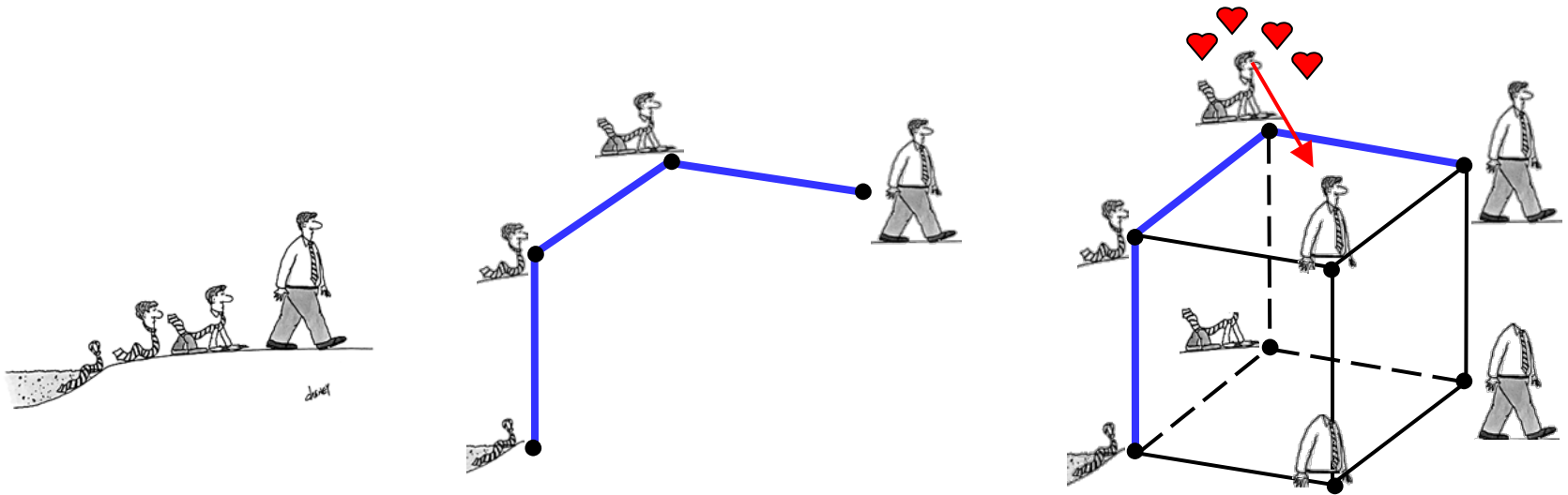


Tracking Evolutionary Trajectories of Sexual Populations



Daniel M. Weinreich

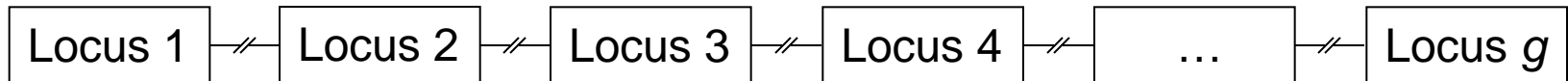
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Today's Question

