PISCES Training Autumn School 2023

Beginner session, LOCEAN (Paris), 9-10 October 2023

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Objectives

The objective of this beginners' session is to learn the fundamentals of the PISCES marine biogeochemistry model, the biogeochemical component implemented in the two ocean model platforms NEMO and CROCO. You will explore different functionalities and tuning possibilities using low computational cost configurations. A presentation will be given to show the modeling choices, the code architecture and the main features of PISCES.

1. You will first install a 1D configuration of NEMO-PISCES, run the code and explore some of the physical and biogeochemical variables produced by the model.
2. Then you will perform sensitivity tests of the model to a set of biogeochemical parameters.
3. Using the ocean platform of your choice, NEMO-PISCES (1D) or CROCO-PISCES (3D), you will carry out sensitivity tests in groups of 3 or 4 people, and present your results.
4. Finally, you will choose one of the proposed scientific questions, explore the results in groups of 3 or 4 and present them.

At the end of each session, there will be an hour or so to discuss the blocking points and answer any questions that may have arisen.

To visualize the results of the simulations you will be producing throughout this session, we suggest using python modules (xarray, matplotlib, numpy). These modules are particularly useful and fast for exploring variables in netcdf files generated by the model. The environment used for the practical work is JupyterLab in which you will open and use Jupyter Notebooks containing documents and live executable python scripts. You will find some python script examples that you will have to adapt to explore the results. If you have any improvements to these scripts, please let us now.

For those doing the practical work on their own, you will need to install python, matplotlib and xarray to use these notebooks. You can also use other visualization tools depending on your work habits.

In order to improve the material and the course of future sessions for beginner users, we welcome any positive or negative feedback from you.

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1. Brief description of PISCES

The PISCES model (Aumont et al., 2015) is constructed on the assumption that phytoplankton growth is directly limited by the external availability in nutrients (Monod, 1942). This choice was mostly dictated by the computing cost as PISCES has been designed to suit a wide range of temporal and spatial scales, including quasi steady state simulations on the global scale.

The operational version of the model, used in this paractical session, has 24 compartments (Figure 1). Phytoplankton growth can be limited by five different nutrients: nitrate, ammonium, phosphate, silicate and iron. Four living pools are represented : two phytoplankton size classes/groups (nanophytoplankton and diatoms) and two zooplankton size classes (microzooplankton and mesozooplankton). Diatoms differ from nanophytoplankton by their need in Si, by higher requirements in Fe (Sunda and Huntsman, 1995) and by higher half-saturation constants because of their larger mean size. For all living compartments, the ratios between C, N and P are kept constant to the values proposed by Takahashi et al. (1985). On the other hand, the internal contents in Fe of both phytoplankton groups and in Si of diatoms are prognostically simulated as a function of the external concentrations in nutrients and of the light level. The Chl/C ratio is modeled using a modified version of the photoadaptation model by Geider et al. (1998). All the elemental ratios of zooplankton are kept constant.

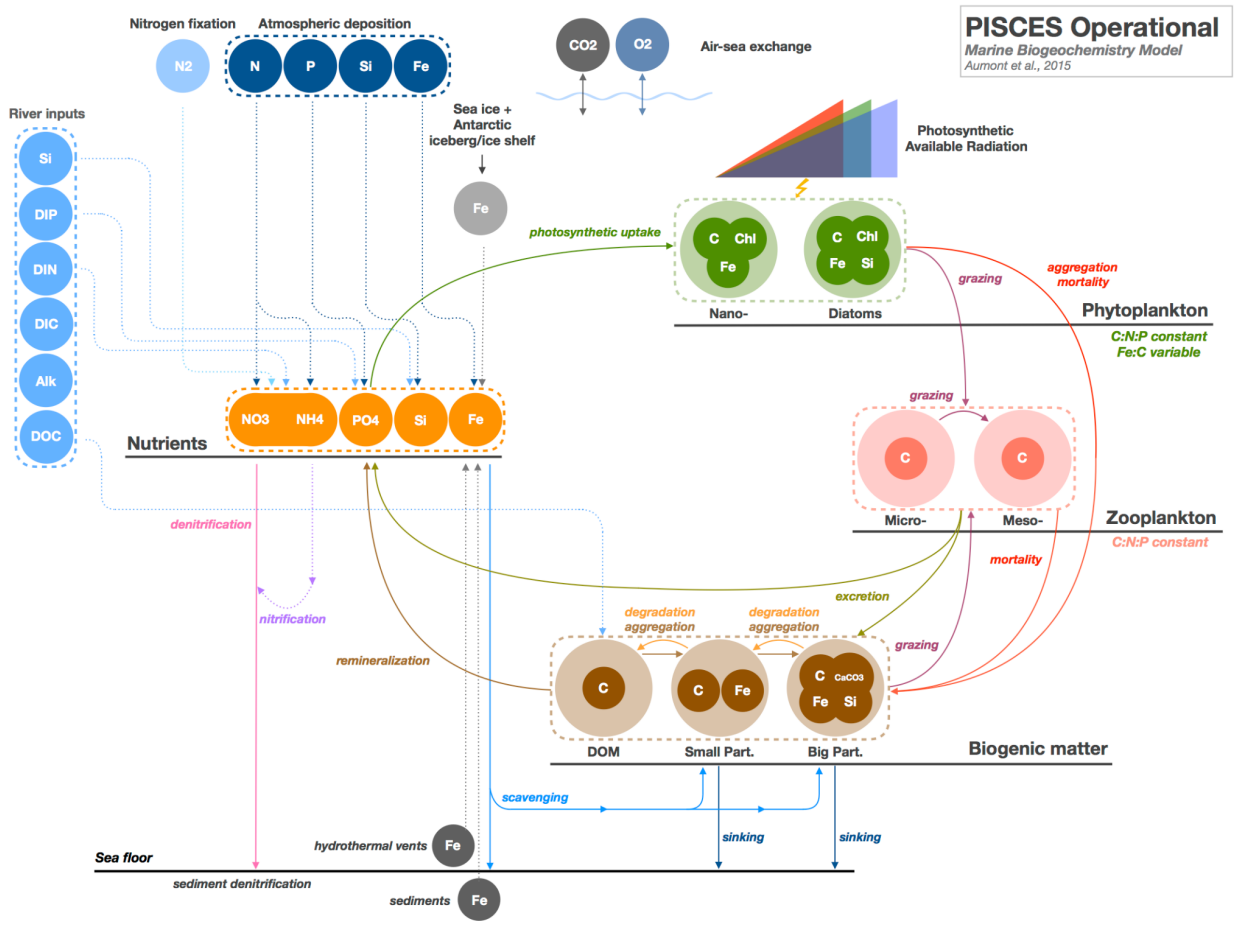


Figure 1. Schematic of PISCES operational (24 tracers)

There are three non-living compartments: semi labile dissolved organic matter (with timescales of several weeks to several years), small and big sinking particles. The two particle size classes differ by their sinking speeds (2 m/d for the small size class and 50 to 200 m/d for the large size class). As for the living compartments, constant Redfield ratios are imposed for C/N/P. However, the iron, silicon and calcite pools of the particles are fully simulated. As a consequence, their ratios relative to organic carbon are allowed to vary. The impact of ballast minerals on particles sinking speeds is not accounted for in the model (e.g., Armstrong et al., 2002).

