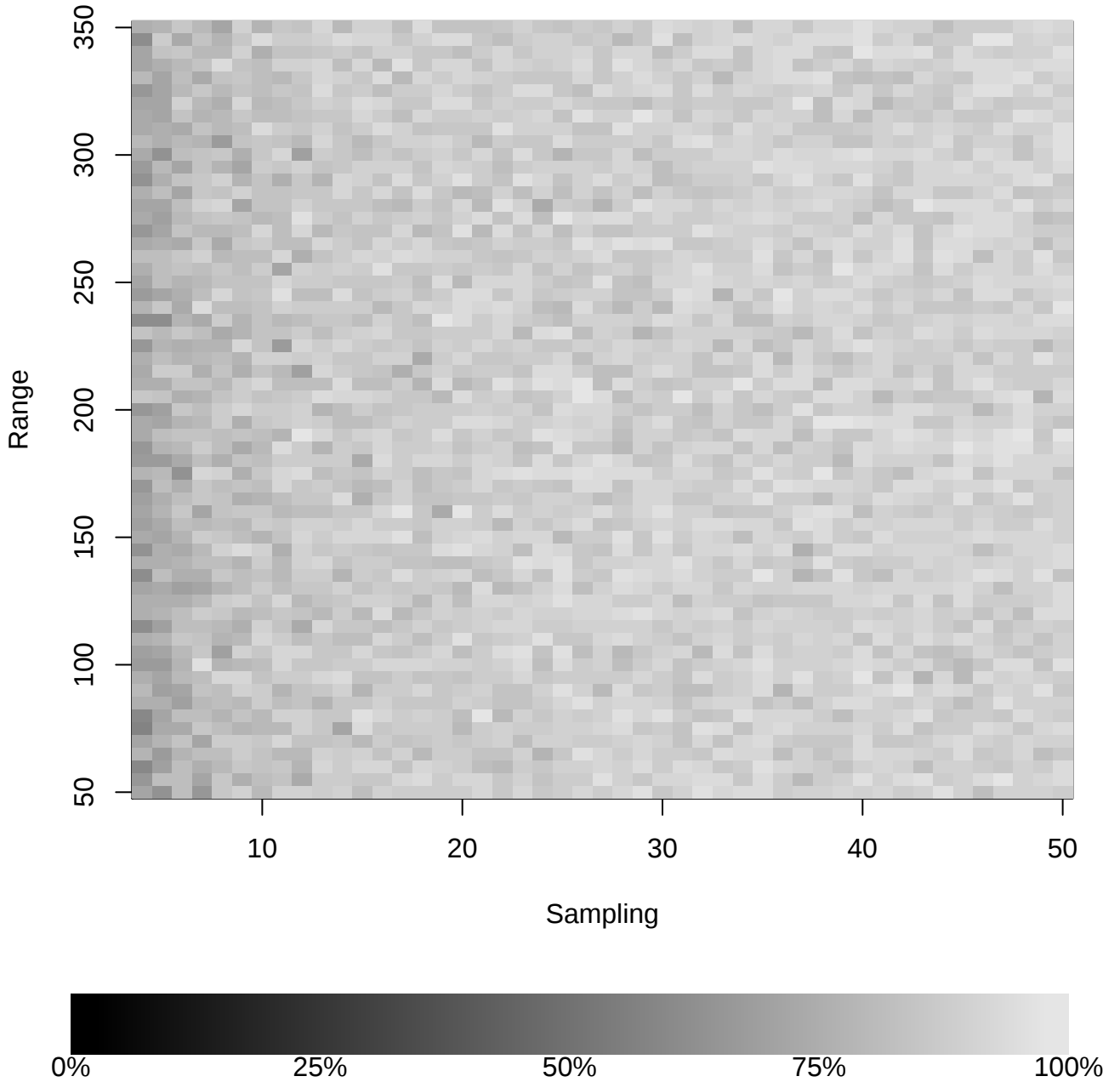


In the format provided by the authors and unedited.

