

# Manual for *HierAdmix*

## 1. Introduction

*HierAdmix* is a software that can be used to reconstruct the 4-way admixture history considering the complex admixture structure. It could automatically select the optimal admixture model between the hierarchical admixture model and the sequential admixture model. *HierAdmix* is an extension of the *MultiWaver* series software.

## 2. Input Files

The format of input ancestral tracts file is same as *MultiWaver* series software. Each line represents an ancestral tract with the genetic distance of start point, the genetic distance of end point, and from which ancestry the tract originates. The unit of first two columns are both in Morgan. Here takes the first few rows of “Hier.seg” as an example:

0	0.01113699	Anc3
0.01113699	0.02255031	Anc2
0.02255031	0.02763909	Anc3
0.02763909	0.03211435	Anc4
0.03211435	0.08753307	Anc3
0.08753307	0.09612572	Anc4
0.09612572	0.11396293	Anc3
.....	.....	.....

## 3. Output Files

The format of output model file is same as *MultiWaver* series software. Here takes the output file “Hier.txt” as an example, which is inferred based on the input file “Hier.seg”:

```
Best Model:      Hierarchical Admixture Model
Anc3      147(G)      0.700884
Anc4      147(G)      0.299116
Anc2      143(G)      0.791475
Anc1      143(G)      0.208525
Anc3_Anc4  50(G)      0.601598
Anc2_Anc1  50(G)      0.398402
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Bootstrapping details
Bootstrapping support ratio:100.0% (100/100)
Anc3      [142, 151](G) [0.691954, 0.7065]
Anc4      [142, 151](G) [0.29304, 0.306569]
Anc2      [139, 148](G) [0.78313, 0.79797]
Anc1      [139, 148](G) [0.200576, 0.214962]
Anc3_Anc4 [47, 52](G) [0.59403, 0.608446]
Anc2_Anc1 [47, 52](G) [0.390023, 0.404444]
```

#### 4. Arguments and Options

Arguments	Type	Description	Note
--input	string	Input file name	required
--lower	float	Lower bound to discard short tracts	optional, default = 0
--bootstrap	int	Number of bootstrapping	optional, default = 0
--ci	float	Confidence level of bootstrapping confidence interval	optional, default = 0.95
--left	string	The specified left part of admixture model, e.g., Anc1_Anc2	optional, default=None
--right	string	The specified right part of admixture model, e.g., Anc3_Anc4	optional, default=None
--output	string	Prefix of output file	optional, default="out"
-h	none	Print help message	none

#### 5. Notes

A special hierarchical admixture model needs special attention, within which the admixture proportions of two populations of left-side are same, and the admixture proportions of two populations of right-side are same too. In this case, the admixture time doesn't have an unique solution and the inference results of *HierAdmix* can be unreliable.

#### 6. Questions and Trouble-shooting

Questions and suggestions are welcome, feel free to contact Shi Zhang [19121640@bjtu.edu.cn](mailto:19121640@bjtu.edu.cn) or Rui Zhang [zhangrui2018@picb.ac.cn](mailto:zhangrui2018@picb.ac.cn).