Manual for MultiWaverX

1. Introduction

MultiWaver series software was designed to infer population admixture history in case of various and complex scenarios. The earlier versions of *MultiWaver* considered only autosomal admixture events. Here, we developed a updated version *MultiWaverX* to model the detailed sex-biased admixture events in case of the continuous and discrete gene flow.

Functions of MultWaver 2.0 were also implemented in this new version, which can be invoked with specific parameters.

The MultiWaverX software is available at https://github.com/Shuhua-Group/MultiWaverX.

2. Getting Started

The executable file is already included in the bin folder.

```
$ tar -zvxf MultiWaverX.tar.gz
$ cd MultiWaverX/bin
```

To recompile from the source code, you can type the following commands:

```
$ cd MultiWaverX/src
$ make clean
$ make all
```

Then the executable software is in the bin file. You can type the following command for help:

```
$ MultiWaverX/bin/MultiWaverX -h
```

3. Arguments and Options

Arguments	Type	Description	Note
-i/--input	string	Input of the autosomal ancestral tracks	required
-o/--output	string	Output file	required
-g/--log	string	Log file of software	optional, no default
-l/--lower	double	Lower bound to discard short tracks	optional, default 0
-a/--alpha	double	Significance level to reject null hypothesis in LRT (Discrete model)	optional, default 0.001
-e/--epsilon	double	Epsilon to check whether a parameter converge or not (Discrete model)	optional, default 1.0e-6
-p/--minProp	double	Minimum survival proportion for a wave at the final generation (Discrete model)	optional, default 0.05
-m/--maxIter	integer	Maximum number of iterations to scan for waves of admixture events	optional, default 10000
-w/--waves	integer	Maximum number of discrete model waves	optional, default 2
-c/--ci	double	Value for the bootstrapping confident interval	optional, default 0.95
-b/--bootstrap	double	Number of bootstrapping	optional, default 0
-t/--thread	integer	Number of threads	optional, default 1
-C/--chr	string	Chromosome type, "A" for Autosome, "X" for X chromosome	optional, default A
-x/--inputX	string	Input of the X chromosome ancestral tracks	optional, required if -C = X
-M/--mode	string	Model parameter : [DMode] Discrete model only. [CMode] Continuous model only. [MixMode] Consider all models together.	optional, default MixMode

Options	Description	Note
-s/--simple	Run in simple mode (Discrete model)	optional
-h/--help	Print this help	optional

4. Input Files

The segmental tracks of autosome and X chromosome are in the same format. Each line represents an acestral track with the start point, end point, and from which ancestry the track originates. The start and end points units are in Morgan.

For example:

autosomal segment tracks

```
0              0.02508272     Anc1
0.02508272     0.02704873     Anc2
0.02704873     0.04892998     Anc1
0.04892998     0.06442661     Anc2
......
2.79991492     2.95633422     Anc1
2.95633422     3              Anc2
```

X chromosomal segment tracks

```
0              0.06672769     Anc1
0.06672769     0.13400564     Anc2
0.13400564     0.1504261      Anc1
0.1504261      0.16002571     Anc2
......
1.9738108      1.98508333     Anc2
1.98508333     2              Anc1
```

5. Output Files

After inputting the following commands:

```
MultiWaverX –i A.seg –C X –x X.seg –b 100 –o test.txt –g test.log
```

We can get two output files: results summary file and log file.

5.1 Results summary file

```
Best Model:     GA
Bootstrapping support ratio: 100% (100/100)
```

```
        Anc1: 99(G) 0.800238
        Anc2: 99(G) 0.199762
        ----------------------------------------------------------------
Bootstrapping details

GA
Bootstrapping supporting ratio: 100% (100/100)
        Anc1: 96~104(G) 0.778284~0.813219
        Anc2: 96~104(G) 0.186781~0.221716
        ----------------------------------------------------------------

Best Model for X:        GA
Bootstrapping support ratio: 100% (100/100)
        Anc1: 99(G) 0.775026     p = 0.547258
        Anc2: 99(G) 0.224974     p = 0.310685
        ----------------------------------------------------------------
Bootstrapping details

GA
Bootstrapping supporting ratio: 100% (100/100)
        Anc1: 99~99(G) 0.753251~0.797996     p: 0.504202~0.588074     100%
(100/100)
        Anc2: 99~99(G) 0.202004~0.246749     p: 0.147181~0.483166     100%
(100/100)
        ----------------------------------------------------------------
```

The format of summary file is similar to that of *MultiWaver 2.0*. Besides the optimal admixture model of autosome and corresponding parameters, the last two parts show the admixture model of X chromosome and estimated parameters, where p is the male-proportion during the admixture.

5.2 Log file

This file records the detailed result of each bootstrapping procedure.

6. Questions and Suggestions

Questions and suggestions are welcome. Feel free to contact zhangrui2018@picb.ac.cn.