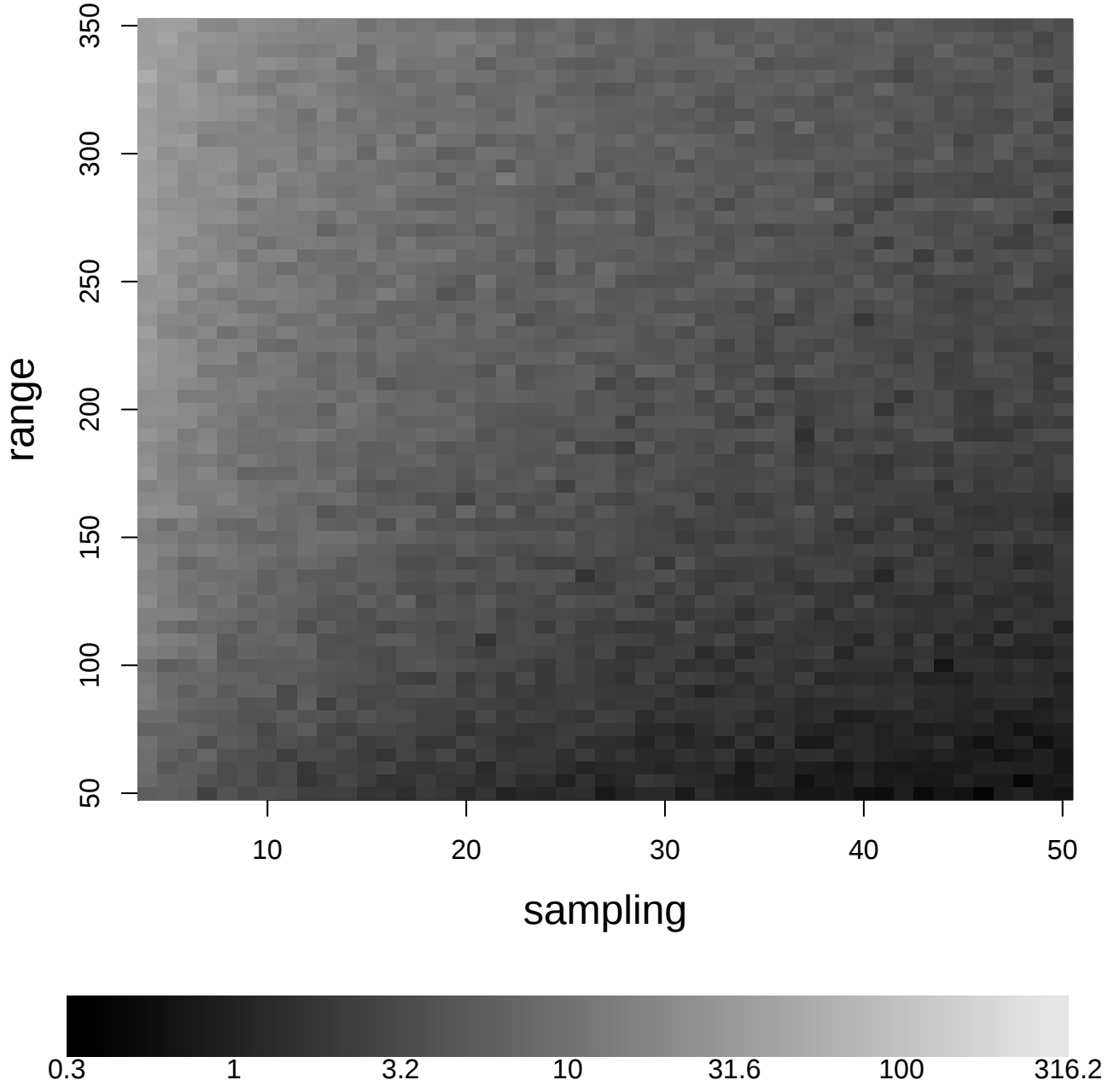
A statistical estimator for determining the limits of contemporary and historic phenology

William D. Pearse ^{1,2,3*}, Charles C. Davis⁴, David W. Inouye ^{5,6}, Richard B. Primack⁷
and T. Jonathan Davies^{1*}

