Supplementary Material
Passive air sampling detects environmental DNA transfer from water into air

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Fish density

X_t

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

E $\qquad$ ω

Visual model

$\lambda_t = X_t \cdot E_t$
$N_t \sim$ Negative Binomial(λ_t, ϕ)
$\phi = 20$

(1)

Water model

$W_t = X_t \cdot \omega$ $\qquad \eta_j, \varepsilon_{ij}, \delta_{ijb} \longrightarrow$

(2)

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)

W_t $\qquad\qquad\qquad\qquad$ A_{tjb}

qPCR water model $\qquad\qquad\qquad$ **qPCR air model**

$U_t = (W_t \cdot F)/V$
$Z_{tr} \sim$ Bernoulli(ψ_t)
$\psi_t = 1 - exp(-U_t \cdot \theta)$
$Y_{trp} \sim$ Normal(μ_{tp}, σ_t) if $Z_{tr} = 1$
$\mu_{tp} = \beta0 + \beta1_p \cdot \ln(U_t)$
$\sigma_t = \exp(\gamma0 + \gamma1 \cdot \ln(U_t))$

(4)

$Q_{tjb} = (A_{tjb} \cdot S_{tj})/(V \cdot P)$
$Z_{tjbr} \sim$ Bernoulli(ψ_{tjb})
$\psi_{tjb} = 1 - exp(-Q_{tjb} \cdot \theta)$
$Y_{tjbrp} \sim$ Normal$(\mu_{tjb}, \sigma_{tjb})$ if $Z_{tjbr} = 1$
$\mu_{tjb} = \beta0 + \beta1_p \cdot \ln(Q_{tjb})$
$\sigma_{tjb} = \exp(\gamma0 + \gamma1 \cdot \ln(Q_{tjb}))$

(5)

$\phi0, \phi1$
$\beta0, \beta1_p$
$\gamma0, \gamma1$

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
$\beta0, \beta1$	intercept and slope between μ and DNA concentration (K and U or Q)
σ	standard deviation of qPCR Ct values
$\gamma0, \gamma1$	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

$Z_{kr} \sim$ Bernoulli(ψ_k)
$(\psi_k) = 1 - exp(-K_k \cdot \theta)$
$Y_{kr} \sim$ Normal(μ_k, σ_k) if $Z_{kr} = 1$
$\mu_k = \beta0 + \beta1_p \cdot \ln(K_k)$
$\sigma_k = \exp(\gamma0 + \gamma1 \cdot \ln(K_k))$

