Modeling copepod diversity, biogeography, and life history

Andrew J. Pershing
University of Maine/ Gulf of Maine Research Institute

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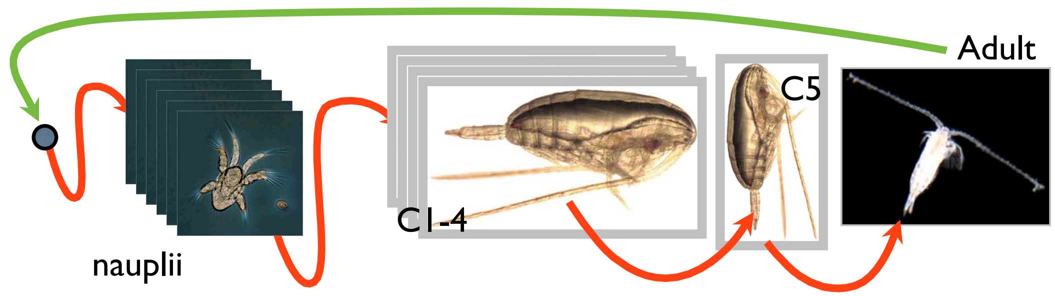
Outline

- “Standard” copepod models
  - Forecasting with ensemble Kalman smoother
- Mass-stage model
  - copepod biogeography & diversity

Copepod Models

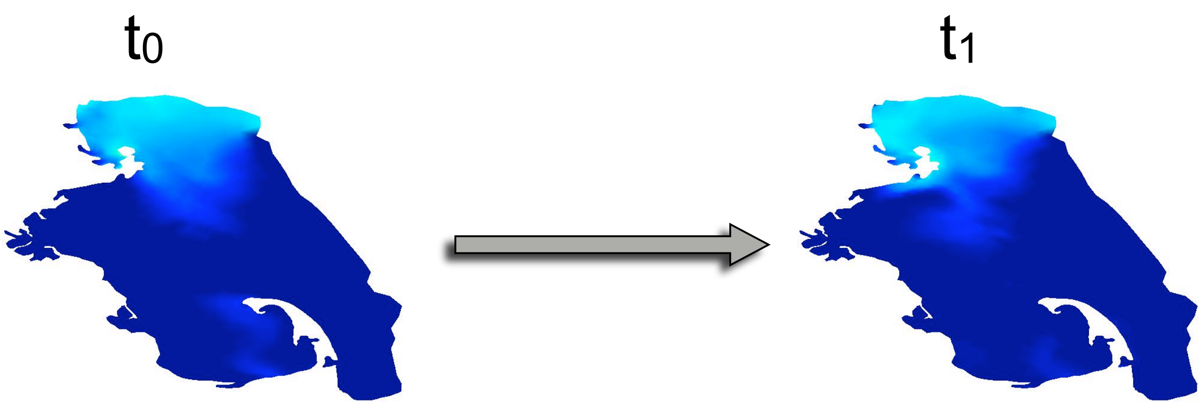
- “Standard” models
  - C_j=abundance of stage j
  - development rate
    - function of temperature
    - developmental diffusion requires substaging
  - egg production
    - function of food
  - mortality
    - ???
    - temp, food, season, density?



Pershing et al. (2009a) MEPS 378:227-243
(2009b) MEPS 378:245-257

Data Assimilation

- Problems
  - don't know initial or boundary conditions
  - unrepresented processes



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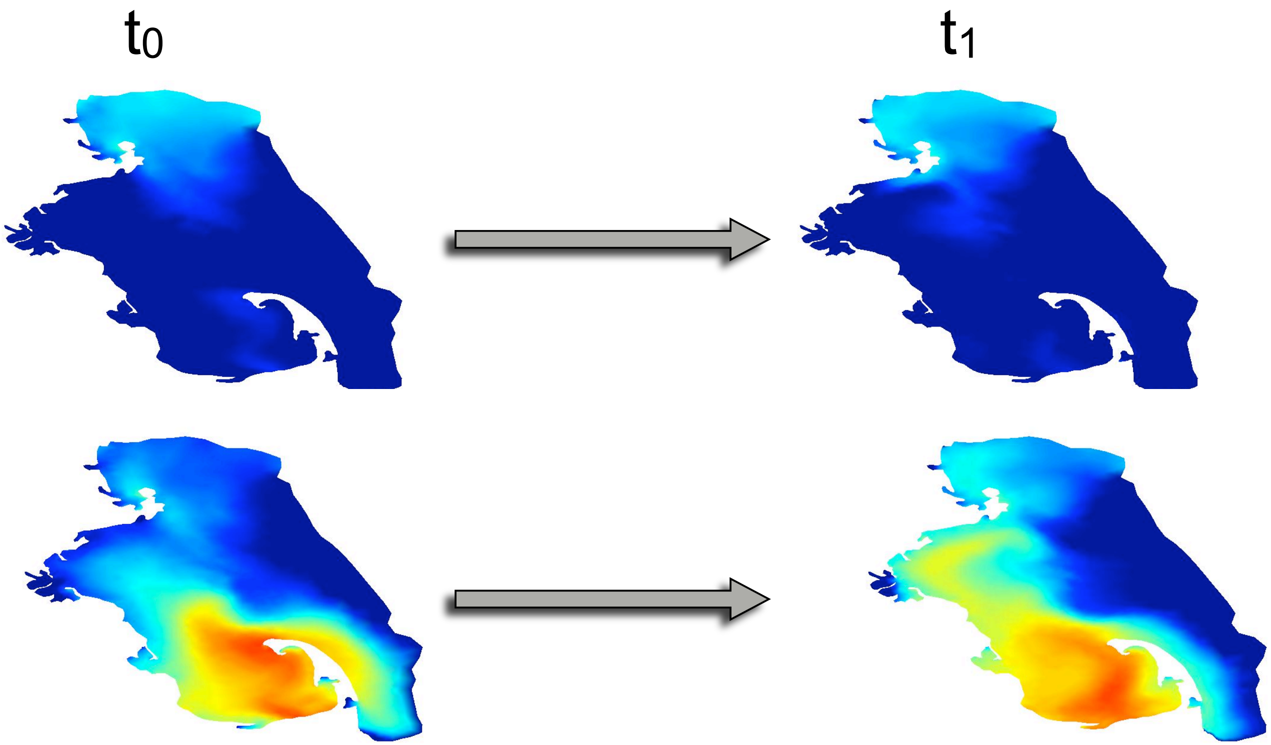

