COLONY (Mac)

1. Introduction

This is a very brief readme file for the Mac version of COLONY. It describes mainly how to run COLONY on a Mac. It cannot replace the ColonyUsersGuide.PDF file, which gives much more details about the methods, inputs and outputs of COLONY and is thus highly recommended to read before starting the use of COLONY.

The zipped Mac COLONY package includes the following files:

1) colony2s.out
2) colony2p.out
3) Readme.pdf
4) ColonyUsersGuide.PDF
5) colony2.dat
6) ColonyUpdateHistory.txt
7) ColonyBatchRun.f90
8) ColonyBatchRun.out

The first and second files are the binaries for serial and parallel (using MPI) run of COLONY in **OS X Mavericks** (version 10.9) or higher, the third is what you are reading, the fourth is a detailed description of the COLONY program, the fifth is an example dataset (example 1 described in the fourth file), the 6th is the brief updating history of Colony, and the 7th and 8th are the Fortran source code and binary for batch run of COLONY.

Executables colony2s.out, colony2p.out and ColonyBatchRun.out are compiled from relevant fortran 2008 codes with gfortran. The 1st is statically linked, while the latter two are linked with gfortran, openmp and openMPI dynamic libraries.

Installation and run of COLONY programs are all better conducted in Mac's x-terminal. It is suggested to open an x-terminal and then to obtain the administrator's privileges by typing

sudo -s

Otherwise, the shell operations (such as unzipping) and COLONY run may have permission problems.

2. Installation

In x-terminal, unzip the downloaded file, and copy everything into your colony program folder on your Mac. Then use command "chmod u+x colony2s.out" to make the binary executable on your Mac. This command should be applied to the other two binaries (colony2p.out and ColonyBatchRun.out) as well.

Colony2s.out works no matter Gfortran and openMPI are installed on your Mac or not. However, to run binary colony2p.out or ColonyBatchRun.out, you need both Gfortran and openMPI installed on your Mac.

3. Running colony

To make a serial run of COLONY for the example dataset colony2.dat, simply go to the COLONY program folder in the X terminal and type

./colony2s.out

To run your own dataset, you need first to prepare a complete input file, providing all of the data and parameter values in the order and formats described in ColonyUsersGuide.PDF. You can use the default input file name colony2.dat, or any other file names. In the latter case, you need to specify the input file name by typing

./colony2s.out IFN:YourInputFileName

Note IFN (representing Input File Name, all capitals) is the key word, followed by the colon and your file name.

For parallel run with multiple processes, you need gfortran and openMPI (version 1.6.5) installed on your Mac. Most often, these are already installed. If not, you need to download (both free) and install them.

Ensuring openMPI is working properly on your machine, you can start running the example dataset with 4 processes by typing:

mpirun -n 4 ./colony2p.out

For an input file with a name different from the default (colony2.dat), the command line is

mpirun -n 4 ./colony2p.out IFN:YourInputFileName

4. Batch run of multiple input files

ColonyBatchRun.out can be used to make a batch run of multiple input files. The runs can be serial or MPI parallel, as detailed in document ColonyUsersGuide.pdf. For parallel run of ColonyBatchRun.out, you need openMPI installed on your Mac.