qPCR Standard model $\qquad$ **(6)**

State variables

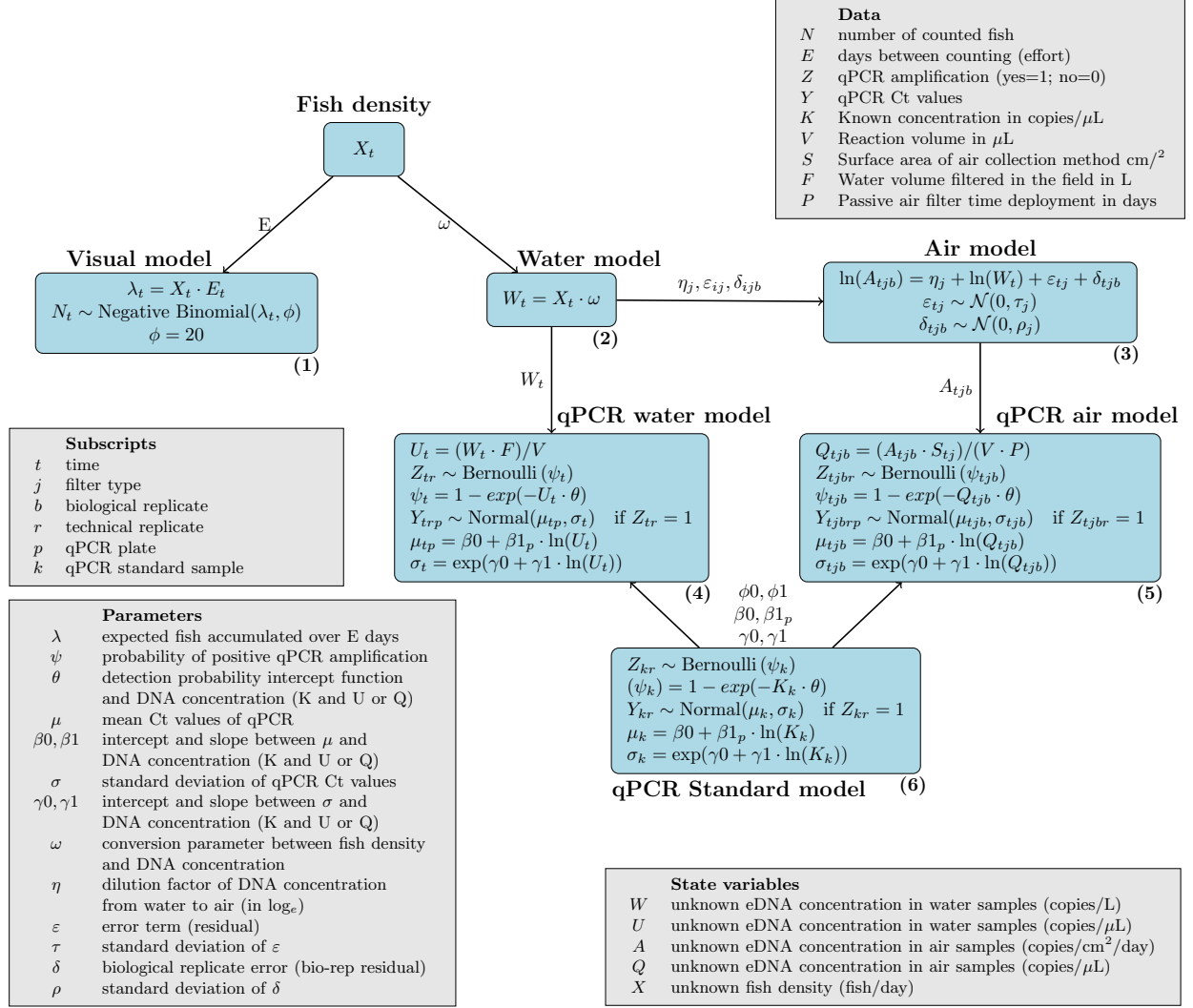|	
W	unknown eDNA concentration in water samples (copies/L)
U	unknown eDNA concentration in water samples (copies/μL)
A	unknown eDNA concentration in air samples (copies/cm^2/day)
Q	unknown eDNA concentration in air samples (copies/μL)
X	unknown fish density (fish/day)