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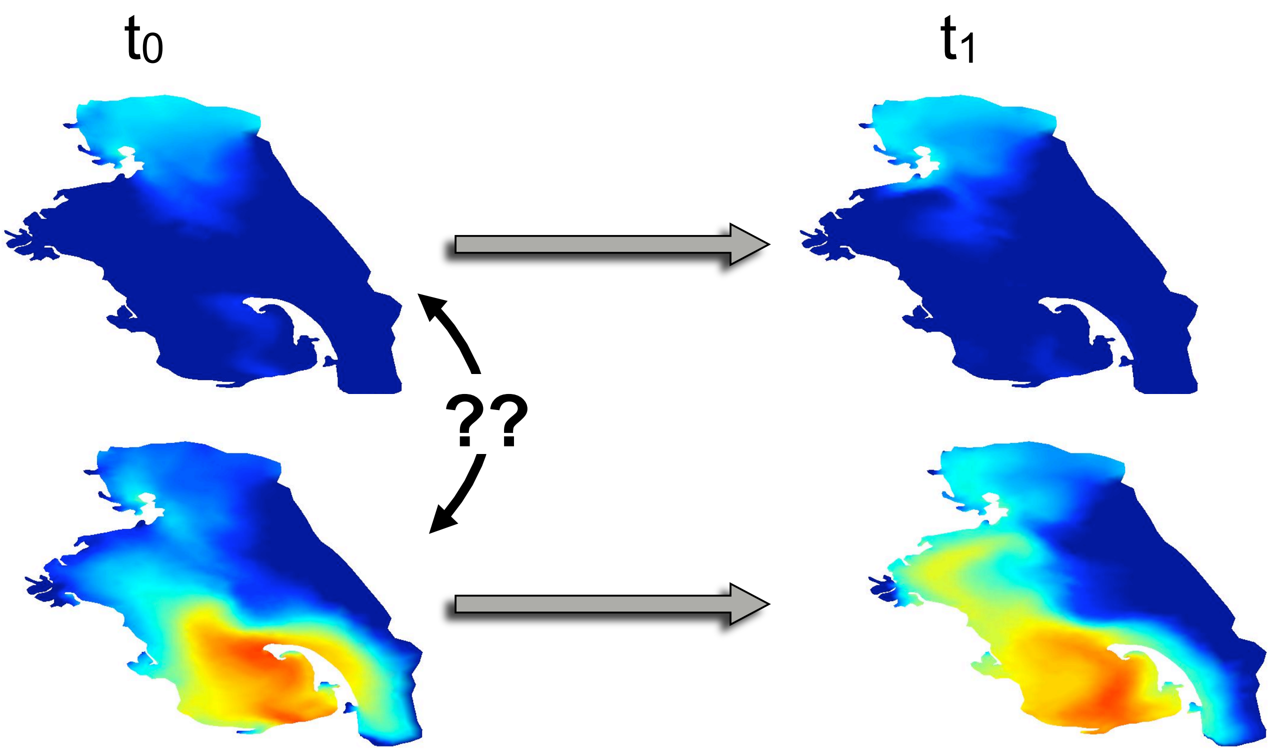
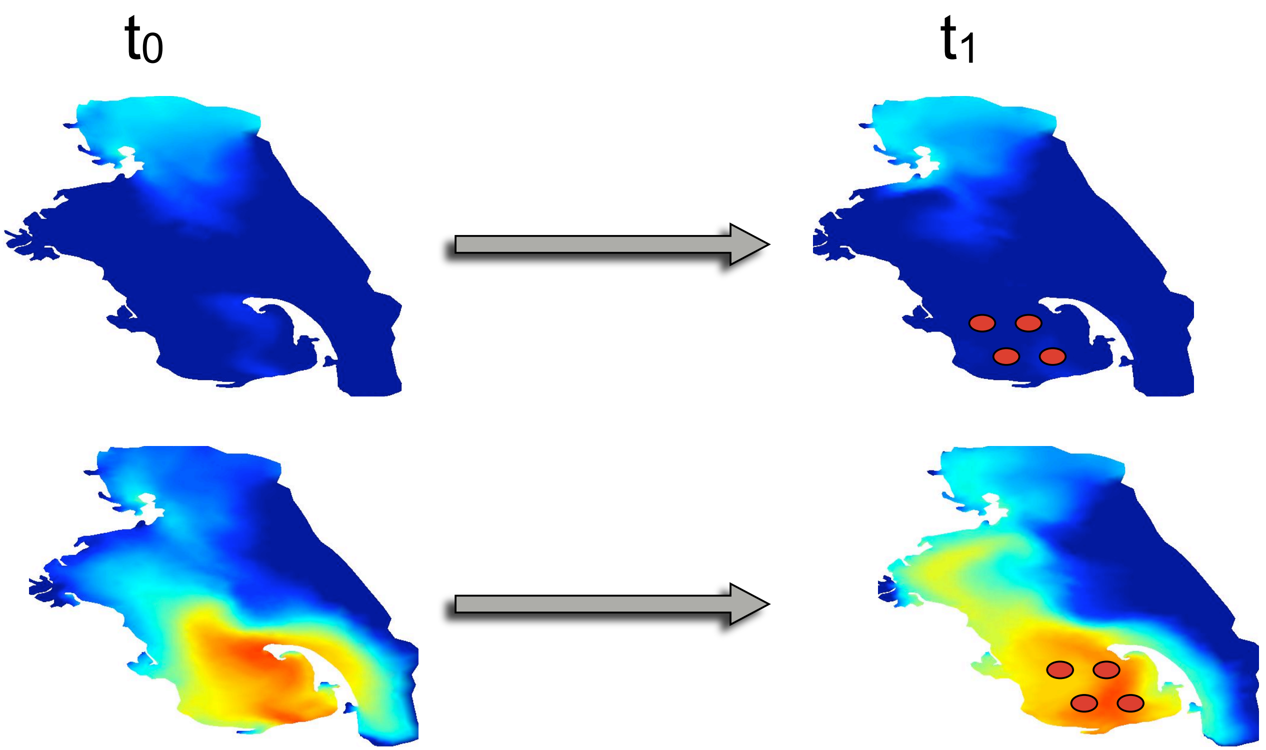


