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Workshop and Conference on Biogeochemical Impacts of Climate and Land-Use Changes on Marine Ecosystems

2 - 10 November 2009

Using ocean ecosystem/biogeochemical models in coupled global climate models, the past, present and future

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NASA
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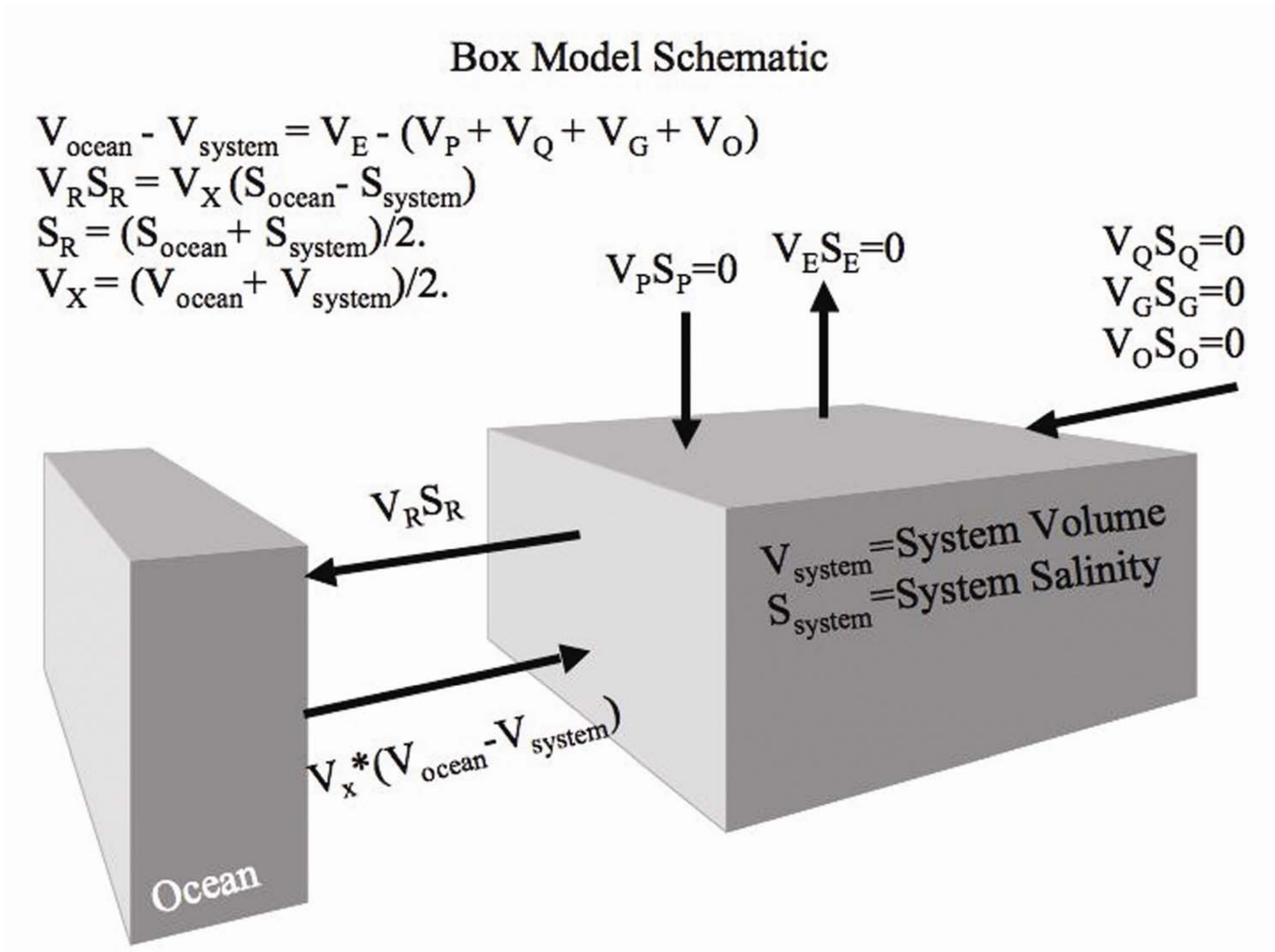

Box Model Schematic
V_ocean - V_system = V_E - (V_P + V_Q + V_G + V_O)
V_R S_R = V_X (S_ocean - S_system)
S_R = (S_ocean + S_system)/2.
V_X = (V_ocean + V_system)/2.
V_P S_P=0
V_E S_E=0
V_Q S_Q=0
V_G S_G=0
V_O S_O=0
V_R S_R
V_system=System Volume
S_system=System Salinity
V_x*(V_ocean-V_system)
Ocean

Box Models

Box Models

One Dimensional (Vertical) Models

Three Dimensional Models

Box Model

$$\frac{dB_i}{dt} = S_i$$

....

....

....

$$\frac{dB_N}{dt} = S_N$$

$$S_{[\mathrm{NO_3}]} = -\tau_{\mathrm{Phyt_{gmax}}}\ \mathrm{Phyt}\,\mathrm{L}_{\mathrm{NO_3}} + \tau_{\mathrm{nitri}}\,[\mathrm{NH}_4];$$

$$S_{[\mathrm{NH_4}]} = -\tau_{\mathrm{Phyt_{gmax}}}\ \mathrm{Phyt}\,L_{\mathrm{NH_4}} - \tau_{\mathrm{nitri}}\,[NH_4] + \tau_{\mathrm{Zoo_{bresp}}}\ \mathrm{Zoo} +$$
$$\tau_{\mathrm{SDET_{remin}}}\ \mathrm{SDET} + \tau_{\mathrm{LDET_{remin}}}\ \mathrm{LDET};$$

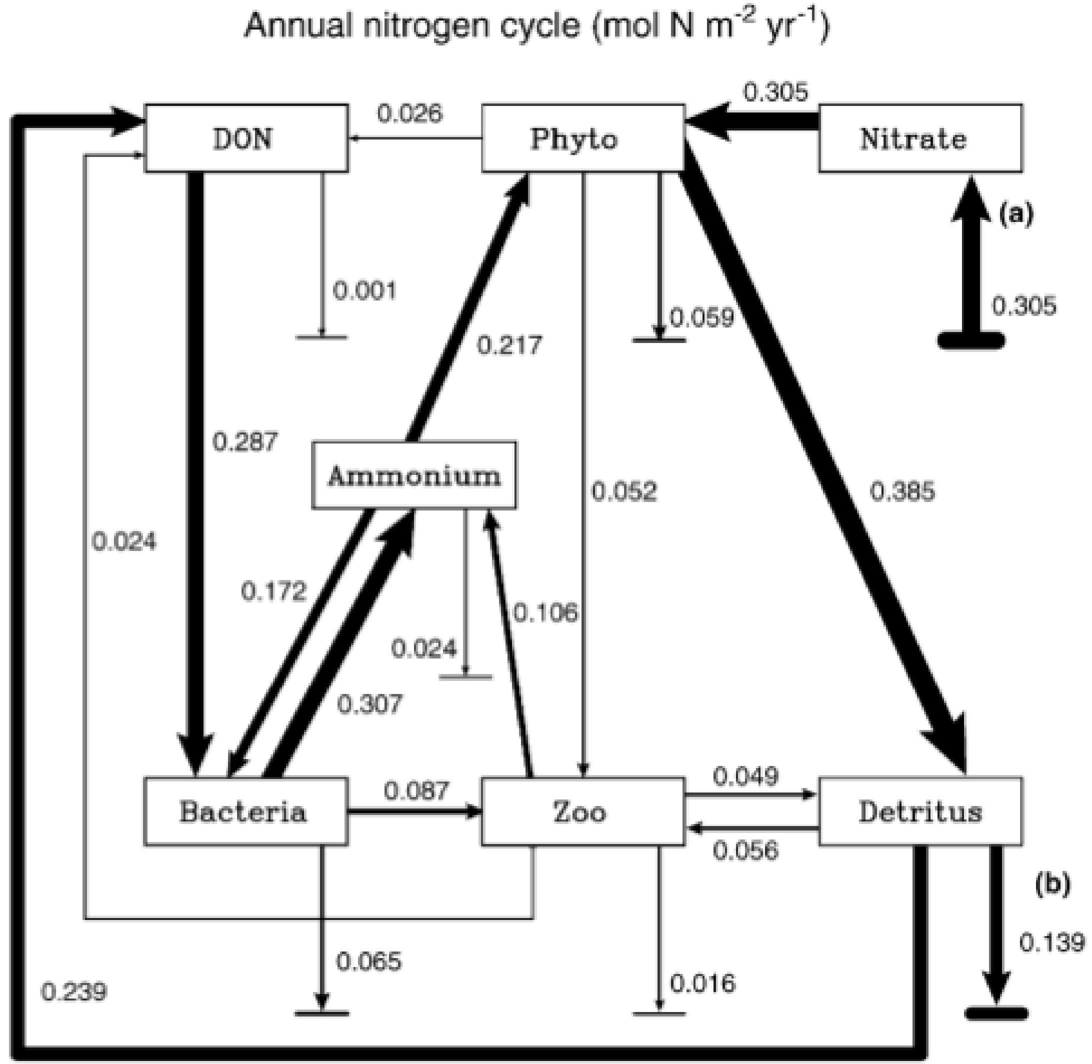
$$S_{\mathrm{SDET}} = \tau_{\mathrm{Zoo_{gmax}}}\ \mathrm{Zoo}(1-\beta)\frac{\mathrm{Phyt}}{K_{\mathrm{Phyt}} + \mathrm{Phyt}} + \tau_{\mathrm{Phyt_{mort}}}\ \mathrm{Phyt} -$$
$$\tau_{\mathrm{coag}}\ \mathrm{SDET}\,(\mathrm{PHYT} + \mathrm{SDET}) - \tau_{\mathrm{SDET_{remin}}}\ \mathrm{SDET};$$

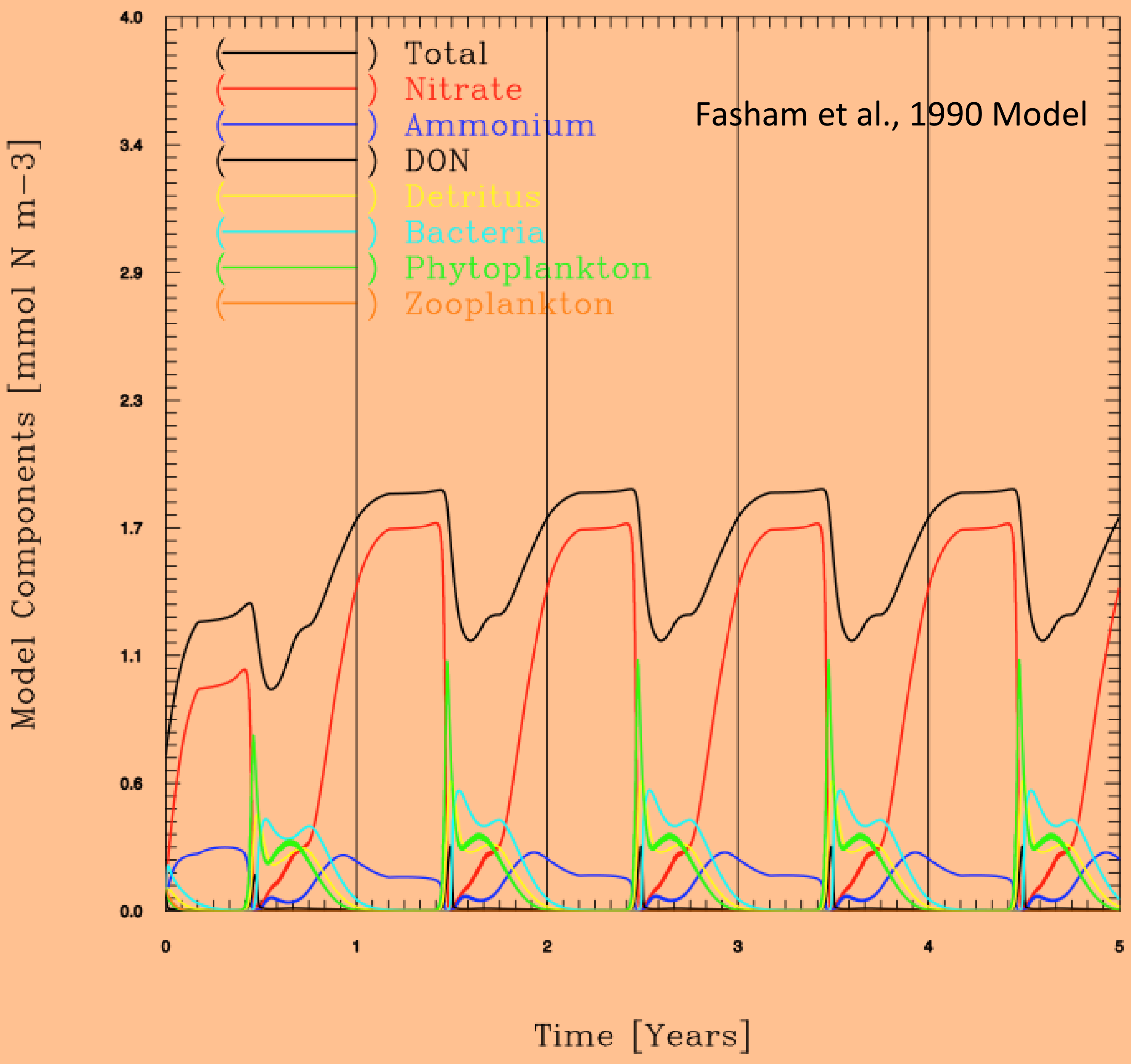
$$S_{\mathrm{LDET}} = \tau_{coag}\,(\mathrm{Phyt} + \mathrm{SDET})^2 - \tau_{\mathrm{LDET_{remin}}}\ \mathrm{LDET};$$

$$S_{\mathrm{Phyt}} = \tau_{\mathrm{Phyt_{gmax}}}\ \mathrm{Phyt}\,L - \tau_{\mathrm{Zoo_{gmax}}}\ \mathrm{Zoo}\frac{\mathrm{Phyt}}{K_{\mathrm{Phyt}} + \mathrm{Phyt}} -$$
$$\tau_{\mathrm{Phyt_{mort}}}\ \mathrm{Phyt} - \tau_{\mathrm{coag}}\ \mathrm{Phyt}\,(\mathrm{Phyt} + \mathrm{SDET});$$

$$S_\theta = L\,\tau_{\mathrm{Phyt_{max}}}\,\theta\left(\frac{V_P\,L\,\theta_{\mathrm{max}}}{V_P^2 + \left(\alpha\,\theta\,\mathrm{PAR}\right)^2} - 1\right)$$

Original Fasham et al., 1990 Mean Nitrogen Budget/Flow

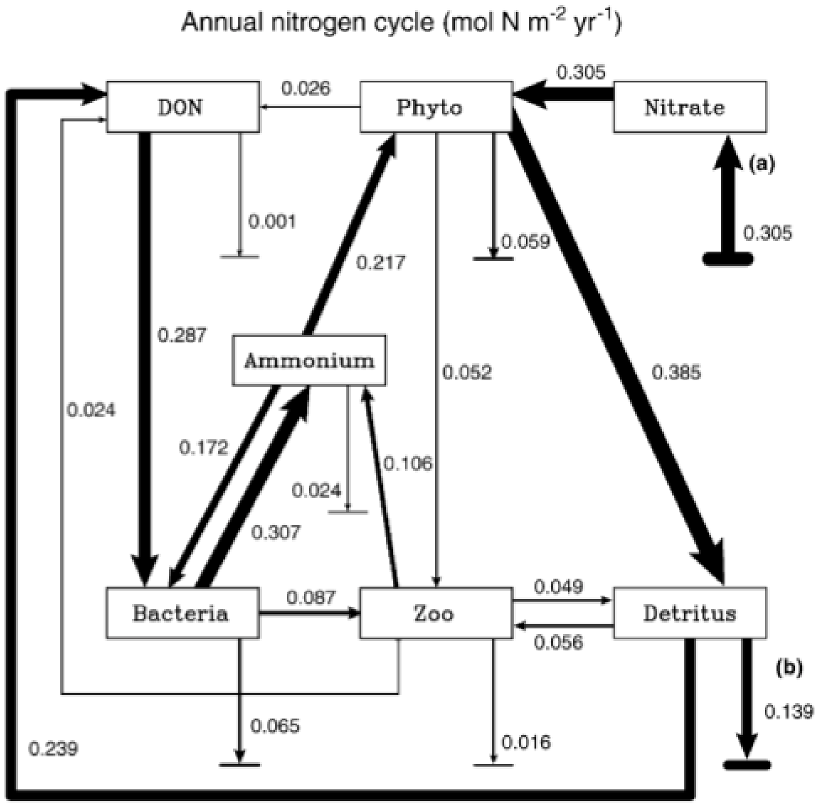




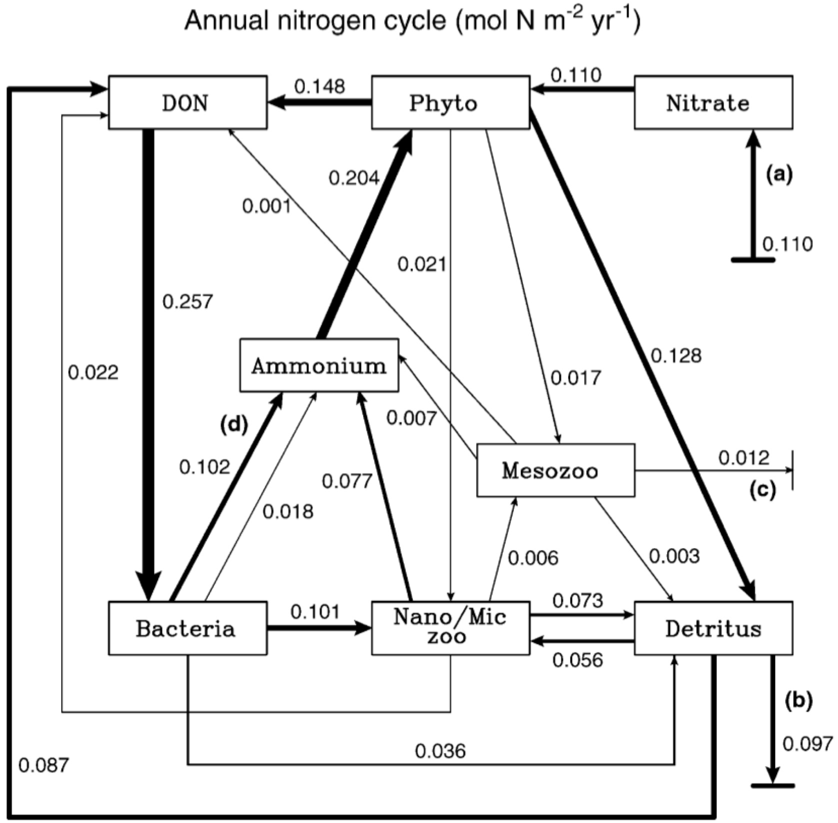
Total
Nitrate
Ammonium
DON
Detritus
Bacteria
Phytoplankton
Zooplankton
Fasham et al., 1990 Model
Model Components [mmol N m−3]
Time [Years]
4.0
3.4
2.9
2.3
1.7
1.1
0.6
0.0
0
1
2
3
4
5

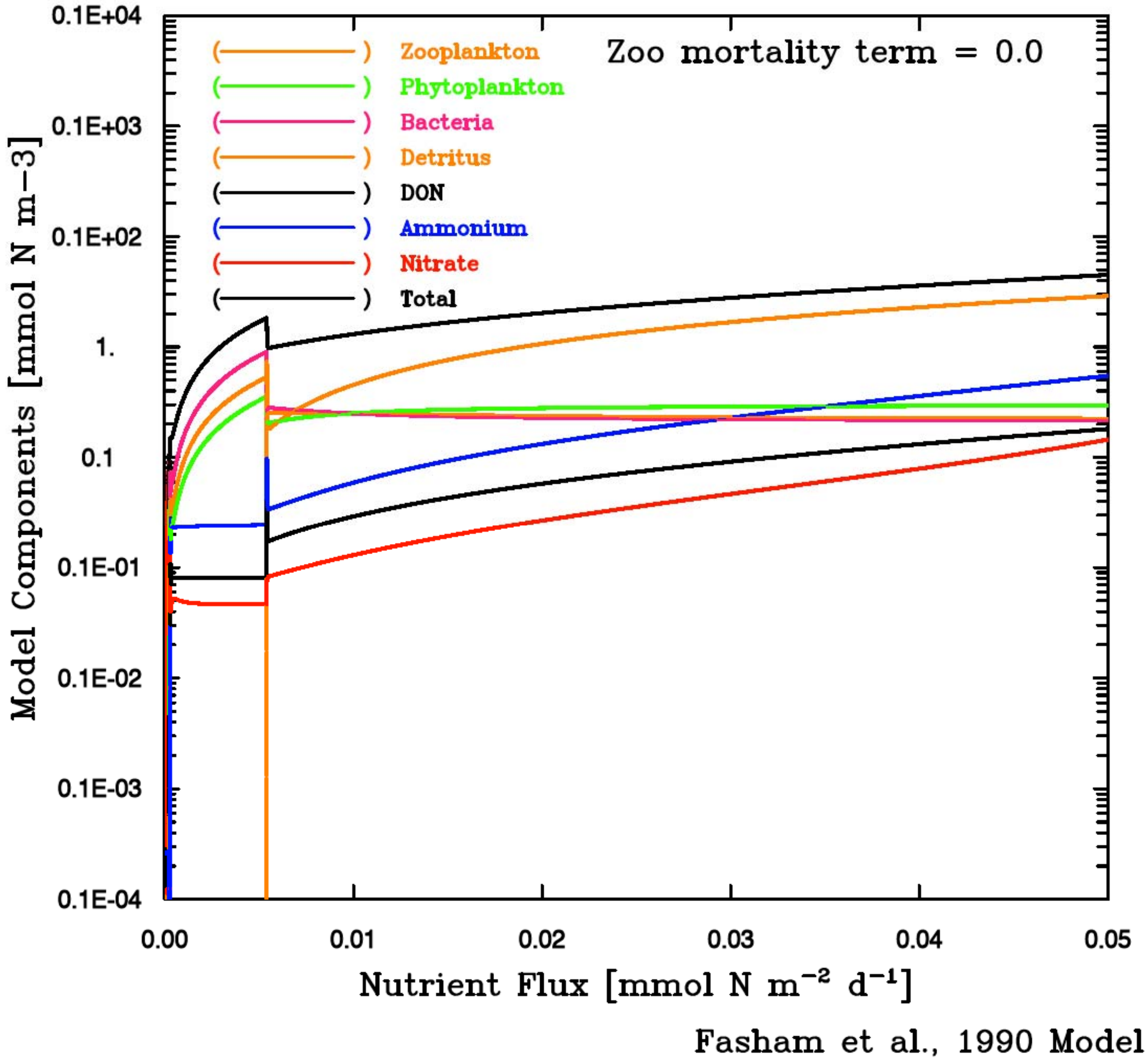
Configuring an ecosystem model using data from the Bermuda Atlantic Time Series (BATS)
Y.H. Spitz, J.R. Moisan, M.R. Abbott, Deep-Sea Research II, 48, 1733-1768, (2001)

