

October 20, 2011

1 Basic description

The aim of this program is to find the best grid possible, corresponding to the fastest treatment.

1 - searching the best regular grid
2 - running a genetic type algorithm, which randomly move borders, in order to

- first decrease as best as possible the standard deviation of the different parts
- then decrease as best as possible the max of those parts, thanks to a transmission of the best characteristics throw successive generations of a evolving population.

2 Files

```
makefile
decoupe.f90
decoupe.manipulation_fichiers.mod.f90
decoupe.traitement.mod.f90
input
```

3 How to use

1 - get the “decoupe” code by copying the directory \$HOMEMARS/./TOOLS/MPI2D_DOMAIN somewhere on your disk.

2 - make

3 - execute decoupe:

Usage: command <fichier bathy><divisions>

- fichier bathy : the bathymetric file, bathy_CONF.nc form,
- divisions : number of different cores assigned to treat the data of the map.

example : decoupe bathy_manga.nc 32

3b - Caparmor use (qsub submission) :
./run <fichier bathy><divisions>

4 - Recover the precious data in the file called bathy_CONF.txt, where the dimensions and coordinates of the grid have been written. Look at the picture of the domain decomposition from bathy_CONF.bmp file.

4b - Caparmor use : result of run script

All informations are gathered into the directory domainNbprocs where you can find the following files :

- bathy_CONF.nc : the bathymetric file
- bathy_CONF.bmp : picture of the spatial decomposition of the domain
- bathy_CONF.txt : file describing the spatial decomposition (dimensions and coordinates of each subgrid) This file (renamed mpi.txt) is read by the code MARS

5 - copy this bathy_CONF.txt file onto \$RDIR/CONF/CONF-CASE[/rank_X] under the name mpi.txt

4 For expert users: define a file named "input"

(If no "input" file is available, the program uses default parameters.)
Composition of the input file:

* Coefficient : Time treatment coefficient between one exchange between two cores

* Min : minimal distance between two borders, and one wet point,.

* Tous actifs : Boolean determining if the whole grid is shared between the cores (true), or if a better combination is searched with a larger grid, in order to have almost the wanted number of active areas, and thus giving up the other ones which are not active (false). Activating this option doesn't mean that all the domains are indeed active, but only that there is not any subdivision of the map leaved apart from the computation. It can be used if the main code doesn't support those partial exclusions of the map.

une dimension : Boolean.

Nbre d'essais : If p is the asked number of procs, test the differents divisions of grids from p to (p + Nbre d'essais) (in the case Tous_actifs == false).

* Population : Number of individuals used in the genetical part.

* Valeur de stab : End the current part of program if a better solution is not found after this number of iterations.

5 !!! Beware !!!

The one dimension switch is exclusive, which means that if it is false, the one dimension solutions will be excluded (for example, prime numbers with the all active option will return no solution in that case).