Data Assimilation

- Solution
  - use available data & model to reconstruct copepod distributions



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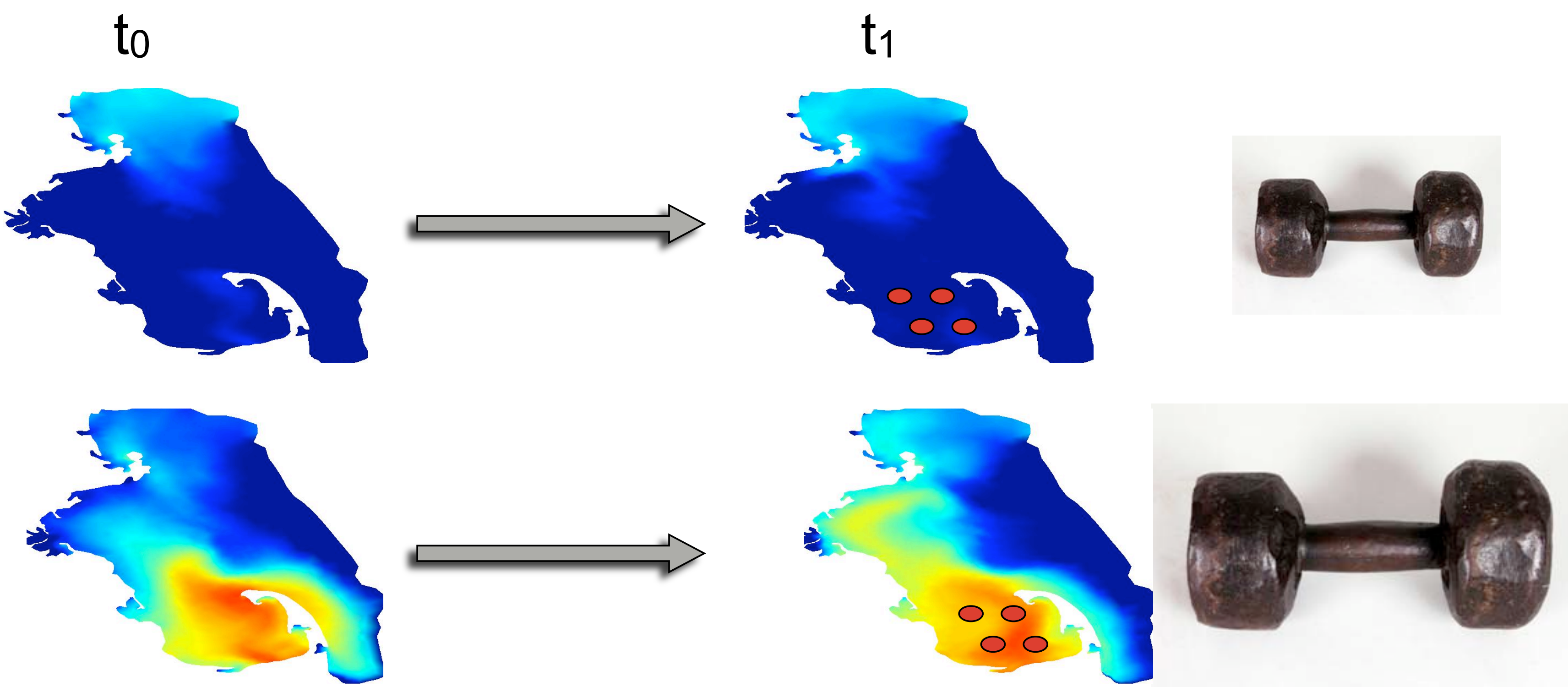

