

PISCES

Basic information on the model options

Objectives of that presentation

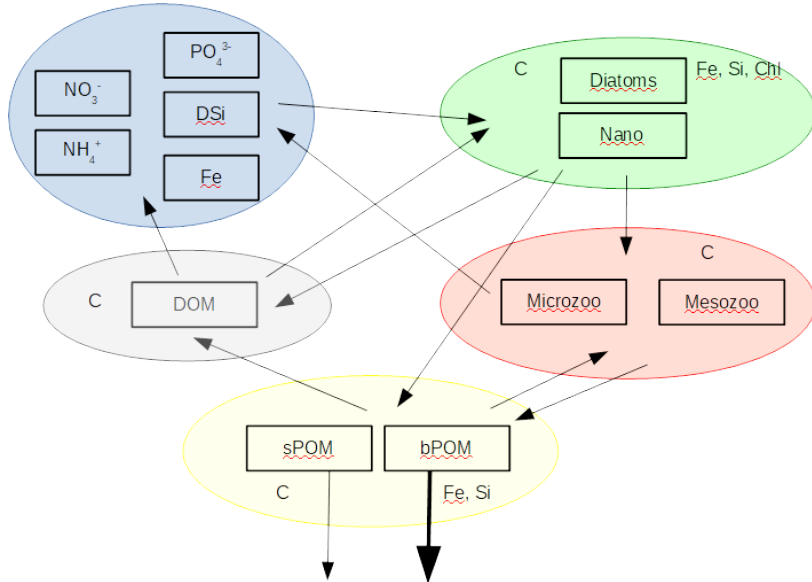
- Not a description of the PISCES model. This is a session for advanced PISCES users!
- Not an exhaustive description of all PISCES secrets
- A brief description of the PISCES optional features that can be activated from the namelist
- It also describes some key parameters that modify the behavior of these features
- This is probably imperfect. Your inputs are welcome to improve that document
- A technical documentation of PISCES is still missing and should come (soon we hope)

PISCES-std vs. PISCES-QUOTA

A first major choice should be made when using PISCES : PISCES-std or PISCES-QUOTA:

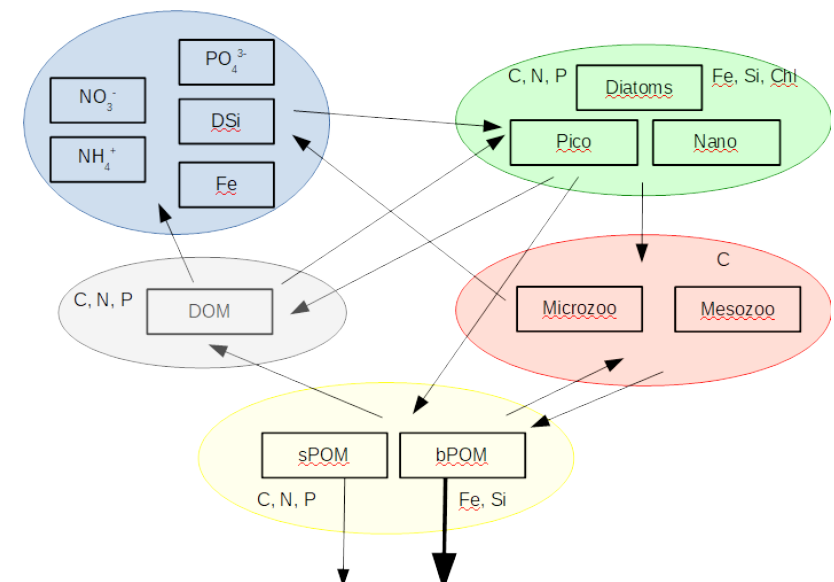
`ln_p4z = .true.`

PISCES-std (24/25 tracers)



`ln_p5z = .true.`

PISCES-QUOTA (39/40 tracers)