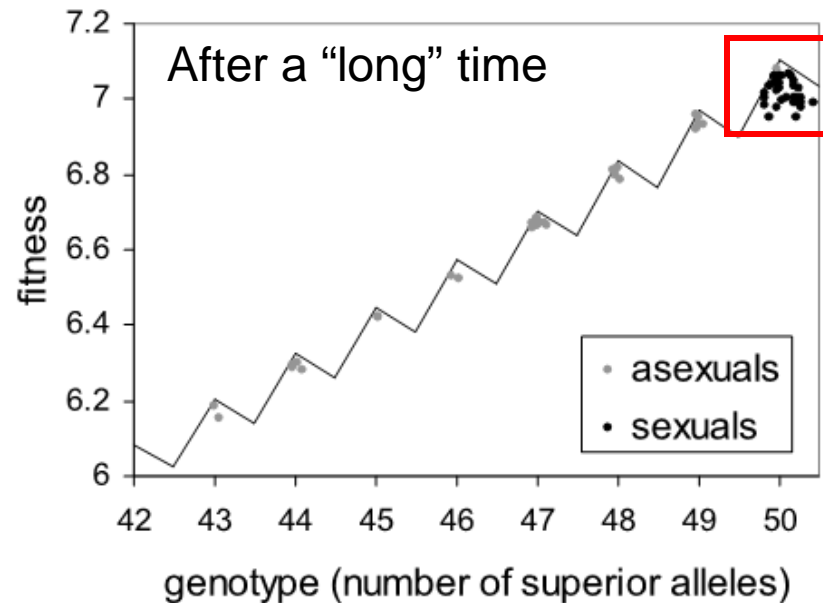
- Nucleotide sequence space provides an instructive framework in which to visualize evolutionary trajectories under SSWM.
 - Extensible
 - Predictive
- Is there an analogous framework in which to visualize trajectories for sexual populations?
 - (I'm not optimistic!)

Genome Structure and the Benefit of Sex



$W_G = \prod w_i$ (thus, no epistasis *among* loci)

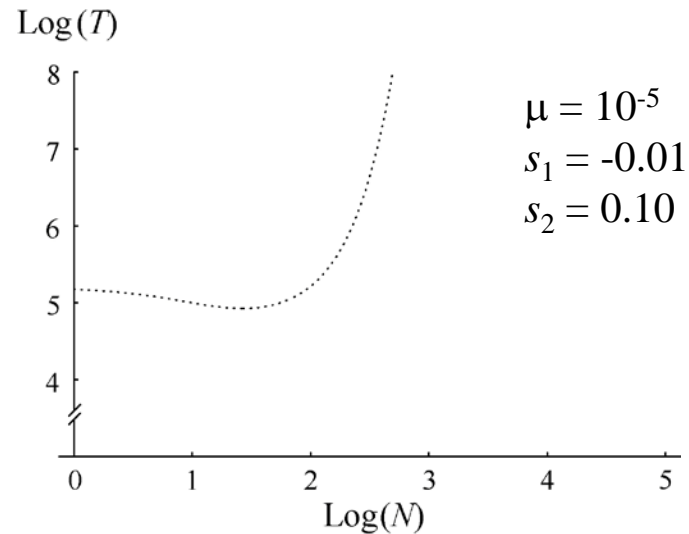
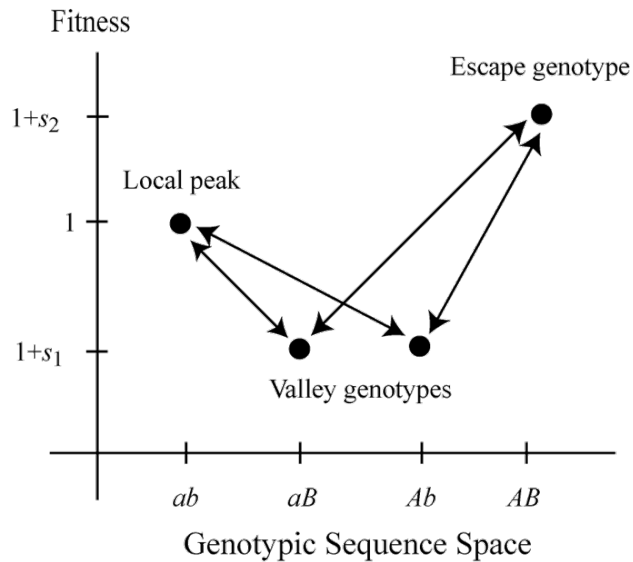
Identical w_i with suboptimal maxima (thus, sign epistasis within loci)



What do these trajectories look like?

