Figure S1. Location of tracked colonies within (A) the Chagos Archipelago and (B) the Diego Garcia atoll. In panel A, tracked colonies are shown in pink circles. In panel B, tracked colonies are within delineated areas: Barton Point (2016-2019) and East Island (2022). In both panels, light grey shading shows water shallower than 100m.
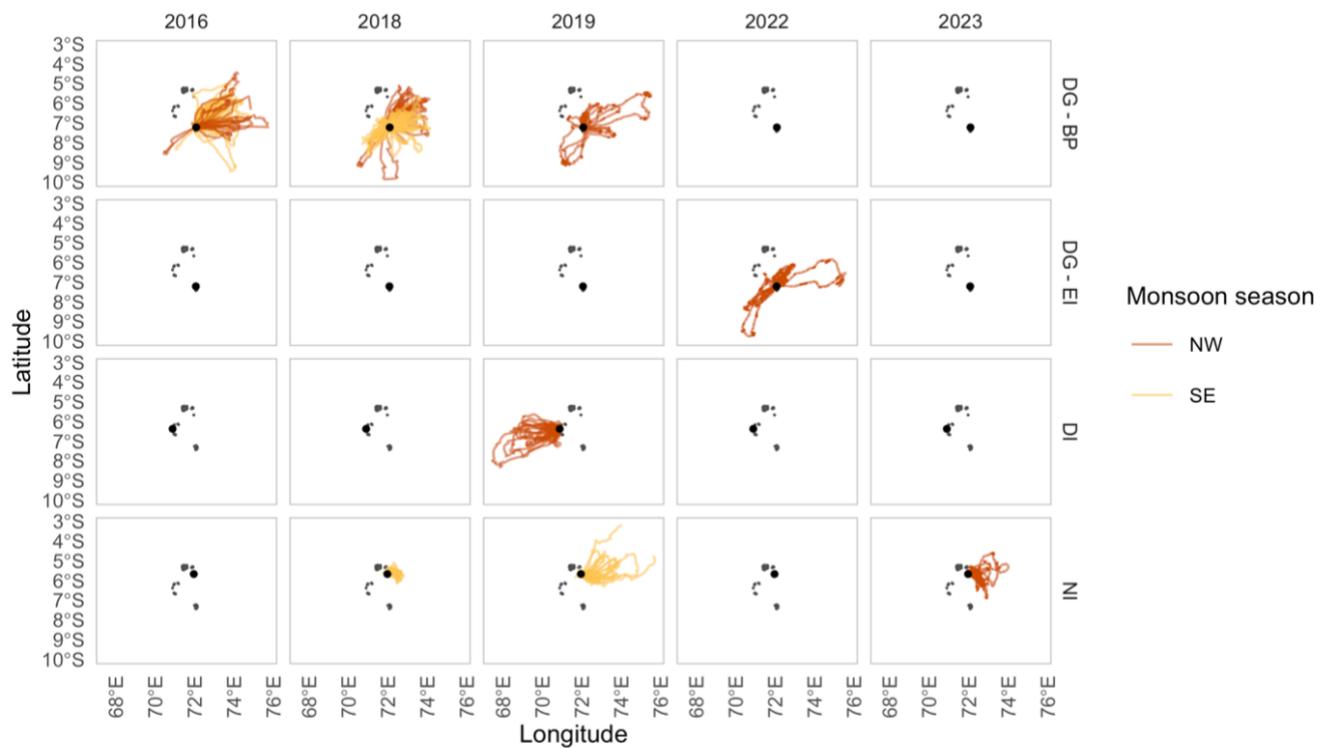

