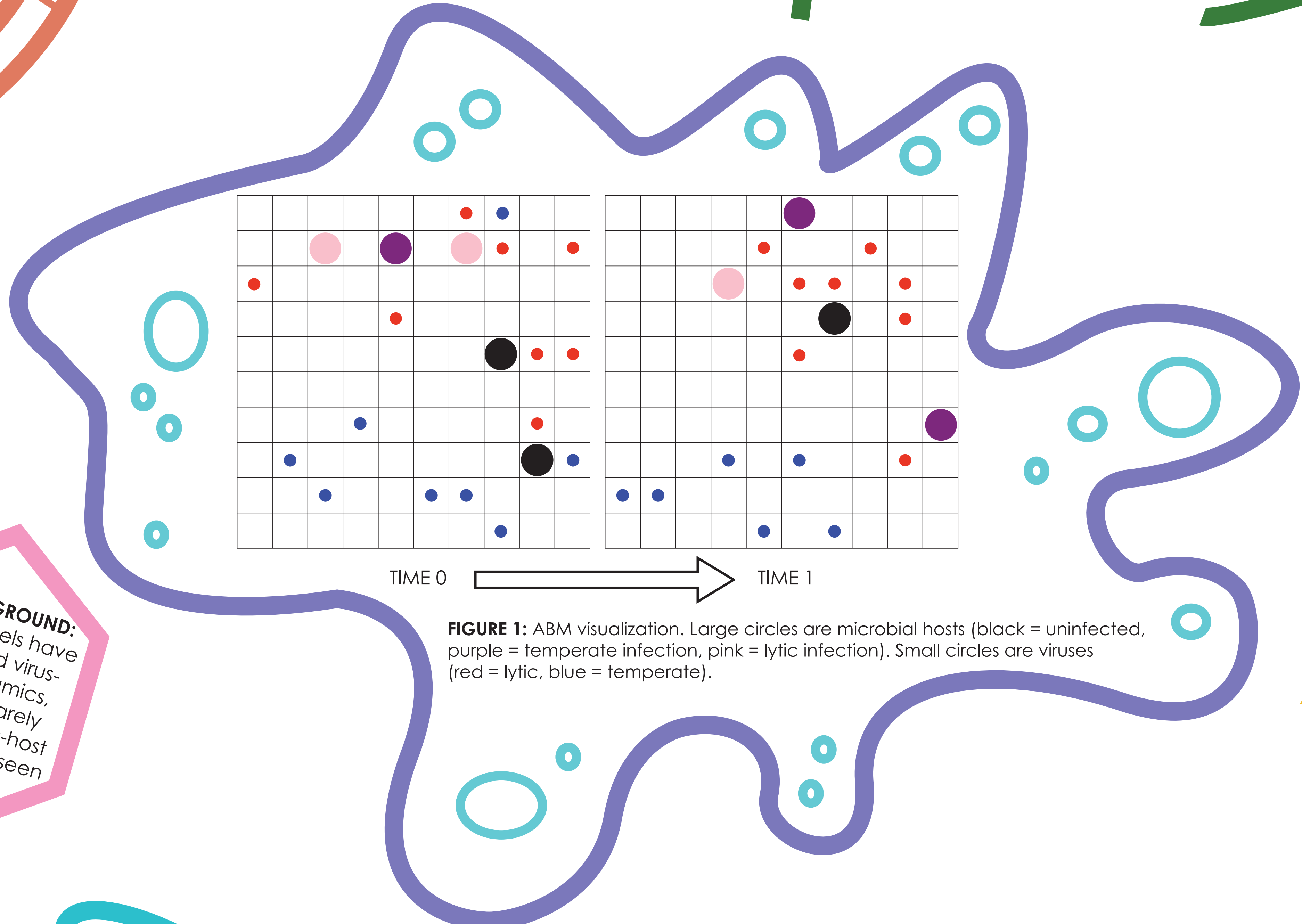


ABSTRACT:
The most widely used theoretical models of virus-host interaction are century-old Lotka-Volterra ordinary differential equations (ODEs). However, our lab identified theoretical and empirical concerns with applying these models to virus-host interactions. While viruses and hosts are able to coexist in nature, coexistence is rarely observed in ODE models, due to the encounter term between viruses and hosts predicting more lysis events than is possible. We therefore created an agent-based model (ABM) that is more realistic than the ODE model to examine virus-host interactions. By probing our ABM, we were able to identify parameter sets for viruses and hosts that led to virus-host coexistence, host proliferation, or systemwide extinction. Future work will continue using the ABM to probe competition dynamics between temperate and lytic viruses, giving insight into the composition and impacts of viral communities across ecosystems from coral reefs to the human gut microbiome.

METHODS:
ABM was made in Python using Mesa. We created virus & host agents with modifiable parameters, then placed agents on a grid to interact. Interactions including natural birth, natural death, infection, lysis, and recovery took place stochastically, with rates centered around modifiable thresholds.

ACKNOWLEDGEMENTS:
Thank you to BIG Summer, QCBio, UCLA, and NSF for giving me this opportunity. Also thank you to the Hopeful Monsters lab, y'all are really cool



BACKGROUND:
Interactions of viruses and their microbial hosts shape our world, so we should better understand their dynamics.

BACKGROUND:
ODE models have examined virus-host dynamics, but they rarely see the virus-host coexistence seen in nature.

QUESTION:
Can we create a virus-host ABM that can represent outcomes such as coexistence, host proliferation & total extinction?

RESULTS:
Our model was able to represent a variety of patterns, including coexistence, host proliferation, and system-wide extinction. While there may be limitations of two-dimensional space, the ABM represents more nuanced interactions than possible with ODEs. Our future research will use the ABM to further explore the competition between lytic and temperate viruses.

