
EMIBD9 (Mac)

Introduction

This document briefly describes how to run EMIBD9 on a Mac machine. It should be read together with the EMIBD9UserGuide.pdf file, which gives much more details about the methods, inputs and outputs of EMIBD9 and is thus highly recommended to read before starting the use of EMIBD9.

The zipped EMIBD9 Mac package includes the following files in 3 subfolders:

- 1) EM_IBD_P
- 2) Readme.pdf
- 3) EMIBD9UserGuide.pdf
- 4) EMIBD9UpdateHistory.txt
- 5) ant377.dat
- 6) ant377.par

The first file is the binary compiled by Gfortran compiler (GNU fortran 6.3.0) under 64bit Mac OS. It is statically linked for a serial run. This binary file is in the subfolder “Bin”.

The 2ed file is what you are reading. The 3rd is a detailed description of the use of EMIBD9 program. The 4th file is a brief updating history of EMIBD9. These 3 documents are in the subfolder “Doc”.

The 5th file is an example genotype data file, and the 6th is the corresponding parameter file. These 2 files are in the subfolder “Example”.

Installation and run of EMIBD9 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 EMIBD9 run may have permission problems.

Installation

In x-terminal, unzip the downloaded file, and copy the 3 subfolders (with content files) into your EMIBD9 program folder on your Mac. Then go to the Bin subfolder, and use command “chmod u+x EM_IBD_P” to make the binary executable on your Mac.

On installation, it is suggested to include the **EMIBD9** program path permanently in the automatic search paths of your shell so that the program can be launched conveniently without specifying the path of the program. Please see EMIBDUserGuide.pdf for details.

Running EMIBD9

To make a serial run of EMIBD9 for the example dataset in subfolder Example, simply open an x terminal and navigate to the Example folder (using command cd), and type

```
*/EM_IBD_P INP:ant377.par
```

where “*” is the path of the EMIBD9 binary files. For example, the path could be “\$HOME/Scratch/EMIBD9/Bin”, and the entire command line is thus “\$HOME/Scratch/EMIBD9/Bin/EM_IBD_P INP:ant377.par”.

If, on installing EMIBD9 program on your computer, you have included the **EMIBD9** program path permanently in the automatic search paths of your shell (as detailed in EMIBD9UserGuide.pdf), then the command line for running the example data simplifies to

```
EM_IBD_P INP:ant377.par
```

On finishing the run, analysis results will be in output file ant377.ibd9 in Example folder.

In the above command line, the key word “INP:” means INPut file. Other key words are listed and explained in the main documentation, EMIBD9UserGuide.pdf.

To run your own dataset, you need to make a project folder, to prepare a parameter input file and a genotype data file, and to save the 2 files in the project folder. Suppose your project folder is “MyPrj”, and in this folder you have a parameter file MyPrj.par and a data file MyPrj.dat. Note the data file name “MyPrj.dat” must be specified in parameter file “MyPrj.par”. You can run the analysis of your data from your project folder, MyPrj, by the X-terminal command line

```
*/EM_IBD_P INP:MyPrj.par
```

On finishing the run, analysis results will be in an output file stored in your project folder, MyPrj.