Figure S2. Red-footed booby foraging tracks among years (columns) at each colony (rows), coloured by monsoon season to indicate the distinct tracking periods.
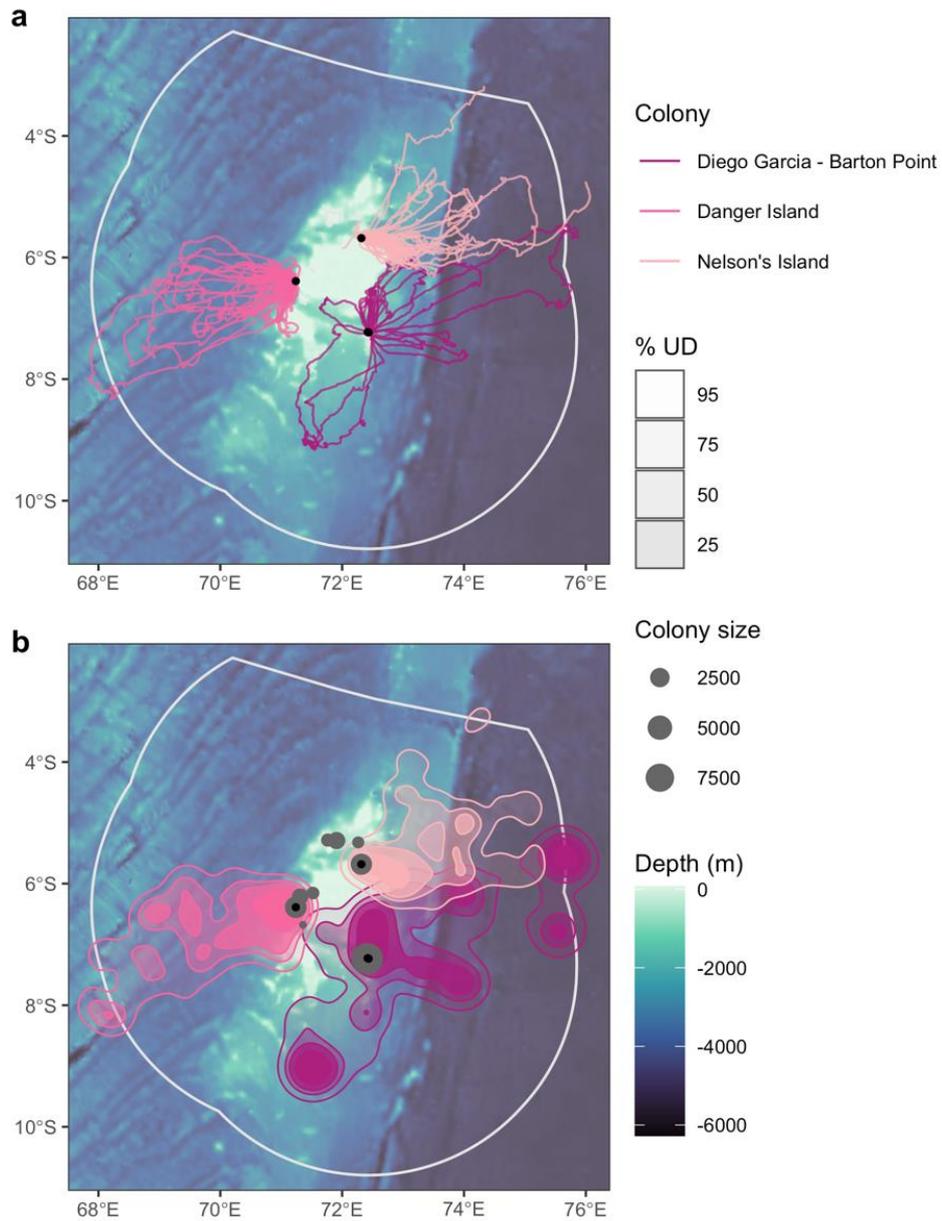
Figure S3. Red-footed booby area use in the Chagos Archipelago during 2019 only, when tracking data exist from Diego Garcia (Barton Point, n = 9), Danger Island (n=27), and Nelson's Island (n = 25). As with results from all years of data, colony foraging areas were largely distinct; there was no overlap among 25% and 50% core areas, and Bhattacharya's affinity among colonies was <0.25.
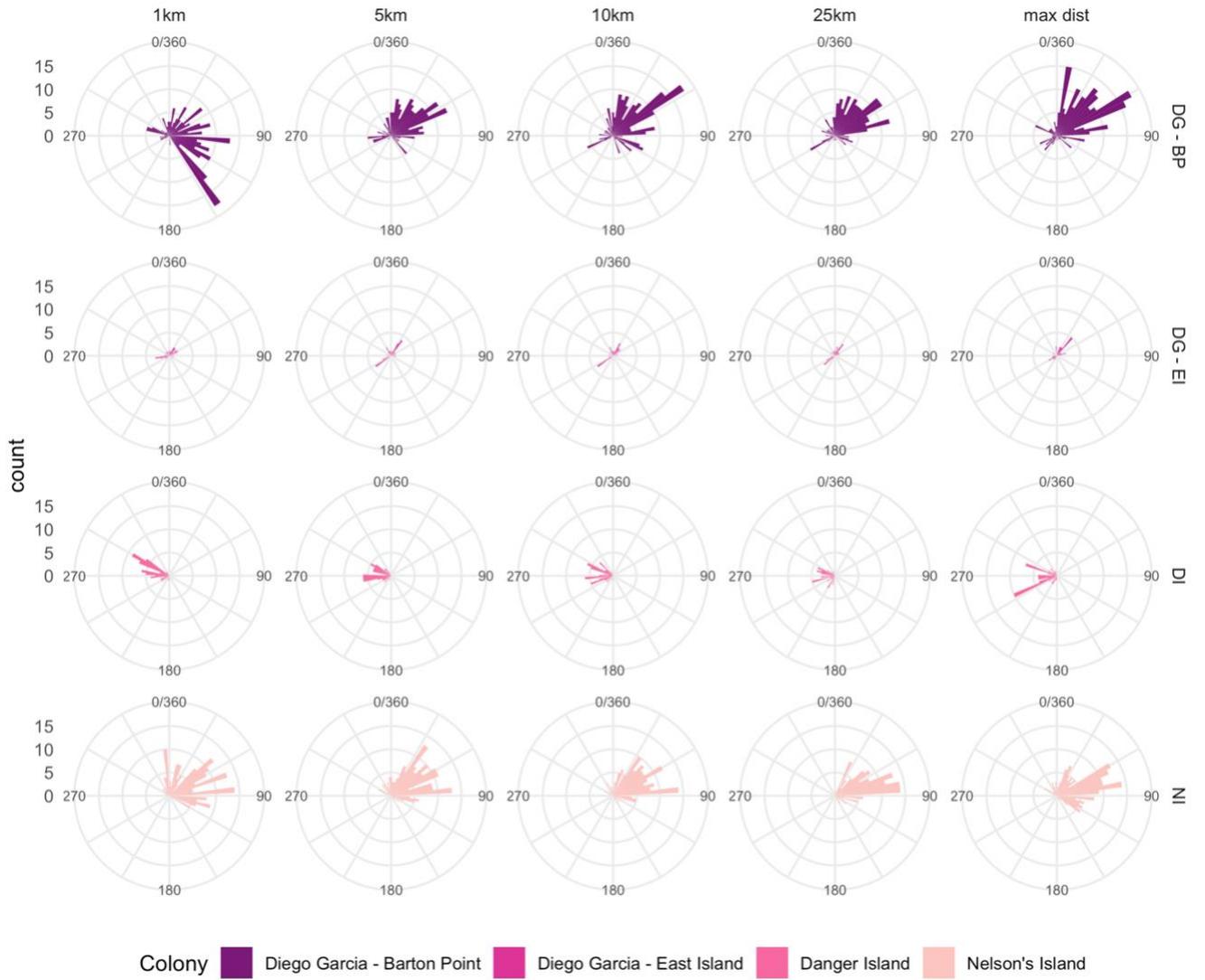
Figure S4. Departure angles of red-footed booby foraging trips calculated at different lengths along the trip.
