Supplementary material

Multiscale relationships between stream temperature and juvenile recruitment in an imperilled freshwater fish

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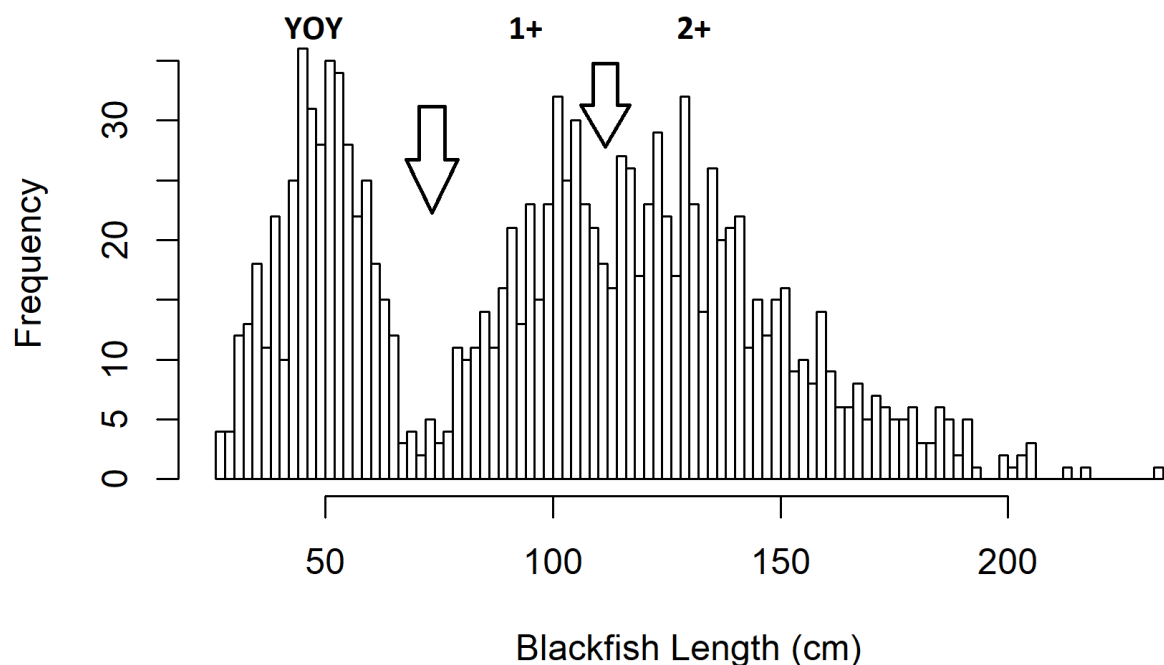[F]Corresponding author. Email: mischa.turschwell@griffithuni.edu.au

Fig. S1. Length frequency histogram of over 1000 blackfish sampled in 2014 used to separate young-of-the-year (YOY) (<70 mm) and 2+ year fish (>115 mm).

Description

Recruitment rate model

Model 1. Bayesian single level regression model

Site-scale recruitment rate was assumed to follow a normal distribution, with the mean related to a single site-scale predictor:

$$y_i \sim N(\mu_i, \tau)$$
$$\mu_i = \beta_0 + \beta_1 X_i$$

where y_i is the logit transformed recruitment rate at the ith site, μ_i is the mean of the posterior distribution estimating juvenile recruitment rate, which is related to a site-scale predictor, X_1 and τ is the precision of the normal distribution. β_0 and β_1 are the intercept and slope respectively and are assumed to follow normal distributions.

