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eDNA concentrations across time and space

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The Model

qPCR – targeted for specific species

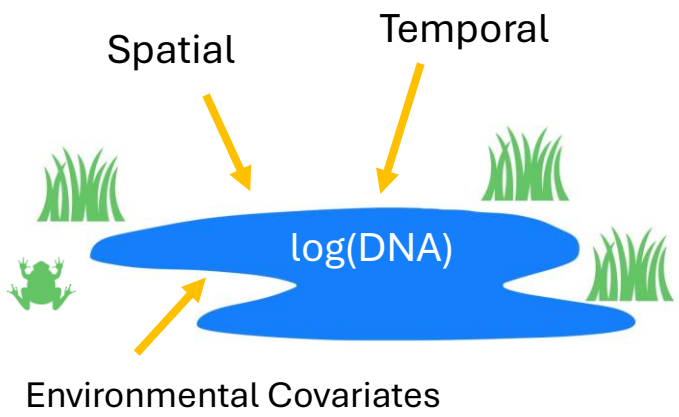
- Important for invasive or elusive species monitoring

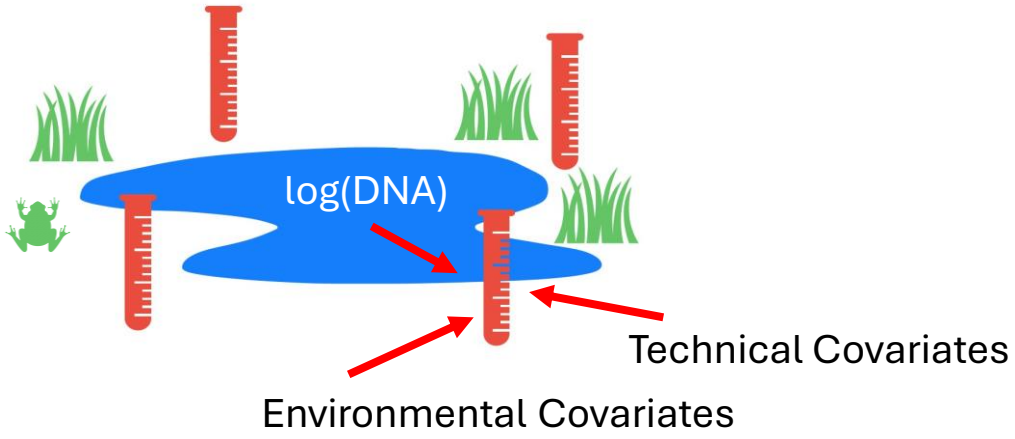
Focus:

- Inferring DNA concentrations in the environment, and linking to environmental covariates

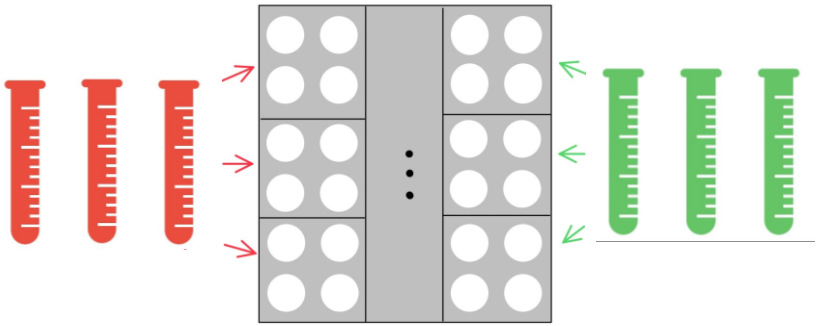
The Model:

- Time series qPCR data
- Accounts for data generating process
- Contamination/Inhibition
- Heteroscedasticity





