

Modelling the Changing Structure of Marine Ecosystems in Response to Changes in the Physical Climate

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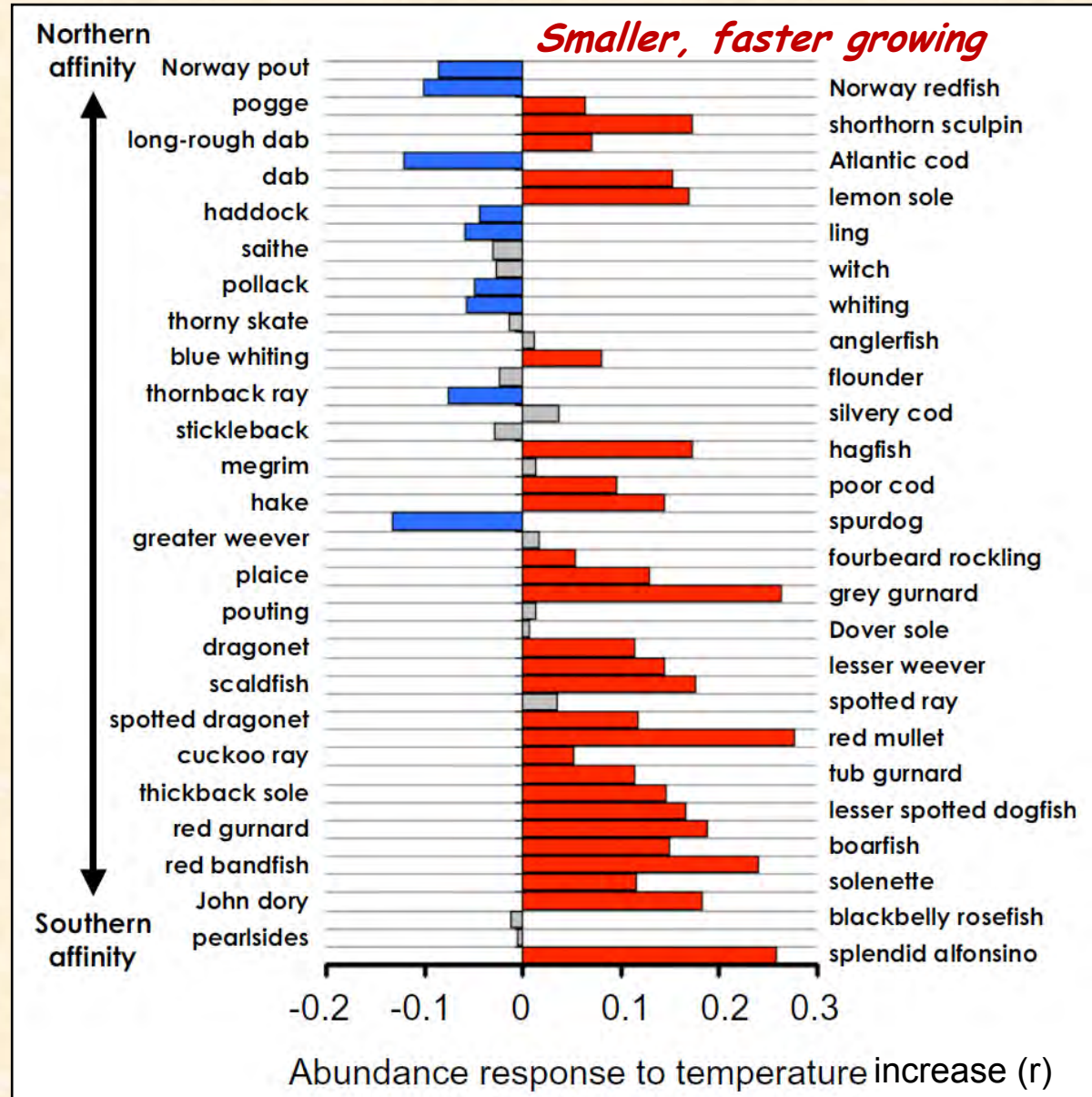
U. Victoria



Changes in Fish Assemblage at Fixed Locations

Simpson et al.,
Continental shelf-wide
response of a fish
assemblage to rapid
warming of the sea,
Current Biology (2011),
doi:10.1016/j.cub.2011.08
.016

Assessed "trends in 172
cells from records of >100
million individuals sampled
over 1.2 million km² from
1980-2008. We
demonstrate responses to
warming in 72% of common
species."

