

Appendix S5

Model evaluation

A warming western boundary current increases the prevalence of commercially disruptive parasites in broadbill swordfish

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Section S1: Prevalence model

Equation S1

The model used to investigate the effect of season for the prevalence dataset is described below:

$$\begin{aligned} \text{logit}(\pi_{ij}) = & \alpha + \beta_1 \times \text{SeasonWinter}_{ij} \\ & + \beta_2 \times \text{SeasonSummer}_{ij} \\ & + \beta_3 \times \text{SeasonSpring}_{ij} \\ & + a_i \\ & + \varepsilon_{ij} \end{aligned}$$

where

$$\begin{aligned} Y_{ij} & \sim \text{Bin}(1, \pi_{ij}) \\ a_i & \sim N(0, \sigma^2_i) \\ \varepsilon_{ij} & \sim N(0, \sigma^2) \end{aligned}$$

Figure S1

The seasonal model of infected swordfish prevalence. Left: Distribution of coefficients, where *SeasonAutumn* is the intercept. Right: The model satisfies residual assumptions. There are no outliers, and there are no issues with variances within and/or between groups.

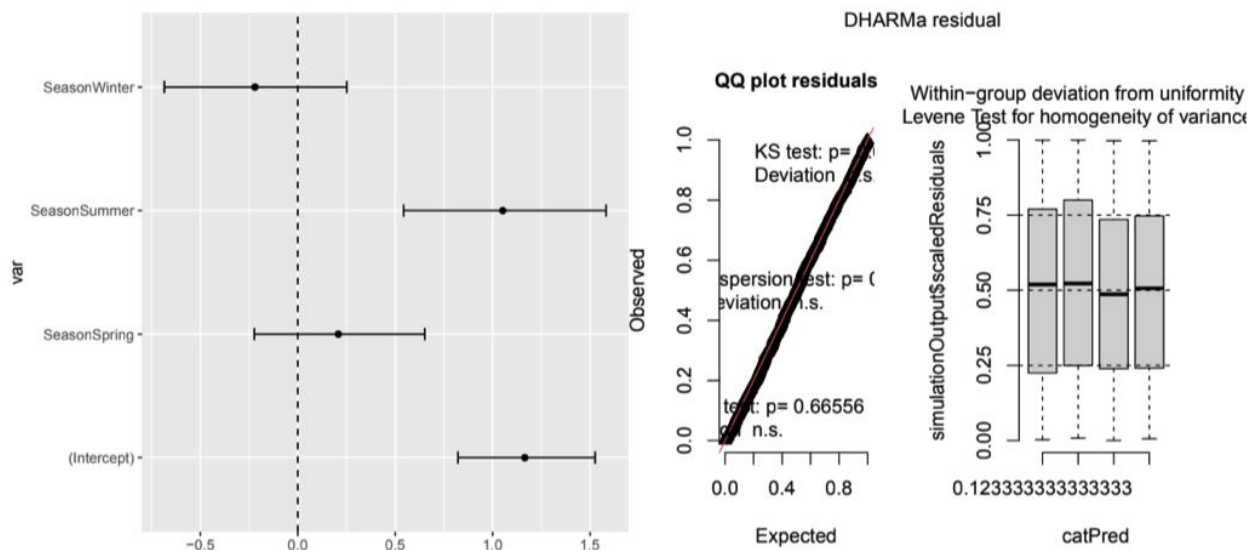


Figure S2

Distribution of coefficients in the best model using environmental covariates. Using Wald-Z significance tests, we get the following predictors in our models, after accounting for correlation between swordfish harvested in the same fishing trip.

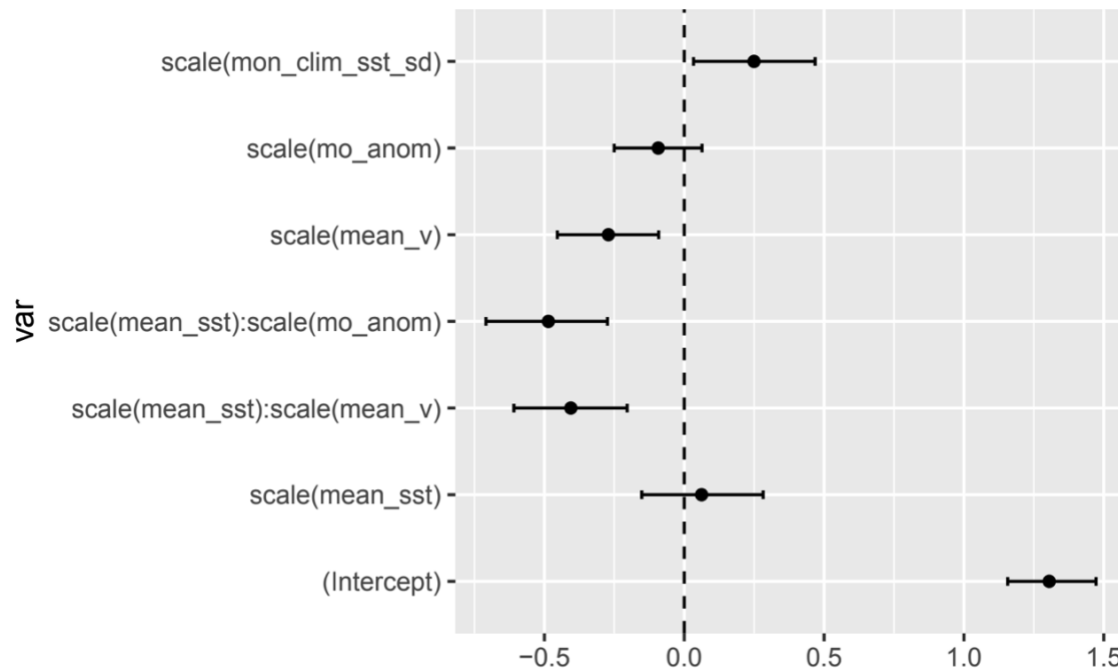


Figure S3

Variance inflation factor (VIFs) of the best model.

