Oikos

OIK-00069

Nabe-Nielsen, J., Tougaard, J., Teilmann, J., Lucke, K. and Forchhammer, M. C. 2013. How a simple adaptive foraging strategy can lead to emergent home ranges and increased food intake. – Oikos 000: 000–000.

Appendix 1

Effects of variations in resource replenishment, memory decay and food patch size on model behavior

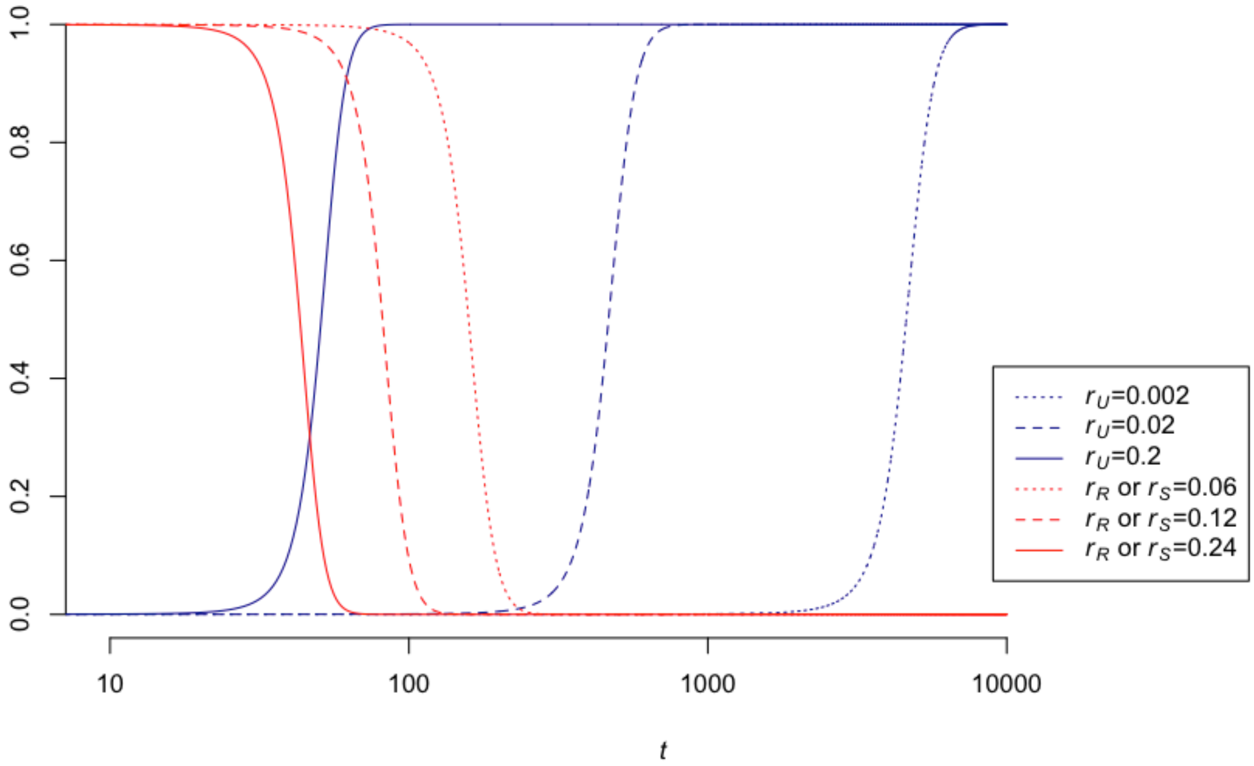
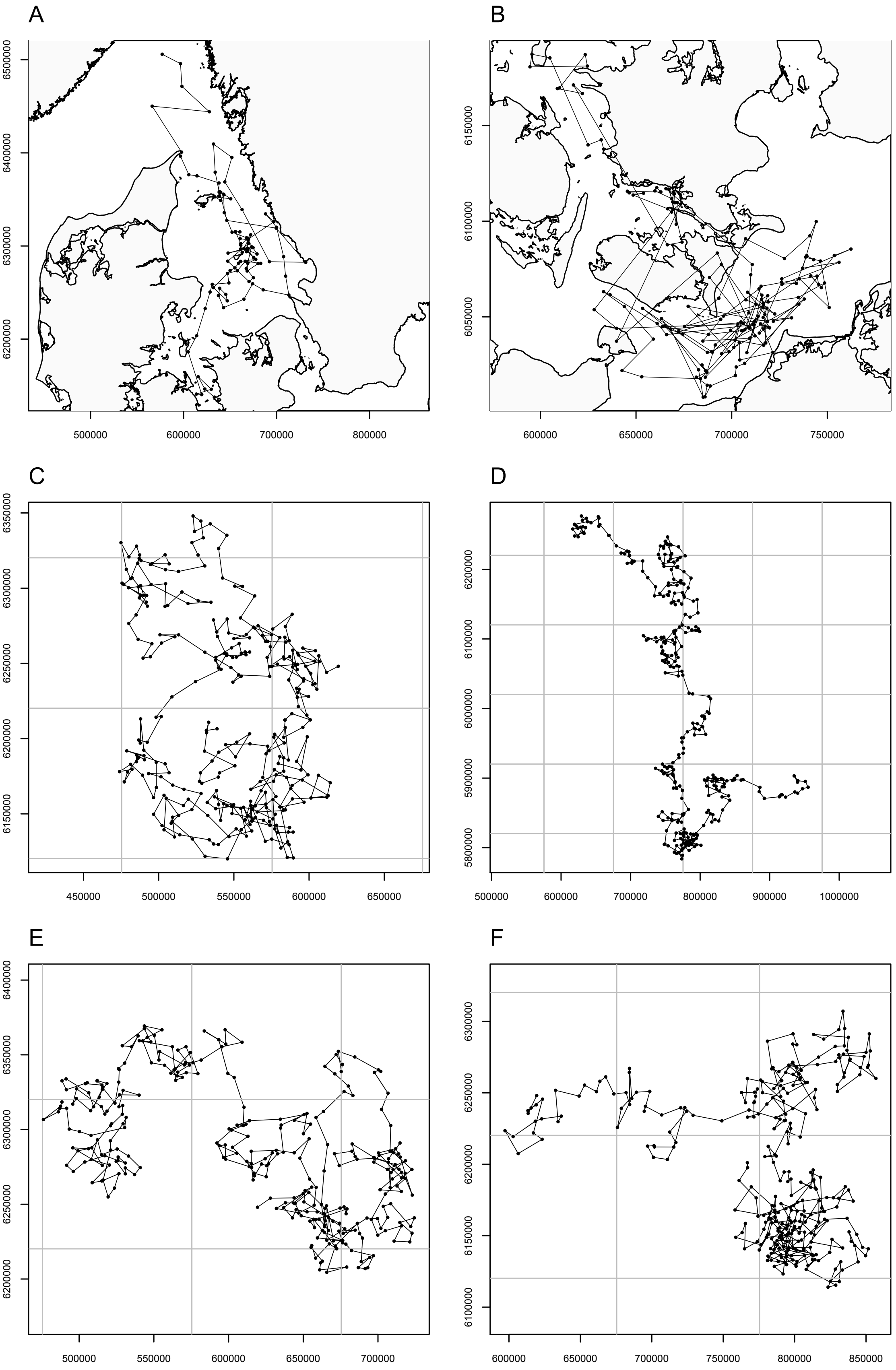


