Supplementary material

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

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![Length frequency histogram](image)

**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 \( i \)th site, \( \mu_i \) is the mean of the posterior distribution estimating juvenile recruitment rate, which is related to a site-scale predictor, \( X_i \) and \( \tau \) is the precision of the normal distribution. \( \beta_0 \) and \( \beta_1 \) 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:

\[ y_{ij} \sim N(\mu_{ij}, \tau) \]
\[ \mu_{ij} = \beta_{j0} + \beta_{j1} X_{j1} \]
\[ \beta_{jk} \sim N(\hat{\beta}_{jk}, \Pi_k) \]

where \( y_{ij} \) is the logit transformed recruitment rate at the \( i \)th site in the \( j \)th segment, \( \mu_{ij} \) is the mean of the posterior distribution estimating juvenile recruitment rate and \( \tau \) is the precision of the normal distribution. \( \beta_{jk} \) represents all slopes and intercepts where \( \beta_{j0} \) 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 \( j \)th segment, \( \beta_{j1} \) 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 \( (X_i) \) in the \( j \)th segment; and \( \Pi_k \) are the precisions of the normal distributions for \( \beta_{jk} \). 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):

\[ \tau \sim \Gamma(2, 0.5) \]
\[ \hat{\beta}_{jk} \sim N(0, 0.001) \]
\[ \Pi_k \sim \Gamma(2, 0.5) \]

**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:

\[ y_{ij} \sim N(\mu_{ij}, \tau) \]
\[ \mu_{ij} = \beta_{j0} + \beta_{j1}X_{ij1} \]
\[ \beta_{jk} \sim N(\hat{\beta}_{jk}, \Pi_k) \]

where \( y_{ij} \) is the logit transformed recruitment rate at the \( i \)th site in the \( j \)th segment, \( \mu_{ij} \) is the mean of the posterior distribution estimating juvenile recruitment rate and \( \tau \) is the precision of the normal distribution. \( \beta_{jk} \) represents all slopes and intercepts where \( \beta_{j0} \) 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 \( j \)th segment, \( \beta_{j1} \) 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 \( (X_i) \) in the \( j \)th segment; and \( \Pi_k \) are the precisions of the normal distributions for \( \beta_{jk} \). 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,

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

where \( \Omega_{k0} \) and \( \Omega_{k1} \), are the intercept and slope of the upper-level relationship, respectively. The fine-scale intercepts (\( \beta_{j0} \)) 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):

\[ \tau \sim \Gamma(2, 0.5) \]
\[ \Pi_k \sim \Gamma(2, 0.5) \]
\[ \Omega_{k,l} \sim \text{MVN}(\mathbf{0}, 0.001\mathbf{I}) \]
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:

\[ y_{ij} \sim \text{Pois}(\lambda_{ij}) \]

\[ \log(\lambda_{ij}) = \beta_{j0} + \beta_{j1}X_{ij1} + \beta_{j2}X_{ij2} \]

where \( y_{ij} \) is the juvenile abundance at the \( i \)th site in the \( j \)th segment, \( \lambda_{ij} \) is the log transformed mean of the posterior distribution estimating juvenile abundance and \( \tau \) is the precision of the normal distribution. \( \beta_{jk} \) represents all slopes and intercepts where, \( \beta_{j0} \) 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 \( j \)th segment, \( \beta_{j1} \) 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 \( j \)th segment; and \( \Pi_k \) are the precisions of the normal distributions for \( \beta_{jk} \). 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,

\[ \beta_{jk} \sim N(\hat{\beta}_{jk}, \Omega_k) \]

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

where \( \Omega_{k0} \) and \( \Omega_{k1} \) are the intercept and slope of the upper-level relationship respectively. The fine-scale intercepts (\( \beta_{j0} \)) 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):

\[ \Omega_k \sim \Gamma(2, 0.5) \]

\[ \Omega_{k,i} \sim \text{MVN}(0, 0.001I) \]
**Fig. S2.** Lower-level slope coefficients ($\beta_{ij2}$) 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**