

Appendix 2. Species area estimates normalized by the number of unique species occurrence localities incorporated in the range model.

Species	C1			C2			C3			C4			C5			C6		
	raw area	# points	normalized	raw area	# points	normalized	raw area	# points	normalized	raw area	# points	normalized	raw area	# points	normalized	raw area	# points	normalized
<i>Austinella scovellei</i>	--	--	--	--	--	--	--	--	--	--	--	123.49	3	41.16	--	--	--	
<i>Catazyga schuchertana</i>	--	--	--	--	--	--	--	--	--	--	--	5464.39	10	546.44	--	--	--	
<i>Dalmanella meeki</i>	--	--	--	--	--	--	2292.43	6	382.07	9038.20	16	564.89	14800.84	40	370.02	3.14	1	3.14
<i>Dalmanella multisepta</i>	3853.11	8	481.64	3814.99	4	953.75	--	--	--	--	--	--	--	--	--	--	--	
<i>Glyptorthis insculpta</i>	--	--	--	--	--	--	--	--	--	--	--	12521.13	49	255.53	425.14	3	141.71	
<i>Hebertella alveata</i>	--	--	--	--	--	--	--	--	--	--	--	131.71	5	26.34	1388.36	7	198.34	
<i>Hebertella occidentalis</i>	3297.12	6	549.52	12522.72	41	305.43	11520.71	22	523.67	11876.83	15	791.79	15218.16	60	253.64	2469.66	16	154.35
<i>Hebertella subjugata</i>	--	--	--	79.21	2	39.61	--	--	--	--	--	1197.84	4	299.46	3.14	1	3.14	
<i>Hiscobeccus capax</i>	--	--	--	--	--	--	--	--	--	--	--	16474.49	69	238.76	2663.68	15	177.58	
<i>Holtedahlinia sulcata</i>	--	--	--	--	--	--	--	--	--	--	--	12544.30	12	1045.36	61.13	2	30.57	
<i>Lepidocyclus perlamellosum</i>	--	--	--	--	--	--	--	--	--	--	--	3689.96	11	335.45	--	--	--	
<i>Leptaena gibbosa</i>	12.44	3	4.15	--	--	--	--	--	--	--	--	--	--	--	--	--	--	
<i>Leptaena richmondensis</i>	--	--	--	--	--	--	--	--	--	1600.86	4	400.22	5478.57	23	238.20	60.43	3	20.14
<i>Plaesiomys subquadrata</i>	--	--	--	--	--	--	--	--	--	--	--	16629.65	50	332.59	955.43	5	191.09	
<i>Platystrophia acutilirata</i>	--	--	--	--	--	--	--	--	--	--	--	11406.07	41	278.20	1038.32	14	74.17	
<i>Platystrophia annieana</i>	--	--	--	--	--	--	--	--	--	--	--	6662.74	11	605.70	--	--	--	
<i>Platystrophia auburnensis</i>	--	--	--	--	--	--	11967.87	16	747.99	--	--	--	--	--	--	--	--	
<i>Platystrophia clarksvillensis</i>	--	--	--	--	--	--	--	--	--	9.22	2	4.61	10048.79	27	372.18	3.14	1	3.14
<i>Platystrophia corryvillensis</i>	--	--	--	--	--	--	3.14	1	3.14	--	--	--	--	--	--	--	--	
<i>Platystrophia crassa</i>	--	--	--	15.55	6	2.59	3.14	1	3.14	--	--	--	--	--	--	--	--	
<i>Platystrophia cummingsi</i>	--	--	--	--	--	--	--	--	--	--	--	155.75	5	31.15	--	--	--	
<i>Platystrophia cypha</i>	--	--	--	4706.10	7	672.30	498.84	5	99.77	5037.88	7	719.70	2672.83	15	178.19	3.14	1	3.14
<i>Platystrophia elkhornensis</i>	--	--	--	--	--	--	--	--	--	--	--	63.88	2	31.94	2580.10	7	368.59	
