A Bayesian framework to model transmissible cancer dynamics within soft-shell clam (*Mya arenaria*) populations

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Background

Bivalve Transmissible Neoplasia (BTN)

Soft-shell Clam

- Transmissible cancer occurs in a few species, including Tasmanian devils, dogs, and several bivalve species.
- In soft-shell clams, a leukemia-like cancer was confirmed to be transmissible in 2015 and is spread through waterborne cancer cells[1]
- Infected clams release cells that can survive for weeks, especially in cold temperatures, leading to seasonality in disease prevalence[2]

Marine Disease Modeling

- Most disease models are built for terrestrial systems, but marine diseases follow different dynamics
- Environmental factors like temperature influence pathogen survival and transmission, shaping seasonal disease dynamics

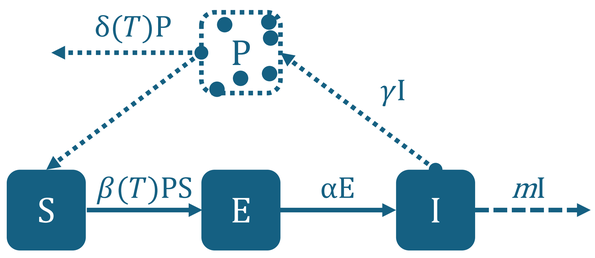
Bayesian Approaches in Disease Modeling

- Bayesian methods combine lab data and field observations.
- We use Stan[3], a probabilistic programming language, to:
  - Efficiently fit ordinary differential equation-based models
  - Estimate key transmission and progression parameters
  - Quantify uncertainty in predictions

Key Objectives

- **Develop a temperature-dependent SEIP model for environmental cancer transmission in soft-shell clams**
- **Estimate transmission, progression, and particle emission rates using Bayesian inference**
- **Test the hypothesis that incorporating seasonal temperature effects allows the model to reproduce observed trends in disease dynamics**

SEIP Model Structure

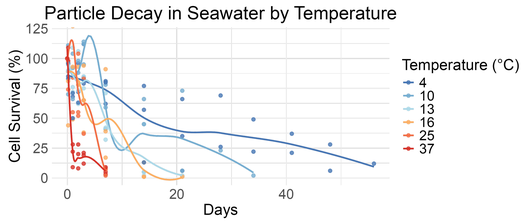


Adapted from a marine infectious disease model[4]:

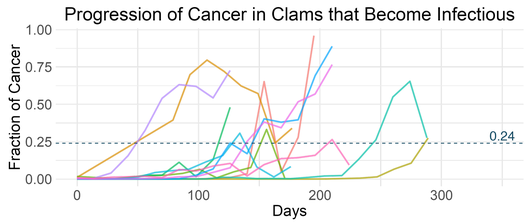
- Susceptible clams (S) become exposed (E) via contact with cancer cells in the water
- Transmission rate (β) varies with temperature
- Infected clams (I) release cancer cells (particles, P) into the environment
- Particle decay rate (δ) is also temperature-dependent

Parameter Priors and Survey Data

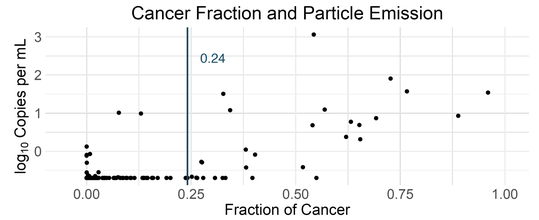
Laboratory Data Used to Inform Model Parameters



Plot A: Cancer cell decay at different temperatures informs the parameter δ and its temperature dependence.



Plot C: Longitudinal data from clams reaching 0.24 cancer fraction. Time to 0.24 informs α; time from 0.24 to death informs m.



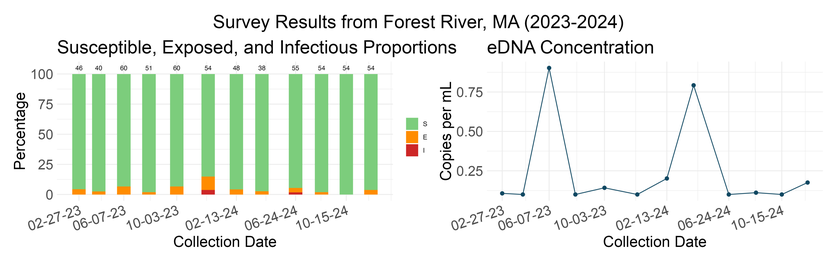
Plot B: Cancer fraction vs. particle release per clam. A changepoint indicates infectiousness; later emissions inform γ.

Parameter	Description	Data/Plot	Prior Mean
β*	Progression rate (S → E)	-	~ 0.02 day^{-1}
α	Progression rate (E → I)	C	~ 0.01 day^{-1}
m	Mortality rate (I → death)	C	~0.03 day^{-1}
γ	Particle emission rate	B	~ 11.90 $copies/mL/day$
δ	Particle decay rate in seawater	A	~ (0.12 - 0.16) day^{-1}

* Estimated by the model; partially informed by lab-based temperature progression (not shown)

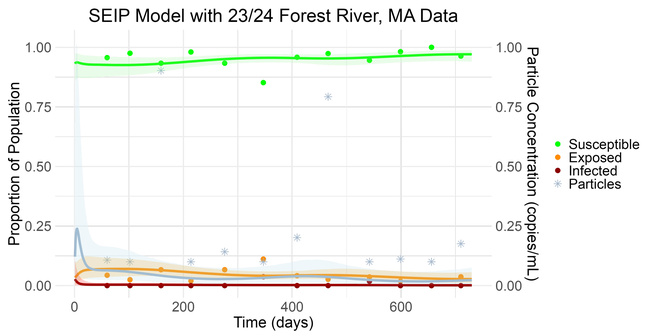
Observational Data

- Field surveys conducted bi-monthly along the East Coast
- Approximately 50 clams were per time point.
- eDNA from seawater enables quantification of cancer cell concentration



Preliminary ODE Model Fit to Survey Data

Parameter	Posterior Median [95% CI]
β	0.011 [0.005, 0.022]
α	0.009 [0.005, 0.012]
m	0.158 [0.060, 0.501]
γ	4.573 [1.763, 10.098]
$\delta(15℃)$	0.418 [0.161, 1.157]

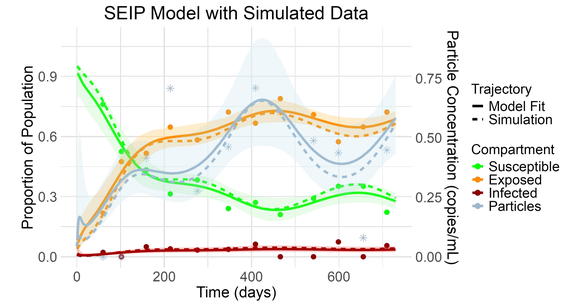


Captures overall disease dynamics, but misses some observed patterns

Discussion

Discrepancies between the model and field data may be due to:

- Observation error or overdispersion in eDNA data due to detection limits
- Biological processes not included in the model (e.g., spawning)
- Insufficient seasonality enforced in the model



Future Work

- Compare model outputs and assess sensitivity to identify key transmission parameters
- Generate predictions for 2025 and validate against future survey data
- Apply to additional sites to identify differences in transmission across populations

Other Survey Locations

Acknowledgments

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