Nutrients are supplied to the ocean from three different sources : atmospheric dust deposition, rivers and sediment mobilization. These sources are explicitly modeled and are extensively described in Aumont et al. (2015). Thus only the main aspects are presented here. Iron deposition from the atmosphere has been estimated from the climatological monthly maps of dust deposition simulated by the model of Tegen and Fung (1995) assuming constant values for the iron content and the solubility (e.g., Jickells and Spokes, 2001 ; Moore et al., 2004). River discharge of carbon is taken from the Global Erosion Model of Ludwig et al. (1996). Supplies of Fe, N, P and Si are derived from the same model output by considering globally constant Fe/P/N/Si/C ratios in the rivers. Reductive mobilization of iron from marine sediments has been recognized as a significant source to the ocean (e.g., Johnson et al., 1999 ; de Baar and de Jong, 2001). Unfortunately, almost no quantitative information is available to describe this potentially important source. In a way similar to Moore et al., 2004, we have very crudely parameterized this input of iron.

PISCES has been used, at the global scale, to study past climates (Bopp et al. 2003), to understand the mechanisms that explain interannual variability in marine productivity (Aumont et al. 2008) or ocean-atmosphere carbon fluxes (Rodgers et al. 2008), to assess the impact of climate change or ocean acidification on marine ecosystems and air-sea carbon fluxes (Bopp et al. 2001, Orr et al. 2005), to evaluate geo-engineering strategies to mitigate climate change (Aumont and Bopp, 2006, Dutreuil et al. 2009)…

2. The 1D NEMO-PISCES vertical configuration

In the tuning session, we use a 1D (vertical) configuration of NEMO-PISCES version 4.2 (https://zenodo.org/record/7139521).

In the 1D configuration, the size of the domain is 1x1x75, 75 being the number of vertical grid levels. The user has to set in the namelist configuration (`namelist_cfg`) the boolean flag `ln_c1d` to `.true.` (`&namdom` section) and to provide the longitude and latitude coordinates of the station, `rn_lat1d`, `rn_lon1d` (`&namc1d` section), and the ocean depth at the given point `rn_bathy` (`&namusr_def` section). Input data (initial state and forcings) at the location under consideration are required ; the initial states must be set to values of dimension 1x1x75. This 1D configuration is based on the NEMO C1D_PAPA reference configuration in which the horizontal and vertical grids are defined.

The one-dimensional vertical model only considers the vertical – z, sigma or partial steps – coordinate and time as independent variables in the primitive equations, with no horizontal variations. All horizontal derivatives are set to zero. Thus, in this one-dimensional vertical configuration, there is no (both lateral and vertical) advection, no lateral mixing on tracers nor dynamics.

Temperature and salinity are thus only controlled by vertical diffusion equations and the density, needed for the turbulent mixing closure scheme, is computed using an equation of state of sea water :

- $\partial_t T = \partial_z (K_z \partial_z T) + 1/(\rho C_p) F(z)$

with *F(z)* the penetrating solar flux. Bulk flux surface boundary conditions for *T(z=0,t)* are imposed (not detailed here). Vertical advection of temperature is not taken into account ($\partial_z(w.T) = 0$) as w=0 over the entire water column. The vertical mixing coefficient K_z is computed using a vertical mixing scheme (not detailed here) depending on the option selected in the dynamical namelist (Turbulent Kinetic Energy (TKE), K-profile-parameterization (KPP), Richardson or constant vertical mixing).

- $\partial_t S = \partial_z (K_z \partial_z S)$

Surface boundary conditions for *S(z=0,t)* are applied (not detailed here).

For passive biogeochemical tracers *C(z,t)*, only biogeochemical sources and sinks are taken into account together with vertical diffusion processes:

- $\partial_t C = \partial_z (K \partial_z C) + SMS_{bio}(z,t)$

SMS_{bio} means “sources” minus “sinks”. Surface boundary conditions are applied depending on the biogeochemical tracer (see Aumont et al., 2015 for details).

The 1D configuration stations

In this session, you will explore the behavior of the NEMO-PISCES 1D configuration model at different JGOFS observation sites (Figure 2). You will start by setting up the 1D configuration at the BATS (Bermuda Atlantic Time-series Study) station. Then, in groups, you will configure and explore the results at the other stations.

1. BATS (64°W, 31.5°N) : https://bats.bios.asu.edu/
2. NABE (20°W,47°N) : http://usjgofs.whoi.edu/research/nabe.html
3. KERFIX (68.25°E, 50.40°S) : http://www.obs-vlfr.fr/cd_rom_dmtt/OTHER/KERFIX/bacteries/kfx_bact_delille.htm.htm
4. HOT (158°W, 22.45°N) : http://hahana.soest.hawaii.edu/hot/
5. DYFAMED (7.52°E, 43.27°N) : http://www.obs-vlfr.fr/cd_rom_dmtt/sodyf_main.htm

