**Supplementary Data SD1.**—Code for the Bayesian logistic regression model used to estimate median length-at-birth for long-finned pilot whales (*Globicephala melas edwardii*) stranded on the New Zealand coast. The model was fitted using Stan (Stan Development Team 2021) in R (R Development Core Team 2021)

```
data {
  int<lower=1> n; // total number of observations
  int<lower=0,upper=1> Y[n]; // response variable
  vector[n] X; // continuous predictor variable
 vector[n] weights; // weights
  real prior_mean_m ; // mean for normal prior on m
real<lower=0> prior_sd_m ; // standard deviation for normal prior on m
  real<lower=0> prior_sd_w ; // standard deviation for normal prior on w
}
parameters {
  real m ; // m = L50 = median length at birth
  real<lower=0> w ; // w = rate parameter, lower bound because postnatal
definitely longer on average
}
model {
  for(i in 1:n) {
   target += weights[i] * bernoulli logit lpmf( Y[i] | w * ( X[i] - m ) ) ;
  }
  target += normal_lpdf( m | prior_mean_m , prior_sd_m ) ;
  target += normal lpdf( w \mid 0 , prior sd w ) ;
}
generated quantities {
  real log_lik[n] ;
  for (i in 1:n) {
     log_lik[i] = weights[i] * bernoulli_logit_lpmf(Y[i] | w * ( X[i] - m )) ;
  }
}
```

**Supplementary Data SD2.**—Prior predictive simulation of p (probability of birth) given x (length) for long-finned pilot whales (*Globicephala melas edwardii*) stranded on the New Zealand coast based on prior distributions for Bayesian logistic regression model parameters  $m = l_{50} \sim N(171, 20)$  and  $w = \omega \sim N^+(0, 1)$ . The simulation was fitted using Stan (Stan Development Team 2021) in R (R Development Core Team 2021)



R code for SD2:

```
# Function for calculating P(y = 1) given x, w, and m
sim_hof2 <- function(x, m, w) {
    eta = w * ( x - m )</pre>
  inv_logit (eta)
}
# set number of simulations
nsim = 500
# draw values of m and w from priors, calculate P, and make plot
expand grid( x = 50:250,
              data.frame(m = rnorm(nsim, 171, 20),
                          w = abs(rnorm(nsim, 0, 1)),
                          group = 1:nsim)) %>%
  mutate(p = sim hof2(x = x, m = m, w = w)) \$>\$
  # group_by(group) %>%
  ggplot() +
    aes(x = x, y = p, group = group) +
    geom line(alpha = 3/50)
```

**Supplementary Data SD3.**—Posterior distribution of the difference in estimated median length-at-birth (mean with 66% and 95% highest posterior density intervals) between male and female long-finned pilot whales (*Globicephala melas edwardii*) stranded on the New Zealand coast (n = 169)



**Supplementary Data SD4.**—Sex versus seven linear body measurements of long-finned pilot whales (*Globicephala melas edwardii*) stranded on the New Zealand coast (1948 – 2017). Total length (male: n = 188, female n = 519); Ujaw anus (male: n = 43, female n = 119); Ujaw genital (male: n = 64, female n = 186); Ujaw dorsal (male: n = 71, female n = 184); Ujaw pectoral (male: n = 80, female n = 216); Ujaw blowhole (male: n = 68, female n = 176); and Ujaw gape (male: n = 48, female n = 113). Colors represent the individuals' sex: female = red, male = blue. Cor = Spearman's rank correlation coefficients. All measurements in cm



**Supplementary Data SD5.**—Sex versus total body length, four appendage measurements, axillary girth, snout and genital slit length of long-finned pilot whales (*Globicephala melas edwardii*) stranded on the New Zealand coast (1948 – 2017). Total length (male: n = 188, female n = 519); Height dorsal (male: n = 31, female n = 91); Pectoral length (male: n = 67, female n = 183); Pectoral width (male: n = 38, female n = 87); Fluke width (male: n = 53, female n = 139); Axill girth (male: n = 44, female n = 125); Snout length (male: n = 26, female n = 80); and Genital slit (male: n = 14, female n = 37). Colors represent the individuals' sex: female = red, male = blue. Cor = Spearman's rank correlation coefficients. All measurements in cm



## LITERATURE CITED

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