Figure A1. Effects of changes in resource replenishment, r_U, on $U[c]$ (blue lines; cf. Eq. 3) and of changes in reference memory decay, r_R, or satiation memory decay, r_S, on M_R and M_S (red lines; cf. Eq. 5). Time t is measured in 30-min steps. When $r_U = 2 \times 10^{-1}$ food is replenished in a patch before the animal forgets its location.


A
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B
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6100000
6200000
500000
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800000
900000
1000000
E
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6350000
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Figure A2. Movement tracks for satellite-tracked and simulated porpoises, including at most one position per day. Numbers in axes show distances in metres (and UTM coordinates for (A) and (B)). (A**)** 97 positions from 97 days for animal number 1999-06421 (mean speed: 18.2 km h^{-1}) and (B): 160 positions from 201 days for animal 2006-06421 (mean speed: 24.1 km h^{-1}) (Fig. 2). (C): 313 positions for animal simulated with $r_S = 0.05$ and $r_R = 0.1$ (mean speed: 19.2 km h^{-1}). (D): 313 positions for animal simulated with $r_S = 0.10$ and $r_R = 0.1$ (mean speed: 22.8 km h^{-1}). (E): 313 positions for animal simulated with $r_S = 0.05$ and $r_R = 0.09$ (mean speed: 21.5 km h^{-1}). (F): 313 positions for animal simulated with $r_S = 0.10$ and $r_R = 0.09$ (mean speed: 17.4 km h^{-1}). Grey squares in the panels corresponding to simulated tracks (C–F) indicate the 100 × 100 km blocks (covering 1000 × 1000 grid cells) that each contained 1000 randomly distributed 13-cell food patches. All simulations used $r_U = 0.2$.