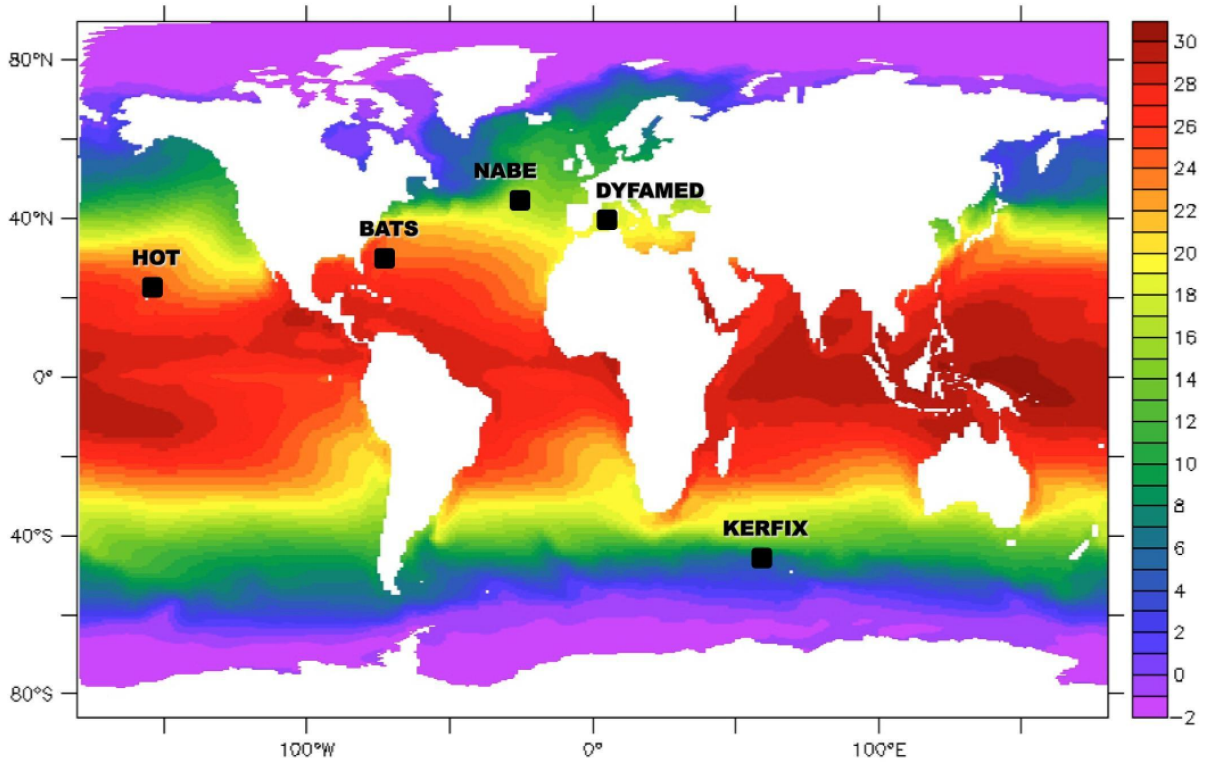


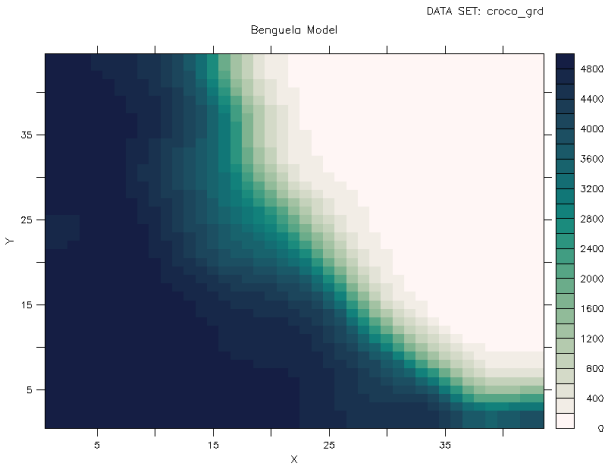
Figure 2: Mean SST from World Ocean Atlas and position of JGOFS sites

3. The CROCO-PISCES Benguela LR configuration

The Benguela Low-Resolution configuration is used to test and implement new parameterizations in CROCO. We will use it here to perform 3D sensitivity experiments for those interested in using PISCES with CROCO. This configuration has a resolution of 1/3° with a small number of grid points, 43 x 44, and a vertical discretization of 32 sigma levels. This configuration allows to study, at low computational cost, the ocean dynamics and biogeochemistry of the Benguela coastal region, which is home to an upwelling of cold, nutrient-rich deep waters that support high marine productivity.

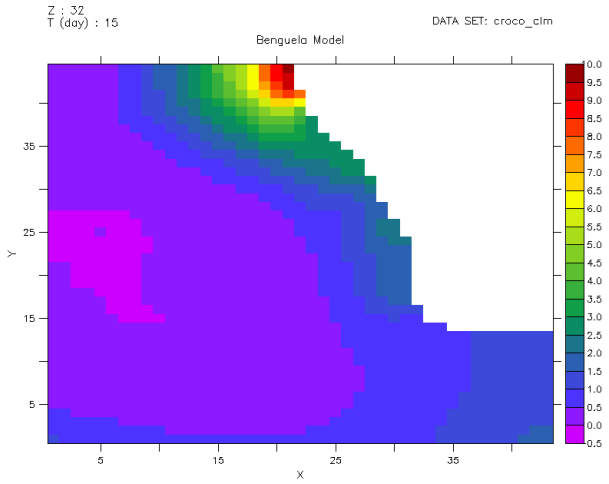
Details on the CROCO code, compilation and pre-processing will not be described here. We will briefly focus on the netcdf input files of the configuration. Netcdf input files are created using the CROCO preprocessing tools (see https://www.croco-ocean.org/documentation/).

- `croco_grd.nc` : 2D (x,y) grid file containing the bottom topography (h), land mask (mask_rho) and other grid parameters.

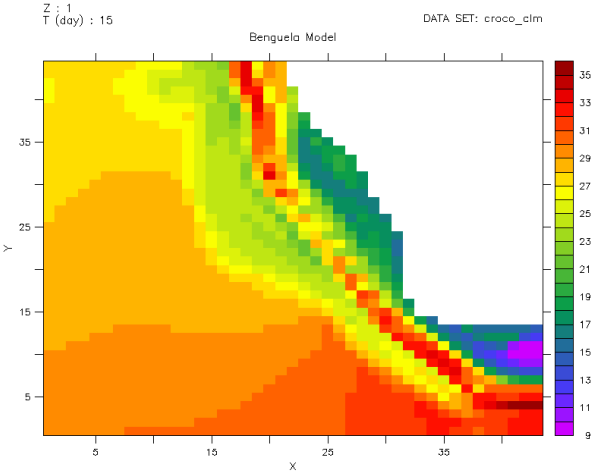


Final bathymetry at RHO-points (meter)

- `croco_clm.nc` : 4D (x,y,z,t) U,V,T,S,zeta in the model domain from World Ocean Atlas + nutrients (NO3, PO4, Si, Fer) + oxygen (O2) + DIC, DOC, TALK (carbonates). Only values near the 4 open boundaries are used, the other PISCES variables (e.g. phyto, zoo,…) are set to constant values at the boundaries.



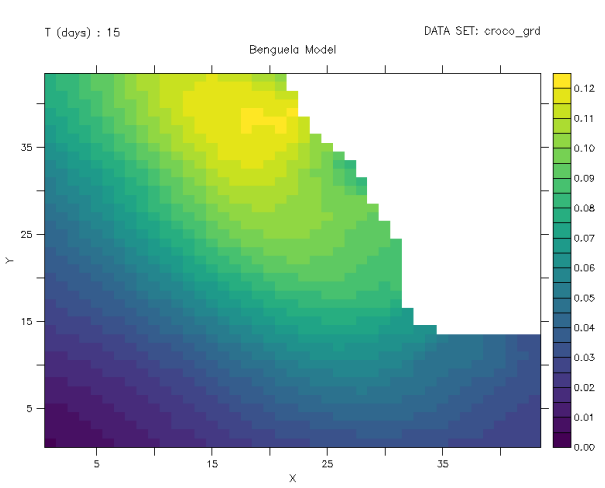
surface NO3 (mmol/m3)



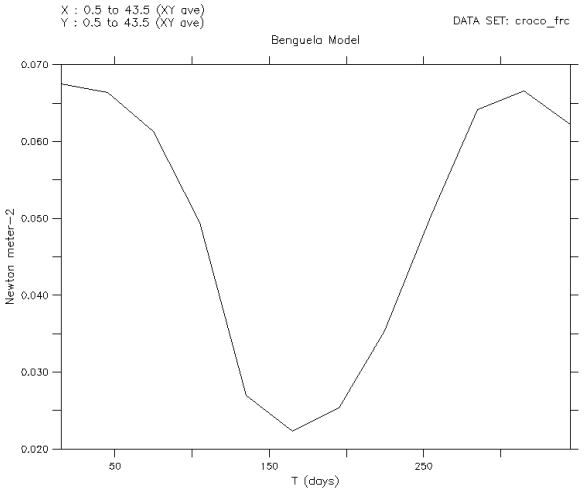
Bottom NO3 (mmol/m3)

- `croco_runoff.nc` : 1D file (t) with river outflow. Here this river input is not considered

- `croco_frc.nc` : 3D (x,y,t) atmospheric forcing file containing the wind stress, heat and freshwater fluxes. Climatological forcing (12 months) from Quikscat (Wind stress) and COADS (fluxes) ocean values are interpolated over land.