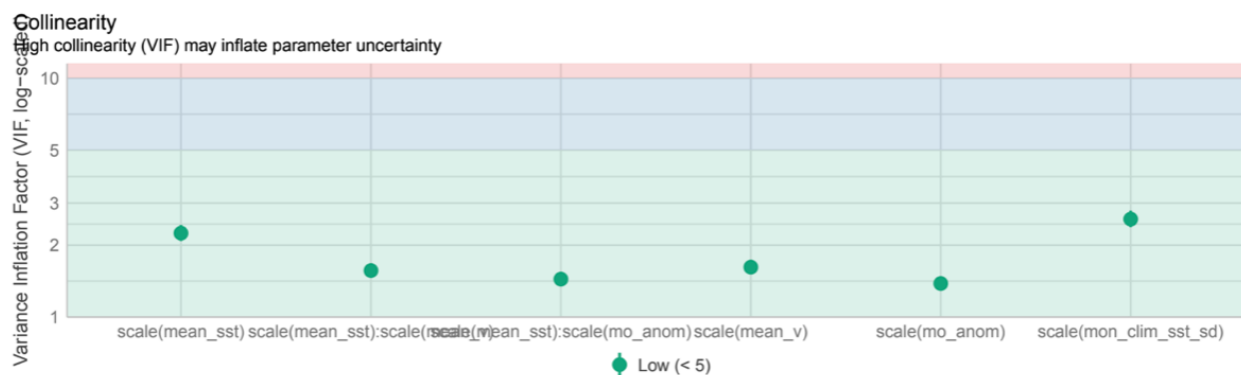


Figure S4

Log likelihood values of models fit with different optimizers. All available optimizers to fit the model converge to identical log likelihood values, meaning the model is not sensitive to optimizer choice. We used Nelder-Mead (i.e., the default) in the final model.

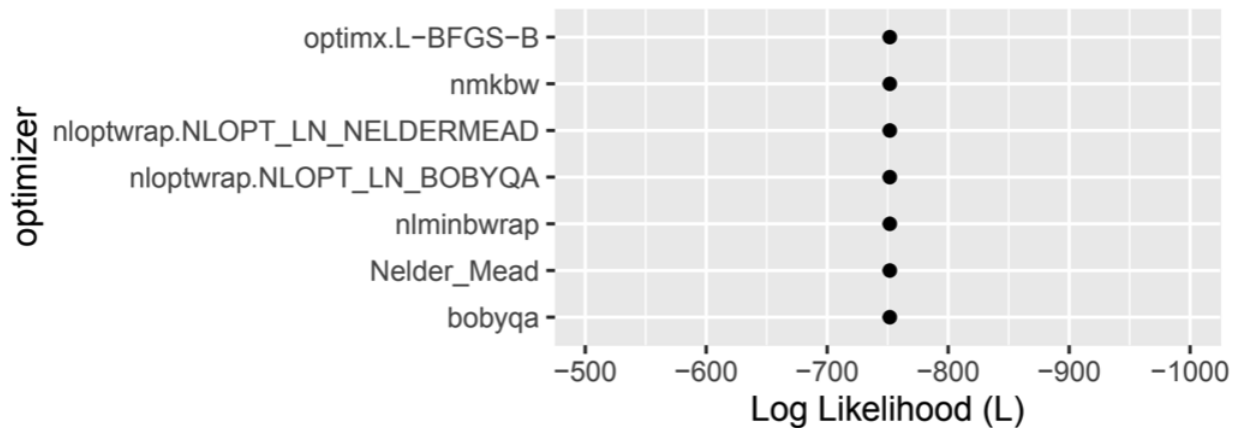


Figure S5

Estimates and 95% confidence/credible intervals of coefficients from the best model, refit with different modelling frameworks available for binomial GLMMs. For the STAN model, we used diffuse priors. All models yielded similar estimates and CIs, meaning the results are not sensitive to the model fitting routine. Methods of parameter estimation:

- `glmmADMB`: AD Model Builder software to estimate maximum likelihood
- `glmmTMB`: Template Model Builder to estimate maximum likelihood
- `glmer`: Laplace Approximation to estimate maximum likelihood
- `glmmPQL`: Estimates penalised quasi-likelihood
- `stan_glmer`: Stan software for Bayesian estimation via Markov Chain Monte Carlo sampling
- `fitme`: Laplace Approximation to estimate maximum likelihood

