

# Marine Biogeochemistry in NEMO System

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# The NEMO System



- The current system (in FORTRAN 90):

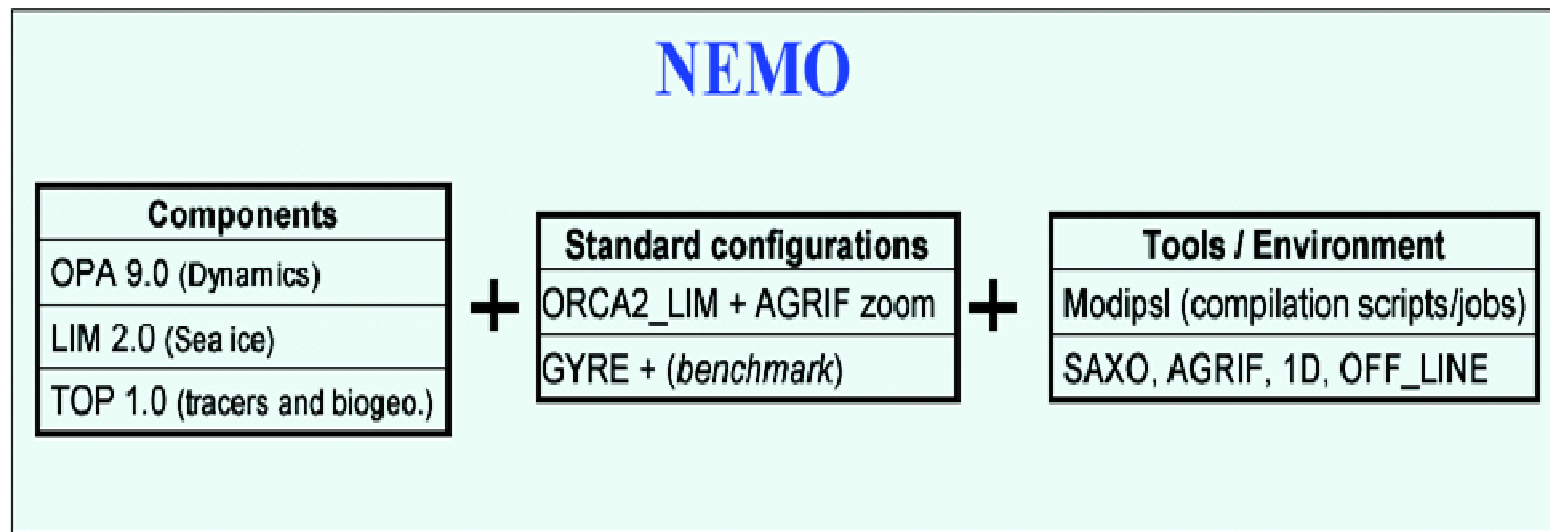
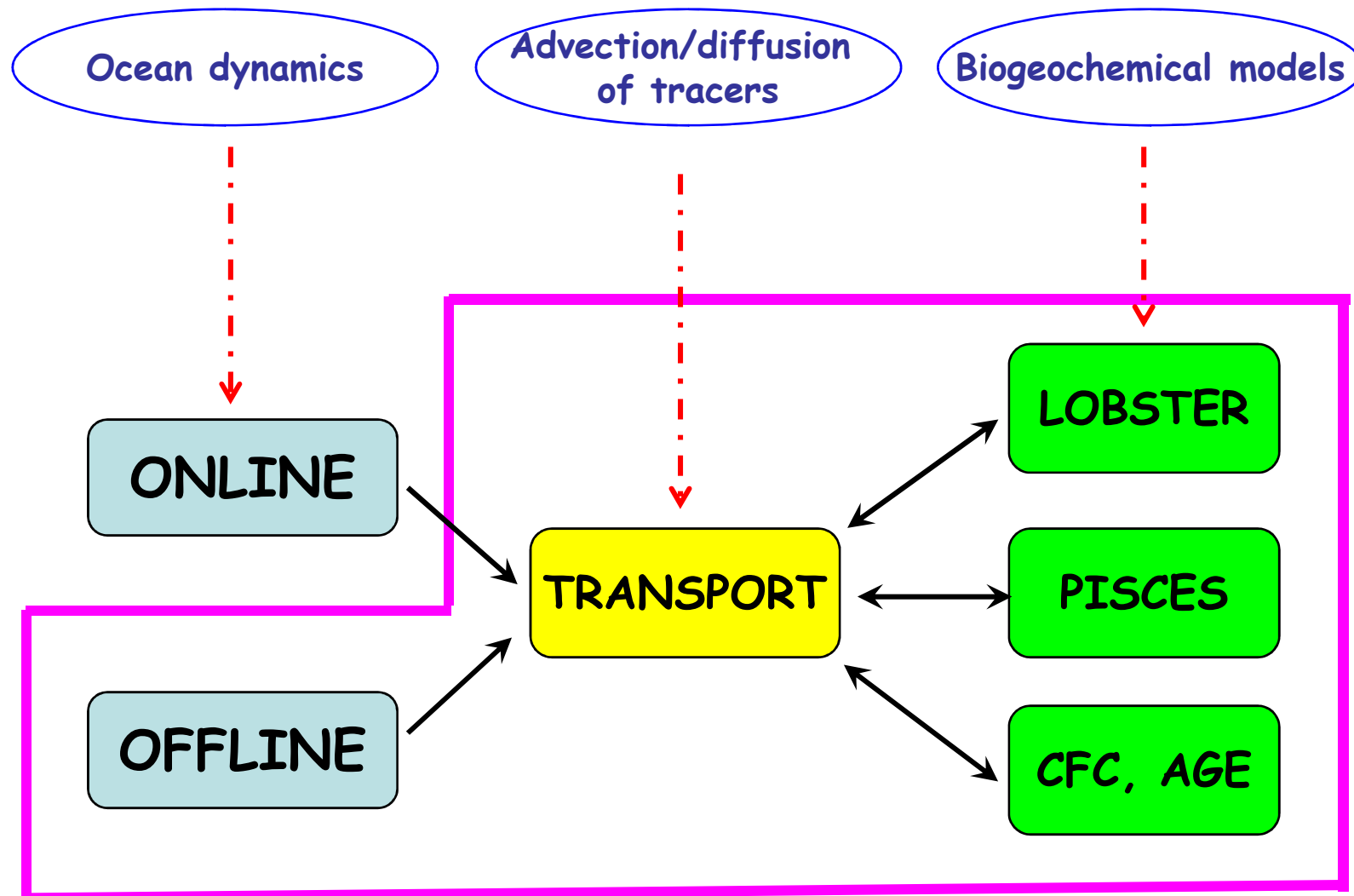