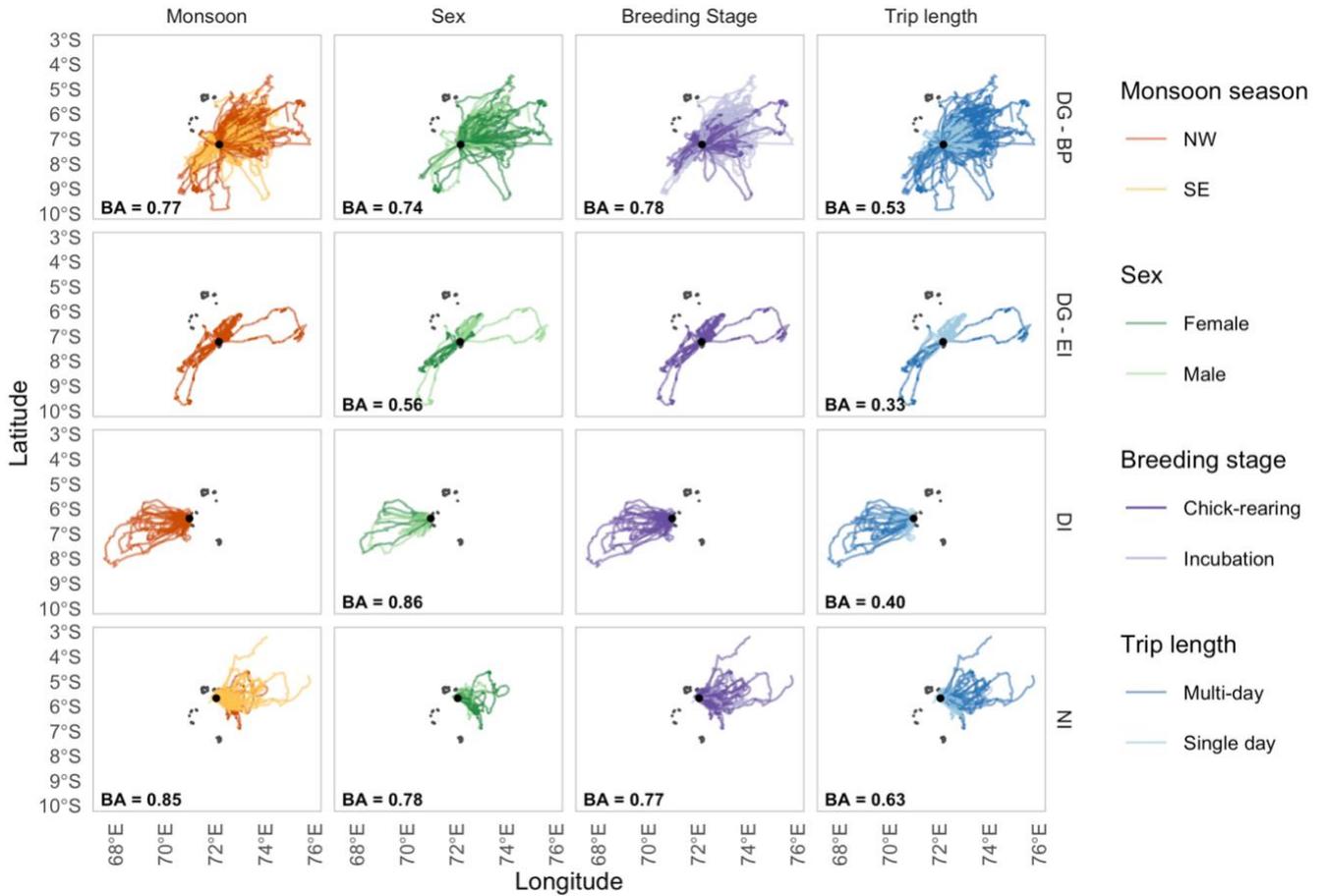
Figure S5. Red-footed booby foraging tracks between levels of intra-colony effects (columns) at each colony (rows). Total individuals = 207, full sample sizes shown in Table 1. Note, to facilitate pairwise comparisons we only show chick-rearing and incubating birds in the column of breeding stages (i.e., excluding pre-egg, n=8; & unknown breeders n=3), and males and females in the column of sexes (i.e., excluding birds of unknown sex, n=100). Bhattacharya's affinity is presented for each pair-wise comparison based on utilisation distributions, for which 0 = no overlap and 1 = complete overlap.