1 cell per patch

r_U = 0.002

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	2.91	3.61	3.23	3.56	2.64	3.17	3.50	2.78
	0.10	3.50	3.24	3.01	3.08	3.17	2.74	3.34	3.77
	0.15	3.50	2.85	3.27	3.58	3.14	3.95	2.74	3.65
	0.20	3.23	3.72	4.42	3.46	2.99	3.66	2.97	3.20
	0.25	3.41	5.09	3.32	3.58	3.11	3.40	2.98	3.09

r_U = 0.02

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.52	2.96	3.33	3.38	3.13	3.30	3.30	3.04
	0.10	3.36	3.95	3.54	2.96	3.12	3.45	2.72	3.14
	0.15	2.89	3.57	3.31	3.17	3.70	3.54	3.26	3.56
	0.20	4.31	4.44	4.57	3.25	3.27	2.98	3.45	3.01
	0.25	5.05	3.73	3.77	3.91	3.58	3.84	3.34	3.79

r_U = 0.2

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.38	4.00	3.06	2.84	4.08	3.17	3.37	3.07
	0.10	3.24	3.23	3.24	3.03	2.75	3.58	3.35	2.86
	0.15	3.30	3.28	3.33	2.98	3.33	3.01	2.98	3.29
	0.20	4.84	3.35	3.67	4.08	3.45	3.63	3.72	3.03
	0.25	6.48	3.91	4.31	3.06	3.46	3.58	3.22	3.39

5 cells per patch

r_U = 0.002

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.00	3.06	3.02	2.94	3.22	3.20	3.03	3.04
	0.10	3.37	3.30	3.59	3.66	3.14	3.06	3.37	3.33
	0.15	4.92	3.95	4.27	3.25	3.29	3.96	3.60	3.23
	0.20	6.29	8.18	3.92	6.67	3.60	3.43	3.70	3.75
	0.25	11.71	5.35	4.75	4.62	4.88	3.45	4.63	5.44

r_U = 0.02

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.06	3.17	2.86	3.39	2.86	2.99	3.27	2.67
	0.10	3.75	3.46	3.31	3.41	3.04	2.87	3.08	2.96
	0.15	5.65	4.30	3.65	4.82	3.85	4.01	3.05	2.99
	0.20	5.83	7.00	4.92	4.11	4.42	3.53	3.54	3.99
	0.25	7.30	6.16	5.93	6.18	5.32	4.09	4.97	4.73

r_U = 0.2

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.26	2.73	3.55	3.05	3.45	3.46	3.22	3.08
	0.10	4.59	3.40	3.26	2.88	2.88	2.93	3.10	2.88
	0.15	4.16	5.15	5.07	4.54	4.10	3.71	2.70	3.07
	0.20	8.42	7.22	4.93	4.40	3.74	4.92	4.59	4.50
	0.25	8.43	9.93	9.53	6.08	5.54	5.00	5.11	4.43

9 cells per patch

r_U = 0.002

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.47	3.56	2.92	3.47	3.18	3.17	3.11	3.08
	0.10	3.84	3.69	3.16	3.26	2.85	2.99	3.18	3.50
	0.15	6.55	4.28	3.34	3.47	2.92	3.04	3.45	3.54
	0.20	8.90	5.26	6.59	4.95	5.48	4.71	3.93	3.44
	0.25	9.15	6.73	6.96	7.71	4.77	7.59	5.31	5.14

r_U = 0.02

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.34	3.82	3.48	3.46	2.83	3.80	3.57	3.58
	0.10	5.07	3.59	3.06	2.83	3.42	3.10	2.72	3.40
	0.15	5.17	4.11	4.04	4.49	4.63	3.18	3.38	4.22
	0.20	7.64	6.69	6.49	6.65	5.48	4.36	4.55	3.52
	0.25	5.86	7.04	10.20	11.76	5.44	6.76	5.27	4.51

