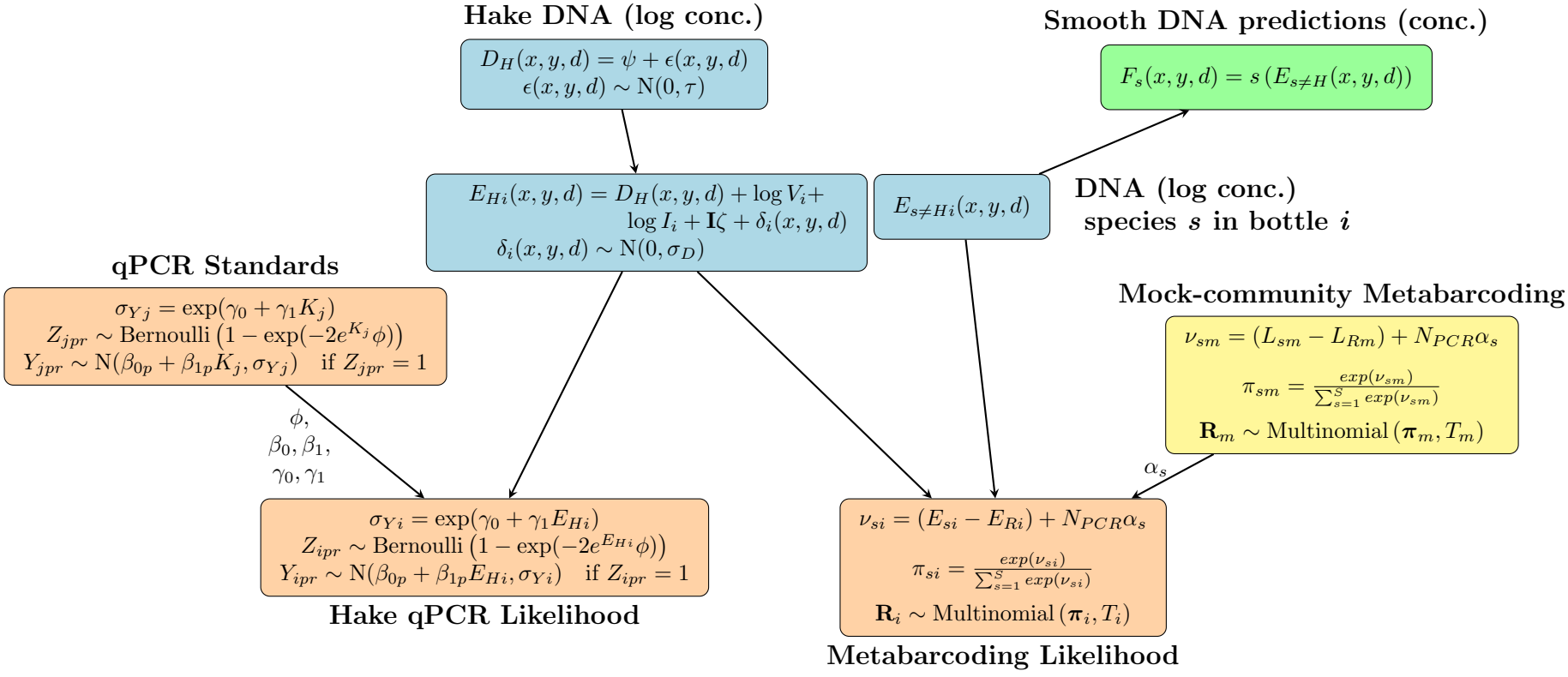

Subscripts

s = species (H = Hake)
x = northing
y = easting
d = depth
i = biological replicate
r = technical replicate
p = qPCR plate
m = mock community sample
j = qPCR standard aliquote sample

Parameters

ψ = mean hake eDNA concentration
δ = biological replicate random effect
V_i = volume filtered and aliquote dilution offset
ϕ = qPCR amplification parameter
σ_Y = standard deviation of qPCR Ct values
β_{0p}, β_{1p} = intercept and slope defining mean qPCR - DNA concentration relationship
$\gamma 0, \gamma 1$ = intercept and slope defining standard deviation of qPCR - DNA concentration relationship
α_s = amplification efficiency relative to reference species
π = predicted sequence proportions at the end of PCR
ν = sequence proportions at the end of PCR (additive log-ratio)
ζ = ethanol wash effect
τ =
η = spatial field
ε = depth specific spatial field

Observations

Z = qPCR amplification (yes=1; no=0)
Y = qPCR Ct values
K = Known DNA conc. (log (copies/μL))
L = Known DNA conc. (log (copies/μL))
R = metabarcoding sequencing reads
T = total number sequencing reads