Installing msmsPlay

Download and in this zip file: <https://si.biostat.washington.edu/sites/default/files/modules/ComputationalResources.zip>

To run:

java -cp msms3.2rc-b163.jar at.mabs.gui.MSMSPlay

Drift

0 generations

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0

-ej 0.0 1 2

40 generations

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0

-ej 0.001 1 2

**Where do we specifying the number of generations ago the two populations split?**

400 generations

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0

-ej 0.01 1 2

4000 generations

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0

-ej 0.1 1 2

40000 generations

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0

-ej 1 1 2

Amish (ish)

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0

-ej 0.00035 1 2

-n 2 0.02

Growth

-N 1e4 -ms 300 10000 -s 1

-N 1e4 -ms 300 10000 -s 1 -G 1

-N 1e4 -ms 300 10000 -s 1 -G 10

-N 1e4 -ms 300 10000 -s 1 -G 100

-N 1e4 -ms 300 10000 -s 1 -G 1000

Bottleneck

-N 1e4 -ms 300 10000 -s 1 -I 1 300 0 -en 0.1 1 0.1 -en 0.11 1 1

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0 -ej 0.1 1 2

-en 0.09 1 0.1 -en 0.1 1 1

**How does this compare to the setting where there are no –en parameters?**

Migration

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 1

-ej 1 1 2

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 10

-ej 1 1 2

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 100

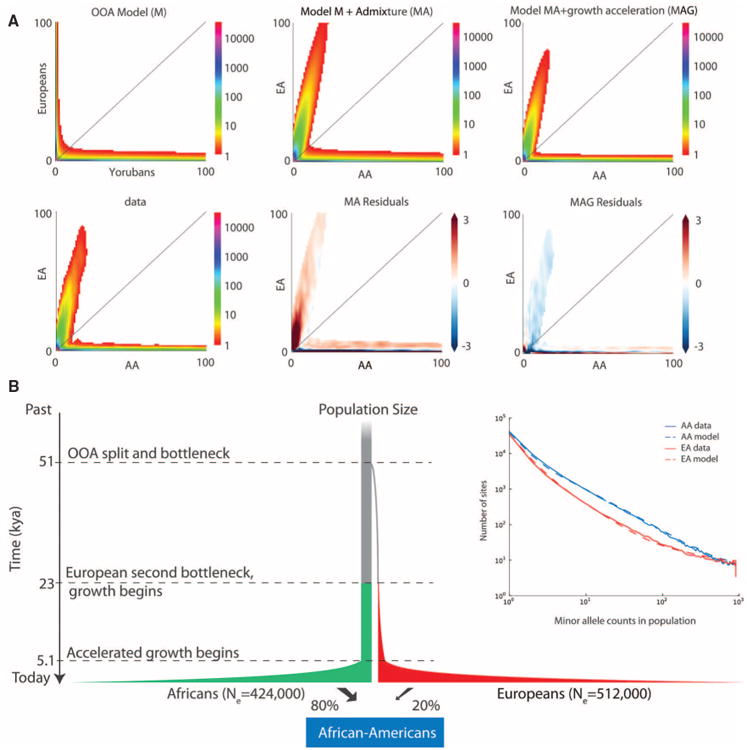
-ej 1 1 2

Assymetrical Migration

-N 1e4 -ms 300 10000 -s 1 -I 2 150 150 0

-ej 1 1 2

-m 2 1 1



Tennessen et al. (2012)

-N 7310 -ms 4878 1000 -s 1 -I 2 2176 2702 0 -n 1 58.002735978 -n 2 70.041039672 -eg 0 1 482.46 -eg 0 2 570.18 -em 0 1 2 0.731 -em 0 2 1 0.731 -eg 0.006997264 1 0 -eg 0.006997264 2 89.7668 -em 0.006997264 1 2 0.7310 -em 0.006997264 2 1 0.7310 -en 0.006997264 1 1.98002736 -eg 0.031463748 2 0 -en 0.031463748 2 0.141176471 -en 0.03146375 2 0.254582763 -em 0.03146375 1 2 4.386 -em 0.03146375 2 1 4.386 -em 0.069767442 1 2 0 -em 0.069767442 2 1 0 -ej 0.069767442 2 1 -en 0.069767442 1 1.98002736 -en 0.20246238 1 1

Recombination

-N 1e4 -ms 300 100 -t 400

-r 400

**If my mutation rate is 10-8 mutations per base pair, what is the sequence length we are simulating here?**

**How many centiMorgans are we simulating?**

Questions:

Please simulate two populations of 15 individuals each with an ancestral effective population size of 10000, a gene length of 1KB, and a population split of 1000 years ago (assuming 25 years per generation).

Please simulation three populations of 50 individuals each with an ancestral effective population size of 10000, a gene length of 1MB, and the first population split at 100000 years ago (1 and 2,3) and the second at 50000 years ago (2 and 3). Population 3 also had a population expansion starting 10000 years ago where it tripled in size.