MULTIPLE APPROACHES TO COUPLING THE CHESAPEAKE BAY EUTROPHICATION MODEL WITH HIGHER TROPHIC LEVELS

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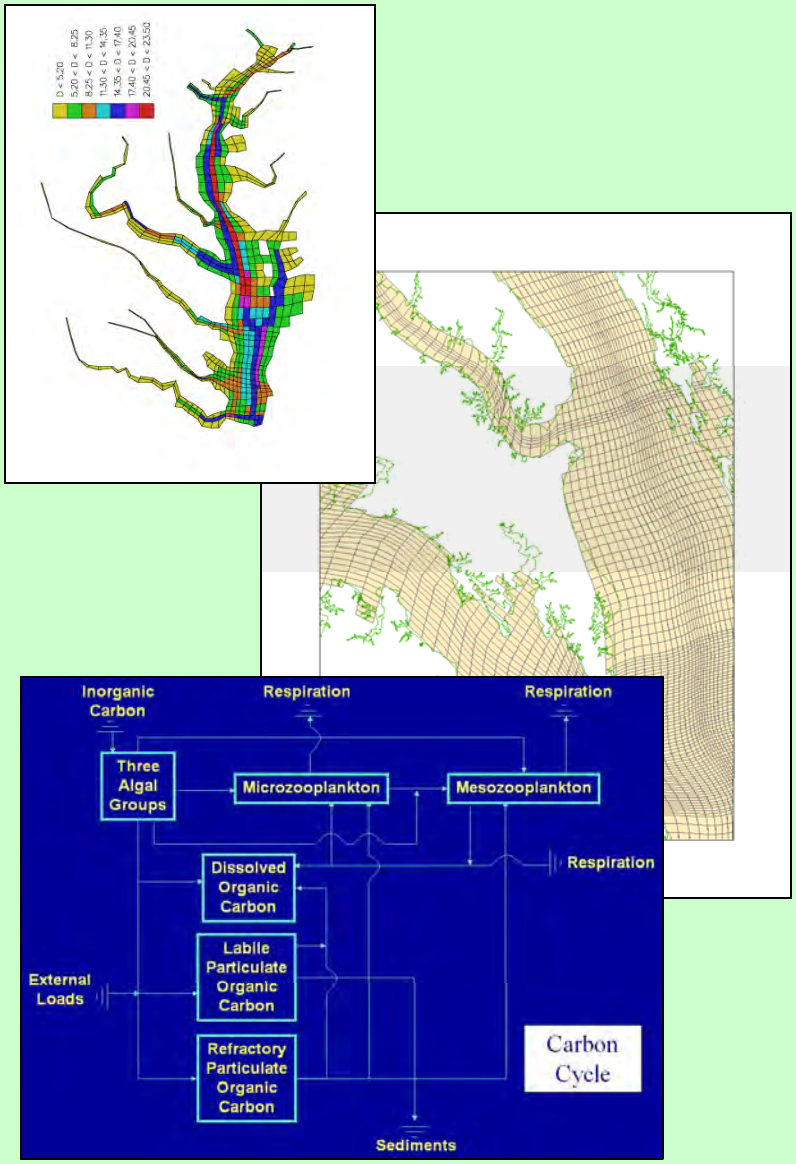
Primary motivation is to examine "top-down" effects

- Conventional eutrophication models are "bottom-up." (nutrients control everything)
- Investigate effect of oysters, menhaden as a supplement to controls on nutrient loads.

- Chesapeake 2000 Agreement
  - By 2010, achieve, at a minimum, a tenfold increase in native oysters
  - By 2004, assess the effects of different levels of filter feeders such as menhaden, oysters, and clams, on Bay water quality and habitat

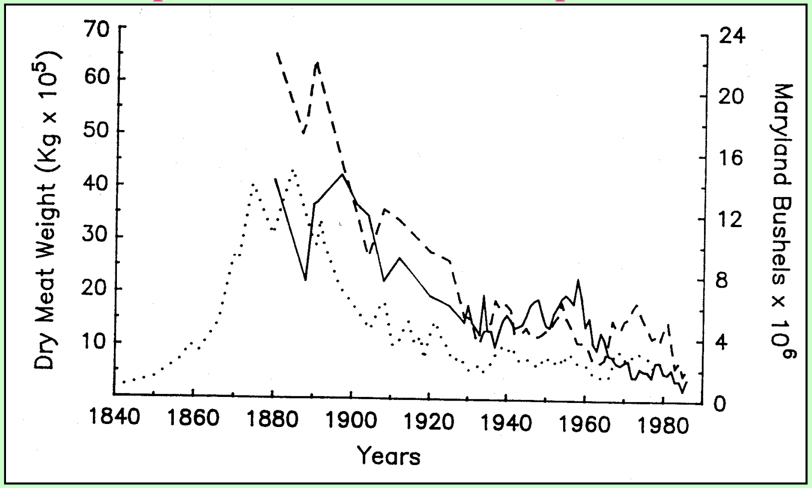
ICM Chesapeake Bay Model



- Coupled to a 3-D hydrodynamic model.
- Operates on multiple grids of 4,000 to 50,000 cells.
- Time steps ≈ 15 minutes.
- Multiple cycles including C, N, P.
- Ultimately carbon based.

