Tutorial for practical sessions 1 and 2.

January 17th and 18th

1. Purpose

Through this tutorial, we will review the basic instructions to work in practical sessions 1 and 2 of CROCO / PISCES.

For this, the first step is to enter the calculation server used in the first week of the Summer School where a simple simulation of the Benguela domain was configured and launched. To do this, follow the basic instructions of the NLHPC cluster.

2. A Discord server has been configured for these practical sessions

The objectives of this server are:

a) Propose a tool for the course participants to interact easily and quickly with the assistants/teachers and other students.

b) Post figures, scripts, and comments that may be of interest to the session.

c) Request help during practical work. Chat rooms and voice rooms have been created for this.

You can join this server through the following link:

https://discord.gg/4SErKYek

During each personal work session, there will be assistants and teachers who will answer your questions or requests for help, either by chat or by voice exchange (with or without screen sharing).

You can find the files associated with this tutorial in the folder

http://mosa.dgeo.udec.cl/CROCO2022/AdvancedCourse

3. Practice 1 (day one, 17th January)

General objective:

Prepare the CROCO-PISCES input files in the Benguela configuration using Matlab scripts and explore the outputs using ferret scripts.

a) Open Matlab according to the instructions indicated in Tutorial_01, section 7.2. If you work with Octave, follow the instructions in Tutorial_01 indicated in section 7.3.

Then write:

>> make_clim_pisces

You should get the following:

```
Add_po4: creating variables and attributes for the OA file
Add_po4: creating variables and attributes for the Climatology file
Add_sio3: creating variables and attributes for the OA file
Add_sio3: creating variables and attributes for the Climatology file
Add_o2: creating variables and attributes for the OA file
Add_o2: creating variables and attributes for the Climatology file
Add_dic: creating variables and attributes for the OA file
Add_dic: creating variables and attributes for the Climatology file
Add_talk: creating variables and attributes for the OA file
```

Then write:

>> make_ini_pisces

You should get the following:

```
nitrate ...

 Ext_tracers: ro = 0 km - default value = NaN
   ext_tracers_ini: time index: 1 of total: 12
   ext_tracers_ini: horizontal interpolation of seasonal data
   ext_tracers_ini: vertical interpolation

phosphate ...

 Ext_tracers: ro = 0 km - default value = NaN
   ext_tracers_ini: time index: 1 of total: 12
   ext_tracers_ini: horizontal interpolation of seasonal data
   ext_tracers_ini: vertical interpolation
```

Then write:

>> make_dust

<u>You should get the following:</u>

```
 Read in the grid...
 Creating file
Getting dust for time index 1
Getting dust for time index 2
Getting dust for time index 3
Getting dust for time index 4
Getting dust for time index 5
Getting dust for time index 6
Getting dust for time index 7
Getting dust for time index 8
Getting dust for time index 9
Getting dust for time index 10
Getting dust for time index 11
Getting dust for time index 12
```

b) In your Benguela_LR Configuration go to *crocotools_param.m* and "activate" **makepisces = 1**

```
%  initial/boundary data options (1 = process)
%  (used in make_clim, make_biol, make_bry,
%   make_OGCM.m and make_OGCM_frcst.m)
%
makeini    = 1;   % initial data
makeclim   = 1;   % climatological data (for boundaries and nudging layers)
makebry    = 1;   % lateral boundary data
makenpzd   = 0;   % initial and boundary data for NChlPZD and N2ChlPZD2 models
makebioebus= 0;   % initial and boundary data for BioEBUS model
makepisces = 1;   % initial and boundary data for PISCES model
```

c) Open cppdefs.h and edit **"define BIOLOGY"**

```
                        /* Applications */
# define  BIOLOGY
# undef  FLOATS
# undef  STATIONS
# undef  PASSIVE_TRACER
# undef  SEDIMENT
# undef  BBL
```

d) In cppdefs.h **"define PISCES"**

```
                    /*   Choice of Biology models    */
# ifdef BIOLOGY
#  define  PISCES
#  undef  BIO_NChlPZD
#  undef  BIO_N2ChlPZD2
#  undef BIO_BioEBUS
```

e) Compile the code (as we made changes in cppdefs.h)

