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### Data S2

### Data and code necessary to implement the hierarchical joint model outlined in Equations 2.1 – 2.5, Appendix S1.

### Author(s) [of the material provided in DataS2.zip]

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### File list (files found within DataS2.zip)

Hierarchical\_model\_interface.R

Hierarchical\_joint\_model.stan

qPCR\_results.csv

trap\_data.csv

**Description**

Hierarchcial\_model\_interface.R – R interface to the hierarchical model written in Stan. Includes data pre-processing, as well as the stan() function (rstan() package) used to read and compile the Stan code and fit the models on the dataset.

Hierarchical\_joint\_model.stan – Joint model (Keller et al., Appendix S1, *Eq. 2.1* – *2.5*) specification written in Stan. Accessed via R interface.

qPCR\_results.csv – Quantitative PCR data used to fit the models. Data include sample ID (Sample), site sampled (Site), date of eDNA sample collection (Date), biological replicate (Bio\_rep), qPCR results from each of three technical replicates (Replicate 1 – Replicate 3), and site region (Region). Each row corresponds to one environmental sample/water bottle.

trap\_data.csv – Trap data used to fit the models. Data include the full site name (Full\_site\_name), site ID (Site), date of trap sample collection (Date), ID of trap sample (TrapID), number of crabs trapped in trap sample (Count), latitude of trap sample (Latitude), and longitude of trap sample (Longitude).