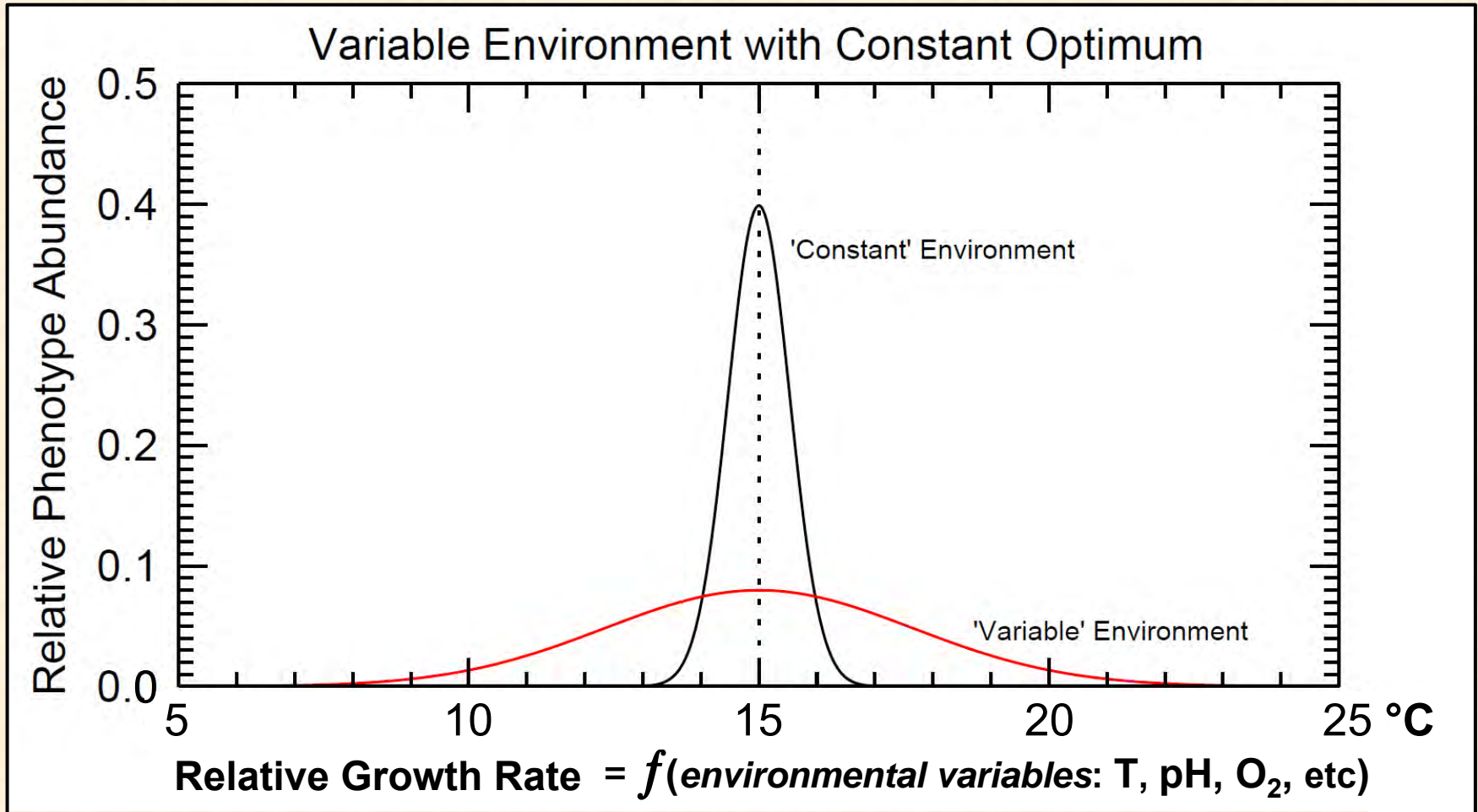


Are Our Standard Compartment Ecosystem Models Adequate?

- Current planktonic food web models have a 'fixed' structure, and few parameter values vary over time in response to a changing environment (exception - "optimality" or "adaptive" models of Markus Pahlow, S. Lan Smith, A. Merico,...)
- Try a model where adaptation is formulated in terms of the distribution of species or phenotypes as a function of traits (e.g., intrinsic growth rate) which in turn are functions of environmental variables: Temp, pH, O_2 , pCO_2 , etc.

e.g. maybe a simple 'Complex Adaptive System' model

Ecological Adaptation to a Changing Climate



Key reference: *Norberg et al. 2001. Phenotypic diversity & ecosystem functioning in changing environments: A theoretical framework, US Proc. Natl. Acad. Sci. 98 (20), 11376-11381.*

Change in Biomass $P(x_i, t)$

of species or phenotype i as a function of environmental variable x_i for a step change in environmental 'fitness', i.e. a regime shift in the environment

$$\frac{dP(x_i, t)}{dt} = P(x_i, t) [(v(x_i)H(x_i - x_m) - m_i)]$$

where :

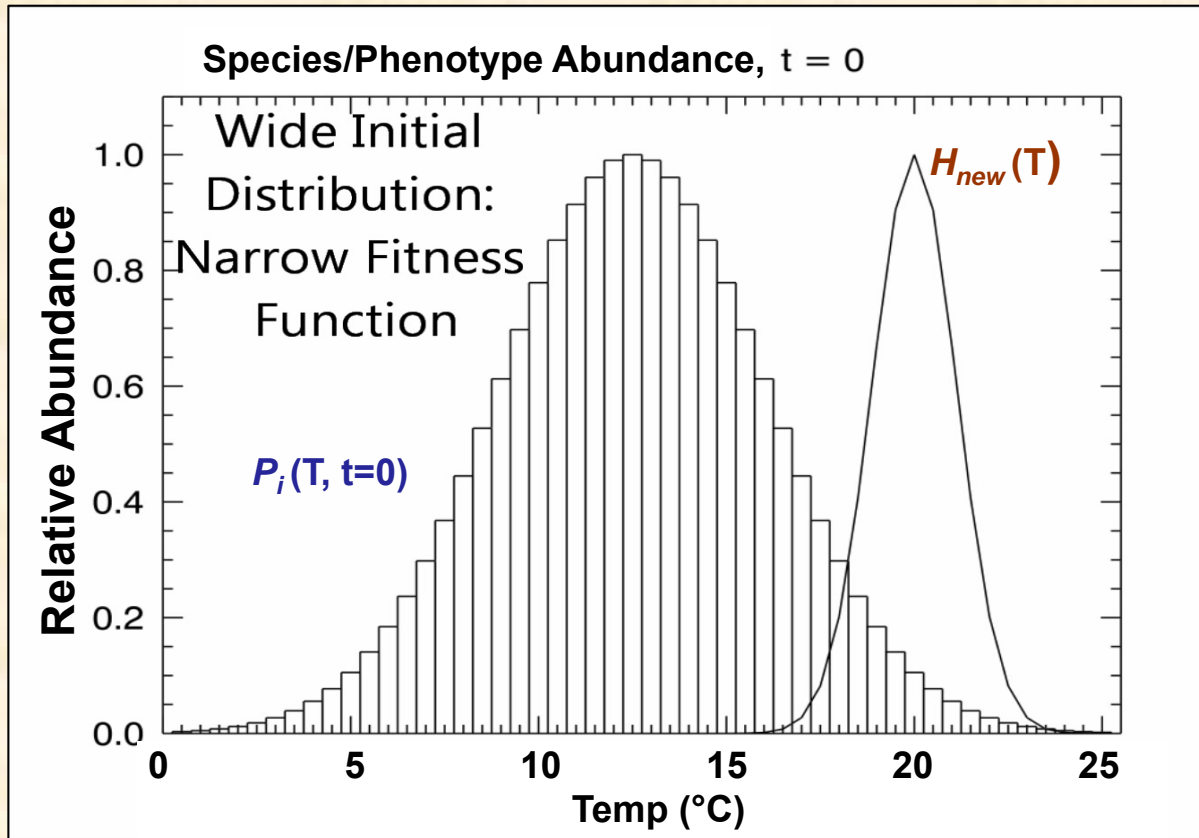
- $v(x_i)$ is the intrinsic growth rate (a 'trait') for phenotype i , as a function of the environmental variable x_i (e.g. pH, O_2 , SST, etc)
- $H(x_i)$, the 'fitness function' is maximum at x_m

$$H(x_i) = \frac{1}{2} \left[1 + \cos \left(\frac{2\pi(x_i - x_m)}{w} \right) \right] \text{ over } [-\pi, \pi], w = \text{width of 'cos' at } H = 0.5$$

- m_i is the linear mortality coefficient for phenotype i , and
- total biomass $B(t) = \int P(x_i, t) dx_i$ is currently controlled by a 'logistic' equation

So far, ignores diffusion, immigration, emigration, plasticity, genetic adaptation (evolution), etc.

