

Special Issue on the Mathematics of Planet Earth

*Read about the application of mathematics and computational science to issues concerning invasive populations, Arctic sea ice, insect flight, and more in this Planet Earth **special issue**!*

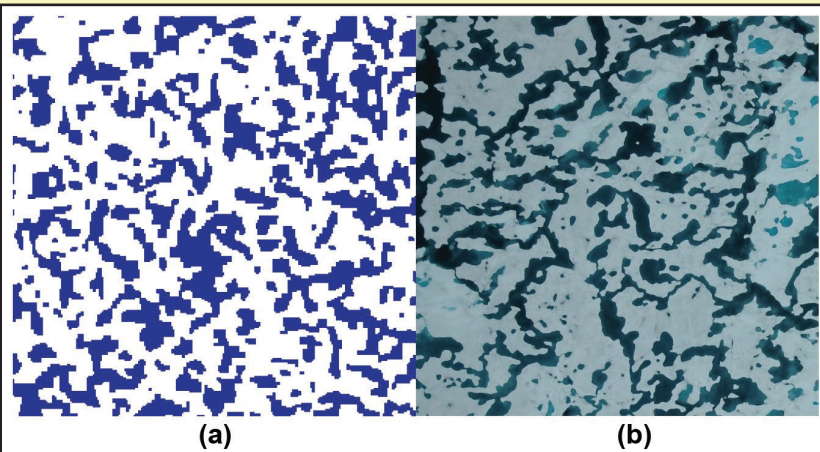


Figure 3. Comparison of real Arctic melt ponds with metastable equilibria in our melt pond Ising model. **3a.** Ising model simulation. **3b.** Real melt pond photo. Figure 3a courtesy of Yiping Ma, 3b courtesy of Donald Perovich.

Vast labyrinthine ponds on the surface of melting Arctic sea ice are key players in the polar climate system and upper ocean ecology. Researchers have adapted the Ising model, which was originally developed to understand magnetic materials, to study the geometry of meltwater's distribution over the sea ice surface. In an article on page 5, Kenneth Golden, Yiping Ma, Courtenay Strong, and Ivan Sudakov explore model predictions.

Controlling Invasive Populations in Rivers

By Yu Jin and Suzanne Lenhart

Flow regimes can change significantly over time and space and strongly impact all levels of river biodiversity, from the individual to the ecosystem. Invasive species in rivers—such as bighead and silver carp, as well as quagga and zebra mussels—continue to cause damage. Management of these species may include targeted adjustment of flow rates in rivers, based on recent research that examines the effects of river morphology and water flow on rivers' ecological statuses. While many previous methodologies rely on habitat suitability models or oversimplification of the hydrodynamics, few studies have focused on the integration of ecological dynamics into water flow assessments.

Earlier work yielded a hybrid modeling approach that directly links river hydrology with stream population models [3]. The hybrid model's hydrodynamic component is based on the water depth in a gradually varying river structure. The model derives the steady advective flow from this structure and relates it to flow features like water discharge, depth, velocity, cross-

sectional area, bottom roughness, bottom slope, and gravitational acceleration. This approach facilitates both theoretical understanding and the generation of quantitative predictions, thus providing a way for scientists to analyze the effects of river fluctuations on population processes.

When a population spreads longitudinally in a one-dimensional (1D) river with spatial heterogeneities in habitat and temporal fluctuations in discharge, the resulting hydrodynamic population model is

$$\begin{aligned} N_t &= -A_t(x, t) \frac{N}{A(x, t)} + \frac{1}{A(x, t)} \left(D(x, t) A(x, t) N_x \right)_x - \frac{Q(t)}{A(x, t)} N_x + rN \left(1 - \frac{N}{K} \right) \\ N(0, t) &= 0 \quad \text{on } (0, T), x = 0, \\ N_x(L, t) &= 0 \quad \text{on } (0, T), x = L, \\ N(x, 0) &= N_0(x) \quad \text{on } (0, L), t = 0 \end{aligned} \quad (1)$$

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Modeling Resource Demands and Constraints for COVID-19 Intervention Strategies

By Erin C.S. Acquesta, Walt Beyeler, Pat Finley, Katherine Klise, Monear Makvandi, and Emma Stanislawski

As the world desperately attempts to control the spread of COVID-19, the need for a model that accounts for realistic trade-offs between time, resources, and corresponding epidemiological implications is apparent. Some early mathematical models of the outbreak compared trade-offs for non-pharmaceutical interventions [3], while others derived the necessary level of test coverage for case-based interventions [4] and demonstrated the value of prioritized testing for close contacts [7].

