TUTORIAL 06:
CREATE MY CROCO CLIM CONFIG WITH NESTING

In this tutorial, we do all the steps to run a CROCO configuration with a zoom. We will connect to the LENGAU,cluster and run Matlab to create climatological CROCO input files using CROCO tools. We will then run the nested simulation on the CHPC cluster.

STEP 1: Logging onto the Lengau HPC cluster and go into your CROCO working directory

→ From a terminal/konsole, execute the following instruction:

```
ssh -X login@lengau.chpc.ac.za
```

Replace **login** with your corresponding account number.

→ Reserve one interactive processor to do the pre-processing steps (Step 4 from **#TUTORIAL01**):

```
[login@login2 ~]$ qsubi1
[login@cnode0220 ~]$
```

→ Go into your **croco** directory (**lustre/croco**):

```
[login@cnode0220 ~]$ cd lustre/croco
[login@cnode0220 croco]$
```

→ Go into your **Run_Clim** working directory. If it does not exist (or if you want to recreate your grid), repeat the Step 2 from **#TUTORIAL02** (edit **create_config.bash** and execute it):

```
[login@cnode0220 ]$ cd Run_Clim
[login@cnode0220 Run_Clim]$
[login@cnode0220 Run_Clim]$
```

OR

```
[login@cnode0220 ]$ ./create_config.bash
[login@cnode0220 ]$ cd Run_Clim
[login@cnode0220 Run_Clim]$
```

STEP 2: Creating CROCO input files for the parent grid

→ It is done with **MATLAB**

→ Launch **MATLAB** with the command **matlab -nodesktop** (or the alias **mat**):

```
[login@cnode0220 Run_Clim]$ matlab -nodesktop &
[login@cnode0220 Run_Clim _LR]$
```

CROCO PARENT FILES

→ Execute the command start and open **crocotools_param.m**:

```
>> start
>> edit crocotools_param
```

➥ Activate the creation of graphics after each pre-processing step by changing **makeplot=0** to **makeplot=1** at line 131.

→ Create your Parent CROCO grid, initial conditions, surface and lateral forcings by repeating the steps detailed in Step 2 from **#TUTORIAL03**):

```
>> make_grid
>> make_forcing; (otional) make_QSCAT_clim; make_bulk;
>> make_clim; (otional) make_bry; make_ini;
>>
```

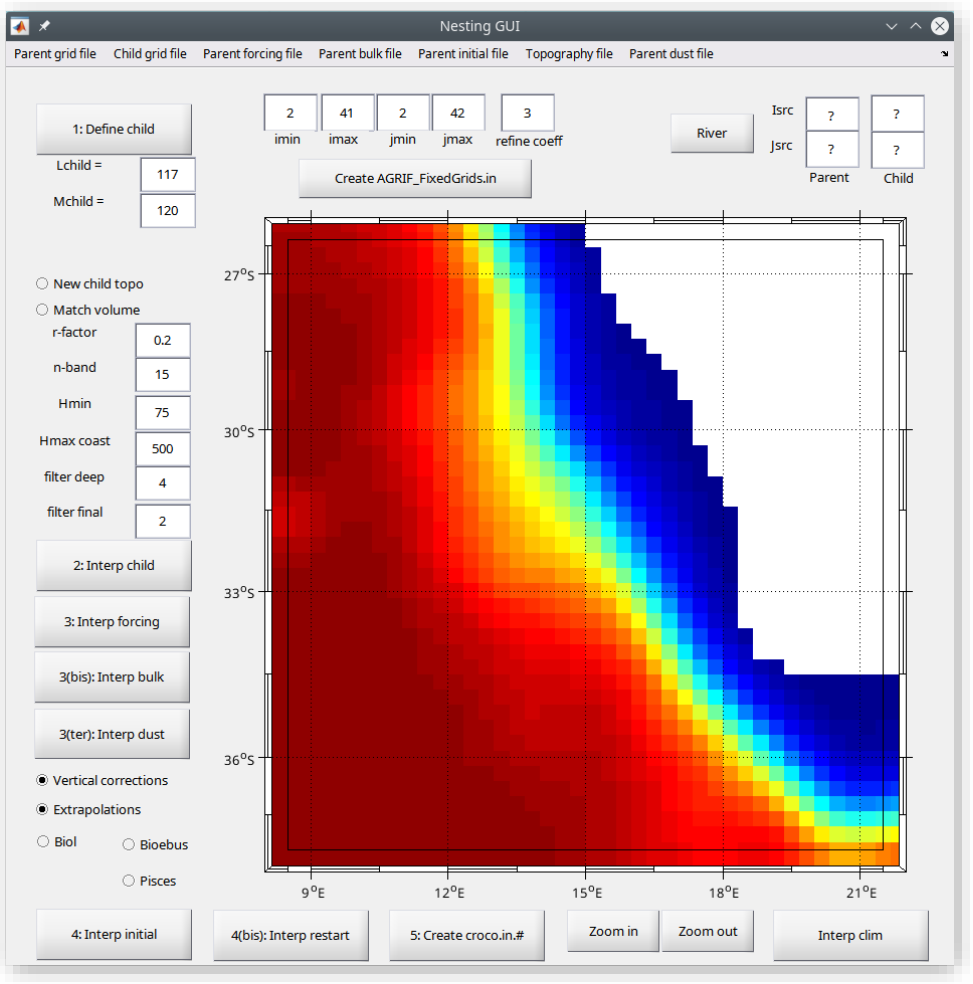
➥ Parameters for these scripts can be found in **crocotools_param.m**

➥ Remember LLm0,MMm0, and N

STEP 3: Creating CROCO input files for the nested domain

→ It is done in **MATLAB** with the nestgui tool:

```
>> nestgui
>>
```



❶ Click on **Define child**: it allows you to draw a rectangle on the map to define the position of your zoom. You can choose to use the same topography as for the parent or use a new topography interpolated from etopo2 (New child topo checkbox).

