

Anne Chao and Lou Jost. 2012. Coverage-based rarefaction and extrapolation: standardizing samples by completeness rather than size. *Ecology* 93:2533–2547. <http://dx.doi.org/10.1890/11-1952.1>

APPENDIX F. Beetle species frequency data (Janzen 1973a, b) and computational details for two examples

Table F1: Beetle species frequency counts in two sites (Janzen 1973a, b)
Osa second-growth site (140 species, $n = 976$);
Osa old-growth site (112 species, $n = 237$).

Osa second-growth site						Osa old-growth site	
i	f_i	i	f_i	i	f_i	i	f_i
1	70	11	3	57	2	1	84
2	17	12	2	60	1	2	10
3	4	14	2	64	1	3	4
4	5	17	1	71	1	4	3
5	5	19	2	77	1	5	5
6	5	20	3			6	1
7	5	21	1			7	2
8	3	24	1			8	1
9	1	26	1			14	1
10	2	40	1			42	1

Table F2: Size- and coverage-based rarefied richness (with s.e.), extrapolated richness (with s.e.) and species richness ratio (with s.e.) for Janzen’s data in Table F1. Reference sample (denoted by black dot ●): old-growth site ($S_{obs} = 112$ species, $n = 237$); second-growth site ($S_{obs} = 140$ species, $n = 976$).

Columns 2 and 6 give the richness $\hat{S}_m$ ($m < n$) for the rarefied sample of size m , and $\hat{S}_{n+m^*}$ for the extrapolated sample of size $n+m^*$ in shaded parts; see Eqs. 5 and 7. (In the old-growth site, extrapolated results for $m^* \leq n$ are in yellow-shaded parts, and extrapolated results for $m^* > n$ are in gray-shaded parts.)

Columns 4 and 8 give the coverage estimate $\hat{C}_m$ ($m < n$) for the rarefied sample, and $\hat{C}_{n+m^*}$ for the extrapolated sample (in shaded parts); see Eqs. 4b and 9. (In the old-growth site, extrapolated results for $m^* \leq n$ are in yellow-shaded parts, and extrapolated results for $m^* > n$ are in gray-shaded parts.)

Columns 3 and 7 give s.e. for each richness estimate by a bootstrap method (Appendix C) using 200 replications.

Column 9 gives species richness ratio of column 2 to column 6 and its s.e. using an approximation formula given in the main text.

Fig. 3a in the main text (size-based rarefaction and extrapolation)

Rarefaction: plot richness $\hat{S}_m$ with respect to m , $m < n$;

Extrapolation: plot richness $\hat{S}_{n+m^*}$ (shaded part in this table) with respect to $n+m^*$ for $m^* \leq n$;

Both parts join smoothly at the reference point (n, S_{obs}) .

Fig. 3c in the main text (coverage-based rarefaction and extrapolation)

Rarefaction: plot richness $\hat{S}_m$ with respect to $\hat{C}_m$, $m < n$;

Extrapolation: plot richness $\hat{S}_{n+m^*}$ with respect to $\hat{C}_{n+m^*}$ for $m^* \leq n$;

Both parts join smoothly at the reference point $(\hat{C}_n, S_{obs})$, see Eq. 4a.

Fig. 3b in the main text

The three species richness ratios for $m = 100, 237$, and 500 shown in Fig. 3b are underlined in bold.

Fig. 3d: see Table F3.

