



September 2025

PISCES

Basic information on the model

PISCES

- PISCES is a standard biogeochemical and plankton ecosystem model of varying complexity
 - Mostly PFT framework but with some trait-based formalism (size, lability, ...)
 - Upper trophic levels (above mesozooplankton) are not explicitly modeled
- PISCES should be coupled to an OGCM:

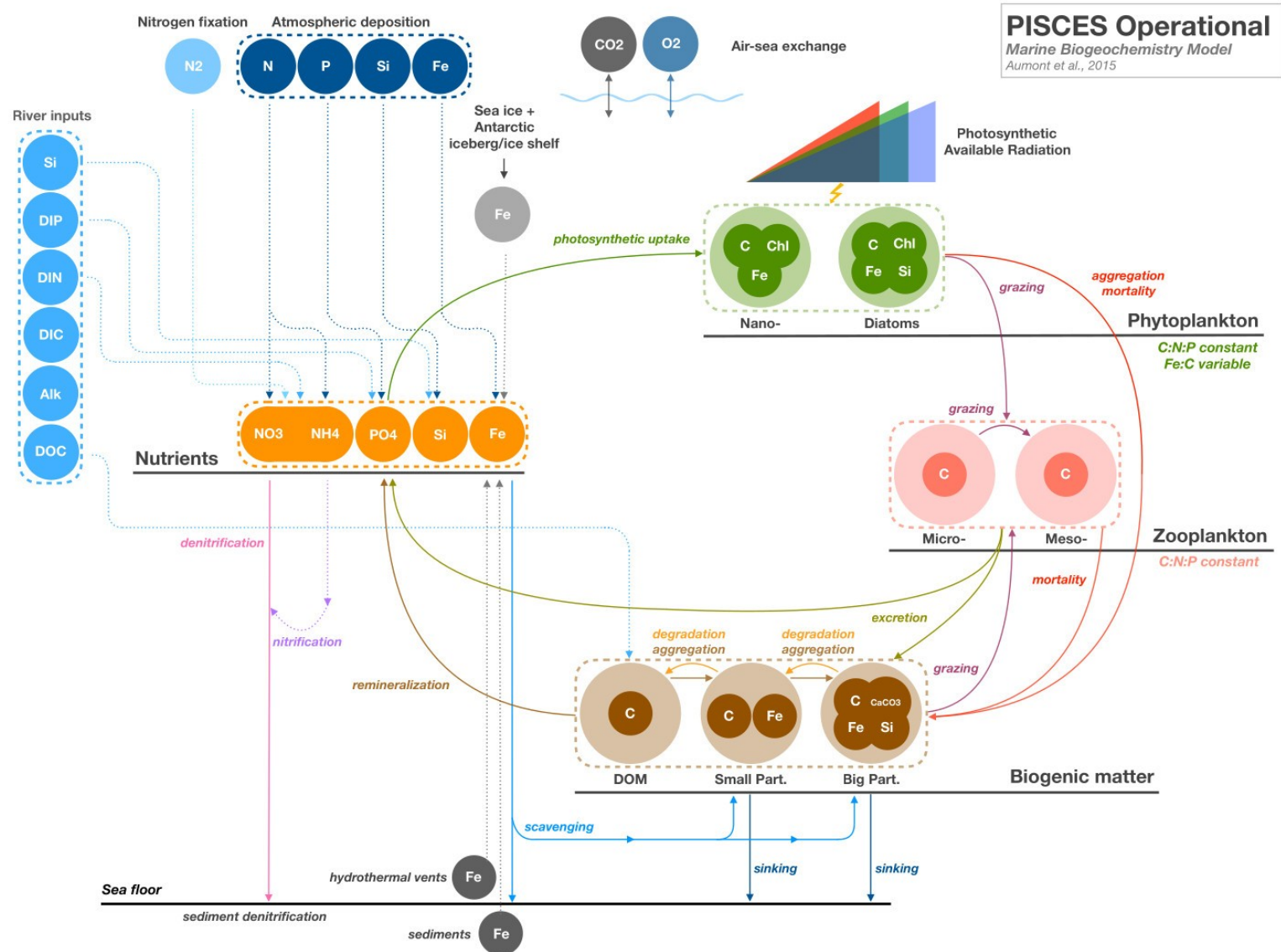


- PISCES is using explicit temporal integration in the ocean
 - Sediment module used implicit integration (Rosenbrock schemes)
- PISCES is coded in Fortran 90
- Works only in 1D-V and 3D (no 0D or 2D version)