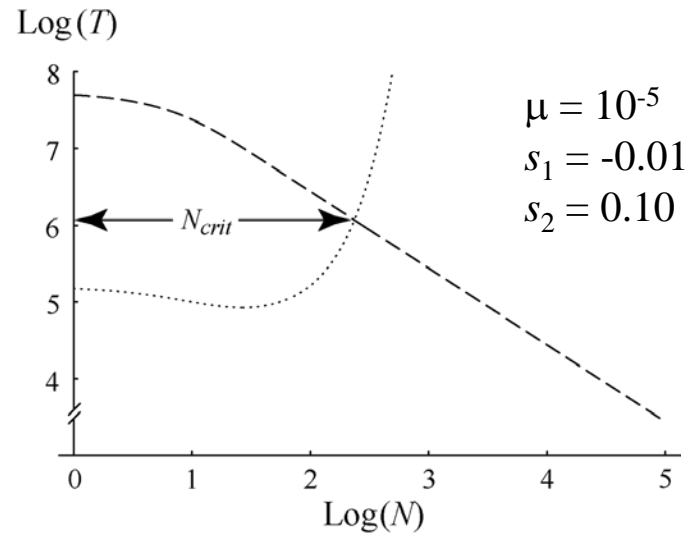
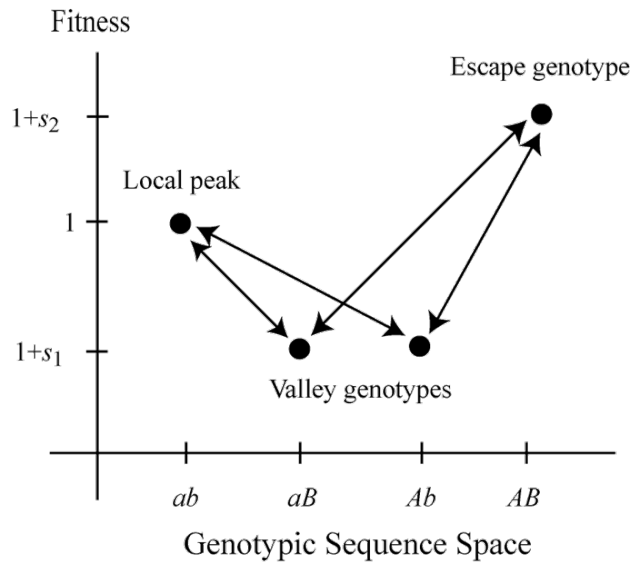
(Watson, Weinreich and Wakeley 2010)

Time Between Adjacent Peaks



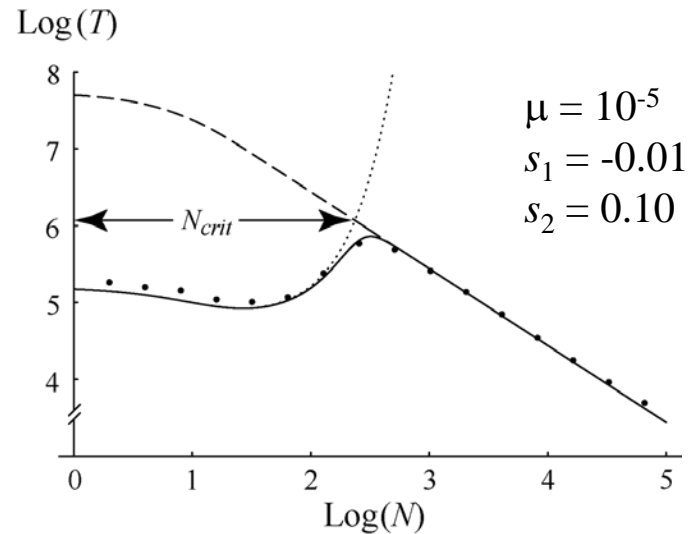
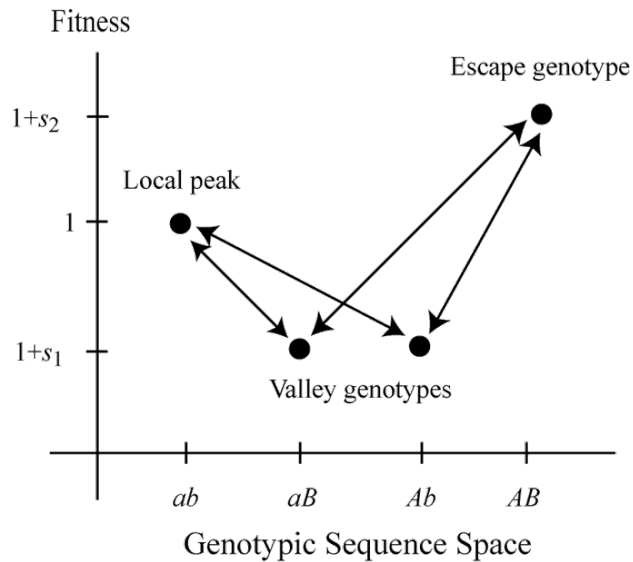
(Carter and Wagner 2002, Iwasa et al 2004, Weinreich and Chao 2005)