Sample size	Richness in old-growth site	Richness s.e. in old-growth site	Coverage in old-growth site	Sample size	Richness in second-growth site	Richness s.e. in second-growth site	Coverage in second-growth site	Species richness ratio (s.e.)
5	4.65	0.06	0.15	5	4.68	0.02	0.15	0.99 (0.01)
10	8.69	0.18	0.24	10	8.69	0.06	0.26	1.00 (0.02)
25	19.22	0.58	0.35	25	18.06	0.24	0.47	1.06 (0.04)
50	34.09	1.29	0.45	50	29.08	0.53	0.63	1.17 (0.05)
75	46.99	2.03	0.51	75	37.41	0.77	0.70	1.26 (0.06)
100	58.62	2.77	0.55	100	44.30	0.98	0.75	1.32 (0.07)
150	79.55	4.21	0.60	150	55.44	1.38	0.80	1.43 (0.08)
200	98.63	5.60	0.63	200	64.43	1.75	0.84	1.53 (0.10)
237 •	112.00 •	6.63 •	0.65 •	237	70.19	2.01	0.85	1.60 (0.10)
300	133.63	8.39	0.67	300	78.83	2.43	0.87	1.70 (0.12)
400	165.26	11.31	0.70	400	90.58	3.07	0.89	1.82 (0.14)
500	193.86	14.45	0.73	500	100.83	3.67	0.90	1.92 (0.16)
600	219.72	17.81	0.75	600	110.11	4.25	0.91	2.00 (0.18)
700	243.11	21.35	0.78	700	118.72	4.80	0.92	2.05 (0.20)
800	264.26	24.99	0.80	800	126.80	5.34	0.92	2.08 (0.22)
900	283.38	28.68	0.82	900	134.45	5.87	0.93	2.11 (0.23)
950	292.24	30.52	0.83	950	138.12	6.13	0.93	2.12 (0.24)
976	296.68	31.48	0.83	976•	140.00 •	6.27 •	0.93 •	2.12 (0.24)
				1000	141.71	6.40	0.93	
				1100	148.62	6.93	0.93	

1300	161.45	8.03	0.94
1500	173.07	9.19	0.94
1700	183.59	10.40	0.95
1900	193.10	11.64	0.95
2000	197.52	12.28	0.96

Table F3: Sample size, species richness (with s.e.) and species richness ratio (with s.e.) by matching coverage for Janzen's data in Table F1. Reference sample (denoted by black dot ●): old-growth site ($S_{obs} = 112$ species, $n = 237$); second-growth site ($S_{obs} = 140$ species, $n = 976$). See Table F2 for more description. Extrapolated values are shown in shaded parts (In the old-growth site, extrapolated results for $m^* \leq n$ are in yellow-shaded parts, and extrapolated results for $m^* > n$ are in gray-shaded parts.) The three species richness ratios for coverage = 0.55, 0.65, and 0.73 shown in Fig. 3d are underlined in bold.

Coverage in old-growth site	Coverage in second-growth site	Sample size in old-growth site	Sample size in second-growth site	Richness in old-growth site	Richness s.e. in old-growth site	Richness in second-growth site	Richness s.e. in second-growth site	Species richness ratio (s.e.)
0.04	0.03	1	1	1.00	0.00	1.00	0.00	1.00 (0.00)
0.11	0.10	3	3	2.88	0.02	2.90	0.01	0.99 (0.01)
0.15	0.15	5	5	4.65	0.06	4.68	0.02	0.99 (0.01)
0.19	0.20	7	7	6.32	0.11	6.36	0.03	0.99 (0.02)
0.25	0.24	11	9	9.46	0.22	7.93	0.06	1.19 (0.03)
0.30	0.30	17	12	13.82	0.38	10.14	0.09	1.36 (0.04)
0.35	0.35	24	15	18.56	0.57	12.18	0.13	1.52 (0.05)
0.40	0.40	35	18	25.47	0.87	14.08	0.17	1.81 (0.07)
0.45	0.44	50	22	34.09	1.29	16.42	0.23	2.08 (0.08)
0.50	0.50	67	28	43.03	1.81	19.61	0.32	2.19 (0.10)
<u>0.55</u>	<u>0.55</u>	<u>100</u>	<u>35</u>	<u>58.62</u>	<u>2.77</u>	<u>22.94</u>	<u>0.42</u>	<u>2.56 (0.13)</u>
0.60	0.60	139	43	75.14	3.94	26.35	0.52	2.85 (0.16)
<u>0.65●</u>	<u>0.65</u>	<u>237●</u>	<u>56</u>	<u>112.00●</u>	<u>6.63●</u>	<u>31.25</u>	<u>0.68</u>	<u>3.58 (0.23)</u>
0.70	0.70	387	75	161.32	10.76	37.41	0.77	4.31 (0.30)
0.72	0.72	487	85	190.30	13.78	40.31	0.98	4.72 (0.36)
<u>0.73</u>	<u>0.73</u>	<u>500</u>	<u>89</u>	<u>193.86</u>	<u>14.45</u>	<u>41.41</u>	<u>1.02</u>	<u>4.68 (0.37)</u>
0.76	0.76	637	110	228.65	18.85	46.76	1.22	4.89 (0.42)
0.78	0.78	687	125	240.20	20.66	50.22	1.35	4.78 (0.43)
0.80	0.80	787	150	261.63	24.40	55.44	1.38	4.72 (0.46)
0.82	0.82	887	175	281.00	28.25	60.14	1.76	4.67 (0.49)
0.83	0.83	976	190	296.68	31.48	62.75	1.88	4.73 (0.52)

