Duke
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GENETIC DRIFT:

Sampling error over many generations

Long-term effects of drift

- Start with a variable population, 2 alleles
  - p(A) = 0.5, q(a) = 0.5 as an example
- After many, many generations,
  - p(A) = 0 or 1
- Reason: once you get to 0 or 1, there's **no variation** (one allele is gone), so can't "drift" back…

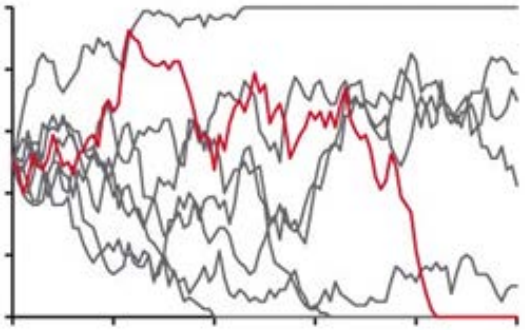

Figure 7.15 Evolutionary Analysis, 4/e

Long-term effects of drift

- What if you start with a variable population, and 2 alleles?
  - p(A) = 0.6, q(a) = 0.4

Analogy:
Blindfolded man walking aimlessly

- 0.0

1.0

Analogy:
Blindfolded man walking aimlessly

- 0.0

1.0

Analogy:
Blindfolded man walking aimlessly

- 0.0

1.0

Probability of "long-term" outcome is predictable

- In one generation, roughly equally likely for allele to go up or down in frequency
  - p(A) may go up or down
- BUT long-term "loss" or "fixation" of allele is more predictable
  - If p(A)=0.5, equally likely
  - If p(A)<0.5, more likely that allele to be lost
  - If p(A)>0.5, more likely that allele to be fixed

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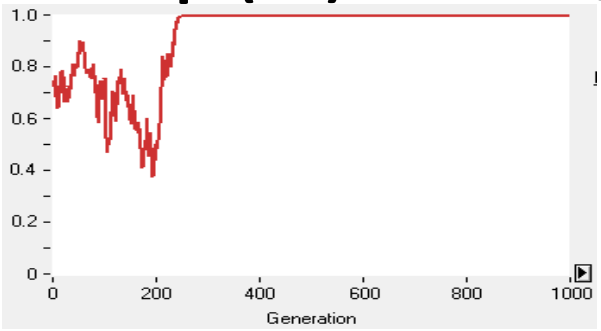
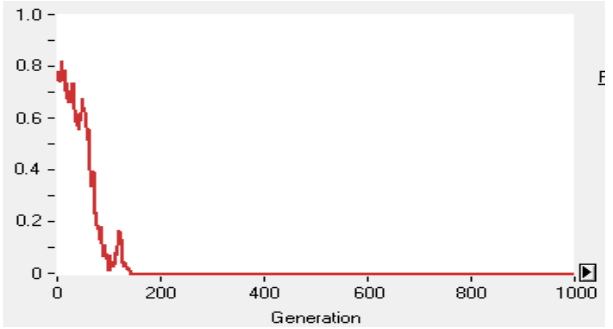
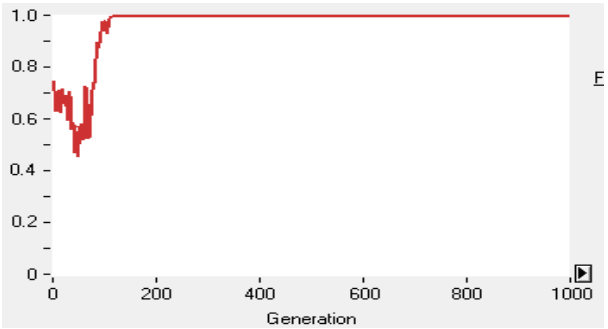
  - If p(A)<0.5, more likely that allele to be lost
  - If p(A)>0.5, more likely that allele to be fixed
- Probability of *eventual* fixation of A equals p(A)!

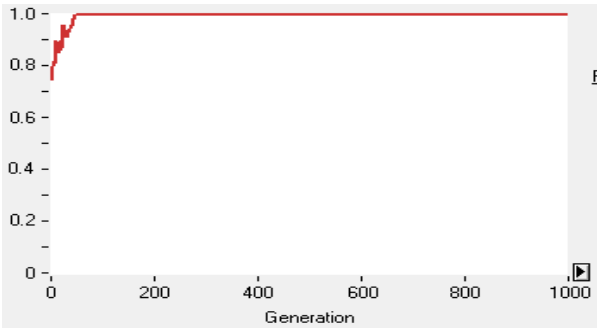
4 sample runs of AlleleA1

p(A)=0.75, Population size = 100









Species vs. populations

- Examples so far looked at what happened in one population
- What happens if look at whole species, which includes some “isolated” populations?