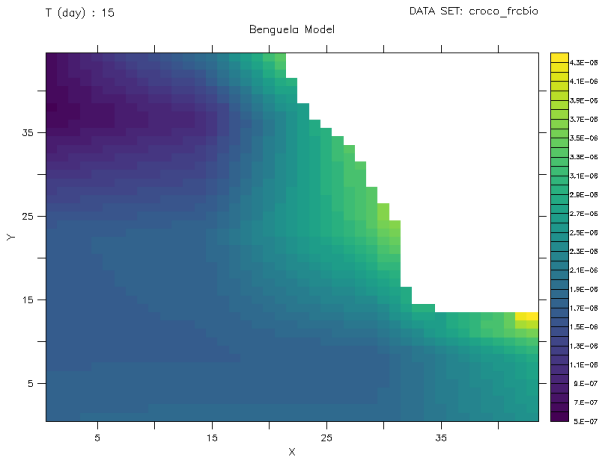


Meridional wind stress (January) N/m2



Seasonal cycle of meridional wind stress

- `croco_ini.nc` : 3D (x,y,z) initial condition file (here january, so identical to 1st file of croco_clm.nc)
- `croco_frcbio.nc` : 3D (x,y,t) iron dust deposition file (climatological)



Fe dust deposition (nmol/m3)

PRACTICAL SESSION

Session 1 : Setting up the 1D configuration of NEMO-PISCES

***Warning*: avoid copying / pasting (or verify them VERY carefully) the command lines indicated in the pdf document of the TP in your terminal because, depending on the environment, this may introduce errors.**

1. System prerequisites

- Fortran compiler
- MPI implementation
- Netcdf package installed on your computing machine
- XIOS package installed on your computing machine
- An arch file set to your computing machine (this just sets paths to XIOS, netcdf and the compiling option which depends on your compiler)

Information to install the necessary environment (libraries, dependencies) to run the NEMO ocean model on your computing machine can be found at :
https://forge.ipsl.jussieu.fr/nemo/chrome/site/doc/NEMO/guide/html/install.html

2. Provided :

- Ocean and biogeochemical boundary and initial conditions and atmospheric forcing at each station
- Namelists of the 1D NEMO-PISCES configuration adapted to each station

You need to copy the tarball of the provided files to the working directory of your computing machine and extract the contents:

- `tar xvzf PISCES_2023.tgz`

A `PISCES` folder should be installed in your working directory (i.e., `$WORK/PISCES/`).

3. Instructions

3.1 Compile XIOS

The outputs of NEMO are managed by the external library XIOS. This library allows a lot of flexibility in the choice of the output variables and output frequencies (amongst other things).

Information on the XIOS library can be found at : https://forge.ipsl.jussieu.fr/ioserver

Before running NEMO, we need to first compile the XIOS library.

- Connect to your computing system and go to your working directory and download the XIOS library :

```
cd $WORK
svn co http://forge.ipsl.jussieu.fr/ioserver/svn/XIOS/trunk@2331 xios
```

- Setup your arch files (one for the environment (`.env`), another for the compiler (`.fcm`) and a last one for the path (`.path`)):

```
cd $WORK/xios/arch
```

In the `arch` directory, examples of arch files can be found, e.g., `arch-X64_JEANZAY.*`

- Compile XIOS referring to the set of your arch files (example here for `X64_JEANZAY`):

```
cd $WORK/xios/
./make_xios --arch X64_JEANZAY --full --prod --job 8
```

XIOS is now compiled.

3.2 Compile and create NEMO executable

Before running NEMO-PISCES, you need to compile the code on your computing machine.

- Go to the NEMO directory :

```
cd $WORK/PISCES/NEMO/
```

- Extract the NEMO code from the tarball file :

```
tar zxvf NEMOGCM.tgz ;  cd NEMOGCM
```

In the `NEMOGCM`, directory, you can see the first level tree structure of NEMO :

- `arch` contains the compilation settings
- `cfgs` contains the reference configurations of NEMO
- `doc` contains the documentation
- `ext` contains external dependencies, e.g., the two-way nesting package of AGRIF
- `mk` contains the compilation scripts
- `src` contains the Fortran model routines, ie.e, the source code
- `tests` contains idealized test-cases
- `tools` contains the pre and post-processing tools

As for XIOS, you need to set the arch file relative to your computing machine environment to compile NEMO. See the NEMO user guide for instructions on setting up your archive file: https://sites.nemo-ocean.io/user-guide/install.html#download-and-install-the-nemo-code

here we used the `arch/CNRS/arch-X64_JEANZAY.fcm`

- **In your arch file, you must ensure that the path to XIOS refers to your XIOS directory** (i.e., `$WORK/xios`). Indeed, as NEMO is compiled with the XIOS library, the `makenemo` compilation script refers to this arch file to create the executable.

- Create and compile the code for the 1D configuration :

The 1D configuration is made upon the reference NEMO configuration `C1D_PAPA` in which the horizontal and vertical grids are defined.

```
./makenemo -n ORCA_1D_PISCES -r GYRE_PISCES -m X64_JEANZAY -j 0 add_key "key_mpi2"

./makenemo -n ORCA_1D_PISCES -r GYRE_PISCES -m X64_JEANZAY clean

cp cfgs/C1D_PAPA/MY_SRC/* cfgs/ORCA_1D_PISCES/MY_SRC/.

./makenemo -n ORCA_1D_PISCES -r GYRE_PISCES -m X64_JEANZAY -j 4
```

4. The NEMO-PISCES 1D configuration

In the 1-D configuration, the size of the domain is 1x1x75, 75 being the number of vertical levels. The user must set several parameters in the namelist of the configuration (`namelist_cfg`):

- the `ln_c1d` flag to `.true.` in the `&namdom` section
- the longitude (`rn_lon1d`) and latitude (`rn_lat1d`) coordinates of the station in the `&namc1d` section
- the depth of the ocean at the given point `rn_bathy` in the `&namusr_def` section

Input data (initial state and forcings) at the location under consideration are required, initial states being set to values of dimension 1x1x75.

Note that in the following, the settings of the 1D configuration namelists have already been done.

