Simulations with `ms`

Here we describe how we produce samples from a spatially distributed population that evolves under the stepping-stone model using the program `ms` [1]. For all simulations, we first construct a regular triangular grid (V, E) of $n_x \times n_y$ demes (vertices) with coordinates (x_α, y_α).
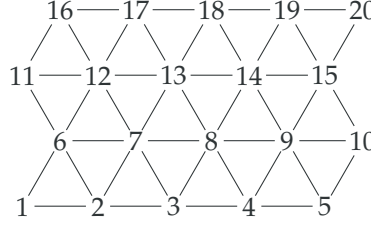

Figure 1   This is a 5×4 regular triangular grid. If line weights are proportional to migration rate, this pattern corresponds to uniform migration with equal deme sizes.

The spatial information is not explicitly used by `ms` and instead we set $m_{\alpha\beta} = 0 = m_{\beta\alpha}$ for all pairs of demes such that $(\alpha, \beta) \notin E$. We also specify the relative size of each deme, p_α, and the migration rates across each edge in the two opposite directions, $m_{\alpha\beta}$ and $m_{\beta\alpha}$. Migration is not necessarily symmetric but is conservative [i.e., it preserves deme sizes.]

Spatial structure due to constant migration

Here edges in the middle of the habitat have migration rate that is a factor of magnitude lower than the rate of the edges on either side. [The rates range from 0.3 to 3.] This patterns is a barrier to actual migration and it results in a barrier to effective migration.
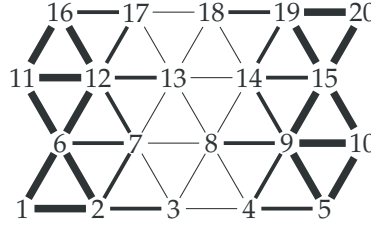

Figure 2   Barrier to migration. If line weights are proportional to migration rates, this patterns corresponds to a barrier across the middle of the habitat.

```
ms 20 1 -s 1 -I 20 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0
-m 1 2 3.0 -m 2 1 3.0 -m 1 6 3.0 -m 6 1 3.0 -m 2 3 1.7 -m 3 2 1.7
-m 2 6 3.0 -m 6 2 3.0 -m 2 7 1.7 -m 7 2 1.7 -m 3 4 0.3 -m 4 3 0.3
-m 3 7 0.3 -m 7 3 0.3 -m 3 8 0.3 -m 8 3 0.3 -m 4 5 1.7 -m 5 4 1.7
-m 4 8 0.3 -m 8 4 0.3 -m 4 9 1.7 -m 9 4 1.7 -m 5 9 3.0 -m 9 5 3.0
-m 5 10 3.0 -m 10 5 3.0 -m 6 7 1.7 -m 7 6 1.7 -m 6 11 3.0 -m 11 6 3.0
-m 6 12 3.0 -m 12 6 3.0 -m 7 8 0.3 -m 8 7 0.3 -m 7 12 1.7 -m 12 7 1.7
-m 7 13 0.3 -m 13 7 0.3 -m 8 9 1.7 -m 9 8 1.7 -m 8 13 0.3 -m 13 8 0.3
```

```
-m 8 14 0.3 -m 14 8 0.3 -m 9 10 3.0 -m 10 9 3.0 -m 9 14 1.7
-m 14 9 1.7 -m 9 15 3.0 -m 15 9 3.0 -m 10 15 3.0 -m 15 10 3.0
-m 11 12 3.0 -m 12 11 3.0 -m 11 16 3.0 -m 16 11 3.0 -m 12 13 1.7
-m 13 12 1.7 -m 12 16 3.0 -m 16 12 3.0 -m 12 17 1.7 -m 17 12 1.7
-m 13 14 0.3 -m 14 13 0.3 -m 13 17 0.3 -m 17 13 0.3 -m 13 18 0.3
-m 18 13 0.3 -m 14 15 1.7 -m 15 14 1.7 -m 14 18 0.3 -m 18 14 0.3
-m 14 19 1.7 -m 19 14 1.7 -m 15 19 3.0 -m 19 15 3.0 -m 15 20 3.0
-m 20 15 3.0 -m 16 17 1.7 -m 17 16 1.7 -m 17 18 0.3 -m 18 17 0.3
-m 18 19 1.7 -m 19 18 1.7 -m 19 20 3.0 -m 20 19 3.0
```