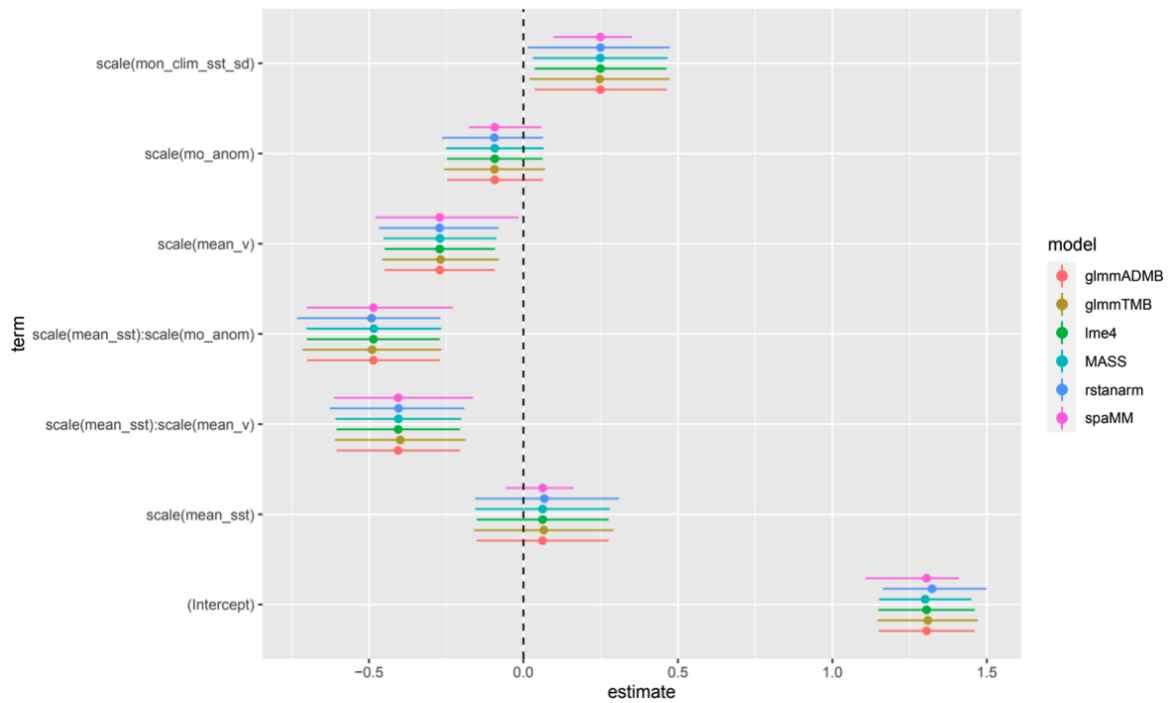


Figure S6

Simulation-based approach of checking scaled residuals from the fitted model. Left: Uniform QQ-plot shows no significant deviations assumptions. Right: Residuals vs fitted values with smooth splines indicate no significant deviations from model assumptions.

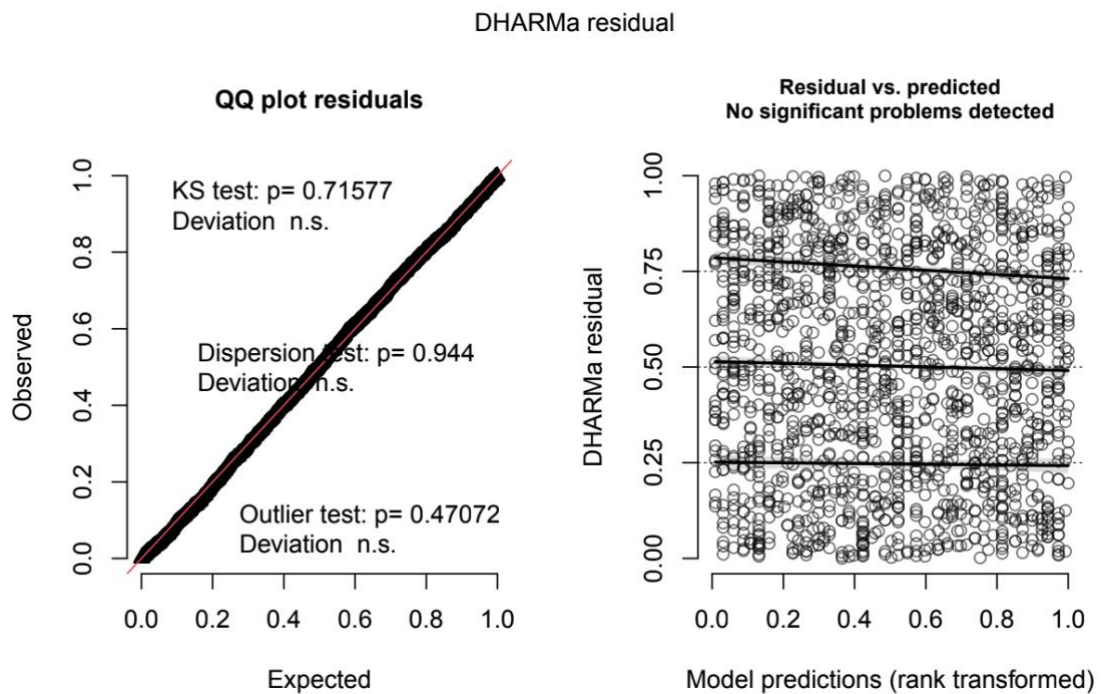


Figure S7

Assessing spatial correlation in the residuals. Top left: Correlogram +/- 95% CIs. There are no significant deviations from 0, meaning no evidence of autocorrelation. Top right: Sample variogram of model residuals. Bottom left: Sample variogram of model residuals for each direction. All variograms are plotted with a cubic regression spline. Variograms suggest no spatial correlation in residuals. Plotting the residuals over the spatial domain (plot not shown due to confidentiality of fishing locations) depicts no clustering of positive or negative residuals.

