

Evolution 5

- send answer to iClicker Question 2A now
- Population Genetics III
 - Violations of HWE assumptions
 - small population
 - mutation, migration, non-random mating
 - natural selection
 - examples
- iClicker Question 2B

Due in lab next week:

⇒ pre-lab for Skulls & Evolution (lab manual p. 13 and on-line)

⇒ HMNH lab report (Just answer questions 1 thru 5).

- iClicker registration is now working!
- Don't forget the on-line "Tree Building Survey" - see course website for Evolution 6.

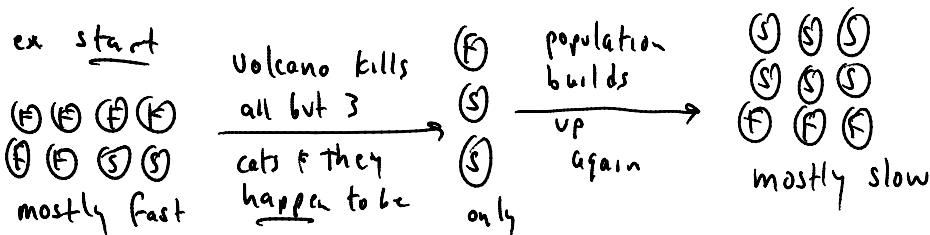
Violations of HWE assumptions

① Very large population size Violation = limited population size

= a randomly-selected small sampleⁿ of the population

starts a new population ("bottleneck" or "founder effect")

* since small - likely to be non-representative



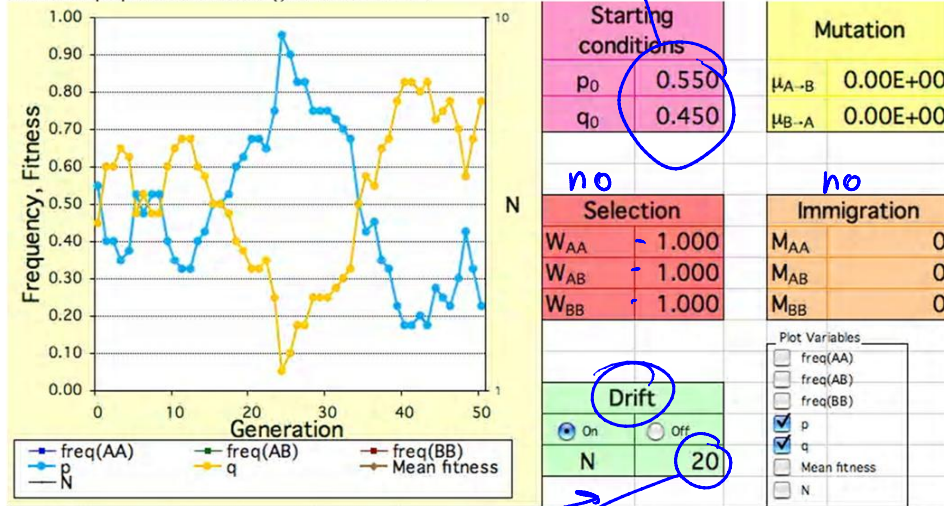
* this is evolution (genetic change over time)

but not adaptation (due to luck or chance not genotype)

Population Genetics Simulations II

Violations of the Hardy-Weinberg Assumptions:

a) Small population size ("genetic DRIFT")



- random changes in allele freqs.
Surviving allele is by luck (not fitness)

Smaller N \rightarrow more variation
different every time

\rightarrow # of randomly-selected survivors in each generation

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⑤ no migration : violation = individuals enter or leave population
so that allele freqs change

⑥ no mutation : violation = new alleles created by mutation

(Some $p \rightarrow r$)

- * essential for evolution (creates variation)
- * only changes allele freqs very slowly

④ random mating : violation

all organisms contribute equally to gene pool
but mate choice depends on genotype

ex. slow x slow ; v. fast x v. fast ; fast x fast
but never slow x fast, etc

- changes genotype freqs, but not allele freqs.