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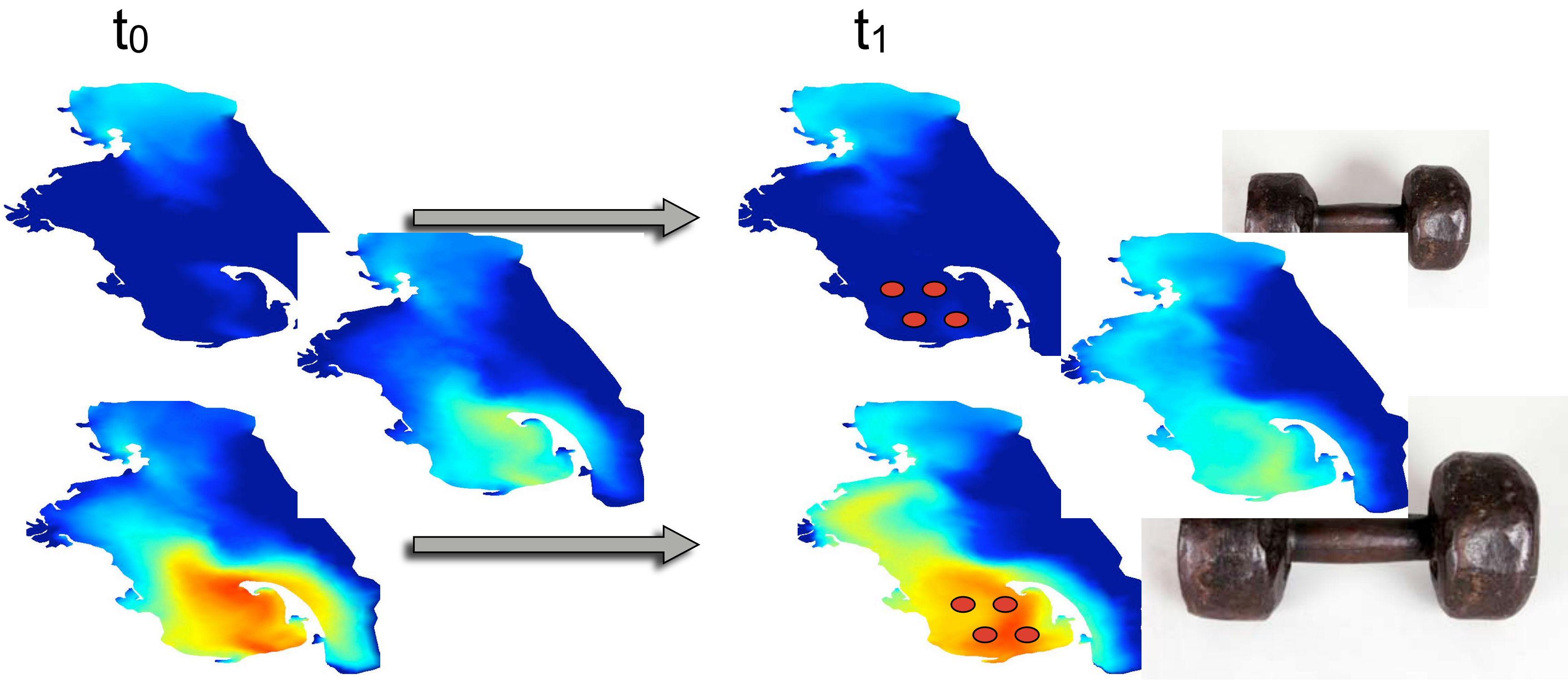
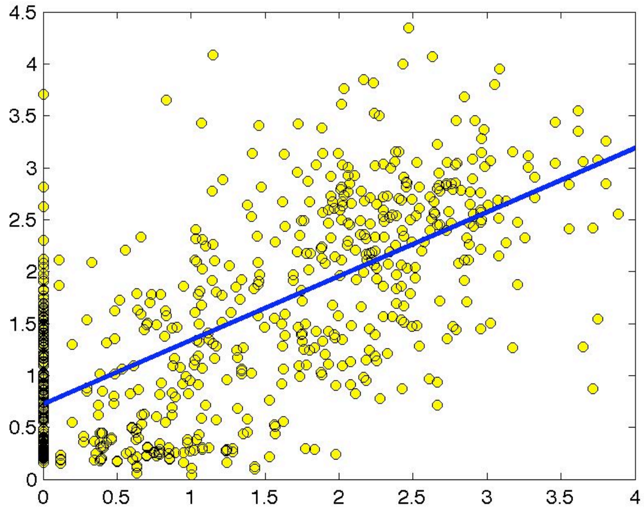
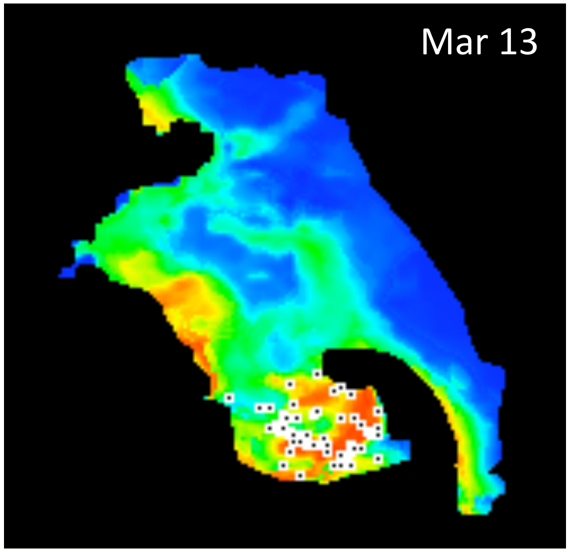