Time Between Adjacent Peaks



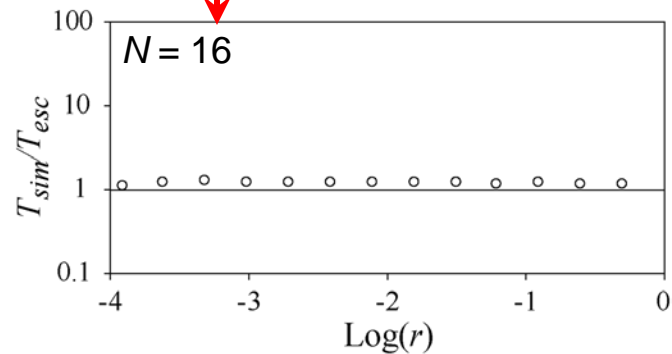
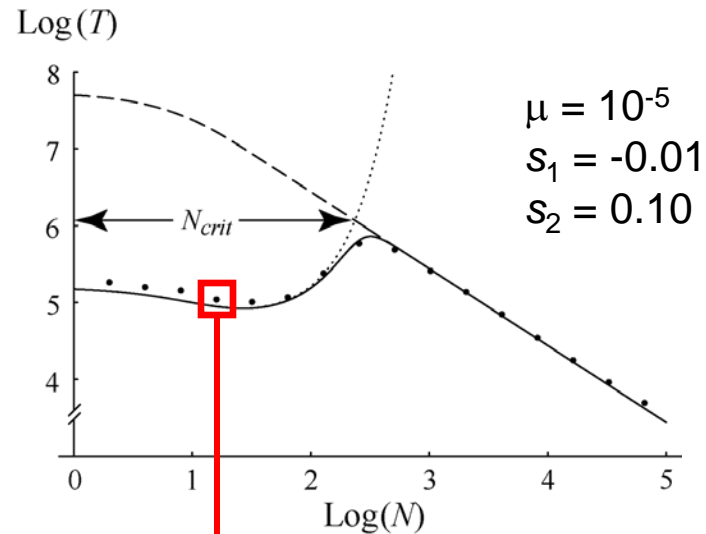
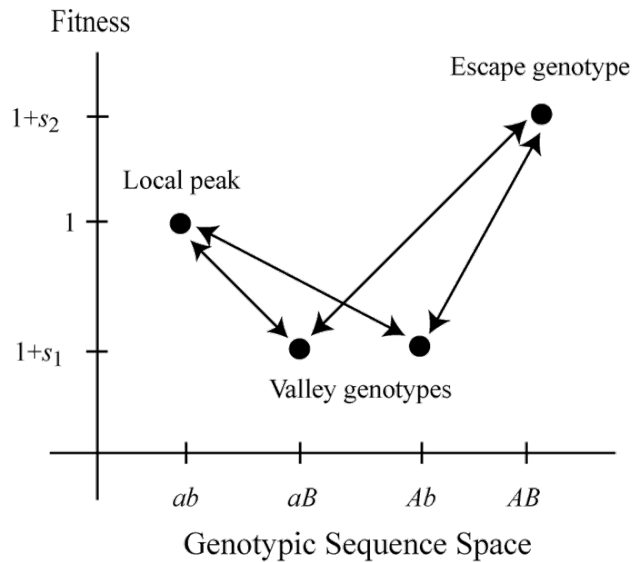
(Carter and Wagner 2002, Iwasa et al 2004, Weinreich and Chao 2005)