Figure 1: Directed acyclic graph (DAG) of joint Bayesian model for linking salmon migration dynamics from visual observation, water and air eDNA concentration.
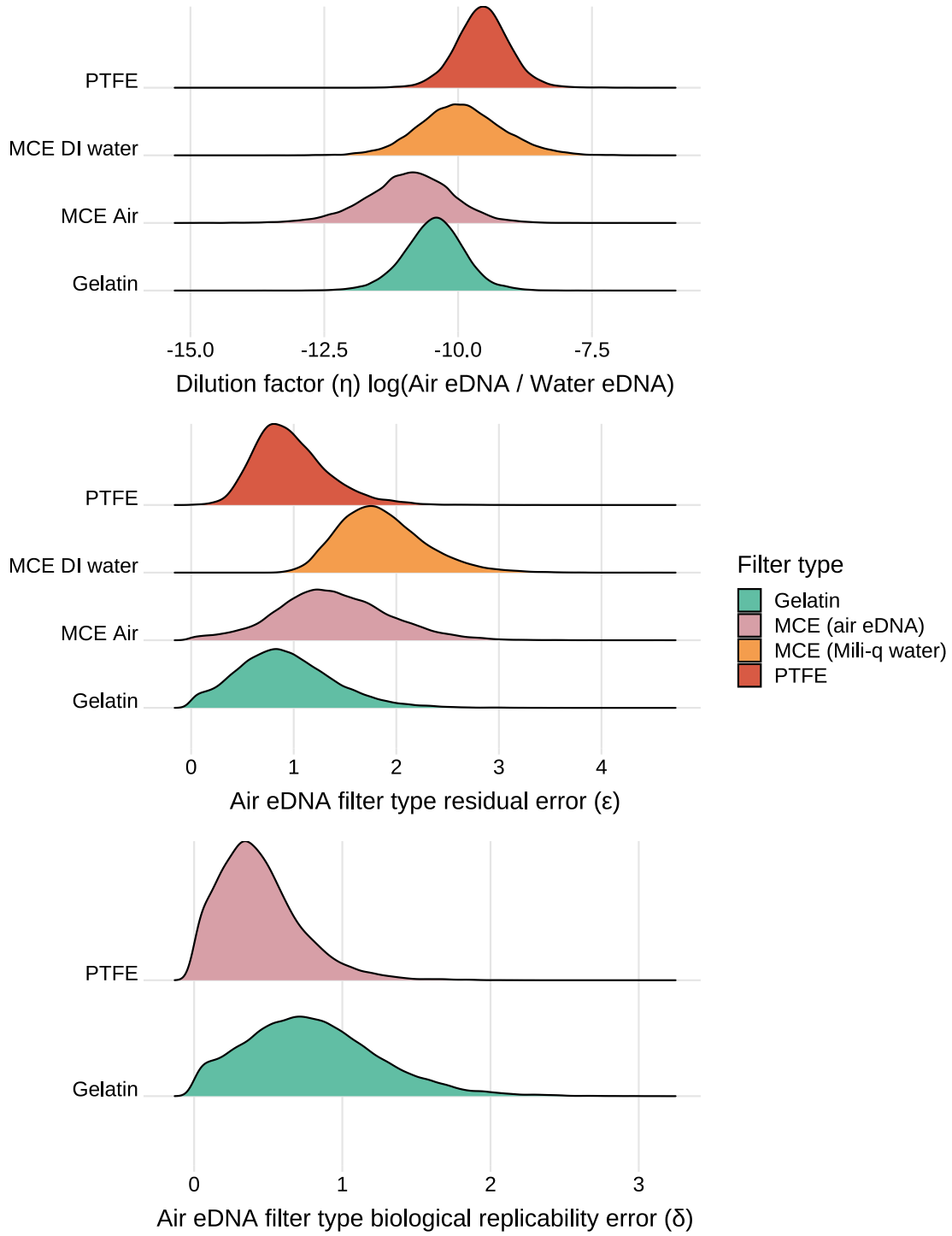
Figure 2: Density plots showing posterior distributions of: (A) water-to-air dilution factors (η), illustrating the magnitude of concentration reduction between aquatic and atmospheric matrices; (B) standard deviation (SD) of the residual error values (τ), representing the congruence (lower = better) between estimated eDNA concentrations between air and water; and (C) standard deviation (SD) of the biological replicability error (ρ), quantifying measurement consistency (lower = better) between technical replicates of two air filters (PTFE and gelatin filters). Each parameter is estimated for each of four different air eDNA collection methods (differentiated by colors).
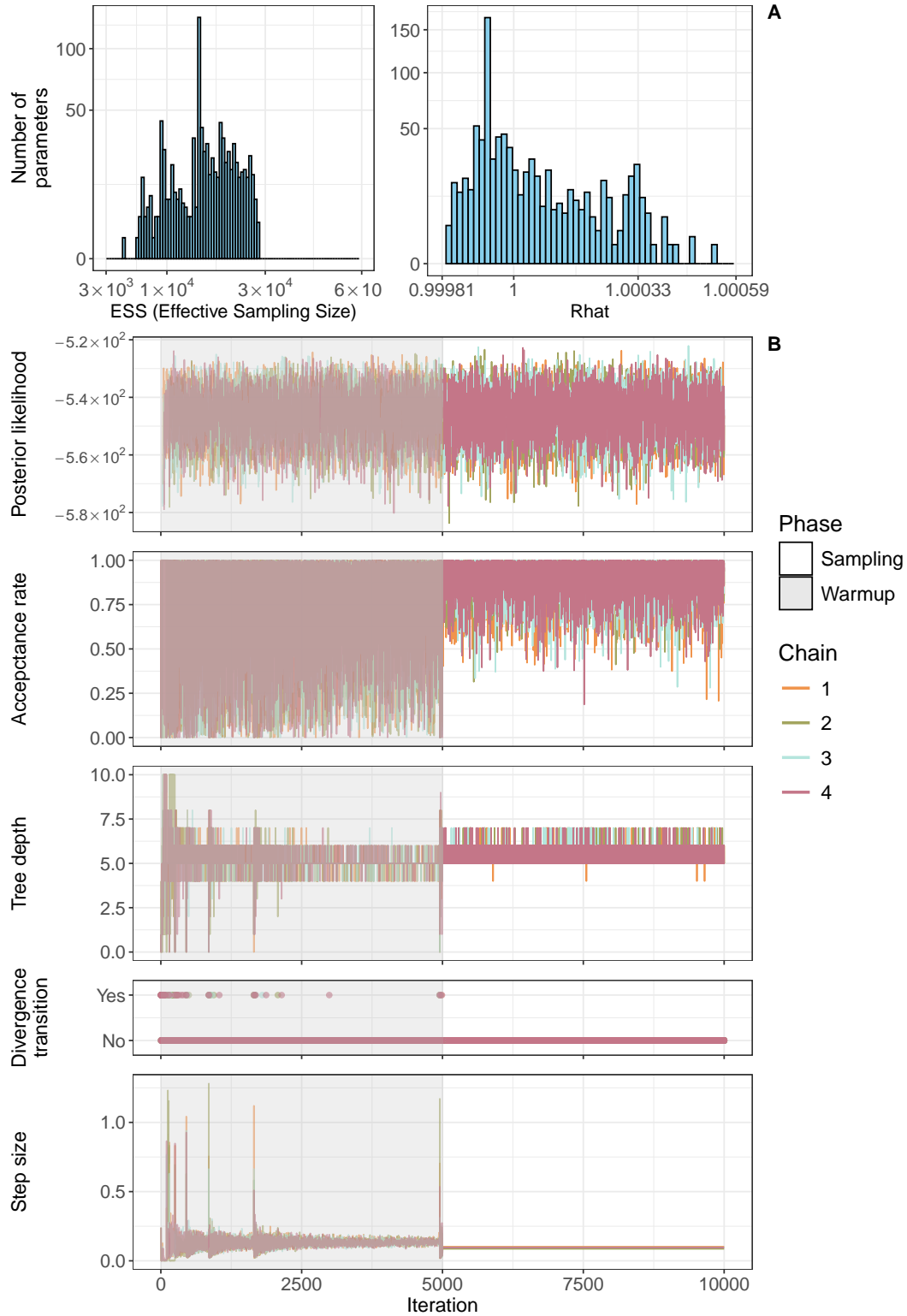
Figure 3: Bayesian model convergence diagnostics indicating (A) the distributions of effective sample size (ESS, left) and $\hat{R}$ values (right) for all parameters and (B) convergence metrics across iterations, including