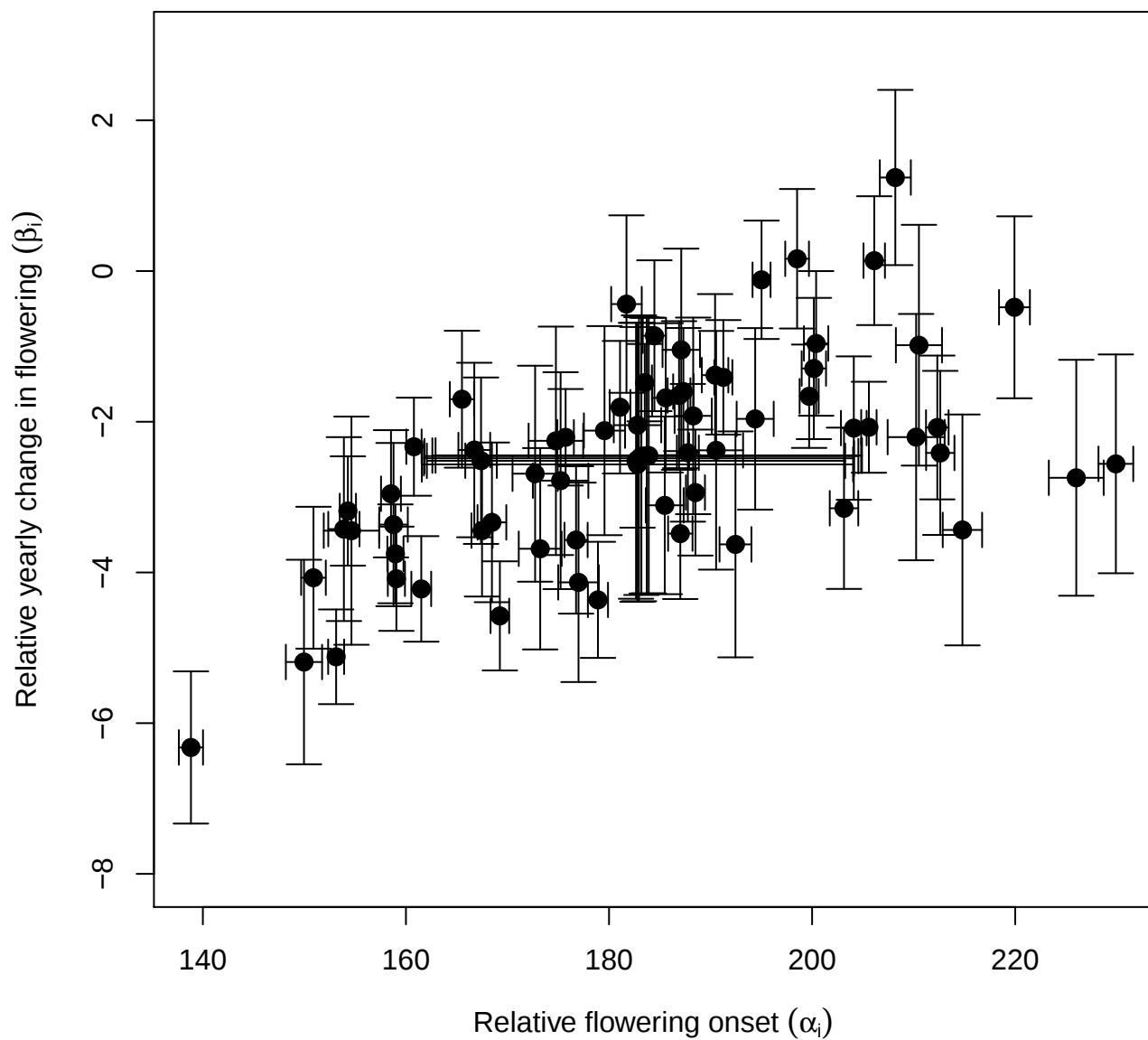
¹Department of Biology, McGill University, Montréal, Québec H3A 1B1, Canada. ²Department of Biological Sciences, Université du Québec à Montréal, Montréal, Québec H2X 1Y4, Canada. ³Department of Biology and Ecology Center, Utah State University, 5305 Old Main Hill, Logan, UT 84322, USA. ⁴Department of Organismic and Evolutionary Biology and Harvard University Herbaria, Harvard University, 22 Divinity Avenue, Cambridge, MA 02138, USA. ⁵Department of Biology, University of Maryland, College Park, MD 20742, USA. ⁶Rocky Mountain Biological Laboratory, PO Box 519, Crested Butte, CO 81224, USA. ⁷Biology Department, Boston University, 5 Cummington Street, Boston, MA 02215, USA. *e-mail: will.pearse@usu.edu; j.davies@mcgill.ca