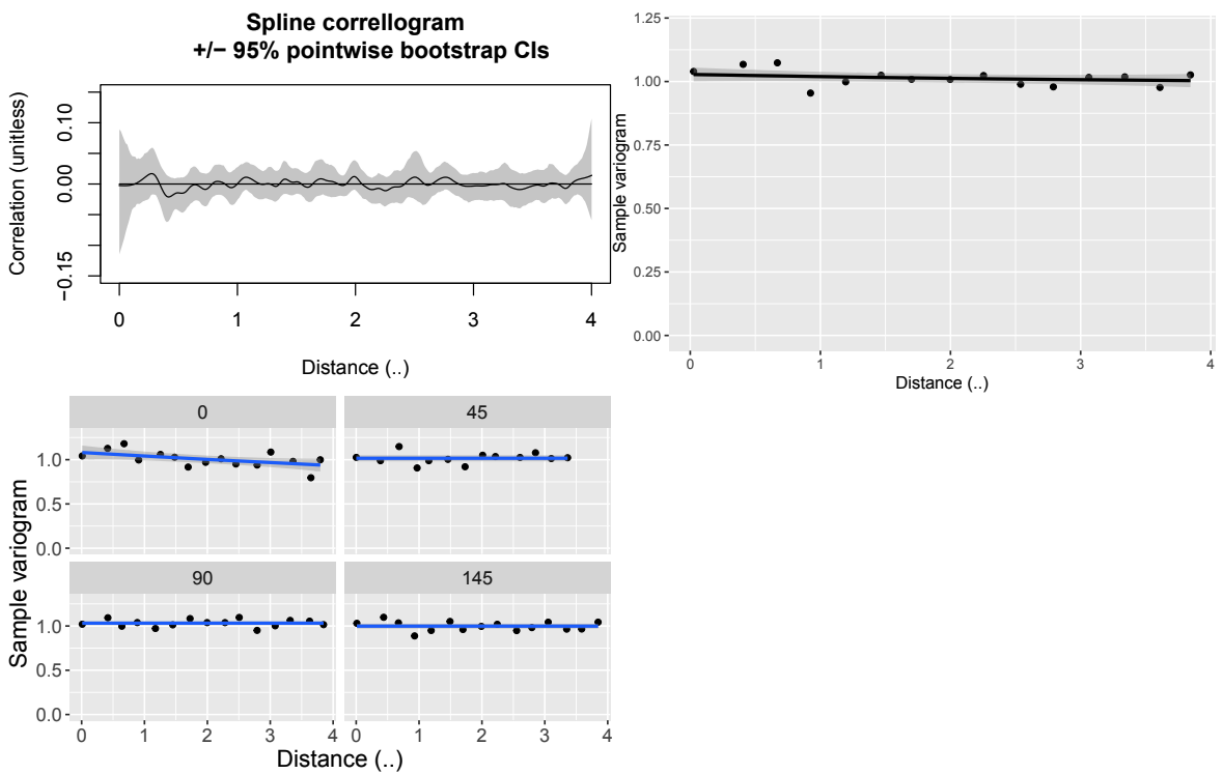
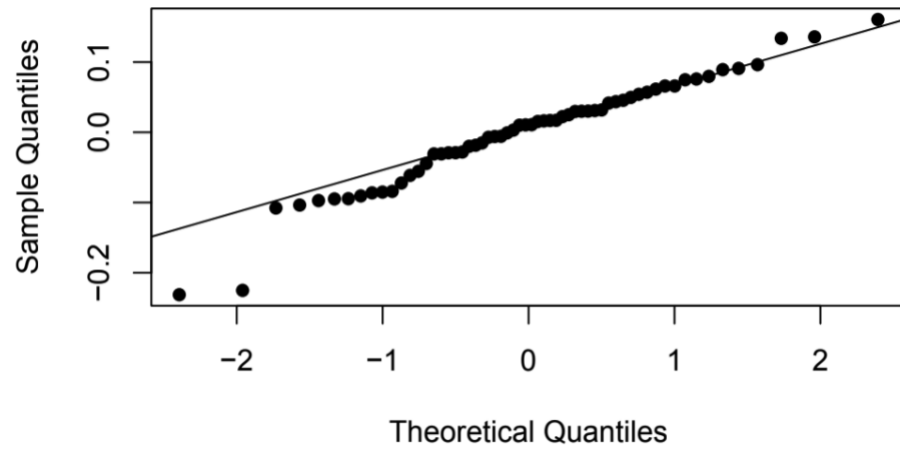


Figure S8

Assessing normality of the random effect. The random effect estimates are more-or-less normally distributed.



