Table S6. Model estimates of the proportion of species that fell into each (mis)alignment category comparing with or without neighbors. Separate models were fit for each (mis)alignment category and scale.

(Mis)alignment	Scale level	Neighbor treatment	Estimated proportion	95% CI
i. aligned present	plot	without neighbors	0.18	0.13, 0.2
i. aligned present	plot	with neighbors	0.10	0.07, 0.1
i. aligned present	grid	without neighbors	0.49	0.32, 0.7
i. aligned present	grid	with neighbors	0.15	0.07, 0.3
i. aligned present	site	without neighbors	0.60	0.3, 0.8
i. aligned present	site	with neighbors	0.13	0.03, 0.4
ii. sink	plot	without neighbors	0.35	0.24, 0.5
ii. sink	plot	with neighbors	0.43	0.3, 0.6
ii. sink	grid	without neighbors	0.44	0.3, 0.6
ii. sink	grid	with neighbors	0.79	0.64, 0.9
ii. sink	site	without neighbors	0.40	0.16, 0.7
ii. sink	site	with neighbors	0.87	0.6, 1
iii. dispersal limitation	plot	without neighbors	0.11	0.07, 0.2
iii. dispersal limitation	plot	with neighbors	0.07	0.04, 0.1
iii. dispersal limitation	grid	without neighbors	0.03	0.01, 0.1
iii. dispersal limitation	grid	with neighbors	0.00	0, 0
iii. dispersal limitation	site	without neighbors	0.00	0, 0
iii. dispersal limitation	site	with neighbors	0.00	0, 0
iv. aligned absent	plot	without neighbors	0.27	0.19, 0.4
iv. aligned absent	plot	with neighbors	0.34	0.25, 0.4
iv. aligned absent	grid	without neighbors	0.00	0, 0.2
iv. aligned absent	grid	with neighbors	0.00	0, 0.3

Table S6. Model estimates of the proportion of species that fell into each (mis)alignment category comparing with or without neighbors. Separate models were fit for each (mis)alignment category and scale.

(Mis)alignment	Scale level	Neighbor treatment	Estimated proportion	95% CI
iv. aligned absent	site	without neighbors	0.00	0, 0
iv. aligned absent	site	with neighbors	0.00	0, 0