Laboratory



qPCR survey pipeline

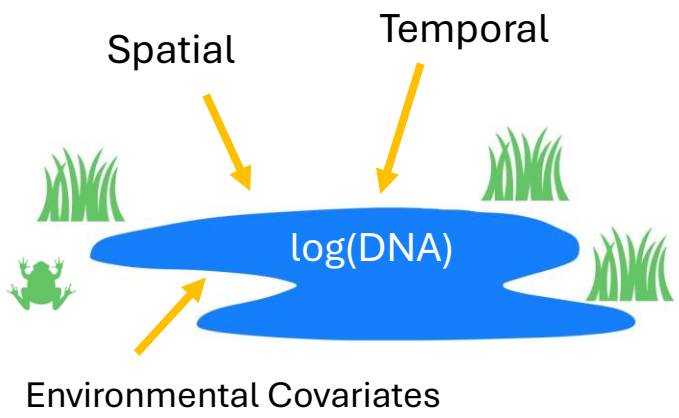
1. DNA availability:
   Across sites $i = 1, \dots, S$ and time-points $t = 1, \dots, T$.
2. DNA collection:
   In samples $m = 1, \dots, M$.
3. DNA analysis:
   On plates p = 1,…,P for replicates k = 1, …, K

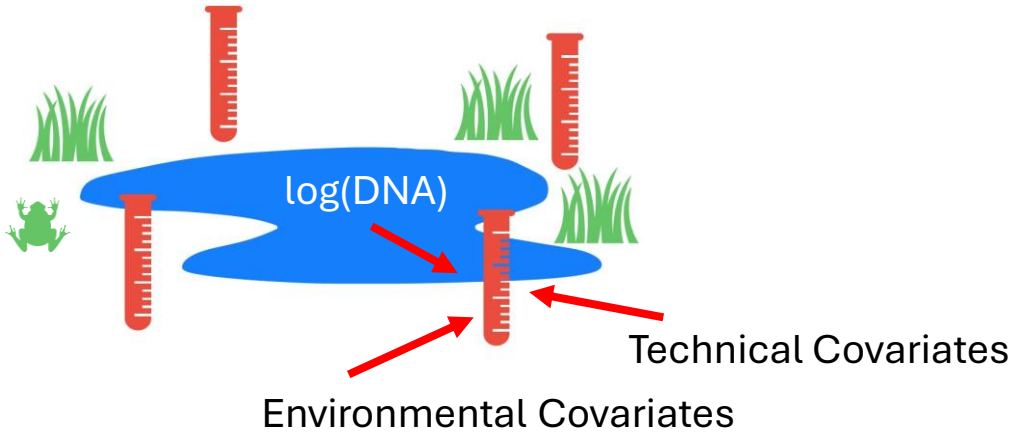
Previous work:

- [Espe et al. 2022] – artemis package
- [Shelton et al. 2022] – spatial model for Pacific Hake

Our focus:

- Time series qPCR data
- Modelling contamination and inhibition in the lab
- qPCR output heteroscedasticity





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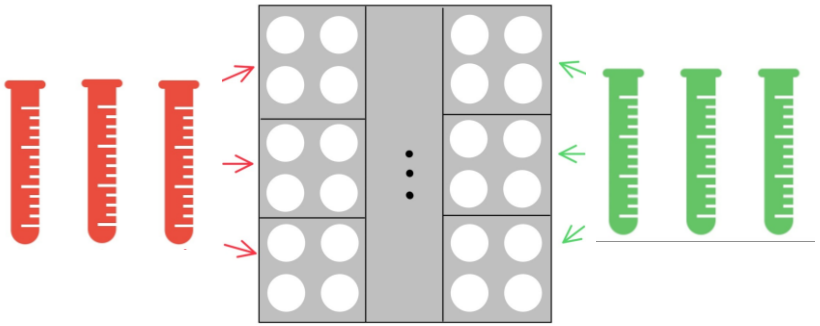

