

## Project # 4



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## *Dacus oleae*

This week's project deals with the olive fruit fly *Dacus oleae*



## *Dacus oleae*

- ▶ *Dacus oleae* is a pest found in Mediterranean regions
- ▶ Females oviposit eggs into ripening olives, resulting in either unusable olives or reduced use of olive oils
- ▶ Of economic concern



# Soluble esterases and experiments

- ▶ locus A catalyzes degradation of acetylcholine
- ▶ locus B catalyzes degradation of pseudocholine
- ▶ homozygotes at locus A more susceptible to dimethoate (insecticide)
- ▶ no detectable selection at locus B

# Selection in wild populations

Krimbas and Tsakas (Evolution, 1971) studied allele frequencies of wild populations in Greece

Are differences due to drift?

	Year		
	1966	1967	1968
Number of $A_1$ alleles	206	142	230
Sample size of $A$ alleles	474	312	400
Number of $B_1$ alleles	292	179	280
Sample size of $B$ alleles	469	281	409

# Questions

1. What would your estimate of the effective population size be if you based it on allele frequency changes at locus  $A$ ?
2. What would your estimate of the effective population size be if you based it on allele frequency changes at locus  $B$ ?
3. Is there evidence that the estimate of effective population size depends on the locus that you select?
4. What is your best estimate of the effective population size?
5. Are the observed allele frequency changes plausibly accounted for by genetic drift, or might natural selection be involved?

## Variance in allele frequency

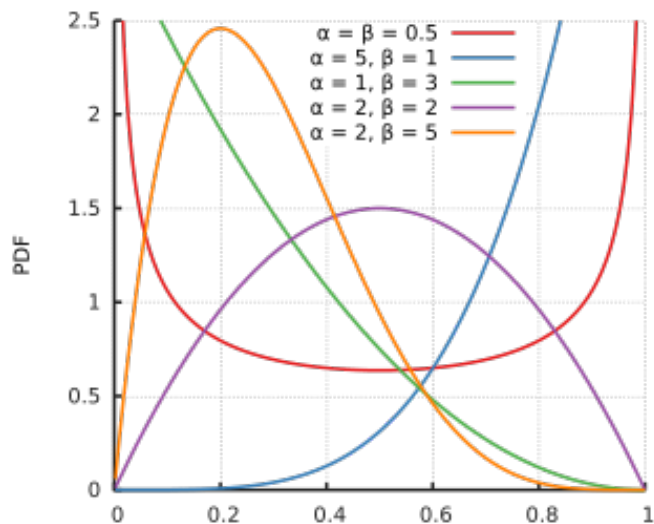
$$\text{Var}(p_{t+1}) = \frac{p_t(1-p_t)}{2N_e}$$

$$P(p_{t+1}|p_t) \sim \text{Beta}(\nu p_t, \nu(1 - p_t))$$

$$\nu = \frac{1-\theta}{\theta}$$



## Beta distribution



$$\text{Var}(p_{t+1}) = \theta p_t(1 - p_t)$$

$$N_e = \frac{1}{2\theta}$$

## JAGS code for one locus

```
p[1] ~ dunif(0, 1)
for (i in 1:2:n_years) {
  p[i] ~ dbeta(nu*p[i-1], nu*(1-p[i-1]))
}
nu <- ((1.0 - theta)/theta)
theta ~ dunif(0, 1)
ne <- 1.0/(2.0*theta)
```

## Other Hints

- ▶ Use the JAGS values of DIC to compare models with  $N_e$  estimated separately for each locus or a single value of  $N_e$  for the combined data.
- ▶ Assume that the number of alleles is drawn from a binomial distribution with a probability equal to the allele frequency and a sample size equal to the number of alleles sampled.

# References

- ▶ Krimbas, Costas B., and Spyros Tsakas. "The genetics of *Dacus oleae*. V. Changes of esterase polymorphism in a natural population following insecticide control-selection or drift?." *Evolution* (1971): 454-460.