<i>Platystrophia forestei</i>	--	--	--	--	--	--	--	--	--	--	--	73.98	2	36.99	--	--	--	
<i>Platystrophia hopensis</i>	3.14	1	3.14	6242.97	12	520.25	3.14	1	3.14	--	--	--	--	--	--	--	--	
<i>Platystrophia laticosta</i>	--	--	--	9103.77	29	313.92	10179.77	19	535.78	3.14	1	3.14	1897.06	7	271.01	--	--	--
<i>Platystrophia moritura</i>	--	--	--	--	--	--	--	--	--	--	--	36.93	2	18.46	2985.89	13	229.68	
<i>Platystrophia morrowensis</i>	--	--	--	--	--	--	4.39	2	2.20	--	--	--	--	--	--	--	--	
<i>Platystrophia ponderosa</i>	3.14	1	3.14	15325.98	60	255.43	14391.90	65	221.41	15561.65	22	707.35	--	--	--	--	--	
<i>Platystrophia sublaticosta</i>	--	--	--	51.18	4	12.80	3.14	1	3.14	--	--	--	--	--	--	--	--	
<i>Plectorthis aequivalis</i>	--	--	--	69.16	2	34.58	3.14	1	3.14	--	--	--	--	--	--	--	--	
<i>Plectorthis fissicosta</i>	--	--	--	515.43	6	85.91	--	--	--	--	--	--	--	--	--	--	--	
<i>Plectorthis neglecta</i>	--	--	--	17.34	2	8.67	--	--	--	--	--	--	--	--	--	--	--	
<i>Plectorthis plicatella</i>	--	--	--	353.46	6	58.91	--	--	--	--	--	--	--	--	--	--	--	
<i>Rafinesquina alternata</i>	3941.69	1	3941.69	9814.65	20	490.73	12509.84	42	297.85	8590.29	24	357.93	16159.25	37	436.74	1906.47	4	476.62
<i>Retrorsirostra carleyi</i>	--	--	--	--	--	--	--	--	--	2703.02	11	245.73	2092.48	12	174.37	--	--	--
<i>Rhynchotrema denatum</i>	--	--	--	--	--	--	--	--	--	169.90	4	42.48	12956.01	24	539.83	933.58	12	77.80
<i>Sowerbyella rugosa</i>	3625.58	7	517.94	--	--	--	--	--	--	--	--	--	--	--	--	--	--	
<i>Strophomena concordensis</i>	--	--	--	--	--	--	--	--	--	20.21	2	10.10	254.59	3	84.86	--	--	--
<i>Strophomena maysvillensis</i>	3.14	1	3.14	30.42	1	30.42	--	--	--	--	--	--	--	--	--	--	--	
<i>Strophomena nutans</i>	--	--	--	--	--	--	--	--	--	--	--	2736.76	10	273.68	--	--	--	
<i>Strophomena planoconvexa</i>	3.14	1	3.14	6078.76	10	607.88	--	--	--	--	--	--	--	--	--	--	--	
<i>Strophomena planumbona</i>	--	--	--	--	--	--	--	--	--	3.14	1	3.14	13873.07	24	578.04	3.14	1	3.14
<i>Strophomena sulcata</i>	--	--	--	--	--	--	--	--	--	--	--	2452.97	7	350.42	47.83	2	23.91	
<i>Strophomena vetusta</i>	--	--	--	--	--	--	--	--	--	--	--	6727.71	8	840.96	631.86	3	210.62	
<i>Tetraphalerella neglecta</i>	--	--	--	--	--	--	--	--	--	--	--	5384.29	10	538.43	--	--	--	
<i>Thaerodonta clarksvillensis</i>	--	--	--	--	--	--	--	--	--	--	--	7281.95	25	291.28	22.59	2	11.29	
<i>Zygospira cincinnatiensis</i>	55.37	2	27.69	112.85	5	22.57	--	--	--	--	--	--	--	--	--	--	--	
<i>Zygospira modesta</i>	4475.88	10	447.59	11319.79	19	595.78	10396.34	18	577.57	12730.94	29	439.00	14796.82	35	422.77	1240.48	7	177.21

