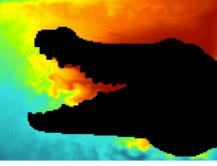
CROCO – training 2024 PSF Barcelonette



Introduction to CROCO and Parallelization



Outline



- 1. Available Parallelization options in CROCO
- 2.MPI Concept and techniques
- 3.MPI Basic setup in Croco
- 4. Advanced MPI CPP options in CROCO
- 5. SUMMARY FOR MPI // in CROCO

Available paradigms in CROCO



1.MPI Parallelization

designed for distributed systems, such as clusters of supercomputers where each node has its own memory. Each process in MPI operates in its own memory space, which requires explicit message passing to communicate between them. This makes it ideal for distributed memory environments.

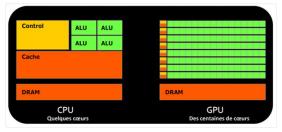
2. OPENMP Parallelization

designed for shared-memory systems, typically multiprocessor or multicore computers with shared memory. The threads created by OpenMP share the same memory and can communicate directly without message passing.

Coming soon...



- no hybrid MPI/OpenMP version
- GPU version under development



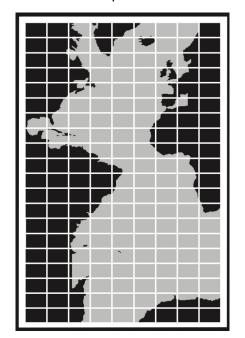
* MPI // is preferred!

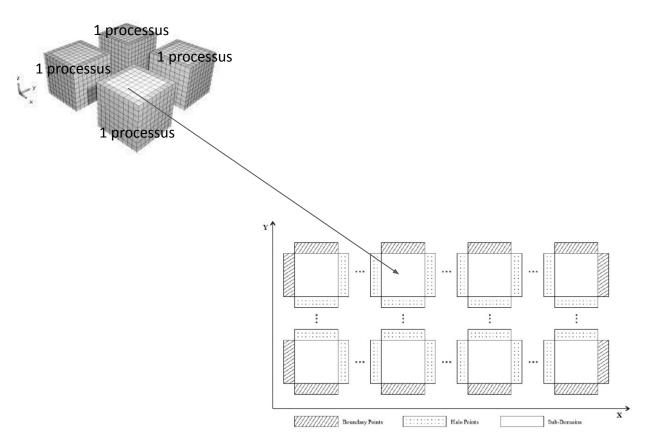
Concept and techniques: domain decomposition



MPI 4 processus

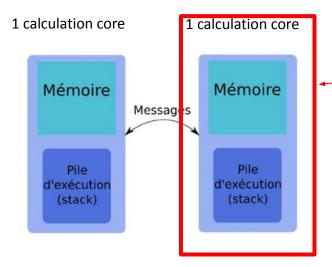
MPI 9x20 processus





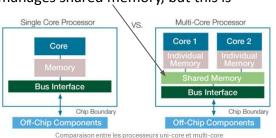
MPI (Message Passing Interface): distributed memory

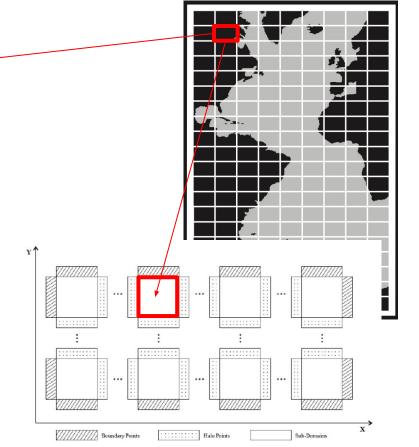




- => compute cores do not have access to a common memory
- => exchanges via network message
- => in practice, MPI also manages shared memory, but this is

transparent to the user.





How to configure MPI in CROCO



STEP1: edit files

1) param.h

Specify tiles number in xi and eta directions => NP XI, NP ETA,

maximum of tiles number in ETA direction is preferred

```
Domain subdivision parameters
                Maximum allowed number of parallel threads;
 NSUB_X,NSUB_E Number of SHARED memory subdomains in XI- and
                                                ETA-directions:
 NNODES
              Total number of MPI processes (nodes):
 NP_XI,NP_ETA Number of MPI subdomains in XI- and ETA-directions;
     integer NSUB_X, NSUB_E, NPP
#ifdef MPI
     integer NP_XI, NP_ETA, NNODES
     parameter (NP_XI=1, NP_ETA=4, NNODES=NP_XI*NP_ETA)
     parameter (NPP=1)
     parameter (NSUB_X=1, NSUB_E=1)
#elif defined OPENMP
     parameter (NPP=4)
ifdef AUTOTILING
     common/distrib/NSUB_X, NSUB_E
else
     parameter (NSUB_X=1, NSUB_E=NPP)
# endif
                                            param.h
     parameter (NPP=1)
```

Variables in param.h:

- NP_XI: decompostion in XI direction
- NP_ETA : decomposition in ETA direction
- NNODES: number of cores (="NP XI*NP ETA", except with MPI_NOLAND)
- NPP = 1
- NSUB_X and NSUB_ETA, number of sub-tiles (almost always =1)

2) cppdefs.h:

activate MPI => #define MPI

STEP2 : compile

./jobcomp

STEP3: execute

Processor Numbers= NNODES

- mpirun -n 4.7croco (or mpiexec or other)

Online documentation:

https://croco-ocean.gitlabpages.inria.fr/croco_doc/model/model.parallel.html

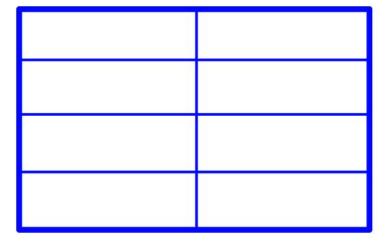
Example of MPI domains



Example 1:

