

qPCR Standard model

$$\begin{aligned} Z_{ik} &\sim \text{Bernoulli}(1 - \exp(-2 \cdot K_{ik} \cdot \phi)) \\ Y_{ik} &\sim \text{Normal}(\mu_{ik}, \sigma_{ik}) \quad \text{if } Z_{ik} = 1 \\ \mu_{ik} &= \beta 0_{ip} + \beta 1_{ip} \cdot \ln K_{ik} \\ \sigma_{ik} &= \exp(\gamma 0 + \gamma 1 \cdot \ln K_{ik}) \end{aligned}$$

ϕ
 $\beta 0, \beta 1$
 $\gamma 0, \gamma 1$

qPCR Unknown model

$$\begin{aligned} Z_{ijdbtr} &\sim \text{Bernoulli}(1 - \exp(-2 \cdot C_{ijdbt} \cdot \phi)) \\ Y_{ijdbtr} &\sim \text{Normal}(\mu_{ijdbt}, \sigma_{ijdbt}) \quad \text{if } Z_{ijr} = 1 \\ \mu_{ijdbt} &= \beta 0_{ip} + \beta 1_{ip} \cdot \ln C_{ijdbt} \\ \sigma_{ijdbt} &= \exp(\gamma 0 + \gamma 1 \cdot \ln C_{ijdbt}) \end{aligned}$$

$\ln C_{ijdbt}$

Covariates

$$\begin{aligned} \ln C_{ijdbt} &= \psi_i + \delta 0_{ijdbt} \cdot \ln D_{ijdb} + \rho_{ijdbt} + \omega_{ijdbt} + \xi 0_{ijdbt} \\ \ln D_{ijdb} &= \psi_i + \delta 1_{ijdb} \cdot \ln D_{ijdb} + \xi 1_{ijdb} \end{aligned}$$

$\ln D_{ijdb}$

Metabarcoding model

$$\begin{aligned} R_{ijdb} &\sim \text{Multinomial}(\pi_{ijdb}, T_{jdb}) \\ \pi_{ijdb} &= \frac{e^{\nu_{ijdb}}}{\sum_{i=1}^I e^{\nu_{ijdb}}} \\ \nu_{ijdb} &= (\ln D_{ijdb} - \ln D_{jdb, i=\text{ref}}) + NPC_R \cdot \alpha_i \end{aligned}$$

$\ln D_{ijdb}$

Spatial model

$$\ln D_{xyz} = \tau + \eta(s) + \varepsilon_d(s)$$

Latent parameters

ψ = mean hake eDNA concentration
 $\delta 0, \delta 1$ = offset from mean hake
 ρ = biological replicate random effect
 ω = ethanol wash effect
 $\xi 0, \xi 1$ = error
 μ = mean Ct values of qPCR
 ϕ = probability of positive qPCR amplification
 σ = standard deviation of qPCR Ct values
 $\beta 0, \beta 1$ = intercept and slope between μ and eDNA concentration (K and C)
 $\gamma 0, \gamma 1$ = intercept and slope between σ and eDNA concentration (K and C)
 α = amplification efficiency relative to reference species
 π = sequence proportions at the end of PCR [0,1]
 ν = sequence proportions at the end of PCR
 τ = scalar intercept
 η = spatial field
 ε = depth specific spatial field

Mock metabarcoding model

$$\begin{aligned} R_{im} &\sim \text{Multinomial}(\pi_{im}, T_m) \\ \pi_{im} &= \frac{e^{\nu_{im}}}{\sum_{i=1}^I e^{\nu_{im}}} \\ \nu_{im} &= (\ln D_{im} - \ln D_{m, i=\text{ref}}) + NPC_R \cdot \alpha_i \end{aligned}$$

α_i

State variables

C = unknown eDNA concentration
 D = unknown eDNA concentration

Subscripts

i = species
 j = station
 d = depth
 b = biological replicate
 t = aliquot replicate
 r = technical replicate
 p = qPCR plate
 m = mock community aliquote sample
 k = qPCR standard aliquote sample

Data

Z = qPCR amplification yes/no (0,1)
 Y = qPCR Ct values
 K = Known concentration in copies/ μL
 R = metabarcoding sequencing reads
 T = total number sequencing reads