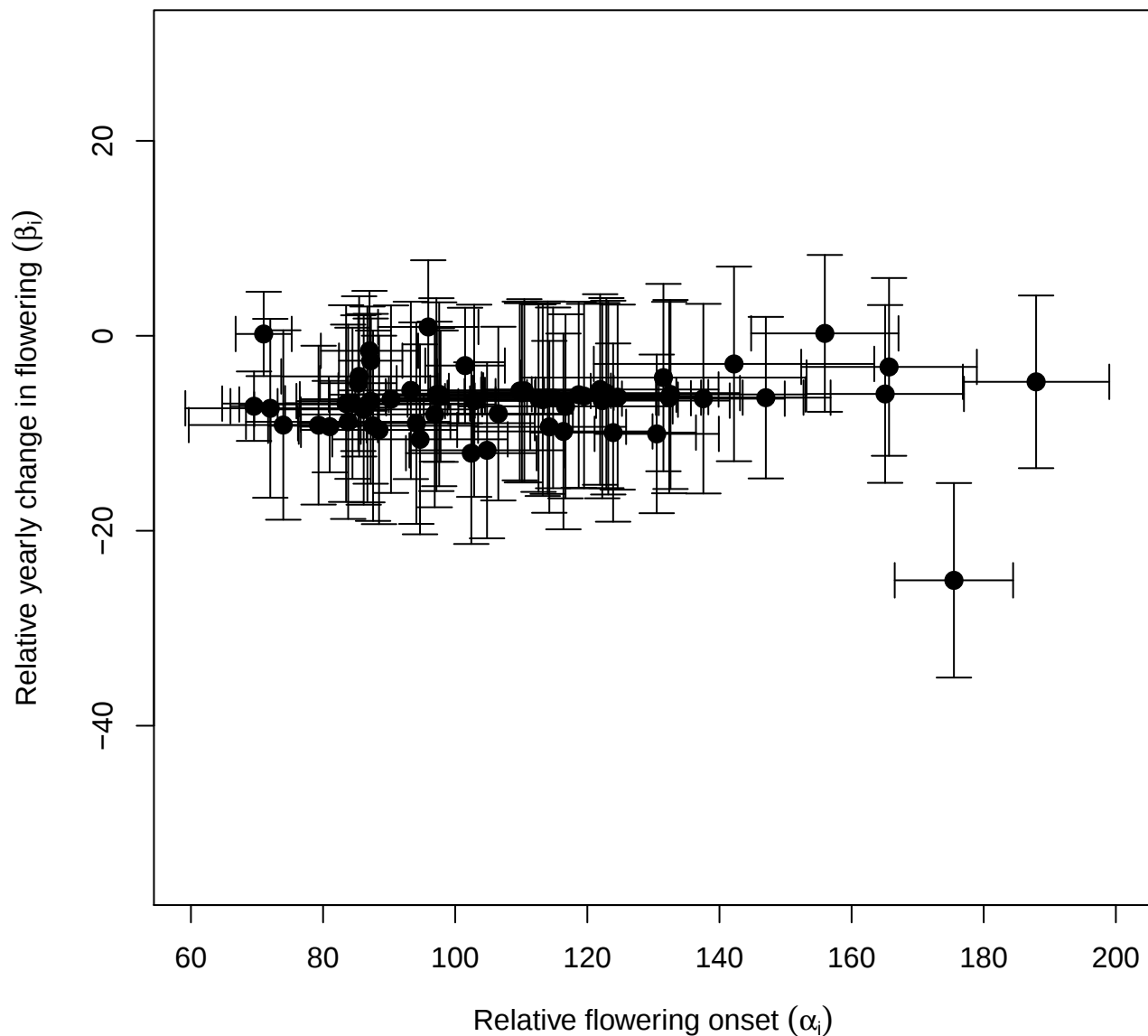
Supplementary Figure 1: Power analysis of our approach to estimating the onset of a process. The percentage of simulations under each parameter combination where the 95% confidence intervals of our estimated start of the process overlapped the true start. The horizontal axis shows the number of sampled units in the simulation, the vertical axis the range over which observations were simulated. The scale for the percentages is shown at the bottom. 50 simulations were carried out under each parameter combination. Because 95% confidence-intervals were used, a power (β) of 80% would be considered ideal performance, and over 93% of parameter combinations had confidence intervals that overlapped the true onset of 0.