Original Fasham et al., 1990

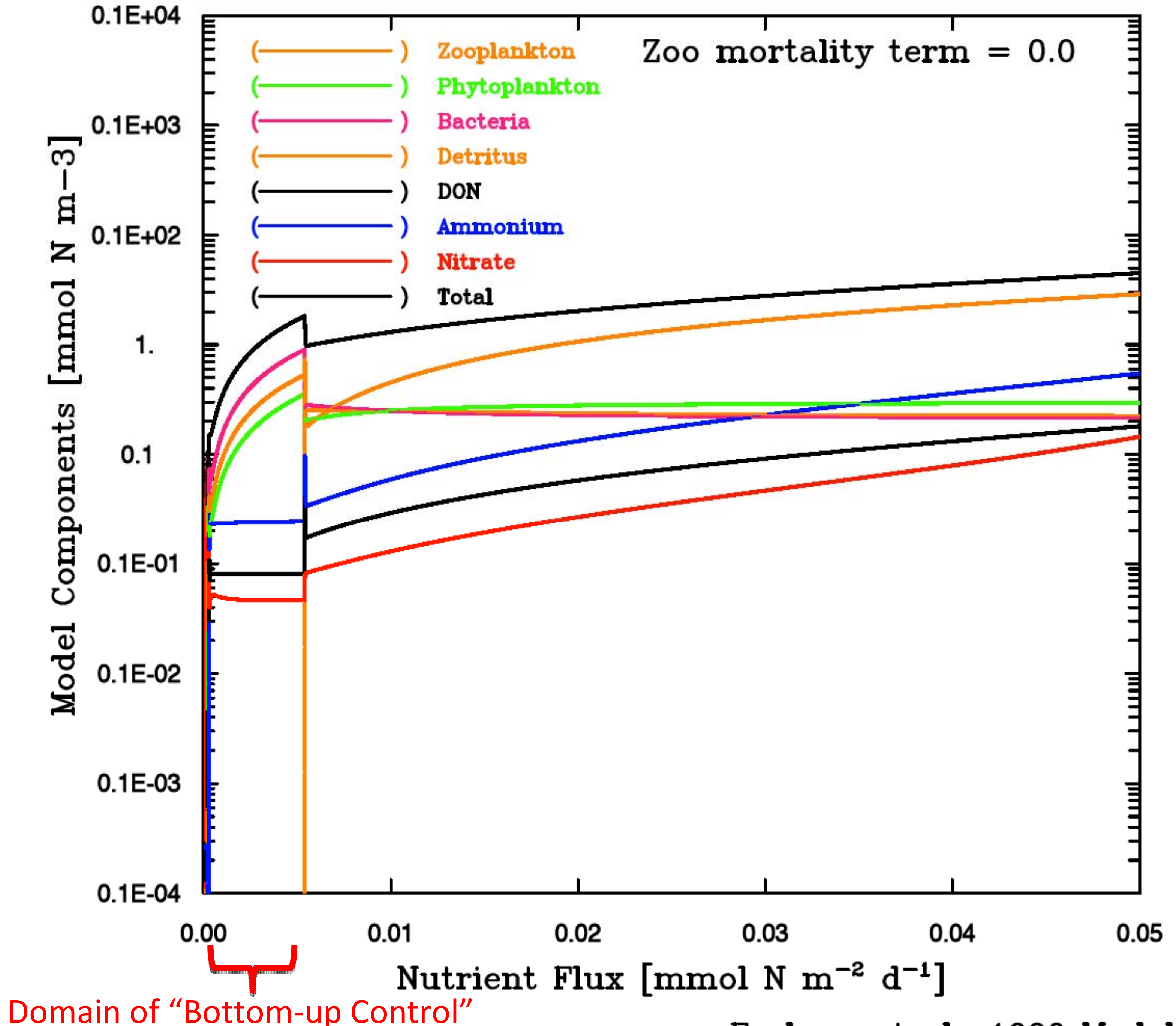


New model with data assimilation

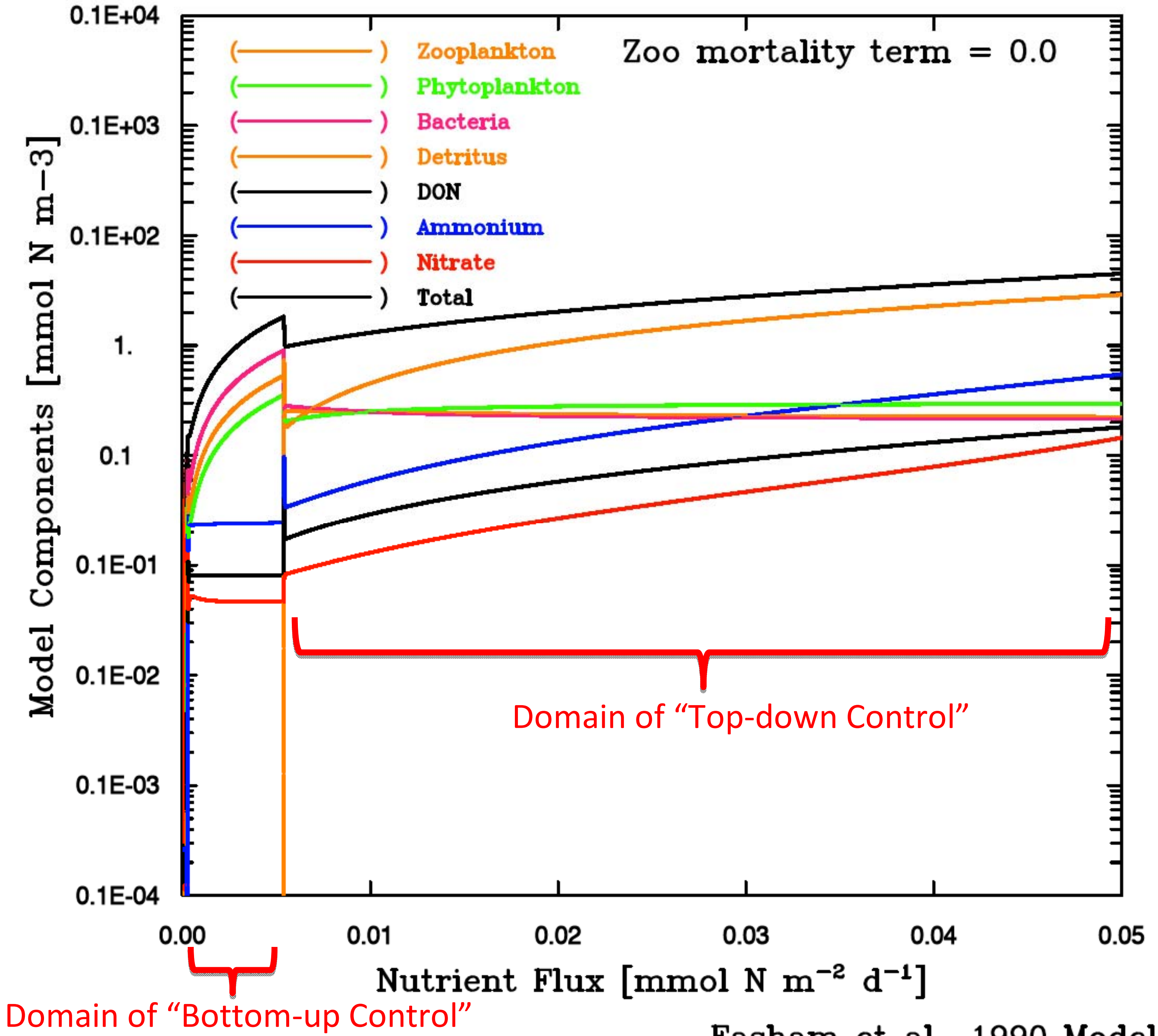




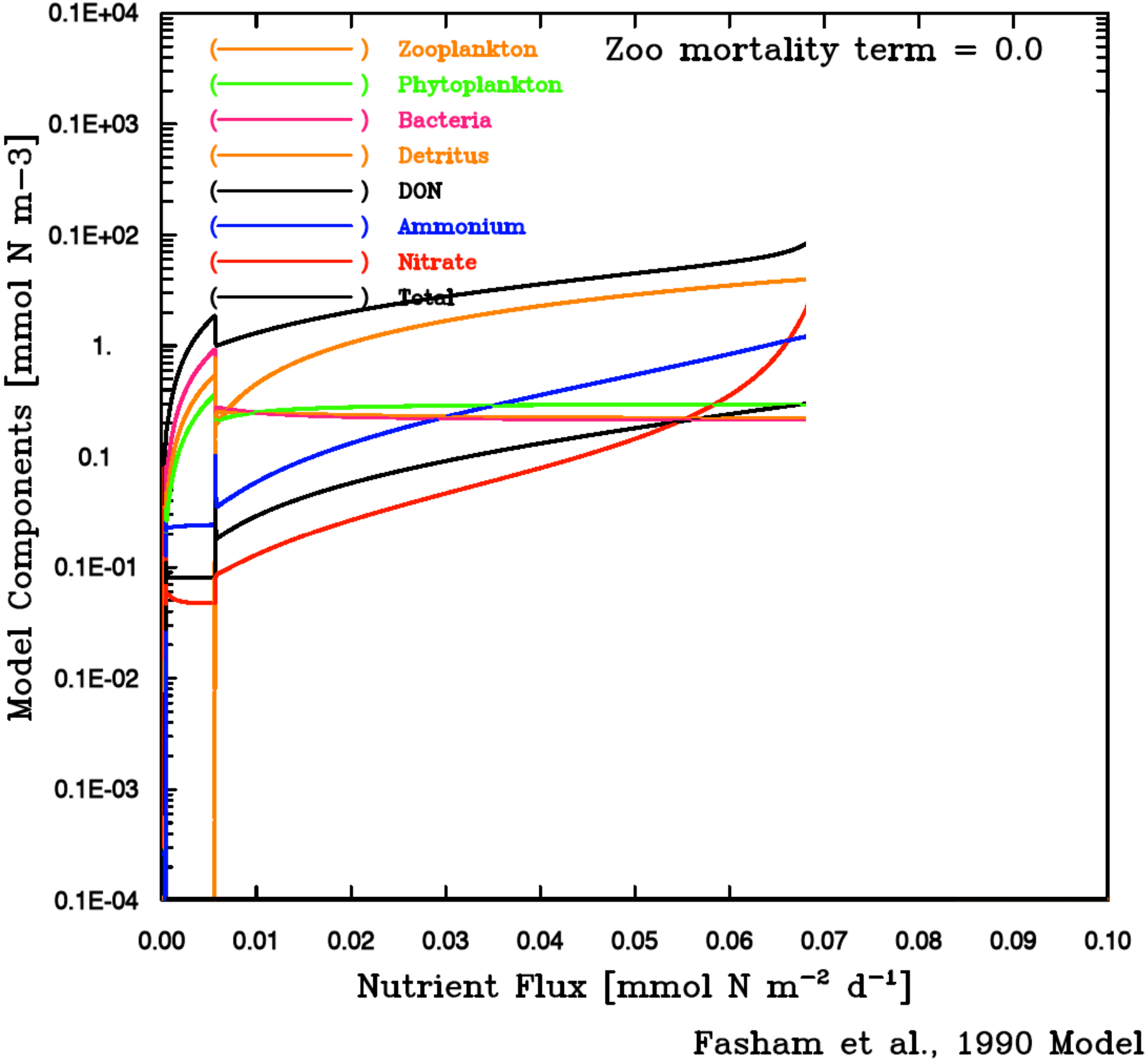
Zooplankton
Phytoplankton
Bacteria
Detritus
DON
Ammonium
Nitrate
Total
Zoo mortality term = 0.0
0.1E+04
0.1E+03
0.1E+02
1.
0.1
0.1E-01
0.1E-02
0.1E-03
0.1E-04
0.00
0.01
0.02
0.03
0.04
0.05
Model Components [mmol N m−3]
Nutrient Flux [mmol N m⁻² d⁻¹]
Fasham et al., 1990 Model

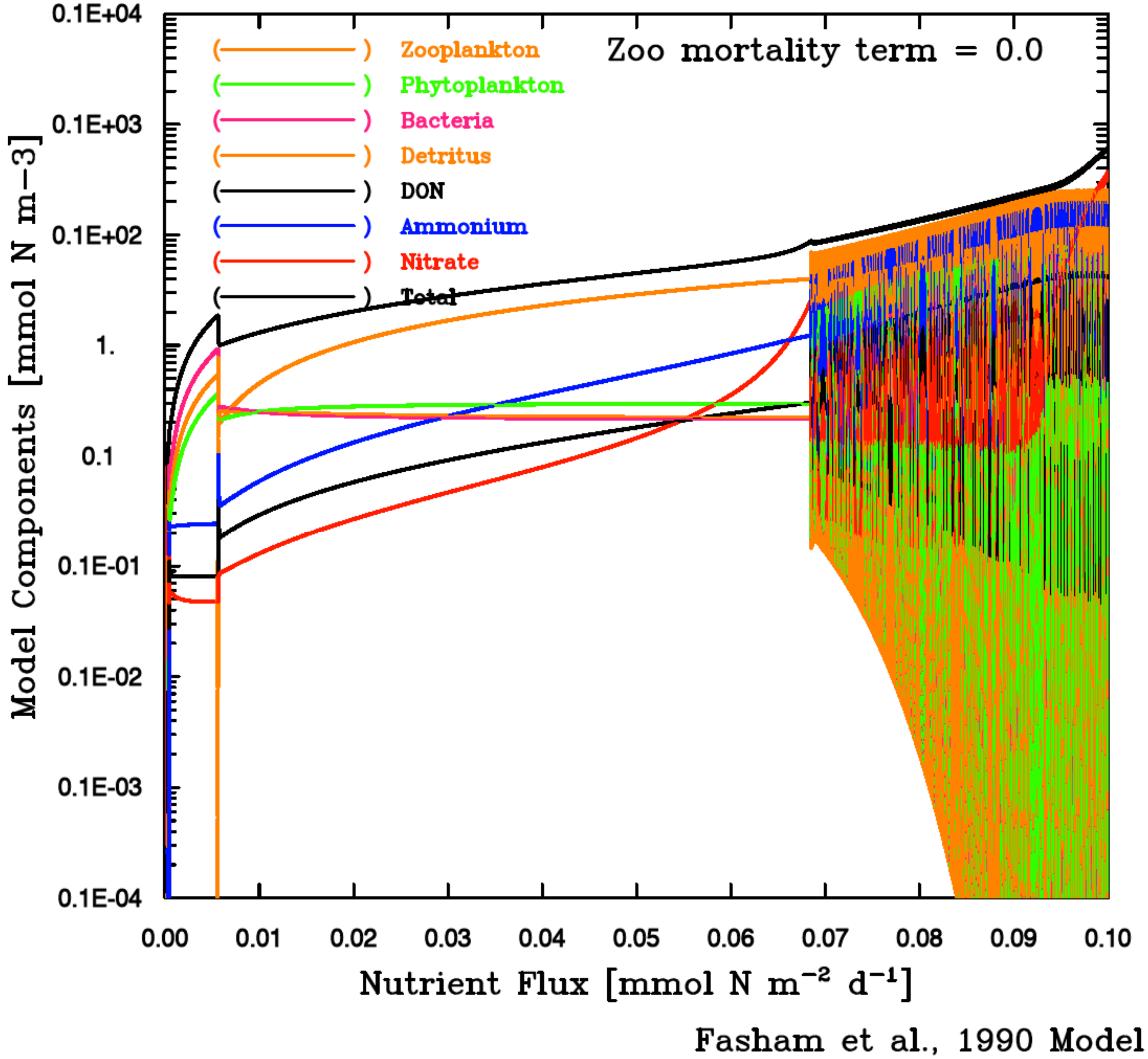


Fasham et al., 1990 Model

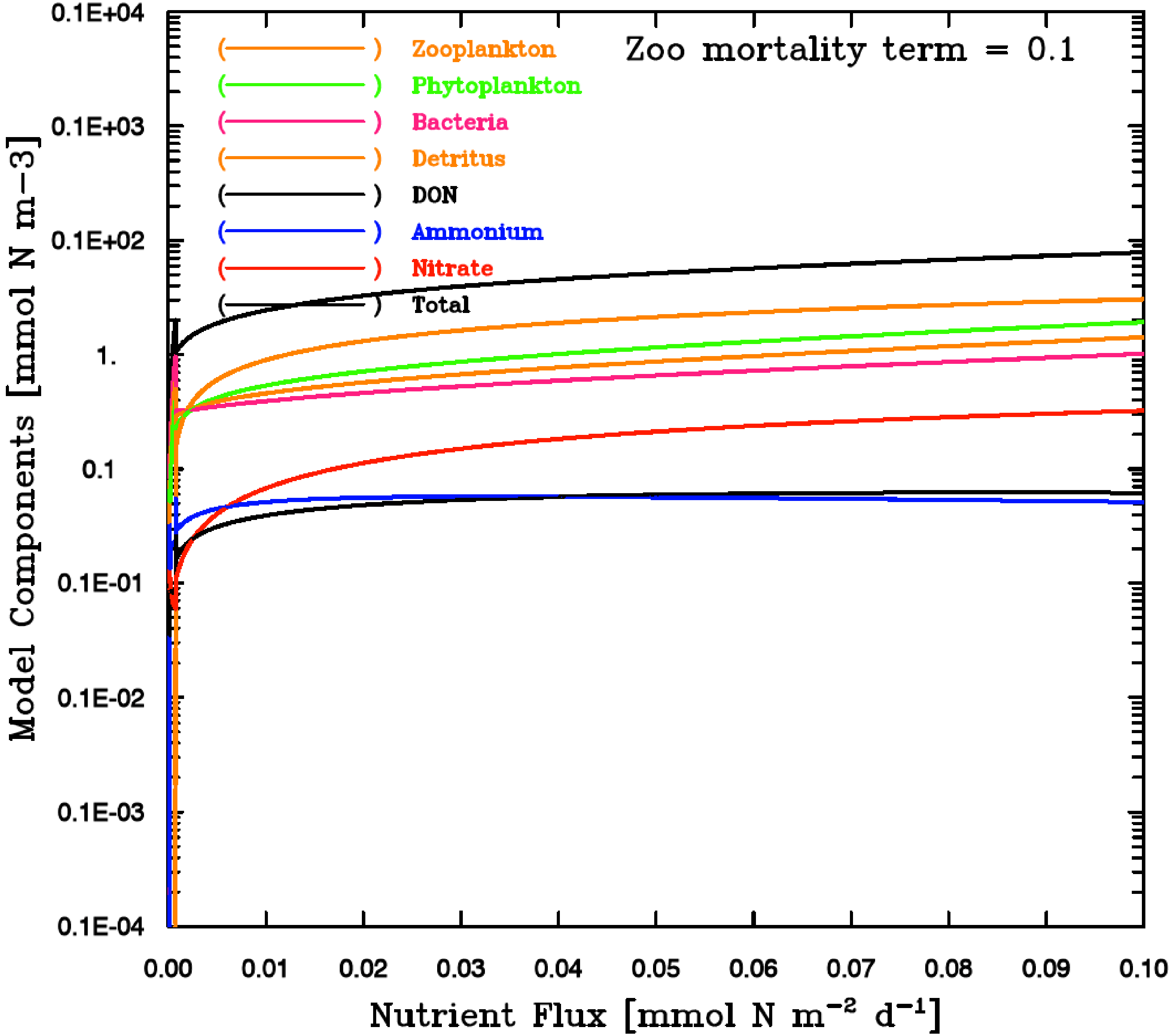


Fasham et al., 1990 Model

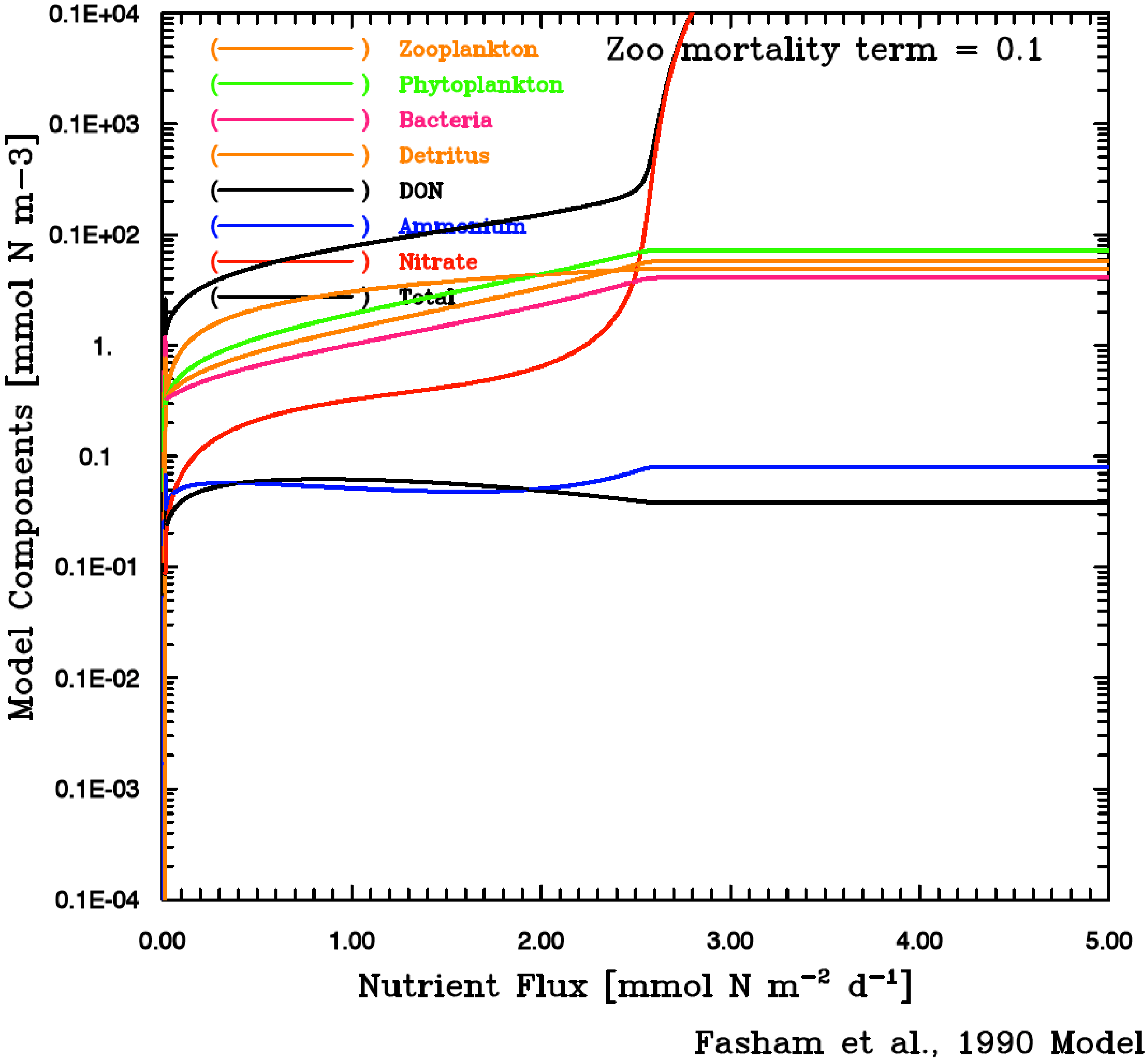

Zooplankton
Phytoplankton
Bacteria
Detritus
DON
Ammonium
Nitrate
Total
Zoo mortality term = 0.0
0.1E+04
0.1E+03
0.1E+02
1.
0.1
0.1E-01
0.1E-02
0.1E-03
0.1E-04
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0.07
0.08
0.09
0.10
Model Components [mmol N m−3]
Nutrient Flux [mmol N m⁻² d⁻¹]
Fasham et al., 1990 Model



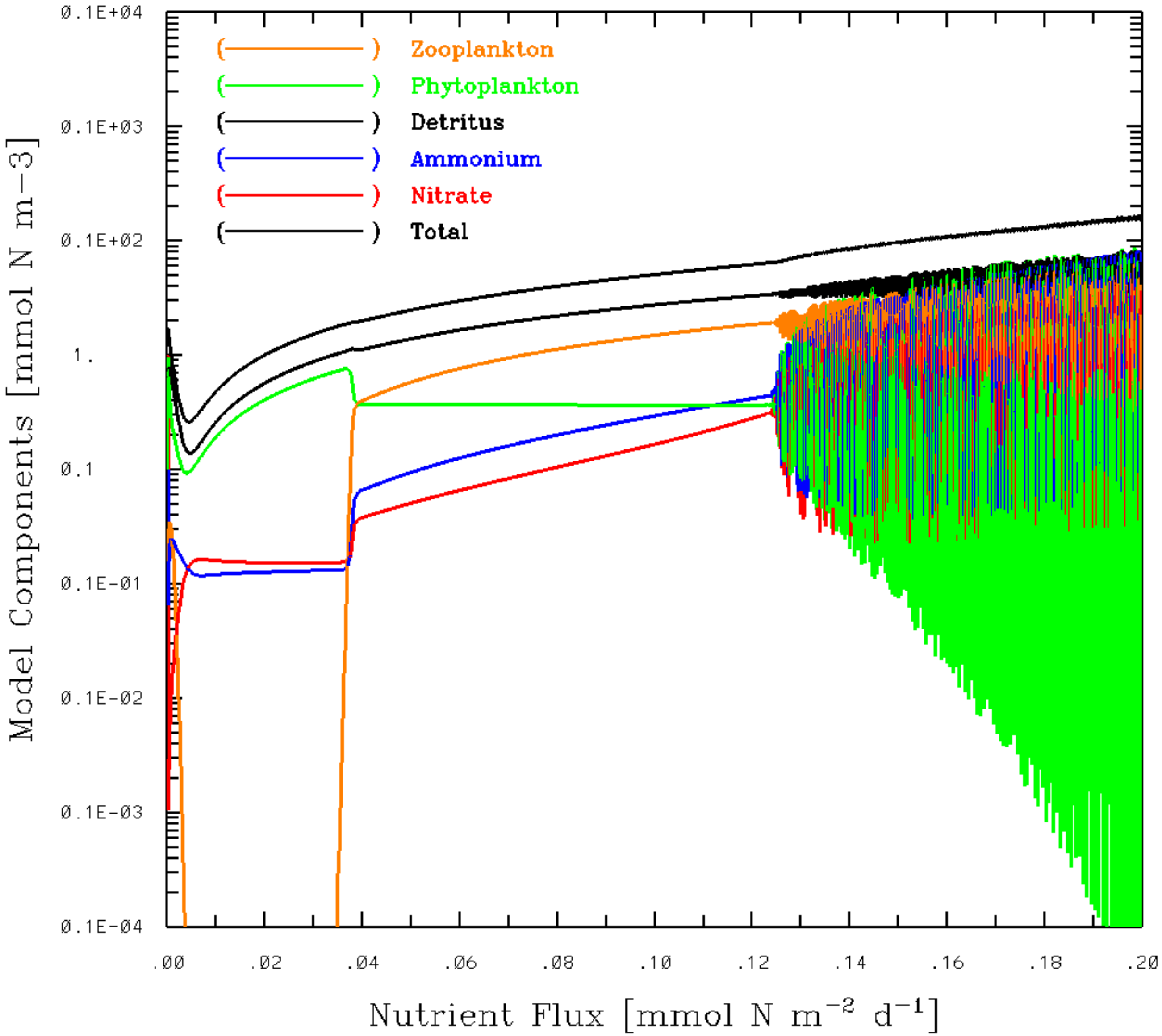
Zooplankton
Phytoplankton
Bacteria
Detritus
DON
Ammonium
Nitrate
Total
Zoo mortality term = 0.0
Model Components [mmol N m−3]
0.1E+04
0.1E+03
0.1E+02
1.
0.1
0.1E-01
0.1E-02
0.1E-03
0.1E-04
0.00
0.01
0.02
0.03
0.04
0.05
0.06
0.07
0.08
0.09
0.10
Nutrient Flux [mmol N m⁻² d⁻¹]
Fasham et al., 1990 Model



