


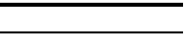


**Table S-1.** Formulas for four eDNA dispersal models

|   | Plume model   | Universal decay model   | Universal decay with lag model  | Constant model  |
|---|---|---|---|---|
| Model component   |        |      |    |  |
| $P_B(x)$<br>Proportion of eDNA in the bank samples                          | $P_B(x) = P_{max}(1 - \exp(-\gamma\sqrt{x}))$   | $P_B(x) = P_0$  | $P_B(x) = P_0$  | $P_B(x) = P_0$  |
| $Q(x)$<br>Quantity of eDNA across two bank samples and one midstream sample | $Q(x) = \frac{\beta_0 F \left( P_B(x)(1 - r_b) + (1 - P_B(x))(1 - r_m) \right)^x}{V^q}$ | $Q(x) = \frac{\beta_0 F \left( P_B(x)(1 - r_b) + (1 - P_B(x))(1 - r_m) \right)^x}{V^q}$ | $Q(x) = \frac{\beta_0 F \left( 1 - \exp(-z\sqrt{x}) \right) \left( P_B(x)(1 - r_b) + (1 - P_B(x))(1 - r_m) \right)^x}{V^q}$ | $Q(x) = \frac{\beta_0 F}{V^q}$  |
| $M(x)$<br>Amount of eDNA found in any given midstream sample                | $M(x) = Q(x)(1 - P_B(x))$   | $M(x) = Q(x)(1 - P_B(x))$   | $M(x) = Q(x)(1 - P_B(x))$   | $M(x) = Q(x)(1 - P_B(x))$   |
| $B(x)$<br>Amount of eDNA found in any given bankside sample                 | $B(x) = \frac{P_B(x)Q(x)}{2}$   | $B(x) = \frac{P_B(x)Q(x)}{2}$   | $B(x) = \frac{P_B(x)Q(x)}{2}$   | $B(x) = \frac{P_B(x)Q(x)}{2}$   |
| $R_M(x)$<br>Midstream sample detection rate                                 | $R_M(x) = \frac{e^{\alpha_0} M(x)^{\alpha_1}}{e^{\alpha_0} M(x)^{\alpha_1} + 1}$        | $R_M(x) = \frac{e^{\alpha_0} M(x)^{\alpha_1}}{e^{\alpha_0} M(x)^{\alpha_1} + 1}$        | $R_M(x) = \frac{e^{\alpha_0} M(x)^{\alpha_1}}{e^{\alpha_0} M(x)^{\alpha_1} + 1}$  | $R_M(x) = \frac{e^{\alpha_0} M(x)^{\alpha_1}}{e^{\alpha_0} M(x)^{\alpha_1} + 1}$    |
| $R_B(x)$<br>Bankside sample detection rate                                  | $R_B(x) = \frac{e^{\alpha_0} B(x)^{\alpha_1}}{e^{\alpha_0} B(x)^{\alpha_1} + 1}$        | $R_B(x) = \frac{e^{\alpha_0} B(x)^{\alpha_1}}{e^{\alpha_0} B(x)^{\alpha_1} + 1}$        | $R_B(x) = \frac{e^{\alpha_0} B(x)^{\alpha_1}}{e^{\alpha_0} B(x)^{\alpha_1} + 1}$  | $R_B(x) = \frac{e^{\alpha_0} B(x)^{\alpha_1}}{e^{\alpha_0} B(x)^{\alpha_1} + 1}$    |

Model graphic legend: vertical axis = eDNA abundance or detection rate; horizontal axis = distance downstream from fish; thick line = midstream samples; thin line = bankside samples.

$x$  = distance downstream;  $\beta_0$  is a stream-specific coefficient;  $F$  = the number of fish;  $r_b$  and  $r_m$  = eDNA decay rates at the banks and midstream, respectively;  $V$  = velocity;  $q$  is a velocity scaling coefficient;  $P_{max}$  is the maximum proportion of eDNA found at the banks;  $\gamma$  is a lateral dispersal rate coefficient;  $\alpha_0$  and  $\alpha_1$  are rate and shape parameters, respectively, for the detection rate ~ eDNA quantity relationship;  $P_0$  is the constant proportion of eDNA found near the banks;  $z$  is a lag coefficient