5. Run the model

Go to the run directory for the BATS station

```
cd $WORK/PISCES/NEMO/Runs/BATS/
```

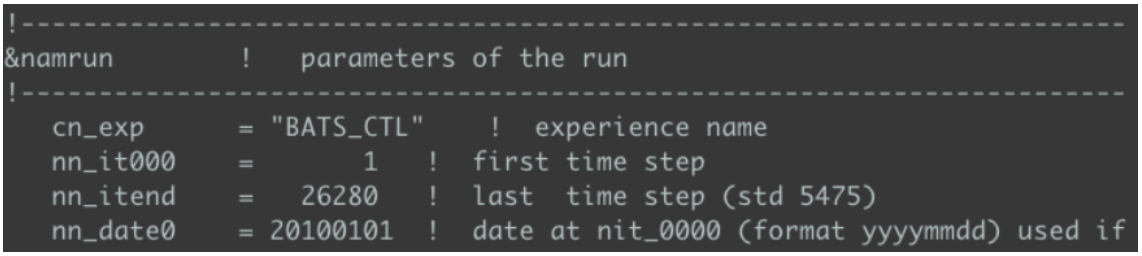
Copy some shared files needed to run the 1D configuration

```
cp /$WORK/PISCES/NEMO/Runs/Shared/* .
```

Explore the run directory and observe the 1D station-specific configuration settings in the namelist files :

1. namelist_cfg

- Set the name of your experience



- Set the 1D configuration option

```
!-----------------------------------------------------------------------
&namdom        !   time and space domain
!-----------------------------------------------------------------------
   ln_linssh   = .true.    !  =T  linear free surface  ==>>  model level are fixed in time
   !
   rn_Dt      = 3600.     !  time step for the dynamics
   !
   ln_c1d      = .true.    !  Single column domain (1x1pt)             (T => fill namc1d)
```

- Ocean depth at the station

```
!-----------------------------------------------------------------------
&namusr_def    !   GYRE user defined namelist
!-----------------------------------------------------------------------
   rn_bathy    =  4556.    ! depth in meters
/
```

- Geographical coordinates of the station

```
!-----------------------------------------------------------------------------
&namc1d        !   1D configuration options
!-----------------------------------------------------------------------------
   rn_lat1d    =    31.5   !  Column latitude
   rn_lon1d    =    -64.   !  Column longitude
/
```

- Initialisation files of temperature and salinity

```
!-----------------------------------------------------------------------
&namtsd        !    Temperature & Salinity Data  (init/dmp)            (default: OFF)
!-----------------------------------------------------------------------
   !                     ! =T  read T-S fields for:
   ln_tsd_init = .true.          !  ocean initialisation

   cn_dir      = './'      !  root directory for the T-S data location
   !___________!_________________________!___________________!___________!_____________!_______!___________
   !           !  file name              ! frequency (hours) ! variable  ! time interp.!  clim  ! 'yearly'/
   !           !                         !  (if <0  months)  !   name    !   (logical) !  (T/F) ! 'monthly'
   sn_tem      = 'InitTS_l75_BATS'    ,         -1.       ,'temp',  .false.     , .true.,  'yearly'  ,    ''
   sn_sal      = 'InitTS_l75_BATS'    ,         -1.       ,'salt',  .false.     , .true.,  'yearly'  ,    ''
/
```

- Atmospheric forcing files at the station

```
!-----------------------------------------------------------------------
&namsbc_blk    !   namsbc_blk  generic Bulk formula                  (ln_blk =T)
!-----------------------------------------------------------------------
   !                   !  bulk algorithm :
   ln_NCAR    = .true.     ! "NCAR"      algorithm   (Large and Yeager 2008)

   cn_dir = './'  !  root directory for the bulk data location
   !___________!_____________     _____________ !___________________!___________!_____________!_______!___________!
   !           !       file name               ! frequency (hours) ! variable  ! time interp.!  clim  ! 'yearly'/ !
   !           !                               !  (if <0  months)  !   name    !   (logical) !  (T/F) ! 'monthly' !
   sn_wndi     = 'CORE2_NY_Forcings_6h_BATS.nc',         6.        , 'U_10_MOD',   .false.   , .true. , 'yearly'  ,
   sn_wndj     = 'CORE2_NY_Forcings_6h_BATS.nc',         6.        , 'V_10_MOD',   .false.   , .true. , 'yearly'  ,
   sn_qsr      = 'CORE2_NY_Forcings_1d_BATS.nc',        24.        , 'SWDN_MOD',   .false.   , .true. , 'yearly'  ,
   sn_qlw      = 'CORE2_NY_Forcings_1d_BATS.nc',        24.        , 'LWDN_MOD',   .false.   , .true. , 'yearly'  ,
   sn_tair     = 'CORE2_NY_Forcings_6h_BATS.nc',         6.        , 'T_10_MOD',   .false.   , .true. , 'yearly'  ,
   sn_humi     = 'CORE2_NY_Forcings_6h_BATS.nc',         6.        , 'Q_10_MOD',   .false.   , .true. , 'yearly'  ,
   sn_prec     = 'CORE2_NY_Forcings_1m_BATS.nc',        -1.        , 'PRC_MOD1',   .false.   , .true. , 'yearly'  ,
   sn_snow     = 'CORE2_NY_Forcings_1m_BATS.nc',        -1.        , 'SNOW'    ,   .false.   , .true. , 'yearly'  ,
   sn_slp      = 'CORE2_NY_Forcings_6h_BATS.nc',         6.        , 'SLP'     ,   .false.   , .true. , 'yearly'  ,
/
```

- Chlorophyll for bio penetration

```
!-----------------------------------------------------------------------
&namtra_qsr    !   penetrative solar radiation                    (ln_traqsr =T)
!-----------------------------------------------------------------------
   !                     !  type of penetration                    (default: NO selection)
   ln_qsr_rgb  = .true.      !  RGB light penetration (Red-Green-Blue)

   cn_dir      = './'      !  root directory for the chlorophyl data location
   !___________!_____________________!___________________!___________!_____________!_______!___________!
   !           !  file name          ! frequency (hours) ! variable  ! time interp.!  clim  ! 'yearly'/ !
   !           !                     !  (if <0  months)  !   name    !   (logical) !  (T/F) ! 'monthly' !
   sn_chl      ='CHLA_BATS'          ,       -1.        , 'CHLA'    ,   .true.    , .true. , 'yearly'  , '
/
```

- Runoff at the station, if needed, e.g., at DYFAMED

```
!-----------------------------------------------------------------------
&namsbc_rnf    !   runoffs                                        (ln_rnf =T)
!-----------------------------------------------------------------------
   ln_rnf_mouth = .false.    !  specific treatment at rivers mouths
      rn_hrnf     =  15.e0    !  depth over which enhanced vertical mixing is used    (ln_rnf_mouth=T)
      rn_avt_rnf  =   1.e-3   !  value of the additional vertical mixing coef. [m2/s] (ln_rnf_mouth=T)
   rn_rfact    =   1.e0    !  multiplicative factor for runoff

   cn_dir = './'  !  root directory for the location of the runoff files
   !___________!_____________!___________________!___________!_____________!________!___________!_________
   !           !  file name  ! frequency (hours) ! variable  ! time interp. !  clim  ! 'yearly'/ ! weights
   !           !             !  (if <0  months)  !   name    !   (logical)  !  (T/F) ! 'monthly' ! filename
   sn_rnf      = 'runoff_DYFAMED.nc',    -1.    , 'sorunoff',   .true.     , .true. , 'yearly'  , ''       ,
   sn_cnf      = 'runoff_DYFAMED.nc',     0.    , 'socoefr0',   .false.    , .true. , 'yearly'  , ''       ,
/
```