PISCES-std vs. PISCES-QUOTA

`ln_p4z = .true.`

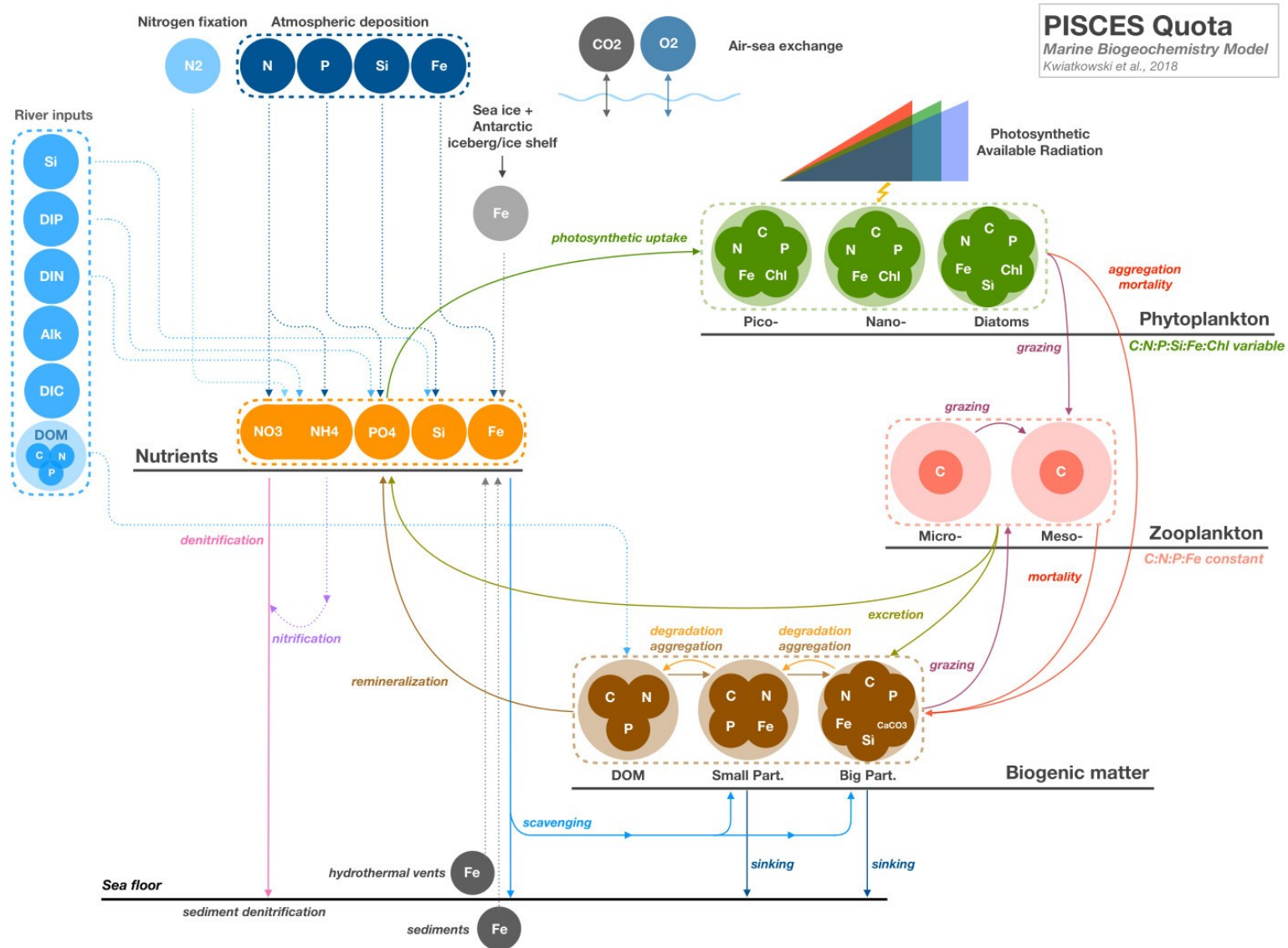
PISCES-std (24/25 tracers)