r_U = 0.2

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.69	3.21	2.83	3.51	3.60	3.26	3.13	3.41
	0.10	3.95	3.39	3.26	3.34	2.99	3.10	3.69	3.75
	0.15	5.89	4.27	4.45	3.32	3.72	3.69	3.53	2.48
	0.20	7.86	4.55	7.65	3.77	3.80	4.33	4.51	3.59
	0.25	8.31	8.10	4.81	6.42	6.89	8.04	6.55	4.81

13 cells per patch

r_U = 0.002

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.27	2.76	3.28	2.77	3.12	2.90	3.09	3.22
	0.10	3.26	3.20	3.43	3.06	3.00	3.34	3.52	3.36
	0.15	4.13	2.94	3.95	3.27	4.49	3.39	3.39	3.39
	0.20	5.85	3.32	3.86	3.46	4.89	3.33	4.36	3.82
	0.25	12.26	4.16	8.41	3.99	6.83	3.07	4.59	4.23

r_U = 0.02

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	3.22	3.15	3.58	3.29	3.54	2.78	2.87	3.35
	0.10	3.60	3.36	3.17	3.55	3.14	3.30	3.26	3.15
	0.15	4.11	3.72	4.42	3.22	3.47	3.15	3.58	3.64
	0.20	5.52	3.11	5.76	3.32	5.22	4.99	5.83	3.63
	0.25	6.12	4.68	4.97	3.48	8.15	3.38	5.44	4.16

r_U = 0.2

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	2.89	2.94	2.94	3.43	3.46	3.24	3.41	2.87
	0.10	3.61	3.37	3.90	2.63	4.31	2.96	2.82	3.96
	0.15	4.96	3.52	4.68	5.30	3.32	3.16	3.63	3.83
	0.20	5.97	5.13	4.30	5.71	3.93	4.29	3.56	3.42
	0.25	7.13	9.70	6.25	4.79	4.64	4.45	4.69	3.96

Table A1. Mean residence times (days) for different combinations of r_R, r_S and r_U and for landscapes with 1000 patches covering either 1, 5, 9 or 13 cells each. Each simulation was run for 15 000 half-hour time steps, and residence times were calculated based on the time spent within a 5-km circle around each point in the tracks. The parameters $r_R = 0.10$ and $r_S = 0.15$ resulted in the residence times that most closely corresponded to the mean residence time observed for satellite-tracked animals (2.9 days) in simulations with 13 cell patches (i.e. with the lowest squared deviation from the observed mean across the three r_U-values.