Response to a Shift in T

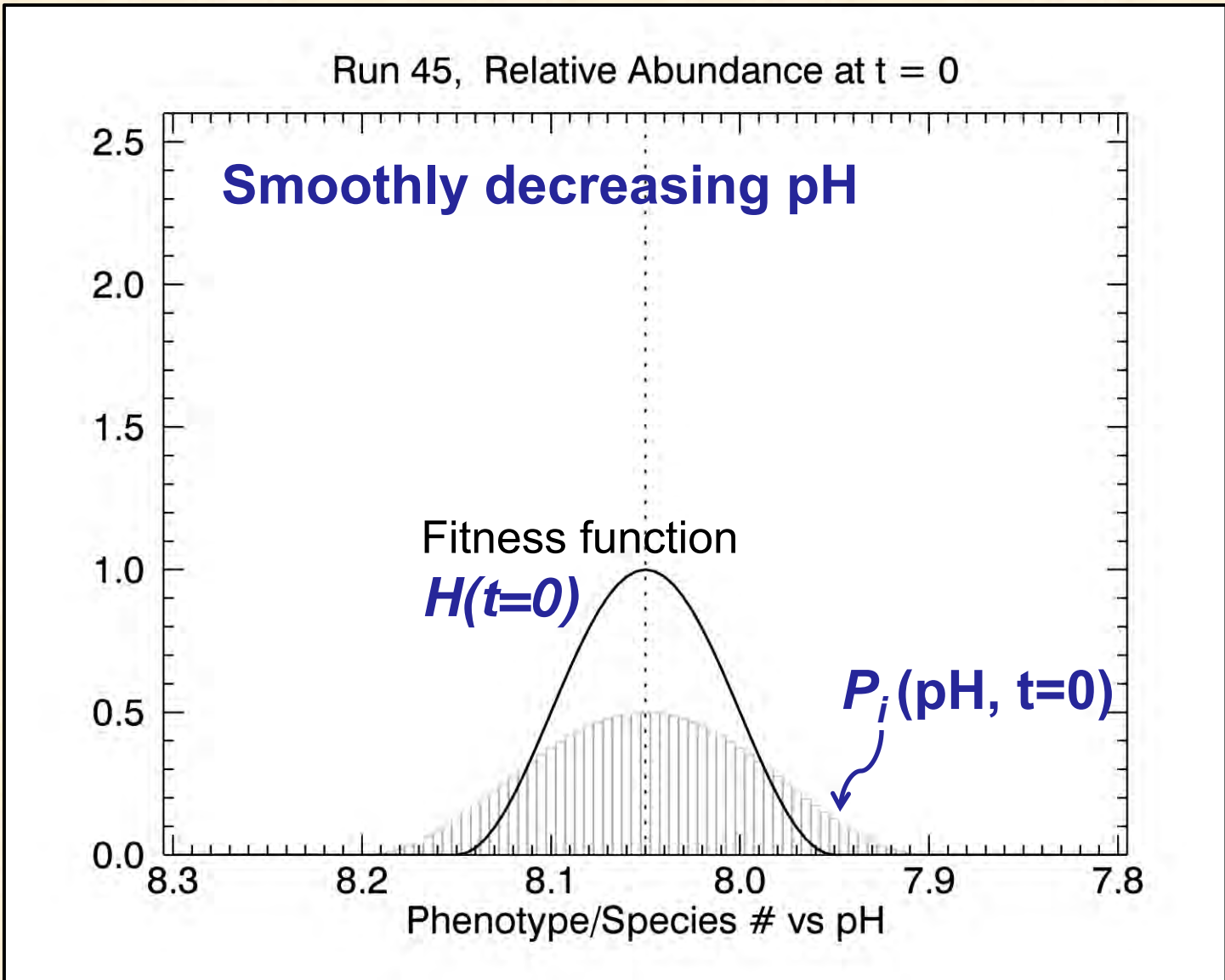


$$T_{old}(H_{max}) = 12.5^{\circ}C$$

$$T_{new}(H_{max}) = 20^{\circ}C$$

Success & rate of adaptation depend on the degree of overlap of the initial distribution $P(x_i, 0)$ of species or phenotypes and the new fitness function $H(x_i, t)$

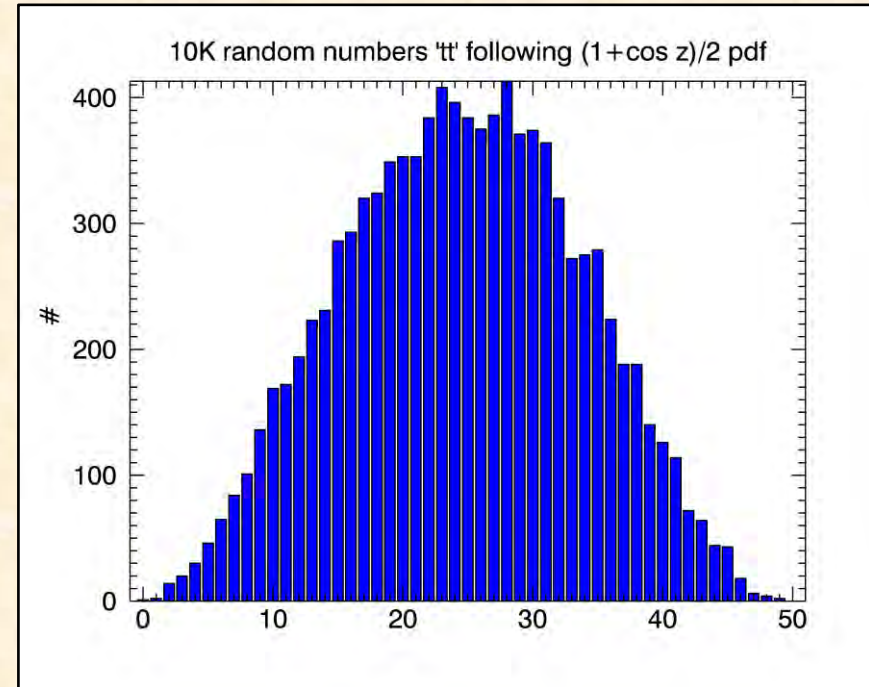
Response to Decreasing pH (1)