Time Between Adjacent Peaks



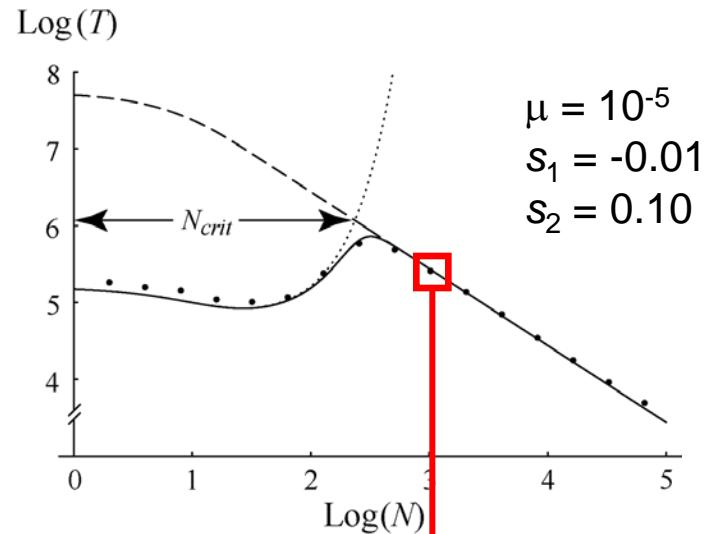
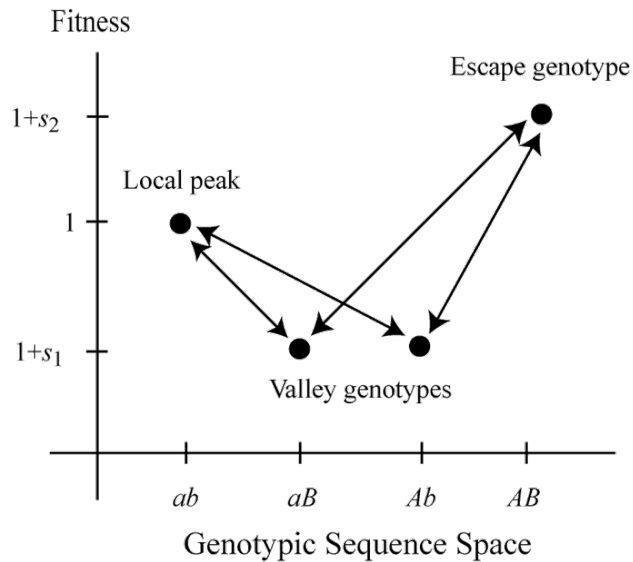
(Carter and Wagner 2002, Iwasa et al 2004, Weinreich and Chao 2005)

What about Recombination?

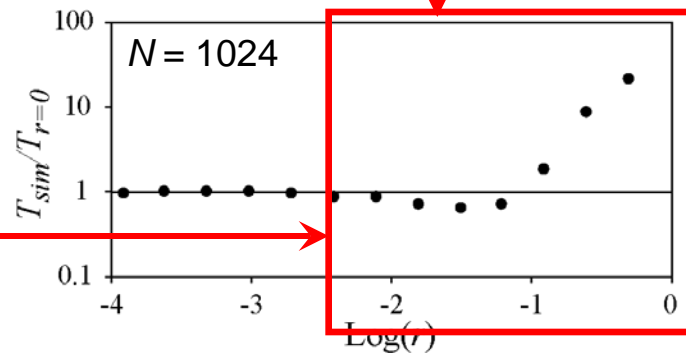


(Weinreich and Chao 2005)

What about Recombination?