0.84	208	65.73	2.01
0.86	258	73.21	2.38
0.88	335	83.17	2.91
0.90	470	97.88	3.79
0.92	766	124.10	5.50
0.93●	976●	140.00 ●	6.27 ●
0.94	1332	163.39	8.42
0.96	2145	203.54	12.91
0.97	2500	216.58	15.01

Table F4: Size- and coverage-based rarefied richness (with s.e.), extrapolated richness (with s.e.) and species richness ratio (with s.e.) for Baker et al.'s (2002) bird species data. Reference sample (denoted by black dot ●): Woodland plot ($S_{obs} = 69$ species, $n = 2482$); heath plot ($S_{obs} = 40$ species, $n = 1295$).

Columns 2 and 6 give the richness $\hat{S}_m$ ($m < n$) for the rarefied sample of size m , and $\hat{S}_{n+m^*}$ for the extrapolated sample of size $n+m^*$ in shaded parts; see Eqs. 5 and 7.

Columns 4 and 8 give the coverage estimate $\hat{C}_m$ ($m < n$) for the rarefied sample, and $\hat{C}_{n+m^*}$ for the extrapolated sample (in shaded parts); see Eqs. 4b and 9.

Columns 3 and 7 give s.e. for each richness estimate by a bootstrap method (Appendix C) using 200 replications.

Column 9 gives species richness ratio of column 2 to column 6 and its s.e. using an approximation formula given in the main text.

Fig. 4a in the main text (size-based rarefaction and extrapolation)

Rarefaction: plot richness $\hat{S}_m$ with respect to m , $m < n$;

Extrapolation: plot richness $\hat{S}_{n+m^*}$ (shaded part in this table) with respect to $n+m^*$ for $m^* \leq n$;

Both parts join smoothly at the reference point (n, S_{obs}).

Fig. 4c in the main text (coverage-based rarefaction and extrapolation)

Rarefaction: plot richness $\hat{S}_m$ with respect to $\hat{C}_m$, $m < n$;

Extrapolation: plot richness $\hat{S}_{n+m^*}$ with respect to $\hat{C}_{n+m^*}$ for $m^* \leq n$;

Both parts join smoothly at the reference point ($\hat{C}_n, S_{obs}$), see Eq. 4a

Fig. 4b in the main text

The three species richness ratios for $m = 200, 500$ and 1295 shown in Fig. 4b are underlined in bold.

Fig. 4d: see Table F5.

Sample size	Richness in woodland plot	Richness s.e. in woodland plot	Coverage in woodland plot	Sample size	Richness in heath plot	Richness s.e. in heath plot	Coverage in heath plot	Species richness ratio
5	4.48	0.02	0.2378	5	3.81	0.05	0.4684	1.17 (0.02)
10	7.96	0.05	0.3907	10	6.14	0.11	0.6099	1.30 (0.02)
25	15.19	0.16	0.6246	25	10.81	0.22	0.7500	1.40 (0.03)
50	22.51	0.29	0.7719	50	15.78	0.34	0.8437	1.43 (0.04)
100	30.97	0.47	0.8728	100	21.47	0.51	0.9170	1.44 (0.04)
150	36.22	0.58	0.9131	150	24.81	0.63	0.9462	1.46 (0.04)
200	39.98	0.67	0.9349	200	27.10	0.72	0.9611	1.48 (0.05)
300	45.20	0.81	0.9581	300	30.18	0.86	0.9755	1.50 (0.05)
400	48.75	0.93	0.9698	400	32.26	0.96	0.9823	1.51 (0.05)
500	51.40	1.04	0.9767	500	33.82	1.05	0.9862	1.52 (0.06)
600	53.50	1.13	0.9811	600	35.06	1.14	0.9888	1.53 (0.06)
700	55.24	1.22	0.9841	700	36.08	1.22	0.9906	1.53 (0.06)
800	56.71	1.31	0.9863	800	36.96	1.30	0.9919	1.53 (0.06)
900	57.99	1.39	0.9880	900	37.72	1.38	0.9929	1.54 (0.07)
1000	59.13	1.47	0.9893	1000	38.40	1.46	0.9937	1.54 (0.07)
1100	60.14	1.54	0.9903	1100	39.00	1.54	0.9943	1.54 (0.07)
1200	61.07	1.62	0.9912	1200	39.54	1.62	0.9949	1.54 (0.08)
1295	61.87	1.69	0.9918	1295●	40.00 ●	1.69 ●	0.9954 ●	1.55(0.08)
1400	62.70	1.76	0.9925	1400	40.46	1.79	0.9958	1.55(0.08)
1600	64.11	1.90	0.9934	1600	41.23	1.98	0.9966	1.55(0.09)
1800	65.37	2.05	0.9940	1800	41.87	2.19	0.9972	1.56(0.10)
2000	66.52	2.19	0.9945	2000	42.40	2.41	0.9978	1.57(0.10)
2200	67.59	2.34	0.9948	2200	42.84	2.63	0.9982	1.58(0.11)
2400	68.60	2.49	0.9951	2400	43.20	2.86	0.9985	1.59(0.12)
2482●	69.00 ●	2.56 ●	0.9952 ●	2482	43.33	2.95	0.9986	1.59(0.12)

