

Fish density

X_t

E

ω

Visual model

$$\lambda_t = X_t \cdot E_t$$

$$N_t \sim \text{Negative Binomial}(\lambda_t, \phi)$$

$$\phi = 20$$

(1)

Water model

$$W_t = X_t \cdot \omega$$

(2)

W_t

qPCR water model

$$U_t = (W_t \cdot F) / V$$

$$Z_{tr} \sim \text{Bernoulli}(\psi_t)$$

$$\psi_t = 1 - \exp(-U_t \cdot \theta)$$

$$Y_{trp} \sim \text{Normal}(\mu_{tp}, \sigma_t) \quad \text{if } Z_{tr} = 1$$

$$\mu_{tp} = \beta_0 + \beta_{1p} \cdot \ln(U_t)$$

$$\sigma_t = \exp(\gamma_0 + \gamma_1 \cdot \ln(U_t))$$

(4)

Air model

$$\ln(A_{tjb}) = \eta_j + \ln(W_t) + \varepsilon_{tj} + \delta_{tjb}$$

$$\varepsilon_{tj} \sim \mathcal{N}(0, \tau_j)$$

$$\delta_{tjb} \sim \mathcal{N}(0, \rho_j)$$

(3)

A_{tjb}

qPCR air model

$$Q_{tjb} = (A_{tjb} \cdot S_{tj}) / (V \cdot P)$$

$$Z_{tjbr} \sim \text{Bernoulli}(\psi_{tjb})$$

$$\psi_{tjb} = 1 - \exp(-Q_{tjb} \cdot \theta)$$

$$Y_{tjbrp} \sim \text{Normal}(\mu_{tjb}, \sigma_{tjb}) \quad \text{if } Z_{tjbr} = 1$$

$$\mu_{tjb} = \beta_0 + \beta_{1p} \cdot \ln(Q_{tjb})$$

$$\sigma_{tjb} = \exp(\gamma_0 + \gamma_1 \cdot \ln(Q_{tjb}))$$

(5)

ϕ_0, ϕ_1
 β_0, β_{1p}
 γ_0, γ_1

$$Z_{kr} \sim \text{Bernoulli}(\psi_k)$$

$$(\psi_k) = 1 - \exp(-K_k \cdot \theta)$$

$$Y_{kr} \sim \text{Normal}(\mu_k, \sigma_k) \quad \text{if } Z_{kr} = 1$$

$$\mu_k = \beta_0 + \beta_{1p} \cdot \ln(K_k)$$

$$\sigma_k = \exp(\gamma_0 + \gamma_1 \cdot \ln(K_k))$$

qPCR Standard model (6)

Data

N	number of counted fish
E	days between counting (effort)
Z	qPCR amplification (yes=1; no=0)
Y	qPCR Ct values
K	Known concentration in copies/ μL
V	Reaction volume in μL
S	Surface area of air collection method cm^2
F	Water volume filtered in the field in L
P	Passive air filter time deployment in days

Subscripts

t	time
j	filter type
b	biological replicate
r	technical replicate
p	qPCR plate
k	qPCR standard sample

Parameters

λ	expected fish accumulated over E days
ψ	probability of positive qPCR amplification
θ	detection probability intercept function and DNA concentration (K and U or Q)
μ	mean Ct values of qPCR
β_0, β_1	intercept and slope between μ and DNA concentration (K and U or Q)
σ	standard deviation of qPCR Ct values
γ_0, γ_1	intercept and slope between σ and DNA concentration (K and U or Q)
ω	conversion parameter between fish density and DNA concentration
η	dilution factor of DNA concentration from water to air (in \log_e)
ε	error term (residual)
τ	standard deviation of ε
δ	biological replicate error (bio-rep residual)
ρ	standard deviation of δ

State variables

W	unknown eDNA concentration in water samples (copies/L)
U	unknown eDNA concentration in water samples (copies/ μL)
A	unknown eDNA concentration in air samples (copies/ cm^2/day)
Q	unknown eDNA concentration in air samples (copies/ μL)
X	unknown fish density (fish/day)