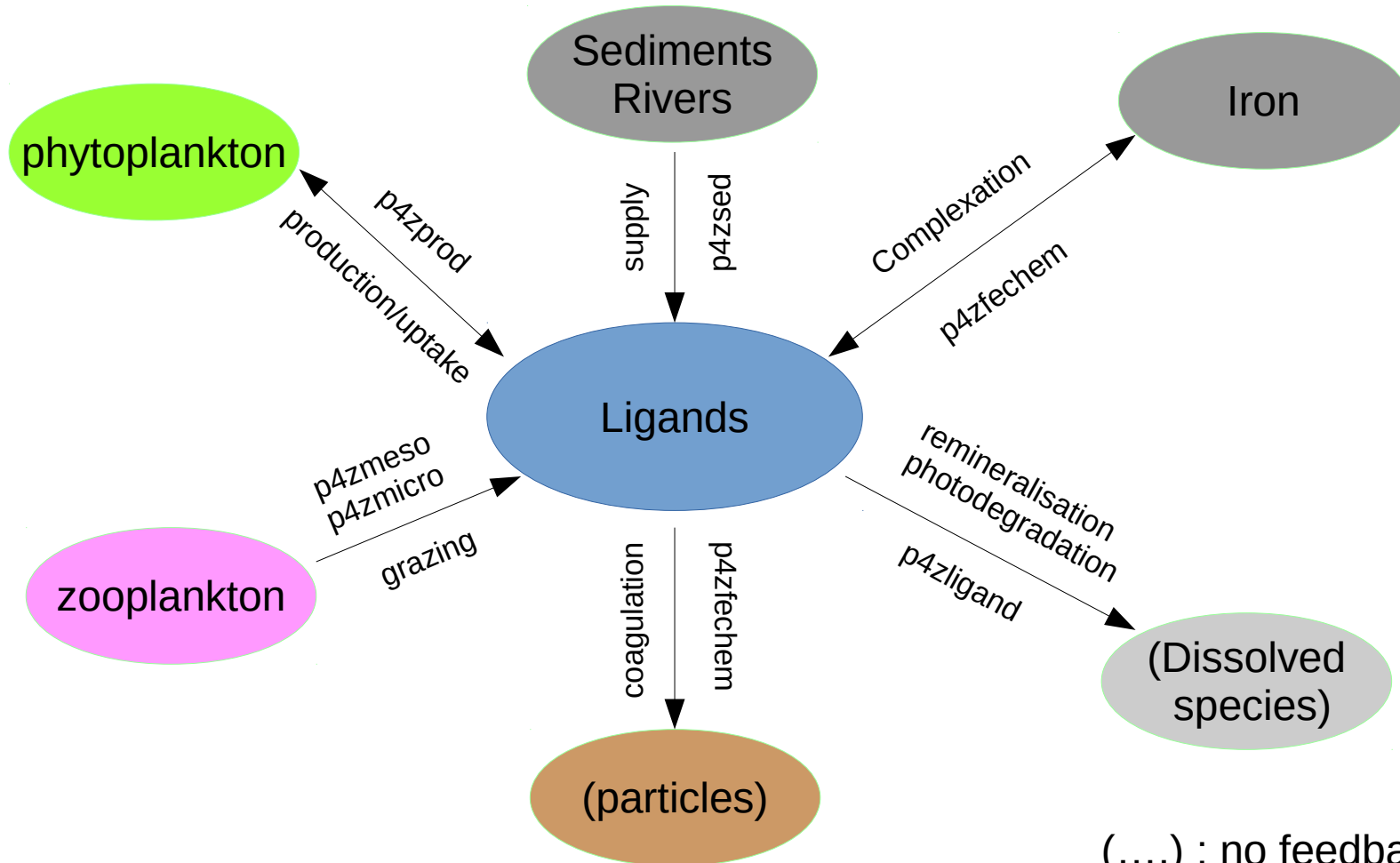
PISCES-std vs. PISCES-QUOTA (2)

- Most of the optional features work in these two main versions of PISCES
- The sediment module cannot be activated with PISCES-QUOTA (no variable stoichiometry in the sediment module)
- PISCES-QUOTA is significantly more expensive than PISCES-std (>2x)
- Many parameterization choices are common to both versions
- The rest of that presentation will be based on PISCES-std

Prognostic ligands

- In the default configuration, concentration of iron ligands is either :
 - 1) set to a constant value defined in the namelist (`ligand`)
 - 2) or to a variable field diagnosed from DOC (`ln_ligvar = .true.`)
- A prognostic description of the ligands can be activated by setting
$$\text{ln_ligand} = \text{.true.}$$
- This adds a new prognostic tracer `jplgw` (25 prognostic tracers)
- `p4zligand` is now called which computes the sinks (rem mineralization, photodegradation)
- Various additional routines have some new codes activated (`p4zprod`, `p4zfechem`, ...)