⑤ no selection violation = natural selection

("artificial selection" = deliberate breeding by humans)

(can be due to human action - just not breeding)

= not all organisms contribute equally to gene pool

* commonplace "fitness" vs. evolutionary fitness

↓
"strength"
"health"
etc.

↳ reproductive fitness - all that matters
for evolution is "# of kids you have"
= how well you pass on your genes

* sometimes connected (ex. cheetahs)
but not the same thing

e) Natural Selection:

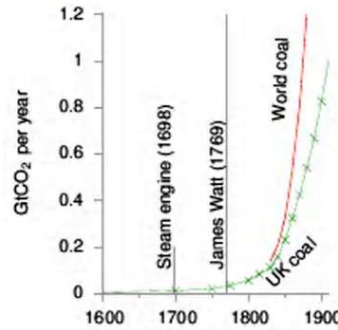
- for example "Industrial Melanism" in the Peppered Moth in England

color controlled by one gene with two alleles *- really this simple*

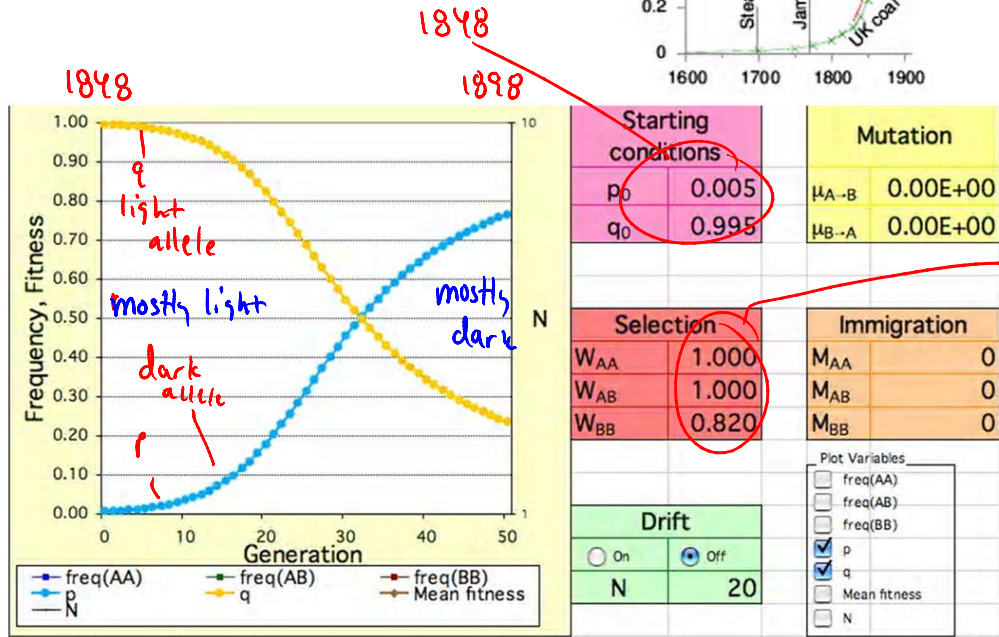
allele	contribution to phenotype	frequency	Genotype	Phenotype
A	dark body (dominant)	p	AA	dark
B	light body (recessive)	q	AB	dark
			BB	light

Data:	% of moths that are DARK	% of moths that are LIGHT	freq (A) (p)	freq (B) (q)
1848	1%	99%	0.005	0.995
1898	95%	5%	0.776	0.224

- In 1848, the trees had clean light bark \Rightarrow dark moths eaten \Rightarrow moths mostly light
- Industrial revolution \Rightarrow coal burning \Rightarrow soot accumulates on trees \Rightarrow trees have dark bark \Rightarrow light moths eaten \Rightarrow moths mostly dark.



Can simulate in Deme:



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Q: why can't you make the recessive allele so away ($q=0$) even though BB's very unfit?

Ⓐ because B's "hide" in carriers (AB) - still dark

∴ "impossible" to completely remove