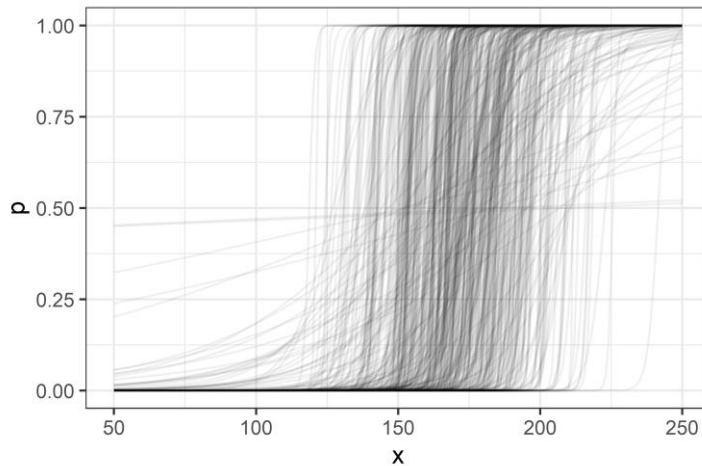


## SUPPLEMENTARY DATA

**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 | 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)



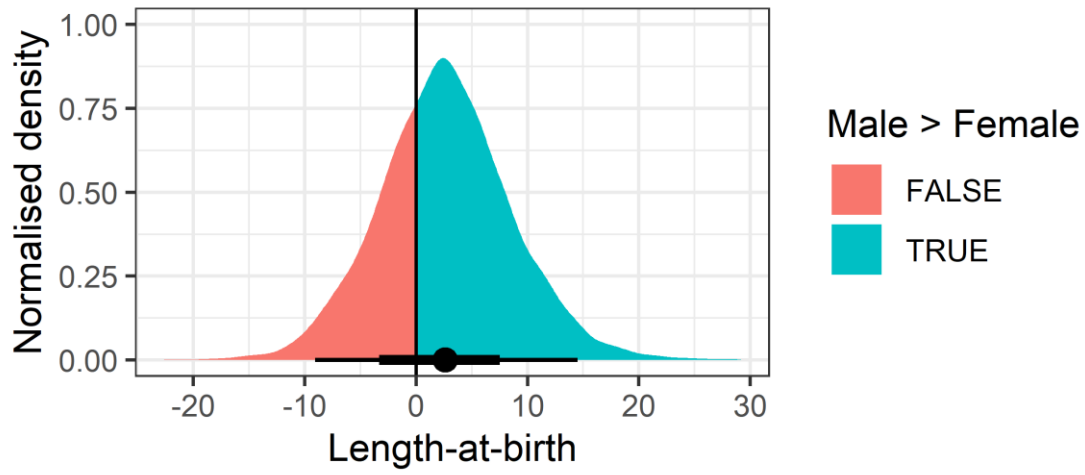
R code for SD2:

```
# Function for calculating P(y = 1) given x, w, and m
sim_hof2 <- function(x, m, w) {
  eta = w * ( x - m )
  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 ( $n = 169$ )







## LITERATURE CITED

- R DEVELOPMENT CORE TEAM. 2021. R: A Language and Environment for Statistical Computing. Foundation for Statistical Computing, R., Vienna, Austria. [www.R-project.org/](http://www.R-project.org/).
- STAN DEVELOPMENT TEAM. 2021. Stan Modeling Language Users Guide and Reference Manual, 2.27. <https://mc-stan.org>