posterior likelihood, acceptance rate, tree depth, divergence transitions, and step size for four MCMC chains. Warmup and sampling phases are distinguished by background shading.
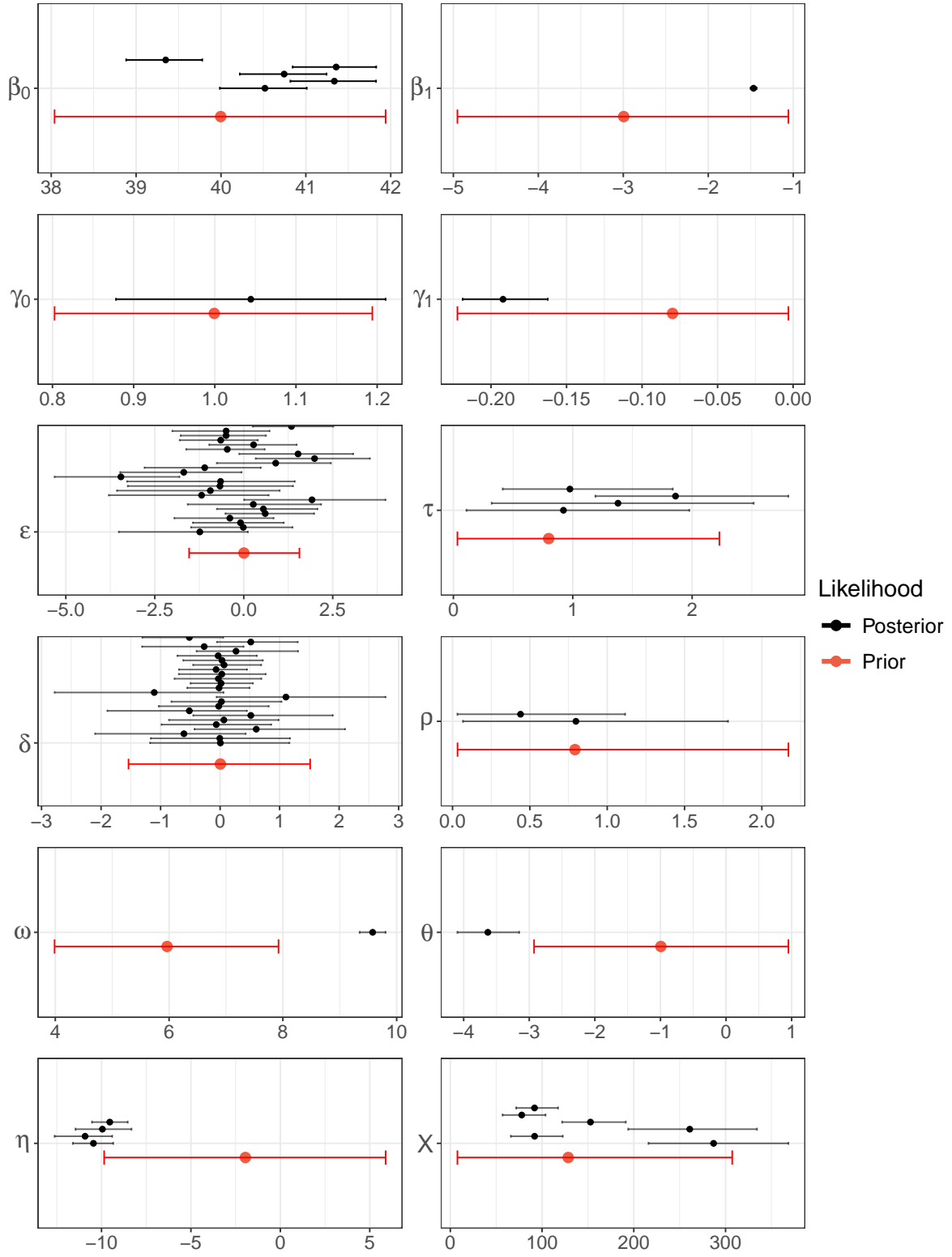
Figure 4: Prior sensitivity analysis for model parameters $(\beta_0, \beta_1, , \gamma_0, \gamma_1, \varepsilon, \tau, \delta, \rho, \omega, \theta, \eta, X)$. Black points and intervals represent posterior means and 95% confidence intervals respectively and red points and intervals show prior mean and 95% confidence intervals respectively.