./jobcomp

f) Launch the simulation according to the instructions in Tutorial_01, section 8.

sbatch run_nlhpc.bash

g) Output files are:

croco_avg.nc
croco_his.nc
croco_rst.nc
croco_diabio_avg.nc
croco_diabio.nc

*** croco_frcbio_avg.nc is an atmospheric deposition forcing of Fe (not an output from PISCES **)*

h) To view the outputs, follow the instructions indicated in Tutorial_01, section 10:

- with the command **ncdump**, we can see the information in the **croco_avg.nc** file

```
ml purge
ml netCDF-Fortran/4.4.4
ncdump -h CROCO_FILES/croco_avg.nc | less
```

- with the command **ncview,** we can preview **croco_avg.nc**

```
ml purge
ml icc/2019.2.187-GCC-8.2.0-2.31.1 impi/2019.2.185 ncview/2.1.7
ncview CROCO_FILES/croco_avg.nc
```

i) If we open **croco_avg.nc** with **ncview**, they should see the following:

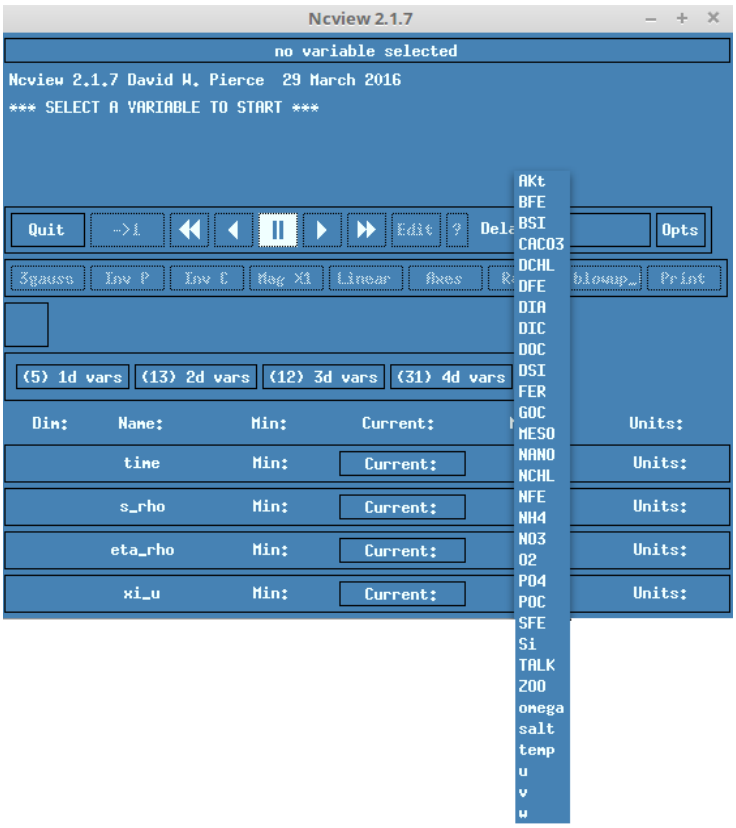


Figure 1: Graphical interface of ncview indicating the biogeochemical variables obtained from CROCO-PISCES (CaCO3, DCHL, NO3, DFE, O2, etc).

