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Current paradigm The 'Mutation-Selection Cycles'



Current attempts to integrate eco-evolutionary processes into General Circulation Models (GCMs) using trait-based models do so following the same general philosophy in two distinct phases:

1. New phenotypes arise, e.g. through genetic mutation. 2. Selection occurs on the phenotypes, modeled as competition among phenotypes in the ecological model.

This general framework could be called the 'Mutation-Selection Cycles', and a wide range of models fall under this category: individual-based models, trait-diffusion processes, adaptive dynamics...

The drawbacks of this framework come from the computational costs (e.g. individual-based models) and **simplifying assumptions** that can be biologically or mathematically problematic (e.g. moments method).

Proof-of-concept Results in a 0D model

A simple chemostat model

In order to test our approach, we use a simple chemostat model with one resource and a washout rate J. The "true" eco-evolutionary dynamics are simulated by implementing an an **individual-based model (IBM)**.

We then compare the dynamics of the mean trait of the population as predicted by the IBM to the solution of the selection gradient equation.



The state of the environment is measured in the bacterial growth rate by the parameter e, and the adequation of the individual to its environment through the evolutionary trait x. We tested different time trajectories of parameter e to simulate different scenarios of environmental change.



Results

approach is best suited for environments change, and provides good approximations of the IBM in all cases. The main discrepancies occur for rapidly changing environments. In these cases, the 'evolutionary rescue' mechanism relies heavily on the standing variation in phenotype, which can't be captured in our framework. This highlights the limitation of the selection gradient equation approach to model adaptive responses to extreme events in short-timescales environmental changes.

The Selection Gradient Equation: Integrating Microbial Evolutionary Processes in General Circulation Models Philippe Cherabier¹, Régis Ferrière^{1,2,3}

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A paradigm shift Modelling a global selection pressure



We propose to assume *a priori* that adaptation through selection occurs, and thus to model it as a supplementary differential equation governing the evolution of a monomorphic trait xwhen the population has a size N:

$$\frac{\mathrm{d}x}{\mathrm{d}t} = \alpha \times N \times P(x)$$

Here, α is the evolutionary rate parameter and P(x) the selection pressure acting on an individual of trait x. There are three desirable properties for function P:

1. Being locally computable.

2. P(x) = 0 if x is an evolutionary stable strategy.

3. Being **biologically meaningful**, i.e. not just a mathematical construct.

Legend value of trait distribution **— — — —** Selection gradient equation Environment parameter Population size

The selection gradient equation under gradual

Application **Results in NEMO-PISCES**

Research question

How does the evolutionary adaptation of the microbial loop feed back into the oceanic carbon cycle under climate change?

Evolutionary trade-off



The trait under study is the bacterial growth efficiency (BGE) ω.

Here, respiration is considered as a proxy for various cell functions, useful for gathering resources: heterotrophic bacteria face a trade-off between yield and resource acquisition, which constrains their adaptation to changing environmental conditions.

The Selection Gradient The relevant mesure for selection pressure

We extend the definition of the invasion fitness (borrowed from the field of adaptive dynamics) for the purpose of deriving the selection pressure. By definition, invasion fitness is the initial growth rate of a mutant population at low density interacting with the resident population at ecological equilibrium. We define the instantaneous invasion fitness as the difference between the mutant and resident growth rates when the mutant population is small, given the current density of the resident population (not necessarily at ecological equilibrium).

We can then define the selection pressure as the gradient of the instantaneous invasion fitness when the mutant trait is infinitesimally close to the resident, the selection gradient.



This so-defined selection gradient possesses the three desirable properties:

1. By definition, a population at a stable strategy can't be invaded by nearby phenotypes. 2. Since the selection gradient is derived from a growth rate in a specific environment, it is locally computable.

3. The selection gradient is a growth rate gradient, and thus informs us on the direction most advantageous for bacteria. It can be used to assess how far a population is from its evolutionary optimum.

Outputs

We implement the selection gradient equations in the global circulation model NEMO coupled with the biogeochemistry model PISCES and compare the outputs to the model without evolution with a fixed BGE of 35%.





Conclusion and perspective

The inclusion of BGE adaptation can substantially upset global ecosystem functions and oceanic carbon stocks. We can note that the bacteria are not always at evolutionary equilibrium, and we can predict that global environmental changes will only exacerbate these Selection gradient differences.









The dos and don'ts Pros and cons of the method



Conclusion



We believe this method is well-suited for integration in Earth-System models (ESM) for the prediction of biogeochemical cycles under climate change. The philosophy behind it already fits current ESM models and allows for dynamical biological parameters constrained by eco-evolutionary processes. The approach assumes that traits are measured at the community level, and generates predictions about the effect of adaptive evolution on inter-annual timescales.

Next steps should focus on implementing the system response to climate change with and without evolution, and extend the eco-evolutionary processes to other compartments such as phytoplankton.

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