Supplemental Information

Tag deployment

Animals were caught on or close to haul-out sites using hand or seine nets. The tags were attached to the fur at the back of the neck using a fast setting two-part epoxy adhesive or Loctite® 422 Instant Adhesive. All permits required to enter protected areas and for animal handling during tagging procedures were obtained from the appropriate authorities. In the UK all animal handling and procedures were carried out under Home Office Licenses 60/3303 and 60/4009. Permits were obtained under the Dutch Nature Protection Act (Natuurbeschermings wet) and Flora and Fauna Act (Flora and Fauna wet) from the provinces of Groningen and Friesland and the Dutch government, respectively. In the Netherlands, protocols were approved by the animal ethics committee (Dier Ethische Commissie, DEC) of the Royal Netherlands Academy of Science (Koninklijke Nederlandse Academie voor Wetenschappen, KNAW). Data was cleaned according to the SMRU protocol where tests on land showed that the over 95% of the cleaned locations had a distance error of <50 m.

The association between tracks of animals and anthropogenic structures

Wind farm boundary

Wind farm boundaries were defined using a buffer of half the median minimum distance between structures.

Pipeline association

Tracks were defined as being associated with pipelines primarily on a visual basis. This is because many locations can occur within a short distance of a pipeline without the animal appearing to follow or use that pipeline. However, all tracks assigned as associated with

pipelines had four of more sequential locations (approximately 24 locations transmitted per day) and at least 2.5 hours within 100m of the pipeline. To estimate the time associated with a pipeline, the tracks were truncated to only include sections which started and ended with at least 2 locations within 100m of the pipelines and for which at least half of the overall locations within 100m of the pipeline of interest.

Activity

State-space model

Locations were regularized onto 0.25 hr (Sheringham Shoal) or 0.5 hr (Alpha Ventus) intervals depending on the temporal resolution of data from the tags. We firstly defined resting and non-resting using behavioral data and then assigned non-resting as foraging and travelling using a state-space model [S1] to obtain three states (z_t) for time periods $t = 1,...N$: resting ($z_t = R$), foraging ($z_t = F$), and travelling ($z_t = T$). The behavioral data (ω_t) were the number of haul-out events during each time step, where a haul-out event is a period of at least 10 minutes for which the tag is dry. Intervals were assigned to resting if they contained any haul-out activity ($\omega_t > 0$) and to non-resting if they were known to contain no haul-out activity $(\omega_t = 0)$.

Non-resting time steps were assigned to the foraging or travelling states based on step distance (the distance travelled during the interval; s_t) and bearing (φ). We also modelled the distribution of step length and bearing for resting states. Following McClintock *et al*. (2013 [S1]), we assumed the step length distribution $s_t \mid \boldsymbol{a}, \boldsymbol{b}, z_t = i \sim \text{Weibull}(a_i, b_i)$:

$$f\left(s_t \mid \boldsymbol{a}, \boldsymbol{b}, z_t = i\right) = \frac{b_i}{a_i}\left(\frac{s_t}{a_i}\right)^{b_i - 1} \exp\left[-\left(s_t / a_i\right)^{b_i}\right]$$

for state-specific scale parameter $a_i > 0$, shape parameter $b_i > 0$, and $i \in \{R, F, T\}$. We assumed a priori that step distance will tend to be longest when travelling and constrained the state-specific scale parameter such that $a_T > a_F > a_R$. For bearing, we assumed a wrapped Cauchy distribution $\phi_t \mid \mathbf{\rho}, z_t = i \sim \text{wCauchy}\left(\phi_{t-1}, \upsilon_i\right)$:

$$f\left(\phi_t \mid \mathbf{\rho}, z_t = i\right) = \frac{1}{2\pi} \frac{1 - \rho_i^2}{1 + \rho_i^2 - 2\rho_i \cos\left(\phi_t - \phi_{t-1}\right)}$$

with bearing $0 \leq \phi_t < 2\pi$ and state-specific mean vector length $0 \leq \rho_i < 1$. Non-resting time steps were assumed to be equally likely to have been travelling or foraging states, and we incorporated memory into the state transition probabilities (ψ) as a first-order Markov process. The model for z_t is then:

$$z_t \mid \mathbf{p}, z_{t-1} = k \sim \text{Categorical}(p_{k,R}, p_{k,F}, p_{k,T})$$

$$p_{k,i} = \frac{\psi_{k,i} f\left(s_t \mid \mathbf{a}, \mathbf{b}, z_t = i\right) f\left(\phi_t \mid \mathbf{\rho}, z_t = i\right) h_{i,t}}{\sum_j \psi_{k,j} f\left(s_t \mid \mathbf{a}, \mathbf{b}, z_t = j\right) f\left(\phi_t \mid \mathbf{\rho}, z_t = j\right) h_{j,t}}$$

where

$$h_{i,t} = \begin{cases} 1 - I\left(\omega_t > 0\right) & \text{if } i = R \\ 1 - I\left(\omega_t = 0\right) & \text{if } i = F \\ 1 - I\left(\omega_t = 0\right) & \text{if } i = T \end{cases}$$

$$\psi_{k,i} = \Pr(z_t = i \mid z_{t-1} = k),$$

$k \in \{R, F, T\}$, and $I\left(q\right)$ is an indicator function taking the value one when argument q is true and zero otherwise.