Fasham et al., 1990 Model



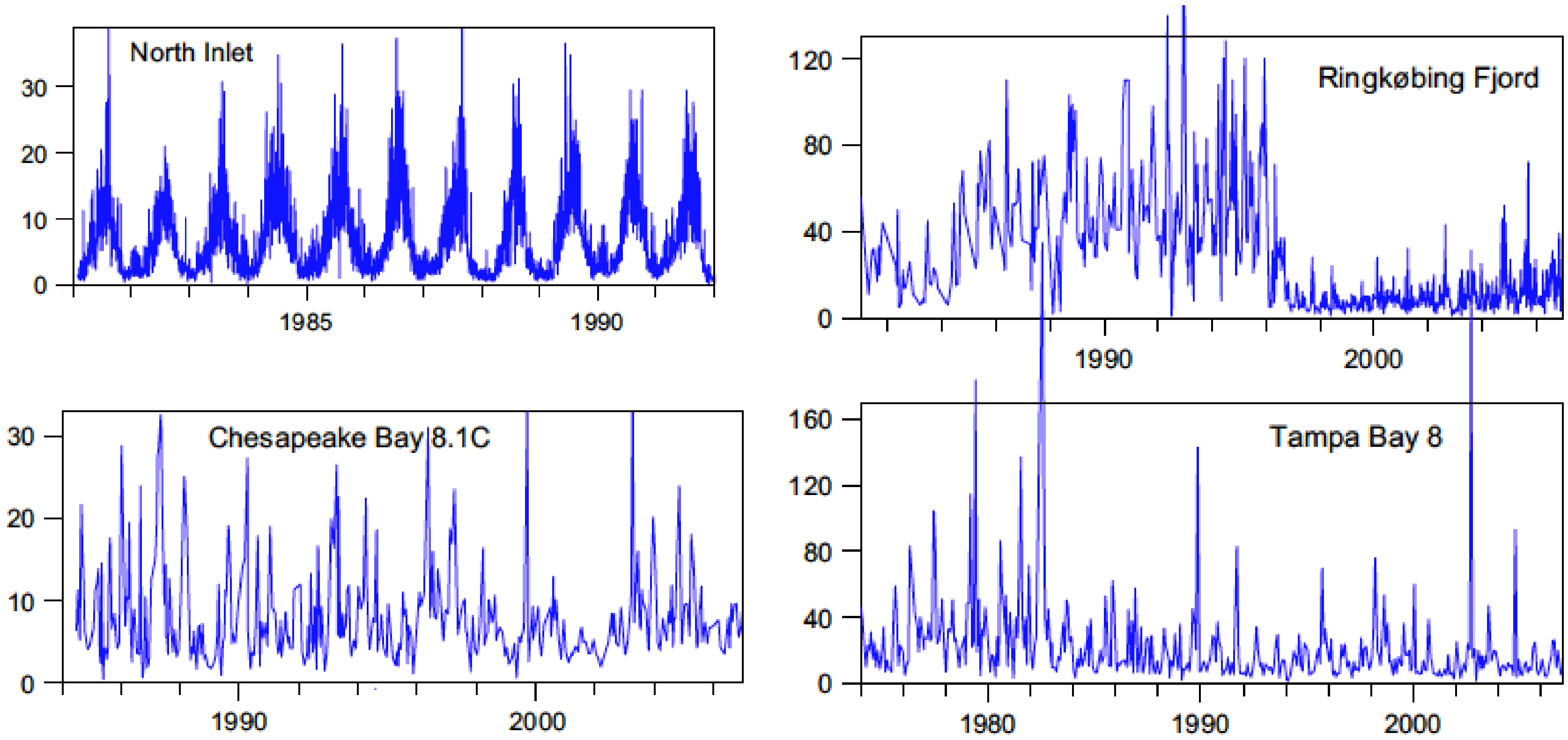
Zooplankton
Phytoplankton
Bacteria
Detritus
DON
Ammonium
Nitrate
Total
Zoo mortality term = 0.1
0.1E+04
0.1E+03
0.1E+02
1.
0.1
0.1E-01
0.1E-02
0.1E-03
0.1E-04
Model Components [mmol N m−3]
0.00
1.00
2.00
3.00
4.00
5.00
Nutrient Flux [mmol N m⁻² d⁻¹]
Fasham et al., 1990 Model

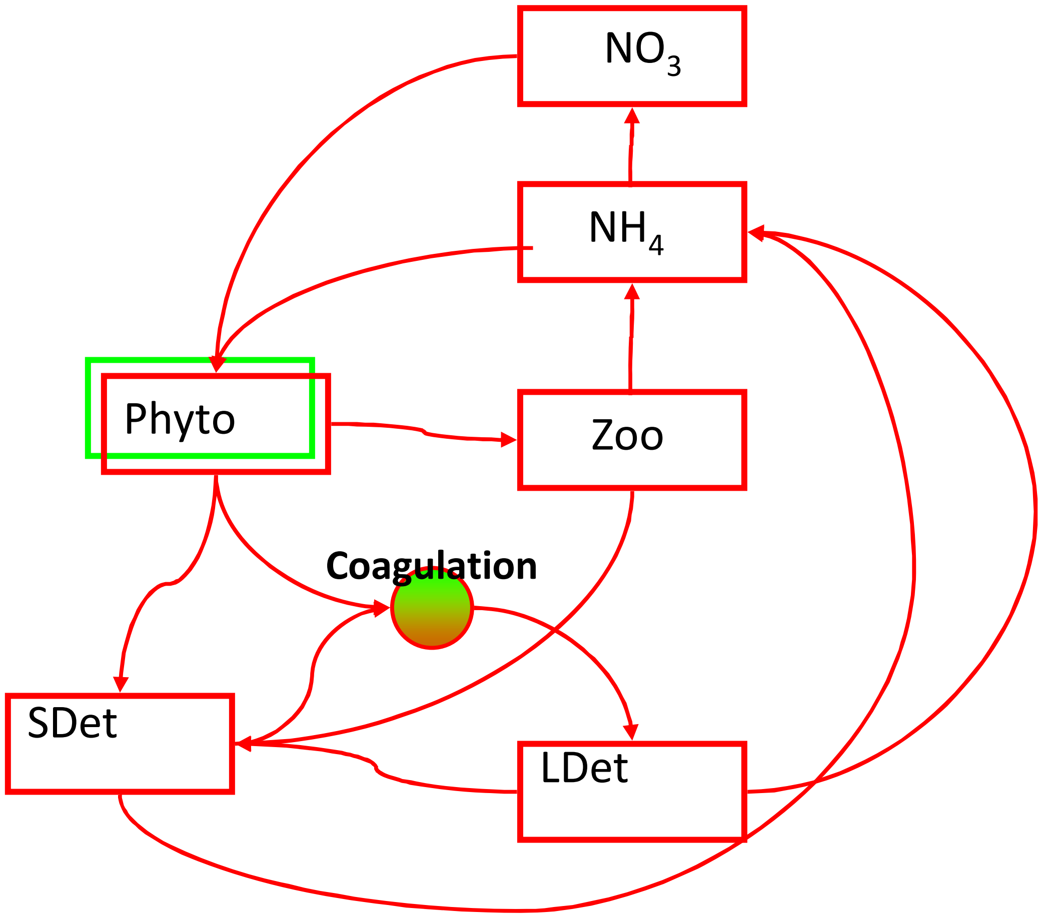


Zooplankton
Phytoplankton
Detritus
Ammonium
Nitrate
Total
0.1E+04
0.1E+03
0.1E+02
1.
0.1
0.1E-01
0.1E-02
0.1E-03
0.1E-04
.00
.02
.04
.06
.08
.10
.12
.14
.16
.18
.20
Model Components [mmol N m−3]
Nutrient Flux [mmol N m^{-2} d^{-1}]

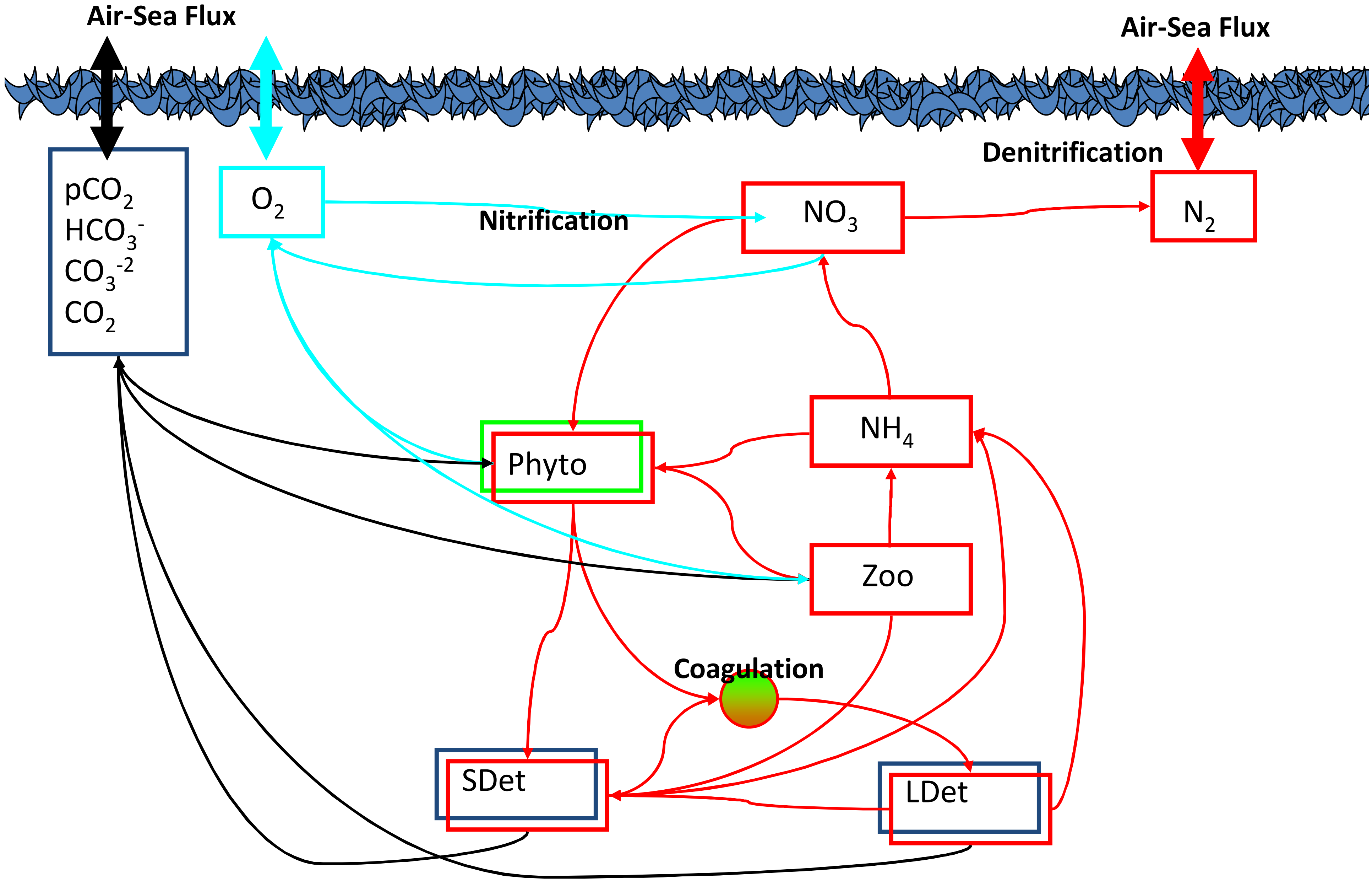
CCS Model

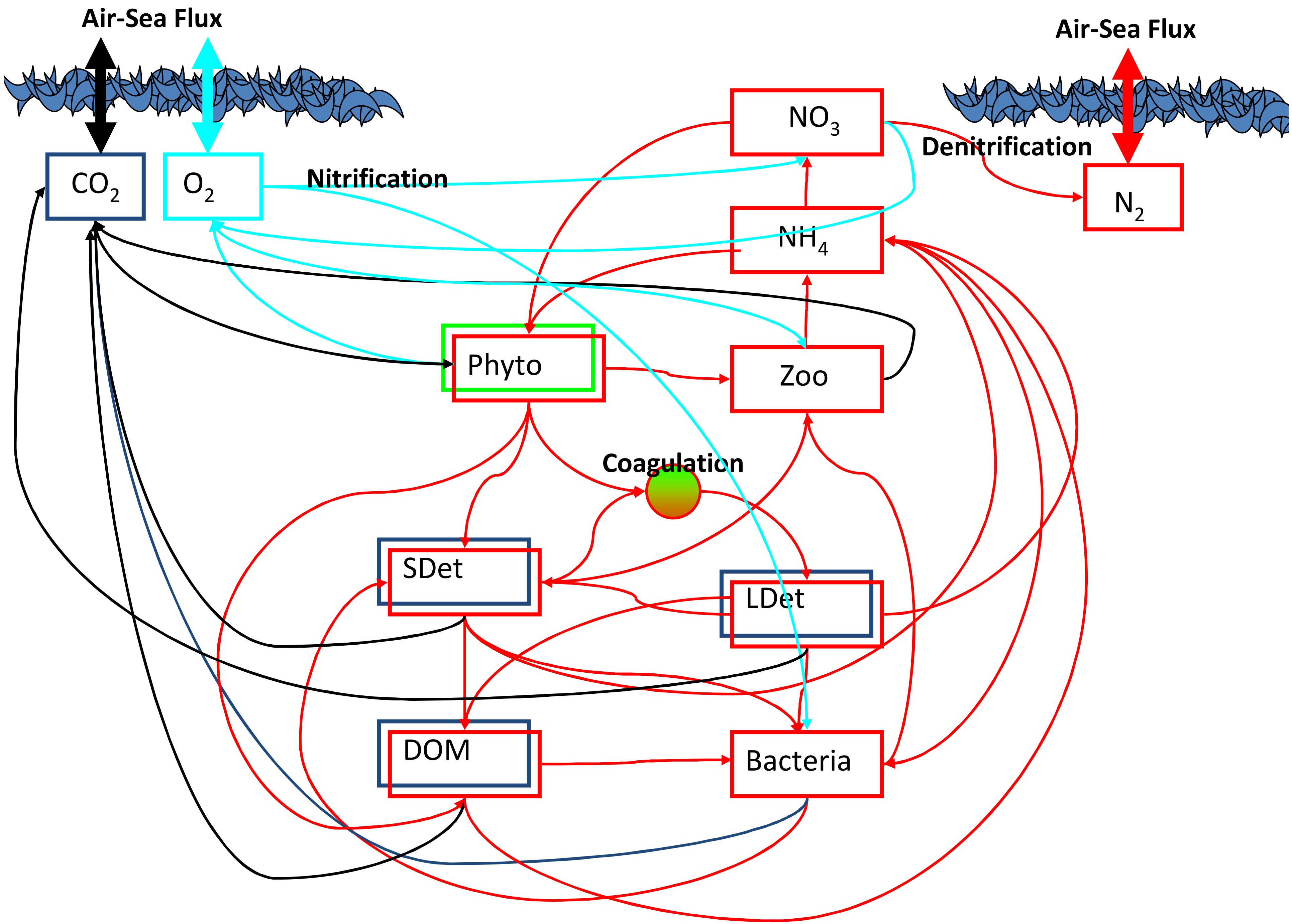
Chlorophyll a time series

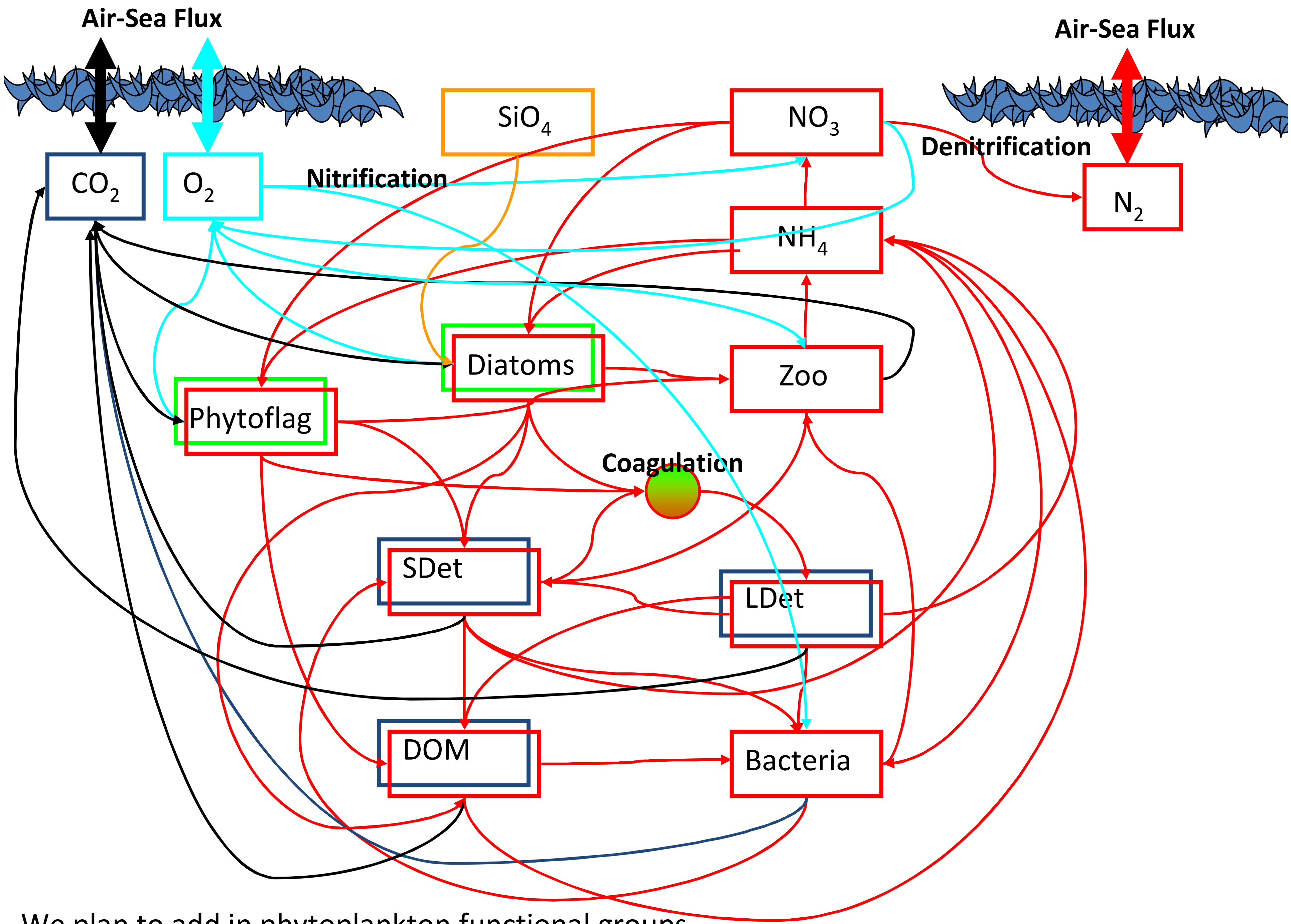




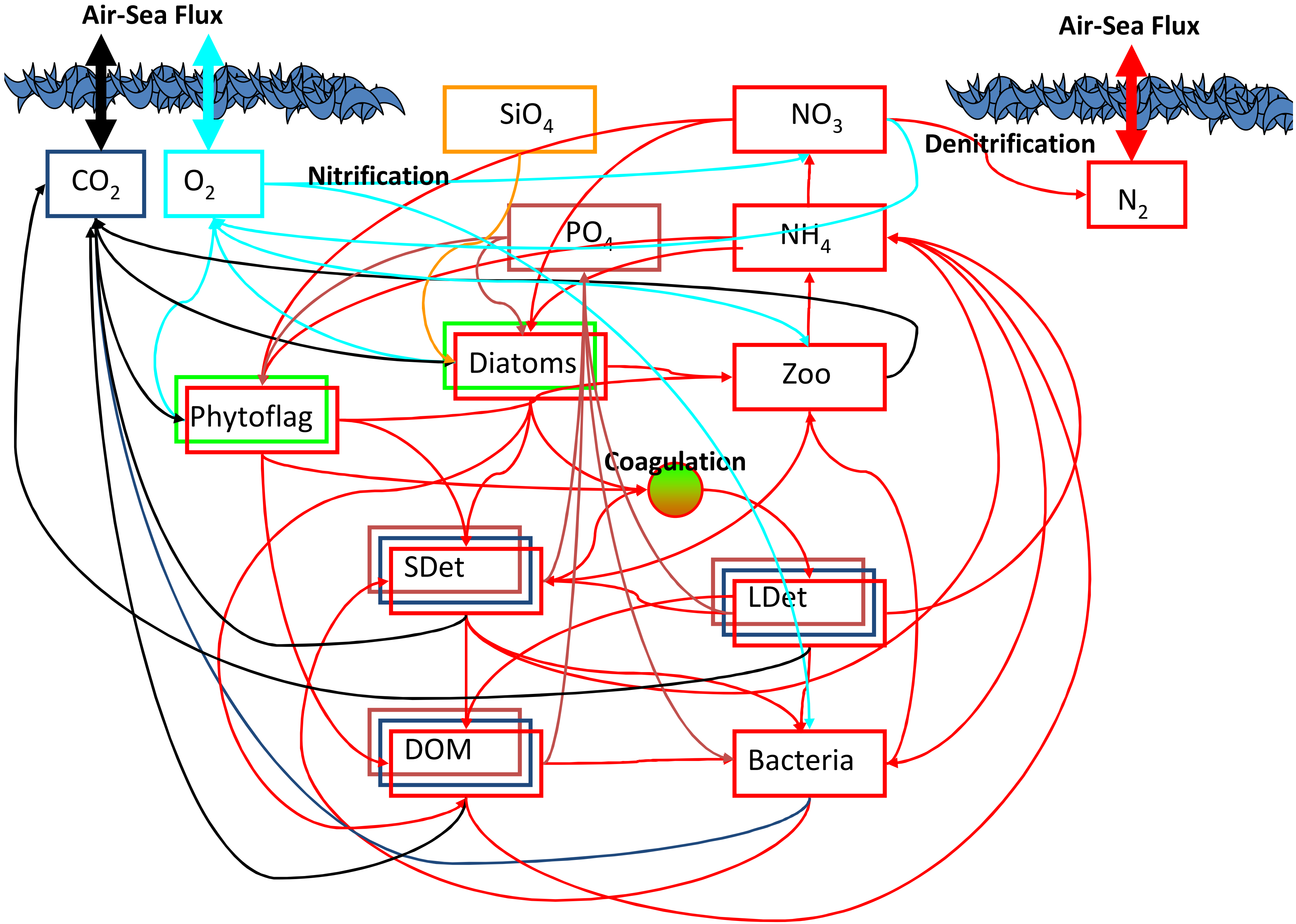
NO3
NH4
Phyto
Zoo
Coagulation
SDet
LDet

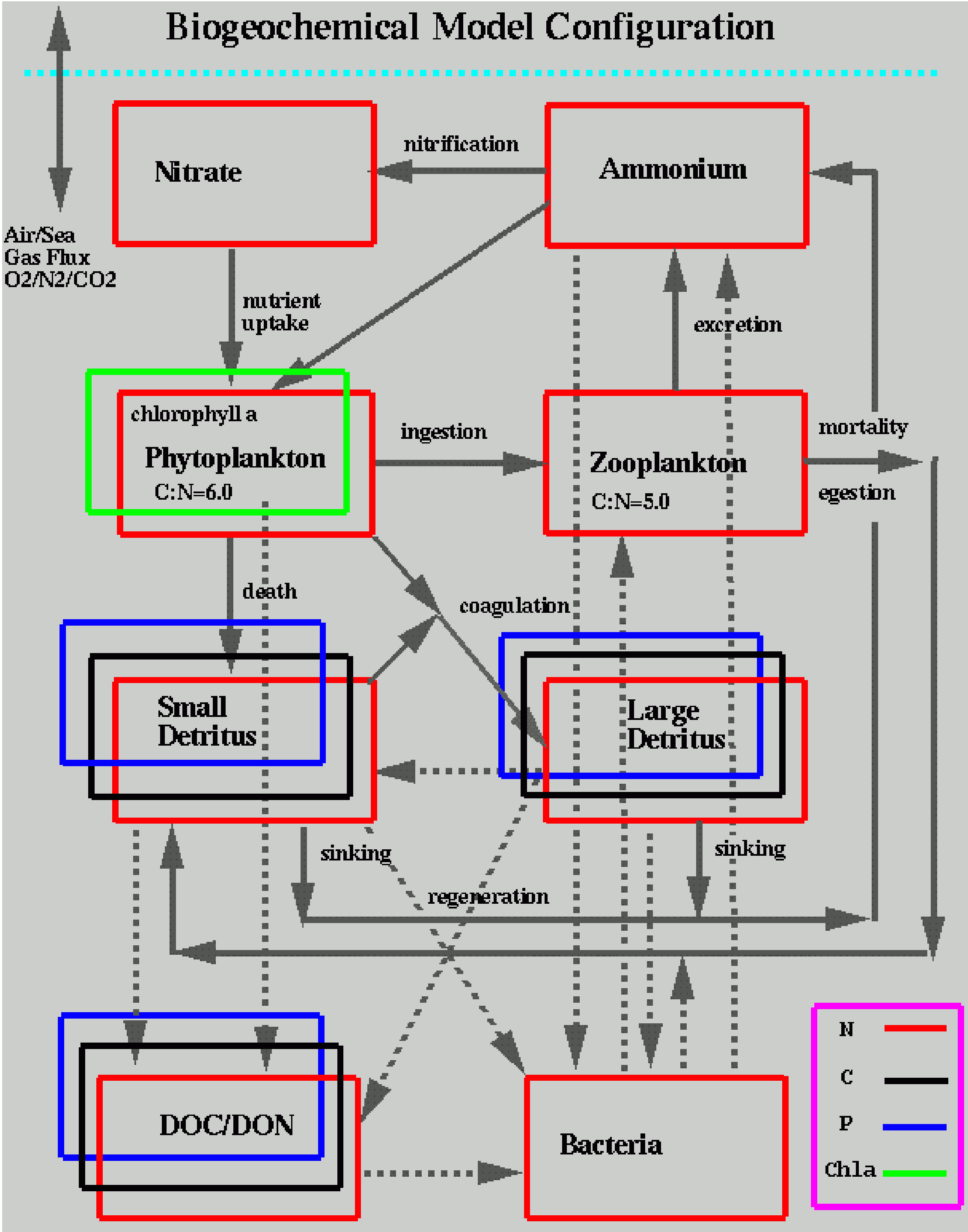

Air-Sea Flux
Air-Sea Flux
Denitrification
pCO2
HCO3-
CO3-2
CO2
O2
Nitrification
NO3
N2
Phyto
NH4
Zoo
Coagulation
SDet
LDet

