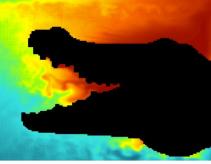
**CROCO – training 2024** 



### TP tests cases



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### **Documentation**



#### **TUTORIALS**

- 1. System requirements
- 2. Download
- 3. Contents & Architecture
- 4. Summary of essential steps
- 5. Test Cases
  - **5.1. BASIN**
  - 5.2. Set up you own test case
- 6. Regional: Preparing your configuration
- 7. Regional: Preprocessing (Matlab)

## 5. Test Cases

- 5.1. BASIN
- 5.2. Set up you own test case



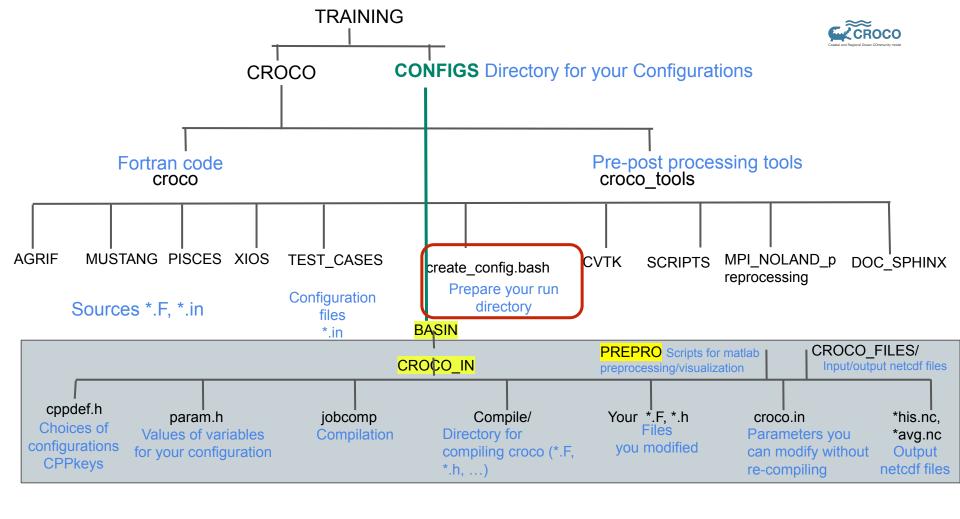
Built with Sphinx using a theme provided by Read the Docs.

# Create config directory for basin testcase



```
ssh -X userX@192.168.1.5
mkdir TRAINING
cd TRAINING
cp -r
/home/COMMONDATA/codes/CROCO .
cp CROCO/croco/create_config.bash .
mkdir CONFIGS
vim create_config.bash
./create_config.bash
```

```
BEGIN USER MODIFICATIONS
# Machine you are working on
 Known machines: Linux DATARMOR IRENE JEANZAY
MACHINE="DATARMOR"
 croco source directory
CROCO_DIR: /home/userX/TRAINING/CROCO/croco
# croco_tools directory
TOOLS_DIR= /home/userX/TRAINING/CROCO/croco_tools
# Configuration name
MY_CONFIG_NAME=
                BASIN
# Home and Work configuration directories
MY CONFIG HOME=
               /home/userX/TRAINING/CONFIGS
MY_CONFIG_WORK=
                /home/userX/TRAINING/CONFIGS
 Options of your configuration
## default option : all—dev for the usual ("all—in") architecture, for forced croco run and/or dev.
#options=( all-dev )
## example for production run architecture
options=(
          (all-dev)
## example for production run architecture and coupling with external models :
#options=( all-prod-cpl )
```



#### Basin test case



### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN

```
3. Edit cppdefs.h for using BASIN case

# define BASIN

# undef REGIONAL

You can also explore the CPP options selected for BASIN case.

You can check the BASIN settings in param.h.
```

This is a rectangular, flat-bottomed basin with double-gyre wind forcing. It produces a western boundary current flowing into a central Gulf Stream which goes unstable and generates eddies if resolution is increased.

# Compilation



### Cd TRAINING/CONFIGS/BASIN

Jobcom should work automatically in Seolane: do not modify it

#### 5. Compile the model:

• By using classical launch command (on individual computers):

```
./jobcomp > jobcomp.log
```

If compilation is successful, you should have a croco executable in your directory.

You will also find a **compile** directory containing the model source files:

- I.F files: original model source files that have been copied from \$croco/OCEAN
- \_\_.f files: pre-compiled files in which only parts defined by cpp-keys are kept
- object files

### **Execution and visualization**



6. Copy the namelist input file for BASIN case:

Cp ~/TRAINING/CROCO/croco/TEST\_CASES/croco.in.Basin .

Eventually edit it.

