

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

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. 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”:

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Best Model:      Hierarchical Multi 2-2 Admixture Model
      A      176(G)  0.603185
      B      176(G)  0.396815
      C      193(G)  0.60126
      D      193(G)  0.39874
      A_B     115(G)  0.535186
      C_D     115(G)  0.464814
      A_B     58(G)   0.638646
      C_D     36(G)   0.472028

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Bootstrapping details
Bootstrapping support ratio:98.0% (98/100)
      A      [174, 178] (G)  [0.596675, 0.607645]
      B      [174, 178] (G)  [0.392355, 0.403325]
      C      [191, 196] (G)  [0.596955, 0.606811]
      D      [191, 196] (G)  [0.393189, 0.403045]
      A_B     [106, 126] (G)  [0.369525, 0.658537]
      C_D     [106, 126] (G)  [0.341463, 0.630475]
      A_B     [41, 68] (G)   [0.511072, 0.717072]
      C_D     [34, 38] (G)   [0.44194, 0.489553]

```

4. 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	/

5. Notes

It should be noted that the model selection of *HiMWA* may be unreliable for admixed populations with extremely biased 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.

6. Questions and Trouble-shooting

Questions and suggestions are welcome, feel free to contact Yuhan Yang
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