Prognostic ligands (2)



Sediment model

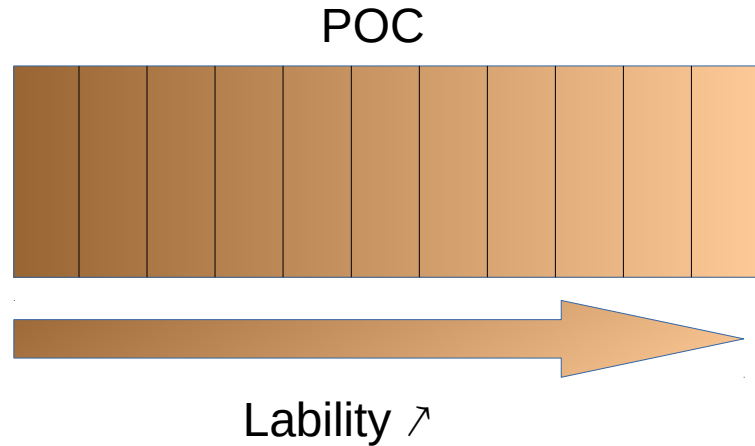
- In the default configuration, exchanges with the sediments are modeled based on a simple metamodel proposed by Middelburg et al. (1996):

$$F_{sed} = F(\text{NO}_3, \text{O}_2, Z, \dots)$$

- A full prognostic diagenetic model is embedded in PISCES and can be activated by setting `ln_sediment = .true.`
- This sediment model can be used in a standalone mode (without PISCES running) but the code needs to be compiled with the CPP key `key_sed_off`
- When running with PISCES, the exchanges between the water column and the sediments can be 1-way or 2-ways: `ln_sed_2way`
- A session is dedicated to this sediment model

Reactivity-continuum for POC

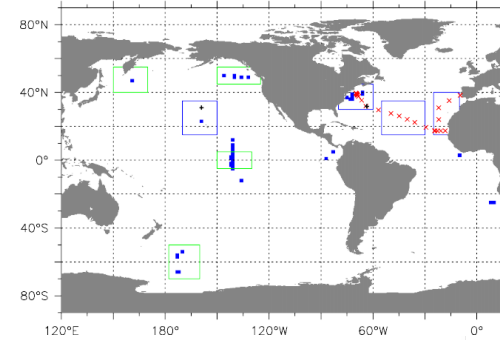
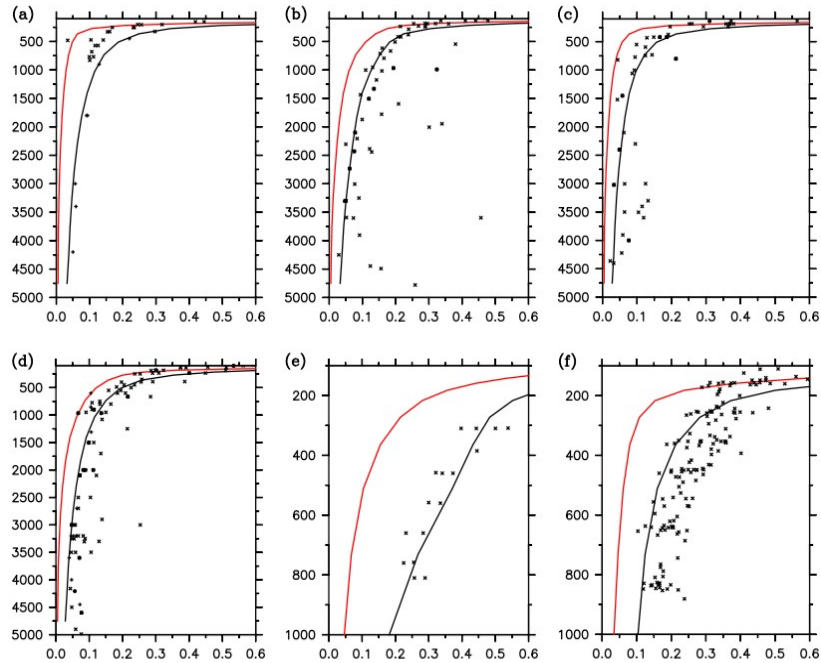
- This parameterization is described in Aumont et al. (2017)