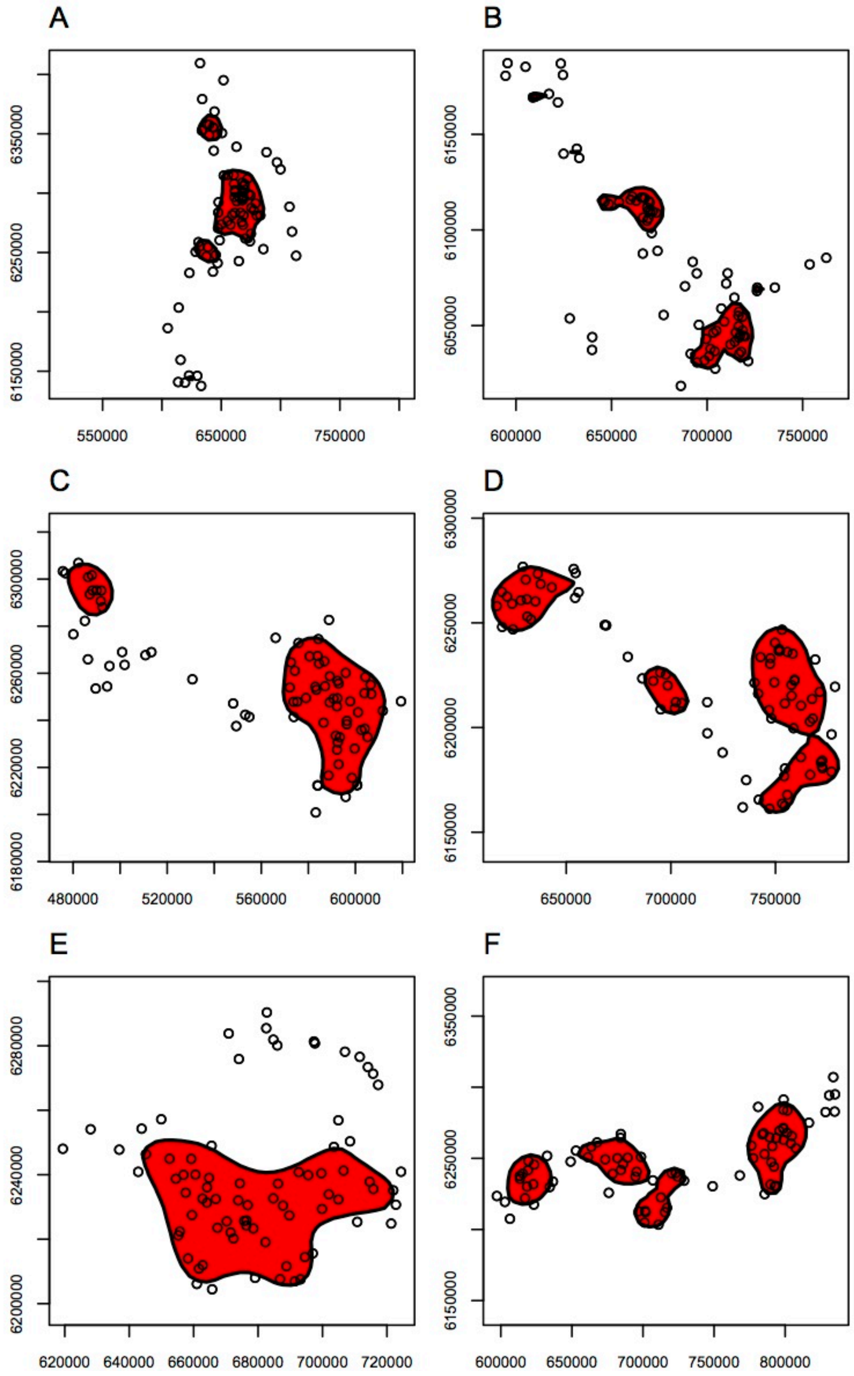

Figure A3. Kernel home ranges for the 50% isopleth. (A): First 80 daily positions from animal 1999-06421. (B): First 80 positions from animal 2006-06421. (C): First 80 daily positions for animal simulated with $r_S = 0.05$ and $r_R = 0.1$. (D): First 80 positions for animal with $r_S = 0.10$ and $r_R = 0.1$. (E): First 80 positions for animal with $r_S = 0.05$ and $r_R = 0.09$. (F): First 80 positions for animal with $r_S = 0.10$ and $r_R = 0.09$.

Appendix B

Calibration of fine-scale movement model using dead-reckoning data

In this appendix we describe the procedure used for calibrating the intrinsic movement part of the simulation model and present summary statistics for the dead-reckoning data set used for model calibration. We also explore how the simulated animal behavior is affected by simplifying the movement model where turning angle is independent of movement speed (Table A2).

The dead-reckoning data set contains movement speeds and changes in turning angles at a 6 s resolution as observed with speed censors and a 3D compass placed on the dorsal fin of a single harbor porpoise (see Wilson et al. 2007 for details). In the current study the data was analyzed using a 30-minute time interval.

Calibration of random walk behavior

The calibration of the intrinsic movement model was performed using a simulation model that included the correlated random walk (CRW) behavior, but without spatial memory behavior. It incorporated a negative correlation between turning angles and a positive correlation between the distances moved. It did not include any kind of environmental variation.