Time-Varying Environmental Forcing

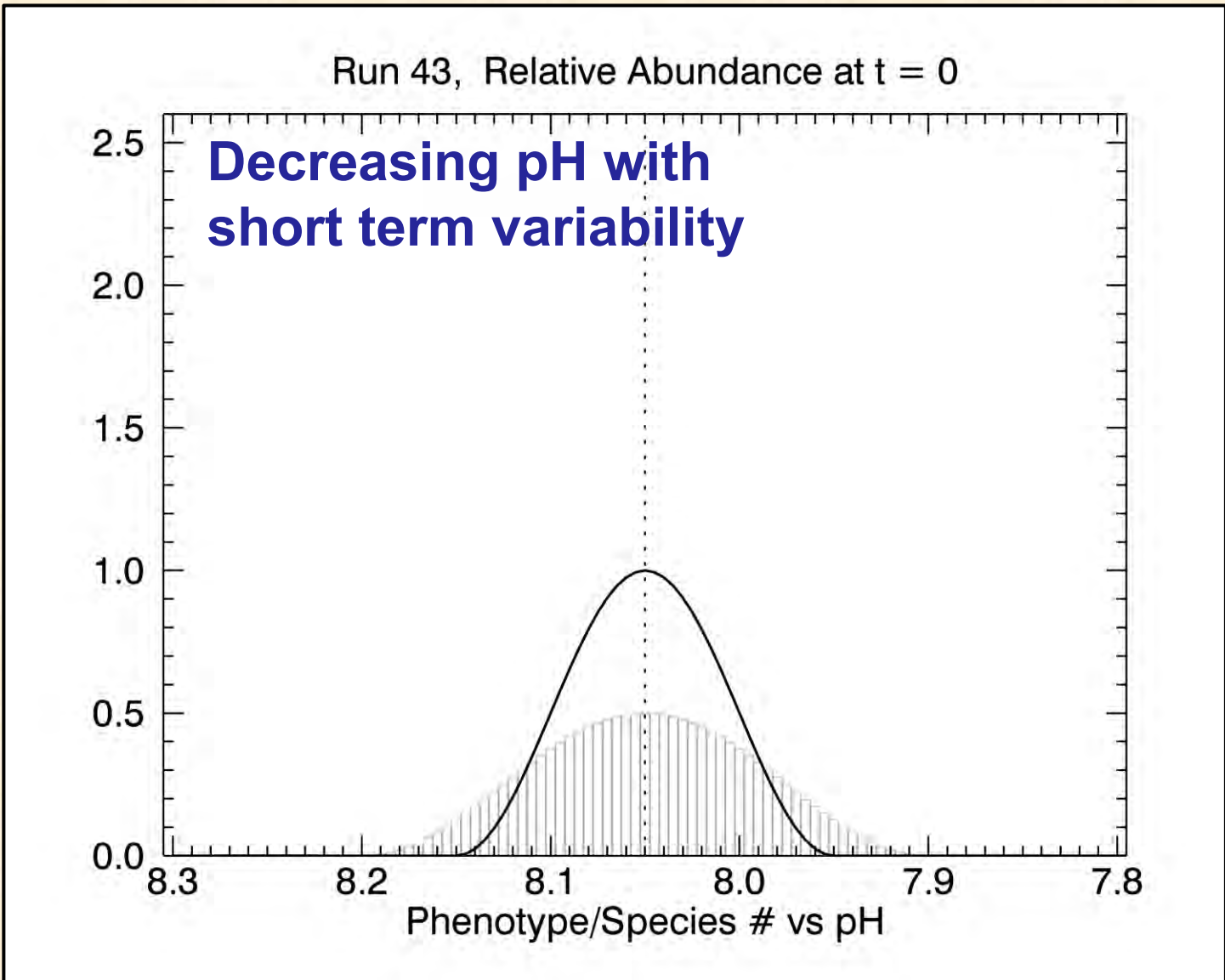
1. At each time t , vary forcing by adding random forcing R_t to the slowly-increasing T_t (or decreasing pH_t)

But this is "too random"



2. So create first order autoregressive variable "AR1":
$$Z_t = a_1 Z_{t-1} + a_2 R_t$$
, where ' a_2 ' can be calculated from ' a_1 ' such that the new distribution Z_t has the same variance about its centre as the original distribution R_t

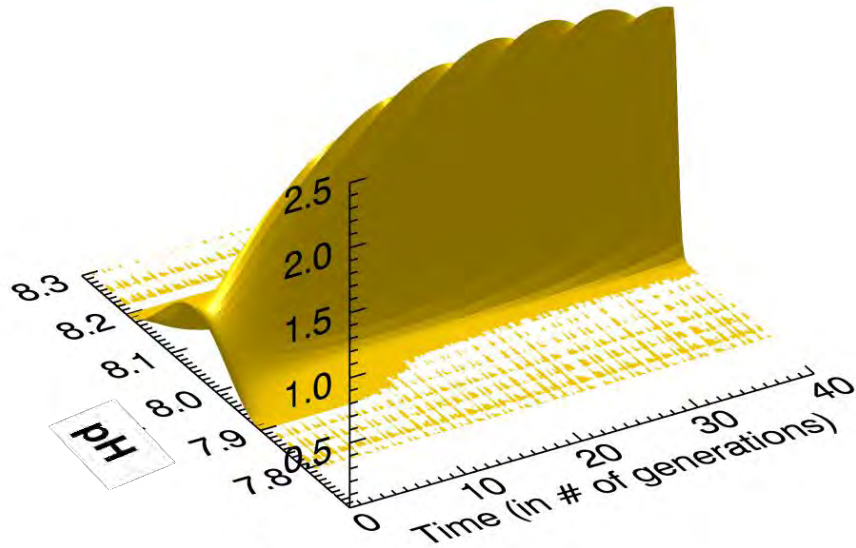
Response to Decreasing pH (2)



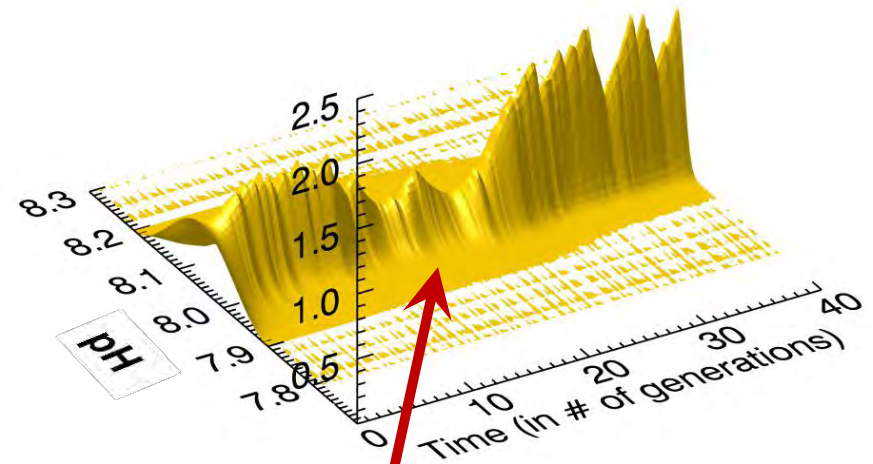
Effect of Variable Forcing in pH

(1 generation = 5 timesteps)