Oysters

Exponential Decline in Population



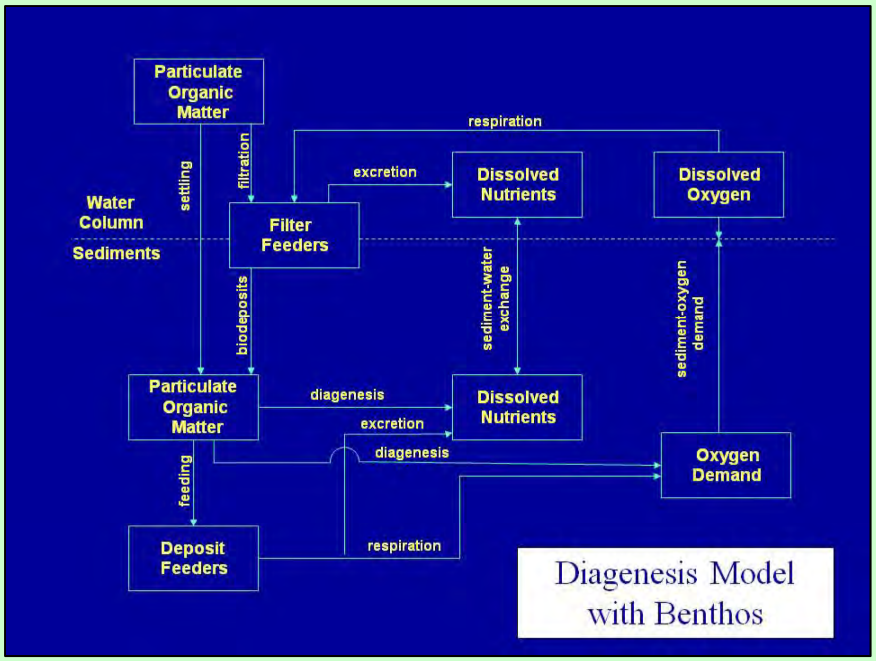
An increase in the oyster population by management and aquaculture could significantly improve water quality by removing large quantities of particulate carbon – Roger Newell, 1988

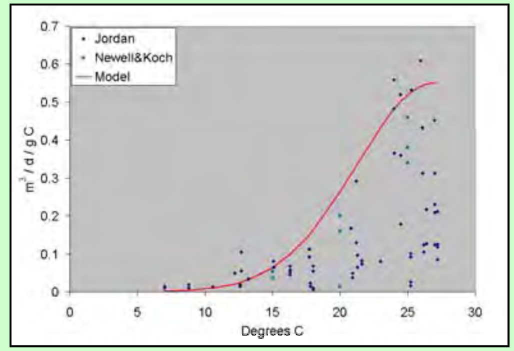
Fundamental Equation

$$\frac{dO}{dt} = \alpha \cdot Fr \cdot POC \cdot O - r \cdot O - \beta \cdot O^2 - hmr \cdot O$$

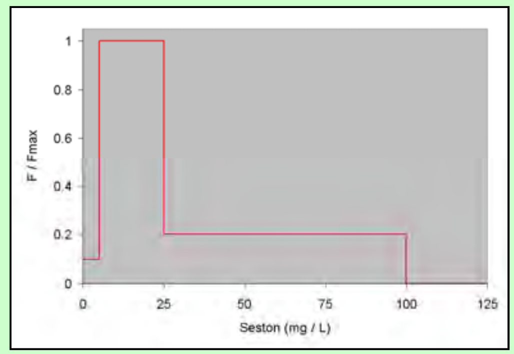
- O = filter feeder biomass (mg C m^{-2})
- α = assimilation efficiency ($0 < \alpha < 1$)
- Fr = filtration rate (m^3 mg^{-1} filter feeder carbon d^{-1})
- POC = particulate organic carbon in overlying water (mg m^{-3})
- r = specific respiration rate (d^{-1})
- β = predation rate (m^2 mg^{-1} filter feeder C d^{-1})
- hmr = mortality rate due to hypoxia (d^{-1})
- t = time (d)

Oysters inserted into sediment diagenesis model. Interact with overlying water column.