The model was calibrated by 1) obtaining initial values of *a* and *b* using first order autoregressive analyses. 2) Log_{10} of the distance moved per time step and the autocorrelation coefficient (R_1 and a in En. 7) were adjusted until the distribution of movement distances closely resembled the ones in Fig. A4. 3) The turning angle distribution and its autocorrelation coefficient (R_2 and b in Eq. 8 when setting $R_3 = \text{N}(0, 0)$) were adjusted until the distribution resembled the one in Fig. A4. 4) It was tested that the model was able to simultaneously produce turning angle and step-length distributions with means and variances corresponding to the ones observed in the dead-reckoning data, and that parameters obtained from multiple simulations were approximately normally distributed around the corresponding values obtained from the dead-reckoning data (Fig. A5). 5) The parameters that controlled the relationship between turning angle and distance moved (R_3 and m in Eq. 8) were adjusted until the model produced the relationship observed in the dead-reckoning data set (Fig. A6). Step 5 affected the autocorrelation and distribution of movement distances and turning angles, and the steps 2–5 were therefore repeated until the model simultaneously produced all the observed relationships.

Effects of dependency between turning angle and movement speed on residence times

Residence times were relatively low in simulations where turning angles did not decrease with movement speed (i.e. by setting $R_3 = \mathrm{N}(0, 0)$), but where all other parameters remained unchanged (as in Table 1). As the relative reduction in residence time was similar across all values of r_R and r_S (Table A2), the model's ability to produce home ranges remains intact when using a more standard CRW model than the one presented in Eq. 8.

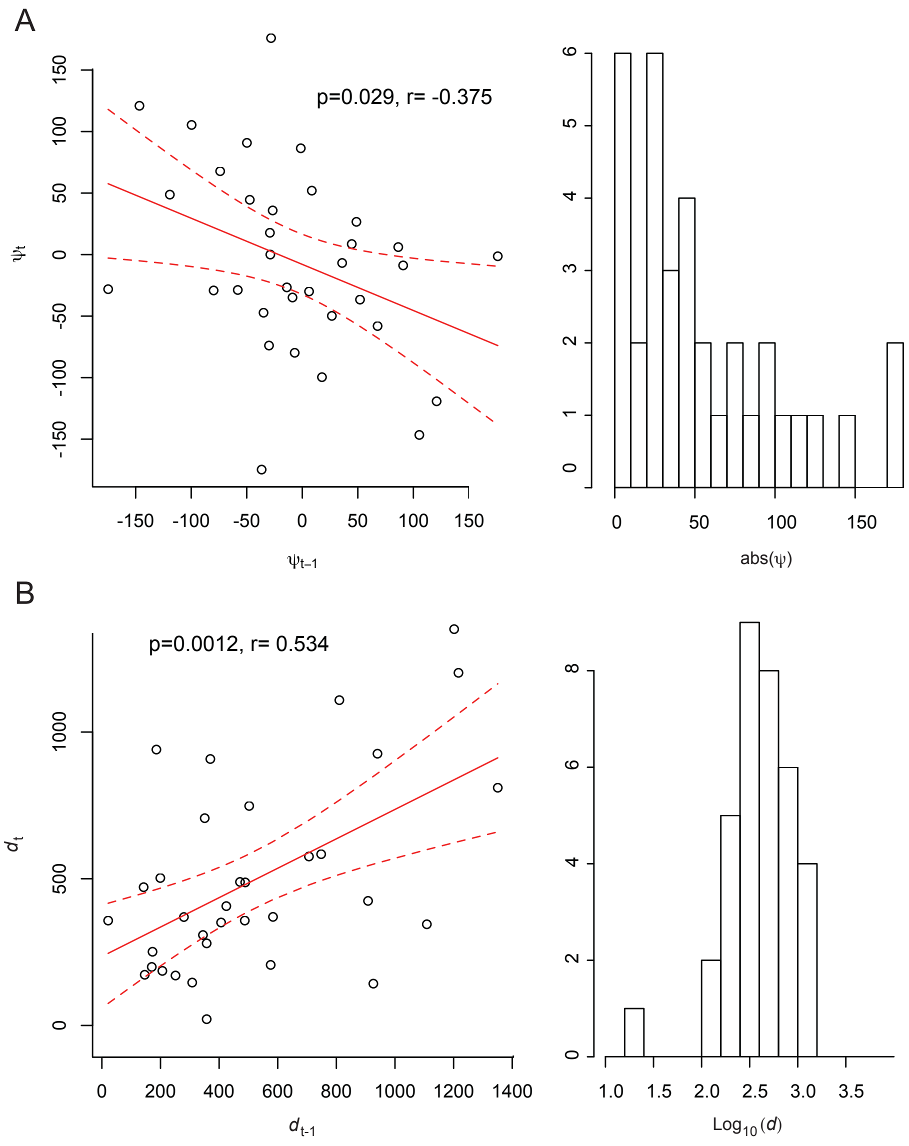

Figure A4. (A): Autocorrelation and distribution of turning angles ψ, and (B): of movement distances d (measured in m per 30 min) in the dead-reckoning dataset. Note that the step-length in the simulation model is based on the logarithm of the movement distances measured in 100-m steps per 30 min, so $\delta = \log_{10}(d / 100)$. Pearson correlation coefficients and the corresponding significance levels are provided.