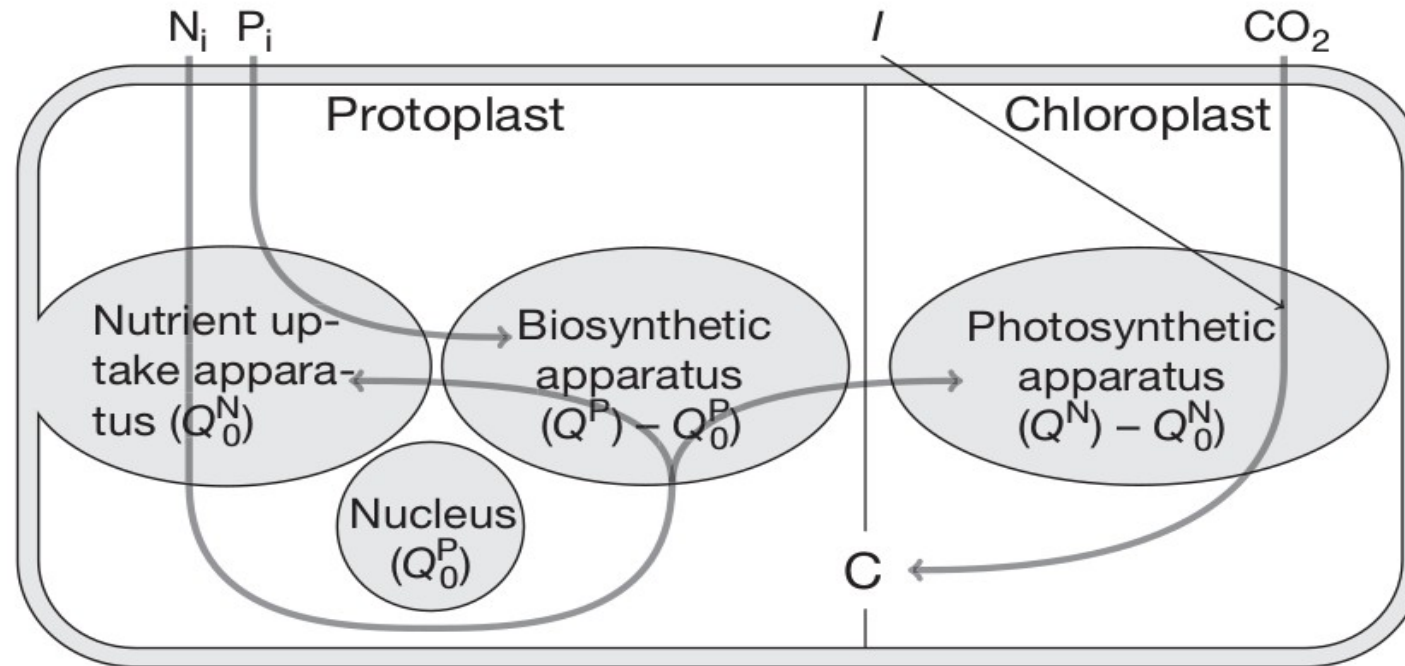
PISCES-std vs. PISCES-QUOTA

`ln_p5z = .true.`

PISCES-QUOTA (39/40 tracers)



PISCES-QUOTA



- Several adaptations of that model when embedded in PISCES:
 - Maximum quotas in P depends on the physiological status of the cells
 - Iron physiology has been added
 - Chlorophyll regulation has been modified

