

POPULATION GENETICS PROBLEM #1

Dan Schoen and Mike Clegg (*Evolution* 39:1242-1349; 1985) studied the transmission of genetic variation from one generation to the next. Focusing just on results from the first experimental design and ignoring the color differences, these are the data they report:

Maternal genotype	Offspring genotype		
	$Est^F Est^F$	$Est^F Est^S$	$Est^S Est^S$
$Est^F Est^F$	267	62	0
$Est^F Est^S$	81	120	44
$Est^S Est^S$	0	143	170

Assume that each offspring included in the sample comes from a different mother as we did in the example with *Zoarces viviparus* in class.¹ Using these data answer the following questions:

1. Do the pollen allele frequencies differ among the three maternal genotypes?²

A χ^2 test or Fisher's exact test in R is quite straightforward, if you follow the example posted earlier.

```
> alleles <- matrix(c(267, 81, 143, 62, 44, 170), nr=3,
+ dimnames=list(c("A1A1", "A1A2", "A2A2"), c("A1", "A2")))
> alleles
      A1  A2
A1A1 267  62
A1A2  81  44
A2A2 143 170
> chisq.test(alleles)
```

¹This means, for example, that there are at total of 329 $Est^F Est^F$ mothers represented in the sample.

²You can use either a classical statistical test, e.g., a χ^2 contingency table or Fisher's exact test to answer this question, or you can do model comparison in WinBUGS, whichever you prefer. Don't be shy about asking for help if you try it with WinBUGS. You'll probably need help figuring out the syntax.

Pearson's Chi-squared test

```
data: alleles
X-squared = 87.6353, df = 2, p-value < 2.2e-16

> fisher.test(alleles)
```

Fisher's Exact Test for Count Data

```
data: alleles
p-value < 2.2e-16
alternative hypothesis: two.sided
```

It's very clear from the results of these tests that the frequency of the A_1 allele in paternal gametes differs significantly among mothers.

It is possible to use model comparison in WinBUGS to get the same result, but the code's reasonably complicated. If you're interested in how to do it, I'll be glad to show you, but I shouldn't have suggested that you might want to try it.

2. Is it reasonable to assume that meiosis is fair in heterozygous mothers?

To determine whether meiosis is fair in heterozygous mothers, we need to determine whether there's evidence that the proportion of heterozygous offspring is different from $1/2$. For this we use a χ^2 goodness of fit test. In R

```
> offspring <- c(81+44, 120)
> offspring
[1] 125 120
> chisq.test(offspring, p=c(0.5, 0.5))
```

Chi-squared test for given probabilities

```
data: offspring
X-squared = 0.102, df = 1, p-value = 0.7494
```

The 81 + 44 is the sum of the homozygous classes. The $p=c(0.5, 0.5)$ says that we expect the two classes with frequency 1/2 and 1/2. Clearly we don't have evidence that the proportion of heterozygous offspring is different from one half, so it's reasonable to conclude that meiosis is fair in heterozygous mothers.³

3. What is the inbreeding coefficient, f , in the maternal plants, and what is the 95% credible interval for f ? Is there evidence for inbreeding in this population? ⁴

The words "credible interval" are a dead giveaway that you have to use WinBUGS for this one. Here's the code and the result.

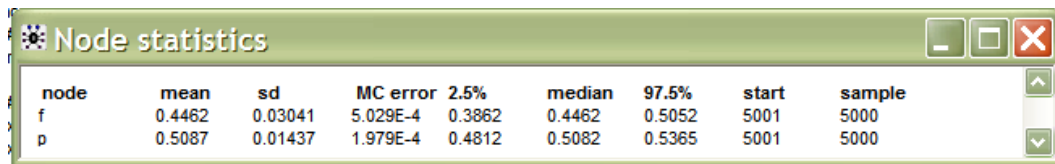
```
model {
  # likelihood
  n[1:3] ~ dmulti(x[], N)

  # genotype frequencies
  x[1] <- p*p + f*p*(1.0-p)
  x[2] <- 2.0*p*(1.0-p)*(1.0-f)
  x[3] <- (1.0-p)*(1.0-p) + f*p*(1.0-p)

  # priors
  p ~ dunif(0, 1)
  f ~ dunif(0, 1)

  # convenience calculation
  N <- sum(n[])
}

list(n=c(329, 245, 313))
```



node	mean	sd	MC error	2.5%	median	97.5%	start	sample
f	0.4462	0.03041	5.029E-4	0.3862	0.4462	0.5052	5001	5000
p	0.5087	0.01437	1.979E-4	0.4812	0.5082	0.5365	5001	5000

³Strictly speaking, of course, we can't conclude that. All we can conclude is that we've failed to reject the null hypothesis that meiosis is fair, which isn't the same thing. Nonetheless, the proportion of heterozygous offspring is very close to 50%, so our best guess is that meiosis is close to fair.

⁴Assume a uniform [0,1] prior for f and p . You'll have to use WinBUGS for this one.

The best estimate of f is its posterior mean, 0.4462, and the 95% credible interval is (0.3862, 0.5052).⁵

4. Given your answers to (1)-(3), what process could explain the pattern of mother-offspring combinations that you see. Be sure to explain *why* the process you propose will produce those results.⁶

f is clearly positive, indicating a substantial deficit of heterozygotes. This suggests that some form of inbreeding is going on. We don't have evidence of anything funny happening in maternal heterozygotes, but the frequency of A_1 in paternal gametes in offspring of A_1A_1 mothers is 0.81 while that in offspring of A_2A_2 mothers is 0.46. This could reflect some kind of interaction between maternal and paternal genotypes in determining fertilization success, but since this is a hermaphroditic plant the easiest explanation is that a substantial fraction of progeny are produced through self-fertilization. This would produce both the correlation between maternal genotype and paternal allele frequency and the deficiency of heterozygotes in the maternal population.

⁵Your numbers may be a little different from these even if you use exactly the same code, because the WinBUGS results are derived from a stochastic simulation.

⁶If you look at the Schoen and Clegg paper, it will be pretty obvious what process is involved. So be sure to make it clear to us that your explanation is independent of what Schoen and Clegg have to say.