

Supporting Tables

Table S1: Migration model results for *Myotis lucifugus*

Shown are results from a Migrate-n analysis of the *Myotis lucifugus* data collected by Carstens & Dewey (2010). Model selection implemented in the program (Beerli and Palczewski 2010) enables evaluation of island models that restrict gene flow among one or more of the described subspecies. The model with the strongest support (P = 1.0) allows gene flow among three of the four subspecies (*M. l. lucifugus*, *M. l. alacensis*, *M. l. relictus*) but finds that none of these exchange migrants with the fourth subspecies (*M. l. carissima*).

Model	lnL (Bezier)	Difference	LBF (thermo)	Prob.
Mlc no mig	-10061.4	0	0	1.000
Mlr no mig	-10193	-131.6	-263.2	0.000
Mla, Mll no mig	-10300.67	-239.27	-478.54	0.000
Mll no mig	-10290.65	-229.25	-458.5	0.000
Mla, Mlr mig	-10322.52	-261.12	-522.24	0.000
Mlc, Mll mig	-10515.44	-454.04	-908.08	0.000
Mla, Mlc no mig	-10580.5	-519.1	-1038.2	0.000
Mlr, Mll mig	-10634.8	-573.4	-1146.8	0.000
Mlc, Mlr mig	-10632.9	-571.5	-1143	0.000
Mla no mig	-10432.84	-371.44	-742.88	0.000
no gene flow	-10874.01	-812.61	-1625.22	0.000

Citations

Beerli P, Palczewski M (2010) Unified framework to evaluate panmixia and migration direction among multiple sampling locations. *Genetics* 185(1):313-26

Carstens BC, Dewey TA (2010) Species delimitation using a combined coalescent and information-theoretic approach: an example from North American *Myotis* Bats. *Syst Biol* 59(4):400-414

Table S2: Specifications for empirical datasets

Specifications for the 19 empirical datasets used in this study. **loc** = number of loci, **bp/loc** = average number of base pairs per locus, **SNPs/loc** = average number of SNPs per locus, **N** = number of tips per tree, **ST** = whether species tree analysis was used, **n-isl** = whether an n-island model was used, **IM** = whether an IM model was used, **delim** = whether species delimitation was investigated, **inference** = the type of model inferred.

Study	loc	bp/loc	SNPs/loc	N	focal taxon	ST	n-isl	IM	delim	inference
Barker et al. (2012)	5	437	19	173	Anuraa	no	yes	yes	no	IM
Camargo et al. (2012)	4	577	51	79	Squamata	yes	no	yes	yes	IM
Carstens et al. (2013)	5	849	24	145	Angiosperm	yes	no	yes	no	expansion
Dhami et al. (2012)	6	323	25	93	Aves	no	no	yes	no	IM
Duvernell et al. (2013)	6	973	113	219	Actinopterygii	yes	no	no	no	isolation only
Fernández-Mazuecos & Vargas (2013)	3	1331	52	119	Angiosperm	yes	no	yes	no	IM
Giaria et al. (2014)	15	622	23	53	Mammalia	yes	no	no	yes	isolation only
Halas & Simons (2014)	8	545	75	200	Actinopterygii	yes	no	no	yes	isolation only
Hambäck et al. (2013)	3	876	127	62	Insecta	yes	no	no	yes	isolation only
Harrington & Near (2012)	4	943	105	120	Actinopterygii	yes	no	yes	yes	isolation only
Hung et al. (2012)	13	567	25	36	Aves	yes	no	yes	yes	isolation only
Jackson & Austin (2012)	8	556	56	151	Squamata	yes	no	yes	no	IM
Leache et al. (2013)	10	704	17	47	Squamata	yes	no	yes	yes	IM
Muir et al. (2012)	6	864	91	111	Angiosperm	no	no	yes	no	IM
Reilly et al. (2013)	14	445	9	51	Caudata	yes	no	no	no	isolation only
Satler et al. (2013)	6	863	141	57	Arachnida	yes	no	no	yes	isolation only
Talavera et al. (2013)	7	851	67	42	Insecta	yes	no	no	yes	isolation only
Werneck et al. (2012)	13	716	174	261	Squamata	yes	yes	yes	no	IM
Wielstra et al. (2013)	4	570	33	335	Caudata	yes	no	no	no	isolation only

Table S3: Parameter estimates from PHRAPL analysis of simulated datasets

Panels A and B give additional details (beyond those in Fig. S9) about parameter estimates for migration and coalescence time, respectively, when 81 models are analyzed. For each of the eight treatments, four values are given for each parameter: raw value = the estimated parameter value calculated by model averaging values of that parameter across all models containing that parameter; weight = a weight applied to each parameter calculated summing AIC weights across all models that contain the given parameter; estimate = the weighted parameter estimate calculated by taking the product of the raw value and weight; true value = the parameter value of the underlying simulated model.

