Manual for *HiMWA*

1. Introduction

HiMWA is a software that can be employed to reconstruct recent refined four-way admixture histories, distinguishing between hierarchical multiple-wave admixture models and sequential admixture models. *HiMWA* represents an extension of the *MultiWaver* series and *HierarchyMix* software.

2. Input Files

Ancestral tracts can be obtained from standard local ancestry inference (LAI) tools such as *RFMix2* or *FLARE*. To facilitate reproducibility and broader application, we provide example scripts (flare2seg.py and msp2seg.py) that convert LAI outputs into *HiMWA*-compatible segment files.

The format of input ancestral tracts file is same as *HierarchyMix*. Each row represents an ancestral tract characterized by the following parameters: (1) the genetic distance of start-point (in Morgans), (2) the genetic distance of end-point (in Morgans), (3) the ancestry of origin, (4) the index of admixed haplotype, and (5) the chromosome label. All genetic positions are specified in Morgans (M) with decimal precision. Here takes the first few rows of "example.seg" as an example:

```
0          0.0121778      A        hap0    1
0.0121778      0.01284813      B        hap0    1
0.01284813     0.02511697      A        hap0    1
0.02511697     0.04025596      B        hap0    1
0.04025596     0.06880797      A        hap0    1
0.06880797     0.0747312       B        hap0    1
0.0747312      0.07882828      D        hap0    1
0.07882828     0.0839206       B        hap0    1
```

3. Running *HiMWA*：

HiMWA can be executed using a single command line. A minimal example is:

python HiMWA.py --input example.seg --output example

Optional arguments allow more refined analyses. For example, bootstrap resampling and tract-length filtering can be specified as:

python HiMWA.py --input example.seg --output example --bootstrap 100 --lower 0.003 --lowerEF 0.02

4. Output Files

The format of output model file is same as *MultiWaver* series and *HierarchyMix* software. Here takes the output file "example.txt" as an example, which is inferred based on the input file "example.seg":
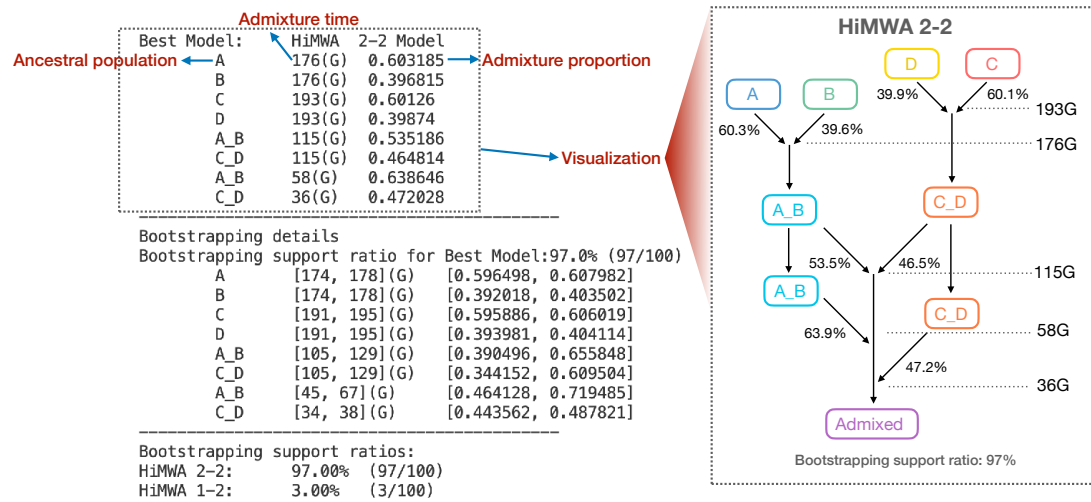
5. Arguments and Options

Arguments	Type	Description	Note
--input	string	Input file name	required
--output	string	Prefix of output file	optional, default = 'out'
--lower	float	Lower bound to discard short tracts	optional, default = 0
--lowerEF	float	Lower bound to discard short tracts of admixed ancestral population	optional, default = 0
--bootstrap	int	Number of bootstrapping	optional, default = 0
--ci	string	Confidence level of bootstrapping confidence interval	optional, default = 0.95
-h	/	Print help message	/

6. Notes

It should be noted that the model selection of *HiMWA* may be unreliable for admixed populations with extremely biasd admixture proportions. Furthermore, in scenarios with multiple recent admixture waves, the inferred times of recent admixture events by *HiMWA* may be overestimated. It is advised to correct the overestimation of the admixture times referring the strategy in this study under specific model configurations.

7. Questions and Trouble-shooting

Questions and suggestions are welcome, feel free to contact Yuhan Yang yhyang22@m.fudan.edu.cn.