

Population Genetics Homework - Week 7

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Intro

I went ahead and adjusted the `run_simulation` function so that the output will include time to coalescence (TTC) from both the finite island and 1-d step models (island and step) for a sequence of inputs.

The output will include times for both models, and the ratio between them (island/step). When `m` is variable, `n_pop` will be set at 10. Conversely, when `n_pop` is variable `m` will be set at 0.02.

```
rat.n <- data.frame(island = NA, step = NA, ratio = NA, n_pops = NA, m = NA)
n_pop <- seq(6, 30, by = 3)
m <- 0.02
run_simulation(n_pop, m, 1000, rat.n)
rat.n <- rat
rat.n
```

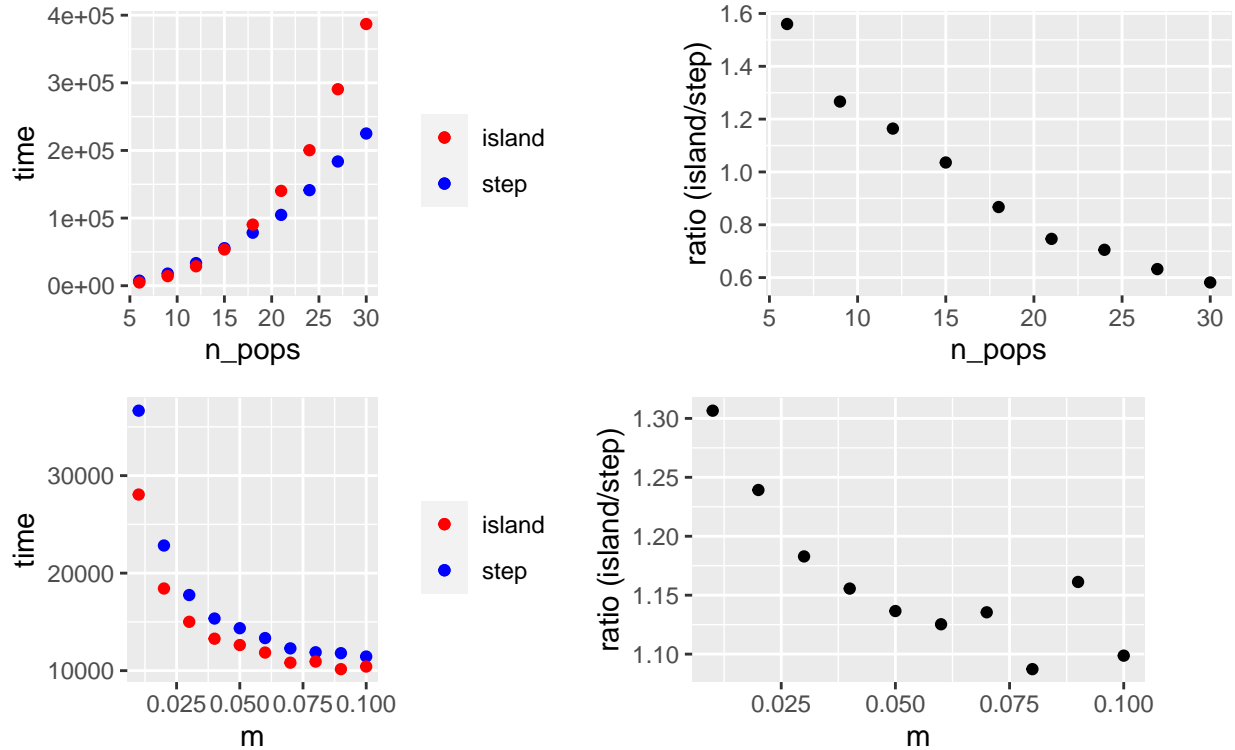
| ## | island | step | ratio | n_pops | m |
|------|------------|------------|-----------|--------|------|
| ## 1 | 7455.564 | 4778.816 | 1.5601279 | 6 | 0.02 |
| ## 2 | 17923.262 | 14151.745 | 1.2665054 | 9 | 0.02 |
| ## 3 | 33417.081 | 28705.691 | 1.1641274 | 12 | 0.02 |
| ## 4 | 55503.167 | 53583.269 | 1.0358302 | 15 | 0.02 |
| ## 5 | 78361.060 | 90366.051 | 0.8671515 | 18 | 0.02 |
| ## 6 | 104717.970 | 140249.837 | 0.7466531 | 21 | 0.02 |
| ## 7 | 141292.696 | 200355.125 | 0.7052113 | 24 | 0.02 |
| ## 8 | 183695.704 | 290577.596 | 0.6321744 | 27 | 0.02 |
| ## 9 | 225041.119 | 386976.189 | 0.5815374 | 30 | 0.02 |

```
rat.m <- data.frame(island = NA, step = NA, ratio = NA, n_pops = NA, m = NA)
n_pop <- 10
m <- seq(0.01, 0.1, by = 0.01)
run_simulation(n_pop, m, 1000, rat.m)
rat.m <- rat
rat.m
```

| ## | island | step | ratio | n_pops | m |
|------|----------|----------|----------|--------|------|
| ## 1 | 36659.32 | 28058.31 | 1.306540 | 10 | 0.01 |
| ## 2 | 22834.13 | 18425.76 | 1.239250 | 10 | 0.02 |
| ## 3 | 17755.41 | 15010.23 | 1.182888 | 10 | 0.03 |
| ## 4 | 15345.62 | 13279.21 | 1.155612 | 10 | 0.04 |
| ## 5 | 14351.95 | 12627.61 | 1.136552 | 10 | 0.05 |
| ## 6 | 13340.67 | 11854.91 | 1.125329 | 10 | 0.06 |
| ## 7 | 12284.13 | 10818.44 | 1.135481 | 10 | 0.07 |
| ## 8 | 11884.82 | 10931.00 | 1.087257 | 10 | 0.08 |

```
## 9 11792.82 10155.42 1.161234 10 0.09
## 10 11448.18 10419.64 1.098712 10 0.10
```

Usually working out a pattern quantitatively is preferable, but the patterns are so clear that plots will work nicely. I'll be plotting island TTC, step TTC, and ratios for each sequence of variations.



Analysis

It appears that an increase in the number of populations rapidly increases TTC. In contrast, increasing migration rate rapidly decreases TTC. This makes sense, as both higher a n_pop and a lower migration rate imply a more structured metapopulation.

Each model, however, responds to changes in either variable differently;

- While both models predict a lower TTC at lower n_pops, the island TTC is higher *in relation* to the step TTC (and vis versa).
- While both models predict a higher TTC at lower migration rates, the step TTC is lower *in relation* to the island TTC.

These relationships made more sense once I considered why migration is different for each model. The island model will predict relatively lower TTCs at high migration and/or higher numbers of population because migration is going to be more impactful when any island can migrate to any other. A step model is going to be more “bogged down” by a higher number of islands because migration from any one island to any other is difficult.