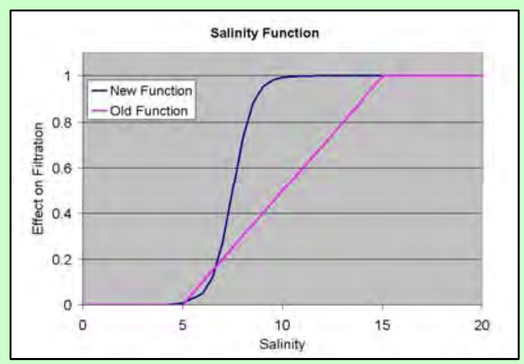




Temperature Effects

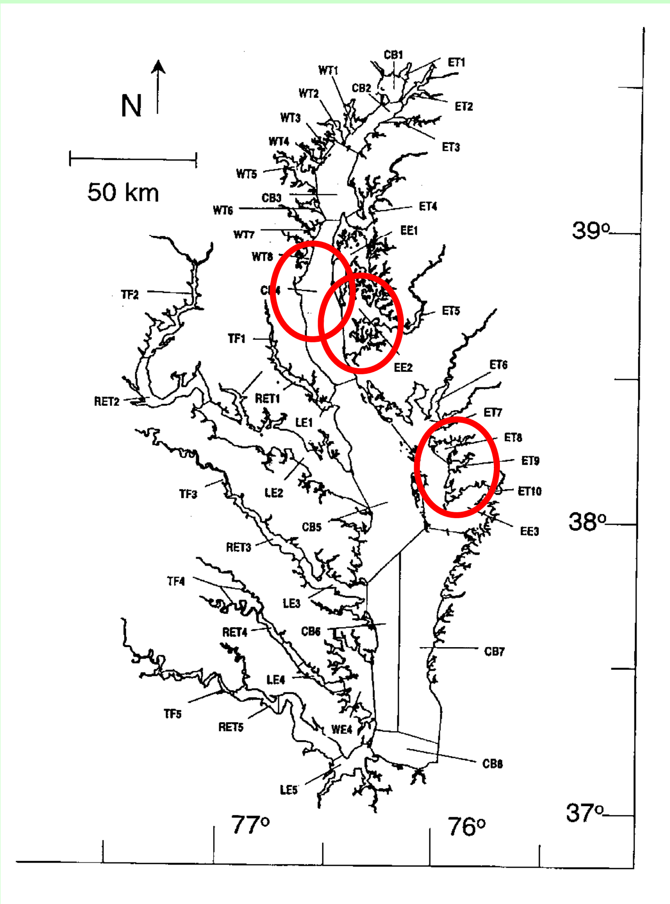


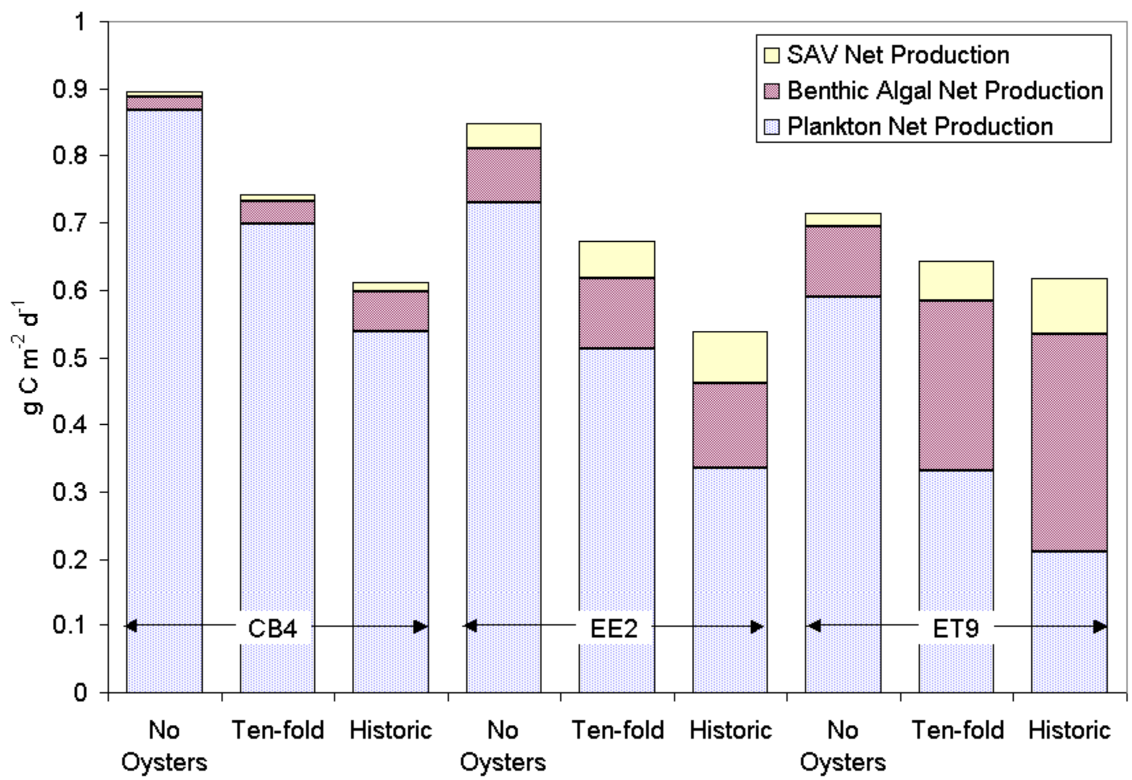
Solids Feedback



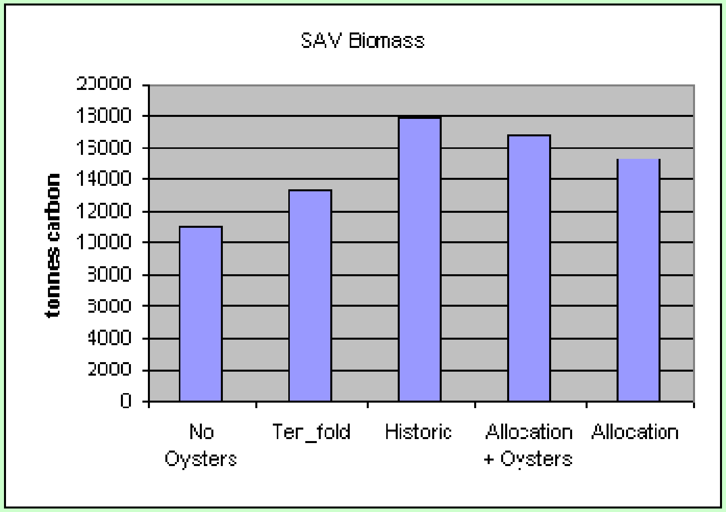
Salinity Effects

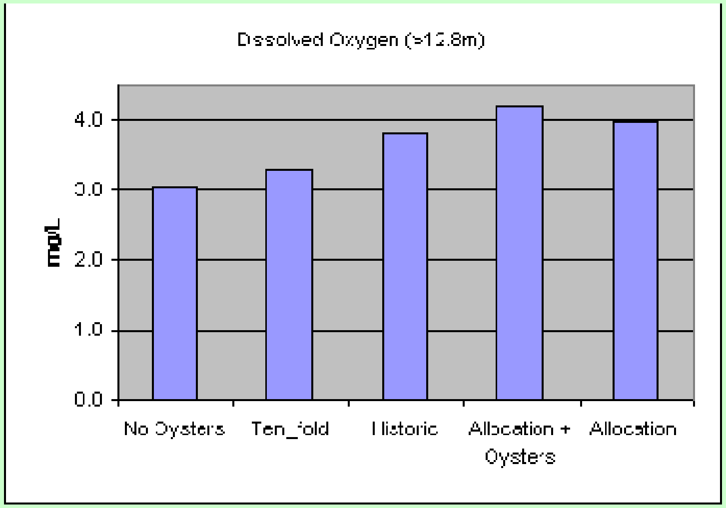
Results from Three Regions





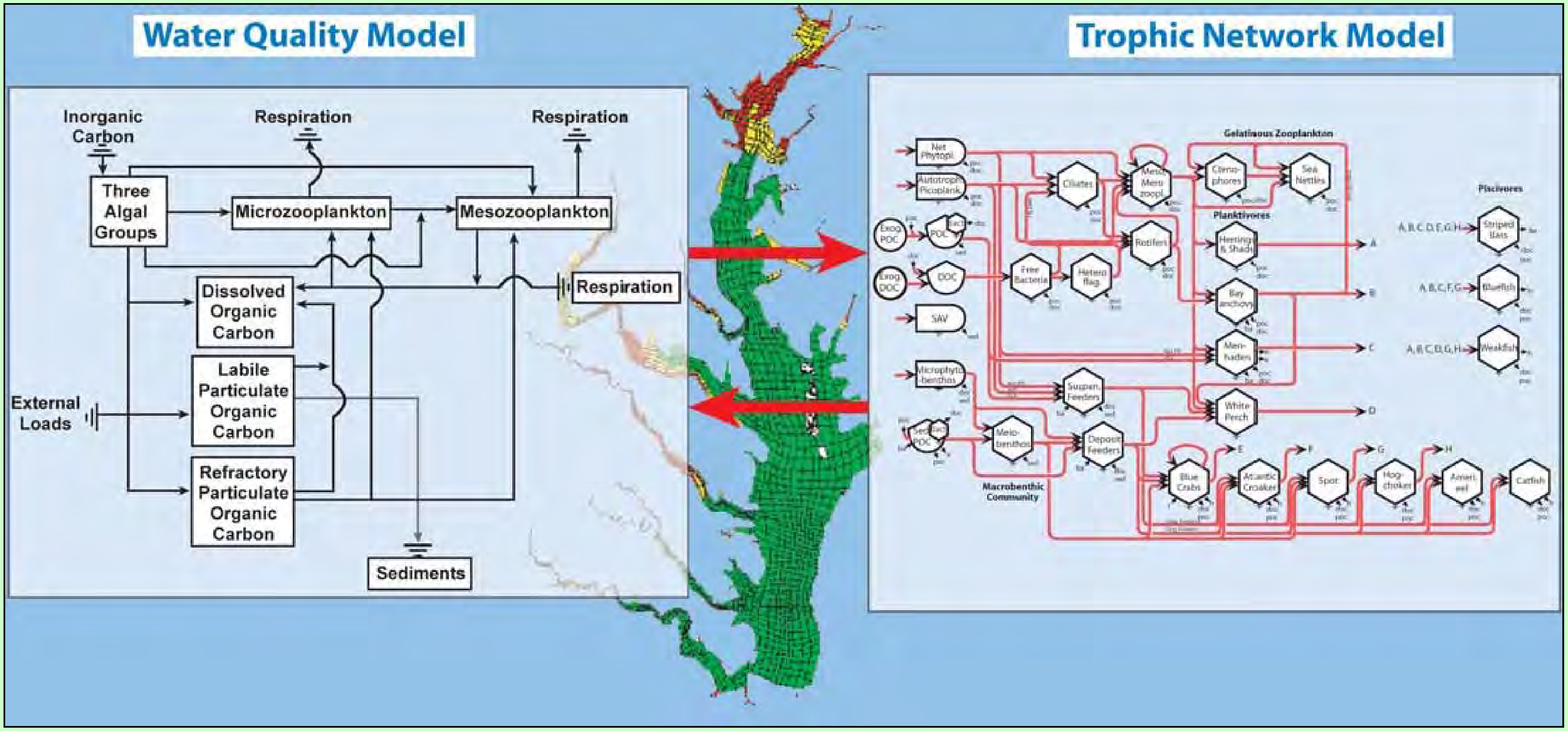
Conclusions





- The greatest ecosystem service of feasible oyster restoration appears to be SAV restoration.
- Other ecosystem services provided by oysters include nitrogen removal and dissolved oxygen enhancement.
- Oysters have larger impact on their local environment than system-wide.

Coupling Network with Eutrophication Models

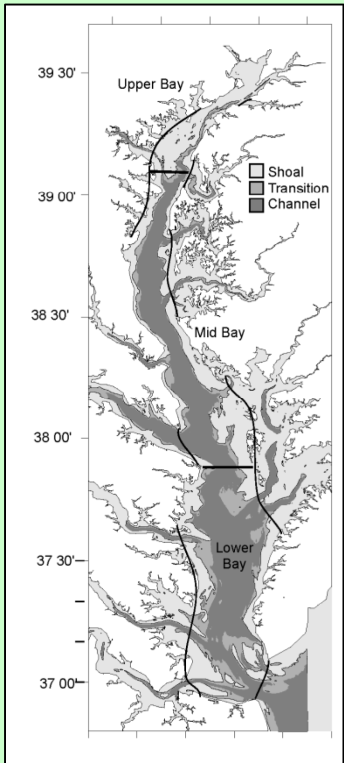


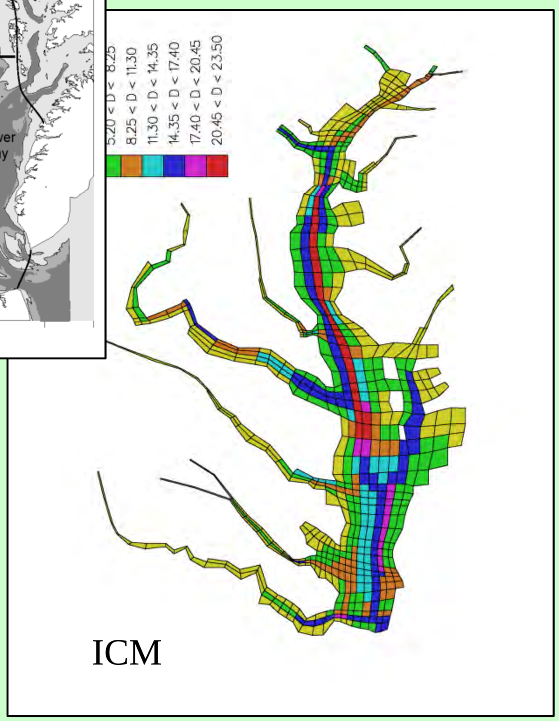
Concerns and Challenges

- Address management issues including:
  - Can fisheries management remediate water quality problems such as excess chlorophyll?
  - How does nutrient management in a watershed affect production and biomass in adjacent water bodies?
- Basic network models are steady-state applications to large regions. This must be reconciled with temporally and spatially-detailed WQM's.
- Eutrophication and fisheries models use different time scales, spatial scales, and "currencies."
- "Look for the hooks." What are the basic commonalities between the two approaches?

Our Approach

Ecopath





ICM

- Couple existing Chesapeake Bay *CE-QUAL-ICM* eutrophication model with existing *Ecopath with Ecosim* network model (courtesy Jim Hagy) for Chesapeake Bay upper trophic levels.
- Identify commonalities, linkages between the models.
- Examine a simple case of increasing menhaden predation on phytoplankton.