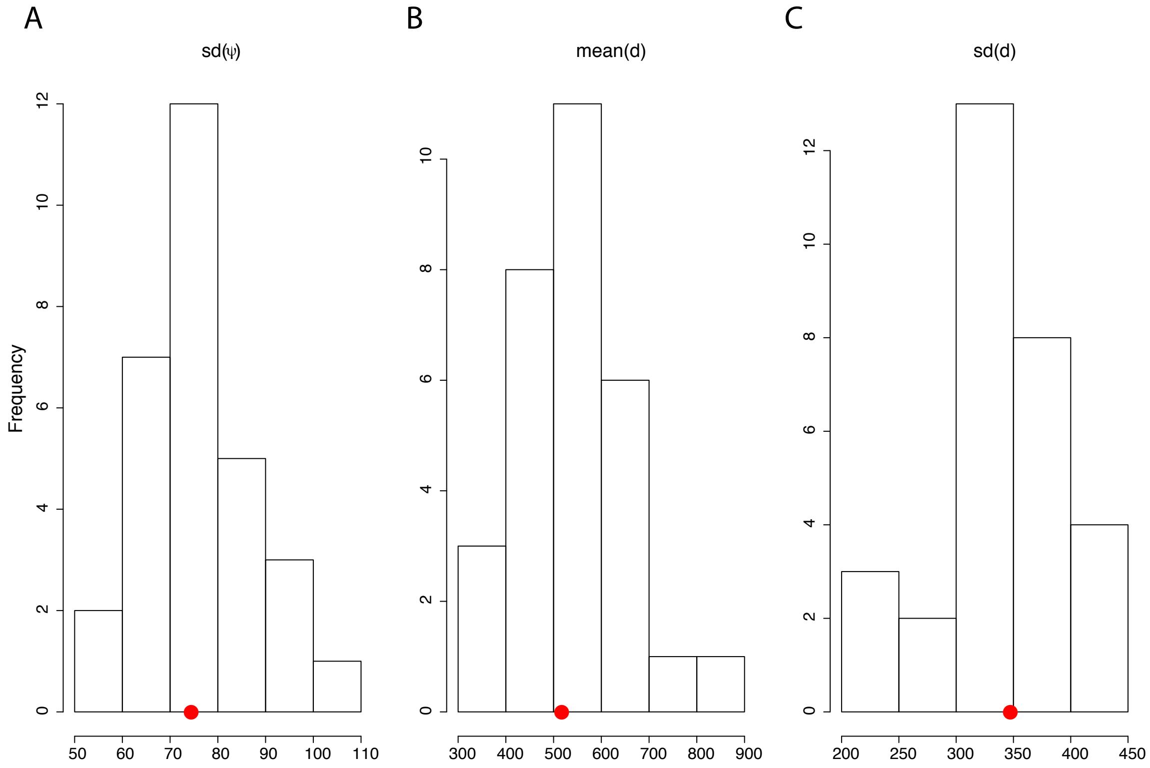

Figure A5. Calibration of correlated random walk model. Red points show (A): standard deviation in turning angle, (B): mean distance moved per 30 minutes, and (C): standard deviation in movement distance in the dead-reckoning data. Histograms show the distribution of the same parameters in 30 simulations with 1500 half-hour steps each, based on the parameters used in the paper.