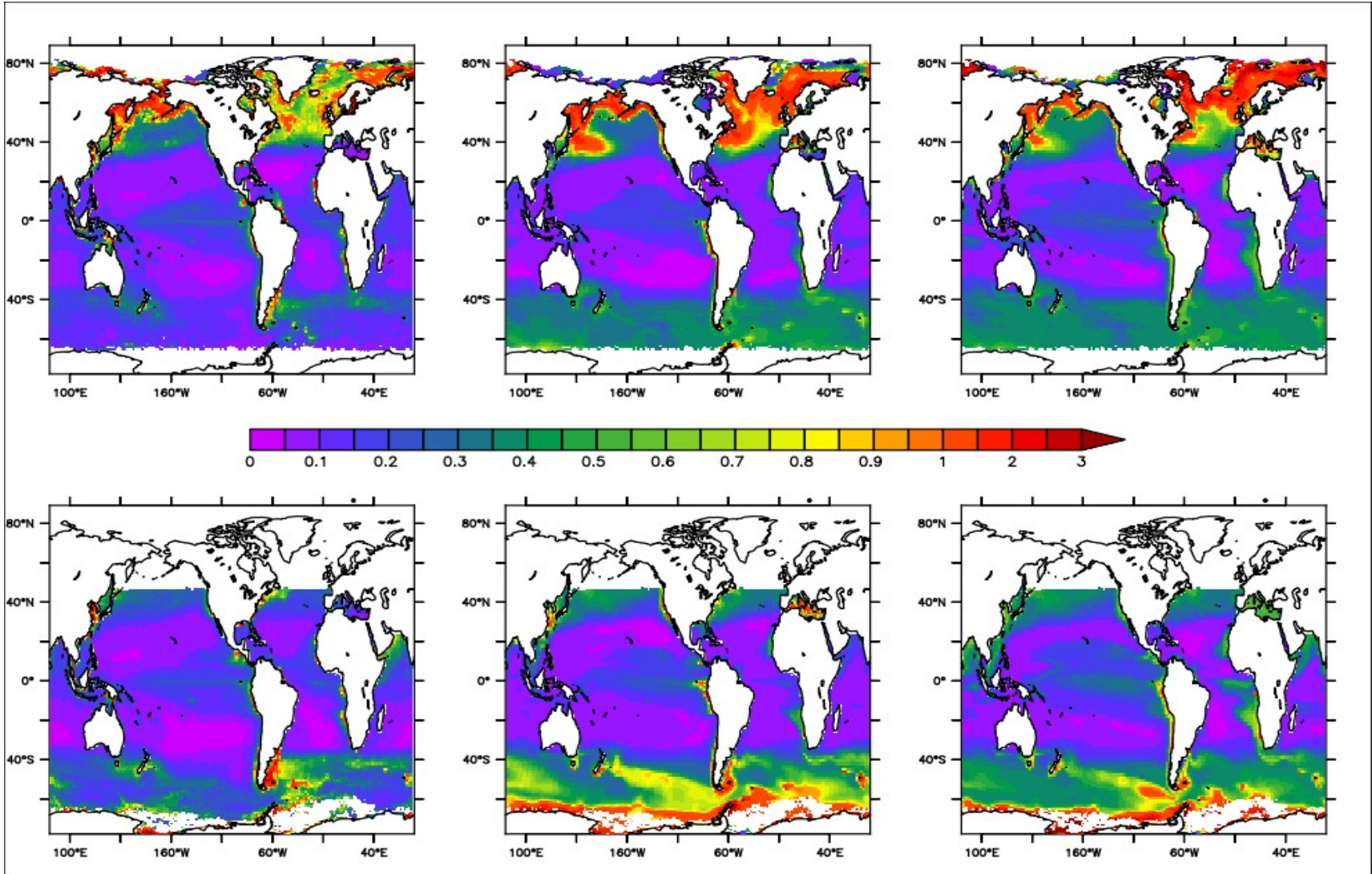
Chlorophyll distribution

Satellite

PISCES-v2

PISCES-QUOTA

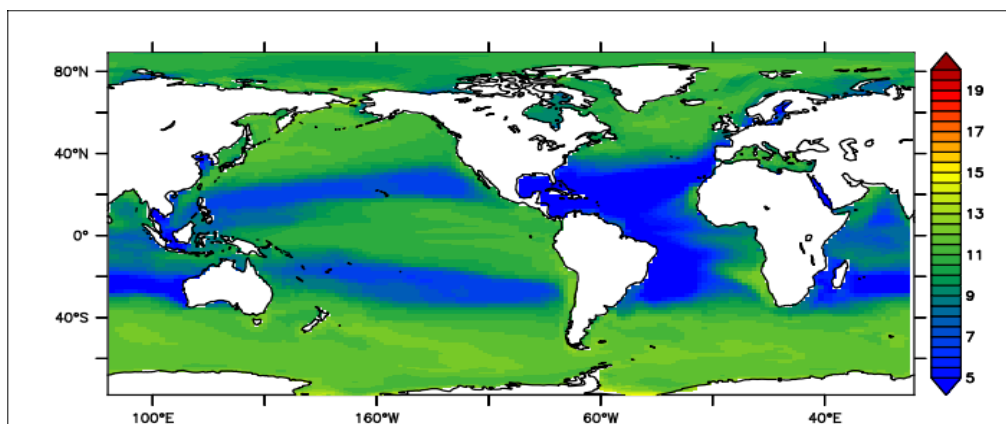
AMJ



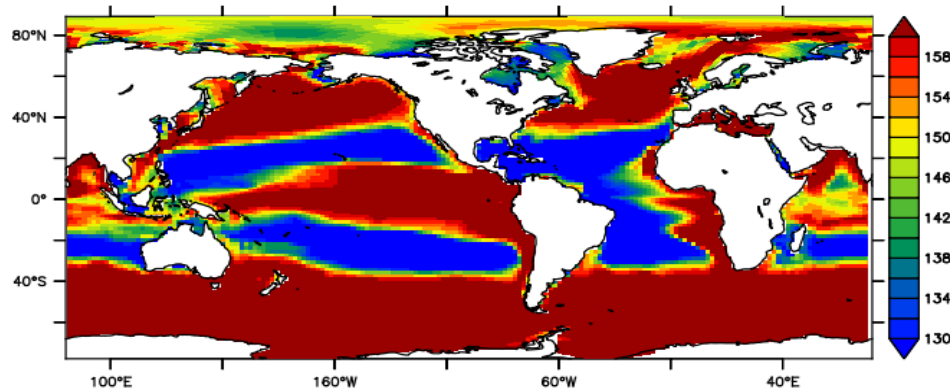
NDJ

C/N/P ratios

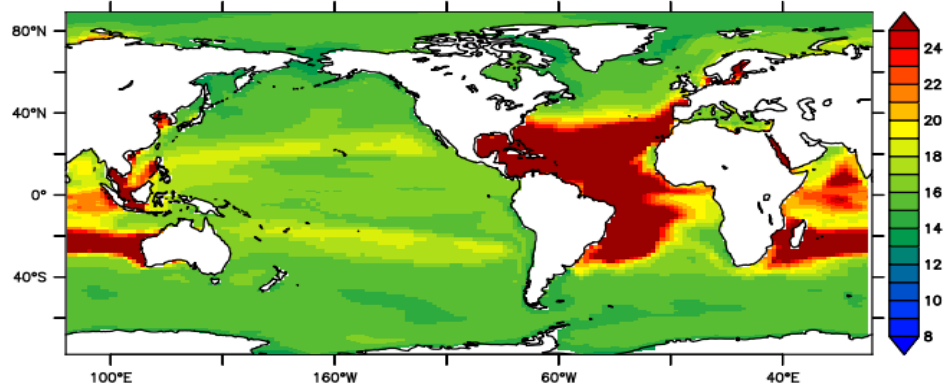
P/C



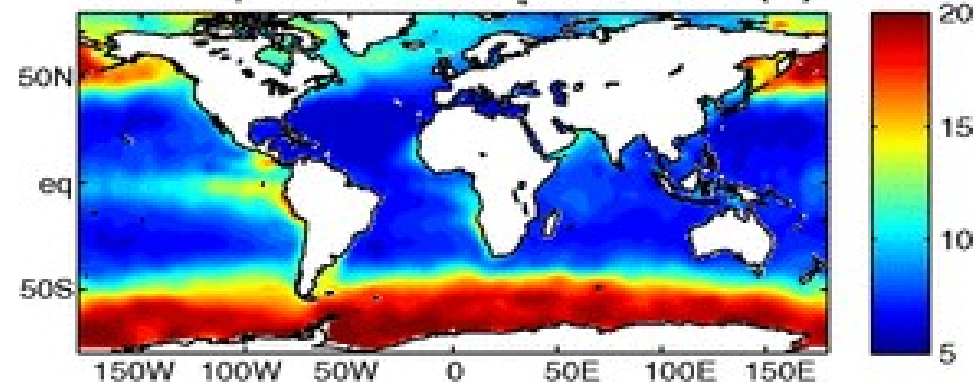
