Evolution:

Quantifying genetic variation
Factors that alter allele frequencies

Genetic drift

Altered allele frequency due to random fluctuation...

Result: loss of variation (a.k.a. loss of heterozygosity)
Drosophila experiment:

Wildtype x forked bristle mutant

\[ + = p = 0.5 \]
\[ \text{forked (f) } = q = 0.5 \]

Pick at random:
4 males x 4 females, 100 parallel crosses

\[ \text{Expected: } p^2 + 2pq + q^2 \]

\[ \text{Observed, after 16 generations: } \]
Consequence of random genetic drift: heterozygotes are exchanged for homozygotes

...drift towards homozygosity

Ultimately:

How likely is the *Drosophila* result if 4000 males and females are chosen?
Calculating rate of loss due to drift

Rate of drift (loss of alleles) $\alpha$

Loss of heterozygosity per generation $= \frac{H_t}{...}$

Effect of inbreeding:

**Founder effect**: small population established from small initial sample

e.g., achromatopsia in Pingelap atoll
What counters the trend towards homozygosity?

Mutation

Mutation rate $\mu$:

If initial frequency ($A$) = $p_0$, then frequency ($A$) after 1 generation –

$p_1 =$
Mutation rate vs. genetic drift:

To counter loss of allele $a$ (rate: $1/N$) from drift… would need mutation rate $\mu$ such that $\mu \geq 1/N$