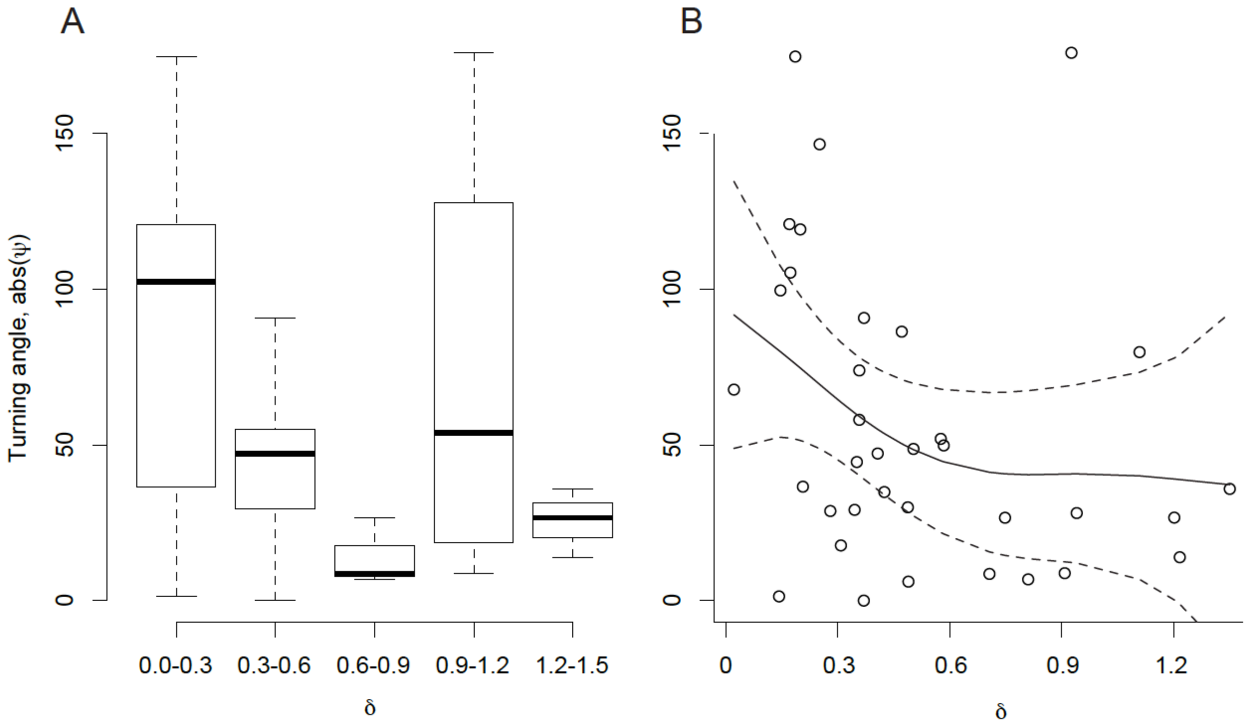

Figure A6. Relationship between turning angles ψ_t and movement distance δ_t per half-hour interval in dead-reckoning dataset. Curves in B are based on a GAM fit with a 95% confidence band.

		r_R							
		0.05	0.06	0.07	0.08	0.09	0.10	0.11	0.12
r_S	0.05	2.797 (-3%)	2.306 (-22%)	2.038 (-31%)	2.343 (-32%)	1.968 (-43%)	2.151 (-34%)	2.200 (-36%)	1.983 (-31%)
	0.10	2.069 (-43%)	2.340 (-31%)	2.418 (-38%)	2.464 (-6%)	2.020 (-53%)	2.069 (-30%)	2.277 (-19%)	2.424 (-39%)
	0.15	2.414 (-51%)	2.570 (-27%)	2.089 (-55%)	2.434 (-54%)	2.203 (-34%)	2.446 (-23%)	1.930 (-47%)	2.633 (-31%)
	0.20	2.882 (-52%)	2.907 (-43%)	3.146 (-27%)	3.650 (-36%)	2.501 (-36%)	2.581 (-40%)	2.853 (-20%)	2.245 (-34%)
	0.25	3.402 (-52%)	3.489 (-64%)	3.619 (-42%)	3.865 (-19%)	2.689 (-42%)	3.099 (-30%)	2.463 (-47%)	3.384 (-14%)

Table A2. Residence times in simulation with no dependency of turning angle on movement speed (i.e. setting R_3 = N(0,0) in Eq. 8) and percent change in residence time relative to standard simulations based on 13-cell patches and with r_U=0.2 (Table A1).

Appendix reference

Wilson, R. P. et al. 2007. All at sea with animal tracks; methodological and analytical solutions for the resolution of movement. – Deep-Sea Res. Part II 54: 193–210.