N/C



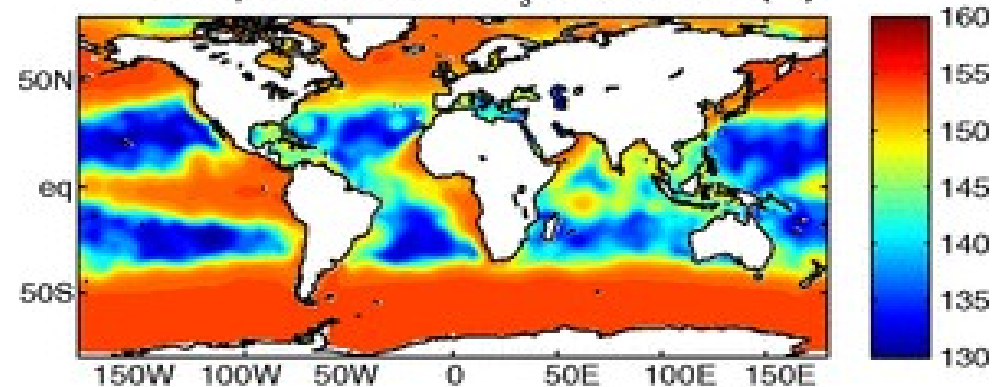
N/P



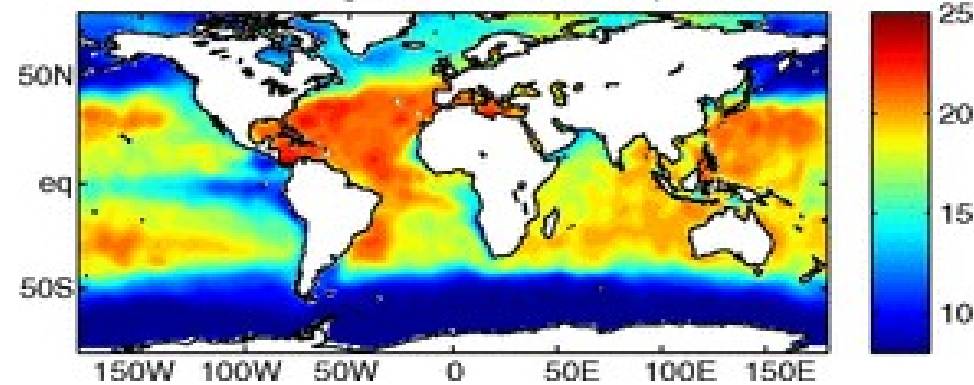
P:C predicted from PO_4 concentration (‰)



N:C predicted from NO_3 concentration (‰)



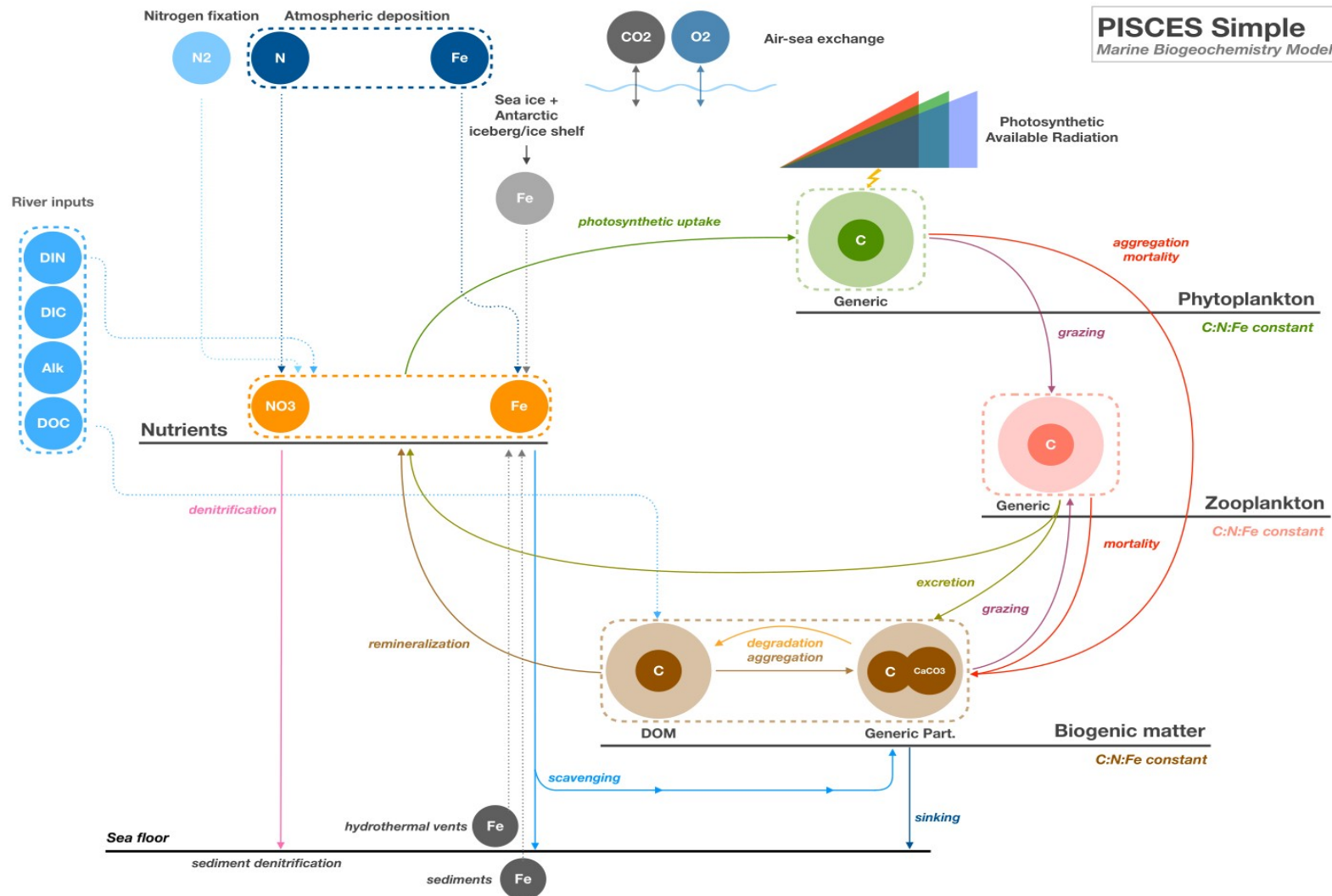
N:P resulting from P:C and N:C predictions