j) If we click on **NO3**, we would see the following

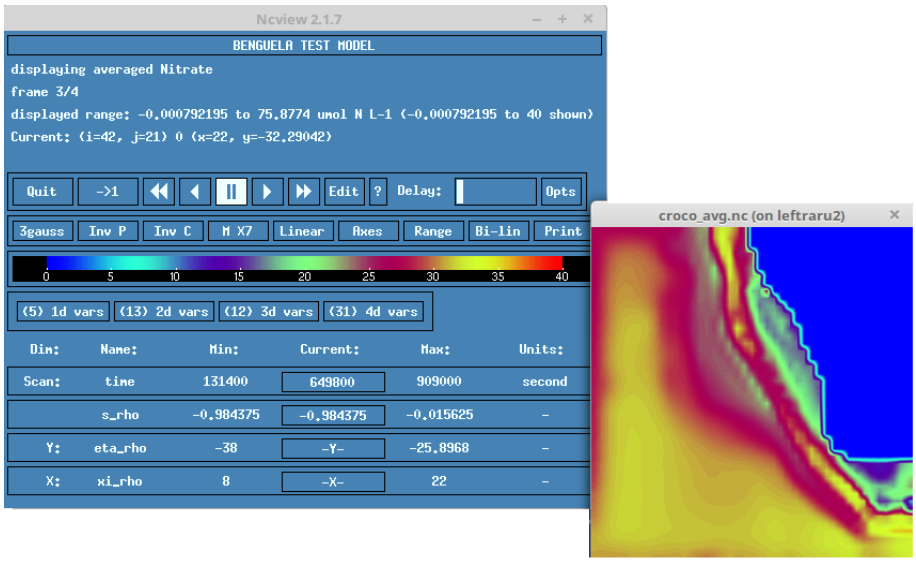


Figure 2: Nitrate at deep level (s_rho: -0.984375).

k) If we open **croco_diabio_avg**.nc with **ncview**, we should see the following:

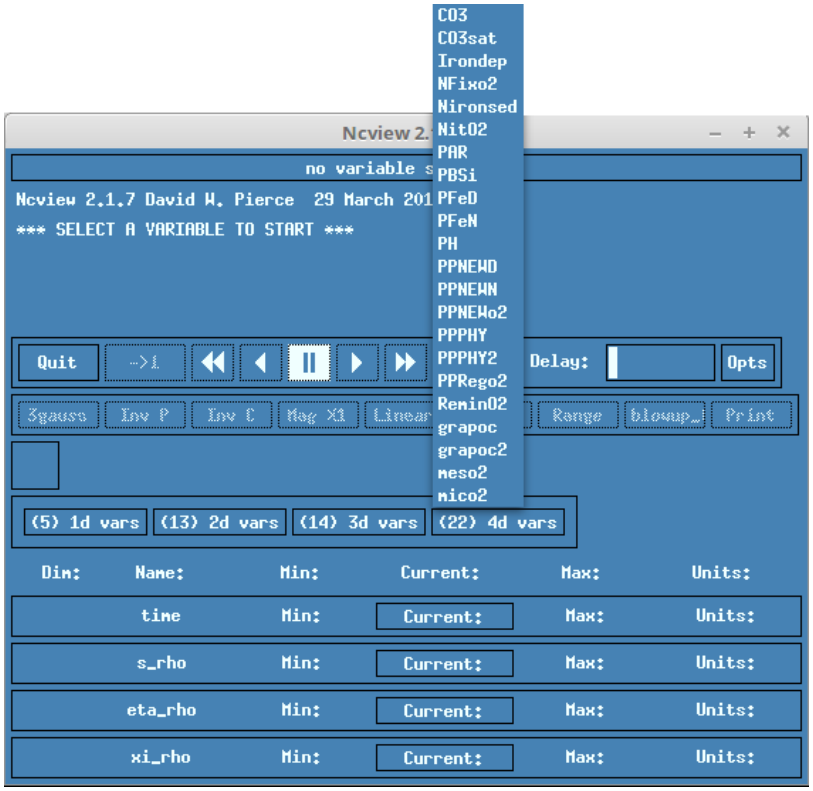


Figure 3: Graphic interface of ncview indicating the Diagnostic variables obtained from PISCES.

l) If we open **croco_frcbio_avg**.nc with **ncview**, we should see the following:

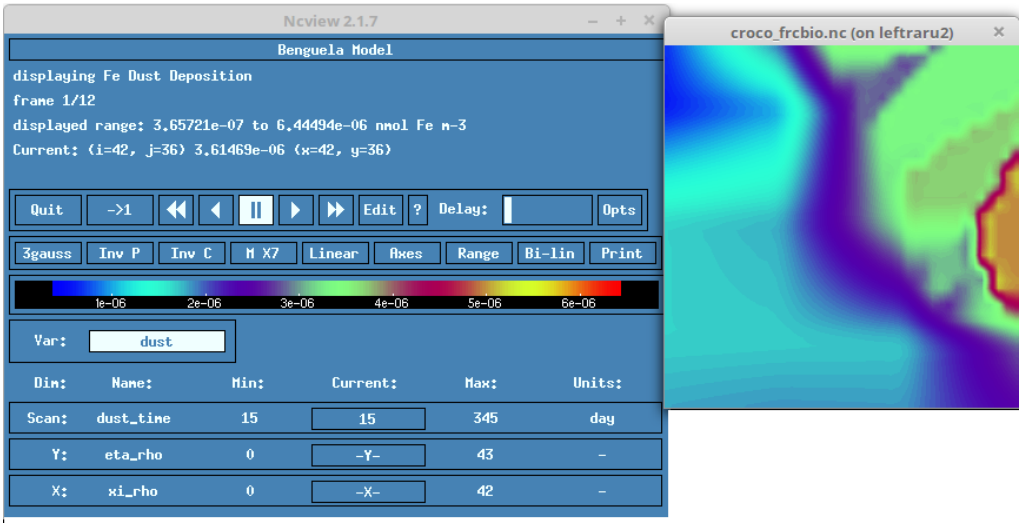


Figure 4: Atmospheric Fe deposition.

3.1. Viewing the outputs

General objective:

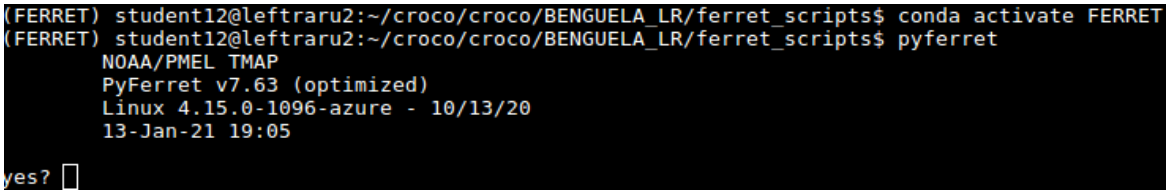
To visualize the results of the simulations that you will carry out throughout this session, you can use Ferret (PyFerret v7.63).

Ferret scripts are particularly convenient and fast for exploring the CROCO generated variables in netcdf format.

To load the Ferret sofware, we must write:

ml Miniconda3/4.5.12
conda activate FERRET
pyferret

You will see the following:



I) Activity 1

a) Exploratory analysis of surface variables:

From the croco_avg.nc file obtained from the CROCO-PISCES simulation in the BENGUELA_LR Configuration, make the following figures for time t=1d and t=30d: NO3, Total Chlorophyll, Diatoms, Nanophytoplankton, Mesozooplankton, Microzooplankton, PO4 and Oxygen.

Use the ferret script: comp_varsurf_run1_run2.jnl

to run a ferret script , type: **>> go script_name.jnl [enter]**

Example:

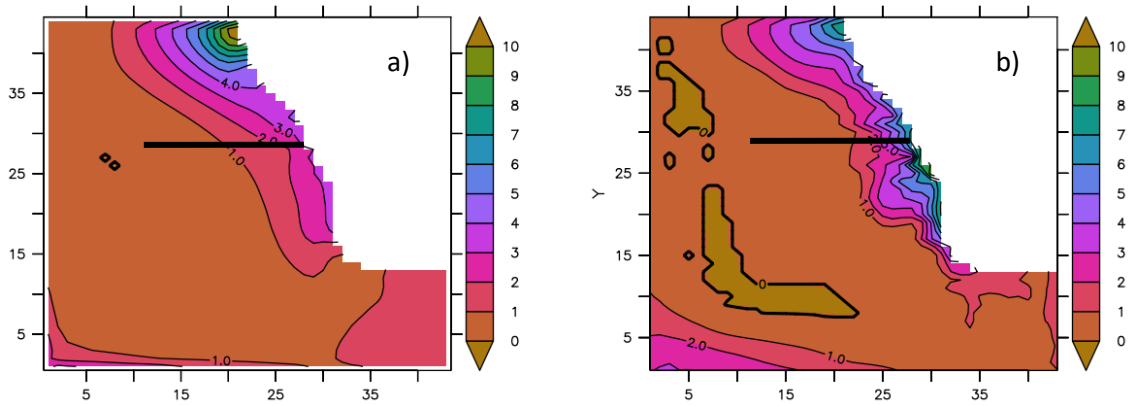


Figure 5: Surface Nitrate (NO3), (a) t=1d and (b) t=30d.