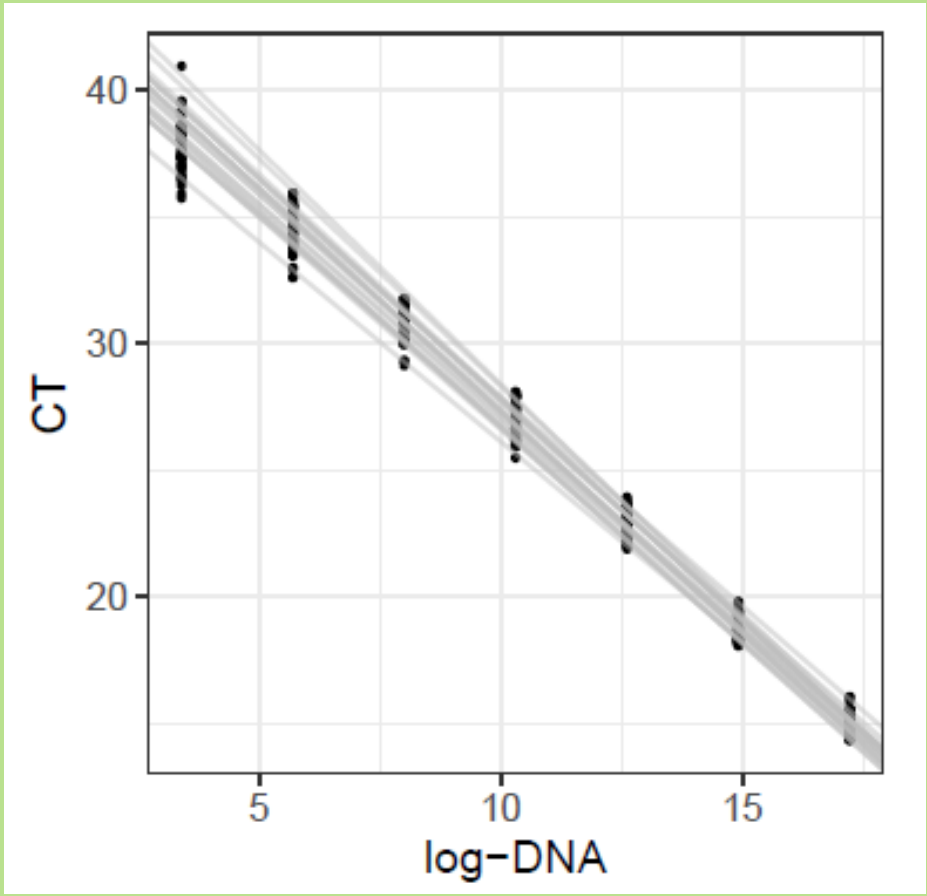

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Simulation study findings

With respect to inferring log-DNA in the environment:

1. Fully modelling the process in three stages reduces bias
2. Failure to account for contamination, inhibition, or heteroscedasticity leads to increased bias even when these effects are small
3. Increasing number of samples (M) and number of technical replicates (K) leads to reduced bias, but in diminishing returns

