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.

Compile

We have provided the static version of getAS2Seg and MultiWaver2.1. To recompile, please type the following commands:

\$ cd getAS2Seg

\$ g++ getAS2Seg.cpp -o getAS2Seg

\$ cd ../MultiWaver2.1

\$ make

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></string>	Input of the ancestral tracks [required]
-l/lower	[double]	Lower bound to discard short tracks [optional, default 0]

-b/bootstrap	[integer]	Number of bootstrapping [optional, default 100]
-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]
-t/thread	[integer]	Number of threads [optional, default 1]
-o/output	<string></string>	Prefix of output [required]

Options	Descriptions
-h/help	Print help message, 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).