To complete the Bayesian specification of the likelihood structure, the following 'uninformative' prior distribution was used (Gelman *et al*. 2004):

$$\beta_0 \sim N(0, 0.001)$$
$$\beta_1 \sim N(0, 0.001)$$
$$\tau \sim \Gamma(2, 0.5)$$

Model 2. Bayesian random effects model

At the lower level of the model, site-scale recruitment rate was assumed to follow a normal distribution, with the mean related to a single site-scale predictor:

$$y_{ij} \sim N\left(\mu_{ij}, \tau\right)$$
$$\mu_{ij} = \beta_{j0} + \beta_{j1} X_{ij1}$$
$$\beta_{jk} \sim N(\widehat{\beta}_{jk}, \Pi_k)$$

where y_{ij} is the logit transformed recruitment rate at the ith site in the jth segment, μ_{ij} is the mean of the posterior distribution estimating juvenile recruitment rate and τ is the precision of the normal distribution. β_{jk} represents all slopes and intercepts where β_{j0} are the intercepts of the lower-level model and with the mean-centring of the predictor variables, represents the estimated segment juvenile recruitment rate given mean lower-level predictors in the jth segment, β_{j1} are the slope terms of the lower-level model that quantify the fine-scale (within segment) relationships between juvenile recruitment rate and the site-scale predictor (X_1) in the jth segment; and Π_k are the precisions of the normal distributions for β_{jk}. The lower-level regression coefficient estimates $\hat{\beta}_{jk}$ are assumed to be normally distributed.

To complete the Bayesian specification of the likelihood structure, the following 'uninformative' prior distributions were used (Gelman *et al*. 2004):

$$\tau \sim \Gamma(2, 0.5)$$

$$\widehat{\beta}_{jk} \sim N(0, 0.001)$$

$$\Pi_k \sim \Gamma(2, 0.5)$$

Model 3. Bayesian hierarchical model

At the lower level of the model, site-scale recruitment rate was assumed to follow a normal distribution, with the mean related to a single site-scale predictor:

$$y_{ij} \sim N\left(\mu_{ij}, \tau\right)$$

$$\mu_{ij} = \beta_{j0} + \beta_{j1}X_{ij1}$$

$$\beta_{jk} \sim N(\widehat{\beta}_{jk}, \Pi_k)$$

where y_{ij} is the logit transformed recruitment rate at the ith site in the jth segment, μ_{ij} is the mean of the posterior distribution estimating juvenile recruitment rate and τ is the precision of the normal distribution. β_{jk} represents all slopes and intercepts where β_{j0} are the intercepts of the lower-level model and with the mean-centring of the predictor variables, represents the estimated segment juvenile recruitment rate given mean lower-level predictors in the jth segment, β_{j1} are the slope terms of the lower-level model that quantify the fine-scale (within segment) relationships between juvenile recruitment rate and the site-scale predictor (X_1) in the jth segment; and Π_k are the precisions of the normal distributions for β_{jk}. We then quantified how the lower-level regression coefficient estimates ($\hat{\beta}_{jk}$) varied systematically with segment maximum weekly maximum temperature (MWMT) (Z_j) at the upper-level of the model,

$$\widehat{\beta}_{jk} = \Omega_{k0} + \Omega_{k1}Z_j$$

where Ω_{k0} and Ω_{k1}, are the intercept and slope of the upper-level relationship, respectively. The fine-scale intercepts (β_{j0}) are estimates of the segment-level recruitment rate given mean lower-level predictors, allowing the upper-level regression of these parameters to quantify the direct relationship between segment MWMT and the mean juvenile recruitment rate.

To complete the Bayesian specification of the likelihood structure, the following 'uninformative' prior distributions were used (Gelman *et al*. 2004):

$$\tau \sim \Gamma(2, 0.5)$$

$$\Pi_k \sim \Gamma(2, 0.5)$$

$$\Omega_{k,l} \sim \text{MVN}(\mathbf{0}, 0.001\text{I})$$

Juvenile abundance model

Model 4. Bayesian hierarchical Poisson model

At the lower level of the model, site-scale juvenile abundance was assumed to follow a Poisson distribution, with the mean related to two site-scale predictors:

$$y_{ij} \sim Pois\left(\lambda_{ij}\right)$$

$$\log\left(\lambda_{ij}\right) = \beta_{j0} + \beta_{j1}X_{ij1} + \beta_{j2}X_{ij2}$$

where y_{ij} is the juvenile abundance at the ith site in the jth segment, λ_{ij} is the log transformed mean of the posterior distribution estimating juvenile abundance and τ is the precision of the normal distribution.