Section S2: Intensity model

Equation S2

The model used to investigate the effect of season is described below:

$$\begin{aligned} \log(\mu_{ij}) = & \alpha + \beta_1 \times \text{SeasonWinter}_{ij} \\ & + \beta_2 \times \text{SeasonSummer}_{ij} \\ & + \beta_3 \times \text{SeasonSpring}_{ij} \\ & + a_i \\ & + \varepsilon_{ij} \end{aligned}$$

where

$$\begin{aligned} Y_{ij} & \sim \text{NB}(\mu_{ij}, k) \\ a_i & \sim N(0, \sigma^2_i) \\ \sigma^2 & = \mu(1 + \mu/k) \end{aligned}$$

Figure S9

The seasonal model of infection intensity. Top left: Simulated residuals for the season model. Assumptions of between and within-group variances are violated, indicated by the failed KS and levene tests. Top right: Simulated residuals after modelling the dispersion between groups via `glmmTMB`. Note that modelling within-group variances with an observation level random effect would fix the KS test problem; however, modelling both the dispersion within and between groups (i.e., with both an OLRE and dispersion formula in the model) resulted in model non-convergence. Therefore, we acknowledge there is significant variance within groups of our final model, and choose the model that models dispersion between groups (top right) and interpret results with caution. Bottom row: Distribution of model coefficients.

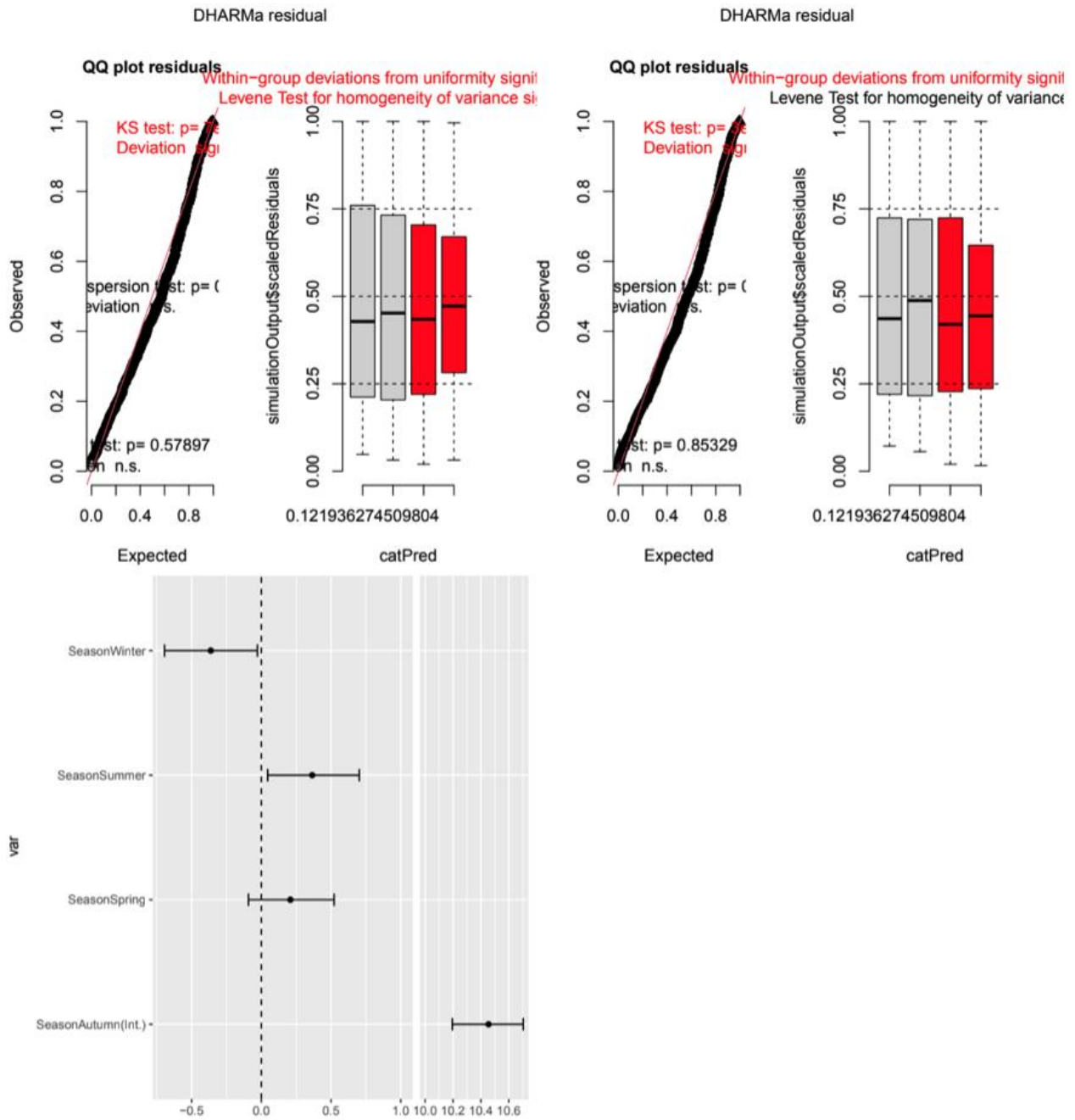


Figure S10

Distribution of coefficients in the best model. Using Wald-Z significance tests, we get the following predictor in our model, after accounting for correlation between swordfish harvested in the same fishing trip.