The Ecopath Basic Equation

$$P_i = Y_i + B_i \cdot M2_i + E_i + BA_i + P_i \cdot (1 - EE_i)$$

P_i = total production rate of group i
Y_i = fishery catch rate of group i
$M2_i$ = total predation rate of group i
E_i = net migration of group i
BA_i = biomass accumulation of group i
B_i = biomass of group i
EE_i = ecotrophic efficiency of group i

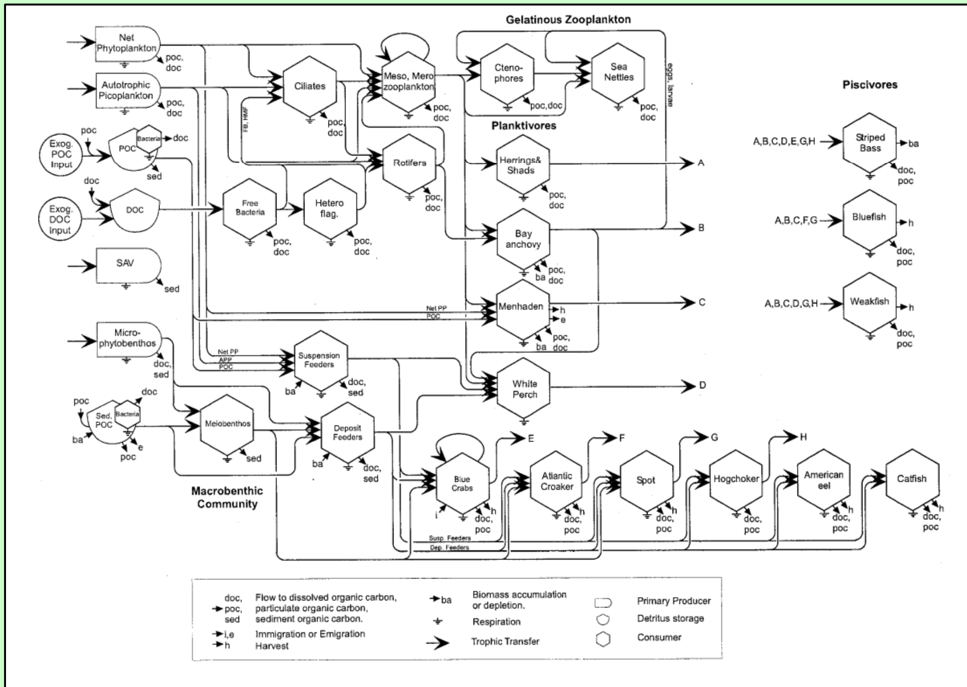
•When the basic equation is written for each group, a matrix of coupled linear equations results.
•One unknown (biomass, production/biomass ratio, consumption/biomass ratio, ecotrophic efficiency) is solved for each group.
•Typically, “ecotrophic efficiency” is solved iteratively so that EE < 1.

The Basic ICM Equation

$$\frac{\delta V_j C_j}{\delta t} = \sum_{k=1}^{n} Q_k C_k + \sum_{k=1}^{n} A_k D_k \frac{\delta C}{\delta x_k} + \sum S_j$$

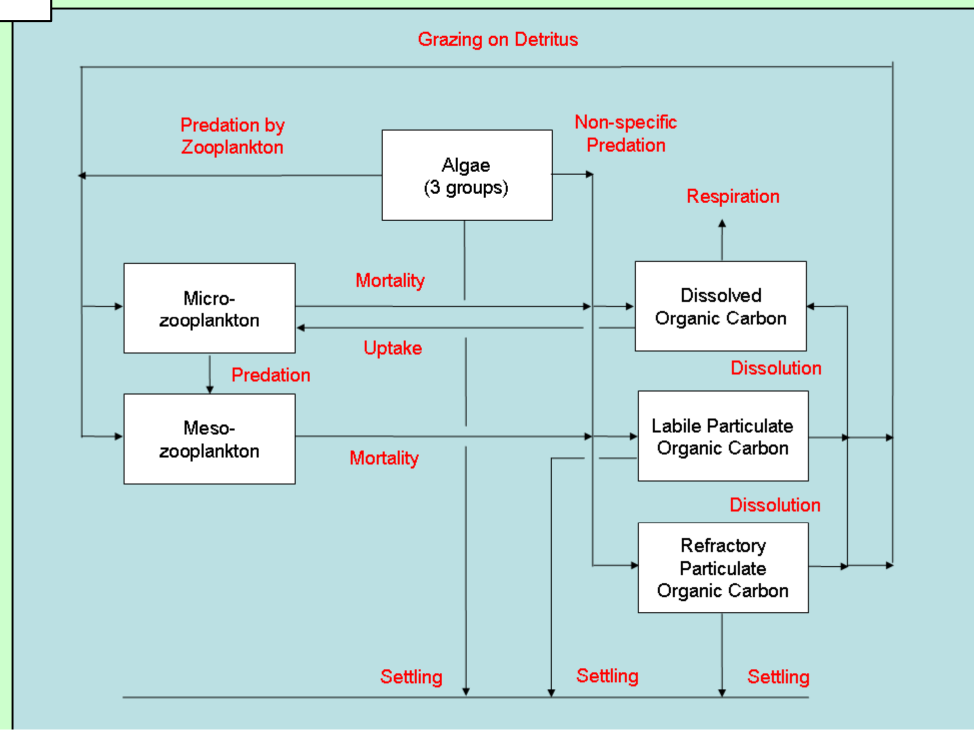
Vj = volume of j^{th} control volume (m^3)
Cj = concentration in j^{th} control volume ($gm\ m^{-3}$)
Qk = volumetric flow across flow face k of j^{th} control volume ($m^3\ sec^{-1}$)
Ck = concentration in flow across flow face k ($gm\ m^{-3}$)
Ak = area of flow face k (m^2)
Dk = diffusion coefficient at flow face k ($m^2\ sec^{-1}$)
n = number of flow faces attached to j^{th} control volume
Sj = external loads and kinetic sources and sinks in j^{th} control volume ($gm\ sec^{-1}$)
t, x = temporal and spatial coordinates

•The model is based on a series of coupled partial differential equations, one for each state variable.
•Biomass/unit volume is the unknown.
•The equations are solved numerically for spatially and temporally-varying biomass.