β_{jk} represents all slopes and intercepts where, β_{j0} are the intercepts of the lower-level model and with the mean-centring of the predictor variables, represents the estimated segment juvenile abundance given mean lower-level predictors in the jth segment, β_{j1} are the slope terms of the lower-level model that quantify the fine-scale (within segment) relationships between juvenile abundance and the site-scale predictors, X_1 (riparian foliage cover, RFC) and X_2 (adult abundance) in the jth segment; and Π_k are the precisions of the normal distributions for β_{jk}. We then quantified how the lower-level regression coefficient estimates ($\hat{\beta}_{jk}$) varied systematically with segment MWMT (Z_j) at the upper-level of the model,

$$\beta_{jk} \sim N(\hat{\beta}_{jk}, \ \Pi_k)$$

$$\hat{\beta}_{jk} = \Omega_{k0} + \Omega_{k1}Z_j$$

where Ω_{k0} and Ω_{k1}, are the intercept and slope of the upper-level relationship respectively. The fine-scale intercepts (β_{j0}) are estimates of the segment-level abundance given mean lower-level predictors, allowing the upper-level regression of these parameters to quantify the direct relationship between segment MWMT and the mean juvenile abundance.

To complete the Bayesian specification of the likelihood structure, the following 'uninformative' prior distributions were used (Gelman *et al*. 2004):

$$\Pi_k \sim \Gamma(2, 0.5)$$
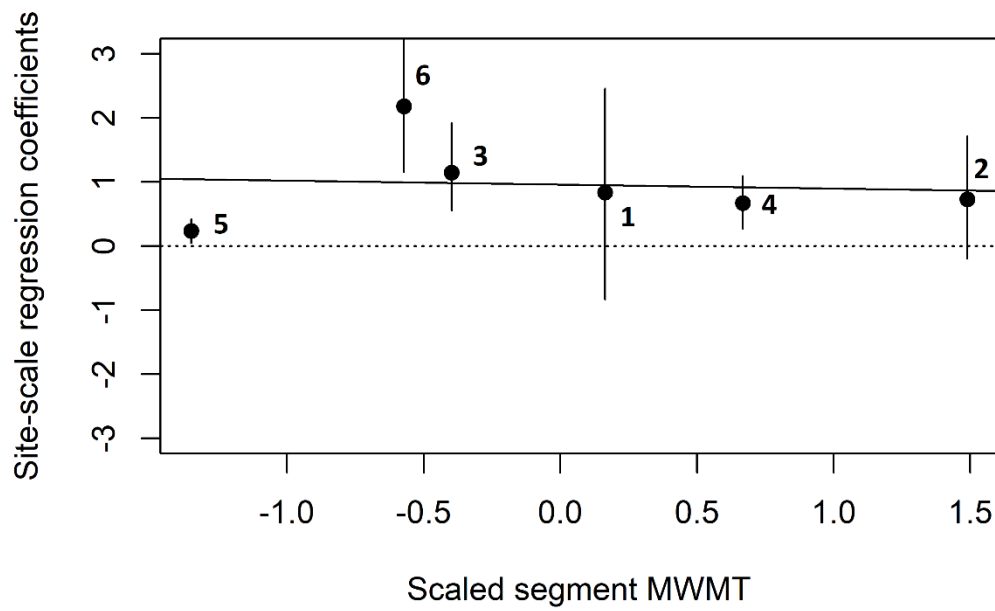
$$\Omega_{k,l} \sim MVN(\mathbf{0}, 0.001\mathbf{I})$$

Fig. S2. Lower-level slope coefficients (β_{j2}) *v*. scaled-segment maximum weekly maximum temperature (MWMT) for the juvenile abundance model. These coefficients quantify how the relationship between fine-scale, log-transformed juvenile abundance and Adult blackfish abundance changes as the MWMT increases. Error bars represent the 95% credible interval of the site-scale relationships and labels represent segment numbers.

Reference

Gelman, A., Carlin, J. B., Stern, H. S., and Rubin, D. B. (2004). 'Bayesian Data Analysis.' Texts in Statistical Science Series. (Chapman & Hall: New York, NY, USA.)