### JOURNAL PUBLICATION CITATION: Keller, A.G., Grason, E.W., McDonald, P.S., Ramón-Laca, A., Kelly, R.P. 2021. Tracking an invasion front with environmental DNA. *Ecological Applications.*

### Data S3

### Data and code necessary to implement the simulation study.

### Author(s) [of the material provided in DataS3.zip]

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### File list (files found within DataS3.zip)

simulation\_interface.R

Simulation\_Joint.stan

Simulation\_Trap-only.stan

Joint\_posterior.csv

**Description**

simulation\_interface.R – R interface to the joint and trap-only models written in Stan used to execute simulations. Includes simulation of qPCR and trap data corresponding to 99 scenarios, as well as the stan() function (rstan() package) used to read and compile the Stan code and fit the simulation models on the dataset. Uses the estimated parameter posterior distributions from the joint model fit using collected data.

Simulation\_Joint.stan – Joint model (Keller et al., *Eq. 1.1* – *1.4*) specification written in Stan. Accessed via R interface. Model estimates, µsim, for each scenario, *i*sim, and uses the median of the posterior distribution (derived from the joint model fit with collected data) for parameters p10, β, and Φ.

Simulation\_Trap-only.stan – Trap-only model (Keller et al., *Eq. 1.4*) specification written in Stan. Accessed via R interface. Model estimates, µsim, for each scenario, *i*sim, and uses the median of the posterior distribution (derived from the joint model fit with collected data) for parameter Φ.

Joint\_posterior.csv – Posterior distributions derived from the joint model (fit using collected data) for estimated µ at each of 20 sampled sites, as well as estimated p10, β, and Φ. Data include the values from the 10,000 sampling iterations for each estimated parameter.