Manual for *MultiWaver 2.1*

MultiWaver 2.1 is a modified version of *MultiWaver 2.0* and it is specially used to estimate the introgression wave utilizing the information output by *ArchaicSeeker 2.0*.

Step1: To estimate the introgression waves, we need to first use the executable file '**getAS2Seg**' to convert the output of *ArchaicSeeker 2.0* into the format of *MultiWaver 2.1*.

getAS2Seg filepath_to_genetic_map seg_output_by_ArchaicSeeker2.0 output_file Archaic

Here, the 'filepath_to_genetic_map' need to have genetic map of chromosomes 1-22, and named as genetic_map_chr*_combined_b37.txt. Archaic can be Altai or Denisova.

Step2: Use the executable file '**MultiWaver2.1**' to estimate the introgression waves.

MultiWaver2.1 -i output_by_getAS2Seg -l threshold -o output_filename

The detailed arguments of *MultiWaver* 2.1 are list as follows:

Arguments	Types	Descriptions
-i/--input	<string>	Input of the ancestral tracks [required]
-l/--lower	[double]	Lower bound to discard short tracks [optional, default 0]
-a/--alpha	[double]	Significance level to reject null hypothesis in LRT [optional, default 0.001]
-e/--epsilon	[double]	Epsilon to check whether a parameter converge or not [optional, default 1.0e-6]
-p/--minProp	[double]	Minimum survival proportion for a wave at the final generation [optional, default 0.05]
-m/--maxIter	[integer]	Maximum number of iterations to scan for waves of admixture events [optional, default 10000]

Options	Descriptions
-h/--help	Print help message, default is OFF
-s/--simple	Run in simple mode, default is OFF

Examples

Step1:

```
getAS2Seg/getAS2Seg  MWexamples/genetic_map_b37/  ../examples/Han.seg  MWexamples/Han
Denisova
```

Step2:

```
MultiWaver2.1/MultiWaver2.1 –i MWexamples/Han.seg –l 0.00015 –o MWexamples/Han
```

The introgression model can be found in MWexamples/Han.sum.

Questions

Questions and suggestions are welcome, feel free to contact Kai Yuan (yorkklause@gmail.com) or Rui Zhang (zhangrui2018@picb.ac.cn).