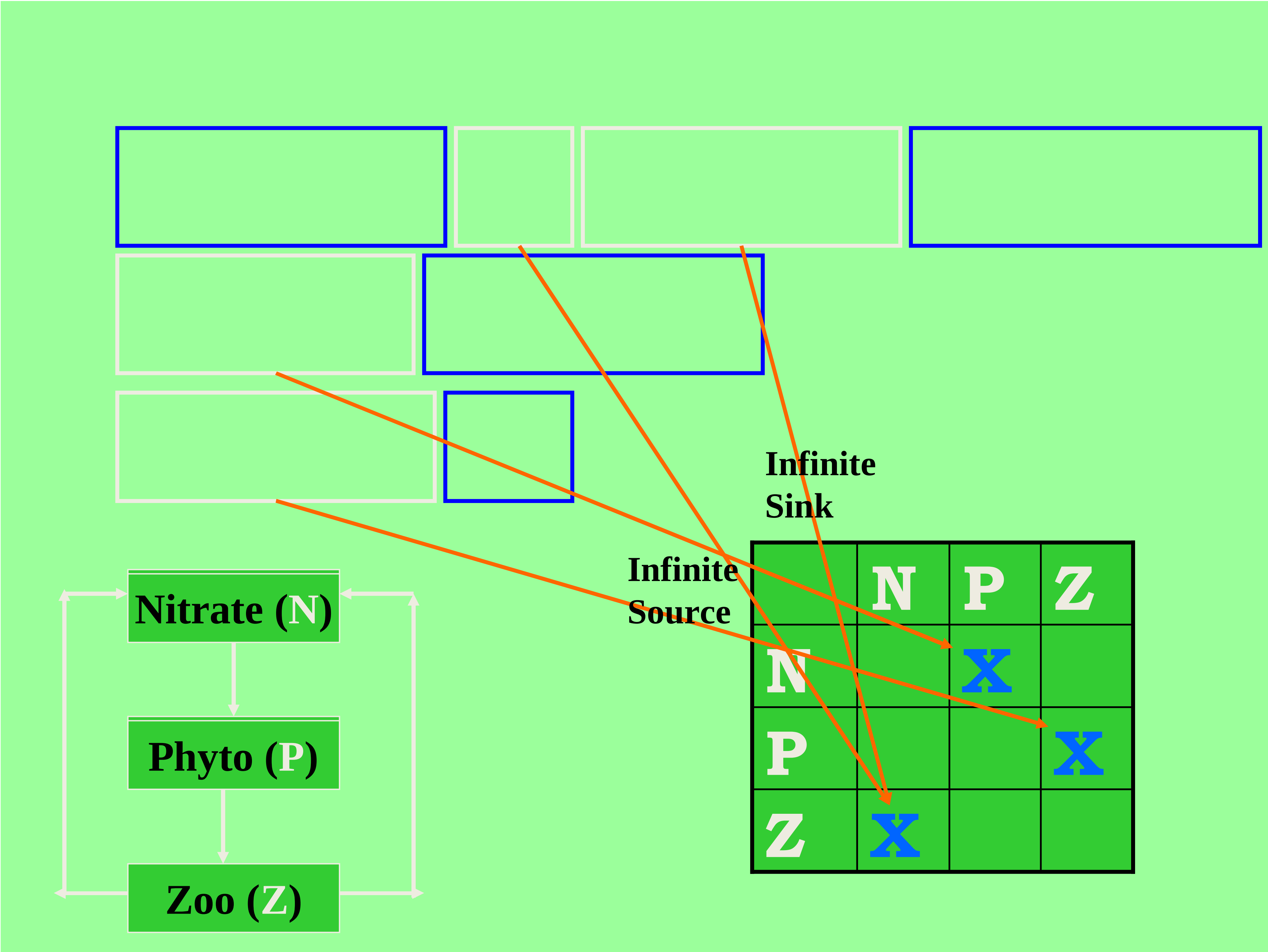

Air-Sea Flux
Air-Sea Flux
NO3
Denitrification
N2
CO2
O2
Nitrification
NH4
Phyto
Zoo
Coagulation
SDet
LDet
DOM
Bacteria



We plan to add in phytoplankton functional groups


Air-Sea Flux
Air-Sea Flux
SiO4
NO3
Denitrification
CO2
O2
Nitrification
N2
PO4
NH4
Diatoms
Zoo
Phytoflag
Coagulation
SDet
LDet
DOM
Bacteria

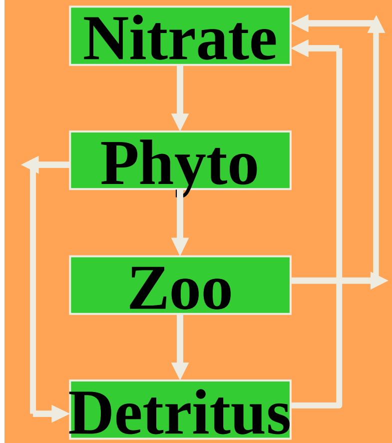

Biogeochemical Model Configuration
Air/Sea
Gas Flux
O2/N2/CO2
Nitrate
nitrification
Ammonium
nutrient
uptake
excretion
chlorophyll a
Phytoplankton
C:N=6.0
ingestion
Zooplankton
C:N=5.0
mortality
egestion
death
coagulation
Small
Detritus
Large
Detritus
sinking
regeneration
sinking
DOC/DON
Bacteria
N
C
P
Chla

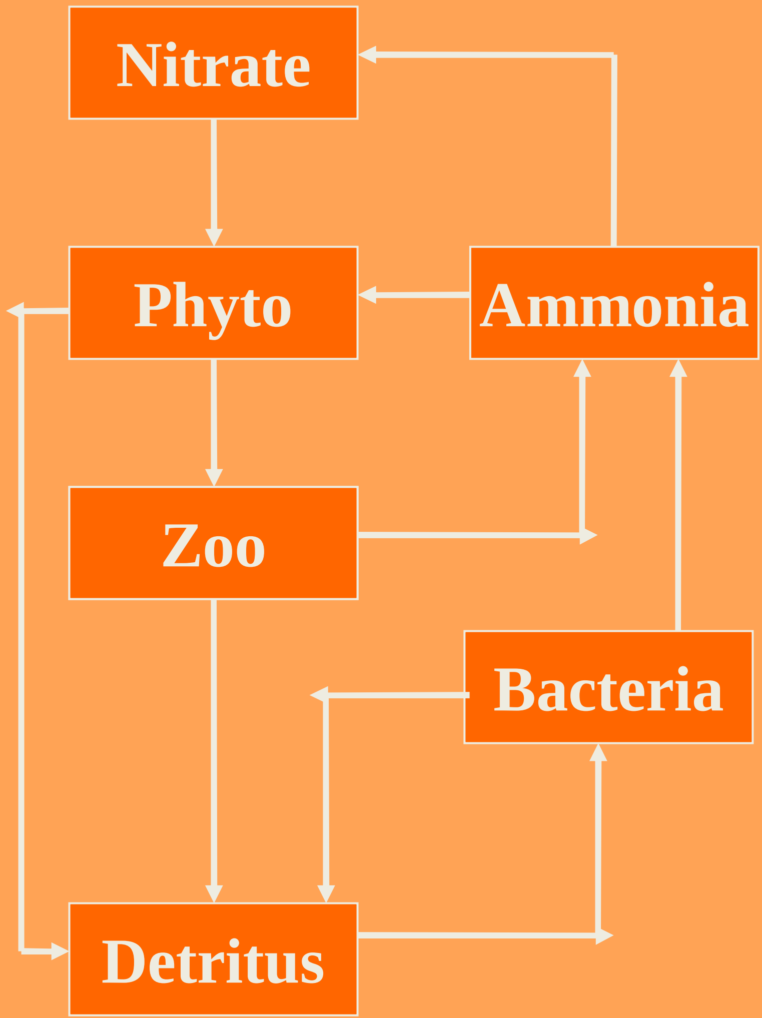


Infinite
Sink
Infinite
Source
Nitrate (N)
Phyto (P)
Zoo (Z)
N
P
Z
N
P
Z
X
X
X

Potential Ecosystem Webs

Food Web Diagrams





Linkage Matrix

	N	D	P	Z
N			X	
D	X			
P		X		X
Z	X	X		

	N	A	D	B	P	Z
N					X	
A					X	
D				X		
B		X	X			
P			X			X
Z		X	X			

```fortran
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
!       ALL OF THE R.H.S. TERMS ARE LISTED HERE
!           the terms below are listed in order of flow from a specific component
!           the inflow fluxes will be established by a matrix sweep at the end
!           Note: The terms [cff] are in [d-1] units specific to the source material/pool
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
!       Deep Water Source/Sink Pool
        bioflo(isrc,iNO3)=(am+hplus)*NO3_deep/(MLD*tbio(0))         ! NO3 injection from ML entrainment [d-1]
!
!       [NO3] nitrate
        bioflo(iNO3,isnk)=(am+hplus)*tbio(iNO3)/(MLD*tbio(iNO3))    ! NO3 dilution from ML entrainment [d-1]
        bioflo(iNO3,iPhyt)=aJ*Q1*tbio(iPhyt)/tbio(iNO3)             ! NO3 uptake by Phyto [d-1]
!
!       [NH4] ammonium
        bioflo(iNH4,isnk)=(am+hplus)*tbio(iNH4)/(MLD*tbio(iNH4))    ! NH4 dilution from ML entrainment [d-1]
        bioflo(iNH4,iBact)=U2/tbio(iNH4)                            ! NH4 uptake by Bact [d-1]
        bioflo(iNH4,iPhyt)=aJ*Q2*tbio(iPhyt)/tbio(iNH4)             ! NH4 uptake by Phyto [d-1]
!
!       [DON] Dissolved Organic Nitrogen
        bioflo(iDON,isnk)=(am+hplus)*tbio(iDON)/(MLD*tbio(iDON))    ! DON dilution from ML entrainment [d-1]
        bioflo(iDON,iBact)=U1/tbio(iDON)                            ! DON uptake by Bact [d-1]
!
!       [DET] Detritus
        bioflo(iDet,isnk)=(am+hplus)*tbio(iDet)/(MLD*tbio(iDet))    ! Det dilution from ML entrainment [d-1]
        bioflo(iDet,isnk)=bioflo(iDet,isnk)+(V*tbio(iDet)/
     &                  (MLD*tbio(iDet)))                           ! Det sinking [d-1]
        bioflo(iDet,iDON)=mu4*tbio(iDet)/tbio(iDet)                 ! Det breakdown to DON [d-1]
        bioflo(iDet,iZoo)=G3/tbio(iDet)                             ! Det ingestion by Zoo [d-1]
!
!       [bact] bacteria
        bioflo(iBact,isnk)=(am+hplus)*Tbio(iBact)/(MLD*tbio(iBact)) ! Bact dilution from ML entrainment [d-1]
        bioflo(iBact,iNH4)=mu3*tbio(iBact)/tbio(iBact)              ! Bact excretion to NH4 [d-1]
        bioflo(iBact,iZoo)=G2/tbio(iBact)                           ! Zoo egestion of Bact [d-1]
!
!       [phyto] phytoplankton
        bioflo(iPhyt,isnk)=(am+hplus)*tbio(iPhyt)/(MLD*tbio(iPhyt)) ! Phyto dilution from ML entrainment [d-1]
        bioflo(iPhyt,iDON)=gamma1*aJ*Q*tbio(iPhyt)/tbio(iPhyt)      ! Phyto exudation to DON [d-1]
!
        bioflo(iPhyt,iDet)=mu1*tbio(iPhyt)/tbio(iPhyt)              ! Phyto mortality to DET [d-1]
!
        bioflo(iPhyt,iZoo)=G1/tbio(iPhyt)                           ! Phyto ingestion by Zoo [d-1]
!
!       [zoo] zooplankton
        bioflo(iZoo,isnk)=hplus*tbio(iZoo)/(MLD*tbio(iZoo))         ! Zoo dilution from ML entrainment [d-1]
        bioflo(iZoo,isnk)=bioflo(iZoo,isnk)+
     &                  (omega*mu5*tbio(iZoo)/tbio(iZoo))           ! Zoo mortality to below MLD [d-1]
        bioflo(iZoo,iNH4)=epsilon*mu2*tbio(iZoo)/tbio(iZoo)         ! Zoo excretion to NH4 [d-1]
        bioflo(iZoo,iNH4)=bioflo(iZoo,iNH4)+
     &                  ((1.-omega)*mu5*tbio(iZoo)/tbio(iZoo))      ! Zoo mort to NH4 [d-1]
        bioflo(iZoo,iDON)=(1.-epsilon)*mu2*tbio(iZoo)/tbio(iZoo)    ! Zoo excretion to DON [d-1]
        bioflo(iZoo,iDet)=(1.-beta1)*G1/tbio(iZoo)                  ! Zoo egestion of Phyto to Det [d-1]
        bioflo(iZoo,iDet)=bioflo(iZoo,iDet)+
     &                  ((1.-beta2)*G2/tbio(iZoo))                  ! Zoo egest of Bact to Det [d-1]
        bioflo(iZoo,iDet)=bioflo(iZoo,iDet)+
     &                  ((1.-beta3)*G3/tbio(iZoo))                  ! Zoo egest of Det to Det [d-1]
!
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

```
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
!       ALL OF THE R.H.S. TERMS ARE LISTED HERE
!           the terms below are listed in order of flow from a specific component
!           the inflow fluxes will be established by a matrix sweep at the end
!           Note: The terms [cff] are in [d-1] units specific to the source material/pool
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
!       Deep Water Source/Sink Pool
        bioflo(isrc,iNO3)=(am+hplus)*NO3_deep/(MLD*tbio(0))       ! NO3 injection from ML entrainment [d-1]
!
!       [NO3] nitrate
        bioflo(iNO3,isnk)=(am+hplus)*tbio(iNO3)/(MLD*tbio(iNO3))   ! NO3 dilution from ML entrainment [d-1]
        bioflo(iNO3,iPhyt)=aJ*Q1*tbio(iPhyt)/tbio(iNO3)            ! NO3 uptake by Phyto [d-1]
!
!       [NH4] ammonium
        bioflo(iNH4,isnk)=(am+hplus)*tbio(iNH4)/(MLD*tbio(iNH4))   ! NH4 dilution from ML entrainment [d-1]
        bioflo(iNH4,iBact)=U2/tbio(iNH4)                           ! NH4 uptake by Bact [d-1]
        bioflo(iNH4,iPhyt)=aJ*Q2*tbio(iPhyt)/tbio(iNH4)            ! NH4 uptake by Phyto [d-1]
!
!       [DON] Dissolved Organic Nitrogen
        bioflo(iDON,isnk)=(am+hplus)*tbio(iDON)/(MLD*tbio(iDON))   ! DON dilution from ML entrainment [d-1]
        bioflo(iDON,iBact)=U1/tbio(iDON)                           ! DON uptake by Bact [d-1]
!
!       [DET] Detritus
        bioflo(iDet,isnk)=(am+hplus)*tbio(iDet)/(MLD*tbio(iDet))   ! Det dilution from ML entrainment [d-1]
        bioflo(iDet,isnk)=bioflo(iDet,isnk)+(V*tbio(iDet)/
     &                   (MLD*tbio(iDet)))                         ! Det sinking [d-1]
        bioflo(iDet,iDON)=mu4*tbio(iDet)/tbio(iDet)                ! Det breakdown to DON [d-1]
        bioflo(iDet,iZoo)=G3/tbio(iDet)                            ! Det ingestion by Zoo [d-1]
!
!       [bact] bacteria
        bioflo(iBact,isnk)=(am+hplus)*Tbio(iBact)/(MLD*tbio(iBact)) ! Bact dilution from ML entrainment [d-1]
        bioflo(iBact,iNH4)=mu3*tbio(iBact)/tbio(iBact)             ! Bact excretion to NH4 [d-1]
        bioflo(iBact,iZoo)=G2/tbio(iBact)                          ! Zoo egestion of Bact [d-1]
!
!       [phyto] phytoplankton
        bioflo(iPhyt,isnk)=(am+hplus)*tbio(iPhyt)/(MLD*tbio(iPhyt)) ! Phyto dilution from ML entrainment [d-1]
        bioflo(iPhyt,iDON)=gamma1*aJ*Q*tbio(iPhyt)/tbio(iPhyt)     ! Phyto exudation to DON [d-1]
!
        bioflo(iPhyt,iDet)=mu1*tbio(iPhyt)/tbio(iPhyt)             ! Phyto mortality to DET [d-1]
!
        bioflo(iPhyt,iZoo)=G1/tbio(iPhyt)                          ! Phyto ingestion by Zoo [d-1]
!
!       [zoo] zooplankton
        bioflo(iZoo,isnk)=hplus*tbio(iZoo)/(MLD*tbio(iZoo))        ! Zoo dilution from ML entrainment [d-1]
        bioflo(iZoo,isnk)=bioflo(iZoo,isnk)+
     &                   (omega*mu5*tbio(iZoo)/tbio(iZoo))         ! Zoo mortality to below MLD [d-1]
        bioflo(iZoo,iNH4)=epsilon*mu2*tbio(iZoo)/tbio(iZoo)        ! Zoo excretion to NH4 [d-1]
        bioflo(iZoo,iNH4)=bioflo(iZoo,iNH4)+
     &                   ((1.-omega)*mu5*tbio(iZoo)/tbio(iZoo))    ! Zoo mort to NH4 [d-1]
        bioflo(iZoo,iDON)=(1.-epsilon)*mu2*tbio(iZoo)/tbio(iZoo)   ! Zoo excretion to DON [d-1]
        bioflo(iZoo,iDet)=(1.-beta1)*G1/tbio(iZoo)                 ! Zoo egestion of Phyto to Det [d-1]
        bioflo(iZoo,iDet)=bioflo(iZoo,iDet)+
     &                   ((1.-beta2)*G2/tbio(iZoo))                ! Zoo egest of Bact to Det [d-1]
        bioflo(iZoo,iDet)=bioflo(iZoo,iDet)+
     &                   ((1.-beta3)*G3/tbio(iZoo))                ! Zoo egest of Det to Det [d-1]
!
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

```
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
!       ALL OF THE R.H.S. TERMS ARE LISTED HERE
!           the terms below are listed in order of flow from a specific component
!           the inflow fluxes will be established by a matrix sweep at the end
!           Note: The terms [cff] are in [d-1] units specific to the source material/pool
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
!       Deep Water Source/Sink Pool
        bioflo(isrc,iNO3)=(am+hplus)*NO3_deep/(MLD*tbio(0))         ! NO3 injection from ML entrainment [d-1]
!
!       [NO3] nitrate
        bioflo(iNO3,isnk)=(am+hplus)*tbio(iNO3)/(MLD*tbio(iNO3))    ! NO3 dilution from ML entrainment [d-1]
        bioflo(iNO3,iPhyt)=aJ*Q1*tbio(iPhyt)/tbio(iNO3)             ! NO3 uptake by Phyto [d-1]
!
!       [NH4] ammonium
```

```
[NO3] nitrate
bioflo(iNO3,isnk)=(am+hplus)*tbio(iNO3)/(MLD*tbio(iNO3))
bioflo(iNO3,iPhyt)=aJ*Q1*tbio(iPhyt)/tbio(iNO3)

[NH4] ammonium
bioflo(iNH4,isnk)=(am+hplus)*tbio(iNH4)/(MLD*tbio(iNH4))
bioflo(iNH4,iBact)=U2/tbio(iNH4)
bioflo(iNH4,iPhyt)=aJ*Q2*tbio(iPhyt)/tbio(iNH4)
```

```
        bioflo(iPhyt,iDet)=mu1*tbio(iPhyt)/tbio(iPhyt)              ! Phyto mortality to DET [d-1]
!
        bioflo(iPhyt,iZoo)=G1/tbio(iPhyt)                           ! Phyto ingestion by Zoo [d-1]
!
!       [zoo] zooplankton
        bioflo(iZoo,isnk)=hplus*tbio(iZoo)/(MLD*tbio(iZoo))         ! Zoo dilution from ML entrainment [d-1]
        bioflo(iZoo,isnk)=bioflo(iZoo,isnk)+
    &                  (omega*mu5*tbio(iZoo)/tbio(iZoo))            ! Zoo mortality to below MLD [d-1]
        bioflo(iZoo,iNH4)=epsilon*mu2*tbio(iZoo)/tbio(iZoo)         ! Zoo excretion to NH4 [d-1]
        bioflo(iZoo,iNH4)=bioflo(iZoo,iNH4)+
    &                  ((1.-omega)*mu5*tbio(iZoo)/tbio(iZoo))       ! Zoo mort to NH4 [d-1]
        bioflo(iZoo,iDON)=(1.-epsilon)*mu2*tbio(iZoo)/tbio(iZoo)    ! Zoo excretion to DON [d-1]
        bioflo(iZoo,iDet)=(1.-beta1)*G1/tbio(iZoo)                  ! Zoo egestion of Phyto to Det [d-1]
        bioflo(iZoo,iDet)=bioflo(iZoo,iDet)+
    &                  ((1.-beta2)*G2/tbio(iZoo))                   ! Zoo egest of Bact to Det [d-1]
        bioflo(iZoo,iDet)=bioflo(iZoo,iDet)+
    &                  ((1.-beta3)*G3/tbio(iZoo))                   ! Zoo egest of Det to Det [d-1]
!
!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!
```

One Dimensional (Vertical) Model

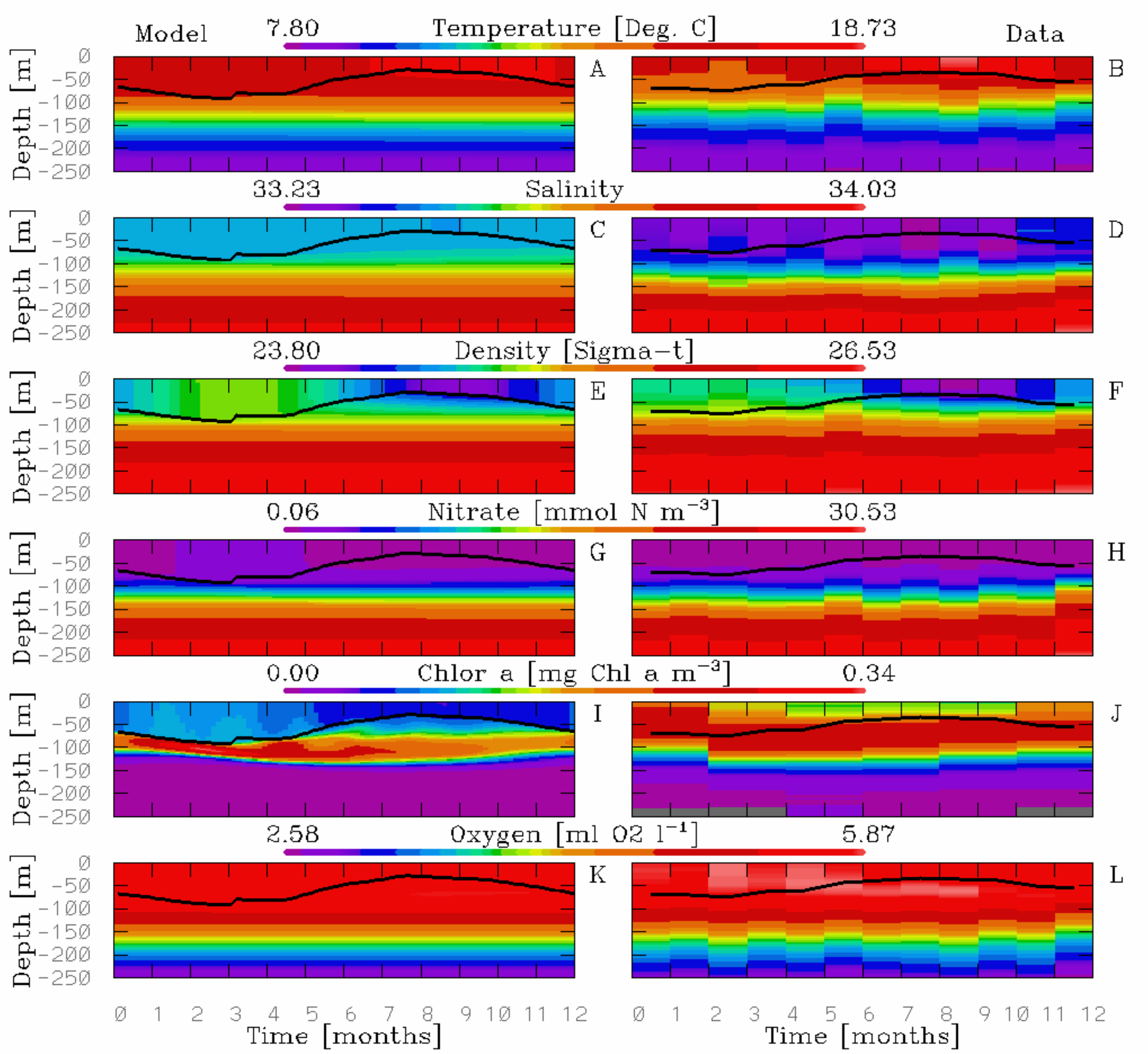
$$\frac{\partial B_i}{\partial t} + (w + w_B)\frac{\partial B_i}{\partial z} - \frac{\partial}{\partial z} K_z \frac{\partial B_i}{\partial z} = S_i$$