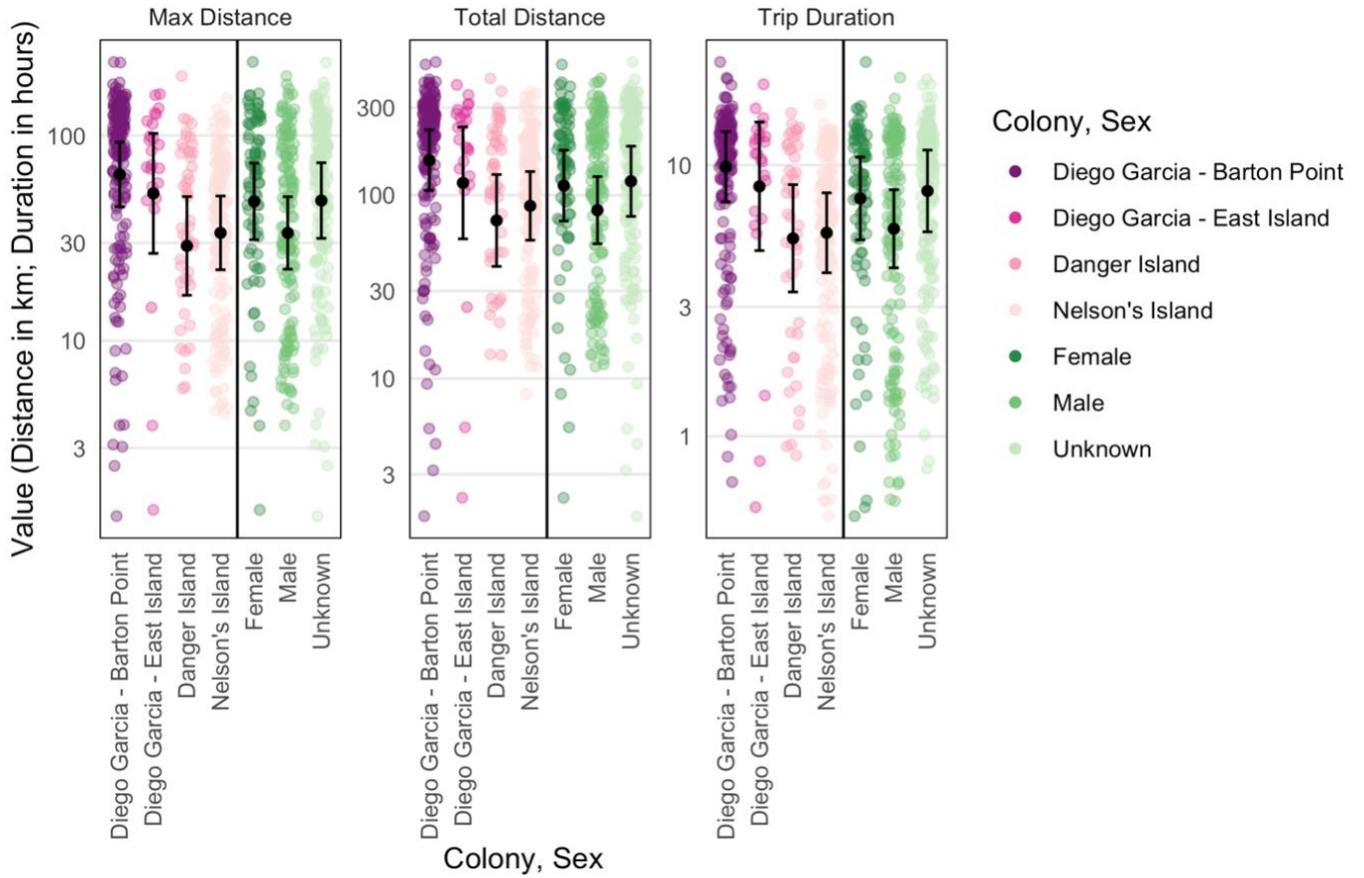**Figure S6.** Colony and sex differences in trip metrics persisted when considering single-day trips, only.

