

Appendix 3. Assessment of spatial autocorrelation in BRT model residuals.

For each species, we tested for spatial autocorrelation by calculating Moran's I statistics on Pearson residuals. For BRT models, we calculated the residuals using the mean of 20 segment-level predictions, and corrected for the bootstrap variance. We also calculated Pearson residuals for a null model including only the mean effect. The "Null Ratio", which measures the reduction in spatial autocorrelation resulting from conditioning on model covariates, is calculated as the Moran's I statistic for the null model divided by that for the BRT models. In both cases, Moran's I was calculated over two distance bands, corresponding to the range of distances between adjacent segments (20-50 km) and between adjacent transects (30-120 km).

Species	Scale	Moran I Statistic	p-Value	Null Ratio
ABDU	segment	0.043	0.005	12.233
ABDU	transect	0.022	0.001	22.634
AGWT	segment	0.022	0.091	23.072
AGWT	transect	-0.009	0.887	43.500
AMWI	segment	0.046	0.003	16.038
AMWI	transect	0.018	0.003	35.358
BUFF	segment	0.029	0.040	19.101
BUFF	transect	0.006	0.154	65.070
BWTE	segment	0.055	0.001	13.793
BWTE	transect	0.037	< 0.001	18.998
CANV	segment	0.046	0.003	11.356
CANV	transect	0.015	0.010	26.021
GADW	segment	0.096	< 0.001	7.299
GADW	transect	0.042	< 0.001	15.183
GGOL	segment	-0.018	0.853	20.608
GGOL	transect	< 0.001	0.468	2816.706
GMER	segment	-0.018	0.845	28.130
GMER	transect	-0.002	0.610	177.650
GSCA	segment	0.039	0.011	13.840
GSCA	transect	0.019	0.002	23.881
GSCO	segment	0.016	0.171	54.310
GSCO	transect	0.034	< 0.001	25.290
MALL	segment	0.066	< 0.001	11.906
MALL	transect	0.026	< 0.001	27.338
NOPI	segment	0.104	< 0.001	7.041
NOPI	transect	0.028	< 0.001	21.967
NSHO	segment	0.061	< 0.001	11.688
NSHO	transect	0.018	0.003	35.621
REDH	segment	0.072	< 0.001	6.867
REDH	transect	0.035	< 0.001	11.513
RNDU	segment	0.024	0.074	15.842
RNDU	transect	0.003	0.284	72.741
RUDU	segment	0.039	0.010	5.979
RUDU	transect	0.016	0.008	10.793