Isolated analyses provide valuable insights, but real-world intervention strategies are interconnected. Contact tracing is the lynchpin of infection control [6] and forms the basis of prioritized testing. Therefore, quantifying the effectiveness of contact tracing is crucial to understanding the real-life implications of disease control strategies.

Contact Tracing Demands

Contact tracers are skilled, culturally competent interviewers who apply their knowledge of disease and risk factors when notifying people who have come into contact with COVID-19-infected individuals. They also continue to monitor the situation after case investigations [1].

Case investigation consists of four steps:

1. Identify and notify cases
2. Interview cases
3. Locate and notify contacts
4. Monitor contacts.

Most health departments are implementing case investigation, contact identification, and quarantine to disrupt COVID-19 transmission. The timeliness of contact tracing is constrained by the length of the infectious period, the turn-around time for testing and result reporting, and the ability to successfully reach and interview patients and their contacts. The European Centre for Disease Prevention and Control approximates that contact tracers spend one to two hours conducting an interview [2]. Estimates regarding the timelines of other steps are limited to subject matter expert elicitation and can vary based on cases' access to phone service or willingness to participate in interviews.

Bounded Exponential

The fundamental structure of our model follows traditional susceptible-exposed-infected-recovered (SEIR) compartmental modeling [5]. We add an asymptomatic population A , a hospitalized population H , and disease-related deaths D , as well as corresponding quarantine states. We define the states $\{S_i, E_i, A_i, I_i, H, R, D\}_{i=0,1}$ for our compartments, such that $i=0$ and $i=1$

correspond to unquarantined and quarantined respectively. Rather than focus on the dynamics that are associated with the state transition diagram in Figure 1, we introduce a formulation for the real-time demands on contact tracers' time as a function of infection prevalence, while also respecting constraints on resources.

When the work that is required to investigate new cases and monitor existing contacts exceeds available resources, a backlog develops. To simulate this backlog, we introduce a new compartment C for tracking the dynamic states of cases:

$$\frac{dC}{dt} = [flow_{in}] - [flow_{out}].$$

Flow into the backlog compartment, represented by $[flow_{in}]$, reflects case identification that is associated with the following transitions in the model:

- The rate of random testing: $q_{rA}(t)A_0(t) \rightarrow A_1(t)$ and $q_{rI}(t)I_0(t) \rightarrow I_1(t)$
- Testing triggered by contact tracing: $q_{tA}(t)A_0(t) \rightarrow A_1(t)$, $q_{tI}(t)I_0(t) \rightarrow I_1(t)$, and $q_{tE}(t)E_i(t) \rightarrow \{A_i(t), I_i(t)\}$
- The population that was missed by the non-pharmaceutical interventions that require hospitalization: $\tau_{IH}(t)I_0(t) \rightarrow H(t)$.

Here, $q_{rs}(t)$ defines the time-dependent rate of random testing, $q_{ts}(t)$ signifies the time-dependent rate of testing that is triggered by contact tracing, and τ_{IH} is the inverse of the expected amount of time for which an infected individual is symptomatic before hospitalization. These terms collectively provide the simulated number of newly-identified positive COVID-19 cases. However, we also need the average number of contacts per case. We thus define function $\mathcal{K}(\kappa, T_s, \phi_\kappa)$ that depends on the average number of contacts a day (κ), the average number of days for which an individual is infectious before going into isolation (T_s), and the likelihood that the individual

See **COVID-19 Intervention** on page 3

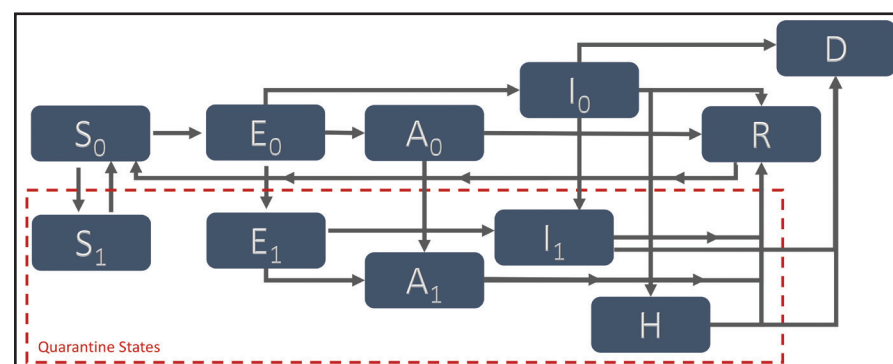


Figure 1. Disease state diagram for the compartmental infectious disease model. Figure courtesy of the authors.

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