Table S1. Trip duration was significantly different among colonies and between males and females (p<0.05). Reference levels in model output are Colony: Barton Point; Monsoon season: NW; Sex: female; Breeding stage: chick-rearing. Estimates are shown on the log-scale.

group		Estimate (log hours)	Standard Error	df	statistic	p-value	
Fixed effects							
	(Intercept)	2.799	0.224	10	12.473	0.0000	***
	Colony (East Island)	-0.270	0.414	5	-0.653	0.5425	
	Colony (Danger Island)	-0.818	0.238	147	-3.442	0.0008	***
	Colony (Nelson's Island)	-0.578	0.144	100	-4.027	0.0001	***
	Monsoon (SE)	-0.207	0.154	68	-1.346	0.1828	
	Sex (M)	-0.490	0.130	150	-3.775	0.0002	***
	Sex (unknown)	0.062	0.147	154	0.422	0.6734	
	Breed Stage (incubation)	0.276	0.145	181	1.911	0.0576	.
	Breed Stage (pre-egg)	0.342	0.285	151	1.202	0.2314	
	Breed Stage (breeding)	0.434	0.451	242	0.963	0.3363	
Random effects							
BirdID	sd__(Intercept)	0.273					
year_f	sd__(Intercept)	0.298					
Residual	sd__Observation	0.894					

