

Some notes about the Carkeek grid samples

From meeting with Ole, Ryan, and Jimmy Aug 25, 2015

1. Three transects are not identical
2. Big differences in communities offshore vs. inshore
3. Could help quantify spread/occurrence; life history variations?

Models

Let:

i = taxon

d = distance from shore

r = distance along shore

l = location (unique site in grid)

Y = who knows? – True count of DNA sequences in environmental sample?

X = counts of DNA sequences in a sequenced sample

π = proportions of DNA sequences in a sequenced sample

β_i = taxon-specific fixed effect; $\beta_1 = 0$

γ_{PCR} = error due to PCR variability (σ_{PCR}^2)

ω = error due to environmental sampling ...?

General relationship between Y and counts of DNA in sequenced sample:

$$\log Y_{i,d,r} \sim \text{Poisson}(X_{i,d,r}) \quad (1)$$

Reasonable Models

1. All DNA communities are identical

$$\log X_{i,d,r} = \beta_0 + \beta_i + \omega_{i,d,r} + \gamma_{PCR} \quad (2)$$

$$\omega_{i,d,r} \sim \text{Normal}(0, \tau^2) \quad (3)$$

$$\gamma_{PCR} \sim \text{Normal}(0, \sigma_{PCR}^2) \quad (4)$$

2. Only off-shore distance matters

$$\log X_{i,d,r} = \beta_0 + \beta_i + \omega_{i,d,r} + \gamma_{PCR} \quad (5)$$

$$\omega_{i,d,r} \sim \text{Normal}(0, \tau_d^2) \quad (6)$$

$$\gamma_{PCR} \sim \text{Normal}(0, \sigma_{PCR}^2) \quad (7)$$

3. Only along-shore distance matters

$$\log X_{i,d,r} = \beta_0 + \beta_i + \omega_{i,d,r} + \gamma_{PCR} \quad (8)$$

$$\omega_{i,d,r} \sim \text{Normal}(0, \tau_r^2) \quad (9)$$

$$\gamma_{PCR} \sim \text{Normal}(0, \sigma_{PCR}^2) \quad (10)$$

4. something else

$$\log X_{i,d,r} = \beta_0 + \beta_i + \omega_{i,d} + \omega_{i,r} + \gamma_{PCR} \quad (11)$$

$$\omega_{i,d} \sim \text{Normal}(0, \tau_d^2) \quad (12)$$

$$\omega_{i,r} \sim \text{Normal}(0, \tau_r^2) \quad (13)$$

$$\gamma_{PCR} \sim \text{Normal}(0, \sigma_{PCR}^2) \quad (14)$$

5. Exponential decay

$$??? = \beta_0 + \beta_1 d + \dots + \beta_n \quad (15)$$