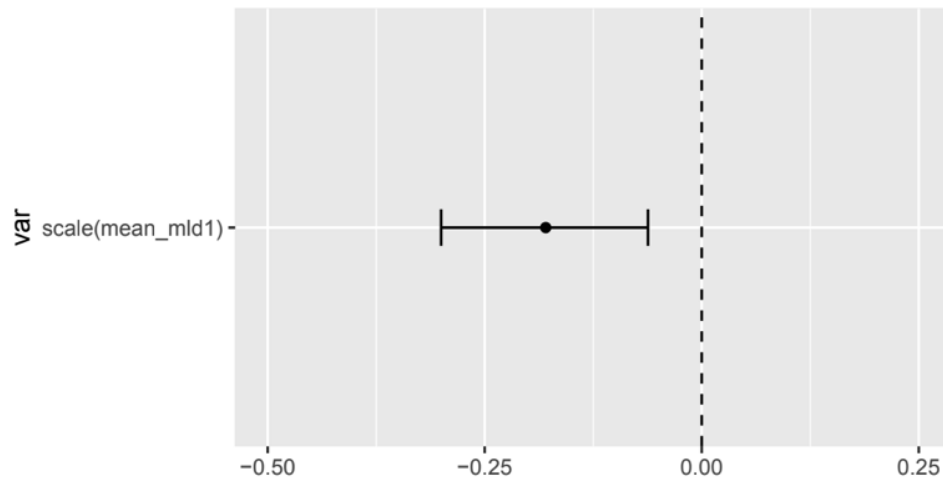


Figure S11

Assessing overdispersion in the model. σ_p is 1.29, meaning the model is slightly overdispersed, particularly at higher predicted spore counts. However, negative binomial models can still perform well with a dispersion ratio of up to ~5 (Payne et al., 2018).

Overdispersion and zero-inflation

Observed residual variance (green) should follow predicted residual variance (blue)

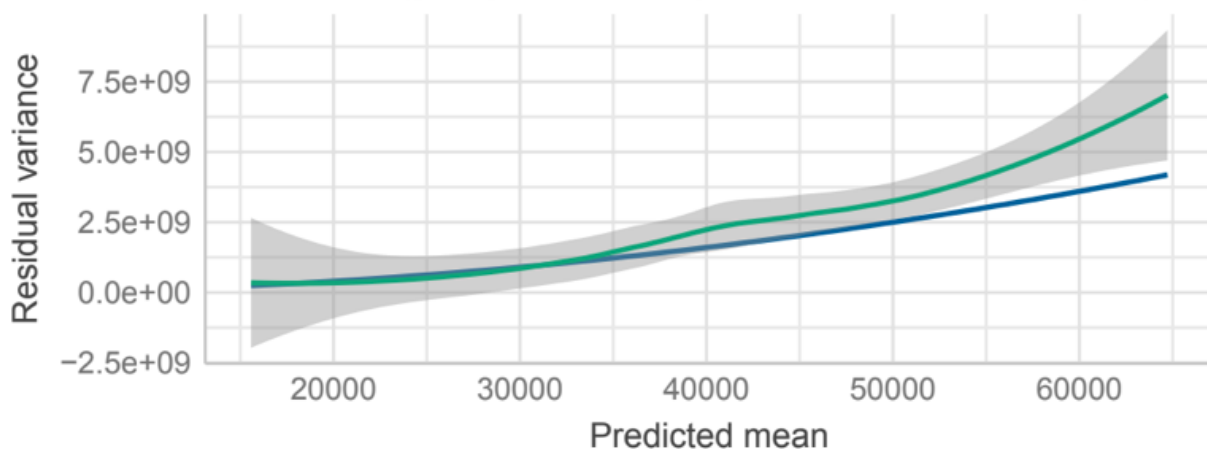


Figure S12

Log likelihood values of models fit with different optimizers. All available optimizers to fit the model converge to identical log likelihood values, meaning the model is not sensitive to optimizer choice. We used Nelder-Mead (i.e., the default) in the final model.

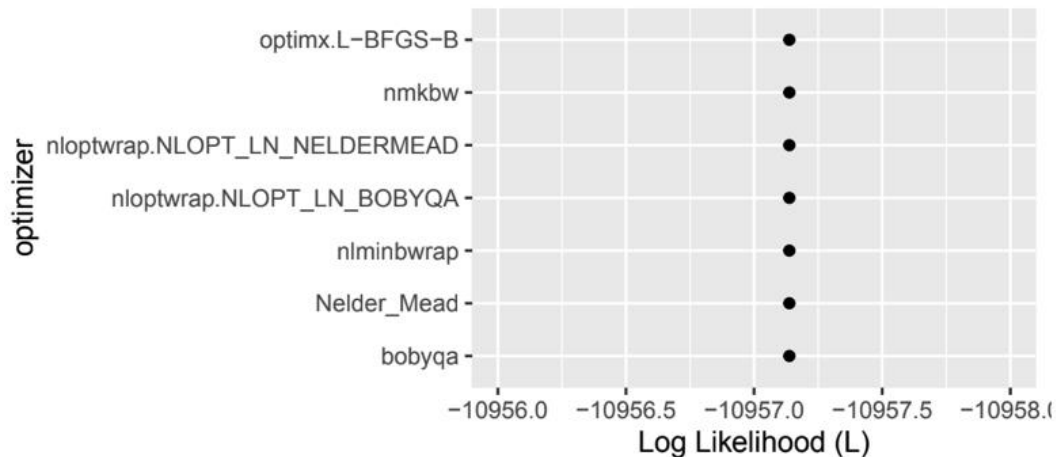


Figure S13

Estimates and 95% confidence/credible intervals of coefficients from the best model, refit with different modelling frameworks available for negative binomial mixed-effects models. All models were fitted with the NB2 parameterisation. For the STAN model, we used diffuse priors. All models yielded similar estimates and CIs, meaning the results are not sensitive to model fitting routine.