Ensemble Kalman Filter

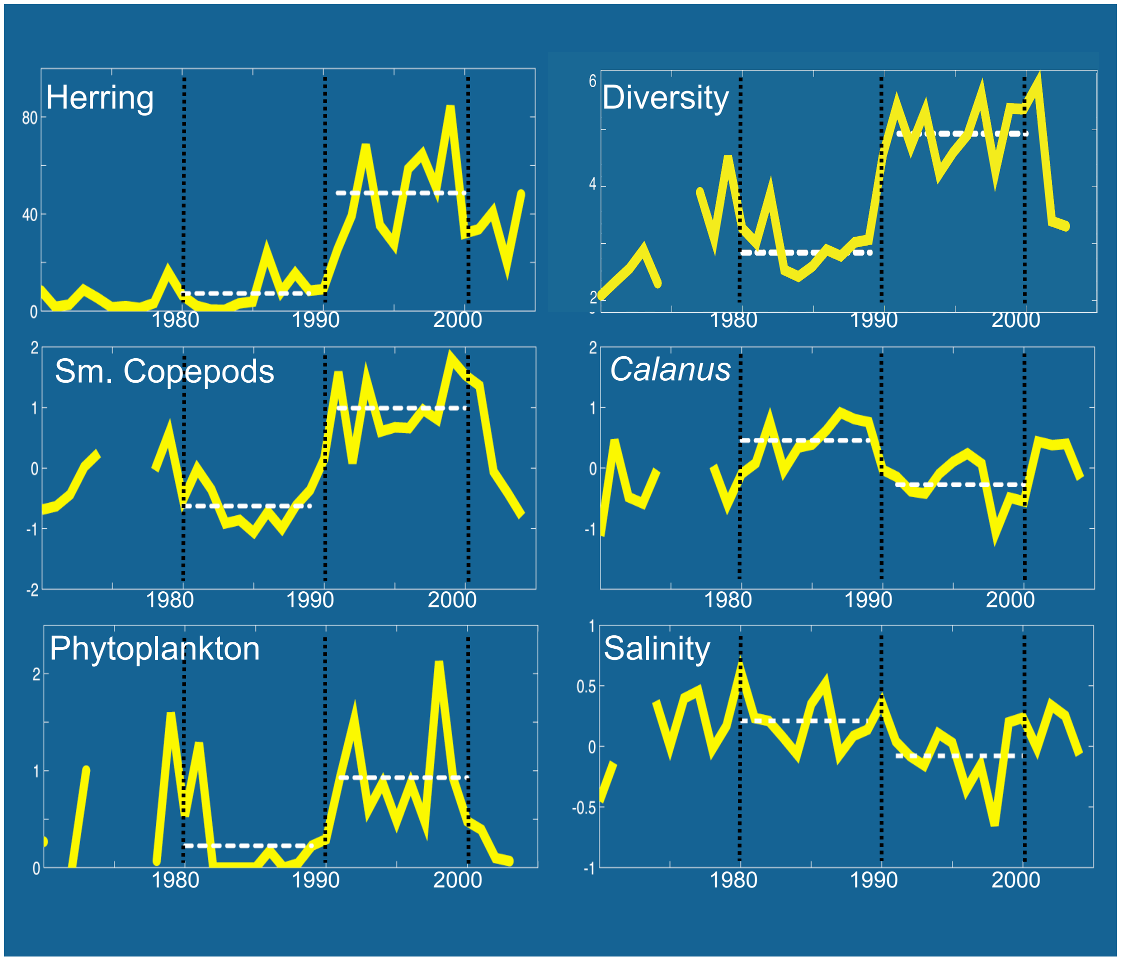
- EnKF
  - ran model with 200 different initial and boundary conditions
  - compared with available PCCS samples
  - 2003-2009