Numer of unique localities/sequence

16

107

88.00

82

189

41

Percent of max localities per sequence

8.47

56.61

46.56

43.39

100.00

21.69

**Appendix 3. Statistical comparison of geographic range size in taxonomic groups across all sequences calculated using the species area method normalized by the number of species occurrence points used to construct range models.**

**1. Geographic range of Maysvillian restricted versus carryover taxa**

	Restricted	Carryover
N	27	34
Mean	155.0	479.0
Std. Dev.	276.0	649.0
SE Mean	53.0	111.0
T-value		-2.62
p-value		0.006

**2. Maysvillian versus Richmondian range size of carryover taxa**

	Maysvillian	Richmondian
N	17	17
Mean	601.0	356.0
Std. Dev.	880.0	251.0
SE Mean	213.0	61.0
T-value		1.10
p-value		0.857

**3. Geographic range size of invader taxa versus carryover taxa in the Richmondian**

	<i>Strophomena</i> native		<i>Strophomena</i> invasive	
	Carryover	Invader	Carryover	Invader
N	17	22	17	31
Mean	356.0	269.0	356.0	240.0
Std. Dev.	251.0	241.0	251.0	231.0
SE Mean	61.0	51.0	61.0	41.0
T-value		-1.10		-1.57
p-value		0.140		0.063

**4. Geographic ranges of Maysvillian carryover taxa versus native descendant species**

	<i>Strophomena</i> native		<i>Strophomena</i> invasive	
	Carryover	Descendants	Carryover	Descendants
N	17	24	17	15
Mean	356.0	170.0	356.0	170.0
Std. Dev.	251.0	186.0	251.0	185.0
SE Mean	61.0	38.0	61.0	48.0
T-value		-2.59		-2.41
p-value		0.008		0.011

**Appendix 4. Statistical comparison of geographic range size in taxonomic groups by sequence calculated using the species area method normalized by the number of species occurrence points used to construct range models.**

**1. Sequence C1: Edenian**

Source	DF	SS	MS	F-value	p-value
Factor	1	4709729	4709729	4.56	0.065
Error	8	8254920	1031865		
Total	9	12964649			

**2. Sequence C2: early Maysvillian**

**Species: Area**

Source	DF	SS	MS	F-value	p-value
Factor	1	231887	231887	2.99	0.103
Error	16	1242757	77672		
Total	17	77672	1474644		

**3. Sequence C3: late Maysvillian**

**Species: Area**

Source	DF	SS	MS	F-value	p-value
Factor	1	250378	250378	448	0.056
Error	12	670054	55838		
Total	13	920432			

**4. Sequence C4: early Richmondian**

***Strophomena* native**

***Strophomena* invasive**

Source	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	577131	288566	5.61	0.023	2	514539	258769	4.51	0.04
Error	10	514795	51480			10	574388	57439		
Total	12	1091927				12	1091927			

**5. Sequence C5: middle Richmondian**

***Strophomena* native**

***Strophomena* invasive**

Source	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	75367	37683	0.65	0.528	2	340589	170295	3.5	0.043
Error	29	1675561	57778			29	1410338	48632		
Total	31	1750927				31	1750927			

**6. Sequence C6: late Richmondian**

***Strophomena* native**

***Strophomena* invasive**

Source	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	9439	4720	0.26	0.776	2	269169	13084	0.75	0.486
Error	18	330218	18345			18	313488	17416		
Total	20	339657				20	339657			

**Appendix 6. Statistical comparison of geographic range size in taxonomic groups across all sequences when Richmondian *Strophomena* species are treated as native descendants.**

**1. Geographic range of Maysvillian restricted versus carryover taxa**

	Species: Area		Species: Linear		Genus: Area		Genus: Linear	
	Restricted	Carryover	Restricted	Carryover	Restricted	Carryover	Restricted	Carryover
N	25	18	25	18	4	17	4	17
Mean	12.3	52.8	39.9	80.5	17.8	57.6	37.8	78.9
Std. Dev.	23.1	30.2	67.5	25.3	30.2	27.9	46.5	31.3
SE Mean	4.6	7.1	13.0	6.0	15.0	6.8	23.0	7.6
T-value		-4.77		-2.76		-2.41		-1.68
p-value		<0.001		0.005		0.037		0.096

**2. Maysvillian versus Richmondian range size of carryover taxa**

	Species: Area		Species: Linear		Genus: Area		Genus: Linear	
	Maysvillian	Richmondian	Maysvillian	Richmondian	Maysvillian	Richmondian	Maysvillian	Richmondian
N	18	20	18	20	17	18	17	18
Mean	52.8	40.7	80.5	64.3	57.6	55.7	78.9	76.0
Std. Dev.	30.2	35.1	25.3	37.7	27.9	33.0	31.3	29.1
SE Mean	7.1	7.8	6.0	8.4	6.8	7.8	7.6	6.9
T-value		1.14		1.57		0.18		0.29
p-value		0.130		0.064		0.430		0.389