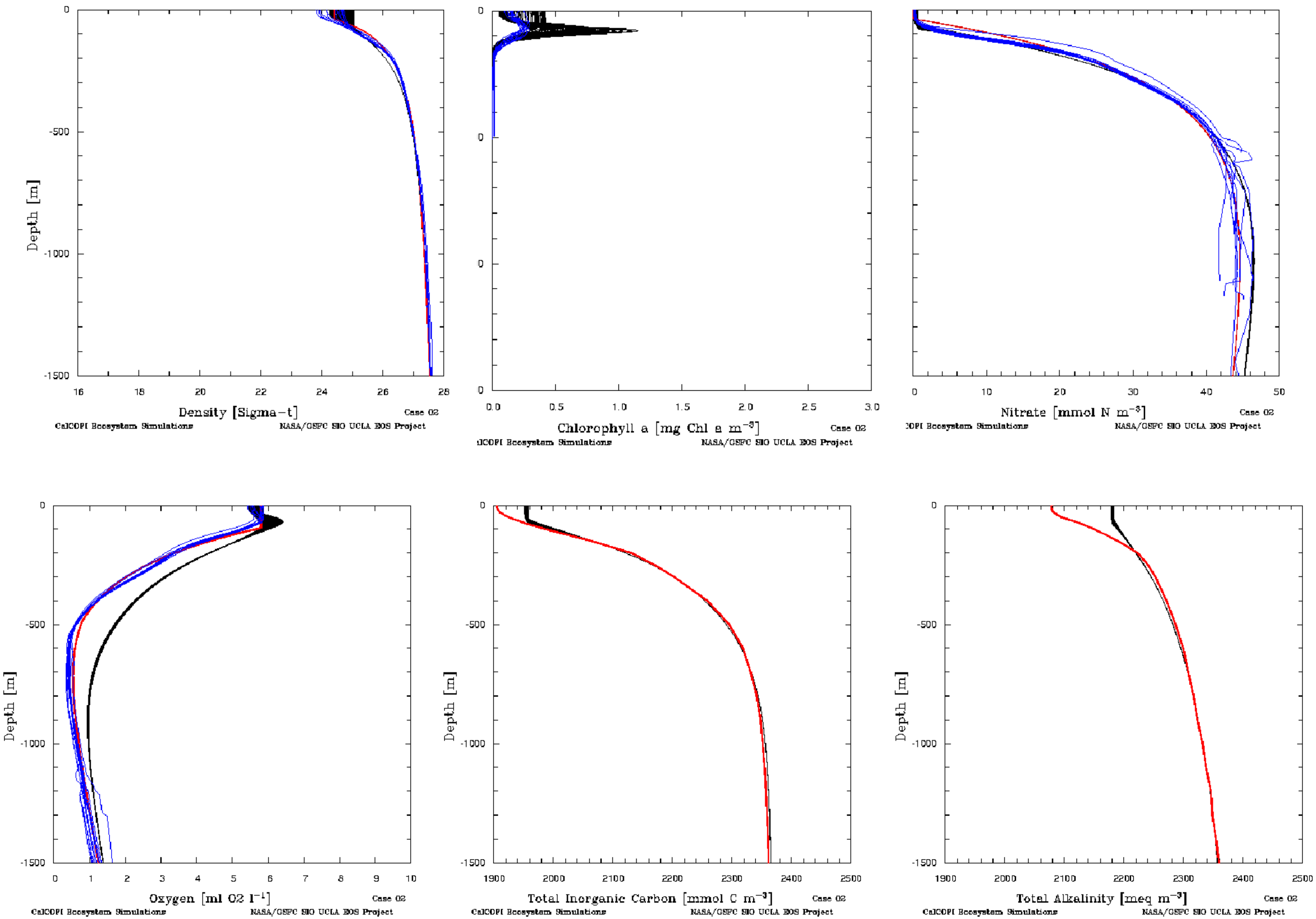
…………..

…………..

…………..

$$\frac{\partial B_N}{\partial t} + (w + w_B)\frac{\partial B_N}{\partial z} - \frac{\partial}{\partial z} K_z \frac{\partial B_N}{\partial z} = S_N$$


Model
Data
7.80 Temperature [Deg. C] 18.73
33.23 Salinity 34.03
23.80 Density [Sigma-t] 26.53
0.06 Nitrate [mmol N m^-3] 30.53
0.00 Chlor a [mg Chl a m^-3] 0.34
2.58 Oxygen [ml O2 l^-1] 5.87
A
B
C
D
E
F
G
H
I
J
K
L
Depth [m]
0 -50 -100 -150 -200 -250
0 1 2 3 4 5 6 7 8 9 10 11 12
Time [months]



Depth [m]
Density [Sigma-t]
Case 02
CalCOFI Ecosystem Simulations
NASA/GSFC SIO UCLA EOS Project
Chlorophyll a [mg Chl a m^{-3}]
Case 02
NASA/GSFC SIO UCLA EOS Project
Nitrate [mmol N m^{-3}]
Case 02
NASA/GSFC SIO UCLA EOS Project
Depth [m]
Oxygen [ml O2 l^{-1}]
Case 02
CalCOFI Ecosystem Simulations
NASA/GSFC SIO UCLA EOS Project
Depth [m]
Total Inorganic Carbon [mmol C m^{-3}]
Case 02
CalCOFI Ecosystem Simulations
NASA/GSFC SIO UCLA EOS Project
Depth [m]
Total Alkalinity [meq m^{-3}]
Case 02
CalCOFI Ecosystem Simulations
NASA/GSFC SIO UCLA EOS Project

Three Dimensional Model

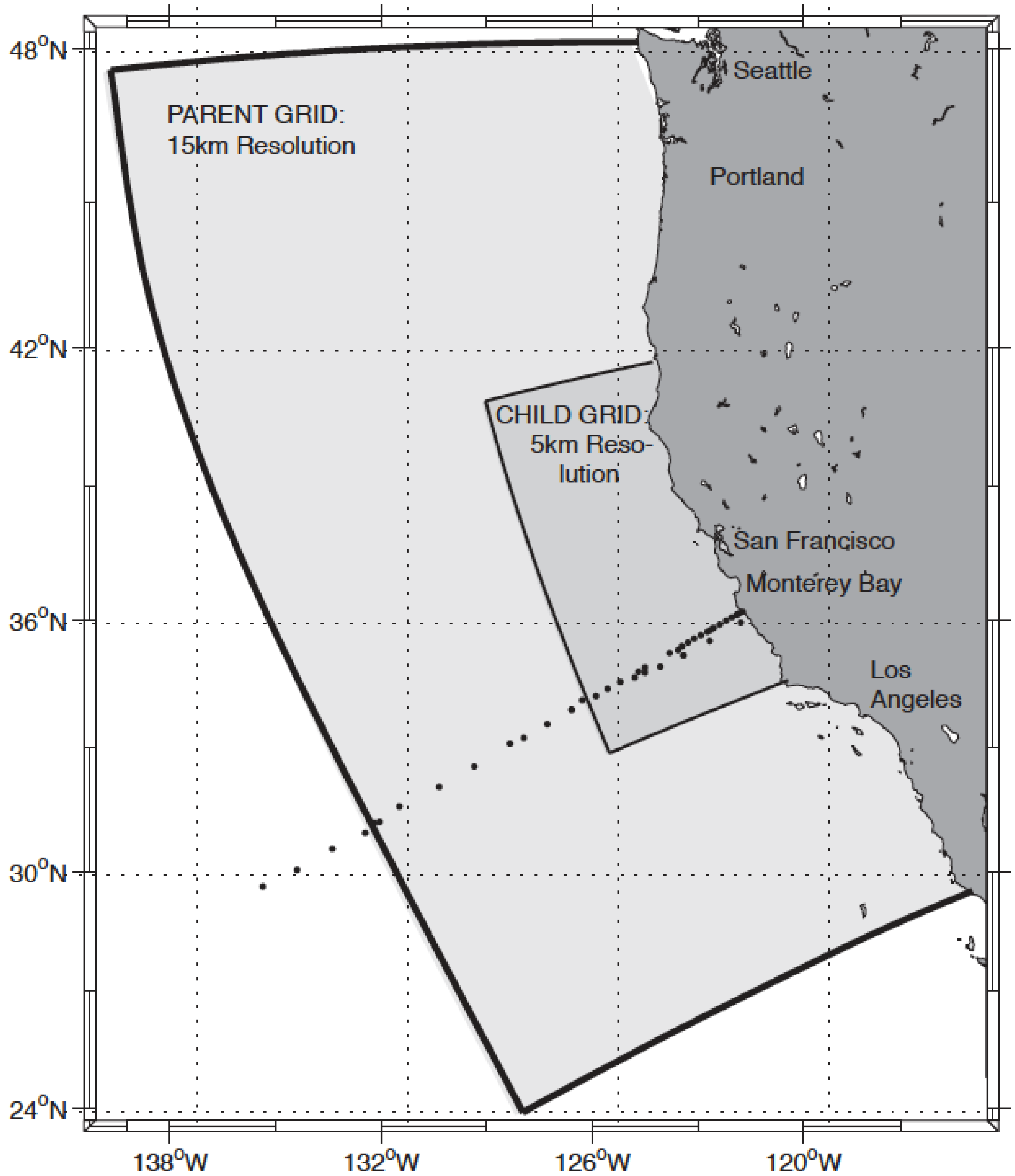
$$\frac{dB_i}{dt} + (\vec{v} + \vec{v}_B) \bullet \nabla B_i - \nabla \bullet (\vec{K} \nabla B_i) = S_i$$

....

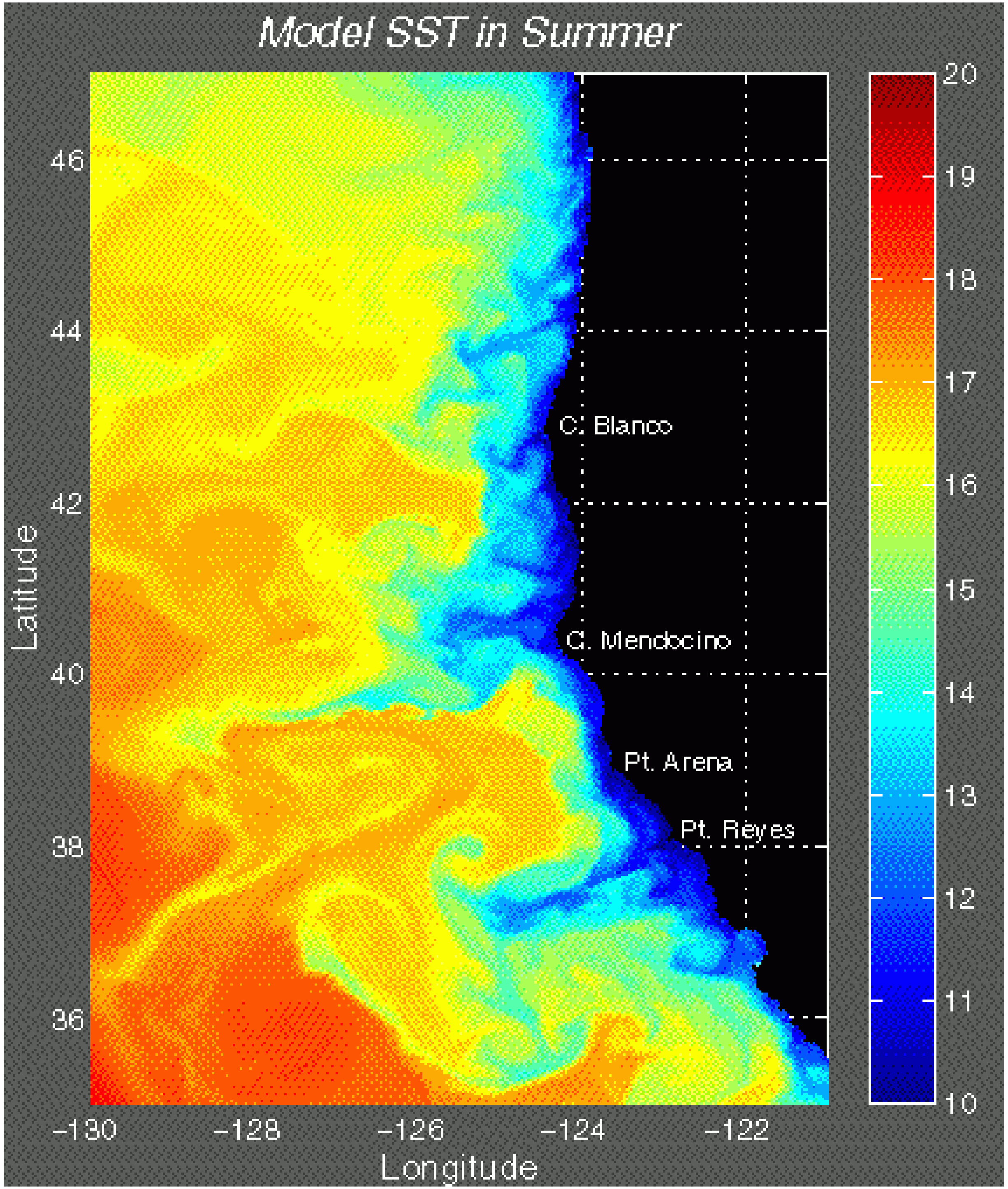
....

....

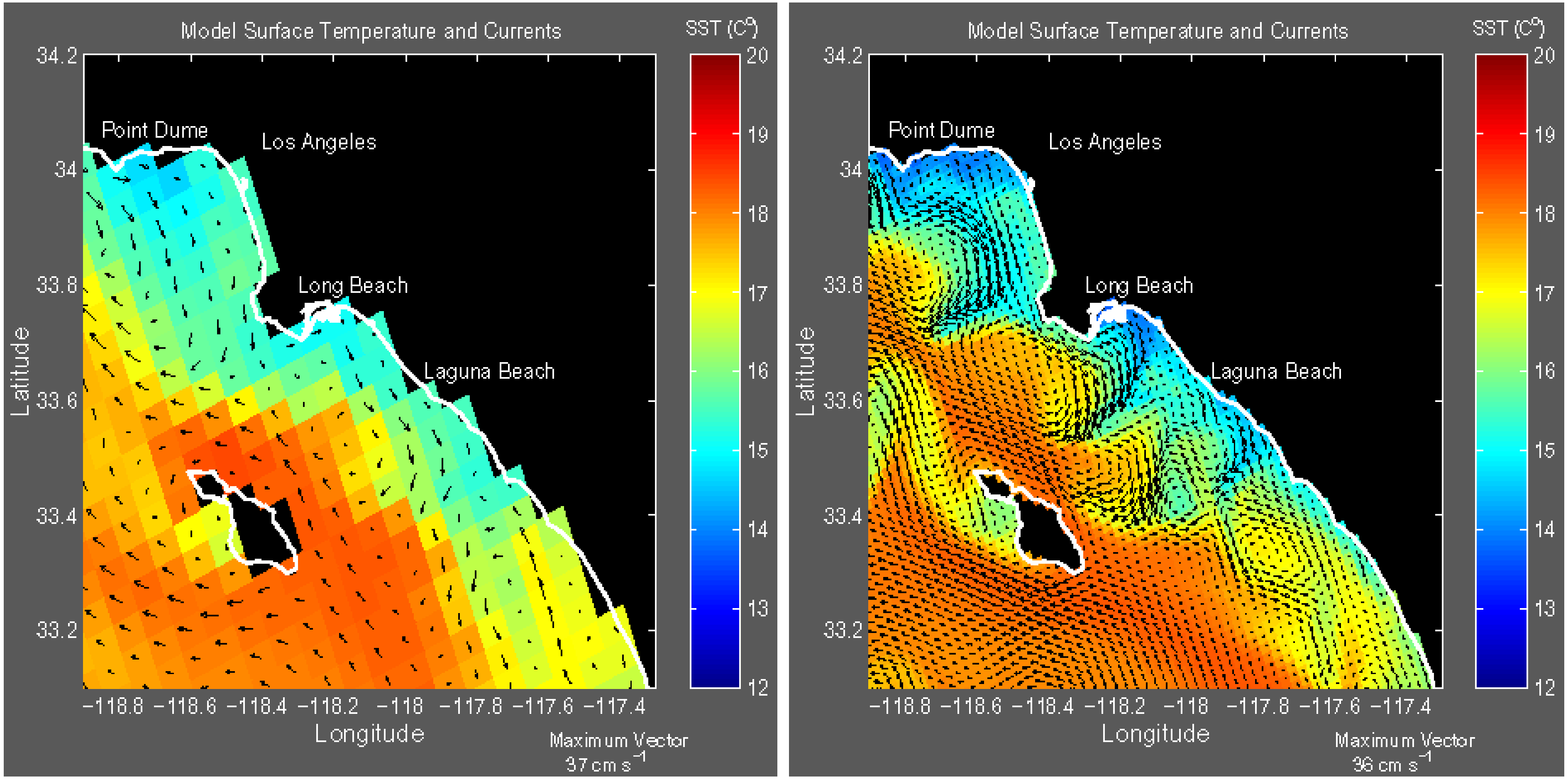
$$\frac{dB_N}{dt} + (\vec{v} + \vec{v}_B) \bullet \nabla B_N - \nabla \bullet (\vec{K} \nabla B_N) = S_N$$



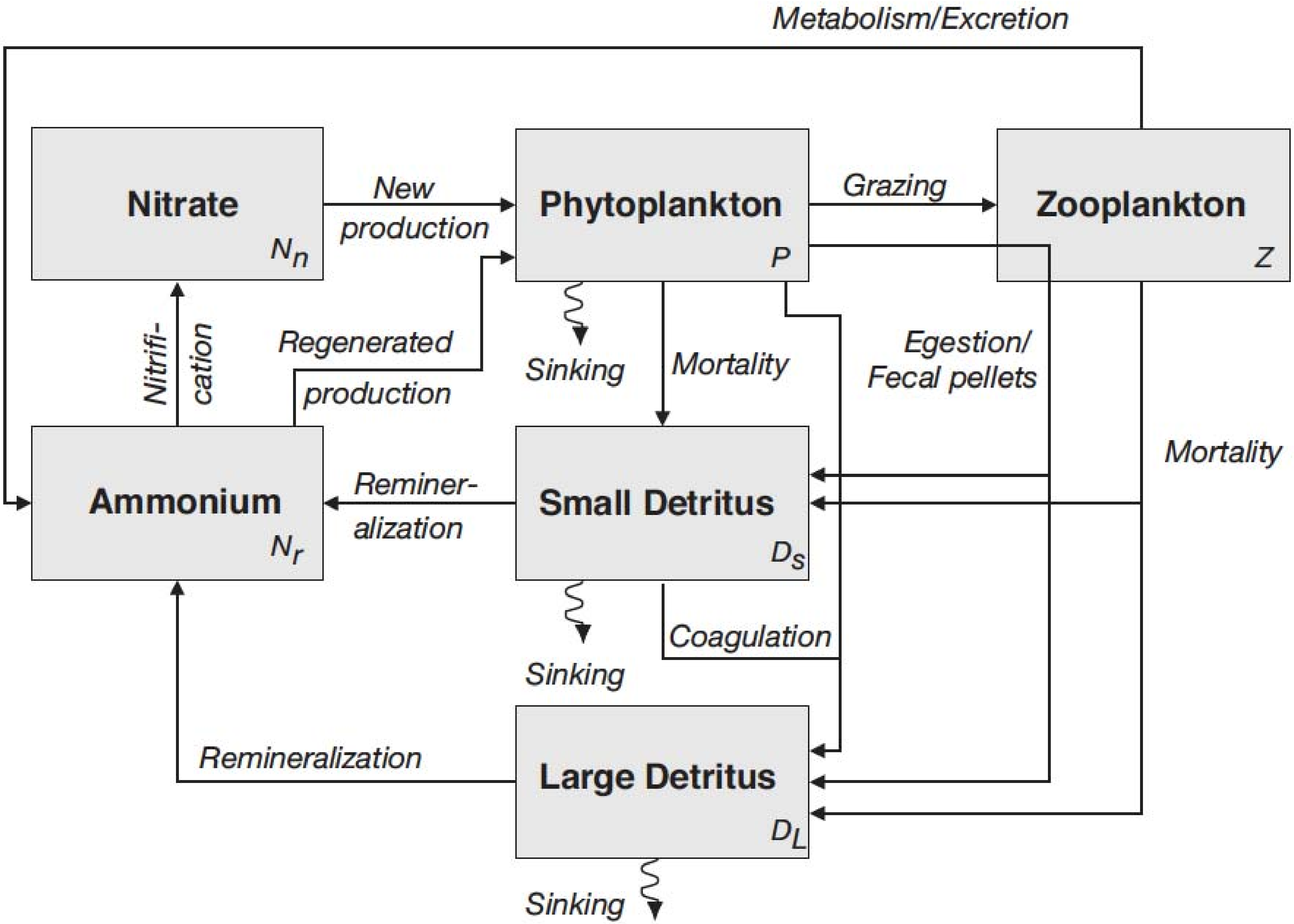
48°N
42°N
36°N
30°N
24°N
138°W
132°W
126°W
120°W
PARENT GRID:
15km Resolution
CHILD GRID:
5km Reso-
lution
Seattle
Portland
San Francisco
Monterey Bay
Los
Angeles



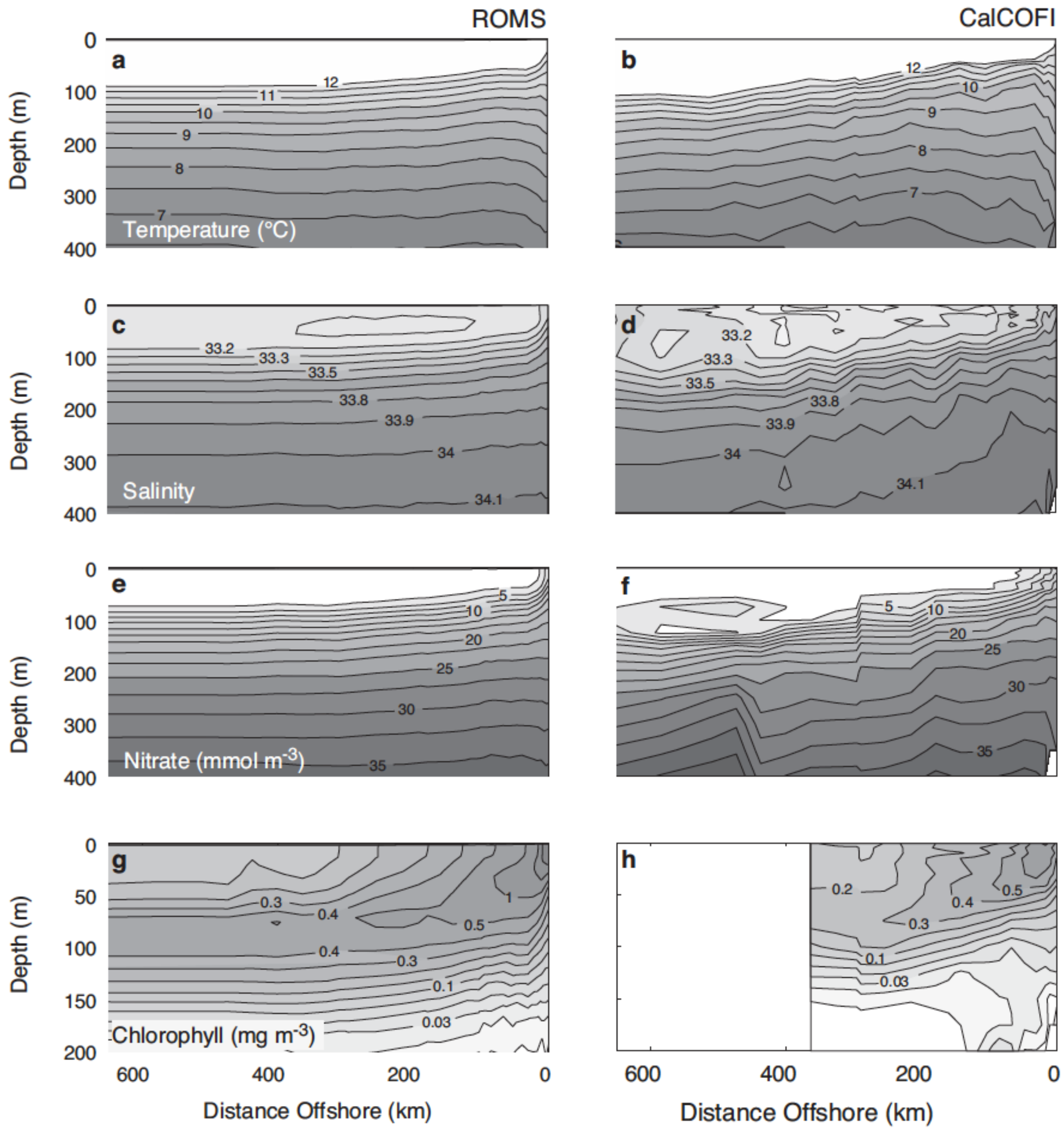
Model SST in Summer
46
44
42
40
38
36
Latitude
-130
-128
-126
-124
-122
Longitude
C. Blanco
C. Mendocino
Pt. Arena
Pt. Reyes
20
19
18
17
16
15
14
13
12
11
10



