.001	-0.51	***
	Link rewiring	0.19	0.04	228	4.66	<0.001	0.22	***
	Species richness	-0.25	0.08	228	-3.02	0.003	-0.21	**
Modularity	Sampling effort	-0.52	0.06	229	-8.17	<0.001	-0.45	***
	Species turnover	0.54	0.04	229	12.52	<0.001	0.56	***
	Species richness	0.50	0.08	229	6.56	<0.001	0.40	***
Network specialization H_2'	Sampling effort	-0.17	0.05	229	-3.39	0.001	-0.18	***
	Species turnover	0.25	0.04	229	5.74	<0.001	0.30	***
	Link rewiring	-0.31	0.04	229	-8.24	<0.001	-0.39	***
Pollinator generality	Sampling effort	0.35	0.06	228	5.52	<0.001	0.29	***
	Species turnover	-0.12	0.04	228	-2.83	0.005	-0.12	**
	Link rewiring	0.24	0.04	228	6.01	<0.001	0.25	***
	Species richness	0.55	0.08	228	6.83	<0.001	0.42	***
Plant generality	Species turnover	-0.13	0.03	230	-4.89	<0.001	-0.18	***
	Species richness	0.67	0.04	230	17.04	<0.001	0.73	***

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