$$\bar{k} = \frac{\int_0^{\infty} k^v e^{-ak} e^{-kt} dk}{\int_0^{\infty} k^{v-1} e^{-ak} e^{-kt} dk} = \frac{v}{(a+t)}$$

- No switch to activate that parameterization. The number of lability classes is set in the namelist by `jc poc` (`jc poc = 1` is equivalent to no variable lability)
- The shape of the gamma function controlling the initial distribution is set by `rshape`

Reactivity-continuum for POC (2)



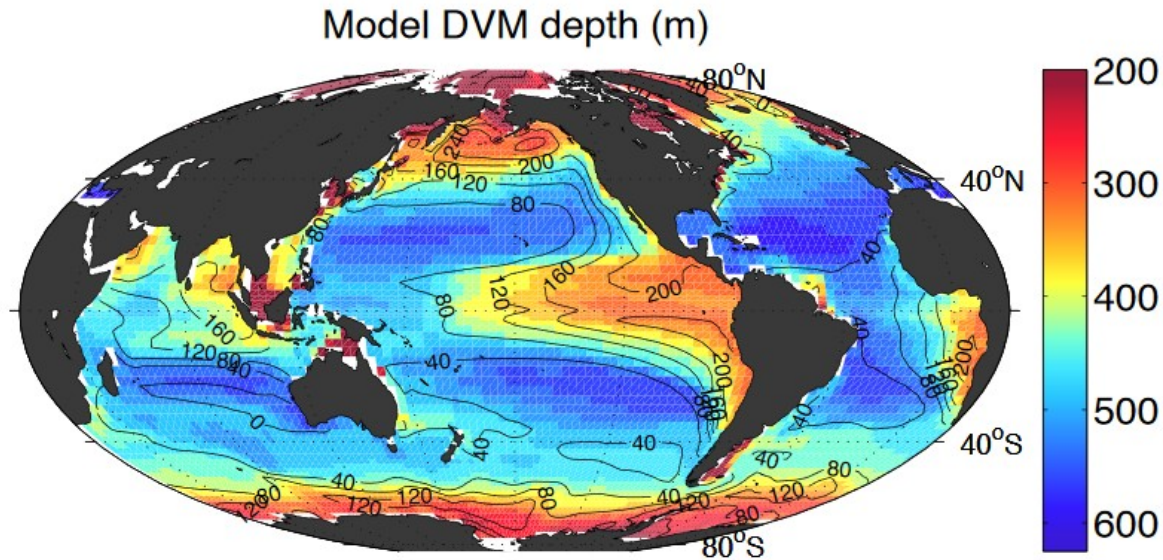
	noRC	RC
<i>n</i>	2656	2656
<i>r</i>	0.7	0.77
RMSE	0.14	0.08
Bias	0.12	0.02
RI	4.9	1.6
MEF	-0.6	0.71

- This parameterization is coded in p4zpoc
- The computing cost is increased by ~10% for 15 lability classes

Diurnal vertical migration of mesozooplankton

- Not a prognostic parameterization ! See Gorgues et al. (2019)
- DVM parameterization is activated by `ln_dvm_meso = .true.`
- Migration depth is parameterized according to Bianchi et al. (2013)

$$Z_{\text{mig}} = F(\text{O}_2, \text{Chl}, T)$$



From Bianchi et al., 2013

Diurnal vertical migration of mesozooplankton (2)

- A constant fraction of mesozoo is prescribed to migrate ($x_{fracmig}$). Microzoo is not migrating
- Organisms are assumed to be at the surface at night and at the migration depth during daytime
- Organisms are supposed to respire, excrete DOM and inorganic nutrients and egest fecal pellets in both habitats (function of daylength and temperature)
- This parameterization is coded in p4zmeso
- The computing cost is only modestly increased

Code structure