Model Surface Temperature and Currents
SST (C°)
Point Dume
Los Angeles
Long Beach
Laguna Beach
Latitude
Longitude
34.2
34
33.8
33.6
33.4
33.2
−118.8 −118.6 −118.4 −118.2 −118 −117.8 −117.6 −117.4
20
19
18
17
16
15
14
13
12
Maximum Vector
37 cm s−1
Model Surface Temperature and Currents
SST (C°)
Point Dume
Los Angeles
Long Beach
Laguna Beach
Latitude
Longitude
Maximum Vector
36 cm s−1

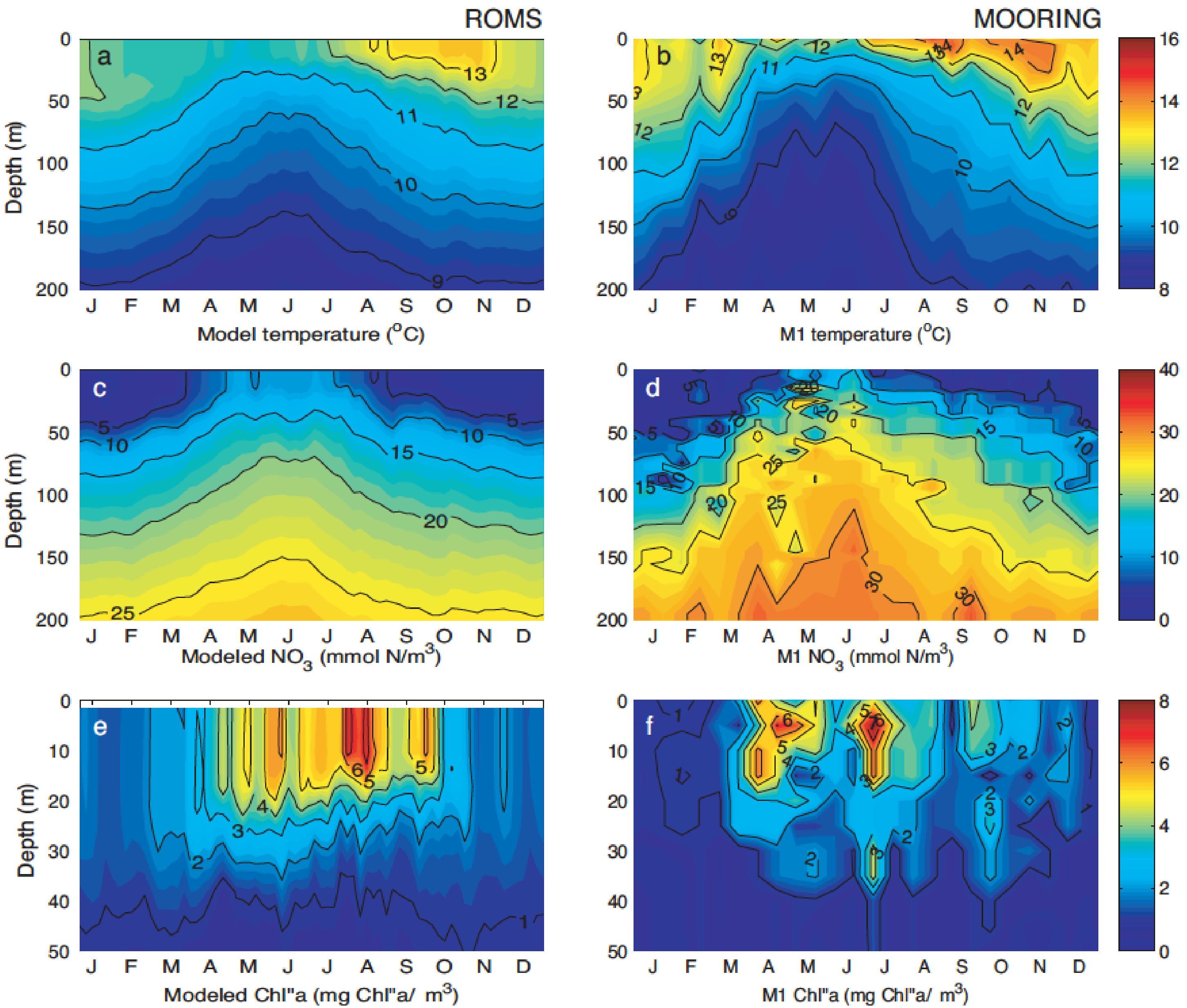


Metabolism/Excretion
Nitrate
N_n
New
production
Phytoplankton
P
Grazing
Zooplankton
Z
Nitrifi-
cation
Regenerated
production
Sinking
Mortality
Egestion/
Fecal pellets
Mortality
Ammonium
N_r
Reminer-
alization
Small Detritus
D_S
Sinking
Coagulation
Remineralization
Large Detritus
D_L
Sinking

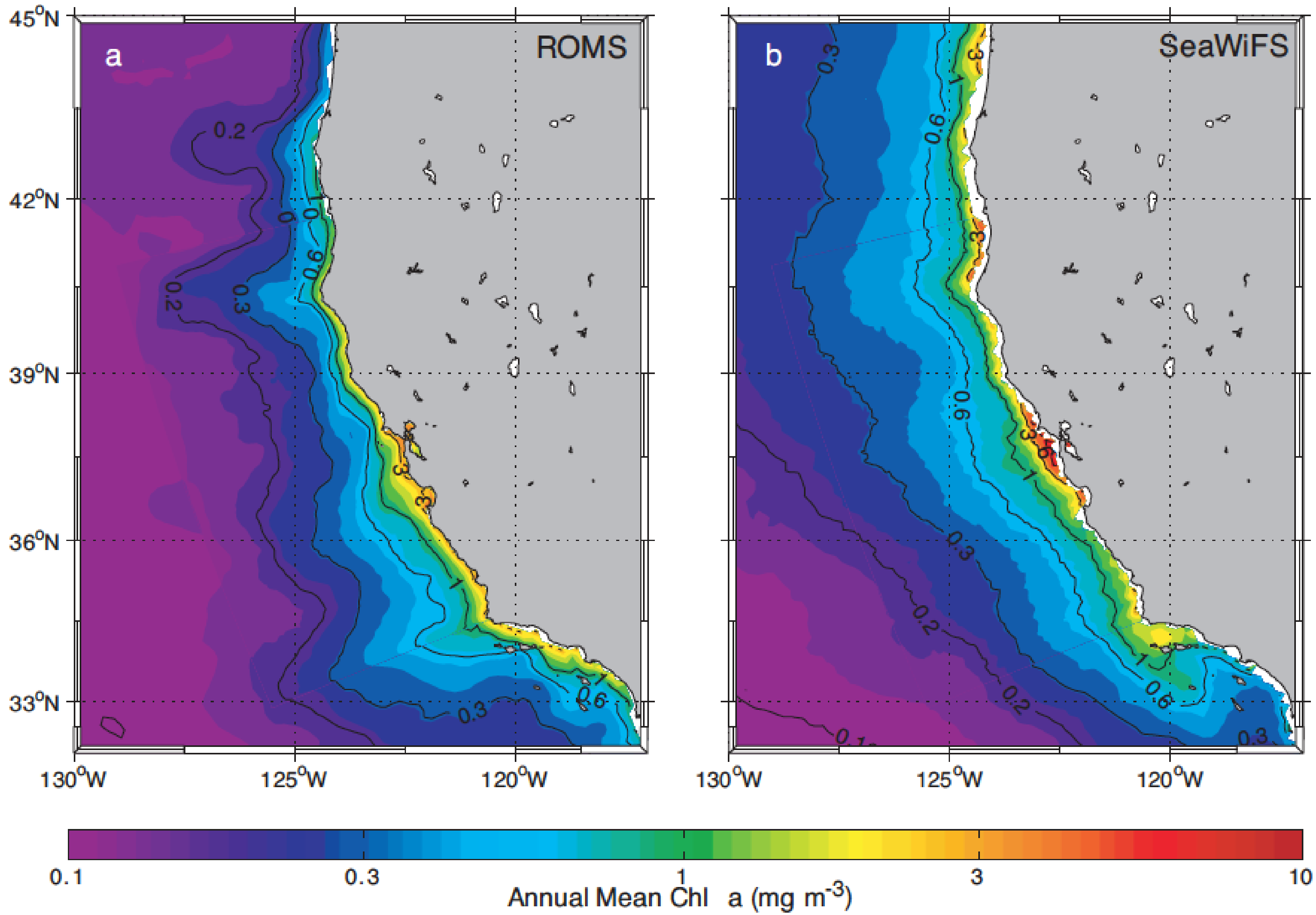


Comparison of vertical section along Line-70 of CalCOFI

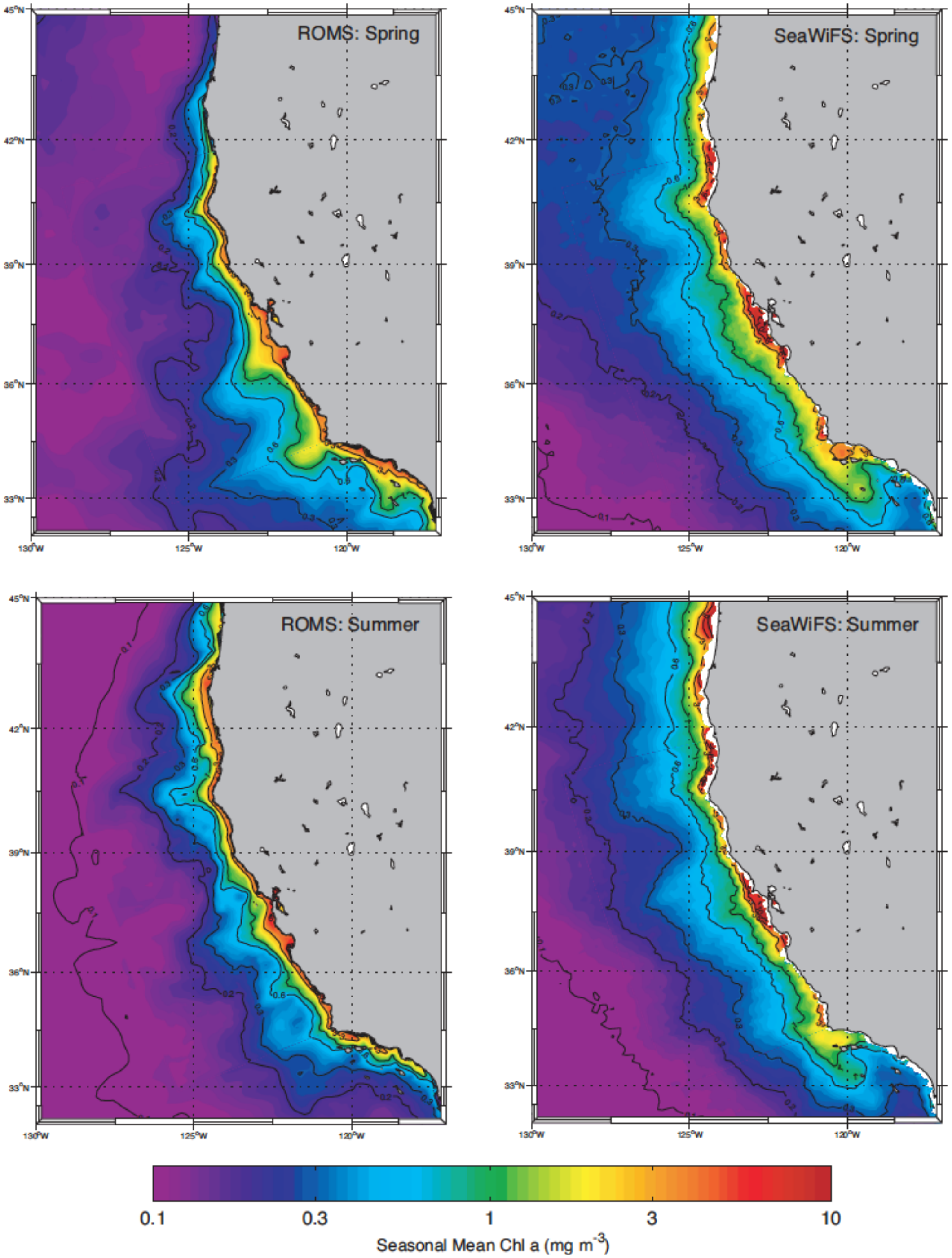
Line 90 CalCOFI

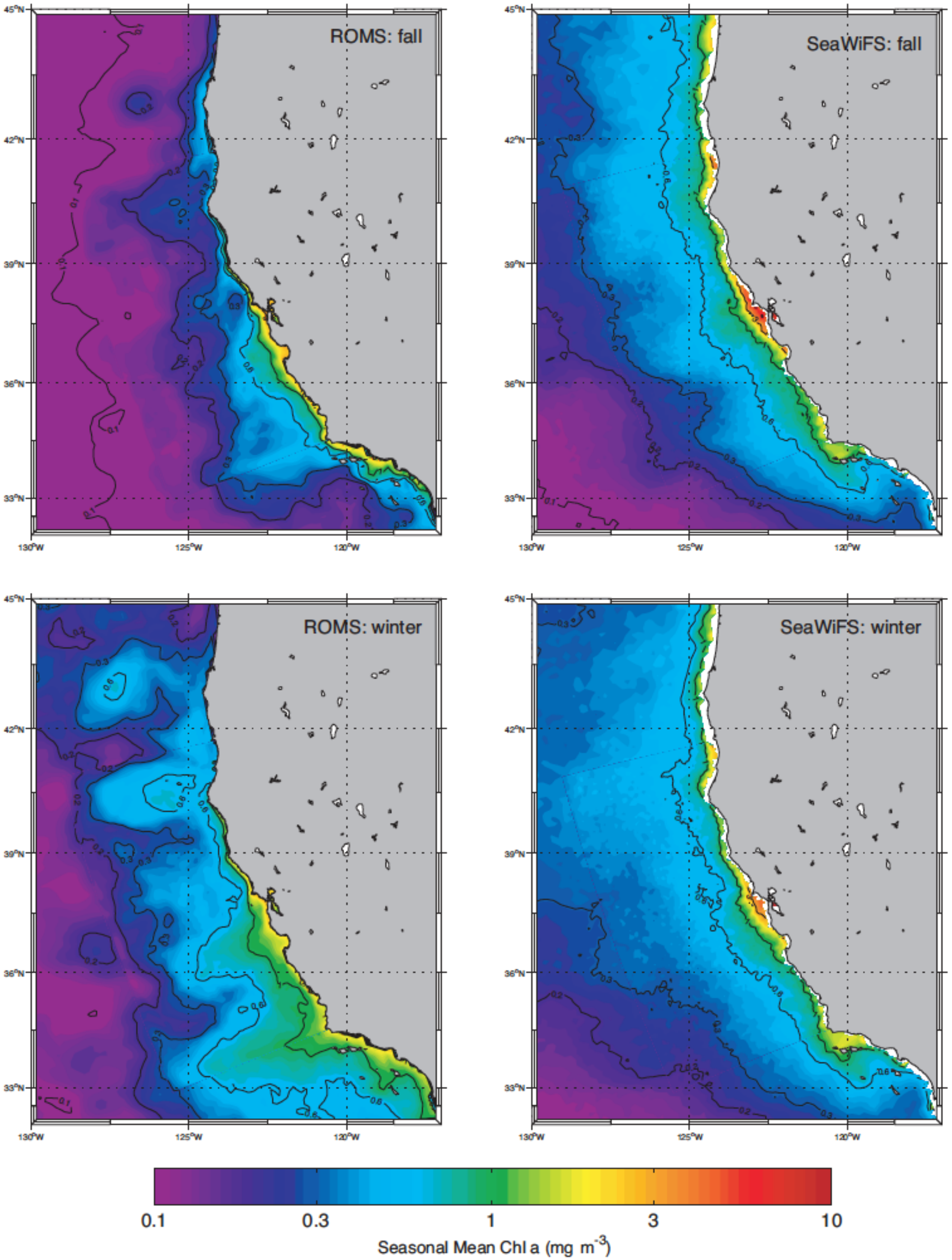


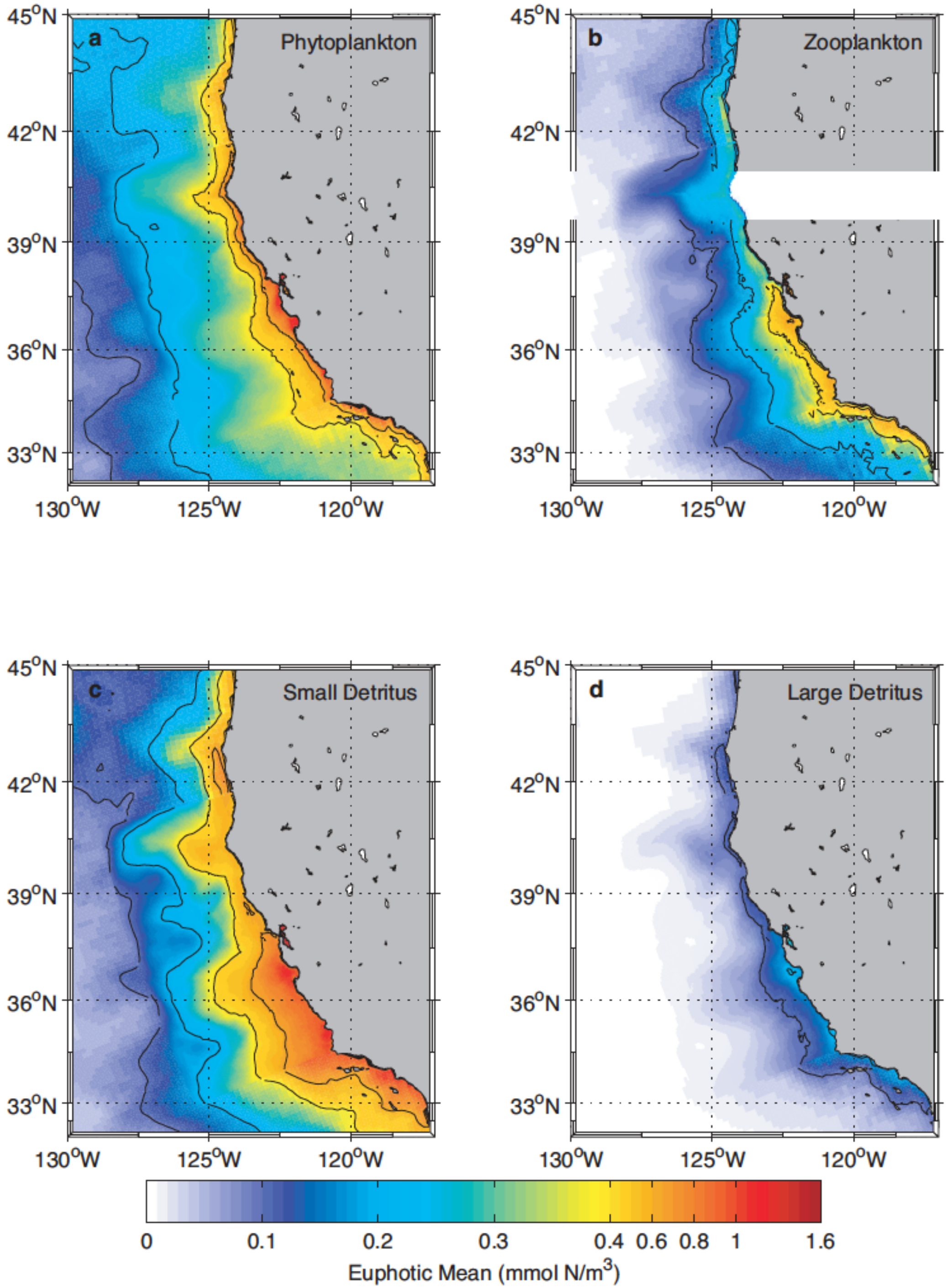
Comparison of the modeled and observed climatological annual cycle of temperature, Nitrate, and chlorophyll at the M1/H3 mooring site in Monterey Bay



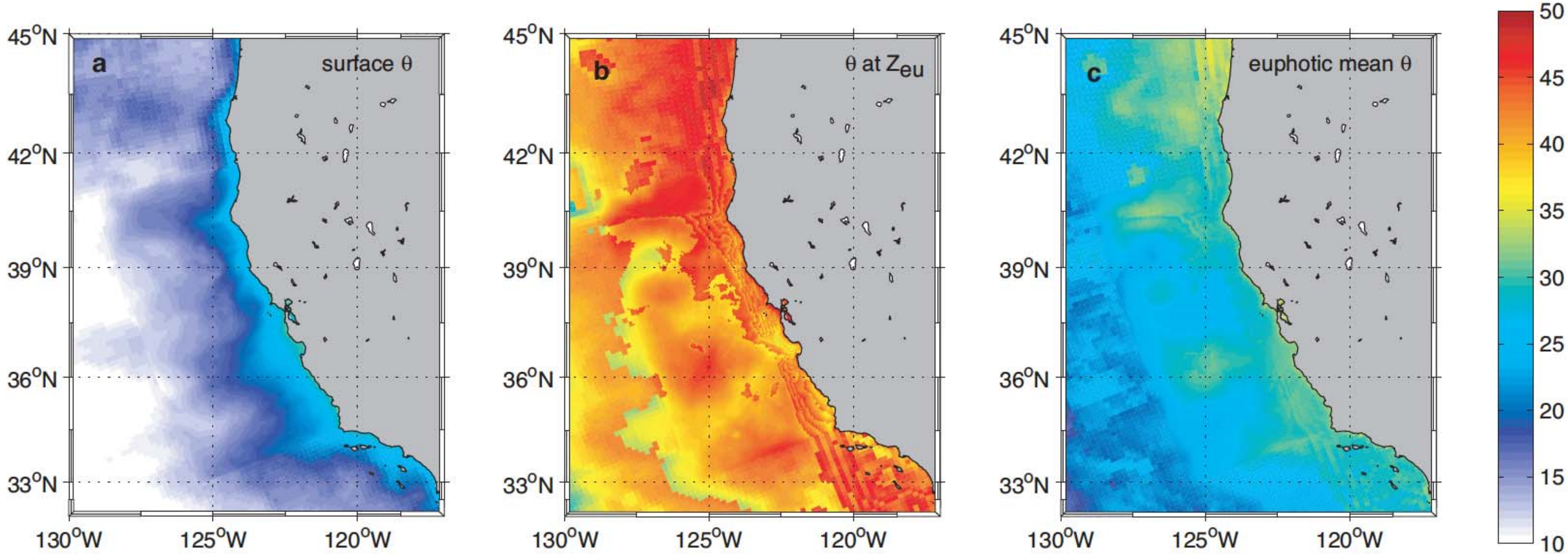
Comparison of (a) observed and (b) modeled annual mean chlorophyll concentraiton in The near surface waters. The observations are based on SeaWiFS, averaged over the period from 1997 to 2002. The model fields are averages of the surface fields.