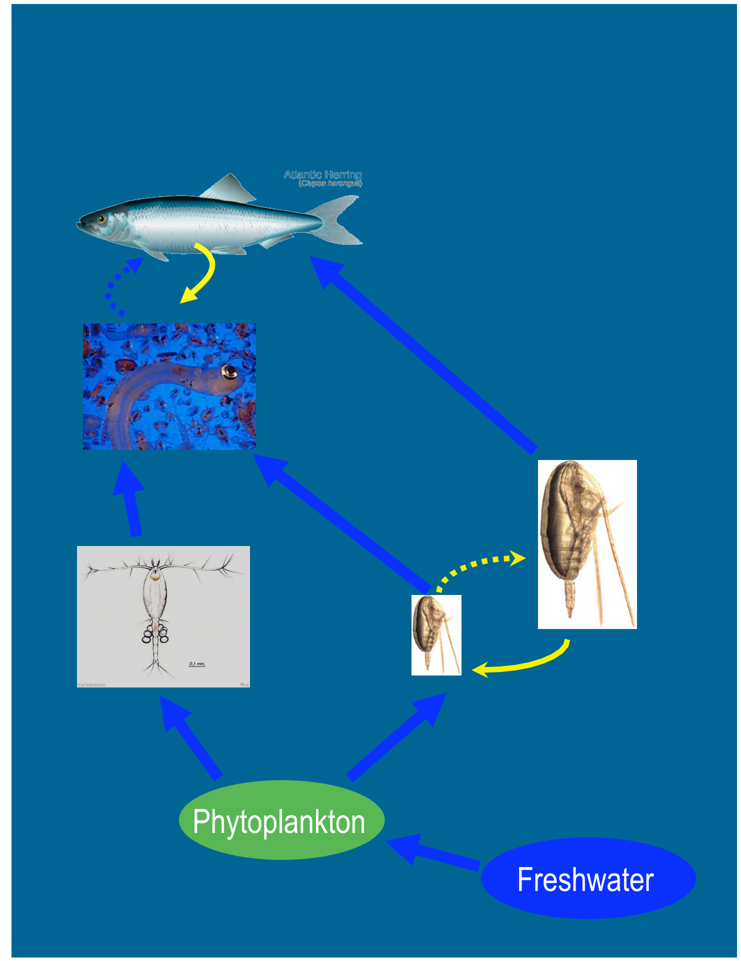


r^2=0.43



Gulf of Maine Regime Shift





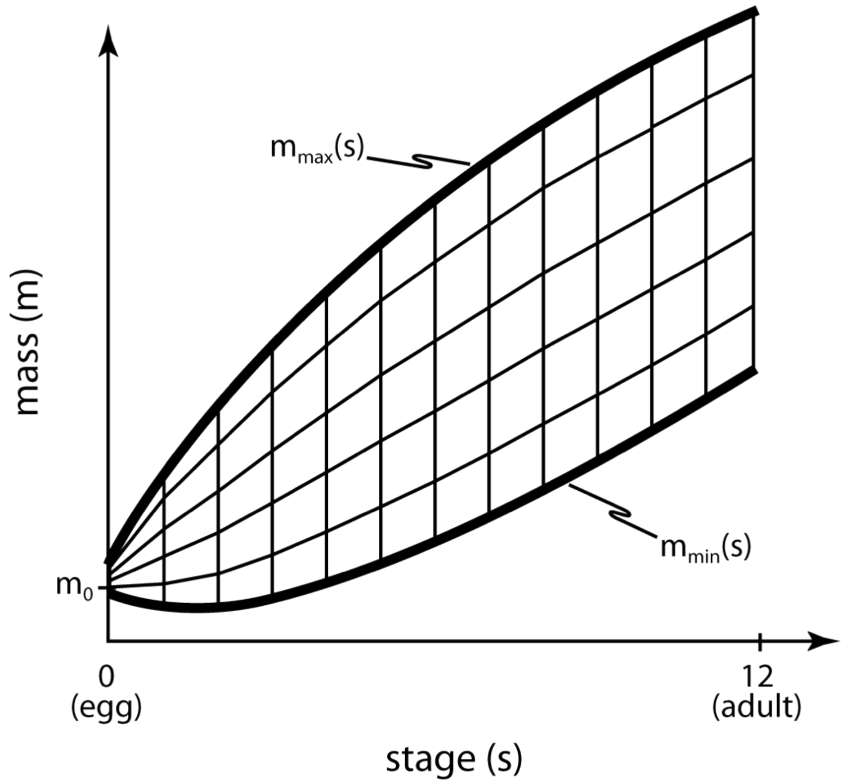
A. J. Pershing et al., ICES Journal of Marine Science 62, 1511 (2005).
C. H. Greene, A. J. Pershing *Science* **315**, 1084 (2007).

Motivation

- Understand 1990s shift in copepod community
  - need to model a community
- Understand patterns of copepod diversity
  - seasonal & interannual
  - spatial
- Predict response of copepod communities in a changing climate

Proposed Model

- Model mass & stage
  - C(s,m)=# of size m, stage s
  - Discretize (s,m) space
  - growth (dm/dt)
  - development (ds/dt)



Development

- Development rate (r):

$$r(s,T) = D_{\lfloor s \rfloor}(T)^{-1}$$

T_c
a_0
a_c
η
κ

- Development time: Belehrádek function

$$D_j(T) = a_j(T + T_c)^{-\beta} \qquad \beta = 2.05$$

- Belehrádek parameters

$$a(s) = \begin{cases} a_0 e^{\eta \lfloor s \rfloor}, & s < 8 \\ a_0 e^{\eta 7} + a_c e^{\kappa \lfloor s \rfloor}, & s \geq 8 \end{cases}$$