8 cores:

- NP_XI=2, NP_ETA=4, NNODES=8
- NPP=1, NSUB_X=1, NSUB_E=1





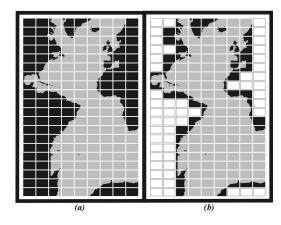
MPI CPP OPTIONS in CROCO For writing output files

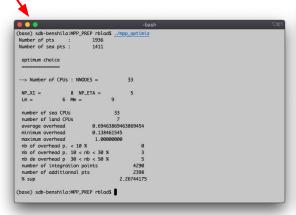
AVOID CALCULATION IN LAND AREAS (1)

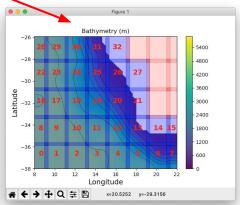


1. Preprocessing In directory CROCO/MPI_NOLAND:

- read README
- compile: edit makefile + make
- edit namelist : grid file name, max number of procs
- execute: /mpp_optimize
- view : ./mpp_plot.py croco grd.nc benguela-008x005_033
- re-read README ...

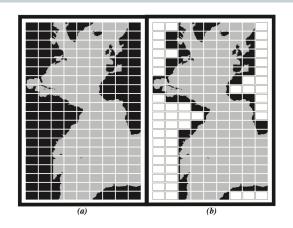






AVOID CALCULATION IN LAND AREAS (2)





2. Three files to edit in CROCO

-cppdefs.h : CPP OPTION: #define MPI_NOLAND

- param.h: insert values for NP_XI, NP_ETA and NPP given by the preprocessing
- MPI_Setup.F: be carefull to the name of grid file (NPP ou NNODES <= NP_XI x NP_ETA)

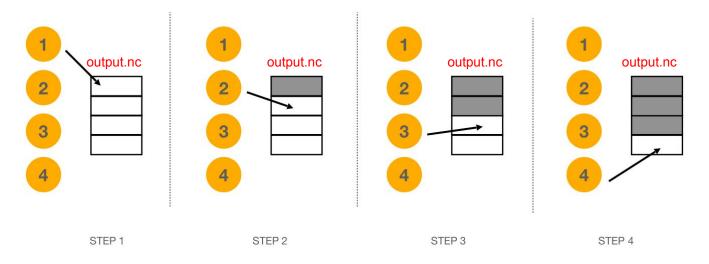
3. Compile and execute

WARNING: grid file as to be called croco_grd.nc (or to be changed in MPI_Setup.F)

Writing MPI 1/4 files: by default



mpirun -np 4 ./croco. (NP_ETA=4)



sequential writing, waiting for each proc to finish before the next one writes

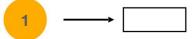
Very inefficient !!!!!!

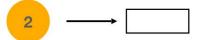
Writing MPI files 2/4: parallel files



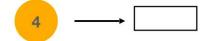
#define PARALLEL_FILES

mpirun -np 4 ./croco. (NP_ETA=4)









Fast, but many output files

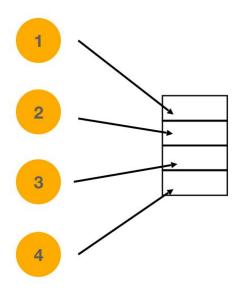
Need to recombine them (cf ncjoin utility)

Writing MPI 3/4 files: parallel writing



#define KEY NC4PAR

mpirun -np 4 ./croco. (NP_ETA=4)



Fast with a single output file

Requires NetCDF4 library installed with parallel support

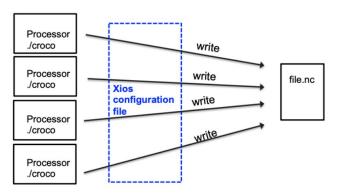
Writing MPI 4/4 files: XIOS

External server developed at IPSL http://forge.ipsl.jussieu.fr/ioserver



XIOS: attached mode

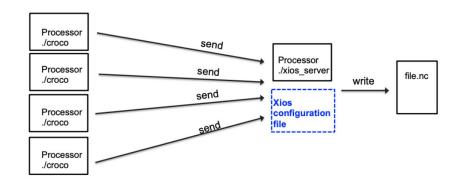
each croco executable compute and write (like a classical library)



Ergonomy AND efficient parallel writing BUT writing overhead

XIOS: detached mode (server mode)

each croco executable compute and send field to the server



- croco executables for computing only
- only xios server writes output
- Flexibility AND efficient parallel writing AND (almost) no overhead

To go further https://croco-ocean.gitlabpages.inria.fr/croco-doc/tutos/tutos.21.xios.html

Writing MPI - SUMMARY -



		Complexity to implement	Disadvantages	Advantages
1	By default	By default	By default	Simple to implement, nothing to do
2	Parallel Files	#define PARALLEL_FILES	many output files, need to recombine them	Simple to implement
3	Parallel writing	#define KEY_NC4_PAR library NETCDF 4 Parallel	installation of NETCDF4 can be tricky	● fast with a single output file
4	XIOS attached mode	#define XIOS, XML file	hard to install XIOS and to use it	very ergonomic and efficientuseful with a big domain
5	XIOS detached mode	#define XIOS, XML file	hard to install XIOS and to use it	 very ergonomic and efficient the best tool with a big domain



Online documentation:

https://croco-ocean.gitlabpages.inria.fr/croco_doc/model/model.parallel.html

Use MPI on your regional configuration with 4 processus (NP_ETA=4)