Supplement. Details of the numerical methods used in R and additional information on model selection and evaluation of sampling biases

Methodological details

The following R syntax was used to (1) compute the derivative of the model describing variation in the prevalence of skull lesions across dolphin age, $\hat{f}'(a)$, and the net rate of change in lesion prevalence with respect to age, $\hat{z}(a)$, and (2) evaluate these functions on a fixed grid of 100 points equally spaced along the full range of age classes:

```r
Data <- read.table("Data.csv", sep="", header=TRUE) #read dataset
library(gamlss) #load gamlss library
mod.cs <- gamlss(lesion ~ cs(age,2), data= Data, family= BI, trace =FALSE) # Fit model to data using GAMLSS
x <- as.vector(mod.cs$mu.x[,2])
y <- mod.cs$mu.fv
sm <- smooth.spline(x, y)  # Fit spline to model; identical to mod.cs
m.grid =100    #Set m points to evaluate functions; m =100
#Set a grid of m evenly-spaced points on which to evaluate the spline:
eval.grid <= seq(from=min(Data[,2]),to=max(Data[,2]),length.out=m.grid)
fit <- predict(sm, x=eval.grid)  #fitted values over range of m grid values
d1 <- predict(sm, x=eval.grid, deriv = 1) #derivative values over range of m grid values
mort <- fit$y*d1$y       #z(a) function over range of m grid values
```

Model selection

Candidate GAMLSS models allowing 4 different binomial-type distributions (binomial, beta-binomial, 0-inflated binomial and 0-inflated beta-binomial) for the response variable were tested over a range of functions: linear, exponential, cubic soothing spline and penalized B-splines (Table S1).
Table S1. Akaike’s Information Criteria (AIC) for the different GAMLSS models being tested. The AIC corresponding to the best model is shown in **bold**. Pb-spline: penalized B-spline; Cs-spline 6 (Cs-spline 4): cubic smoothing spline with 6 (4) effective df. Distributions tested were BI: binomial; BB: beta-binomial; ZIBI: 0-inflated binomial; ZIBB: 0-inflated beta-binomial

<table>
<thead>
<tr>
<th>Model</th>
<th>BI</th>
<th>BB</th>
<th>ZIBI</th>
<th>ZIBB</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linear</td>
<td>387.84</td>
<td>389.84</td>
<td>389.82</td>
<td>391.82</td>
</tr>
<tr>
<td>Pb-spline</td>
<td>384.21</td>
<td>386.17</td>
<td>386.19</td>
<td>388.19</td>
</tr>
<tr>
<td>Cs-spline 6</td>
<td>384.20</td>
<td>386.10</td>
<td>386.09</td>
<td>388.10</td>
</tr>
<tr>
<td>Cs-spline 4</td>
<td><strong>384.09</strong></td>
<td>386.02</td>
<td>386.03</td>
<td>388.03</td>
</tr>
<tr>
<td>Logarithmic</td>
<td>389.77</td>
<td>391.77</td>
<td>391.76</td>
<td>393.76</td>
</tr>
<tr>
<td>Exponential</td>
<td>388.82</td>
<td>390.82</td>
<td>390.83</td>
<td>392.83</td>
</tr>
</tbody>
</table>

**Evaluation of sampling biases**

The potential effect of differences in sampling selectivity between infected and uninfected dolphins on estimates of net rate of change in lesion prevalence with respect to age were evaluated by means of weighted GAMLSS regressions. Fig. S1 compares the original model (assuming no sampling biases) with one obtained assuming that infected animals were 2 times more likely to be incidentally killed in the fishery than uninfected ones. Estimates were clearly reduced in the latter case, but the overall behaviour of the model was similar to that of the original model.

Fig. S1. *Stenella attenuata*. Variation in the net change rate in skull lesion prevalence across dolphin age (continuous lines) with bootstrapped standard error bands (dashed lines) and 95% confidence intervals (grey area). (a) Original Model assuming no sampling biases in favour of infected dolphins. (b) Weighted model assuming that infected dolphins were 2 times more likely to be incidentally caught than uninfected ones.