Supplementary Figure 2: Power analysis of taking the first observation as an estimate of the onset of a process. The first observation was recorded across the same simulations as used for our method (see text and Extended Data Figure 1). The horizontal axis shows the number of sampled units in the simulation, the vertical the range over which observations were simulated. The scale at the bottom shows the estimated onset of the process: note that the true value was 0 in all simulations. For every 1.00 log-unit increase in the range, and every 0.97 log-unit increase in the sampling, the erroneous over-estimate of the onset of the process increases by 1 log-unit ($F_{2,143347} = 30780$, $p \leq 0.0001$, $r_{adj}^2 = 30\%$.)



Supplementary Figure 3: Species' rate change in first-flowering date plotted against overall order of flowering in the Rocky Mountain data. Points are medians and bars represent standard deviations from the posterior distributions of the Bayesian hierarchical model described in the text. Axes labels refer to terms in the model as described in the text.



Supplementary Figure 4: Species' rate change in first-flowering date plotted against overall order of flowering in the NPN data. Points are medians and bars represent standard deviations from the posterior distributions of the Bayesian hierarchical model described in the text. Axes labels refer to terms in the model as described in the text. The species in the bottom-right is *Hamamelis virginiana* (American witch-hazel); this species had few observations (9) and has a latitudinally wide distribution, which may have contributed to its relatively large change in flowering.

	df	SS	MSE	F	Pr(>F)
Species	64	2 756 444	43 069.44	335.83	<0.0001***
Year	1	45 879	45 878.94	357.74	<0.0001***
Log(abundance)	1	6875	6874.92	53.61	<0.0001***
Species–year interaction	64	27 401	428.14	3.34	<0.0001***
Residuals	7099	910 434	128.25		

Supplementary Table 1: Coefficients for the model of the onset of flowering across species in the Colorado Rocky Mountain dataset. $r_{adj}^2 = 75.3\%$, and $p \leq 0.0001$.

	df	SS	MSE	F	Pr(>F)
Species	64	3 422 243	53 472.55	440.46	<0.0001***
Year	1	40 746	40 746.38	335.63	<0.0001***
Log(abundance)	1	1218	1217.77	10.03	0.0015*
Species–year interaction	64	22 045	344.45	2.84	<0.0001***
Residuals	7099	861 826	121.40		

Supplementary Table 2: Coefficients for the model of the mean of flowering across species in the Colorado Rocky Mountain dataset. $r_{adj}^2 = 79.8\%$, $p < 0.0001$.

	df	SS	MSE	F	Pr(>F)
Species	64	4 280 140	66 877.19	316.14	<0.0001***
Year	1	34 881	34 881.24	164.89	<0.0001***
Log(abundance)	1	50 478	50 477.53	238.62	<0.0001***
Species–year interaction	64	39 790	621.72	2.94	<0.0001***
Residuals	7099	1 501 737	211.54		

Supplementary Table 3: Coefficients for the model of the cessation of flowering across species in the Colorado Rocky Mountain dataset. $r_{adj}^2 = 74.1\%$, $p < 0.0001$.