Smoothly decreasing pH

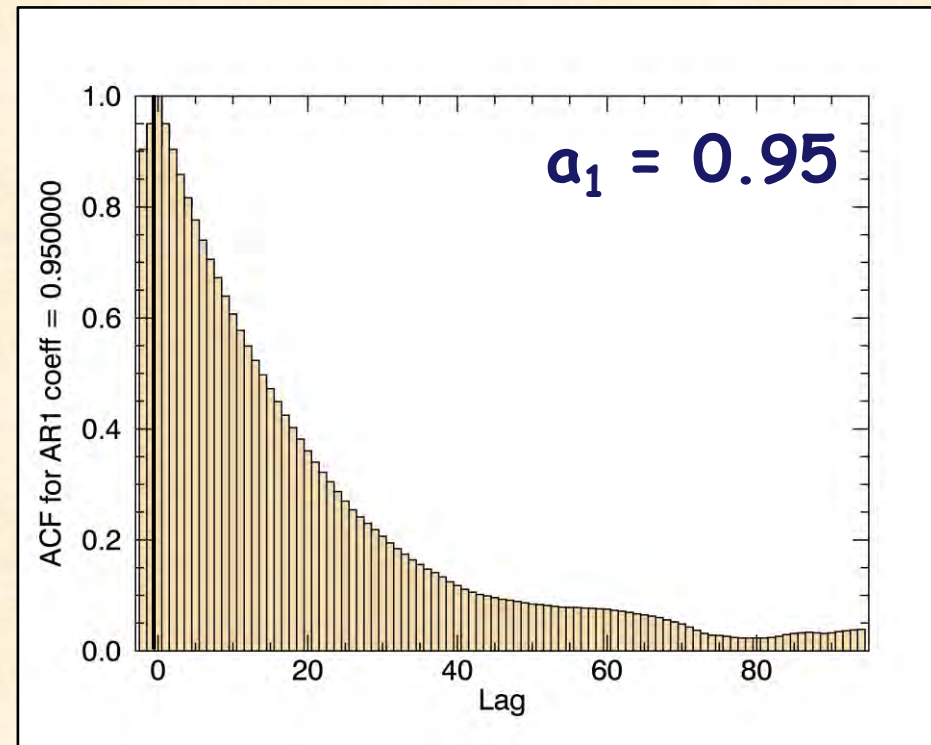
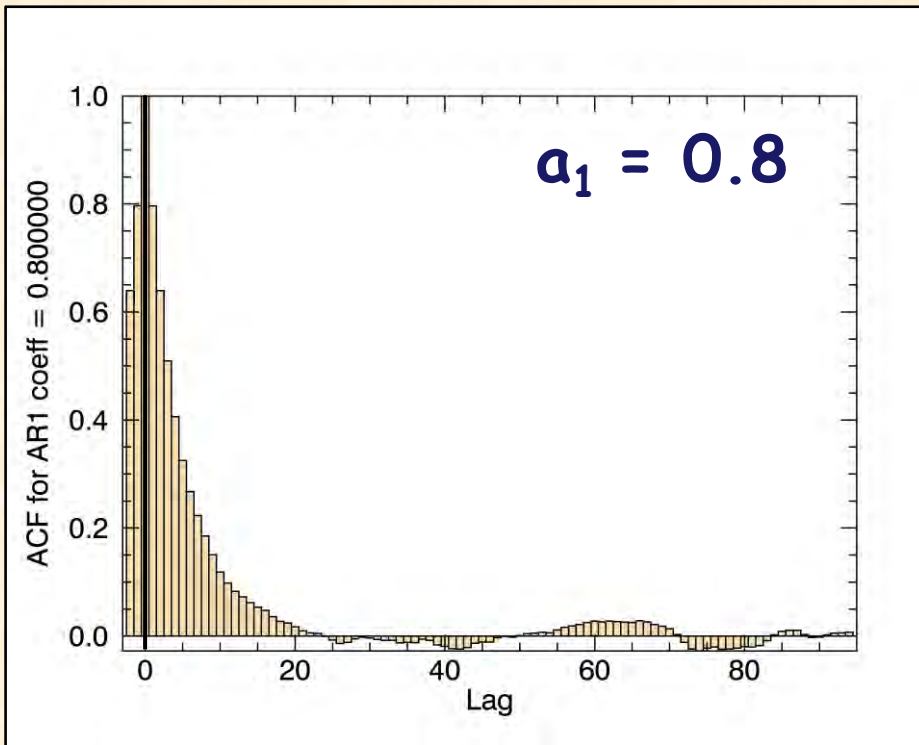


Decreasing pH with short term variability



Demonstrates how an extreme in variability imposed on a smooth decrease in pH over several generations *could* cause local extinction

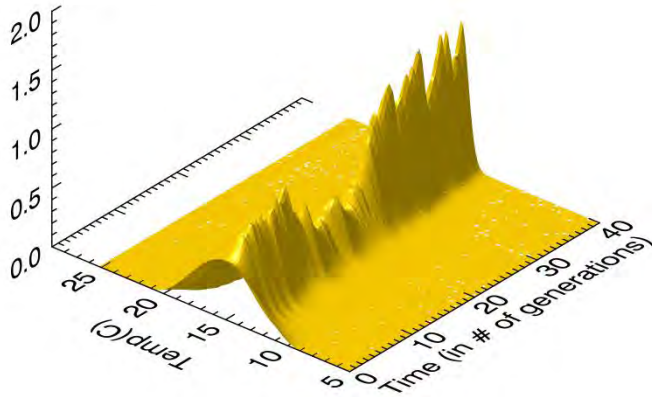
Consider $a_1 = 0.8$ and 0.95



Larger AR1 coefficient a_1 has a longer 'memory'