ECOPATH groups and flows

ICM carbon cycle (water column)



Can we reconcile these disparate representations?

Table 3. Groups modeled in ICM and Ecopath application to Chesapeake Bay.

ICM Variable	Ecopath Variable	ICM Formula
Phytoplankton (spring diatoms, green algae)	Picoplankton, Net Phytoplankton	$B2 + B3$
Submerged Aquatic Vegetation	Submerged Aquatic Vegetation	$PATCH \times SH$
Benthic Algae	Microphytobenthos	BBM
Microzooplankton	Heteroflagellates, Ciliates, Rotifers, Meroplankton	SZ
Mesozooplankton	Mesozooplankton	LZ
Deposit Feeders	Deposit-Feeding Benthos	DF
Filter Feeders	Filter-Feeding Benthos	$SF(1) + SF(2) + SF(3)$
Particulate Organic Carbon	Particulate Organic Carbon	$LPOC + RPOC$
Dissolved Organic Carbon	Dissolved Organic Carbon	DOC
Sediment Organic Carbon	Sediment Carbon	$G1 + G2 + G3$

Table 4. Production-to-biomass ratio derived from ICM variables.

Group	Formula	Units
Phytoplankton	$Palg \times (1 - PRSPalg) - BMalg$	D^{-1}
SAV	$Psav - BMsav - SL$	D^{-1}
Benthic Algae	$Pba - BMba$	D^{-1}
Microzooplankton	$Esz \times (1 - RFsz) \times Rsz - BMsz$	D^{-1}
Mesozooplankton	$Elz \times (1 - RFlz) \times Rlz - BMlz$	D^{-1}
Deposit Feeders	$Gdf - Rdf$	D^{-1}
Filter Feeders	$(TCONff - UCONff - RESPff) / SF$	D^{-1}

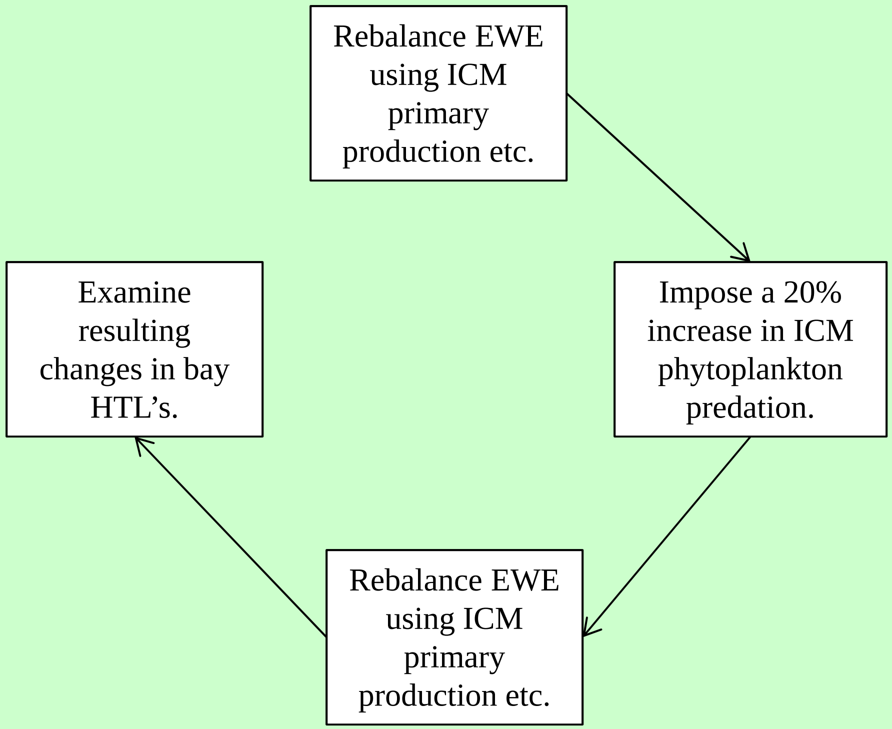
Table 5. Consumption-to-biomass ratio derived from ICM variables.

Group	Formula	Units
Microzooplankton	Rsz	d^{-1}
Mesozooplankton	Rlz	d^{-1}
Deposit Feeders	$xki0 \times (POC1 + POC2 + POC3) / M2$	d^{-1}
Filter Feeders	$FILTCT \times (B2 + B3 + LPOC + RPOC)$	d^{-1}

Yes, with a bit of doing, commonalities can be identified and differing vocabularies can be penetrated.

Two Experiments

- Impose a 20% increase in phytoplankton predation in ICM. Pass resulting production, biomass, etc. to ECOPATH. What changes occur in the network?
- Add a 20% menhaden biomass increase to ICM effects. What changes occur in the network?



Results

Table 19. Mid-bay ICM carbon stocks input to Ecopath.

	ICM Base (g C m^{-2})	ICM Increased Predation (g C m^{-2})
Phytoplankton	3.56	3.42
Benthic Algae	0.11	0.103
SAV	1.28	1.255
Microzooplankton	0.14	0.137
Mesozoplankton	0.53	0.526
Deposit Feeders	1.10	1.095
Filter Feeders	0.42	0.421
DOC	28.20	28.20
POC	10.30	10.30
Sediments	201.70	201.70

Table 20. Alterations in mid-bay Ecopath model required to accommodate increased grazing in ICM.

	Base	Increased Predation
Meiofauna diet fraction from benthic algae	0.175	0.125
Meiofauna diet fraction from sediment POC	0.425	0.475

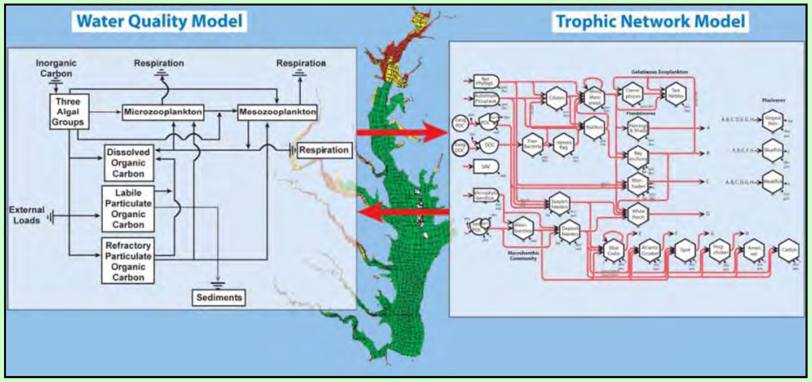
Table 18. Ecopath alterations required to accommodate increased menhaden biomass in the mid bay.