Signif. codes: 0 <= '***' < 0.001 < '**' < 0.01 < '*' < 0.05

square root of the estimated residual variance: 0.9

data's log-likelihood under the model: -661.7

Akaike Information Criterion: 1,349.4

Bayesian Information Criterion: 1,403.8

Table S2. Total distance travelled during a foraging trip was significantly different among colonies and between males and females (p<0.05). Reference levels in model output are Colony: Barton Point; Monsoon season: NW; Sex: female; Breeding stage: chick-rearing. Estimates are shown on the log-scale.

group		Estimate (log km)	Standard Error	df	statistic	p-value	
Fixed effects							
	(Intercept)	5.772	0.240	11	24.008	0.0000	***
	Colony (East Island)	-0.368	0.442	5	-0.832	0.4417	
	Colony (Danger Island)	-0.913	0.256	161	-3.562	0.0005	***
	Colony (Nelson's Island)	-0.591	0.155	112	-3.820	0.0002	***
	Monsoon (SE)	-0.294	0.166	69	-1.778	0.0798	.
	Sex (M)	-0.500	0.140	184	-3.563	0.0005	***
	Sex (unknown)	0.042	0.159	176	0.266	0.7902	
	Breed Stage (incubation)	0.204	0.156	216	1.310	0.1916	
	Breed Stage (pre-egg)	0.227	0.308	184	0.736	0.4629	
	Breed Stage (breeding)	-0.275	0.487	279	-0.565	0.5723	
Random effects							
BirdID	sd__(Intercept)	0.296					
year_f	sd__(Intercept)	0.316					
Residual	sd__Observation	0.966					

Signif. codes: 0 <= '***' < 0.001 < '**' < 0.01 < '*' < 0.05

square root of the estimated residual variance: 1.0

data's log-likelihood under the model: -698.3

Akaike Information Criterion: 1,422.6

Bayesian Information Criterion: 1,477.0

Table S3. Maximum distance from the colony during a foraging trip was significantly different among colonies and between males and females (p<0.05). Reference levels in model output are Colony: Barton Point; Monsoon season: NW; Sex: female; Breeding stage: chick-rearing. Estimates are shown on the log-scale.

group		Estimate (log km)	Standard Error	df	statistic	p-value	
Fixed effects							
	(Intercept)	4.814	0.231	11	20.853	0.0000	***
	Colony (East Island)	-0.275	0.424	5	-0.649	0.5434	
	Colony (Danger Island)	-0.917	0.247	159	-3.711	0.0003	***
	Colony (Nelson's Island)	-0.648	0.150	112	-4.318	0.0000	***
	Monsoon (SE)	-0.281	0.159	68	-1.770	0.0813	.
	Sex (M)	-0.523	0.136	189	-3.844	0.0002	***
	Sex (unknown)	0.030	0.154	176	0.196	0.8448	
	Breed Stage (incubation)	0.232	0.151	218	1.536	0.1259	
	Breed Stage (pre-egg)	0.191	0.299	192	0.641	0.5221	
	Breed Stage (breeding)	-0.142	0.469	277	-0.304	0.7615	
Random effects							
BirdID	sd__(Intercept)	0.325					
year_f	sd__(Intercept)	0.299					
Residual	sd__Observation	0.901					