Galapagos Land Snail

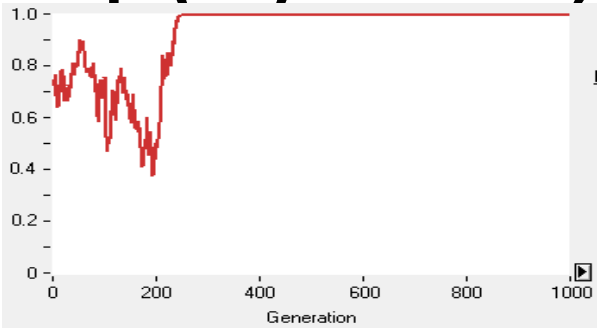
Thought question...

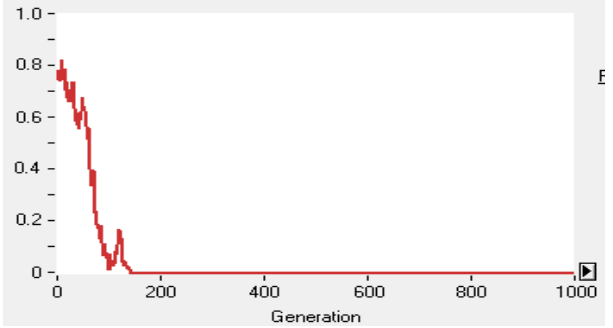
If all 4 populations of Galapagos land snail started with p(A) = 0.75,

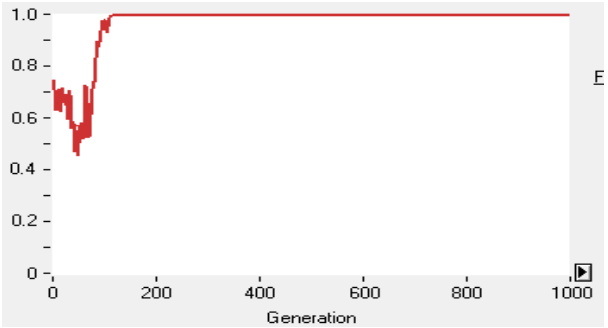
1) What would the allele frequencies be in the populations many years later?
2) What would the AVERAGE p(A) across all populations be many years later?

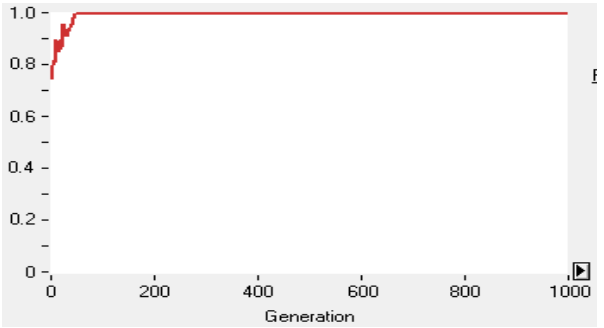
4 sample runs of AlleleA1

p(A)=0.75, Population size = 100









Points to remember

- Drift **eventually leads to allele fixation or loss in every population**
- Starting allele frequency (p(A)) is long-term probability of allele's fixation

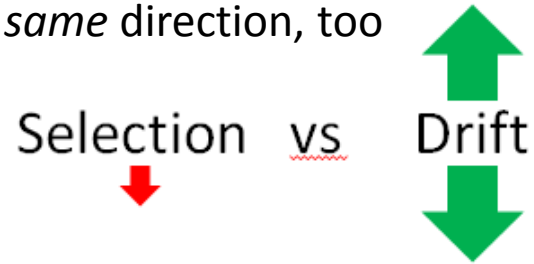
  (1-p(A)) is long-term probability of allele's loss
- If have species with many isolated populations, then individual populations have fixation/ loss, but overall species retains variation with same p(A)

Can genetic drift make "bad" alleles spread (or even be fixed)?