Zebra Mussels

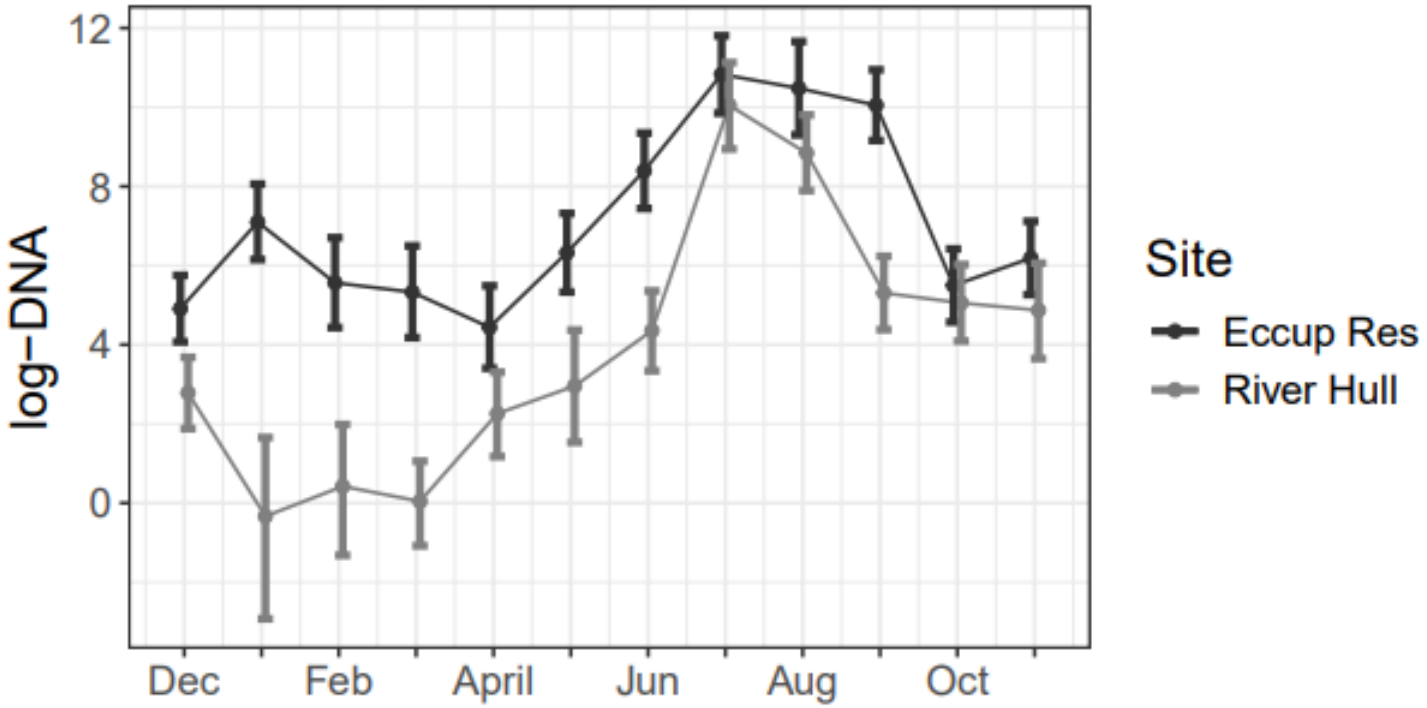
(Dreissena polymorpha)

<u>Study:</u>

Two sites in Yorkshire:
- Eccup Reservoir
- River Hull

Dec 2020-Nov 2021

M=10 samples
K=6 replicates



Sampling covariates:

Covariate	Mean	95% PCI
volume	0.401	(-0.034, 0.844)
pH	-0.032	(-0.298, 0.235)
calcium	0.160	(-0.445, 0.787)

Study design recommendations

Under this modelling framework:

1. Replication of both samples and technical replicates

2. Collecting field negatives would allow for modelling contamination and inhibition at collection stage

Thanks

Code and Manuscript available at:

github.com/millyljones/Spatio-temporal-eDNA

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References

Espe, M.B., Johnston, M., Blankenship, S.M., Dean, C.A., Bowen, M.D., Schultz, A., Schumer, G.: The artemis package for environmental DNA analysis in R. Environmental DNA 4(3), 523–532 (2022) https://doi.org/10.1002/edn3.277

Shelton, A.O., Ramon-Laca, A., Wells, A., Clemons, J., Chu, D., Feist, B.E., Kelly, R.P., Parker-Stetter, S.L., Thomas, R., Nichols, K.M., Park, L.: Environmental DNA provides quantitative estimates of pacific hake abundance and distribution in the open ocean. Proceedings of the Royal Society B 289(1971), 20212613 (2022) https://doi.org/10.1098/rspb.2021.2613