PISCES-simple vs. PISCES-STD

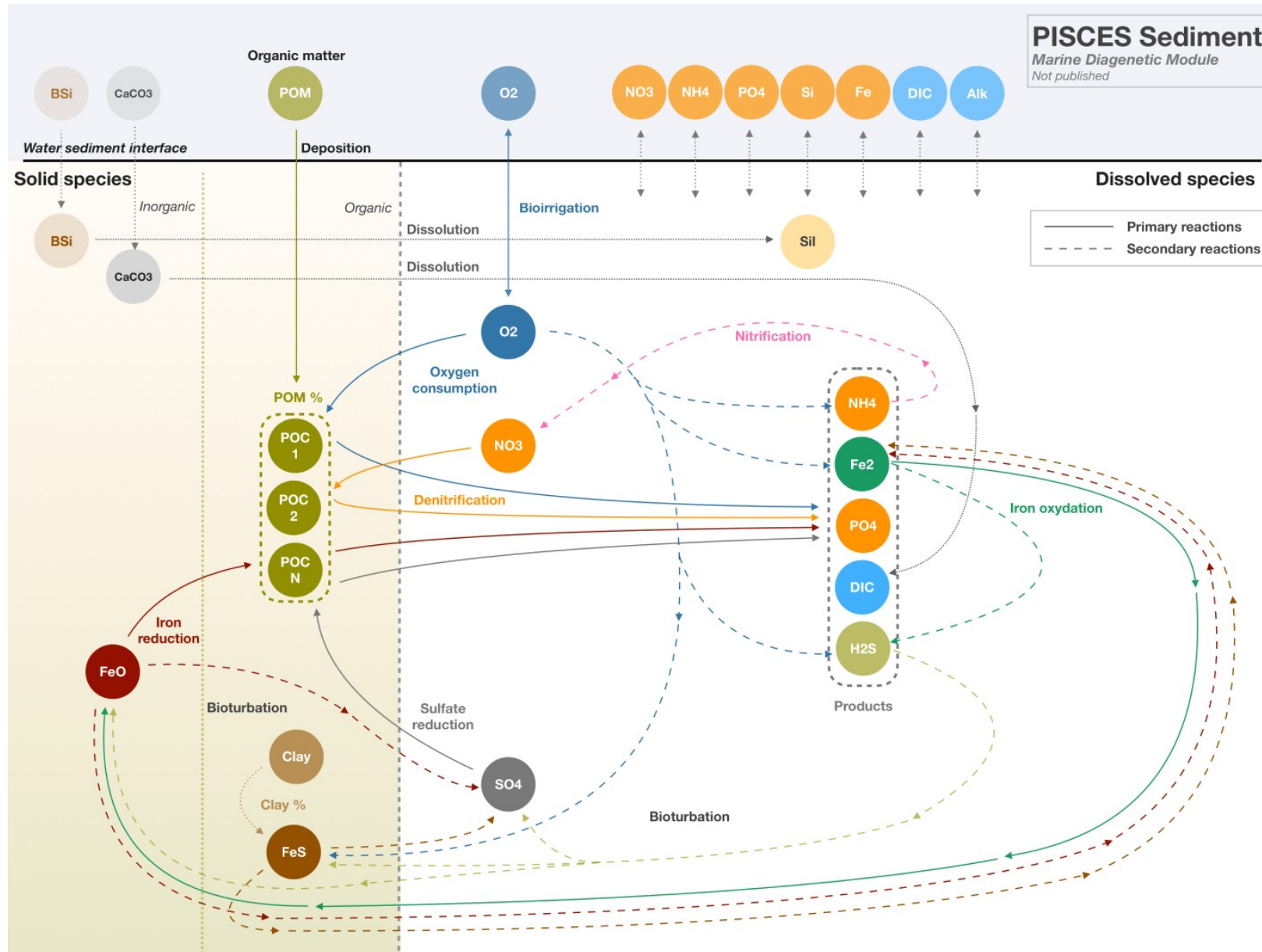
`ln_p2z = .true.`

PISCES-Simple (9 tracers)