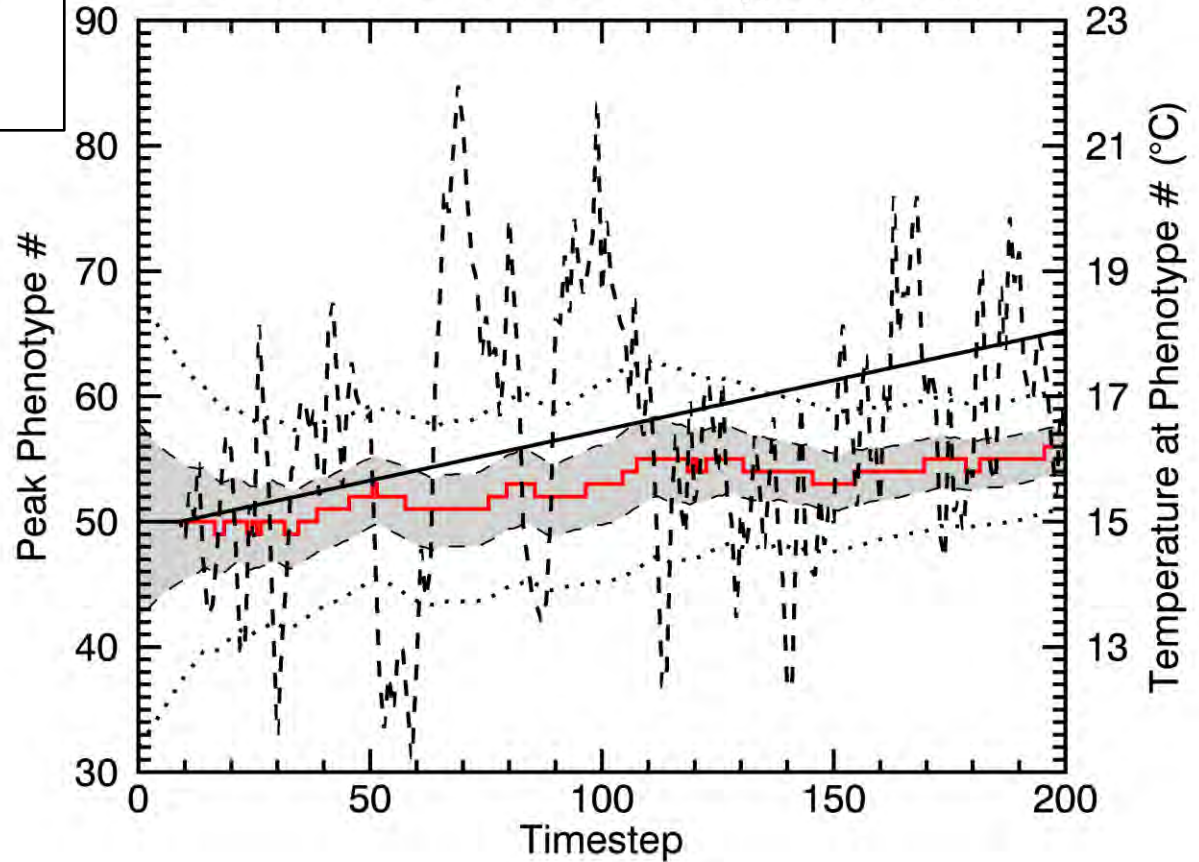
Uniform Warming + Variable Forcing

$$\alpha_1 = 0.8$$

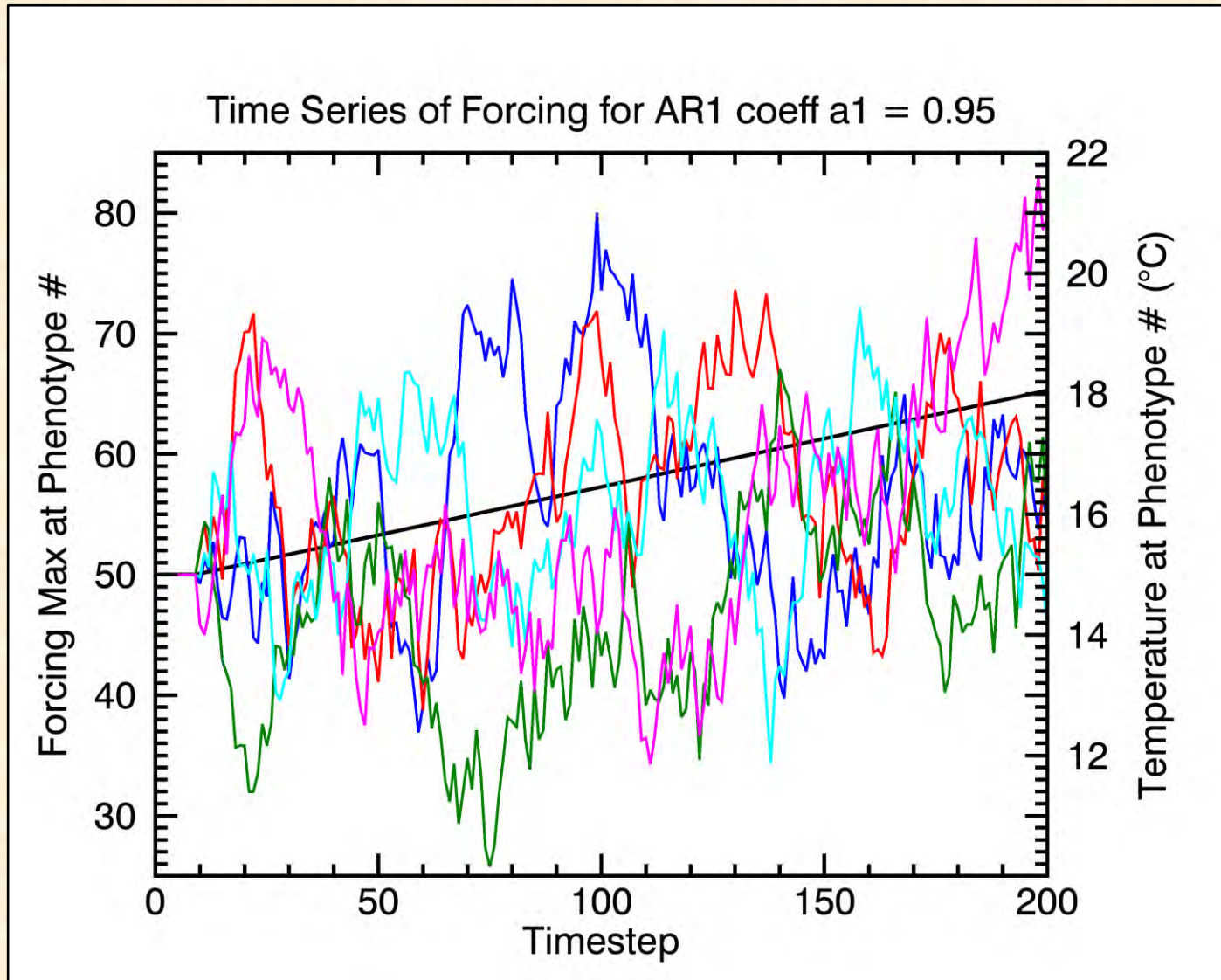


- 'Slow' trend in T
- - - Plus random forcing Z_t
- Peak biomass
- 95% cpdf
- - - 75% cpdf
- █ 25% cpdf
- 5% cpdf