Assuming independence, we therefore have the conditional likelihood:

$$f\left(\mathbf{\phi}, \mathbf{s}, \mathbf{z} \mid \mathbf{\theta}\right) = \prod_{t=1}^{N} f\left(\phi_t \mid \mathbf{\theta}, z_t\right) f\left(s_t \mid \mathbf{\theta}, z_t\right) f\left(z_t \mid \mathbf{\theta}, z_{t-1}\right)$$

where θ is the set of model parameters. Whenever there was a gap of > 4 times the interval between the observed locations surrounding the interpolated location, or if, due to missing data, it was unknown whether there was any haul-out activity within an interval, we ignored the movement data for time step t by setting $f(\phi_t | \theta, z_t) f(s_t | \theta, z_t) = 1$. Latent state assignments for unreliable or missing time steps were therefore based entirely on the Markov property of the state transition probabilities and were excluded from the reported results.

We adopted a Bayesian perspective and fitted this state-space model using a Markov chain Monte Carlo (MCMC) algorithm written in C with vague prior distributions for all parameters. Independent analyses were run for each seal, with two chains starting at different initial values and a burn-in of between 50,000 and 100,000 iterations. Convergence was judged by visual inspection and using the Gelman-Rubin diagnostic [S2]. We used 50,000 iterations for summarizing the posterior distributions.

Activities within wind farms

Using generalized estimating equations, we then investigated the relationship between the proportion of MCMC iterations for which an interval was assigned to foraging and the distance from the nearest structure within the wind farm. Visits to the wind farm that were separated by more than 24 hours were assumed to be independent. By including a working independence structure [S3] parameter estimates were robust to the presence of autocorrelation within visits to the wind farm whilst not explicitly modelling this correlation. We found that the probability of foraging increased significantly with decreasing distance to structures in two of three individuals (df=4, X^2=31.76, P <0.0001; df=4, X^2=236.14, P <0.0001).

Activities at pipelines

For the animals which associated with pipelines, we compared their speed distribution within the vicinity (<100m) of the pipeline section they associated with and that of their whole trip (defined as the period between haul-outs) which included both travelling (typically fast speeds) and foraging. Locations were available at irregular intervals with, in general, a lower frequency than for those animals which used the wind farms. Thus the locations were regularized onto a 1 hour time line and the speed calculated using the distance travelled in each 1 hour. If there was over 1 hour between an interpolated location and the prior or following observed location then that interpolated location and following interpolated location were removed. For two animals, this resulted in less than ten reliable locations within 100m of the pipelines and thus the speed distributions of these animals were not considered.

video_S1.mpg

Video S1. Four of thirteen trips of an individual to Sheringham Shoal. White points show structures including turbines and sub-stations. The seal's track is shown in red with the yellow pointer updating every half an hour of the track.
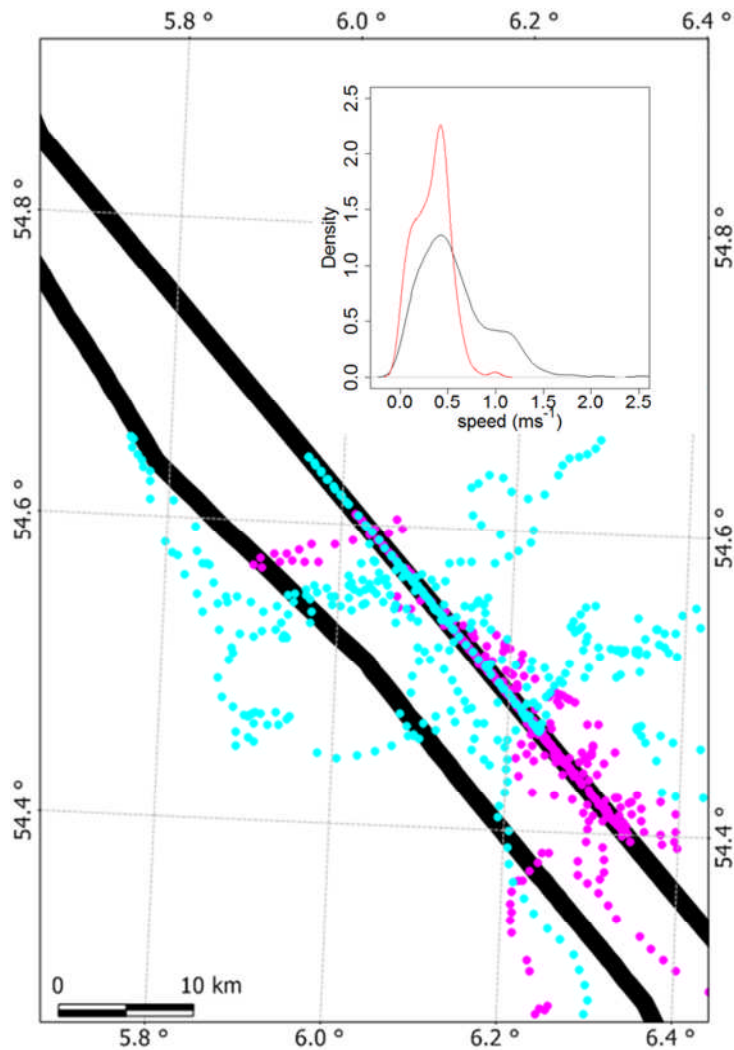
Figure S1. The tracks of an individual around at a pipeline, colored by trip. Also shown is then density distribution of speeds when within 100m of the pipeline (red) and for the rest of the trips (black).

References

1. McClintock, B.T., Russell, D.J.F., Matthiopoulos, J., and King, R. (2013). Combining individual animal movement and ancillary biotelemetry data to investigate population-level activity budgets. Ecology *94*, 838-849.
2. Brooks, S.P., and Roberts, G.O. (1998). Convergence assessment techniques for Markov chain Monte Carlo. Statistics and Computing *8*, 319-335.
3. Pirotta, E., Matthiopoulos, J., MacKenzie, M., Scott-Hayward, L., and Rendell, L. (2011). Modelling sperm whale habitat preference: a novel approach combining transect and follow data. Marine Ecology Progress Series *436*, 257-272.