Growth

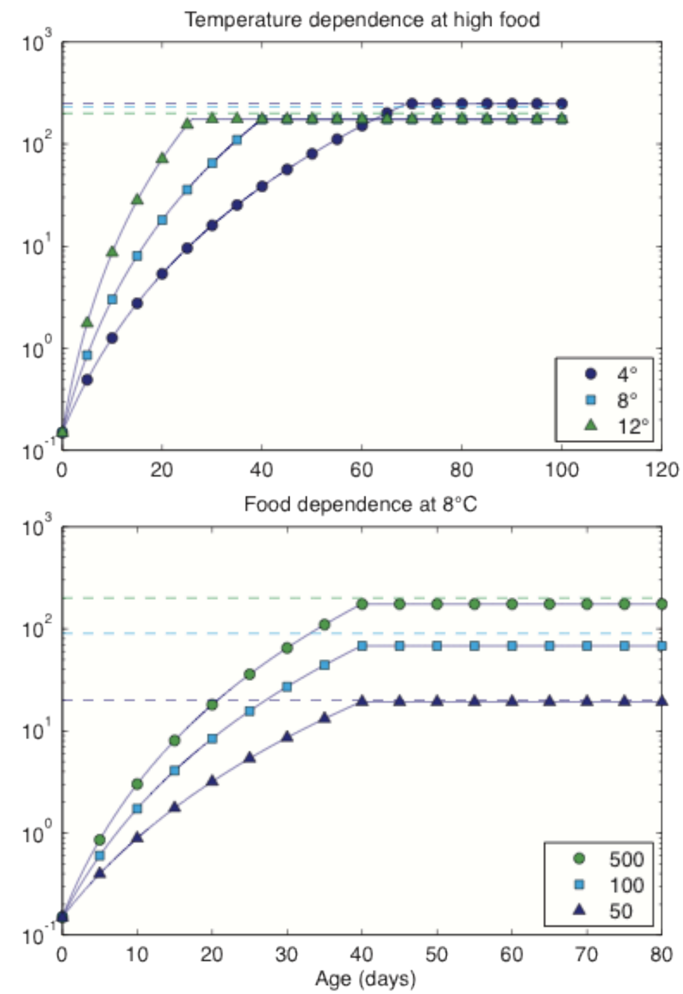
$$g(m,T,F) = Ingestion(m,T,F) - Metabolism(m,T)$$
$$= \gamma(1 - e^{-F/f_c})m^{7/9}Me^{-E_f/T} - m^{3/4}Me^{-E_m/T}$$

- Metabolism---holling function, clearance rate
  - size & temp
- Ingestion
  - size & temp
  - food concentration

γ
f_c
E_f
E_m

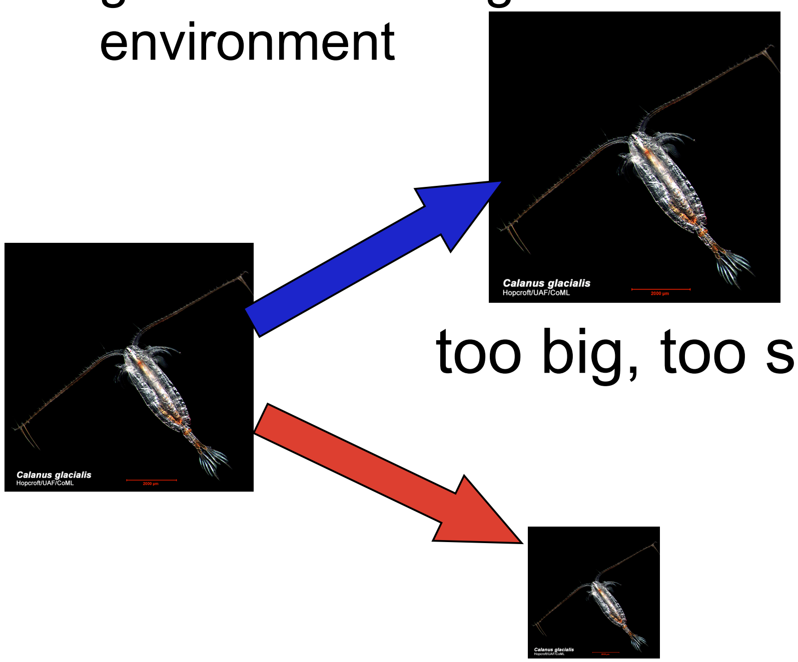
Calanus finmarchicus

- mass-stage model can represent *C. finmarchicus*
- Hypothesis:
  - growth & development structure captures essential features of copepods
  - defines trade-offs that copepods are making to optimize fitness