❷ Click on **Interp child**: it will create the child grid that will be stored in **CROCO_FILES/croco_grd.nc.1**.

⚠ Reload the child grid and then click on **Create AGRIF_Fixed_grid.in** to create the CROCO nesting parameters (position of the nested grid in **AGRIF_Fixed_grid.in**).

❸ Click on **Interp forcing**: it will create the child forcing file that will be stored in **CROCO_FILES/croco_frc.nc.1**.

❸(bis) Click on **Interp bulk**: it will create the child bulk forcing file that will be stored in **CROCO_FILES/croco_blk.nc.1**.

❹ Click on **Interp initial**: it will create the child initial conditions that will be stored in **CROCO_FILES/croco_ini.nc.1**.

❺ Click on **Create croco.in.#** to create the child parameter file **croco_inter.in.1**.

→ exit Matab, you are finished with steps 2 & 3:

```
>> exit
>>
```

→ You can inspect all your input files stored in CROCO_FILES using the **ncdump** or **ncview** tools:

```
[login@cnode0220 Run_Clim]$ cd CROCO_FILES/
[login@cnode0220 CROCO_FILES]$ ls
croco_clm.nc croco_clm.nc.1 croco_frc.nc croco_frc.nc.1
croco_grd.nc croco_grd.nc.1 croco_ini.nc croco_ini.nc.1
[login@cnode0220 Run_Clim]$ cd ..
```

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STEP 4: Compiling CROCO with Nesting capability

→ To compile CROCO, you need to copy my **jobcomp_lengau** file into your Run_Clim directory:

```
cp /mnt/lustre/users/sillig/CROCO_TRAINING_Week1/3_Some_files/jobcomp_lengau .
```

➥ You can check the differences between **jobcomp** and **jobcomp_lengau**:

```
[login@cnode0220 Run_Clim]$ diff jobcomp jobcom_lengau
```

→ Edit the CROCO parameter file **param.h** using **vi** or **nedit**:

```
[login@cnode0220 Run_Clim]$ nedit param.h &
[login@cnode0220 Run_Clim]$
```

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➥ Define your configuration with the appropriate values for (LLm0,MMm0 and N .

➥ Check the parameters for the parallelisation (NP_XI, NP_ETA)

→ Edit the **cppdefs.h** file using **vi** or **nedit**:

```
[login@cnode0220 Run_Clim]$ nedit cppdefs.h &
[login@cnode0220 Run_Clim]$
```

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➥ As in **#TUTORIAL03**, activate your config, MPI parallelization, define which of your **parent** boundaries are open or closed, chose the surface and boundary forcing formulation.

➥ Activate the **Nesting capability** (**#define AGRIF**) and if you want 2 ways interaction between the parent and the child, also activate **#define AGRIF_2WAY**.

→ Compile CROCO using the **jobcomp_lengau** script:

```
[login@cnode0220 Run_Clim]$ ./jobcomp_lengau
[login@cnode0220 Run_Clim]$
```

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STEP 5: Running CROCO

→ To launch your simulation on the Lengau cluster using the PBS Pro job scheduler, you need to copy my **run_croco.pbs** file into your Run_Clim directory:

```
cp /mnt/lustre/users/sillig/CROCO_TRAINING_Week1/3_Some_files/run_croco.pbs .
```

➥ Check the PBS scheduler parameter and put your email address (not mine ⚠)

➥ Check the path of your **Run_Clim** working directory

→ Edit the CROCO parameter files **croco_inter.in** and **croco_inter.in.1**:

```
[login@cnode0220 Run_Clim]$ diff croco_inter.in croco_inter.in.1
[login@cnode0220 Run_Clim]$
```

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➥ Fix your grid parameters at line 8: `THETA_S,  THETA_B,  Hc (m)`

➥ Check the outputs requested.

→ Edit the script **run_croco.pbs** using **vi** or **nedit**:

```
[login@cnode0220 Run_Clim]$ nedit run_croco.pbs &
[login@cnode0220 Run_Clim]$
```

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➥ Check the use configurable section. In particular, check out the time step (DT), the parameters for the parallelisation (NBPROCS) and put NLEVEL=2 (at line 75).

→ Launch your first simulation using the PBD command **qsub**:

```
[login@cnode0220 Run_Clim]$ qsub run_croco.pbs
[login@cnode0220 Run_Clim]$
```

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➥ Your simulation will soon start. You will receive an email.

➥ The model outputs will be stored in the directory: **./SCRATCH**

STEP 6: Visualising model outputs

→ This can be done with **MATLAB**

→ Launch **matlab -nodesktop** (or the alias **mat**) to use the crocotools croco_gui:

```
>> croco_gui
>>
```

➥ Have fun !

→ You can concatenate model outputs to visualize them easily in croco_gui:

```
[login@cnode0220 Run_Clim]$ cd SCRATCH
[login@cnode0220 SCRATCH]$ ncrcat croco_avg_Y2M[1-9].nc.1
croco_avg_Y2M1[0-2].nc.1 croco_avg_Y2.nc.1
```

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STEP 7: Exiting

→ When you are done, exit Matlab and logout from the cluster:

```
[login@cnode0220 Run_Clim]$ exit
logout
qsub: job 4416950.sched01 completed
[login@login2 ~]$ exit
```