**3. Geographic range size of invader taxa versus carryover taxa in the Richmondian**

	Species: Area		Species: Linear		Genus: Area		Genus: Linear	
	Carryover	Invader	Carryover	Invader	Carryover	Invader	Carryover	Invader
N	20	22	20	22	18	29.4	18	22
Mean	40.7	29.4	64.3	62.2	55.7	30.2	76.0	62.2
Std. Dev.	35.1	30.2	37.7	25.4	33.0	6.4	29.1	25.4
SE Mean	7.8	6.4	8.4	5.4	7.8	2.6	6.9	5.4
T-value		1.12		0.21		2.61		1.57
p-value		0.136		0.441		0.006		0.063

**4. Geographic ranges of Maysvillian carryover taxa versus native descendant species**

	Species: Area		Species: Linear	
	Carryover	Descendants	Carryover	Descendants
N	20	24	20	24
Mean	40.7	17.0	64.3	42.8
Std. Dev.	35.1	22.8	37.7	31.7
SE Mean	7.8	4.7	8.4	6.5
T-value		2.60		2.03
p-value		0.007		0.025

**Appendix 7. Statistical comparison of geographic range size in taxonomic groups by sequence when Richmondian *Strophomena* species are treated as native descendants.**

**1. Sequence C1: Edenian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	1	2605	260	52.45	0.152	1	4081	4081	1.93	0.209	1	268	268	0.20	0.673	1	460	460	0.16	0.706
Error	9	9553	1061			9	20048	2228			6	8169	1362			6	17592	2932		
Total	10	12158				10	24128				7	8438				7	18052			

**2. Sequence C2: early Maysvillian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	1	9389	9389	71.06	0.001	1	1530	1530	0.30	0.591	1	2597	2597	3.48	0.121	1	718	718	4.66	0.083
Error	16	8804	550			16	81472	5092			5	3726	745			5	770	154		
Total	17	18194				17	83002				6	6323				6	1488			

**3. Sequence C3: late Maysvillian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	1	5705	5705	9.31	0.019	1	17901	17901	22.11	0.001	1	3638	3638	15.21	0.018	1	6765	6765	109.00	<0.001
Error	12	9366	781			12	9717	810			4	957	239			4	248	62		
Total	13	15072				13	27613				5	4595				5	7012			

**4. Sequence C4: early Richmondian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	7955	3978	6.71	0.014	2	12200	6100	7.39	0.011	1	4792	4792	6.50	0.038	1	1412	1412	3.85	0.100
Error	10	5926	593			10	8250	825			7	5159	737			7	2758	394		
Total	12	13881				12	20450				8	9951				8	4170			

**5. Sequence C5: middle Richmondian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	5186	2593	2.59	0.092	2	2635	1318	1.86	0.174	1	6220	6220	9.36	0.007	1	1625	1625	4.73	0.045
Error	29	29018	1001			29	20579	710			16	10636	665			16	5499	344		
Total	31	34203				31	23214				17	16856				17	7123			

**6. Sequence C6: late Richmondian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	70	35	0.20	0.820	2	520	260	0.42	0.664	1	682	682	2.98	0.112	1	45	45	0.09	0.771
Error	18	3121	173			18	11165	620			11	2514	229			11	5613	510		
Total	20	3191				20	11685				12	3196				12	5658			

**Appendix 8. Statistical comparison of geographic range size in taxonomic groups across all sequences when Richmondian *Strophomena* species are treated as invasive.**

**1. Geographic range of Maysvillian restricted versus carryover taxa**

	Species: Area		Species: Linear		Genus: Area		Genus: Linear	
	Restricted	Carryover	Restricted	Carryover	Restricted	Carryover	Restricted	Carryover
N	25	18	25	18	6	15	6	15
Mean	12.3	52.8	39.9	80.5	18.5	62.6	37.2	84.6
Std. Dev.	23.1	30.2	67.5	25.3	26.6	24.5	42.3	25.3
SE Mean	4.6	7.1	13.0	6.0	11.0	6.3	17.0	6.5
T-value	-4.77		-2.76		-3.50		-2.57	
p-value	<0.001		0.005		0.004		0.021	