	Ecopath Base	Increased Menhaden
Phytoplankton Ecotrophic Efficiency	0.45	0.467
Free Bacteria (g C m^{-2})	2415	2294
Benthic Bacteria (g C m^{-2})	298	283

The only changes in the network resulting from a 20% increase in phytoplankton predation are minor changes in meiofauna diet fraction. This is not surprising since group biomasses are inputs, not unknowns.

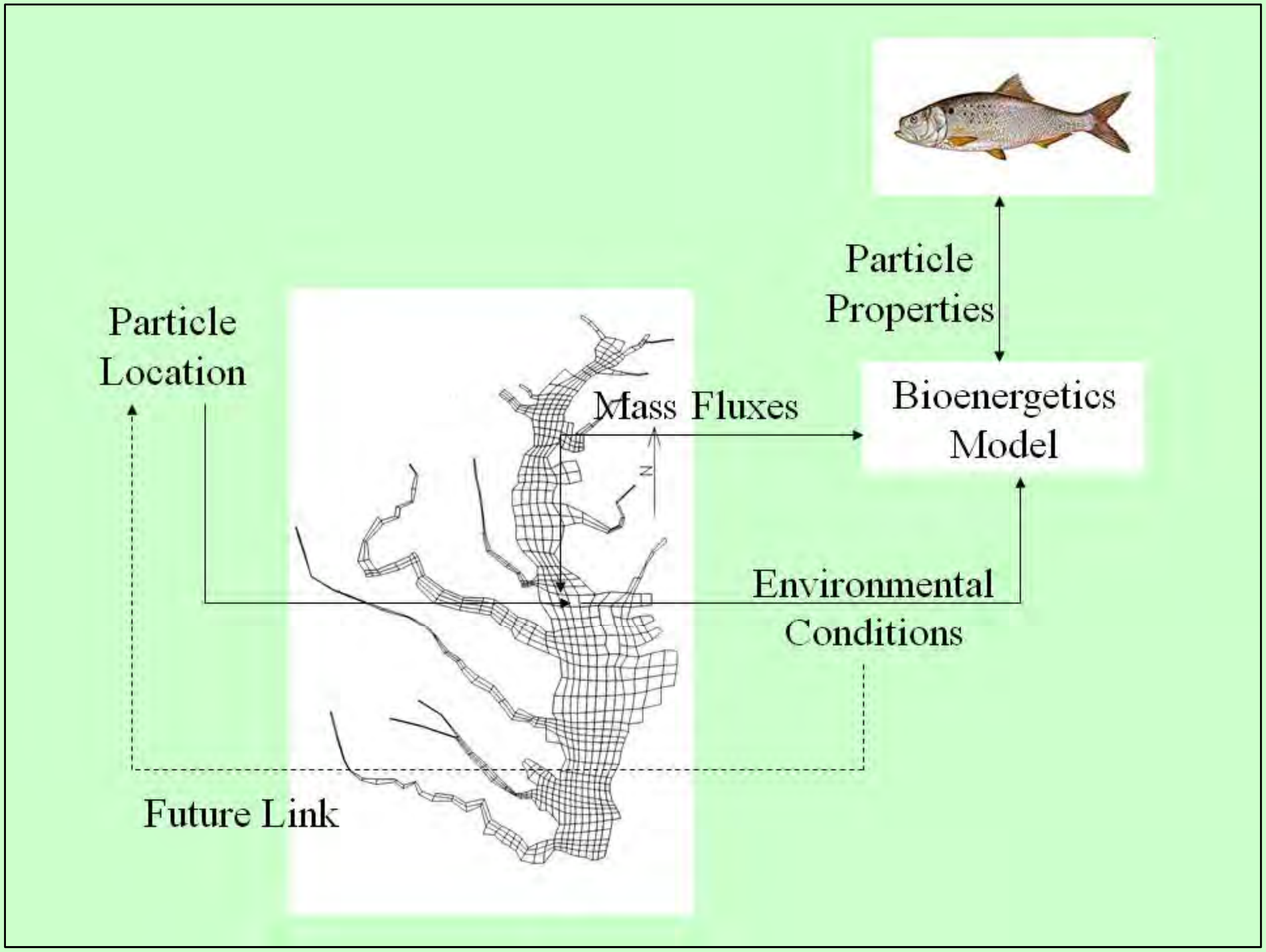
Forcing a menhaden biomass increases results in more changes but not in groups of menhaden predators like striped bass. These would have to be input as well.

Conclusions



- We've made strides in combining eutrophication and network models.
- This approach, as it stands, is unsatisfying. I refer to it as a feasibility tester. It's feasible that a 20% increase in grazing will have minimal impact.
- Ecopath specialists advise we need to go to time-variable Ecosim to obtain realistic results.

Coupling Eutrophication Model with Menhaden Bioenergetics Model



The bioenergetics approach combines

Counts of individual fish

$$\Delta N = \Delta N_{stv} + \Delta N_{suf} + \Delta N_{prd} + \Delta N_{fsh}$$

The total number of individuals lost (ΔN) within a time step (Δt) is the sum of the number lost due to starvation (ΔN_{stv}) and suffocation (ΔN_{suf}), accounted for explicitly as functions of fish condition and model environment, along with the number lost to other natural causes (ΔN_{prd}, primarily predation in the case of menhaden) and those caught by the fishery (ΔN_{fsh}).

Bioenergetics of individual fish

$$\frac{\partial WW}{\partial t} = \left\{ C' - \left[(R' + S') + (F' + U') \right] \right\} \cdot \frac{1}{E_{pred}}$$

$\partial WW / \partial t$ is the rate of wet weight growth (g/s); E_{pred} is the energy density of the fish (J/g). Other variables are the rates of energy uptake of consumption (C'), respiration (R'), specific dynamic action (S'), egestion (F'), and excretion (U').