Spatial structure due to variation in diversity

Here some demes have bigger size and thus lower coalescence rate and higher genetic diversity. In the first version, migration rates are constant but there are differences in effective population size. Since demes in the "east" and "west" of the habitat are 5 times bigger than those in the middle, the effect is a barrier to effective migration that is qualitatively very similar to the barrier in the previous simulation.
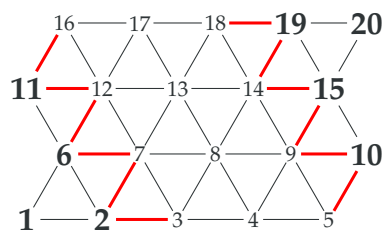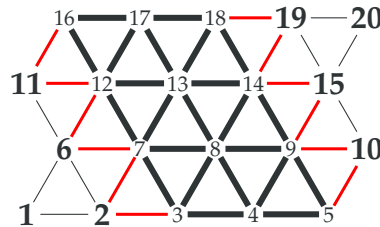

Figure 3 Barrier to effective migration due to differences in effective population size. The demes in bold are 5 times bigger; the edges in red are *directed* — this is necessary to preserve equilibrium in time.

A few edges are directed, with rate $m_{\alpha\beta} = 0.2$ from a big deme to a small deme and rate $m_{\beta\alpha} = 1$ in the other direction. These edges cross the "boundary" between the areas of high and low diversity and their rates are assigned so that migration is conservative: the same number of migrants are exchanged between α and β because $N_\alpha m_{\alpha\beta} = N_\beta m_{\beta\alpha}$.

```
ms 20 1 -s 1 -I 20 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0
-n 1 5.0 -n 2 5.0 -n 3 1.0 -n 4 1.0 -n 5 1.0 -n 6 5.0 -n 7 1.0
-n 8 1.0 -n 9 1.0 -n 10 5.0 -n 11 5.0 -n 12 1.0 -n 13 1.0 -n 14 1.0
-n 15 5.0 -n 16 1.0 -n 17 1.0 -n 18 1.0 -n 19 5.0 -n 20 5.0
-m 1 2 1.0 -m 2 1 1.0 -m 1 6 1.0 -m 6 1 1.0 -m 2 3 0.2 -m 3 2 1.0
-m 2 6 1.0 -m 6 2 1.0 -m 2 7 0.2 -m 7 2 1.0 -m 3 4 1.0 -m 4 3 1.0
-m 3 7 1.0 -m 7 3 1.0 -m 3 8 1.0 -m 8 3 1.0 -m 4 5 1.0 -m 5 4 1.0
-m 4 8 1.0 -m 8 4 1.0 -m 4 9 1.0 -m 9 4 1.0 -m 5 9 1.0 -m 9 5 1.0
-m 5 10 1.0 -m 10 5 0.2 -m 6 7 0.2 -m 7 6 1.0 -m 6 11 1.0 -m 11 6 1.0
-m 6 12 0.2 -m 12 6 1.0 -m 7 8 1.0 -m 8 7 1.0 -m 7 12 1.0 -m 12 7 1.0
-m 7 13 1.0 -m 13 7 1.0 -m 8 9 1.0 -m 9 8 1.0 -m 8 13 1.0 -m 13 8 1.0
```

```
-m 8 14 1.0 -m 14 8 1.0 -m 9 10 1.0 -m 10 9 0.2 -m 9 14 1.0 -m 14 9 1.0

-m 9 15 1.0 -m 15 9 0.2 -m 10 15 1.0 -m 15 10 1.0 -m 11 12 0.2

-m 12 11 1.0 -m 11 16 0.2 -m 16 11 1.0 -m 12 13 1.0 -m 13 12 1.0

-m 12 16 1.0 -m 16 12 1.0 -m 12 17 1.0 -m 17 12 1.0 -m 13 14 1.0

-m 14 13 1.0 -m 13 17 1.0 -m 17 13 1.0 -m 13 18 1.0 -m 18 13 1.0

-m 14 15 1.0 -m 15 14 0.2 -m 14 18 1.0 -m 18 14 1.0 -m 14 19 1.0

-m 19 14 0.2 -m 15 19 1.0 -m 19 15 1.0 -m 15 20 1.0 -m 20 15 1.0

-m 16 17 1.0 -m 17 16 1.0 -m 17 18 1.0 -m 18 17 1.0 -m 18 19 1.0

-m 19 18 0.2 -m 19 20 1.0 -m 20 19 1.0
```