A

treatment	value	$M_{I1} 1 \rightarrow 2$	$M_{I1} 1 \rightarrow 3$	$M_{I1} 2 \rightarrow 1$	$M_{I1} 2 \rightarrow 3$	$M_{I1} 3 \rightarrow 1$	$M_{I1} 3 \rightarrow 2$	$M_{I2} 1 \rightarrow 2$	$M_{I2} 2 \rightarrow 1$
I_shallow	raw value	0.2542	0.1518	0.2542	0.1495	0.1520	0.1496	0.3522	0.3522
	weight	0.4824	0.0359	0.4824	0.0400	0.0367	0.0408	0.7451	0.7451
	estimate	0.1226	0.0055	0.1226	0.0060	0.0056	0.0061	0.2625	0.2625
	true value	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
I_medium	raw value	0.1256	0.1074	0.1256	0.1262	0.1074	0.1262	0.1737	0.1737
	weight	0.0822	0.0045	0.0822	0.0014	0.0045	0.0014	0.3371	0.3371
	estimate	0.0103	0.0005	0.0103	0.0002	0.0005	0.0002	0.0586	0.0586
	true value	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
I_deep	raw value	0.1128	0.1034	0.1128	0.1131	0.1034	0.1132	0.1166	0.1166
	weight	0.0162	0.0003	0.0162	0.0002	0.0003	0.0002	0.1030	0.1030
	estimate	0.0018	0.0000	0.0018	0.0000	0.0000	0.0000	0.0120	0.0120
	true value	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
IM_shallow	raw value	0.3768	0.1478	0.3768	0.4141	0.1477	0.4168	0.5953	0.5953
	weight	0.5929	0.1387	0.5929	0.9514	0.1585	0.9711	0.7908	0.7908
	estimate	0.2234	0.0205	0.2234	0.3940	0.0234	0.4047	0.4707	0.4707
	true value	0.2500	0.1000	0.2500	0.5000	0.1000	0.5000	0.0500	0.0500
IM_medium	raw value	0.3129	0.1399	0.3129	0.4346	0.1381	0.4450	1.7713	1.7713
	weight	0.8815	0.5052	0.8815	0.9207	0.5279	0.9435	0.6002	0.6002
	estimate	0.2758	0.0707	0.2758	0.4001	0.0729	0.4198	1.0632	1.0632

	true value	0.2500	0.1000	0.2500	0.5000	0.1000	0.5000	0.0500	0.0500
IM_deep	raw value	0.2628	0.1498	0.2628	0.4678	0.1517	0.4862	2.1592	2.1592
	weight	0.9194	0.6931	0.9194	0.9049	0.7113	0.9231	0.6079	0.6079
	estimate	0.2417	0.1038	0.2417	0.4233	0.1079	0.4489	1.3125	1.3125
	true value	0.2500	0.1000	0.2500	0.5000	0.1000	0.5000	0.0500	0.0500
M	raw value	0.2998	0.1410	0.2998	0.4744	0.1418	0.4746	2.1237	2.1237
	weight	0.8872	0.5682	0.8872	0.9524	0.5685	0.9528	0.5023	0.5023
	estimate	0.2660	0.0801	0.2660	0.4518	0.0806	0.4521	1.0668	1.0668
	true value	0.2500	0.1000	0.2500	0.5000	0.1000	0.5000	0.0000	0.0000
mixed	raw value	0.1105	0.3751	0.1105	0.3932	0.5771	1.3704	1.4152	1.4152
	weight	0.0000	0.0217	0.0000	0.0216	1.0000	0.9999	0.9807	0.9807
	estimate	0.0000	0.0081	0.0000	0.0085	0.5771	1.3703	1.3880	1.3880
	true value	0.0000	0.0000	0.0000	0.0000	0.5000	1.0000	0.1000	0.1000

B

treatment	value	t_1 1-2	t_1 1-3	t_1 2-3	t_1 1-2-3	t_2 1-2
I_shallow	raw value	0.4818	1.3850	1.4573	1.3555	3.3038
	weight	0.9489	0.0141	0.0292	0.0077	0.8565
	estimate	0.4572	0.0195	0.0426	0.0105	2.8297
	true value	0.5000	0.0000	0.0000	0.0000	1.0000
I_medium	raw value	1.8841	9.2907	9.4525	9.1107	6.8131
	weight	0.9523	0.0178	0.0132	0.0166	0.7582
	estimate	1.7943	0.1657	0.1247	0.1508	5.1658
	true value	1.5000	0.0000	0.0000	0.0000	3.0000
I_deep	raw value	4.3291	9.8565	9.8486	9.9333	11.9858
	weight	0.9917	0.0026	0.0026	0.0031	0.9171

	estimate	4.2933	0.0252	0.0259	0.0305	10.9916
	true value	4.0000	0.0000	0.0000	0.0000	8.0000
IM_shallow	raw value	1.0884	3.8959	4.4827	4.4478	6.4873
	weight	0.8826	0.0414	0.0466	0.0270	0.7527
	estimate	0.9606	0.1613	0.2087	0.1200	4.8832
	true value	0.5000	0.0000	0.0000	0.0000	1.0000
IM_medium	raw value	2.7486	4.2114	3.3912	3.9239	8.2513
	weight	0.6686	0.0934	0.1742	0.0391	0.7185
	estimate	1.8378	0.3934	0.5907	0.1533	5.9285
	true value	1.5000	0.0000	0.0000	0.0000	3.0000
IM_deep	raw value	2.8498	3.7654	1.8187	3.4040	8.0464
	weight	0.6300	0.0414	0.2465	0.0589	0.8399
	estimate	1.7953	0.1557	0.4483	0.2004	6.7582
	true value	4.0000	0.0000	0.0000	0.0000	8.0000
M	raw value	2.8936	3.5286	1.9112	3.7689	8.3953
	weight	0.5050	0.0445	0.3318	0.0761	0.8039
	estimate	1.4612	0.1569	0.6342	0.2869	6.7493
	true value	0.0000	0.0000	0.0000	0.0000	0.0000
mixed	raw value	1.3640	5.2170	2.3846	4.8791	8.2352
	weight	0.9807	0.0017	0.0174	0.0001	0.0200
	estimate	1.3378	0.0090	0.0415	0.0005	0.1647
	true value	1.5000	0.0000	0.0000	0.0000	0.0000