	Mean	SE	SD	2.5%	50%	97.5%	n_{eff}
μ_{spp} :							
α_0	105.04	0.08	4.27	96.99	105.03	113.58	3161
β_0	−5.06	0.03	1.74	−8.62	−5.01	−1.84	3200
σ_{α_i}	28.88	0.05	3.06	23.56	28.64	35.50	3165
σ_{β_i}	6.61	0.04	2.00	3.01	6.50	10.86	3200
μ_{env} :							
τ	−1.20	0.03	1.59	−4.48	−1.19	1.86	3094
π	0.87	0.03	1.75	−2.47	0.84	4.38	3200
μ_{space} :							
x_α	7.85	0.04	2.32	3.08	7.83	12.37	3166
y_α	16.49	0.04	2.35	12.04	16.46	21.22	3200
z_α	1.96	0.02	1.18	−0.36	1.94	4.33	3200
σ_{α_j}	8.55	0.03	1.88	5.29	8.40	12.63	3200
$\mu_{space-time}$:							
x_β	1.42	0.02	1.29	−1.10	1.40	3.89	3200
y_β	1.27	0.03	1.48	−1.57	1.25	4.22	3153
z_β	0.31	0.02	0.93	−1.52	0.29	2.16	3082
σ_{β_j}	2.04	0.02	1.40	0.09	1.85	5.25	3200
ϵ_0	24.51	0.01	0.66	23.30	24.48	25.86	3200
ϵ_β	0.30	0.01	0.73	−1.11	0.31	1.68	3200

Supplementary Table 4: Extended summaries of coefficients from model of the NPN data (for definitions see text) fitted to only data from 2009 and onwards with filtering criteria as described in text (reduced data, conservative criteria). All coefficients are summaries of Bayesian credible intervals taken from 3200 samples across 16 MCMC chains with all $n_{eff} > 3000$ and $\hat{R} = 1$ [1] (see methods for more details). The results are from the same model as presented in the main text, but coefficients are reported for the z -transformed explanatory variables to make the relative importance of coefficients directly comparable [following 1].

	Mean	SE	SD	2.5%	50%	97.5%	n_{eff}
μ_{spp} :							
α_0	105.98	0.06	3.25	99.83	105.89	112.36	3200
β_0	-5.11	0.03	1.56	-8.28	-5.03	-2.16	3068
σ_{α_i}	28.07	0.04	2.23	23.99	27.93	32.98	3200
σ_{β_i}	6.26	0.04	2.05	2.44	6.20	10.38	3194
μ_{env} :							
τ	-1.13	0.03	1.61	-4.34	-1.09	1.96	3200
π	1.25	0.03	1.71	-2.03	1.28	4.71	3200
μ_{space} :							
x_α	8.48	0.04	2.51	3.48	8.47	13.66	3200
y_α	18.23	0.05	2.64	12.95	18.15	23.63	3200
z_α	2.38	0.03	1.50	-0.66	2.41	5.24	3200
σ_{α_j}	8.89	0.03	1.88	5.56	8.76	12.91	3200
$\mu_{space-time}$:							
x_β	3.17	0.02	1.37	0.46	3.20	5.82	3139
y_β	0.71	0.03	1.63	-2.46	0.73	3.96	3200
z_β	-1.03	0.02	1.02	-2.94	-1.05	1.01	3102
σ_{β_j}	2.56	0.03	1.53	0.14	2.50	5.74	3200
ϵ_0	25.35	0.01	0.65	24.10	25.35	26.63	3200
ϵ_β	-0.10	0.01	0.74	-1.59	-0.09	1.34	3099

Supplementary Table 5: Extended summaries of coefficients from the model of the NPN data (for definitions see text) fitted to only data from 2009 and onwards (reduced data, liberal criteria). All coefficients are summaries of Bayesian credible intervals taken from 3200 samples across 16 MCMC chains with all $n_{eff} > 3000$ and $\hat{R} = 1$ [1] (see Methods for more details).

	Mean	SE	SD	2.5%	50%	97.5%	n_{eff}
μ_{spp} :							
α_0	106.94	0.07	4.19	99.04	106.88	115.48	3200
β_0	-7.83	0.04	2.41	-12.58	-7.79	-3.28	3200
σ_{α_i}	29.31	0.05	3.06	23.91	29.11	36.21	3152
σ_{β_i}	9.85	0.05	2.87	4.47	9.78	15.59	3040
μ_{env} :							
τ	-1.94	0.03	1.57	-4.97	-1.95	1.08	3200
π	1.41	0.03	1.56	-1.51	1.37	4.46	3200
μ_{space} :							
x_α	8.57	0.04	2.20	4.18	8.61	12.82	3200
y_α	16.50	0.04	2.39	11.85	16.47	21.16	3063
z_α	1.70	0.02	1.12	-0.47	1.70	3.86	3200
σ_{α_j}	8.90	0.04	1.91	5.55	8.74	13.06	2662
μ_{space} :							
x_β	-0.24	0.02	1.36	-2.80	-0.27	2.53	3009
y_β	-0.35	0.03	1.57	-3.28	-0.42	2.89	3100
z_β	0.78	0.02	1.12	-1.40	0.80	2.94	3200
σ_{β_j}	2.37	0.03	1.64	0.12	2.10	6.13	3133
ϵ_0	23.69	0.01	0.63	22.47	23.67	25.02	3150
ϵ_β	3.56	0.01	0.53	2.39	3.59	4.48	3145