Figure from ESOPA : <http://www.lodyc.jussieu.fr/NEMO>

# TOP : Tracers in the Ocean Paradigm



# OGCM OPA

## ▶ *Online*

- ✓ The tracers models are include with a CPP key *key\_passivetr*
- ✓ The evolution of tracers is computed along with the dynamics
- ✓ No feedbacks from the biogeochemistry on the dynamics
- ✓ 3 entry points : 1 initialization, 1 time stepping, 1 output

## ▶ *Offline*

- ✓ The offline code is a simplified OPA 9 model
- ✓ Fields of advection and diffusion are read from several files instead of being computed
- ✓ No constraint on the time sampling in the inputs files

# Tracer transport model

- ✓ The code is based on the dynamical model : it has been written from the subroutine of T & S
- ✓ Same numerical advection schemes : Arakawa, TVD, MUSCL and diffusion : laplacian or biharmonic
- ✓ Restoring to climatological fields or observations is coded

## *Coupling online with OPA*

- ✓ The transport model can be called every Nth dynamical time step
- ✓ Numerical scheme can be selected independently - parameters are specified in a specific namelist

# Geochemicals models

The geochemical models do not include a description of marine biology activity.

They are generally light with a few processes to describe -

- ✓ Age tracer : 2 tracers whose combination gives the age and the proportion of a specified water mass
- ✓ CFC's : 1 or 2 tracers for CFC-11 and/or CFC-12
- ✓ DIC-12 and DIC-14 : 2 tracers modeled according to OCMIP protocol



# SMS models

## *Coupling with the transport model*

- ✓ For each sms model : 1 specific common file, 1 specific parameter file, 1 specific namelist file
- ✓ 2 entry points : 1 for initialization, 1 for time evolution
- ✓ Time step for sms model = time step for transport model except for PISCES : computational of biological terms can be called several times by time step
- ✓ 2 outputs files : 1 for the tracer concentrations, 1 for the additional biogeochemical fluxes ( optional )



# Code status

- ✓ Full mpp capabilities
- ✓ 1D vertical configuration for online and offline versions
- ✓ AGRIF suitable for TOP and zooming option available but not open boundaries
- ✓ Initialisation from analytical distributions or from files
- ✓ Grid degradation for speed-up offline spin-up
- ✓ Spectral particule model in PISCES ( Kriest parameterisation )
- ✓ Trends in the mixed layer or euphotic layer

# performances

## Performances on NEC-SX8

	# procs	Time step	CPU time/year	Memory size used	GFlops	V. Op. Ratio
ORCA2-LIM-PISCES ( 182 × 149 × 31 ) Online version	1	Ocean : 1h 36 mn Ice : 8 h Transport : 1h 36 mn Bio : 24 mn	3 h 05 mn	3.4 Gb	3.2	99.65%
ORCA2-PISCES ( 182 × 149 × 31 ) Offline version	1	Transport : 7h 18mn Bio : 1h 49 mn	36 mn	2.4 Gb	6.4	99.62%

## Performances on the Earth Simulator for higher resolution models

	# procs	Time step	CPU time/year	Memory size used	GFlops	V. Op. Ratio
ORCA05-LIM-PISCES ( 722 × 511 × 31 ) Online version	64	Ocean : 36 mn Ice : 3 h Transport : 36 mn Bio : 36 mn	3 h	100 Gb	167	99.45%
GYRE-LOBSTER ( 1/27° × 1/27° ) ( 812 × 542 × 31 )	78	Ocean : 5 mn Transport : 5 mn Bio : 5 mn	9 h	73 Gb	171	99.32%

# Future developments

- ✓ Merge of dynamical transport and passive tracer transport models
- ✓ Optimisation of memory for PISCES model : necessary for higher resolution configuration
- ✓ Redesign of biological components : rewriting of LOBSTER and PISCES in F90 and share some processes like gas exchange, optics, chemistry )
- ✓ Include of a sediment model : stand-alone or coupled with PISCES
- ✓ Biological trends in the mixed-layer and in the euphotic layer

## More informations

**Wiki page :**

**<http://www.lodyc.jussieu.fr/NEMO/wiki/index.php/BiogeochemicalComponent>**