2. namelist_top_cfg

- PISCES initial data

```
!-----------------------------------------------------------------------
&namtrc_dta      !    Initialisation from data input file
!-----------------------------------------------------------------------
!         !  file name  ! frequency (hours) ! variable  ! time interp. !  clim  ! 'yearly'/ ! weights  ! rotation ! land/sea mask
!         !             !  (if <0  months)  !   name    !   (logical)  !  (T/F) ! 'monthly' ! filename ! pairing  ! filename
   sn_trcdta(1)  = 'Glodapv2.1_annual_l75_BATS.nc',      -12.         , 'TDIC'    ,    .false.   , .true. , 'yearly'  , ''
   sn_trcdta(2)  = 'Glodapv2.1_annual_l75_BATS.nc',      -12.         , 'Alkalini',    .false.   , .true. , 'yearly'  , ''
   sn_trcdta(3)  = 'WOA2009_monthly_l75_BATS.nc'  ,       -1.         , 'O2'      ,    .true.    , .true. , 'yearly'  , ''
   sn_trcdta(5)  = 'WOA2009_monthly_l75_BATS.nc'  ,       -1.         , 'PO4'     ,    .true.    , .true. , 'yearly'  , ''
   sn_trcdta(7)  = 'WOA2009_monthly_l75_BATS.nc'  ,       -1.         , 'Si'      ,    .true.    , .true. , 'yearly'  , ''
   sn_trcdta(10) = 'PISCES_monthly_l75_BATS.nc'   ,       -1.         , 'DOC'     ,    .true.    , .true. , 'yearly'  , ''       ,
   sn_trcdta(14) = 'PISCES_monthly_l75_BATS.nc'   ,       -1.         , 'Fer'     ,    .true.    , .true. , 'yearly'  , ''       ,
   sn_trcdta(23) = 'WOA2009_monthly_l75_BATS.nc' ,        -1.         , 'NO3'     ,    .true.    , .true. , 'yearly'  , ''
```

- Nutrients from external inputs (surface deposition of dust and nitrogen)

```
!-----------------------------------------------------------------------
&namtrc_bc       !   data for boundary conditions
!-----------------------------------------------------------------------
!               !  file name        ! frequency (hours) ! variable      ! time interp. !  clim  ! 'yearly'/ !
!               !                   !  (if <0  months)  !   name        !   (logical)  !  (T/F) ! 'monthly' !
   sn_trcsbc(5)  = 'DustNew_BATS'    ,       -1          , 'dustpo4'     ,  .true.      , .true. , 'yearly'   ,
   sn_trcsbc(7)  = 'DustNew_BATS'    ,       -1          , 'dustsi'      ,  .true.      , .true. , 'yearly'   ,
   sn_trcsbc(14) = 'DustNew_BATS'    ,       -1          , 'dustfer'     ,  .true.      , .true. , 'yearly'   ,
   sn_trcsbc(23) = 'Ndep_BATS'       ,      -12          , 'ndep2'       ,  .false.     , .true. , 'yearly'   ,
```

3. namelist_pisces_cfg

- Photosynthetically Available Radiation (from a file)

```
!-----------------------------------------------------------------------
&nampisopt     !   parameters for optics
!-----------------------------------------------------------------------
   sn_par      = 'par_fr_gewex_clim_BATS.nc'       ,     24.           , 'fr_par'   ,   .true.
   cn_dir      = './'      !  root directory for the location of the dynamical files
   ln_varpar   =  .true.   ! boolean for PAR variable
   parlux      =  0.43      ! Fraction of shortwave as PAR
/
```

- Nutrients from external inputs (iron from sediments, dust in water column)

```
!-----------------------------------------------------------------------
&nampisbc      !   parameters for inputs deposition
!-----------------------------------------------------------------------
!              !  file name        ! frequency (hours) ! variable  ! time interp. !  clim  ! 'yearly'/ !
!              !                   !  (if <0  months)  !   name    !   (logical)  !  (T/F) ! 'monthly' !
   sn_dust     = 'DustNew_BATS'     ,     -1            , 'dust'      ,  .true.      , .true. , 'yearly'
   sn_ironsed  = 'pmarge_etopo_BATS',    -12.           , 'bathy'     ,  .false.     , .true. , 'yearly'
   ln_ironsed  =  .true.   ! boolean for Fe input from sediments
/
```

Copy the executable in your run directory and run the model and launch the executable

```
cp $WORK/PISCES/NEMO/NEMOGCM/cfgs/ORCA_1D_PISCES/BLD/bin/nemo.exe .

./nemo.exe &
```

The run takes a few minutes to complete.

6. Results

One file has been created : `BATS_CTL_1m_20100101_20121231_nemo.nc`

Now you will explore some physical and biogeochemical variables. For that, you can open the "`1.1.NEMO_PISCES_1D_results`" notebook file. You will need to install python and some modules (matplotlib, xarray and Jupyter Notebook) to use this Notebook file. The Anaconda distribution can be used for this if python and the various packages are not installed on your computer. Finally, you will also need to define the path to the directory in which the file was created, so that you can explore the results.

Session 2 : Sensitivity experiments at BATS

In this session, you will explore the sensitivity of the model to some parameters and see how they impact the solution at the BATS station. To do this, you will modify the values of some biogeochemical parameters in the namelists dedicated to PISCES and compare the results to the run performed in the morning as a control run.

To explore the results of these new simulations, we recommend that you duplicate the `NEMO_PISCES_1D_results.ipynb` file, so as to retain the original document, rename it and adapt the scripts to your needs.

1. Remove all the nutrient supplies.

In the `namelist_top_cfg`, disable the surface deposition of nutrients :

```
!-----------------------------------------------------------------------
&namtrc         !   tracers definition
!-----------------------------------------------------------------------
   jp_bgc       =  24
!
   ln_pisces    =  .true.
!
   ln_trcdta    =  .true.  !  Initialisation from data input file (T) or not (F)
   ln_trcbc     =  .false. !  Enables Boundary conditions
!               !          !                                  !           !        !
!               !    name  !          title of the field      !   units   ! init   ! sbc
   sn_tracer(5)  = 'PO4     ' , 'Phosphate Concentration      ',  'mol-C/L' , .true.  , .true.
   sn_tracer(7)  = 'Si      ' , 'Silicate Concentration       ',  'mol-C/L' , .true.  , .true.
   sn_tracer(14) = 'Fer     ' , 'Dissolved Iron Concentration ',  'mol-C/L' , .true.  , .true.
   sn_tracer(23) = 'NO3     ' , 'Nitrates Concentration       ',  'mol-C/L' , .true.  , .true.
```

Set the name of the experience in `namelist_cfg` (BATS_no_surf_nut, for instance), run the model and compare it to the control simulation.

2. Photosynthetic / Irradiance ratio experiments.

In the `namelist_pisces_cfg`, increase and decrease the `pislopen`, `pisloped` parameters by 50% and compare to CTL.

```
!-----------------------------------------------------------------------
&namp4zprod    !   parameters for phytoplankton growth for PISCES std  - ln_p4z
!-----------------------------------------------------------------------
   pislopen    =  2.       ! P-I slope
   pisloped    =  2.       ! P-I slope  for diatoms
```

Set the name of the experience in `namelist_cfg` (BATS_pislope_inc and BATS_pislope_dec, for instance), run the model and compare to the CTL simulation.

3. Half-saturation constant experiments

In the `namelist_pisces_cfg`, increase and decrease the half-saturation constants of both NO3 and NH4 by 50% for both phytoplankton groups and compare to CTL.

```
!-----------------------------------------------------------------------
&namp4zlim     !   parameters for nutrient limitations for PISCES std  - ln_p4z
!-----------------------------------------------------------------------
   concnno3   =  1.e-6     ! Nitrate half saturation of nanophytoplankton
   concdno3   =  3.E-6     ! Nitrate half saturation for diatoms
   concnnh4   =  1.E-6     ! NH4 half saturation for phyto
   concdnh4   =  3.E-6     ! NH4 half saturation for diatoms
```

Set the name of the experience in `namelist_cfg` (BATS_halfsat, for instance), run the model and compare to the CTL simulation.