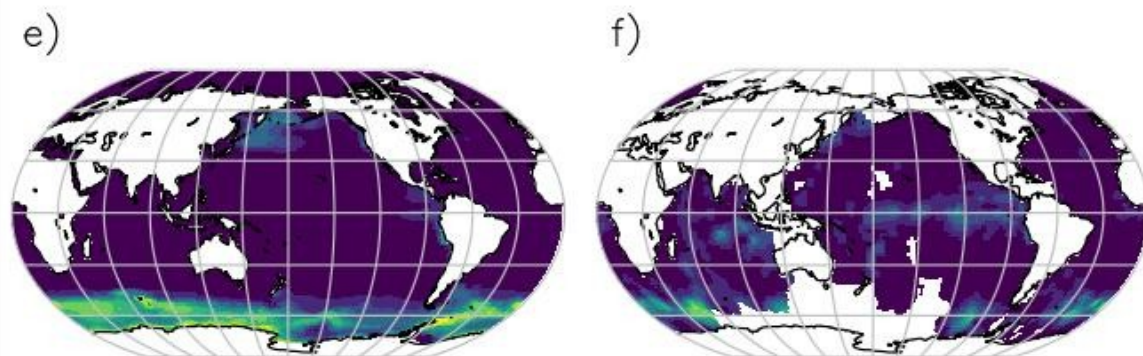
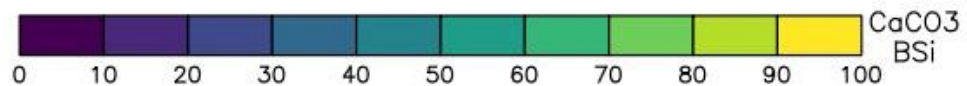
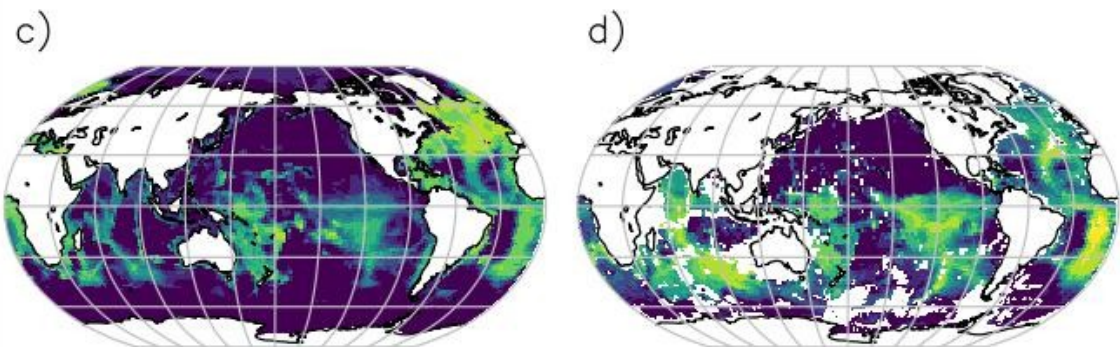
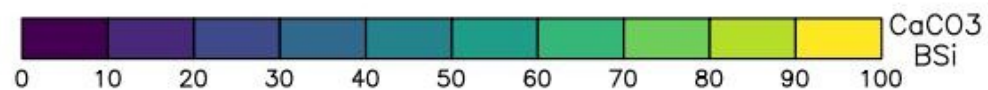
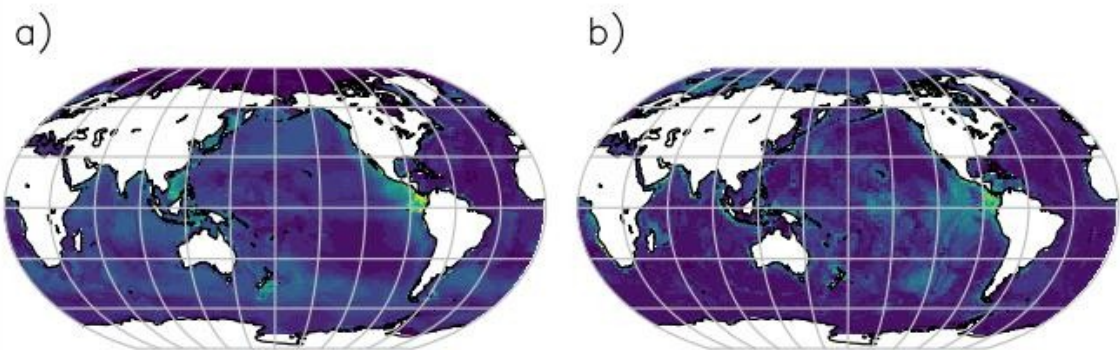