b) Exploratory analysis of longitudinal sections at 30ºS (Fig. 5 indicates the transect)

From the croco_avg.nc file obtained from the CROCO-PISCES simulation in the BENGUELA_LR Configuration, make the following figures for time t=30d: NO3, Total chlorophyll (DCHL + NCHL), Chlorophyll in nanophytoplankton (NCHL), Chlorophyll in diatoms (DCHL), Diatoms and nanophytoplankton.

Use the ferret script: sect_xz_var_croco.jnl

Example:

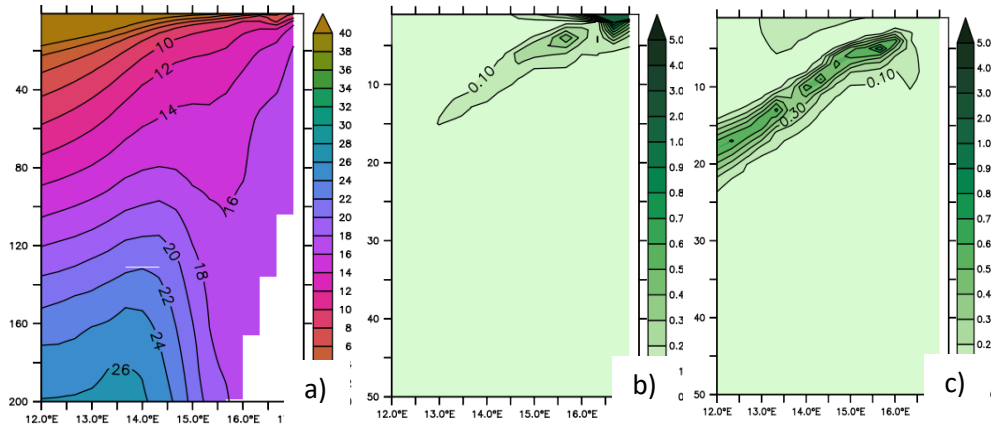


Figure 6: 30°S section, (a) Nitrate, (b) DCHL and (C) NCHL.

II) Activity 2 (day two, 18th January)

- Before you do any new experiment, save the basic simulation in a directory. For this, write the following:

mv croco_avg.nc croco_avg_ref.nc

****croco_avg_ref.nc* is the new name of the original file without modifications.***

- Then create a directory where you keep the original files. For this, write the following:

mkdir REF

After this, move your file ***croco_avg_ref.nc*** to the created directory ***REF.*** For this, write the following:

mv croco_avg.nc croco_avg_ref.nc REF/

Repite this with every sensivity experiment that we will realize during the practice.

a) Iron (Fe) sensivity test

- open ***namelist_pisces_ref*** and modify **ln_ironsed = .false**. (ref = .true.)

```
!''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''''
&nampissbc     !   parameters for inputs deposition
!,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
   ln_dust     =  .true.    ! boolean for dust input from the atmosphere
   ln_river    =  .false.   ! boolean for river input of nutrients
   ln_ndepo    =  .false.    ! boolean for atmospheric deposition of N
   ln_ironsed  =  .true.    ! boolean for Fe input from sediments
   sedfeinput  =  2E-9      ! Coastal release of Iron
   dustsolub   =  0.014     ! Solubility of the dust
   mfrac       =  0.035     ! Fe mineral fraction of dust
   wdust       =  2.0       ! Dust sinking speed
```

Run the simulation:

sbatch run_nlhpc.bash

b) We will obtain the following files:

- *croco_avg.nc*
- *croco_his.nc*
- *croco_rst.nc*
- *croco_diabio_avg.nc*
- *croco_diabio.nc*

*** Don't forget to support first simulation ***

c) From the files obtained by changing ln_ironsed = .false. make the following surface graphs for t = 30d:

1. Standard sim chlorophyll/ new simulation chlorophyll - Standard chlorophyll (difference)
2.-Fe standard simulation / Fe new simulation-Fe standard (difference)
3. Diatoms standard simulation/ new simulation-Standard DIA (difference)
4.-Nano standard sim/ New Nano sim-Standard Nanophytoplankton (difference)
5.-Meso standard sim /Meso new sim-Meso standard (difference)
6. Micro standard sim/ Microzoo new sim-Microzoo standard (difference)
-Use the following script for chlorophyll: *comp_nofesed_run1_run2_chl.jnl*
-Use the following script for the other variables: *comp_nofesed_run1_run2_var.jnl*

Example:

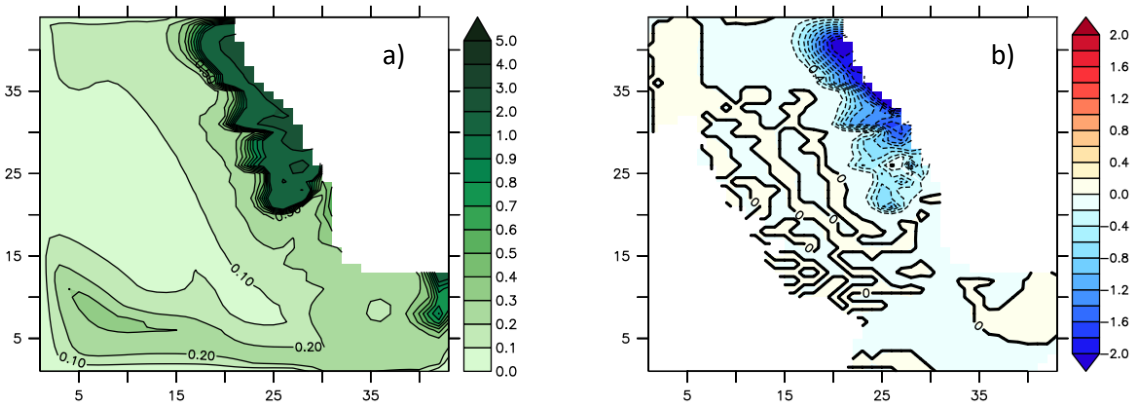


Figure 7: (a) Chl standard simulation and (b) Chl new simulation - Chl standard

*** Don't forget to save this new simulation ***

III) Activity 3

General objective:

Perform sensitivity experiments by changing the values of some PISCES parameters and observe how these modifications affect the different variables in the model.

1) Experiment 1, change of **pislopen** parameter (initial slope of the PI curve in nanophytoplankton)

a) To develop this activity, open **namelist_pisces_ref** and increase the value by 50%. The reference value is 2, therefore its new value must be 3.

```
!-----------------------------------------------------------------------
&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     =  0.004    ! Minimum Chl/c in phytoplankton
   fecnm       =  80E-6    ! Maximum Fe/C in nanophytoplankton
   fecdm       =  80E-6    ! Maximum Fe/C in diatoms
   grosip      =  0.159    ! mean Si/C ratio
/
```

- Run the simulation

sbatch run_nlhpc.bash

b) We will obtain the following files:

- *croco_avg.nc*
- *croco_his.nc*
- *croco_rst.nc*
- *croco_diabio_avg.nc*
- *croco_diabio.nc*

c) From the new netcdf files obtained, use croco_avg.nc and make the following surface figures with t = 30d:

1. Chlorophyll standard sim / Chlorophyll pislopen (+) - Standard chlorophyll (difference).
2. Nitrate standard sim / Nitrate pislopen (+) - Standard nitrate (difference).