Interaction of genetic drift & natural selection

•If the population size is small (i.e., drift is strong), genetic drift **can** sometimes counteract weak selection to spread or fix "bad" allele

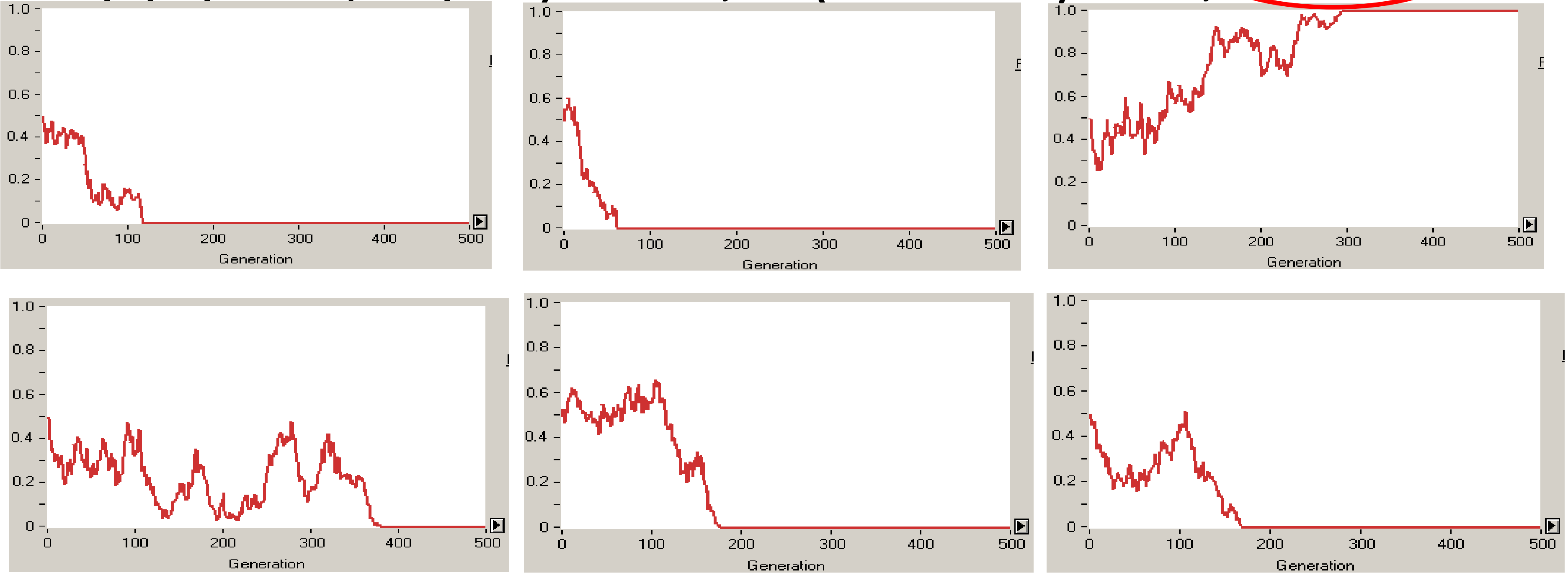
- Won't *always* counteract selection, because drift is random in direction in each generation
  - May push in the *same* direction, too



Selection vs Drift

6 simulations: strong drift, weak selection

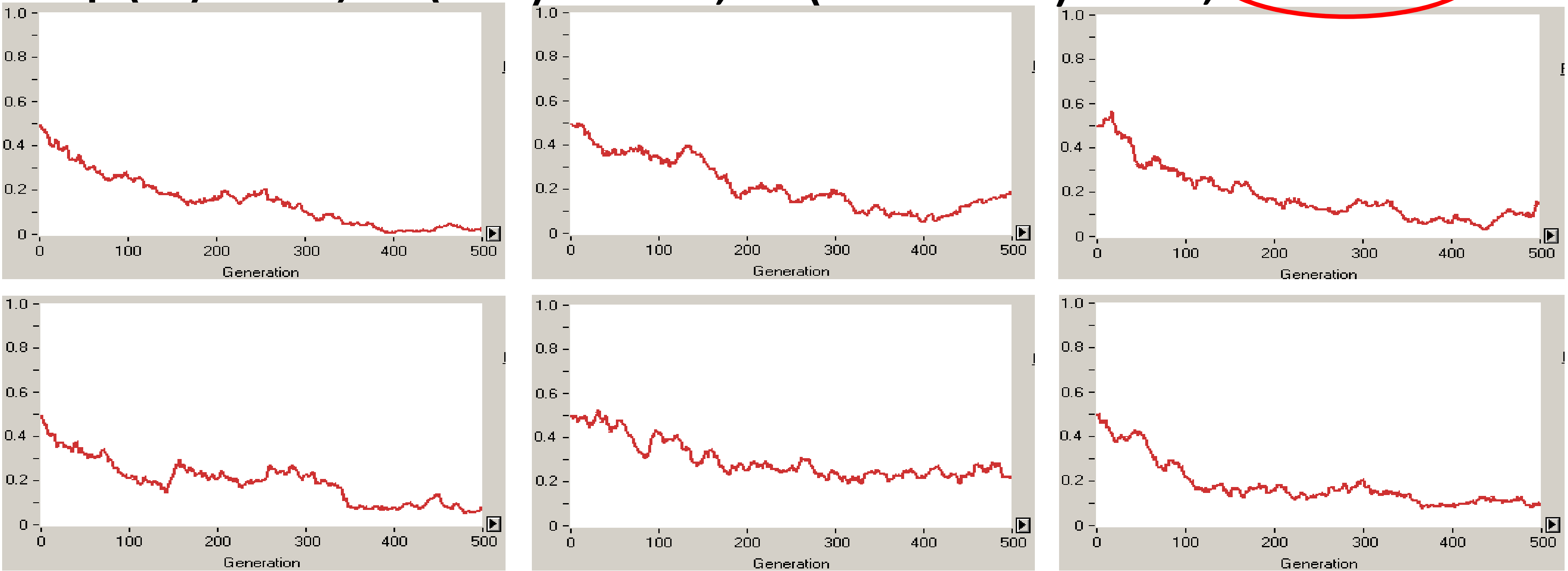
p(A)=0.5, w(AA)=0.98, w(Aa & aa)=1.0, **N=100**