7. Run the model:

./croco croco.in.Basin

If your run is successful you should obtain the following files:

```
basin_rst.nc # restart file
basin_his.nc # instantaneous output file
```

8. Have a look at the results:

ncview basin\_his.nc

## Questions



#### Cd TRAINING/CONFIGS/BASIN

#### 9. Test: some questions:

- What is the size of the grid (see param.h)?
- What are the name of the horizontal directions?
- What is the spatial resolution in both horizontal directions?
- How many vertical levels do you have?
- How are the vertical levels distributed (look for the cpp key NEW\_S\_COORD )?
- What are the initial dynamical conditions (see both cppdefs.h and croco.in)?
- What do the air-sea exchanges look like?

# Parallel compilation and execution



### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN

10. Re-run this case in parallel on 4 CPUs:

To run in parallel, your first need to edit <a href="cppdefs.h">cppdefs.h</a>, <a href="param.h">param.h</a>, and to recompile.

• Edit cppdefs.h:

# define MPI

• Edit param.h:

```
#ifdef MPI
integer NP_XI, NP_ETA, NNODES
parameter (NP_XI=2, NP_ETA=2, NNODES=NP_XI*NP_ETA)
parameter (NPP=1)
parameter (NSUB_X=1, NSUB_E=1)
```

#### Note

MPI tiles should be at least 20x20 points.

· Recompile.

# Parallel compilation and execution



### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN

- Run the model in parallel:
  - By using classical launch command (on individual computers):

```
mpirun -np NPROCS croco croco.in
```

where NPROCS is the number of CPUs you want to allocate. mpirun -np NPROCS is a typical mpi command, but it may be adjusted to your MPI compiler and machine settings.

 OR by using a batch script (e.g. PBS) to launch the model (in clusters), examples are provided:

```
cp ~/croco/croco_tools/job_croco_mpi.pbs .
```

Edit job\_croco\_mpi.pbs according to your MPI settings in param.h and launch the run:

```
qsub job_croco_mpi.pbs
```

• Warning

NPROCS needs to be consistent to what you indicated in param.h during compilation

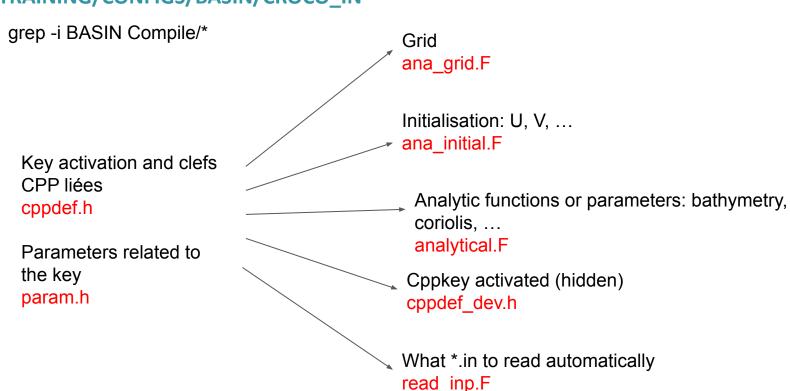


#### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN

grep BASIN Compile/\*



#### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN





#### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN



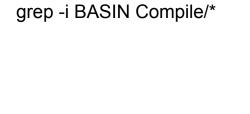
Key activation and clefs CPP liées cppdef.h

Parameters related to the key param.h

```
Grid
 ana_grid.F
                  ana grid.F
# if defined BASIN
                        depth=5000.
                        f0=1.E-4
                        beta=2.E-11
# elif defined SINGLE COLUMN
# if defined BASIN
                        Length XI =3600.0e+3
                        Length ETA=2800.0e+3
# if defined BASIN || defined EQ
                   defined SO
                   defined KH
                   defined AC
                   defined JE
     do j=JstrR.JendR
       do i=IstrR, IendR
         h(i,j)=depth
       enddo
     enddo
```

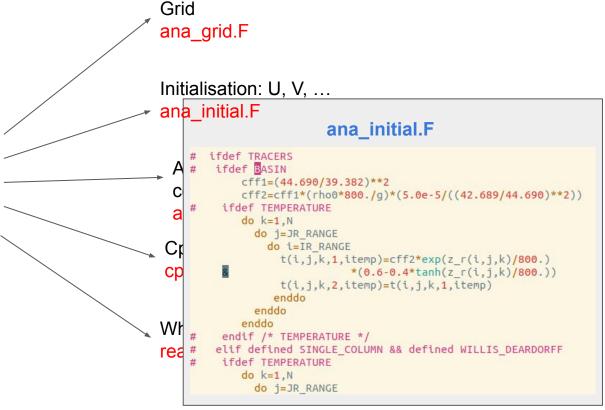


#### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN



Key activation and clefs CPP liées cppdef.h

Parameters related to the key param.h





#### Cd TRAINING/CONFIGS/BASIN/CROCO\_IN

grep -i BASIN Compile/\*

Key activation and clefs CPP liées cppdef.h

Parameters related to the key param.h