4. Zooplankton grazing rate experiments

Decrease by 50% the grazing rates `grazrat` and `grazrat2` of both zooplankton groups simultaneously.

```
!-----------------------------------------------------------------------
&namp4zzoo     !   parameters for microzooplankton for PISCES std      - ln_p4z
!-----------------------------------------------------------------------
   part       =  0.75     ! part of calcite not dissolved in microzoo guts
   grazrat    =  2.0      ! maximal zoo grazing rate
```

```
!-----------------------------------------------------------------------
&namp4zmes     !   parameters for mesozooplankton for PISCES std       - ln_p4z
!-----------------------------------------------------------------------
   part2      =  0.75     ! part of calcite not dissolved in mesozoo guts
   grazrat2   =  0.5      ! maximal mesozoo grazing rate
```

Set the name of the experience in `namelist_cfg` (BATS_grazrat, for instance), run the model and compare to the CTL simulation.

Repeat that step by changing `grazrat2` only and compare it to the previous and CTL tests.

Then reduce by 50% the `mzrat2` parameter.

```
!-----------------------------------------------------------------------
&namp4zmes     !   parameters for mesozooplankton for PISCES std       - ln_p4z
!-----------------------------------------------------------------------
   part2      =  0.75     ! part of calcite not dissolved in mesozoo guts
   grazrat2   =  0.5      ! maximal mesozoo grazing rate
   resrat2    =  0.005    ! exsudation rate of mesozooplankton
   mzrat2     =  0.01     ! mesozooplankton mortality rate
```

What do you observe for the mesozooplankton biomass relative to the CTL simulation?

5. Scavenging rate experiment

Increase the scavenging rate `xlam1` by a factor of 10.

```
!-----------------------------------------------------------------------
&nampisfer     !   parameters for iron chemistry
!-----------------------------------------------------------------------
   ln_ligvar =  .false.    ! variable ligand concentration
   xlam1     =  0.02       ! scavenging rate of Iron by biogenic particles
```

Set the name of the experience in `namelist_cfg` (BATS_scav, for instance), run the model and compare to the CTL simulation.

6. Maximum phytoplankton Fe/C ratio experiment

Divide by 2 the `fecnm` and `fecdm` values

```
!-----------------------------------------------------------------------
&namp4zprod    !   parameters for phytoplankton growth for PISCES std  - ln_p4z
!-----------------------------------------------------------------------
   pislopen    =  2.       ! P-I slope
   pisloped    =  2.       ! P-I slope  for diatoms
   xadap       =  0.       ! Adaptation factor to low light
   excretn     =  0.05     ! excretion ratio of phytoplankton
   excretd     =  0.05     ! excretion ratio of diatoms
   bresp       =  0.033    ! Basal respiration rate
   chlcnm      =  0.033    ! Maximum Chl/C in nanophytoplankton
   chlcdm      =  0.05     ! Maximum Chl/C in diatoms
   chlcmin     =  0.003    ! Minimum Chl/c in phytoplankton
   fecnm       =  60E-6    ! Maximum Fe/C in nanophytoplankton
   fecdm       =  60E-6    ! Maximum Fe/C in diatoms
   grosip      =  0.13     ! mean Si/C ratio
```

Set the name of the experience in `namelist_cfg` (BATS_fec, for instance), run the model and compare to the CTL simulation.

7. Small particle sinking speed experiment

Adjust the sinking speed of small particles (`wsbio`) to the same value as that of the large particles.

```
!-----------------------------------------------------------------------
&nampisbio     !   biological parameters
!-----------------------------------------------------------------------
   nrdttrc     =  1        ! time step frequency for biology
   wsbio       =  2.       ! POC sinking speed
   xkmort      =  2.E-7    ! half saturation constant for mortality
   ferat3      =  10.E-6   ! Fe/C in zooplankton
   wsbio2      =  50.      ! Big particles sinking speed
   wsbio2max   =  50.      ! Big particles maximum sinking speed
```

Set the name of the experience in `namelist_cfg` (BATS_wsbio, for instance), run the model and compare to the CTL simulation.

Session 3 : Sensitivity experiments at different stations

In this session, you will explore the sensitivity of the model at other stations (NABE, KERFIX, DYFAMED, HOT) for the NEMO-PISCES 1D configuration or in the Benguela region for CROCO-PISCES. In groups of 3 or 4, you will compare and interpret the results obtained in relation to the physical and biochemical variables of the control experiment.

For sensitivity experiments with the CROCO-PISCES model, first set up the BENGUELA Low Resolution configuration (see notebook file 3.1.CROCO-PISCES-Setup), run the control experiment and then the sensitivity experiments.

NEMO-PISCES 1D

For the NEMO-PISCES 1D experiments, you will need to create a directory for each station as for BATS, run the model and save the outputs.

1. Repeat the steps at the NABE station.

Compare the results to the CTL simulation. Interpret the differences obtained in relation to those with BATS. Remember to back up the control run at NABE before performing the sensitivity experiments.

2. Repeat these steps at the KERFIX station

Compare the results to the CTL simulation. Interpret the differences obtained in relation to those with BATS. Remember to back up the control run at KERFIX before performing the sensitivity experiments.

3. Repeat these steps at the DYFAMED station

Compare the results to the CTL simulation. Interpret the differences obtained in relation to those with BATS. Remember to back up the control run at DYFAMED before performing the sensitivity experiments.

4. Repeat these steps at the HOT station

Compare the results to the CTL simulation. Interpret the differences obtained in relation to those with BATS. Remember to back up the control run at HOT before performing the sensitivity experiments.

CROCO-PISCES

In these sensitivity tests, you will study the biogeochemical impacts induced by the modification of certain parameters on phytoplankton, chlorophyll and nutrients. To do this, you will run a one-year simulation of CROCO-PISCES with the Benguela Low Resolution configuration.

First, you'll need to run a control simulation, i.e. without modifying the PISCES parameters (see `3.1.CROCO_PISCES_Setup` notebook). Each run lasts about 7 minutes.

1. Suppression of iron flux from sediment

In this first sensitivity test, we investigate the impact of turning off the iron sediment source.

Open the `namelist_pisces_cfg` file and set the sediment Fe input boolean `ln_ironsed` to `.false.` in the `&nampissbc` section.

Rename the experiment by editing the title in the `croco.in` file, `BENGUELA_No_Iron_Sed` for instance.

Run the model, compare and interpret the differences simulated with those of the control experiment.

2. Modification of P-I slope parameters

In this second sensitivity experiment, you will study the impacts induced by changes in P-I slope parameters for diatoms and nanophytoplankton.

- First, increase the P-I slope parameters for diatoms and nanophytoplankton by 50% :

Open the `namelist_pisces_cfg` file and set the `pislopen` and `pisloped` to 3 in the `&namp4zprod` section.

Rename the experiment by editing the title in the `croco.in` file, `BENGUELA_PI_Slope_Inc` for instance.