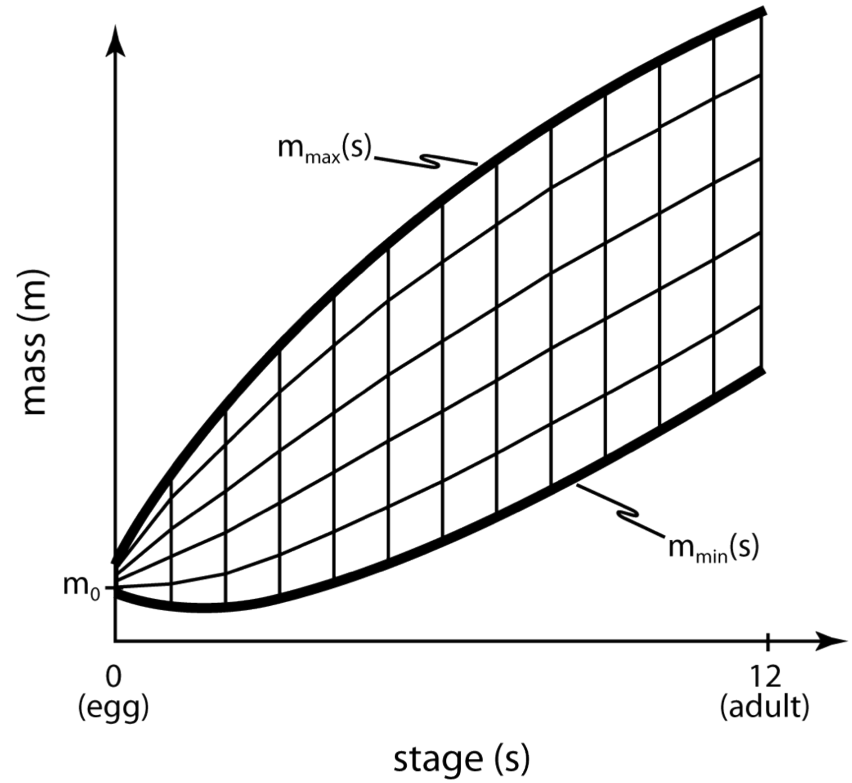
Copepod Adaptation

- Development rate has evolved to balance growth rate in a given environment



too big, too slow

too small, too fast



Mortality

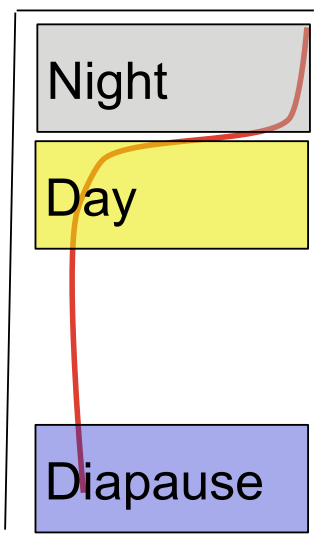
- Simplified predator populations
- Size-structured predation

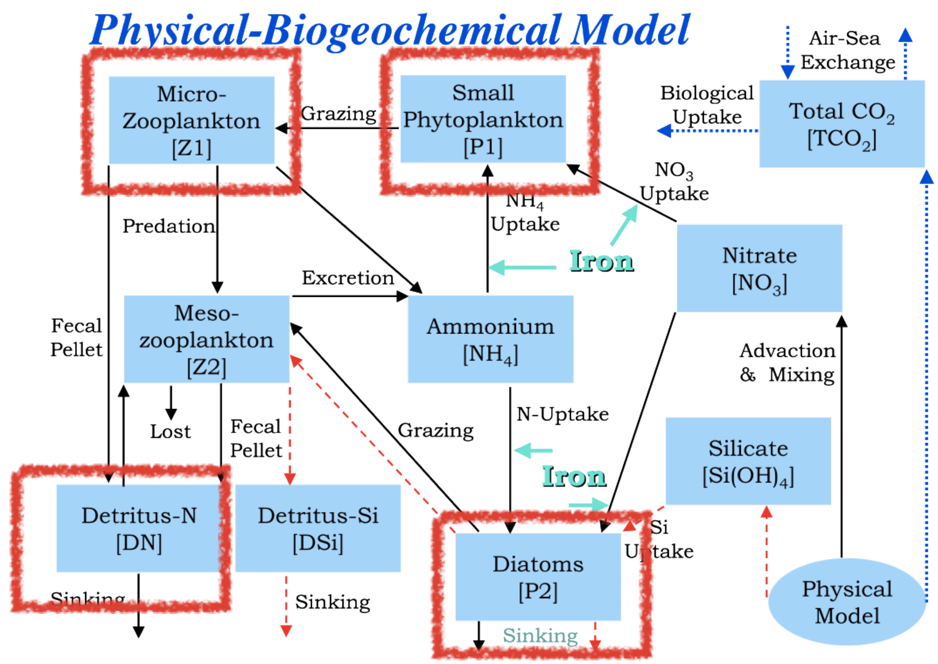
$$\frac{dP_k}{dt} = \rho_k Ing(\|C\|_k)P_k - \mu_k P_k^2$$

$$mortality(C) = \sum_{k=1}^{n} Ing(\|C\|_k)P_k \frac{C}{\|C\|_k}$$

Physics & Food

- ROMS model (1D)
- CoSiNE ecosystem model
- Layered





Plan

- 1. Build models for *Calanus finmarchicus & Pseudocalanus newmani*
  - test framework, develop mortality functions
- 2. Diversity experiments
  - generate random copepod “species”
  - examine how life history, growth, & development change with environment
    - temperate, subtropical, subpolar
  - examine how diversity changes with environment

Seascape Modeling
www.seascapemodeling.org