ROMS: Spring
SeaWiFS: Spring
ROMS: Summer
SeaWiFS: Summer
0.1
0.3
1
3
10
Seasonal Mean Chl a (mg m-3)

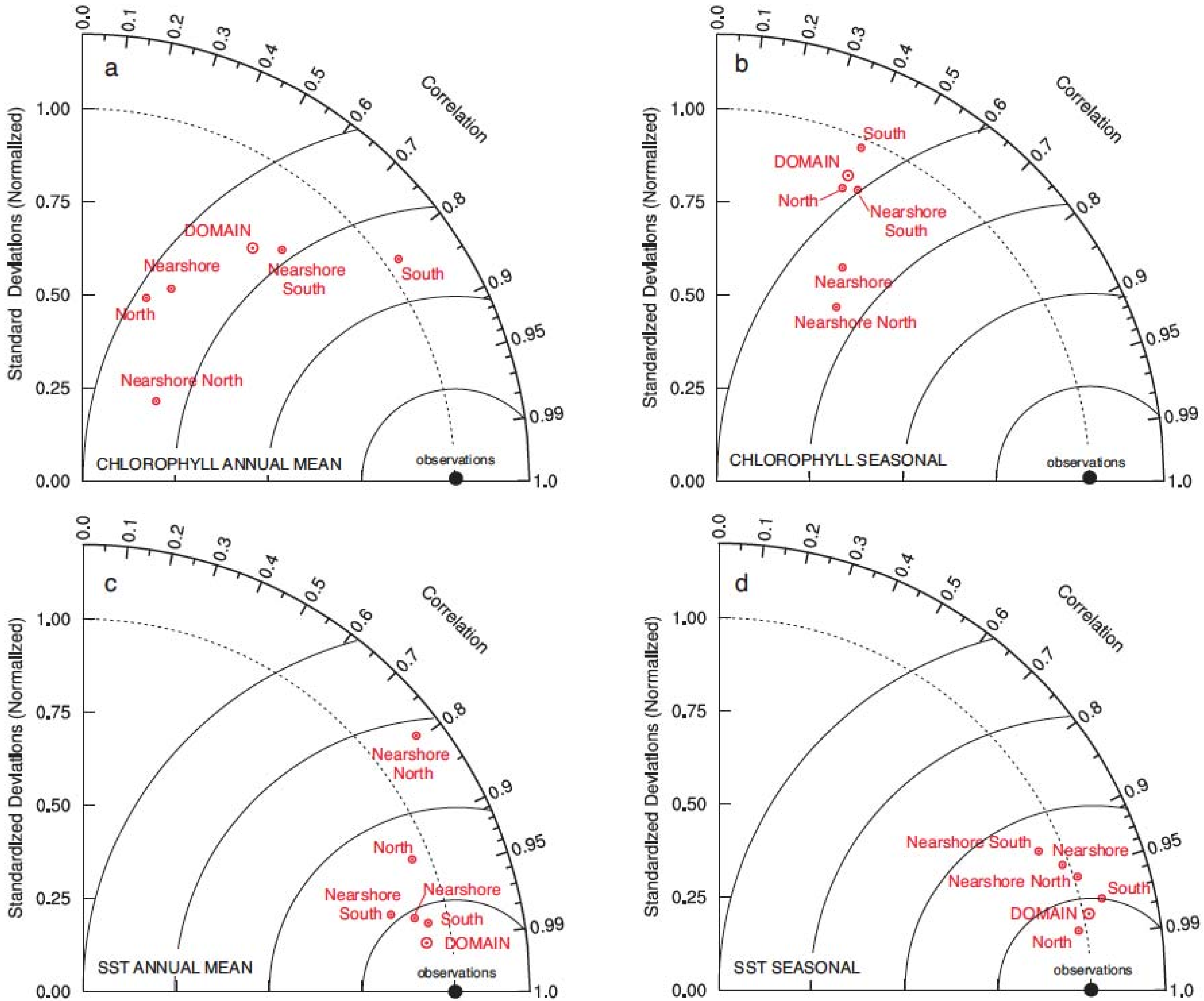

ROMS: fall
SeaWiFS: fall
ROMS: winter
SeaWiFS: winter
45°N
42°N
39°N
36°N
33°N
130°W
125°W
120°W
0.1
0.3
1
3
10
Seasonal Mean Chl a (mg m-3)



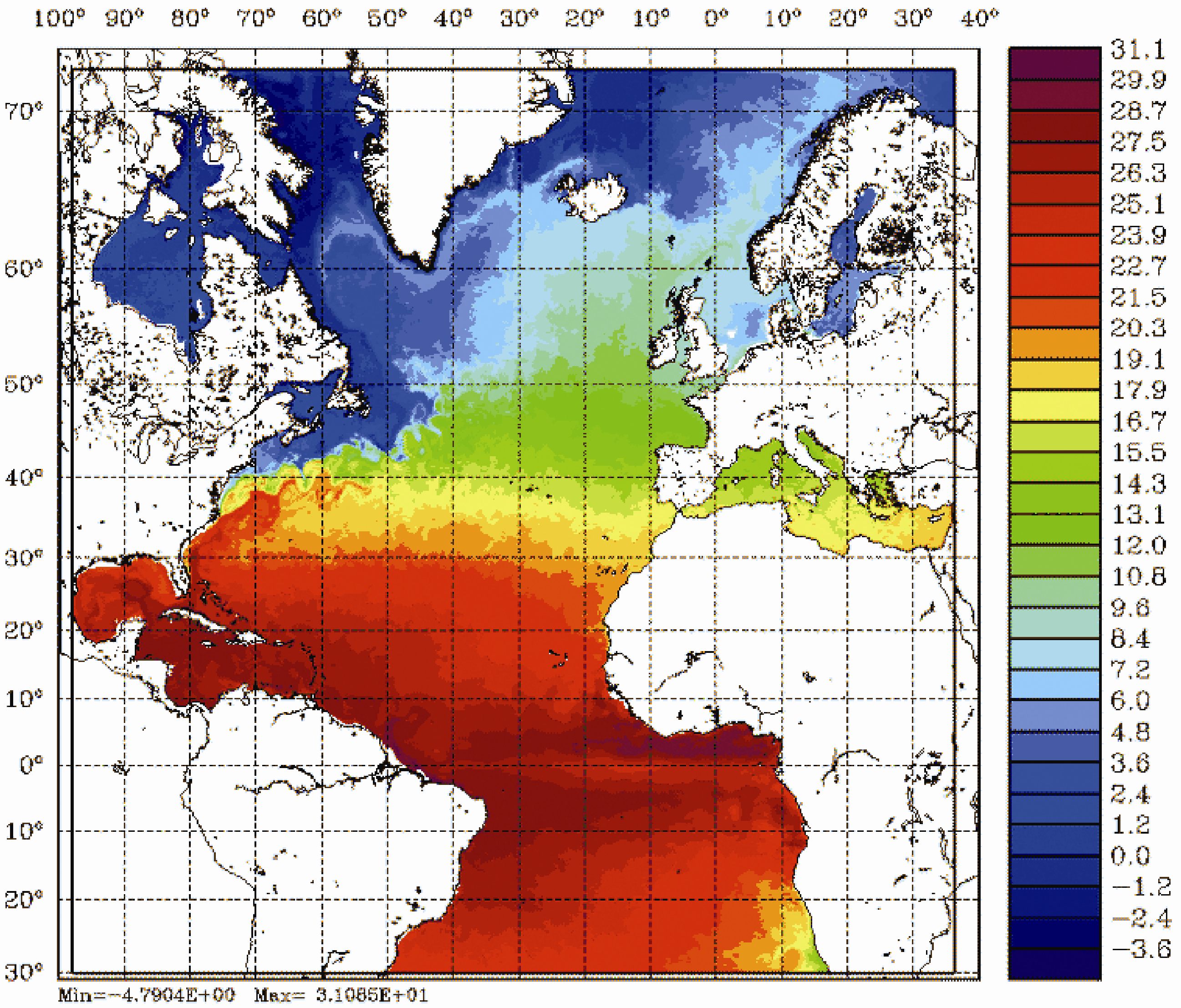
a
Phytoplankton
b
Zooplankton
c
Small Detritus
d
Large Detritus
45°N
42°N
39°N
36°N
33°N
130°W
125°W
120°W
0
0.1
0.2
0.3
0.4
0.6
0.8
1
1.6
Euphotic Mean (mmol N/m³)



Maps of the chlorophyll-to-carbon ratio [ugchl (mg C)$^{-1}$

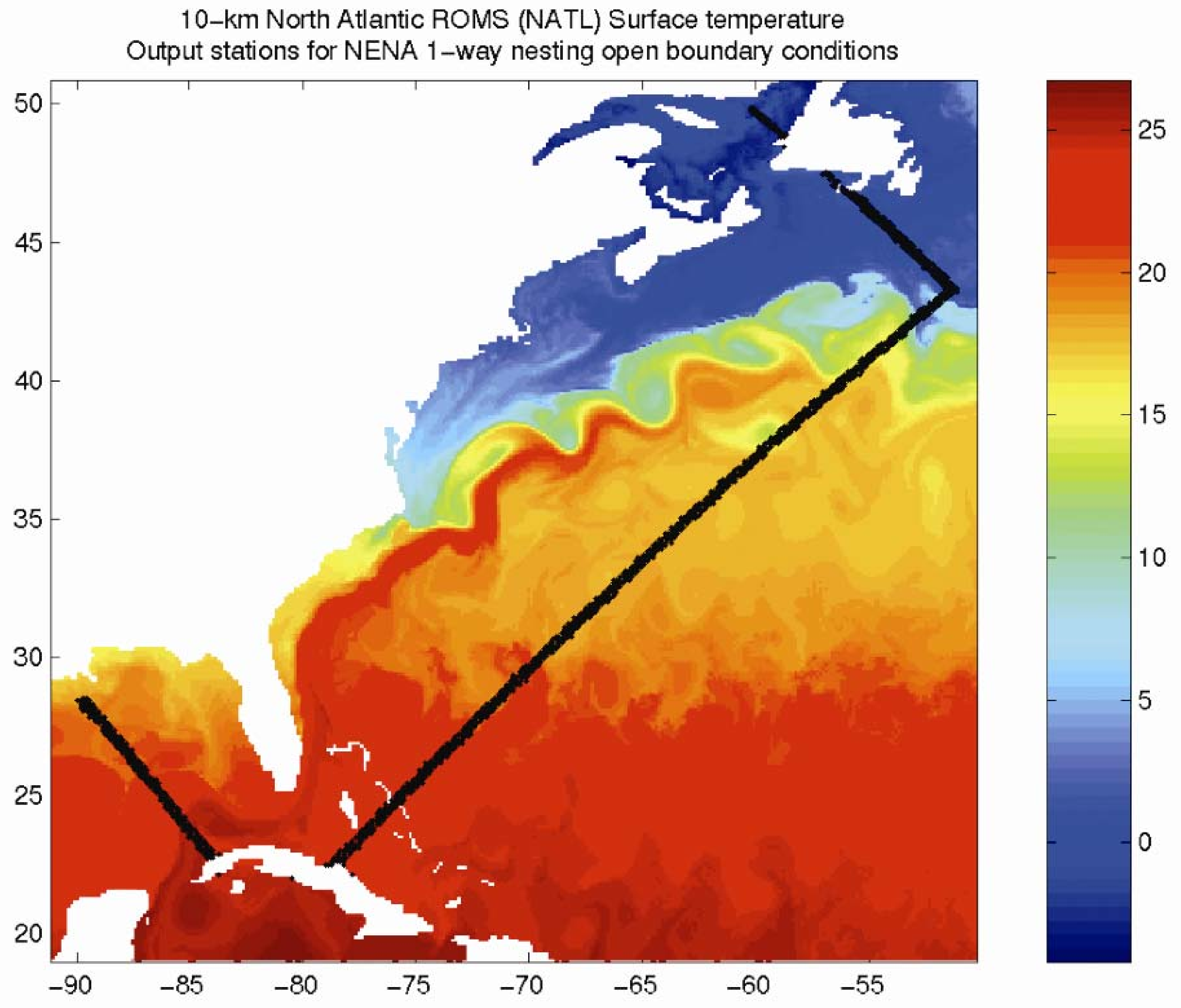


a
CHLOROPHYLL ANNUAL MEAN
b
CHLOROPHYLL SEASONAL
c
SST ANNUAL MEAN
d
SST SEASONAL
Correlation
Standard Deviations (Normalized)
Standardized Deviations (Normalized)
observations
DOMAIN
North
South
Nearshore
Nearshore North
Nearshore South

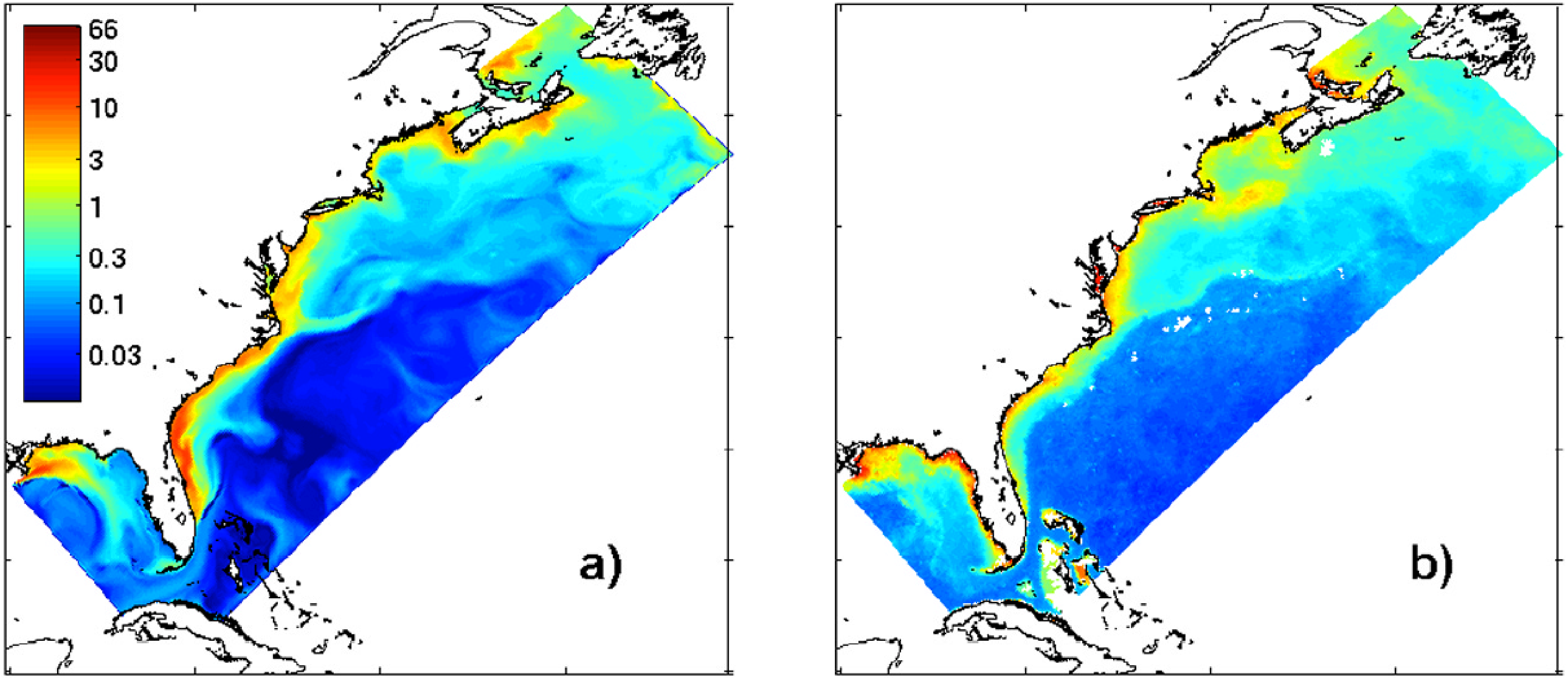


100° 90° 80° 70° 60° 50° 40° 30° 20° 10° 0° 10° 20° 30° 40°
70°
60°
50°
40°
30°
20°
10°
0°
10°
20°
30°
31.1
29.9
28.7
27.5
26.3
25.1
23.9
22.7
21.5
20.3
19.1
17.9
16.7
15.5
14.3
13.1
12.0
10.8
9.6
8.4
7.2
6.0
4.8
3.6
2.4
1.2
0.0
−1.2
−2.4
−3.6
Min=−4.7904E+00 Max= 3.1085E+01

133.00 Day

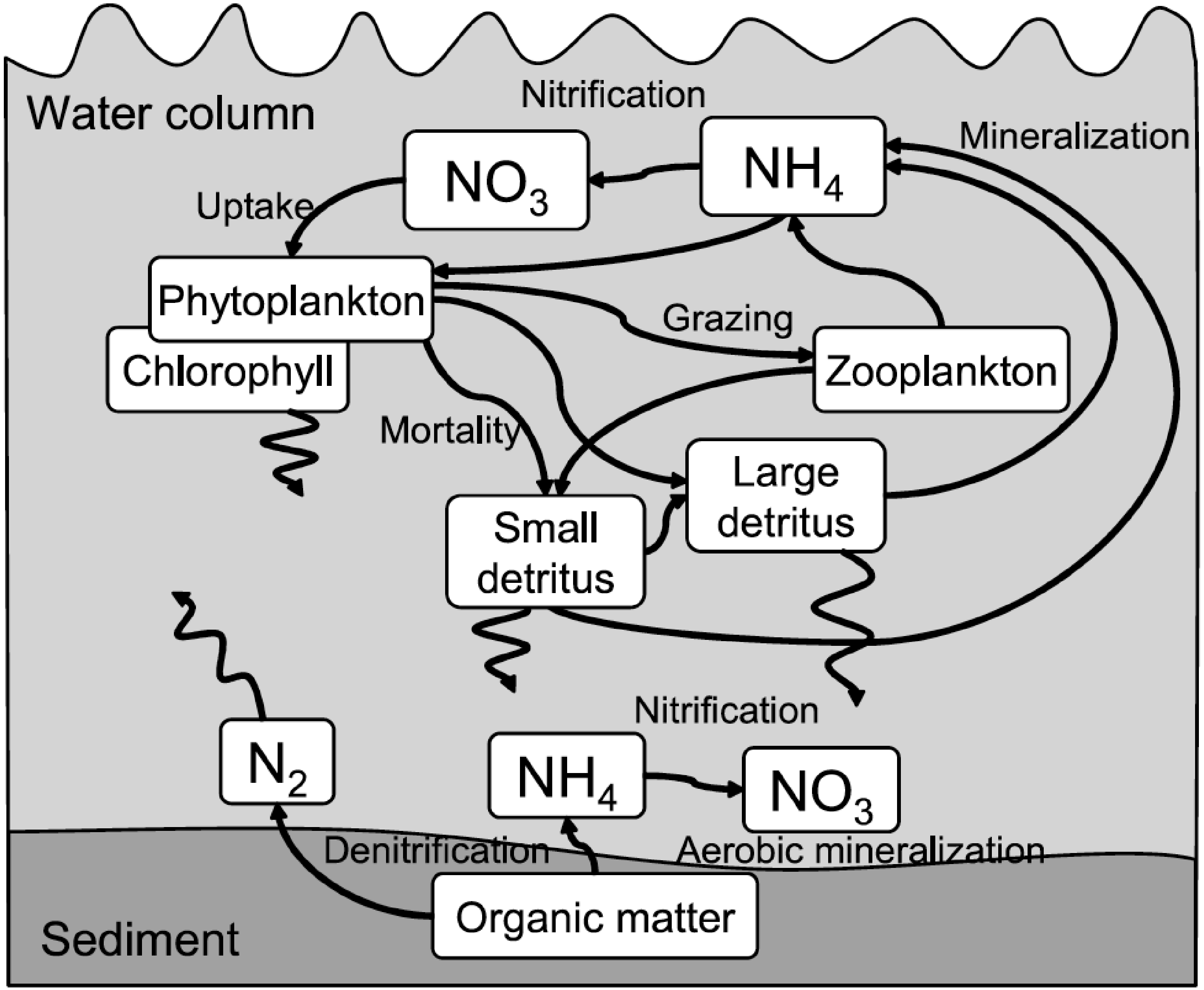

10–km North Atlantic ROMS (NATL) Surface temperature
Output stations for NENA 1–way nesting open boundary conditions
50
45
40
35
30
25
20
−90
−85
−80
−75
−70
−65
−60
−55
25
20
15
10
5
0

Citation: Fennel, K., J. Wilkin, J. Levin, J. Moisan, J. O'Reilly, and D. Haidvogel (2006), Nitrogen cycling in the Middle Atlantic Bight: Results from a three-dimensional model and implications for the North Atlantic nitrogen budget, Global Biogeochem. Cycles, 20, GB3007, doi:10.1029/2005GB002456.

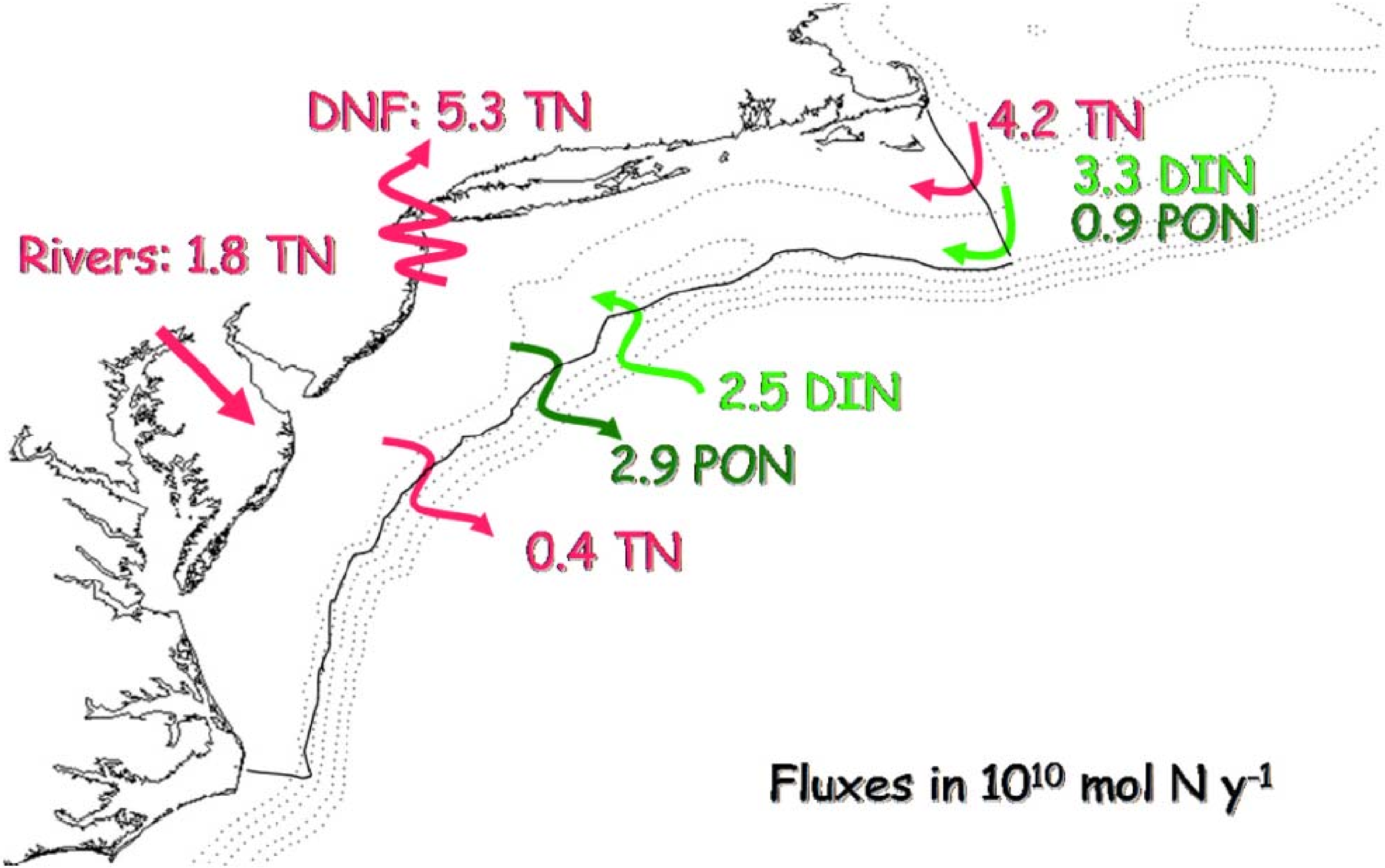


(a) Model-simulated mean surface chlorophyll for July of 1994 and
(b) SeaWiFS mean chlorophyll for July of 2003 (same color scale)

Biological Model Schematic



Nitrogen Budget for the Mid-Atlantic Bight



State-of-the-Art in GBC Modeling:

•Develop the ecosystem model equations (a subjective effort)

•Fit the model solution to observations by using data assimilation (DA) in a 1D-mode to tune the model's parameter set

•Run the model in 3D-mode with fit parameters from 1D DA

[in practice, most models run in an Nx1D configuration]

An example of the various 'parameter sets' obtained from fitting an ecosystem model to observations using 12 different DA schemes

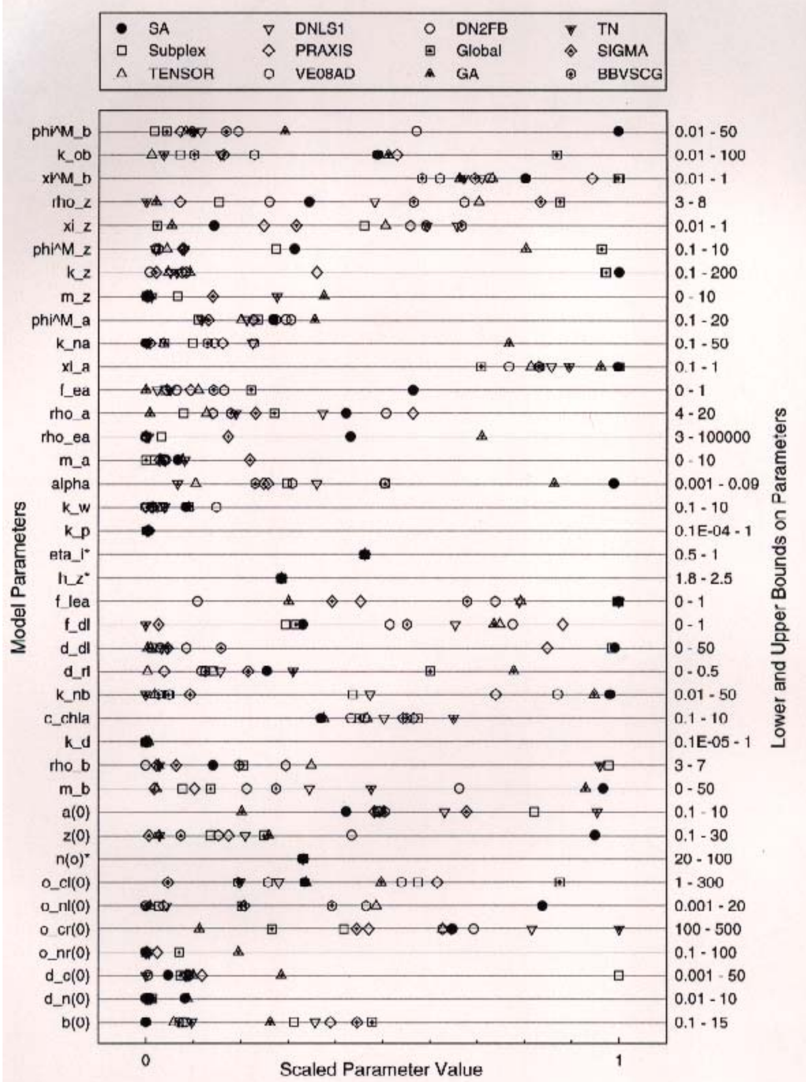


Fig. 5., Vallino, J.J.

