

Pérez Méndez, T., Naves, J., Vázquez, J. F., Fernández-Gil, A., Seijas, J., Albornoz, J., Revilla, E.m Delibes, M. and Domínguez, A. 2014. Estimating the population size of the endangered Cantabrian brown bear through genetic sampling. – Wildlife Biology doi: 10.2981/wlb.00069

Appendix 1

Table A1. Whole population size estimates.

Models / estimators	Estimates (n)	SE	CI95% lower	CI95% upper	CI95% width	Deviance	DF	AIC
Mh Chao	220	29.1	177	294	117	5.98	6	53.6
Mh Poisson2	164	8.7	149	184	35	55.47	10	95.1
Mh Darroch	224	21.6	188	274	86	13.25	10	52.9
Mh Gamma3.5	419	84.5	291	634	343	9.75	10	49.4
CAPWIRE TIRM	223	-	185	270	85			
Number of individual genotypes (n_{minimum}) = 130								

Table A2. Western subpopulation size estimates.

Models / estimators	Estimates (n)	SE	CI95% lower	CI95% upper	CI95% width	Deviance	DF	AIC
Mh Chao	197	26.3	160	265	105	6.33	7	49.25
Mh Poisson2	154	9.2	139	175	36	39.43	10	76.35
Mh Darroch	209	21.8	173	260	87	10.81	10	47.73
Mh Gamma3.5	380	81.1	258	588	330	10.18	10	47.11
CAPWIRE TIRM	204		172	255	102			
Number of individual genotypes (n_{minimum}) = 117								

Table A3. Eastern subpopulation size estimates.

Models / estimators	Estimates (n)	SE	CI95% lower	CI95% upper	CI95% width	Deviance	DF	AIC
Mh Chao	20	12.8	12	>71	>59	1.42	4	23.69
Mh Poisson2	14	2.7	12	22	10	4.46	5	24.73
Mh Darroch	18	7.4	12	47	35	4.12	5	24.39
Mh Gamma3.5	28	23.9	12	>100	>88	4.03	5	24.31
CAPWIRE TIRM	18		12	27	15			
Number of individual genotypes (n_{minimum}) = 13								

Table A4. Population size estimates (excluding the individual captured 13 times).

Models / estimators	Estimates (n)	SE	CI95% lower	CI95% upper	CI95% width	Deviance	DF	AIC
Mh Chao	218	29.1	176	293	117	0.67	2	46.29
Mh Poisson2	182	12.7	161	211	50	11.79	6	49.41
Mh Darroch	265	34.9	209	349	140	1.84	6	39.46
Mh Gamma3.5	455	109.8	295	749	454	5.02	6	42.64
CAPWIRE TIRM	223		188	275	87			
Number of individual genotypes (n_{minimum}) = 129								