**2. Maysvillian versus Richmondian range size of carryover taxa**

	Species: Area		Species: Linear		Genus: Area		Genus: Linear	
	Maysvillian	Richmondian	Maysvillian	Richmondian	Maysvillian	Richmondian	Maysvillian	Richmondian
N	18	20	18	20	15	15	15	15
Mean	52.8	40.7	80.5	64.3	62.6	60.2	84.6	79.9
Std. Dev.	30.2	35.1	25.3	37.7	24.5	29.7	25.3	28.2
SE Mean	7.1	7.8	6.0	8.4	6.3	7.7	6.5	7.3
T-value	1.14		1.57		0.24		0.48	
p-value	0.130		0.064		0.408		0.316	

**3. Geographic range size of invader taxa versus carryover taxa in the Richmondian**

	Species: Area		Species: Linear		Genus: Area		Genus: Linear	
	Carryover	Invader	Carryover	Invader	Carryover	Invader	Carryover	Invader
N	20	32	20	32	15	25	15	25
Mean	40.7	24.9	64.3	55.9	60.2	29.8	79.9	61.5
Std. Dev.	35.1	28.9	37.7	29.3	29.7	31.3	28.2	25.4
SE Mean	7.8	5.1	8.4	5.2	7.7	6.3	7.3	5.1
T-value	1.77		0.86		-3.07		-2.07	
p-value	0.041		0.200		0.002		0.025	

**4. Geographic ranges of Maysvillian carryover taxa versus native descendant species**

	Species: Area		Species: Linear	
	Carryover	Descendants	Carryover	Descendants
N	20	14	20	14
Mean	40.7	18.3	64.3	43.3
Std. Dev.	35.1	22.4	37.7	31.5
SE Mean	7.8	6.0	8.4	8.4
T-value	2.11		1.76	
p-value	0.021		0.440	

**Appendix 9. Statistical comparison of geographic range size in taxonomic groups by sequence when Richmondian *Strophomena* species are treated as invasive.**

**1. Sequence C1: Edenian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	1	2605	260	52.45	0.152	1	4081	4081	1.93	0.209	1	2017	217	1.89	0.219	1	4097	4097	1.76	0.233
Error	9	9553	1061			9	20048	2228			6	642	170			6	13955	2326		
Total	10	12158				10	24128				7	8438				7	18052			

**2. Sequence C2: early Maysvillian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	1	9389	9389	71.06	0.001	1	1530	1530	0.30	0.591	1	2737	2737	3.82	0.108	1	672	672	4.11	0.098
Error	16	8804	550			16	81472	5092			5	3586	717			5	817	163		
Total	17	18194				17	83002				6	6323				6	1488			

**3. Sequence C3: late Maysvillian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	1	5705	5705	9.31	0.019	1	17901	17901	22.11	0.001	1	3638	3638	15.21	0.018	1	6765	6765	109.00	<0.001
Error	12	9366	781			12	9717	810			4	957	239			4	248	62		
Total	13	15072				13	27613				5	4595				5	7012			

**4. Sequence C4: early Richmondian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	7861	3931	6.53	0.015	2	8543	4272	3.59	0.067	1	8614	8614	45.09	<0.001	1	3584	3584	42.79	<0.001
Error	10	602	62			10	11907	1191			7	1337	191			7	586	84		
Total	12	13881				12	20450				8	9951				8	4170			

**5. Sequence C5: middle Richmondian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	4348	2174	2.11	0.139	2	354	177	2.61	0.091	1	4697	4697	6.18	0.024	1	1384	1384	3.86	0.067
Error	29	29855	129			29	19675	678			16	1216	760			16	5740	359		
Total	31	34203				31	23214				17	16856				17	7123			

**6. Sequence C6: late Richmondian**

Source	Species: Area					Species Linear					Genus: Area					Genus Linear				
	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value	DF	SS	MS	F-value	p-value
Factor	2	517	259	1.74	0.204	2	378	189	0.3	0.744	1	845	845	3.95	0.072	1	132	132	0.26	0.619
Error	18	2674	149			18	11307	628			11	2350	214			11	5527	502		
Total	20	3191				20	11685				12	3196				12	5658			