Run 51T Time Series of Phenotype Distribution

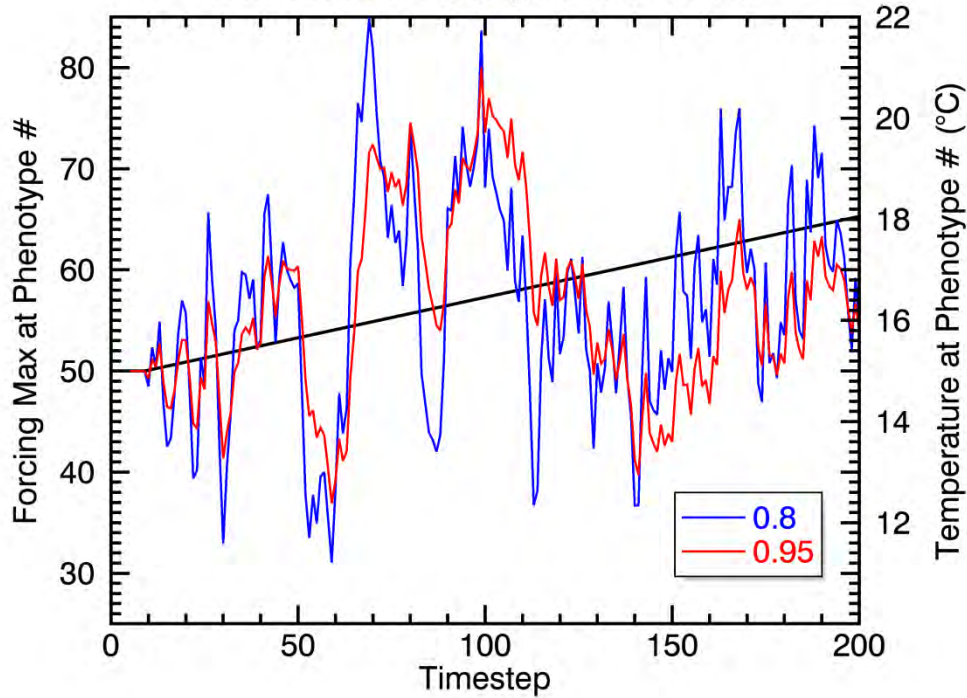


AR1 Forcing Starting at $t = 0, 500, 1000, 1500, 2000$

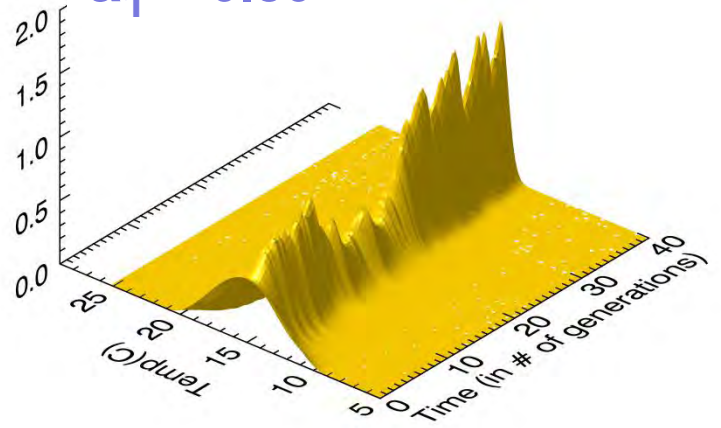


Effect of 'Slower' Variability

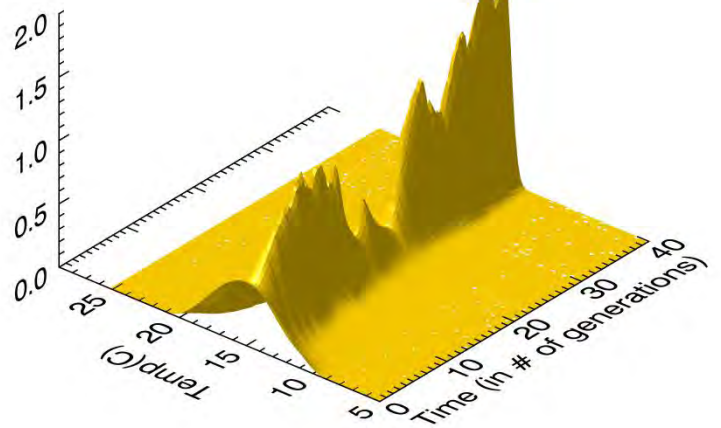
Time Series of Forcing for AR1 coeff a_1