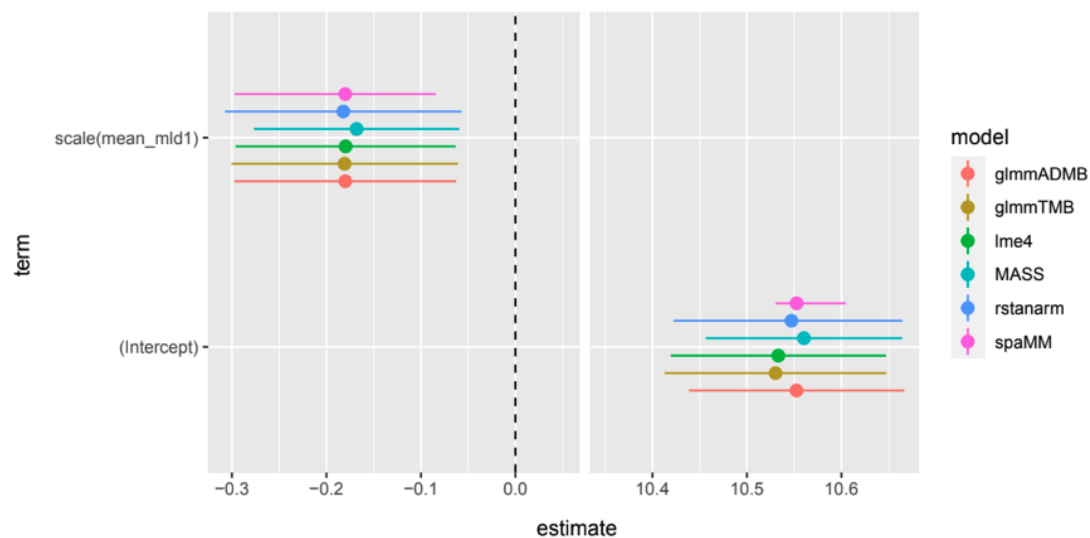


Figure S14

Simulated residuals for the model. Left: QQplot demonstrates slight non-uniformity of the residuals, with a significant Kolmogorov-Smirnov (KS) normality test ($P = 0.004$). This is to be expected since our model is slightly overdispersed ($\sigma_p = 1.29$). Introducing an observation-level-random-effect to the model, to satisfy the KS test, results in model non-convergence, so we leave the model as is. Right: Residuals vs fitted plot, with quantile regressions fit on the 0.25, 0.5 and 0.75 quantile. The spline at the location of the 0.25 quantile deviates from a flat line ($P = 0.03$), indicated by the red colour. However, the effective degrees of freedom of the spline are only 1.9, which in our opinion, is not wiggly enough to warrant refitting the model with a generalised additive mixed model (GAMM). Since this is only a minor violation, combined with the fact that the second and third quartiles satisfy assumptions, we continue the analysis.

