

### qPCR Standard model

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

$\phi$   
 $\beta 0, \beta 1$   
 $\gamma 0, \gamma 1$

### 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

$$\begin{aligned} \ln C_{ijdbt} &= \psi_i + \ln D_{ijdb} + \rho_{ijdbt} + \omega_{ijdbt} + \xi_{ijdbt} \\ \ln D_{ijdb} &= \psi_i + \ln D_{ijdb} + \rho_{ijdbt} \end{aligned}$$

$\ln D_{ijdb}$

### 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

$\psi$  = mean hake eDNA concentration  
 $\rho$  = biological replicate random effect  
 $\omega$  = ethanol wash effect  
 $\xi$  = volume and dilution offset  
 $\mu$  = mean Ct values of qPCR  
 $\phi$  = probability of positive qPCR amplification  
 $\sigma$  = standard deviation of qPCR Ct values  
 $\beta 0, \beta 1$  = intercept and slope between  $\mu$  and eDNA concentration (K and C)  
 $\gamma 0, \gamma 1$  = intercept and slope between  $\sigma$  and eDNA concentration (K and C)  
 $\alpha$  = amplification efficiency relative to reference species  
 $\pi$  = sequence proportions at the end of PCR [0,1]  
 $\nu$  = sequence proportions at the end of PCR  
 $\tau$  = scalar intercept  
 $\eta$  = spatial field  
 $\varepsilon$  = depth specific spatial field

### Mock metabarcoding model

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

$\alpha_i$

### 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/ $\mu\text{L}$   
 $R$  = metabarcoding sequencing reads  
 $T$  = total number sequencing reads