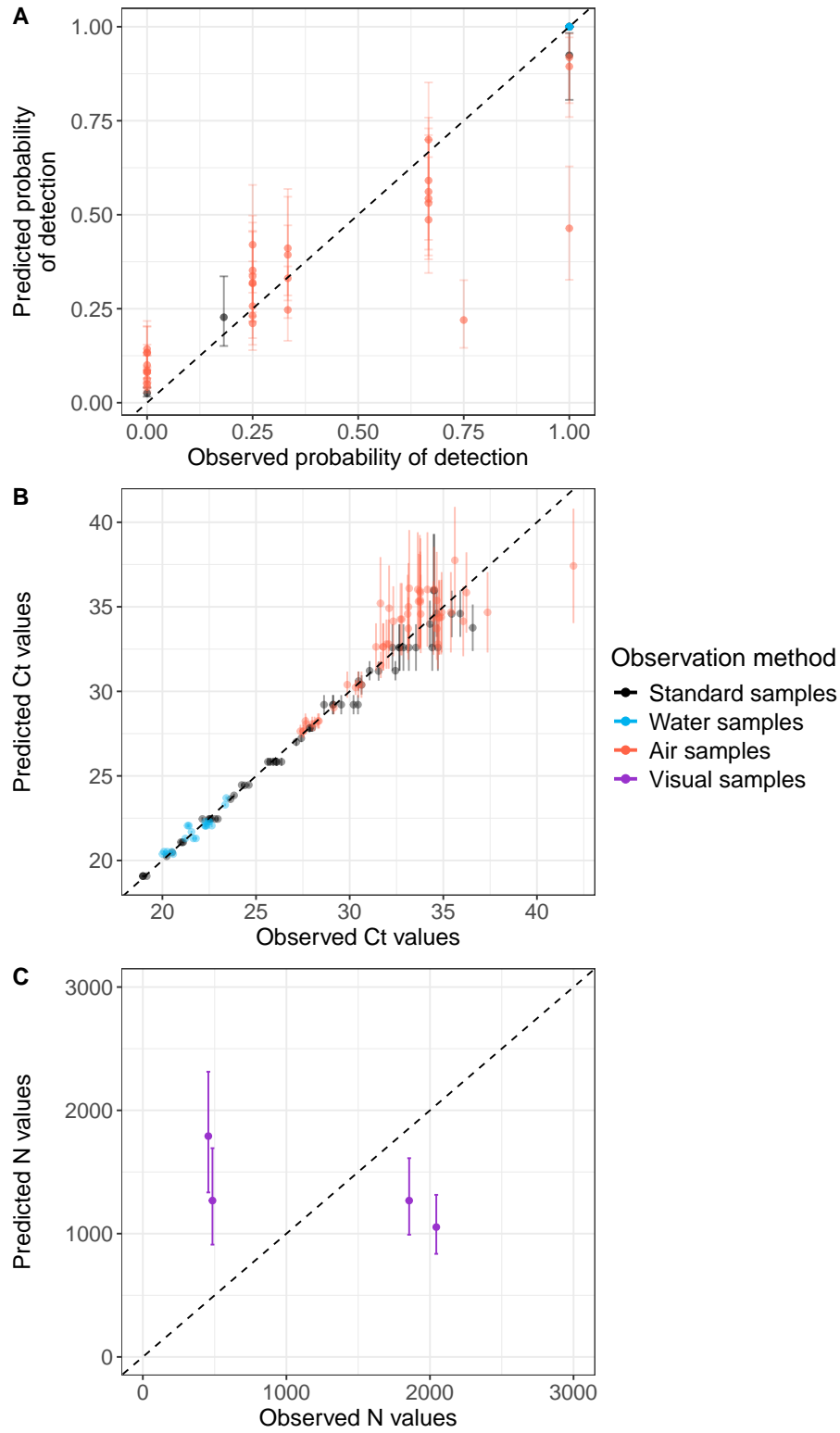
Figure 5: Posterior predictive checks comparing observed vs. model-predicted values for (A) detection probability of air and water samples alongside standard samples, (B) Ct values for air and water samples alongside standard, and (C) visual counts of fish (N).
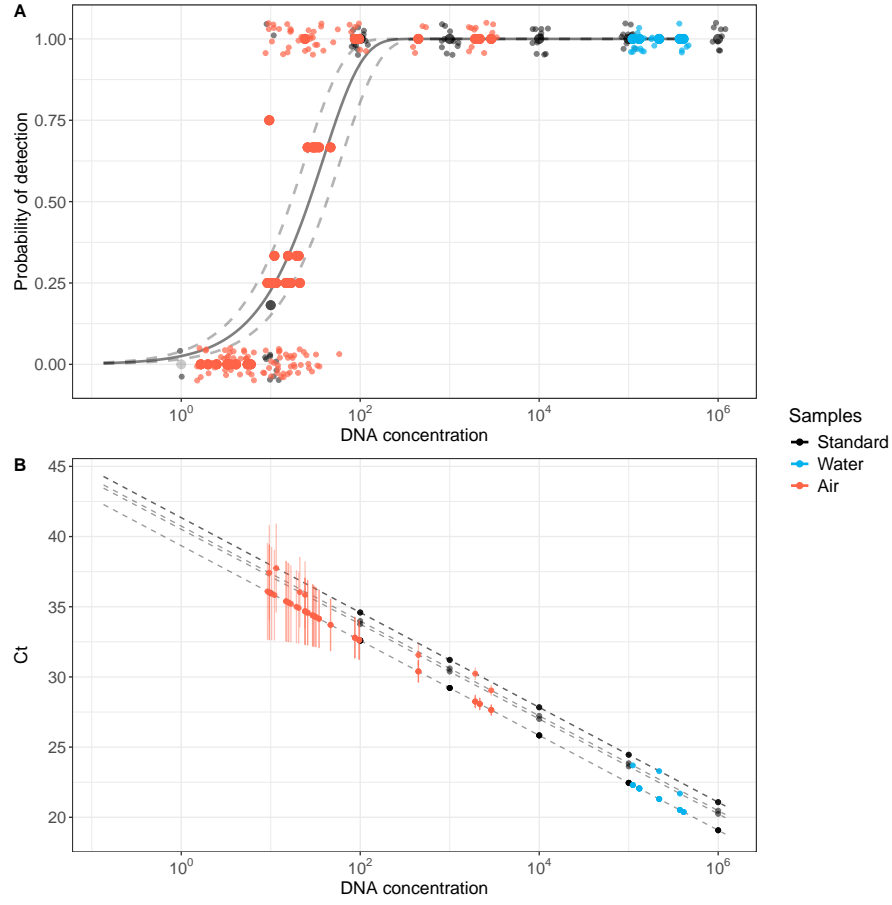
Figure 6: The probability of detection and Ct values along the eDNA concentration from the posterior estimates of the standard samples and water and air environmental samples indicating assay and qPCR machine performance.