In the second version, differences in migration rates compensate for differences in deme size because $N_\gamma m_{\gamma\omega} = N_\omega m_{\omega\gamma}$ for *all* edges $(\gamma, \omega) \in E$. The result is no variation in effective migration although both the deme sizes and the migration rates vary across the habitat.

Figure 4 Uniform effective migration even though there are differences in both population size and in migration rates. The demes in bold are 4 times bigger; the edges in red are *directed* — this is necessary to preserve equilibrium in time.

```
ms 20 1 -s 1 -I 20 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 0

-n 1 5.0 -n 2 5.0 -n 3 1.0 -n 4 1.0 -n 5 1.0 -n 6 5.0 -n 7 1.0

-n 8 1.0 -n 9 1.0 -n 10 5.0 -n 11 5.0 -n 12 1.0 -n 13 1.0 -n 14 1.0

-n 15 5.0 -n 16 1.0 -n 17 1.0 -n 18 1.0 -n 19 5.0 -n 20 5.0

-m 1 2 0.2 -m 2 1 0.2 -m 1 6 0.2 -m 6 1 0.2 -m 2 3 0.2 -m 3 2 1.0

-m 2 6 0.2 -m 6 2 0.2 -m 2 7 0.2 -m 7 2 1.0 -m 3 4 1.0 -m 4 3 1.0

-m 3 7 1.0 -m 7 3 1.0 -m 3 8 1.0 -m 8 3 1.0 -m 4 5 1.0 -m 5 4 1.0

-m 4 8 1.0 -m 8 4 1.0 -m 4 9 1.0 -m 9 4 1.0 -m 5 9 1.0 -m 9 5 1.0

-m 5 10 1.0 -m 10 5 0.2 -m 6 7 0.2 -m 7 6 1.0 -m 6 11 0.2 -m 11 6 0.2

-m 6 12 0.2 -m 12 6 1.0 -m 7 8 1.0 -m 8 7 1.0 -m 7 12 1.0 -m 12 7 1.0

-m 7 13 1.0 -m 13 7 1.0 -m 8 9 1.0 -m 9 8 1.0 -m 8 13 1.0 -m 13 8 1.0

-m 8 14 1.0 -m 14 8 1.0 -m 9 10 1.0 -m 10 9 0.2 -m 9 14 1.0 -m 14 9 1.0

-m 9 15 1.0 -m 15 9 0.2 -m 10 15 0.2 -m 15 10 0.2 -m 11 12 0.2

-m 12 11 1.0 -m 11 16 0.2 -m 16 11 1.0 -m 12 13 1.0 -m 13 12 1.0

-m 12 16 1.0 -m 16 12 1.0 -m 12 17 1.0 -m 17 12 1.0 -m 13 14 1.0

-m 14 13 1.0 -m 13 17 1.0 -m 17 13 1.0 -m 13 18 1.0 -m 18 13 1.0

-m 14 15 1.0 -m 15 14 0.2 -m 14 18 1.0 -m 18 14 1.0 -m 14 19 1.0
```

```
-m 19 14 0.2 -m 15 19 0.2 -m 19 15 0.2 -m 15 20 0.2 -m 20 15 0.2
-m 16 17 1.0 -m 17 16 1.0 -m 17 18 1.0 -m 18 17 1.0 -m 18 19 1.0
-m 19 18 0.2 -m 19 20 0.2 -m 20 19 0.2
```