Run the model, compare and interpret the differences simulated with those of the control experiment.

- Second, decrease the P-I slope parameters for diatoms and nanophytoplankton by 50%

Open the `namelist_pisces_cfg` file and set the `pislopen` and `pisloped` to 1 in the `&namp4zprod` section.

Rename the experiment by editing the title in the `croco.in` file, `BENGUELA_PI_Slope_Dec` for instance.

Run the model, compare and interpret the differences simulated with those of the control experiment.

3. Modification of microzooplankton grazing

In this sensitivity test, we investigate the biogeochemical impacts of decreasing the microzooplankton grazing rate on both phytoplankton groups, chlorophyll and nutrients.

Open the `namelist_pisces_cfg` file and set the `grazrat` to 1.5 in the `&namp4zzoo` section.

Rename the experiment by editing the title in the `croco.in` file, `BENGUELA_Grazrat_Dec` for instance.

Run the model, compare and interpret the differences simulated with those of the control experiment.

Session 3 : Setting up the BENGUELA configuration of CROCO-PISCES

1. Download and compile

Go in the run directory for CROCO

```
cd $WORK/PISCES/CROCO/
```

Extract the code from the tarball file

```
tar zxvf croco-v1.3.tgz
```

Set the run configuration

```
 cd croco-v1.3 ; ./create_config.bash
```

Answer yes to the following questions :

```
Do you want to proceed ? [Y/n] y
```

```
Do you want to proceed without MATLAB tools ? [Y/n] y
```

The error messages at the end are not important, as they are linked to croco_tools, which is not used here.

A directory named `Run_Benguela_LR` has been created.

2. Compile the code

Beforehand, you'll need to define the following information in the `jobcomp` file:

- your Fortran compiler. See informations in the tutorial sections of the CROCO documentation https://croco-ocean.gitlabpages.inria.fr/croco_doc/tutos/tutos.00.env.html
- the path to the xios directory (already compiled for the NEMO 1D configuration). See https://croco-ocean.gitlabpages.inria.fr/croco_doc/tutos/tutos.20.xios.html

```
cd $WORK/PISCES/CROCO/Run_BENGUELA_LR
./jobcomp
```

Create xml files needed for XIOS

```
./process_xios_xml.sh
```

Note: The outputs of CROCO can be managed by using the external library XIOS. This library allows a lot of flexibility in the choice of the output variables and output frequencies (amongst other things). Here you can use the XIOS executable compiled for the NEMO configuration.

Information on the XIOS library and its used can be found at :

- https://forge.ipsl.jussieu.fr/ioserver
- https://www.croco-ocean.org/documentation/

3. Running the model configuration

Copy the input files

```
cd $WORK/PISCES/CROCO/Run_BENGUELA_LR/CROCO_FILES/

ln -sf /$WORK/PISCES/CROCO/Inputs/Run_BENGUELA_LR/* .
```

Run the model configuration

```
cd ..
mpirun -np 4 ./croco > benguela.log &
```

After 7 or 8 minutes, you get the outputs of the reference model experiment :

- `BENGUELA_CTL_1m_pisces.nc`
- `BENGUELA_CTL_1m_aver.nc`

You can change the name of the next experiments by editing the `croco.in` file :

`title: BENGUELA_CTL`

Session 4 : Scientific questions

By group of 3 or 4, you will investigate some scientific questions with the ocean platform of your choice. Four questions are proposed for NEMO-PISCES and 2 questions for CROCO-PISCES. You can choose any scientific question you want, agreeing with the other groups in order to not choose the same question. You will explore the results and prepare a 5-minute presentation on the biogeochemical impacts and the physical and/or biogeochemical mechanisms controlling these changes.

From a practical point of view, in this session, you will have to modify either the code or the namelist file depending on your scientific questions.

NEMO session

First hint : for questions 1, 2 and 3, you will have to modify the Fortran routine `sbcblk.F90` where the atmospheric forcing fields are read.

These atmospheric forcing fields are read by calling the `fld_read` subroutine in the `sbcblk.F90` routine, i.e. :

```
CALL fld_read( kt, nn_fsbc, sf )
```

- The air temperature variable is : `sf(jp_tair)%fnow(:,:,1)`
- The zonal component of the wind is : `sf(jp_wndi)%fnow(:,:,1)`
- The meridional component of the wind is : `sf(jp_wndj)%fnow(:,:,1)`
- The total precipitation is : `sf(jp_prec)%fnow(:,:,1)`

Second hint : Before modifying the routine, you must copy it from the WORK sub-directory to the MY_SRC sub-directory, which is located in the ORCA_1D_PISCES configuration directory.

```
cp $WORK/PISCES/NEMO/Code/NEMOGCM/cfgs/ORCA_1D_PISCES/WORK/sbcblk.F90
$WORK/PISCES/NEMO/Code/NEMOGCM/cfgs/ORCA_1D_PISCES/MY_SRC/.
```

Once the routine has been correctly modified to suit your scientific question, you will have to recompile the code before running your experiments.

Question 1 : What are the impacts of altered physical factors in a context of climate change on the seasonal cycle of nutrients and marine productivity?

You can explore this question at one or different stations : BATS, HOT, NABE, DYFAMED.

You will need to perform :

1. a pre-industrial control simulation
2. a simulation with 2°C atmospheric surface warming and atmospheric CO2 concentration increased to 450 ppm
3. a simulation with 4°C atmospheric surface warming and atmospheric CO2 concentration increased to 800 ppm

To modify the partial pressure of atmospheric CO2, you have to change the `atcco2` value parameter in the `namelist_pisces_cfg` file.

Question 2 : How do a set of physical and biogeochemical variables respond to a halving of the surface wind at the KERFIX station?

You will need to perform :

1. a control simulation where no modifications are added to the forcing files
2. a simulation in which the zonal and meridional wind components used to force the NEMO-PISCES model are divided by a factor of 2 at all time steps

Question 3 : How precipitation influences nutrient and chlorophyll distribution at the NABE station?

You will have to perform :

1. A control simulation in which precipitation forcing remains unchanged
2. A simulation in which precipitation is divided by 2

Question 4 : What are the potential biogeochemical impacts of a significant increase in iron inputs from atmospheric deposition in the Kerguelen region (KERFIX station)?

You will have to perform :

1. a control simulation with both phytoplankton groups
2. a simulation with an increase by a factor of 1000 of Fe dust input

The Fe dust input coefficient is `rn_trsfac(14)` and can be modified in the `namelist_top_cfg`

CROCO session

Question 1 : What are the impacts of the wind stress on marine biogeochemistry in the Benguela region?

You will have to perform :

1. a control simulation with standard seasonal variations in wind stress
2. a simulation with an annual mean wind stress
3. a simulation with a wind stress divided by 2
4. a simulation with a windstress multiplied by 2

To set the appropriate wind stress state, you will have to modify the `croco.in` file to set up the right forcing file, i.e., `croco_frc_uvstr_mean.nc`, `croco_frc_uvstr_half.nc` and `croco_frc_uvstr_doubled.nc`

Question 2 : What is the impact of the diatom group on marine biogeochemistry in the Benguela region?

You will have to perform :

1. a control simulation
2. a simulation in which you will kill the growth rate of diatoms (hint: you can do this with the diatom P-I slope parameter