Supplementary Table 6: Extended summaries of coefficients from model of the NPN data (for definitions see text) presented in main body of text (entire dataset, conservative criteria). All coefficients are summaries of Bayesian credible intervals taken from 3200 samples across 16 MCMC chains with all $n_{eff} > 3000$ and $\hat{R} = 1$ [1] (methods for more details).

	Mean	SE	SD	2.5%	50%	97.5%	n_{eff}
μ_{spp} :							
α_0	107.79	0.06	3.22	101.56	107.75	114.21	3200
β_0	-7.35	0.04	2.30	-11.96	-7.29	-2.96	3200
σ_{α_i}	27.93	0.04	2.25	23.76	27.88	32.66	3200
σ_{β_i}	9.36	0.05	2.87	3.94	9.33	15.04	3200
μ_{env} :							
τ	-1.93	0.03	1.56	-5.11	-1.91	1.11	2843
π	1.65	0.03	1.58	-1.32	1.64	4.81	3200
μ_{space} :							
x_α	8.64	0.04	2.46	3.69	8.69	13.54	3058
y_α	17.92	0.05	2.60	13.01	17.89	23.24	3200
z_α	2.35	0.03	1.44	-0.42	2.32	5.28	3200
σ_{α_j}	9.03	0.03	1.90	5.73	8.91	13.15	3200
$\mu_{space-time}$:							
x_β	1.70	0.03	1.68	-1.59	1.66	4.99	2926
y_β	-0.55	0.03	1.97	-4.14	-0.65	3.52	3200
z_β	-0.98	0.02	1.27	-3.51	-0.97	1.42	3200
σ_{β_j}	4.20	0.03	1.79	0.84	4.16	7.93	3010
ϵ_0	24.61	0.01	0.61	23.43	24.60	25.84	3200
ϵ_β	3.49	0.01	0.53	2.38	3.53	4.45	3200

Supplementary Table 7: Summaries of coefficients from the model of the NPN data (for definitions see text) when fitted to all data (entire dataset, liberal criteria). All coefficients are summaries of Bayesian credible intervals taken from 3200 samples across 16 MCMC chains with all $n_{eff} > 3000$ and $\hat{R} = 1$ [1] (see methods for more details).

	Mean	SE	SD	2.5%	50%	97.5%	n_{eff}
α_0	183.32	0.05	2.56	178.26	183.33	188.32	2700
β_0	-2.48	0.00	0.28	-3.01	-2.49	-1.93	3200
γ	-1.00	0.00	0.14	-1.27	-1.00	-0.72	3127
σ_{α_i}	20.84	0.03	1.86	17.60	20.74	24.72	3200
σ_{β_i}	1.79	0.00	0.25	1.35	1.78	2.33	3200
ϵ_0	11.32	0.00	0.10	11.14	11.32	11.52	3200
ϵ_β	0.22	0.00	0.10	0.03	0.23	0.41	2968

Supplementary Table 8: Model coefficients from the hierarchical model of the Rocky Mountain data (for definitions see text). All coefficients are summaries of Bayesian credible intervals taken from 1600 samples across 16 MCMC chains with all $N_{eff} > 2700$ and $\hat{R} = 1$ [1]; see text for more details.

⁶ Bibliography

- ⁷ [1] A. Gelman, J. B. Carlin, H. S. Stern, & D. B. Rubin. Bayesian Data Analysis. 3rd edition.
⁸ Taylor & Francis, 2014.