

POPULATION GENETICS

SPRING 1999

PROBLEM #3

Due: 9 March 1999

Evolutionary biologists and ecologists often hope that by using molecular markers they will be able to infer things about the pattern of individual movements that would otherwise require marked-release recapture studies. While inferences based on inverting the relationship between F_{st} and $N_e m$ are problematic, more direct approaches are possible. Consider, for example, the following imaginary set of data:¹

Population	Adults		Seedlings	
	A_1	Total	A_1	Total
1	10	55	15	75
2	14	35	17	47
3	28	45	15	35
4	22	35	11	20
5	18	25	20	30

The A_1 columns are the number of A_1 alleles observed in the sample. If we assume that allele frequencies in seedlings differ from those in adults only as a result of migration among these populations, that the allele frequency in migrants is equal to the mean allele frequency across populations, and that the rate of migration into each population is the same, then we can use these data to estimate the migration rate. Using these data and making those assumptions, answer the following two questions:²

1. What is the migration rate into populations in this sample?
2. If each population is composed of exactly 10 males and exactly 90 females,³ what F_{st} would you expect at equilibrium assuming the “infinite alleles” model of migration? What if the population was composed of exactly 50 males and exactly 50 females?

You'll need the following set of priors in WinBUGS:

```
# migration rate
m ~ dunif(0,1);

# allele frequencies in adults
p[1] ~ dunif(0,1);
p[2] ~ dunif(0,1);
p[3] ~ dunif(0,1);
p[4] ~ dunif(0,1);
p[5] ~ dunif(0,1);
```

¹ The data is imaginary, but the situation is inspired by some data Courtney Murren collected as part of her dissertation research.

² As always, include 95% confidence limits with your answers.

³ I say “exactly” so that you know you can take those numbers as given, you don't have to estimate them.