	Description	Prior
	Data	
N	number of fish counted	-
E	elapsed days between counting	-
Z	qPCR amplification (yes=1; no=0)	-
Y	qPCR cycle threshold (Ct)	-
K	known DNA concentration (qPCR standards)	-
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	-
	State processes	
X	unknown fish density in (fish $\cdot$ day^{-1})	$\mathcal{TN}(100, 100; 0, +\infty)$
W	unknown DNA concentration in water in (copies/L)	-
U	unknown eDNA concentration in water samples (copies/μL)	-
A	unknown DNA concentration in air in (copies/cm^2/day)	-
Q	unknown eDNA concentration in air samples (copies/μL)	-
	Transformed parameters	
λ	expected fish accumulated over E days	-
ψ	probability of positive qPCR amplification	-
μ	mean Ct values of qPCR	-
σ	standard deviation of qPCR Ct values	-
	Fixed parameters	
ϕ	overdispersion parameter of Negative Binomial	- ($\phi = 20$)
	Parameters	
ω	conversion parameter between fish density and DNA concentration	$\mathcal{N}(6, 1)$
η	dilution factor of DNA concentration from water to air	$\mathcal{N}(-2, 4)$
ε	time (t) specific error term (residual)	$\mathcal{N}(0, \tau)$
τ	standard deviation of residuals	$\mathcal{TN}(0, 1; 0, +\infty)$
δ	biological replicate error term (residual)	$\mathcal{N}(0, \rho)$
ρ	standard deviation of biological replicate error	$\mathcal{TN}(0, 1; 0, +\infty)$
θ	intercept of the qPCR probability of detection (ψ) relationship and eDNA concentration (K, W, and A)	$\mathcal{N}(-1, 1)$
$\beta0$	intercept of the linear relation between the mean Ct values (μ) and eDNA concentration (K, W, and A)	$\mathcal{N}(40, 1)$
$\beta1$	slope of the linear relation between the mean Ct values (μ) and eDNA concentration (K, W, and A))	$\mathcal{N}(-3, 1)$
$\gamma0$	intercept of the linear relation between the standard deviation of Ct values (σ) and eDNA concentration (K, W, and A)	$\mathcal{N}(1, 0.1)$
$\gamma1$	intercept of the linear relation between the standard deviation of Ct values (σ) and eDNA concentration (K, W, and A)	$\mathcal{N}(0, 0.1)$
	Index	
t	time (days)	-
j	filter type	-
b	biological sample replicate	-
p	qPCR plate	-
k	qPCR standard sample	-
r	qPCR technical replicate	-

Table 1: Data, state processes, parameters, transformed parameters, and subscripts employed in the joint Bayesian model and their prior distributions

Location	Date	Rain Yes/No	Precipitate (mm)	River water discharge (m)
Issaquah Hatchery	2024-10-17	Yes	0.05	4.10
Issaquah Hatchery	2024-10-24	Yes	0.01	4.13
Issaquah Hatchery	2024-10-31	Yes	0.32	4.50
Issaquah Hatchery	2024-11-07	No	0	4.46
Issaquah Hatchery	2024-11-14	Yes	0.29	4.95
Issaquah Hatchery	2024-11-21	No	NA (sheltered bridge)	4.91

Table 2: Meteorological metadata collected from NOAA during the sampling events