PISCES-Sediment

Can be used online/offline/standalone



Solid composition of the upper sediments



Code structure - Main

Initialization

trcnam_pisces.F90
Reading of PISCES namelist

trcini_pisces.F90
Initialization of PISCES tracers
and specific variables

p4zrst.F90
Initialization of PISCES specific variables
From restart

Time stepping

trcsms_pisces.F90
Source Minus Sink management

trcwri_pisces.F90
XIOS call for output data

trcice_pisces.F90
PISCES tracer initialization in sea ice

P4Z
Marine biogeochemical process modules

SED
Diagenetic process modules

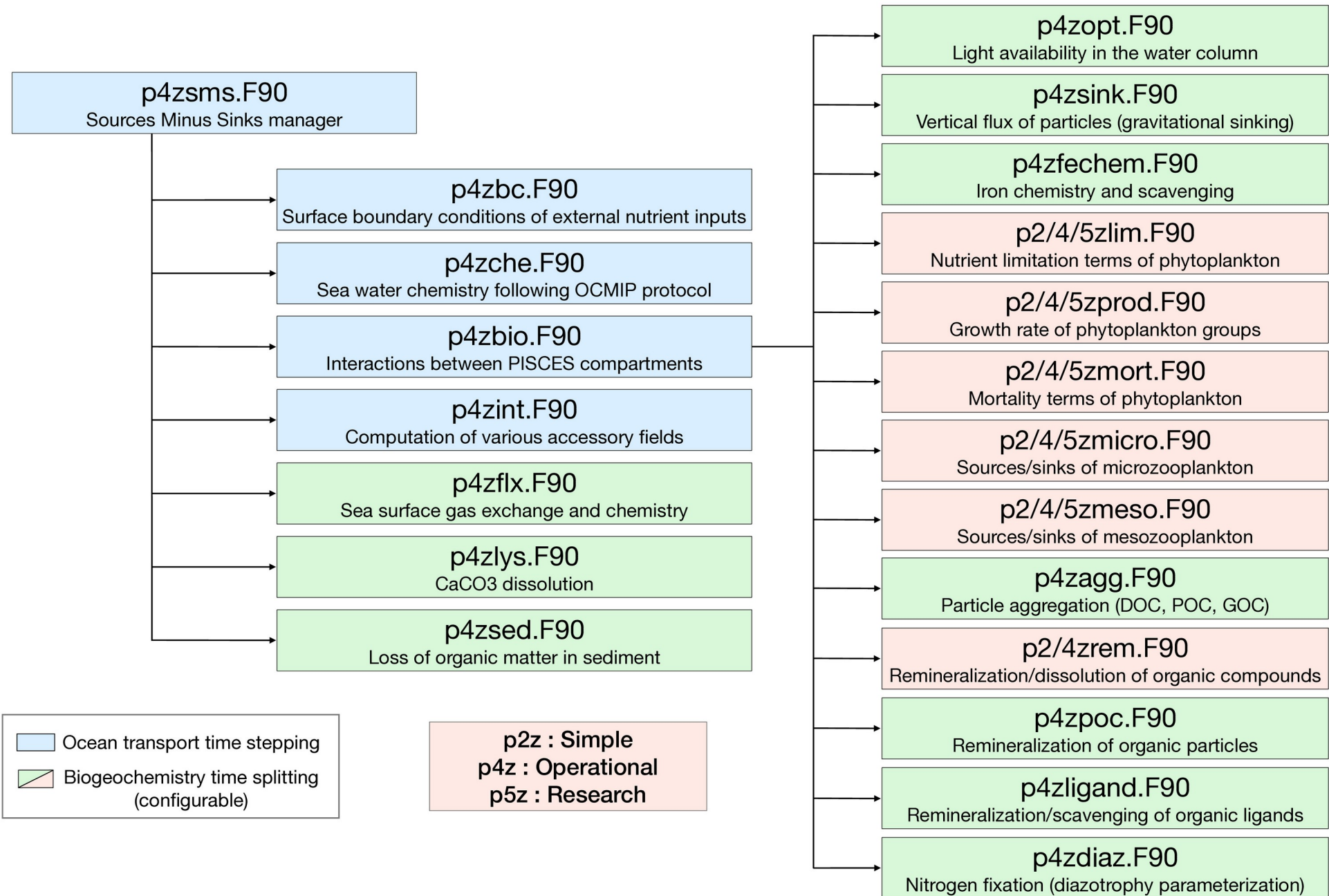
Externalized process modules

trcsink.F90
Vertical gravitational flux of particulate matter

Specific to NEMO

trcbc.F90
Passive tracer boundary conditions

Code structure - SMS



Code structure – Diagenetic module

Initialization

Time stepping

sedini.F90
Initialization of sediment variables
Reading of namelist parameters

sedinitrc.F90
Initialization of sediment state variables

sedstp.F90
Sediment model time-stepping

seddta.F90
Reading of sediment data input

sedchem.F90
Sediment chemistry

sedsol.F90
Biogeochemical reactions in sediment

sedadv.F90
Vertical advection and burial

sedsfc.F90
2 ways exchange at sediment interface

sedbtb.F90
Bioturbation

ROSK.F90
Temporal implicit solver (fast reactions)

sedinorg.F90
Inorganic chemistry

sedorg.F90
Organic chemistry (slow reactions)

Implicit solver (Rosenbrock)