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Ecological Modelling 000 (2002) 000–000

ECOLOGICAL MODELLING

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Modelling the effect of temperature on the maximum growth rates of phytoplankton populations

John R. Moisan [a,*], Tiffany A. Moisan [a,1], Mark R. Abbott [b,2]

[a] *Laboratory for Hydrospheric Processes, NASA/GSFC Wallops Flight Facility, Wallops Island, VA 23337-5099, USA*
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Received 3 January 2001; received in revised form 28 November 2001; accepted 20 December 2001

Abstract

Functional relationships which parameterize growth based on the Eppley temperature relationship for phytoplankton maximal growth rates are increasingly being used in marine and freshwater ecosystem models. In this paper, we demonstrate the effect of using such generalized relationships in modelling studies. Two suites of numerical experiments are carried out to investigate the sensitivity of models to generalized growth relationships. In each experiment, 100 individual species or groups of phytoplankton are allowed to compete under a variety of growth versus temperature relationships. One suite of experiments is carried out within a simple 'chemostat' type model that is forced with seasonally varying temperature and photosynthetically available radiation (PAR) fields. A second suite of experiments is carried out using a biogeochemical mixed-layer model to demonstrate the sensitivity of these models to various temperature versus growth relationships. The key difference in the biogeochemical mixed-layer simulations is in the timing of the ecosystem response to seasonal variability of the mixed-layer depth and temperature. The Eppley growth versus temperature relationship overestimates phytoplankton growth by as much as 80% during the spring when growth rates are crucial to the timing of the spring blooms. This decrease in growth rates causes a delay in the spring phytoplankton bloom which in turn results in significant changes in all other model constituents. The results from both suites of experiments show that it is important to resolve the intrinsic growth dynamics of a population in order to properly resolve the maximum growth rates of phytoplankton populations. The results also present a possible explanation for why phytoplankton are commonly found growing within water colder than their optimal temperature for growth. A dynamic growth versus temperature model is introduced that is capable of resolving the growth dynamics of a population of phytoplankton under a variety of temperature forcing scenarios. This new growth versus temperature model/relationship will be useful in global biogeochemical models and demonstrates the importance of underlying population dynamics in controlling bulk community growth estimates.
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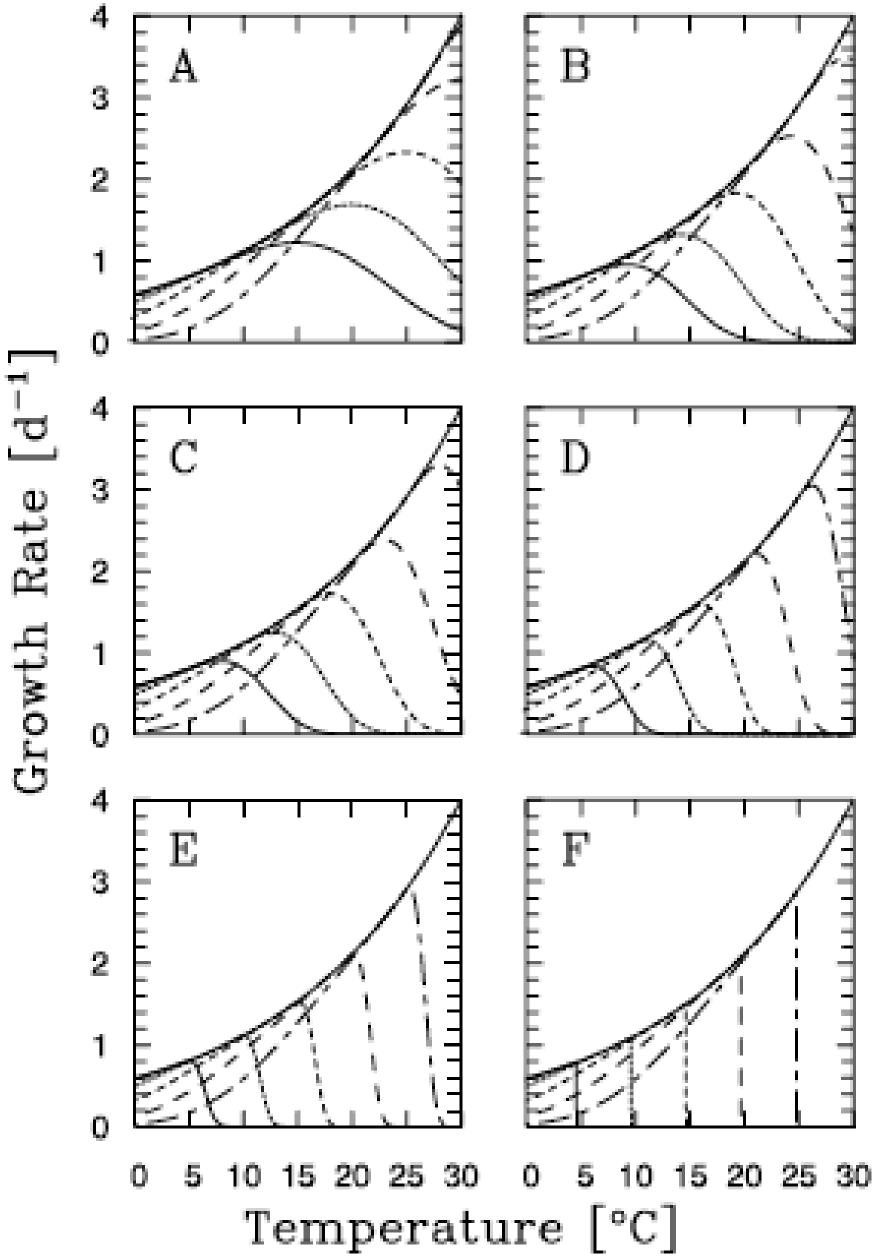
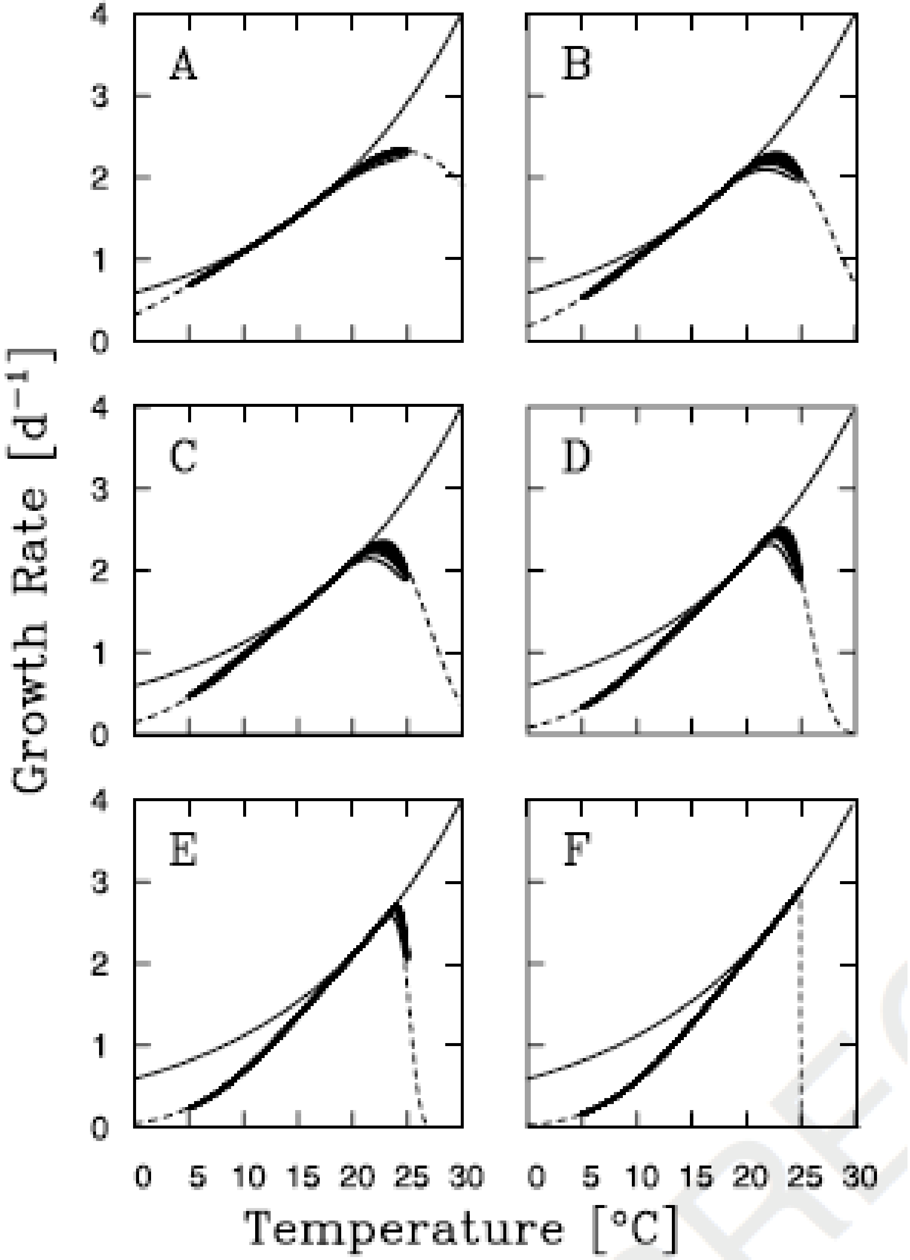
Keywords: Phytoplankton; Temperature; Maximum growth rate; Population

UNCORRECTED PROOF


A
B
C
D
E
F
Growth Rate [d⁻¹]
Temperature [°C]


A
B
C
D
E
F
Growth Rate [d⁻¹]
Temperature [°C]

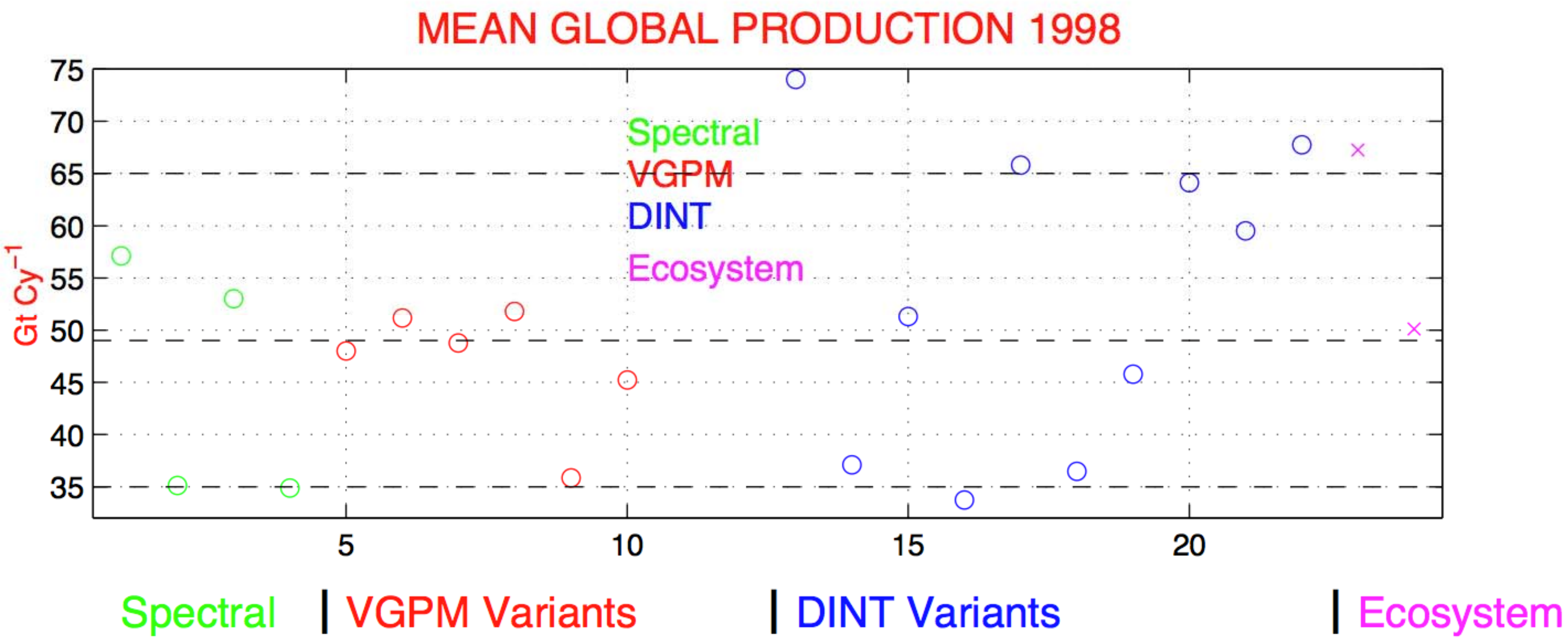


Figure from Carr et al.,

SCIENCE VOL 315 30 MARCH 2007

Emergent Biogeography of Microbial Communities in a Model Ocean

Michael J. Follows,[1*] Stephanie Dutkiewicz,[1] Scott Grant,[1,2] Sallie W. Chisholm[3]

A marine ecosystem model seeded with many phytoplankton types, whose physiological traits were randomly assigned from ranges defined by field and laboratory data, generated an emergent community structure and biogeography consistent with observed global phytoplankton distributions. The modeled organisms included types analogous to the marine cyanobacterium *Prochlorococcus*. Their emergent global distributions and physiological properties simultaneously correspond to observations. This flexible representation of community structure can be used to explore relations between ecosystems, biogeochemical cycles, and climate change.

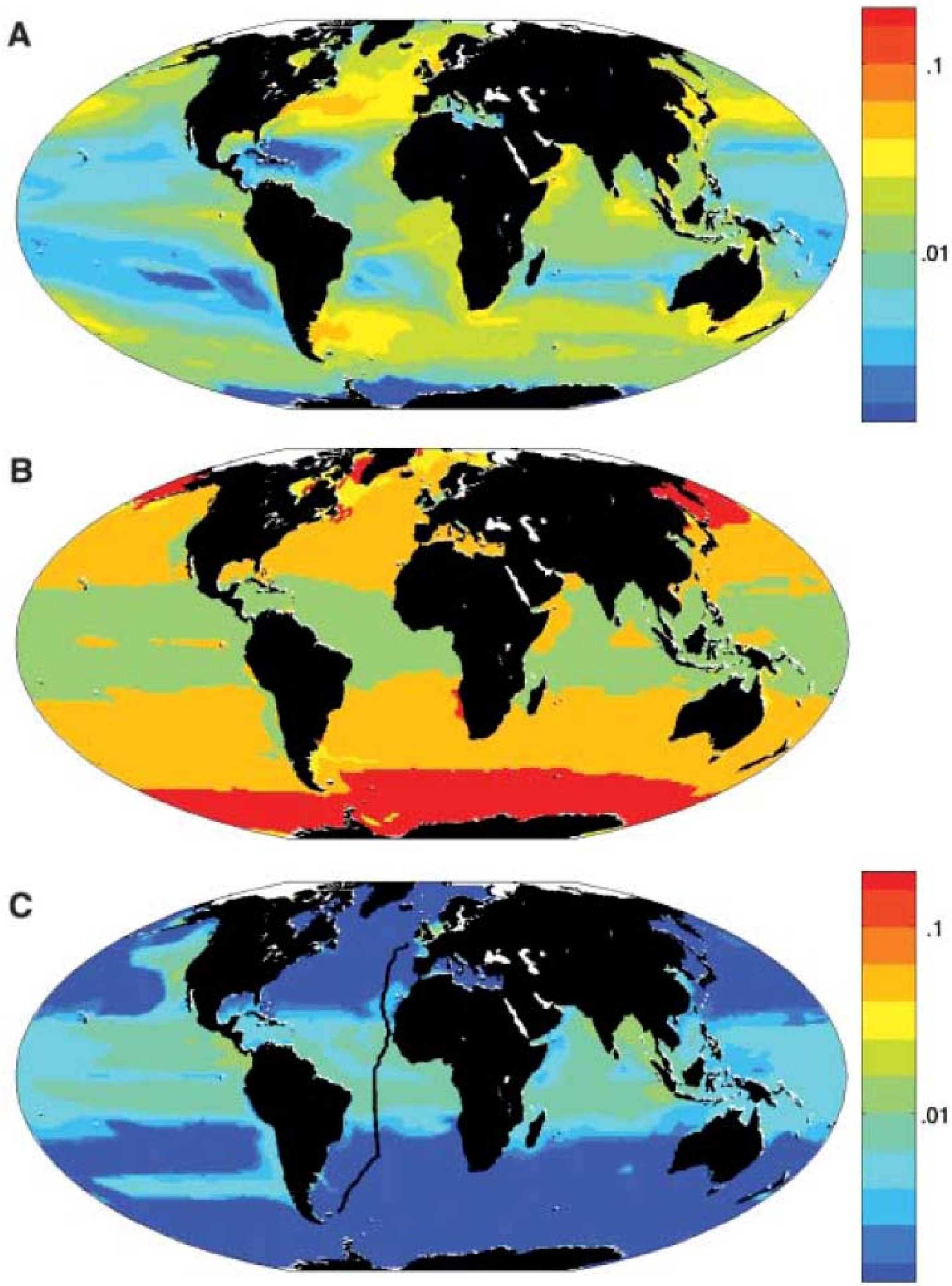
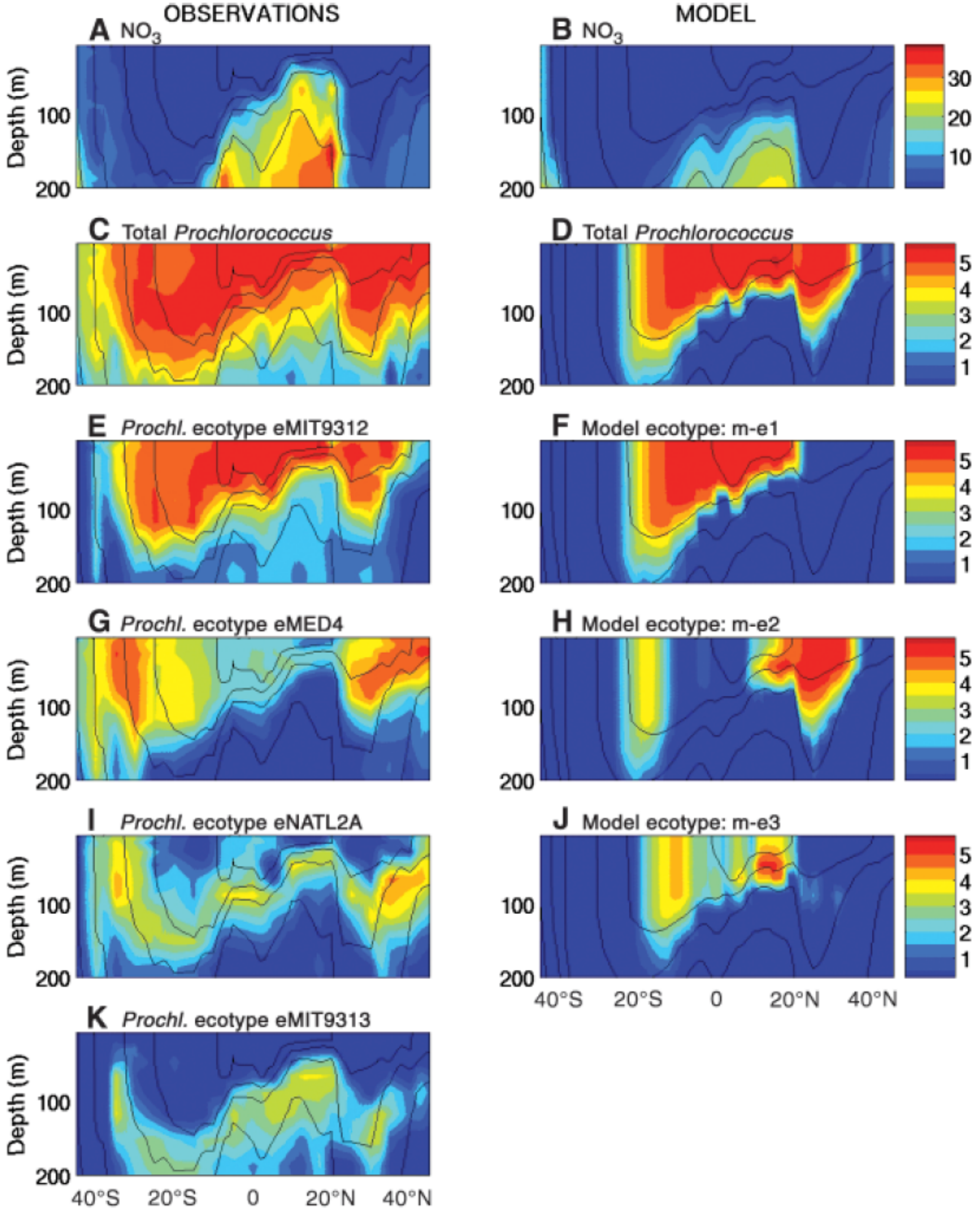
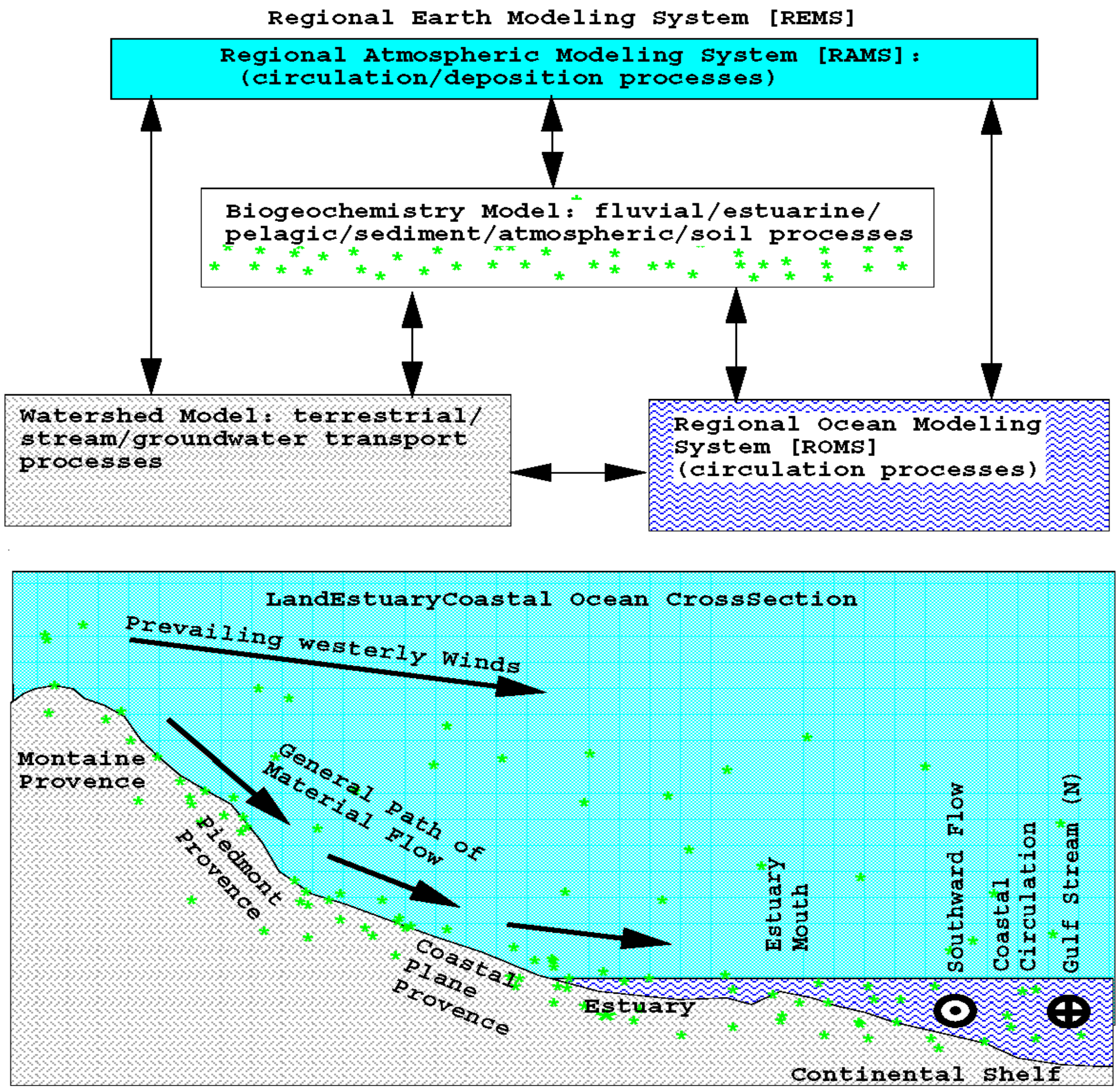


Fig. 1. Annual mean biomass and biogeography from single integration. (**A**) Total phytoplankton biomass (μM P, 0 to 50 m average). (**B**) Emergent biogeography: Modeled photo-autotrophs were categorized into four functional groups; color coding is according to group locally dominating annual mean biomass. Green, analogs of *Prochlorococcus*; orange, other small photo-autotrophs; red, diatoms; and yellow, other large phytoplankton. (**C**) Total biomass of *Prochlorococcus* analogs (μM P, 0 to 50 m average). Black line indicates the track of AMT13.



OBSERVATIONS
MODEL
A NO3
B NO3
C Total Prochlorococcus
D Total Prochlorococcus
E Prochl. ecotype eMIT9312
F Model ecotype: m-e1
G Prochl. ecotype eMED4
H Model ecotype: m-e2
I Prochl. ecotype eNATL2A
J Model ecotype: m-e3
K Prochl. ecotype eMIT9313
Depth (m)
100
200
10
20
30
1
2
3
4
5
40°S
20°S
0
20°N
40°N



Regional Earth Modeling System [REMS]
Regional Atmospheric Modeling System [RAMS]: (circulation/deposition processes)
Biogeochemistry Model: fluvial/estuarine/ pelagic/sediment/atmospheric/soil processes
Watershed Model: terrestrial/ stream/groundwater transport processes
Regional Ocean Modeling System [ROMS] (circulation processes)
LandEstuaryCoastal Ocean CrossSection
Prevailing westerly Winds
Montaine Provence
General Path of Material Flow
Piedmont Provence
Coastal Plane Provence
Estuary
Estuary Mouth
Southward Flow
Coastal Circulation
Gulf Stream (N)
Continental Shelf

Coastal Watersheds on the Atlantic and Gulf Coasts