Use the following ferret script for chlorophyll: *comp_pislopen_surf_run1_run2_chl.jnl*
Use the following ferret script for the other variables: *comp_pislopen_surf_run1_run2_var.jnl*

Example

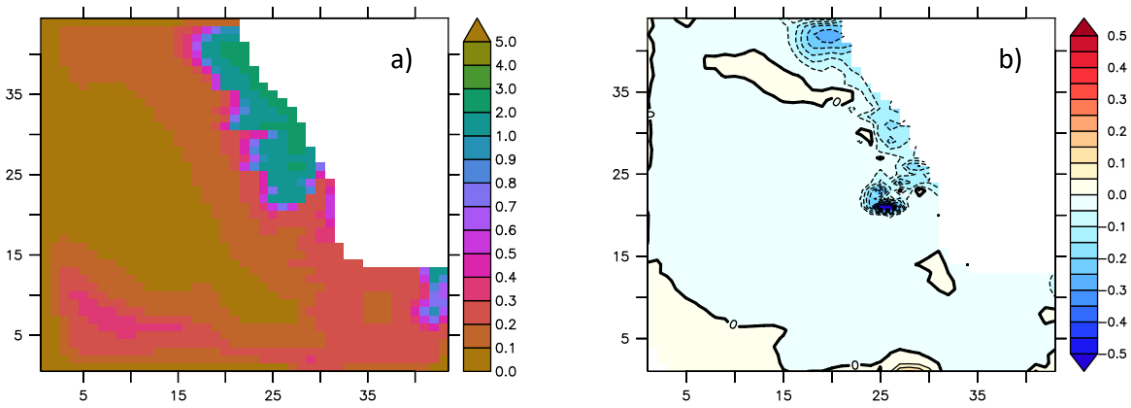


Figure 10: (a) Chl standard sim and (b) Chl pislopen (+) - Standard chl (difference).

d) Exploratory analysis of longitudinal sections at 33ºS
From the new croco_avg.nc file obtained from pislopen (+) experiment, make the following figures for time t=30d:
1. Chlorophyll standard sim / Chlorophyll pislopen (-)/ Chlorophyll pislopen (-) - Standard chlorophyll (difference).

Use the ferret script: *sect_xz_dif_run1_run2_chl.jnl*

*** Don't forget to save the simulation with changes in pislopen (+ 50%) ***

2) Experiment 2, change of **pislopen** parameter (initial slope of the PI curve in nanophytoplankton)

a) To develop this activity, open ***namelist_pisces_ref*** and decreased the value by 50%. The reference value is 2, therefore its new value must be 1.

```
!-----------------------------------------------------------------------
&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     =  0.004    ! Minimum Chl/c in phytoplankton
   fecnm       =  80E-6    ! Maximum Fe/C in nanophytoplankton
   fecdm       =  80E-6    ! Maximum Fe/C in diatoms
   grosip      =  0.159    ! mean Si/C ratio
/
```

-Run the simulation

sbatch run_nlhpc.bash

b) We will obtain the following files:

- *croco_avg.nc*
- *croco_his.nc*
- *croco_rst.nc*
- *croco_diabio_avg.nc*
- *croco_diabio.nc*

c) From the new netcdf files obtained, use croco_avg.nc and make the following surface figures with t = 30d:

1. Chlorophyll standard / Chlorophyll pislopen (-) - Standard chlorophyll (difference).
2. Nitrate standard / Nitrate pislopen (-) - Standard nitrate (difference).

Use the following ferret script for chlorophyll: *comp_pislopen_surf_run1_run2_chl.jnl*
Use the following ferret script for the other variables: *comp_pislopen_surf_run1_run2_var.jnl.*

d) Exploratory analysis of longitudinal sections at 33ºS

From the new croco_avg.nc file obtained from pislopen (-) experiment, make the following figures for time t=30d:

1. Chlorophyll standard sim / Chlorophyll pislopen (-)/ Chlorophyll pislopen (-) - Standard chlorophyll (difference).

Use the ferret script: *sect_xz_dif_run1_run2_chl.jnl*

*** Don't forget to save the simulation with changes in pislopen (- 50%) ***

3) Experiment 3, grazrat2 parameter change (grazing of mesozooplankton)

a) To develop this activity, open ***namelist_pisces_ref*** and decreased the value by 50%. The reference value is 0.75, therefore its new value must be 0.4.

```
!-----------------------------------------------------------------------
&namp4zmes     !   parameters for mesozooplankton for PISCES std       - ln_p4z
!-----------------------------------------------------------------------
   part2       =  0.75     ! part of calcite not dissolved in mesozoo guts
   grazrat2    =  0.75     ! maximal mesozoo grazing rate
   resrat2     =  0.005    ! exsudation rate of mesozooplankton
   mzrat2      =  0.03     ! mesozooplankton mortality rate
   xpref2d     =  1.       ! mesozoo preference for diatoms
   xpref2n     =  0.3      ! mesozoo preference for nanophyto.
   xpref2z     =  1.       ! mesozoo preference for microzoo.
```

-Run the simulation

sbatch run_nlhpc.bash

b) We will obtain the following files:

- *croco_avg.nc*
- *croco_his.nc*
- *croco_rst.nc*
- *croco_diabio_avg.nc*
- *croco_diabio.nc*

c) From the new netcdf files obtained, use croco_avg.nc and make the following surface figures with t = 30d:

1. Diatoms grazrat2 standard sim / Diatoms grazrat2 (-) - Standard diatoms (difference).
2. Nitrate grazrat2 standard / Nitrate grazrat2 (-) - Standard nitrate (difference).
3. Mesozooplankton grazrat2 standard sim / Mesozooplankton grazrat2 (-) - Standard mesozooplankton (difference).
4. Microzooplankton grazrat2 standard sim / Microzooplankton grazrat2 (-) - Standard microzooplankton (difference).

Use the ferret script: *comp_varsurf_run1_run2_grazrate.jnl*

Example:

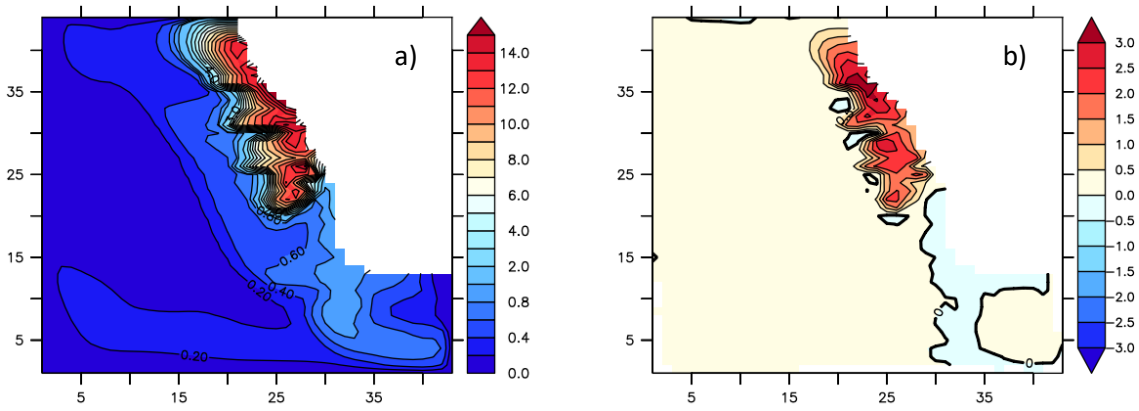


Figure 10: (a) Diatoms standard sim and (b) Diatoms grazrate2 (-) - Standard diatoms (difference).

*** Don't forget to save the simulation with changes in grazrate2 (- 50%) ***

Ferret script list:

1. comp_varsurf_run1_run2.jnl
2. sect_xz_var_croco.jnl
3. comp_nofesed_run1_run2_chl.jnl
4. comp_nofesed_run1_run2_var.jnl
5. comp_pislopen_surf_run1_run2_chl.jnl
6. comp_pislopen_surf_run1_run2_var.jnl
7. sect_xz_dif_run1_run2_chl.jnl
8. comp_varsurf_run1_run2_grazrate.jnl