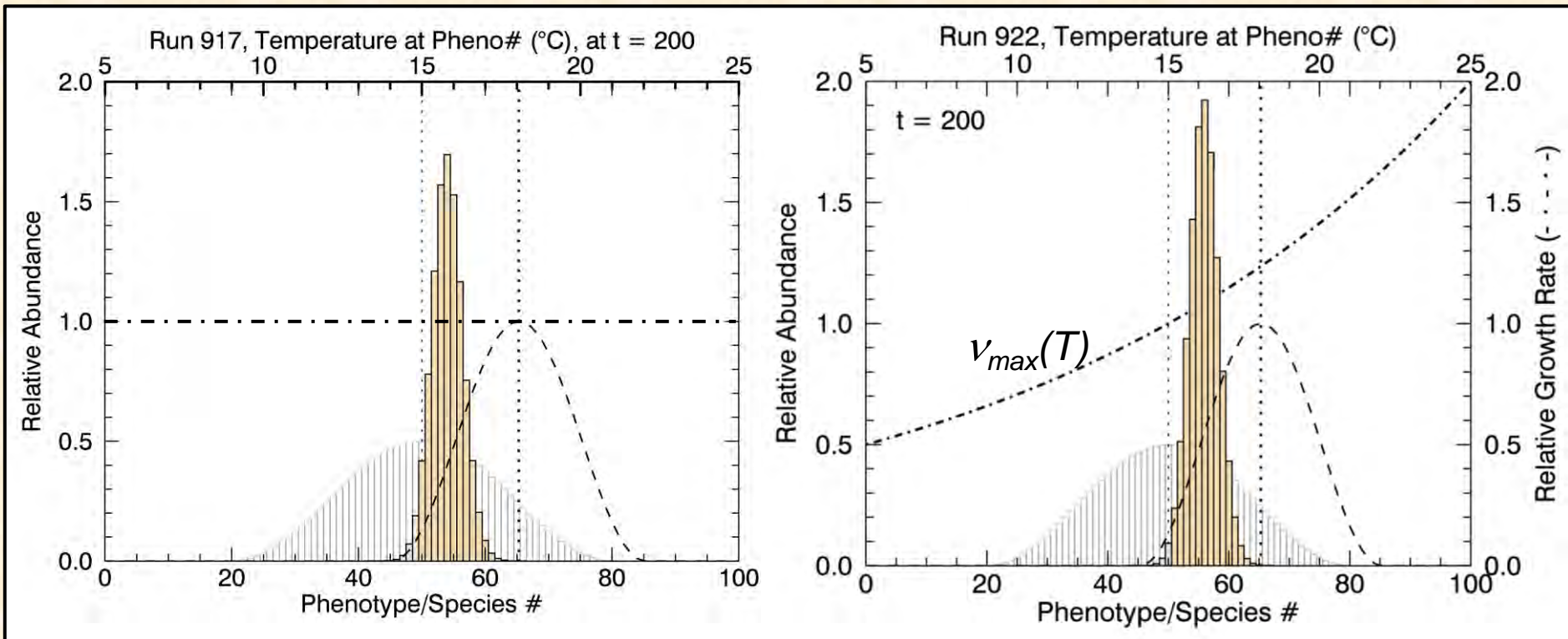
$a_1 = 0.80$



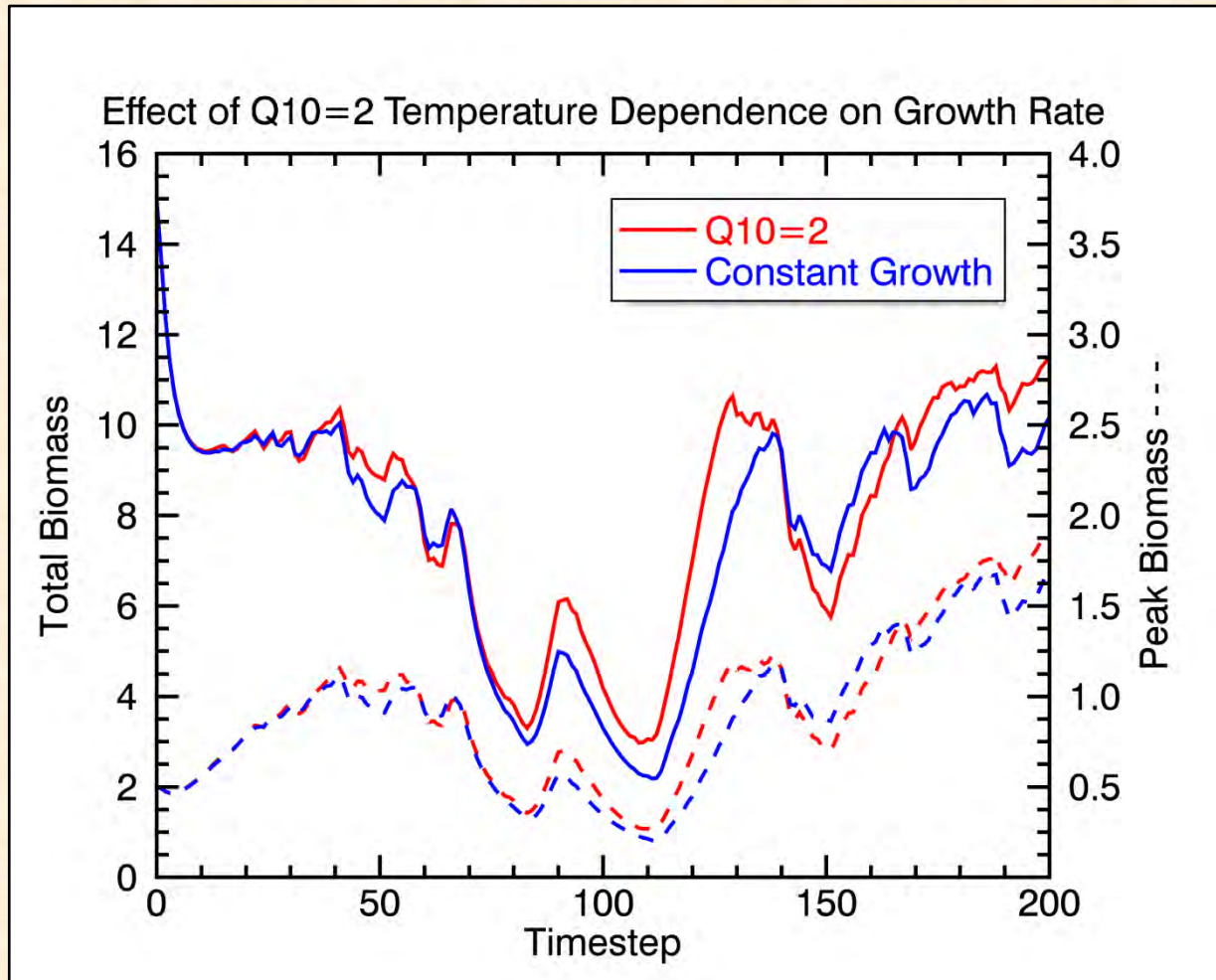
$a_1 = 0.95$



Constant Max Growth Rate vs $Q_{10} = 2$ Increase with T



Effect of Q_{10} Dependence on Total and Peak Biomass



Adding Realism? i.e. Complexity

So far we have started to explore only the effect of change in 1 environmental variable (T or pH) on 1 physiological trait (maximum intrinsic growth rate), of 1 group.

What is next?

1. Add size dependence of phytoplankton as a function of T
2. Develop zooplankton whose size is a function of the size of their prey, via an allometric relationship
3. Start to build a foodweb with these adaptive groups
4. Add multiple stressors, e.g. changing T, pH, O_2 , etc., possibly using Hans Pörtner's 'Optimum Thermal Window' concept.

Thanks

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