Signif. codes: 0 <= '***' < 0.001 < '**' < 0.01 < '*' < 0.05

square root of the estimated residual variance: 0.9

data's log-likelihood under the model: -671.5

Akaike Information Criterion: 1,369.1

Bayesian Information Criterion: 1,423.5

Table S4. Departure time (hours after dawn) was significantly different among colonies, between males and females, and between single and multi-day trips (p<0.05). Reference levels in model output are Colony: Barton Point; Monsoon season: NW; Sex: female; Breeding stage: chick-rearing; Trip length: multi-day.

group		Estimate (hours after dawn)	Standard Error	df	statistic	p-value	
Fixed effects							
	(Intercept)	0.471	0.843	25	0.559	0.5812	
	Colony (East Island)	-0.039	1.312	7	-0.030	0.9772	
	Colony (Danger Island)	2.829	0.911	92	3.107	0.0025	**
	Colony (Nelson's Island)	1.877	0.538	87	3.490	0.0008	***
	Monsoon (SE)	0.555	0.574	39	0.968	0.3392	
	Sex (M)	1.592	0.512	191	3.107	0.0022	**
	Sex (unknown)	0.084	0.564	120	0.149	0.8815	
	Breed Stage (incubation)	0.349	0.575	223	0.607	0.5445	
	Breed Stage (pre-egg)	0.276	1.104	173	0.250	0.8032	
	Breed Stage (breeding)	1.916	1.799	300	1.065	0.2876	
	Trip length (Single day)	1.605	0.498	471	3.224	0.0014	**
Random effects							
BirdID	sd__(Intercept)	0.587					
year_f	sd__(Intercept)	0.813					
Residual	sd__Observation	3.816					

Signif. codes: 0 <= '***' < 0.001 < '**' < 0.01 < '*' < 0.05

square root of the estimated residual variance: 3.8

data's log-likelihood under the model: -1,335.8

Akaike Information Criterion: 2,699.7

Bayesian Information Criterion: 2,758.2

Table S5. Arrival time (hours after dusk) was consistent across all factors. Reference levels in model output are Colony: Barton Point; Monsoon season: NW; Sex: female; Breeding stage: chick-rearing; Trip length: multi-day.

group		Estimate (hours after dusk)	Standard Error	df	statistic	p-value	
Fixed effects							
	(Intercept)	-2.844	0.883	33	-3.219	0.0029	**
	Colony (East Island)	-0.251	1.334	9	-0.188	0.8551	
	Colony (Danger Island)	0.877	0.983	48	0.892	0.3770	
	Colony (Nelson's Island)	0.775	0.598	60	1.297	0.1997	
	Monsoon (SE)	0.259	0.605	30	0.428	0.6719	
	Sex (M)	0.081	0.583	142	0.139	0.8896	
	Sex (unknown)	0.516	0.618	65	0.834	0.4074	
	Breed Stage (incubation)	0.421	0.643	168	0.656	0.5129	
	Breed Stage (pre-egg)	1.768	1.252	142	1.412	0.1601	
	Breed Stage (breeding)	-0.279	1.983	221	-0.141	0.8883	
	Trip length (Single day)	0.445	0.514	466	0.867	0.3865	
Random effects							
BirdID	sd__(Intercept)	1.432					
year_f	sd__(Intercept)	0.671					
Residual	sd__Observation	3.773					

Signif. codes: 0 <= '***' < 0.001 < '**' < 0.01 < '*' < 0.05

square root of the estimated residual variance: 3.8

data's log-likelihood under the model: -1,351.9

Akaike Information Criterion: 2,731.8

Bayesian Information Criterion: 2,790.4