Spatial structure due to a split event

Here the effect of a barrier to effective migration is produced by a past event that zeroes out some migration rates and thus disconnects the "east" and "west" regions of the habitat. The split is instantaneous and occurs $3N_0$ generations back in the past. This creates a barrier in time that is detected as a barrier to effective migration.
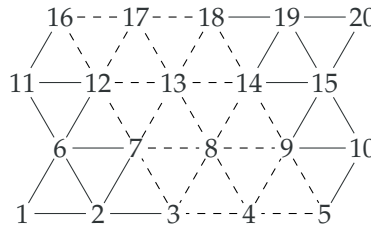

Figure 5 Barrier to effective migration due to a split in time and otherwise uniform migration rates. The dashed edges are disconnected at the same point of time in the past.

```
ms 20 1 -s 1 -I 20 4 3 0 0 0 3 0 0 0 0 0 0 0 0 3 0 0 0 3 4 0
-m 1 2 1.0 -m 2 1 1.0 -m 1 6 1.0 -m 6 1 1.0 -m 2 3 1.0 -m 3 2 1.0
-m 2 6 1.0 -m 6 2 1.0 -m 2 7 1.0 -m 7 2 1.0 -m 5 10 1.0 -m 10 5 1.0
-m 6 7 1.0 -m 7 6 1.0 -m 6 11 1.0 -m 11 6 1.0 -m 6 12 1.0 -m 12 6 1.0
-m 9 10 1.0 -m 10 9 1.0 -m 9 15 1.0 -m 15 9 1.0 -m 10 15 1.0
-m 15 10 1.0 -m 11 12 1.0 -m 12 11 1.0 -m 11 16 1.0 -m 16 11 1.0
-m 14 15 1.0 -m 15 14 1.0 -m 14 19 1.0 -m 19 14 1.0 -m 15 19 1.0
-m 19 15 1.0 -m 15 20 1.0 -m 20 15 1.0 -m 18 19 1.0 -m 19 18 1.0
-m 19 20 1.0 -m 20 19 1.0
-em 3.0 3 7 1.0 -em 3.0 3 8 1.0 -em 3.0 3 4 1.0 -em 3.0 4 3 1.0
-em 3.0 4 8 1.0 -em 3.0 4 9 1.0 -em 3.0 4 5 1.0 -em 3.0 5 4 1.0
-em 3.0 5 9 1.0 -em 3.0 7 12 1.0 -em 3.0 7 13 1.0 -em 3.0 7 8 1.0
-em 3.0 7 3 1.0 -em 3.0 8 7 1.0 -em 3.0 8 13 1.0 -em 3.0 8 14 1.0
-em 3.0 8 9 1.0 -em 3.0 8 4 1.0 -em 3.0 8 3 1.0 -em 3.0 9 8 1.0
-em 3.0 9 14 1.0 -em 3.0 9 5 1.0 -em 3.0 9 4 1.0 -em 3.0 12 16 1.0
-em 3.0 12 17 1.0 -em 3.0 12 13 1.0 -em 3.0 12 7 1.0 -em 3.0 13 12 1.0
-em 3.0 13 17 1.0 -em 3.0 13 18 1.0 -em 3.0 13 14 1.0 -em 3.0 13 8 1.0
-em 3.0 13 7 1.0 -em 3.0 14 13 1.0 -em 3.0 14 18 1.0 -em 3.0 14 9 1.0
-em 3.0 14 8 1.0 -em 3.0 16 17 1.0 -em 3.0 16 12 1.0 -em 3.0 17 16 1.0
-em 3.0 17 18 1.0 -em 3.0 17 13 1.0 -em 3.0 17 12 1.0 -em 3.0 18 17 1.0
-em 3.0 18 14 1.0 -em 3.0 18 13 1.0
```

References

[1] Hudson, R. R. Generating samples under a Wright-Fisher neutral model of genetic variation. *Bioinformatics* **18**, 337–338 (2002).