Table F5: Sample size, species richness (with s.e.) and species richness ratio (with s.e.) for Baker et al.'s (2002) bird species data. Reference sample (denoted by black dot ●): Woodland plot ($S_{obs} = 69$ species, $n = 2482$); heath plot ($S_{obs} = 40$ species, $n = 1295$). See Table F4 for more description. Extrapolated values are shown in shaded parts. The three species richness ratios for coverage = 0.935, 0.977 and 0.995 shown in Fig. 4d are underlined in bold.

Coverage in woodland plot	Coverage in heath plot	Sample size in woodland plot	Sample Size in in heath plot	Richness in woodland plot	Richness s.e. in woodland plot	Richness in heath plot	Richness s.e. in heath plot	Species richness ratio (s.e.)
0.156	0.152	3	1	2.83	0.01	1.00	0.00	2.83 (0.01)
0.274	0.266	6	2	5.24	0.02	1.85	0.01	2.83 (0.02)
0.365	0.351	9	3	7.33	0.04	2.58	0.02	2.84 (0.03)
0.415	0.417	11	4	8.57	0.05	3.23	0.03	2.65 (0.03)
0.477	0.468	14	5	10.26	0.07	3.81	0.05	2.69 (0.04)
0.512	0.509	16	6	11.29	0.09	4.35	0.05	2.60 (0.04)
0.593	0.591	22	9	14.00	0.13	5.73	0.09	2.44 (0.04)
0.702	0.703	35	18	18.57	0.20	8.88	0.16	2.09 (0.04)
0.752	0.750	45	25	21.31	0.25	10.81	0.22	1.97 (0.05)
0.800	0.801	59	36	24.44	0.31	13.29	0.27	1.84 (0.04)
0.860	0.860	90	57	29.63	0.42	16.82	0.36	1.76 (0.05)
0.920	0.920	163	104	37.31	0.59	21.80	0.51	1.71 (0.05)
<u>0.935</u>	<u>0.935</u>	<u>200</u>	<u>126</u>	<u>39.98</u>	<u>0.67</u>	<u>23.39</u>	<u>0.56</u>	<u>1.71 (0.05)</u>
0.940	0.940	217	136	41.04	0.68	24.02	0.59	1.71 (0.05)
0.960	0.960	313	195	45.73	0.81	26.90	0.71	1.70 (0.05)
<u>0.977</u>	<u>0.977</u>	<u>500</u>	<u>313</u>	<u>51.40</u>	<u>1.04</u>	<u>30.50</u>	<u>0.88</u>	<u>1.69 (0.06)</u>
0.980	0.980	572	359	52.96	1.11	31.48	0.94	1.68 (0.06)
<u>0.995●</u>	<u>0.995●</u>	<u>2482●</u>	<u>1295●</u>	<u>69.00●</u>	<u>2.56●</u>	<u>40.00●</u>	<u>1.69●</u>	<u>1.73 (0.10)</u>
	0.996		1400			40.46	1.79	
	0.997		1700			41.56	2.07	
	0.998		2100			42.63	2.48	
	0.999		2482			43.33	2.95	

LITERATURE CITED

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