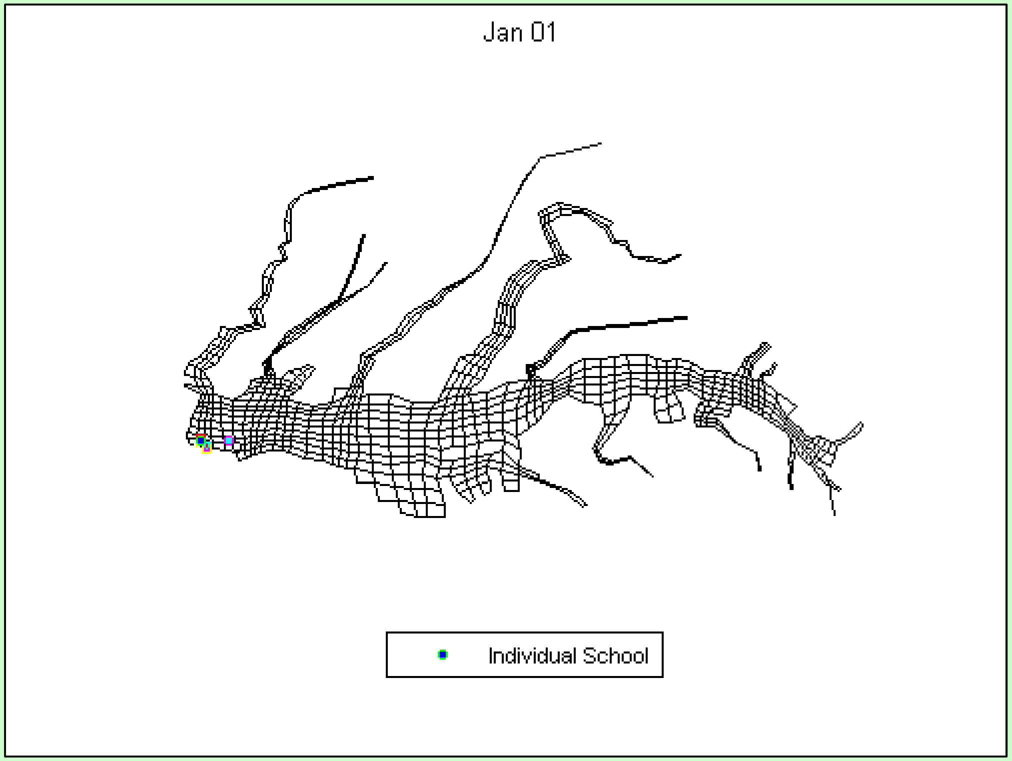
Fish biomass and interactions with water column

$$G'_C = C'_C - \left(R'_C + F'_C + U'_C \right)$$

G'_C is the growth rate in carbon (gC/s) and is a function of carbon uptake (, in gC/s), respiration (, in gC/s), egestion (, in gC/s), and excretion rates (, in gC/s).

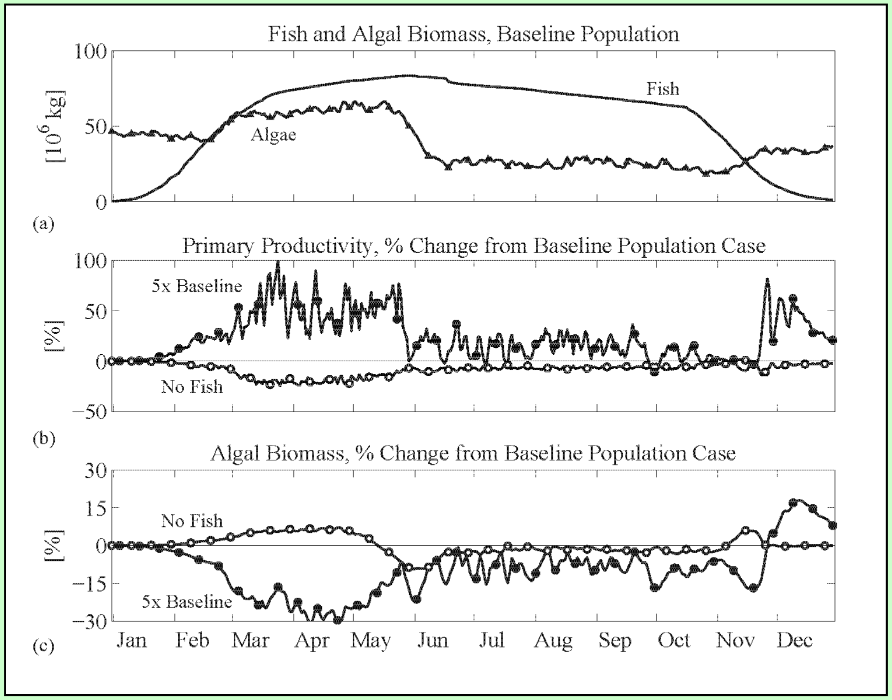
Menhaden Migration

- Menhaden are modeled as schools of identical individuals (age 0, 1 – 2 years, or 3 years).
- 4,000 schools of ≈ 4.4×10^5 individuals.
- Schools enter the bay from January – March, swim upstream, leave the bay commencing October.



Menhaden Effect on Algal Biomass and Production

- Sensitivity Runs
  - Base Run
  - No Menhaden
  - 5 x Increase in Menhaden
- For the range tested, menhaden diminish algal biomass while stimulating production via enhanced nutrient recycling.



Conclusive Conclusions

Oysters

- Mass-balance PDE's are easiest to apply.
- Maybe not the ultimate in biological realism.
- From a management standpoint, these runs were most significant.

Network Model

- A lot was accomplished in terms of linkage.
- Least satisfying, least useful.
- Needs extension to time-varying, two-way linkage.

Menhaden Bioenergetics

- Greatest biological realism.
- Computationally feasible. Seems to be the route for future developments.
- Next step is to incorporate behavior as a response to environment.
- Personally exciting!