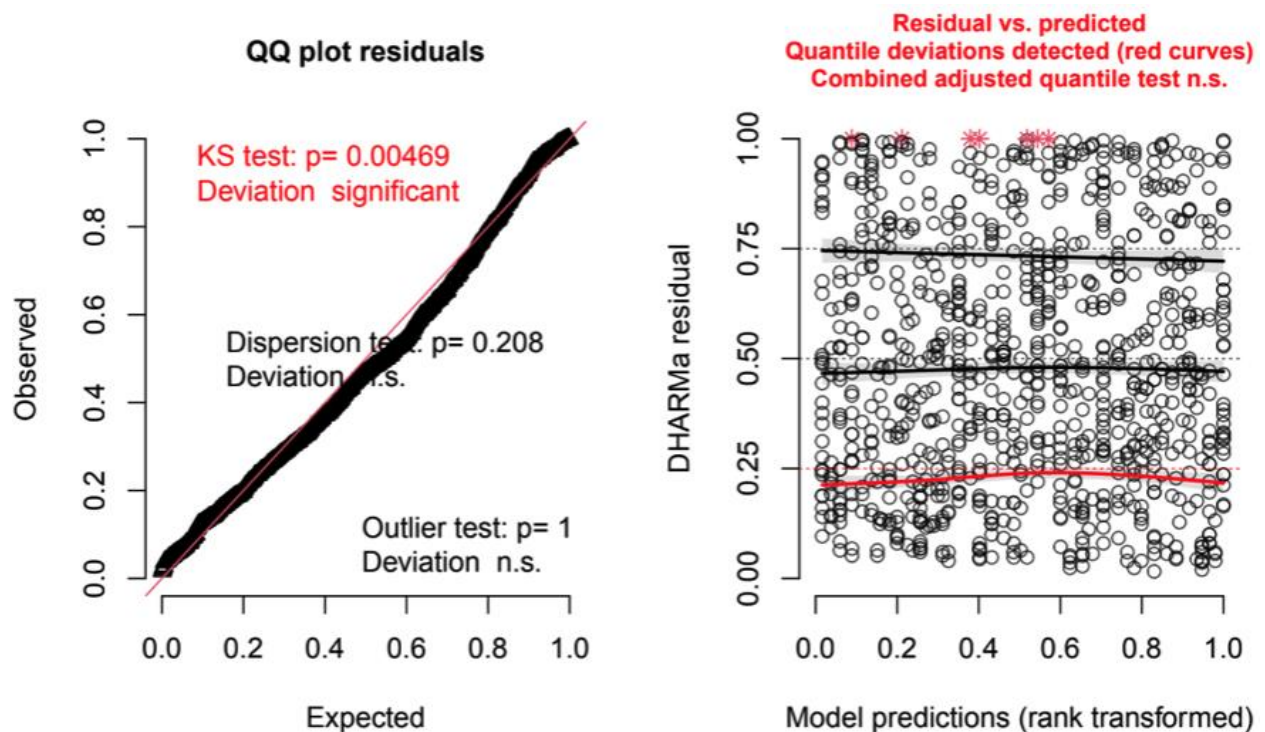


Figure S15

Assessing spatial correlation in the residuals. Top left: Correlogram $\pm 95\%$ pointwise bootstrap CIs. There are no significant deviations from 0, meaning no evidence of autocorrelation. Top right: Sample variogram of model residuals. Bottom left: Sample variogram of model residuals for each direction. All variograms are plotted with a cubic regression spline. Variograms suggest no spatial correlation in residuals. Plotting the residuals over the spatial domain (plot not shown due to confidentiality of fishing locations) depicts no clustering of positive or negative residuals.

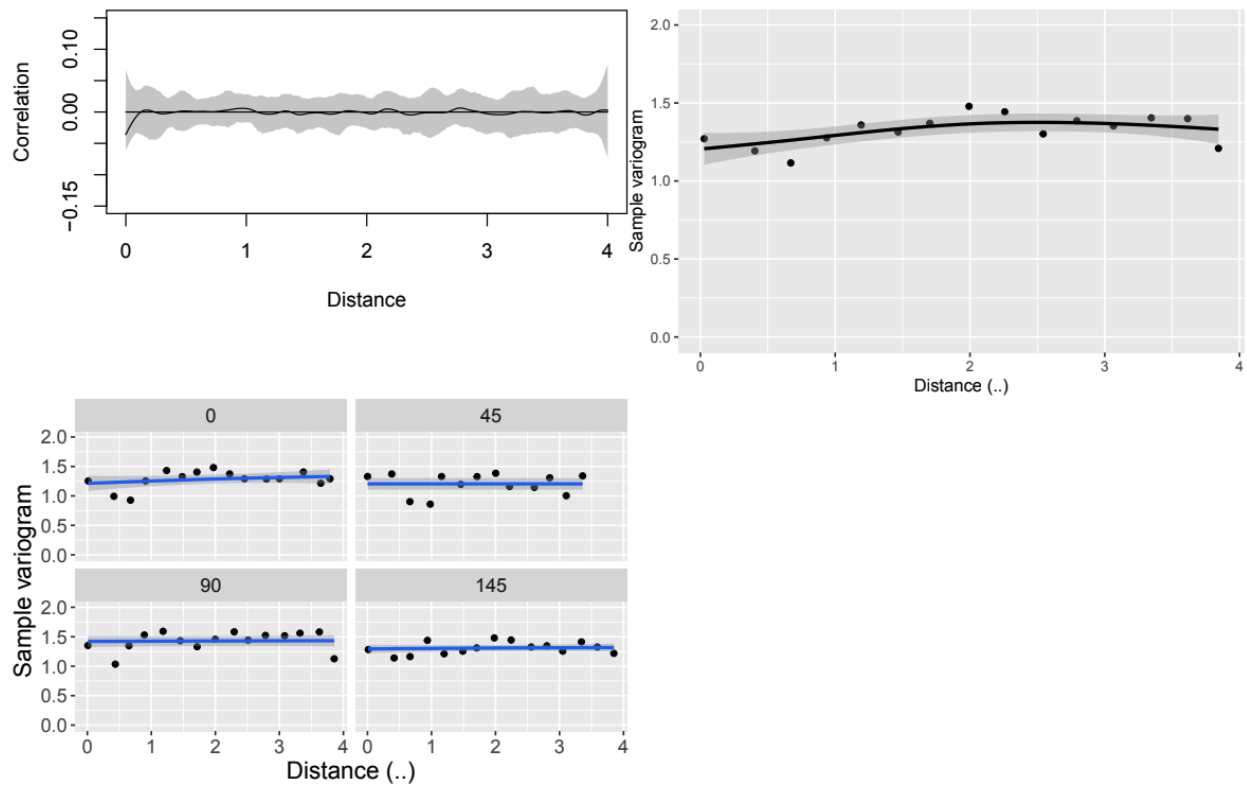


Figure S16

Assessing normality of the random effect: Random effects are more-or-less normally distributed.