Selection vs Drift

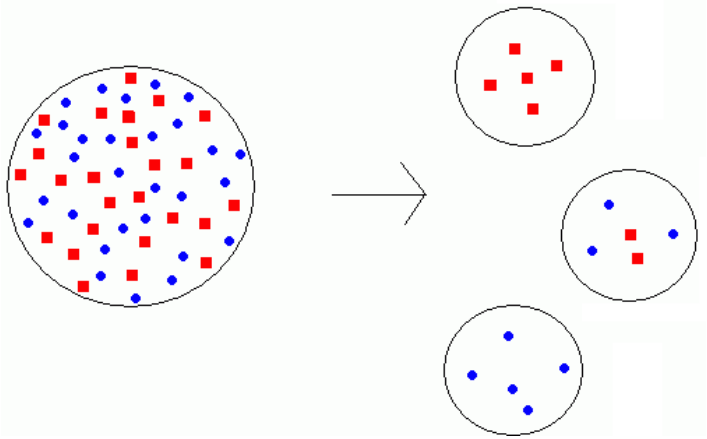
6 simulations: weak drift, weak selection

p(A)=0.5, w(AA)=0.98, w(Aa & aa)=1.0, **N=1000**



“Founder effects”

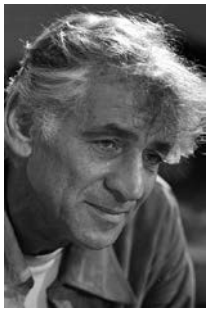
- Strong genetic drift when a new population is established by a very small number of individuals from a larger population
  - Often associated with colonizing islands
  - Sometimes causes spread (or fixation) of even detrimental alleles since drift is strong

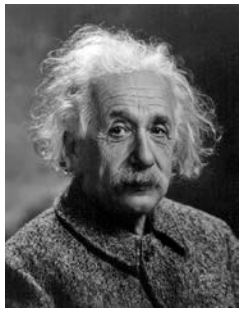


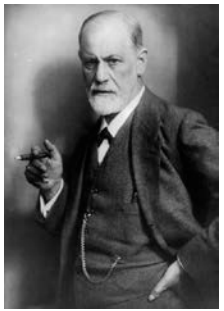
Diseases or traits common in certain human populations from founder effects

- Polydactyly in Amish

- Tay-Sachs disease in Ashkenazi Jews





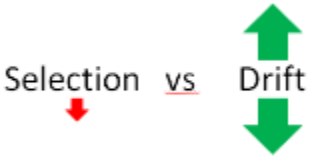


- Huntington's disease in Mauritius

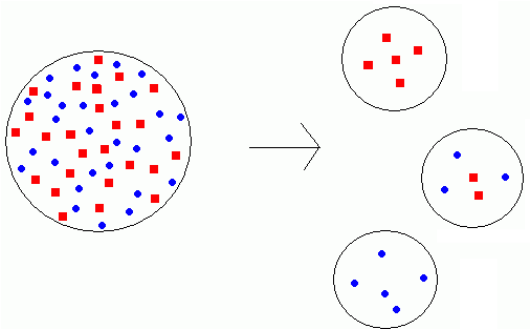
- Red hair among Irish

More points to remember

- In small populations, genetic drift can sometimes overpower weak selection
  - Might spread or fix “bad” alleles



- Founder effects– special case of genetic drift



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