Can we visualize
these trajectories?

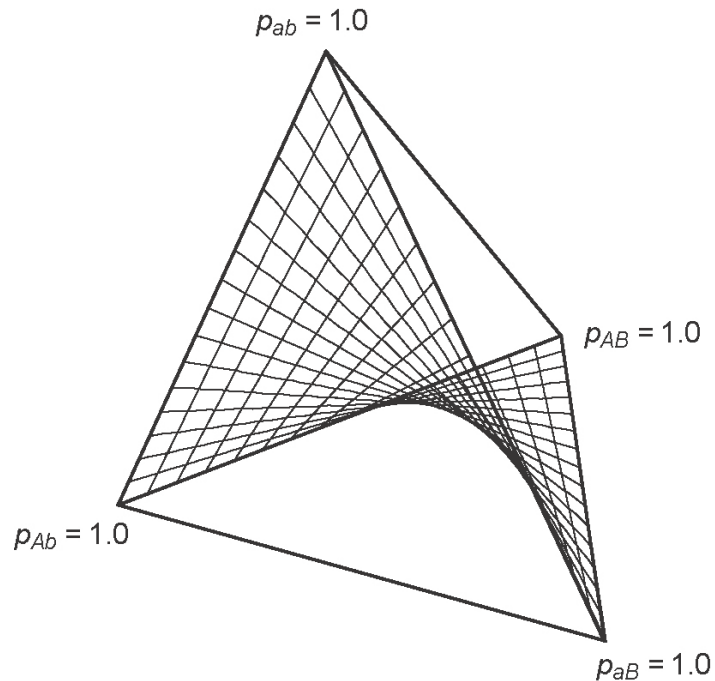


(Weinreich and Chao 2005)

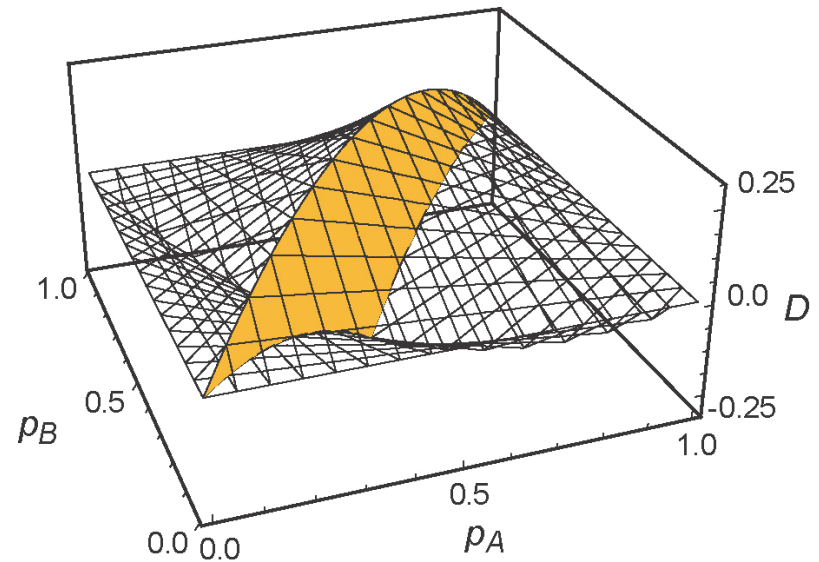
Need to Track Frequencies

- Genotype frequencies? Somewhat ugly because each difference equation depends on all four state variables.
- We thought to try allele frequencies and linkage disequilibrium because this respects the genetics of mutation and recombination, which act atomically on loci and breakpoints between loci.
 - $\Delta_r p_A = \Delta_r p_b = 0$
 - $\Delta_r D = -r \cdot D$
 - $\Delta_\mu p_A = \mu(1 - 2p_A)$
 - $\Delta_r D = -4D(1 - \mu)\mu$

Alternative Spaces

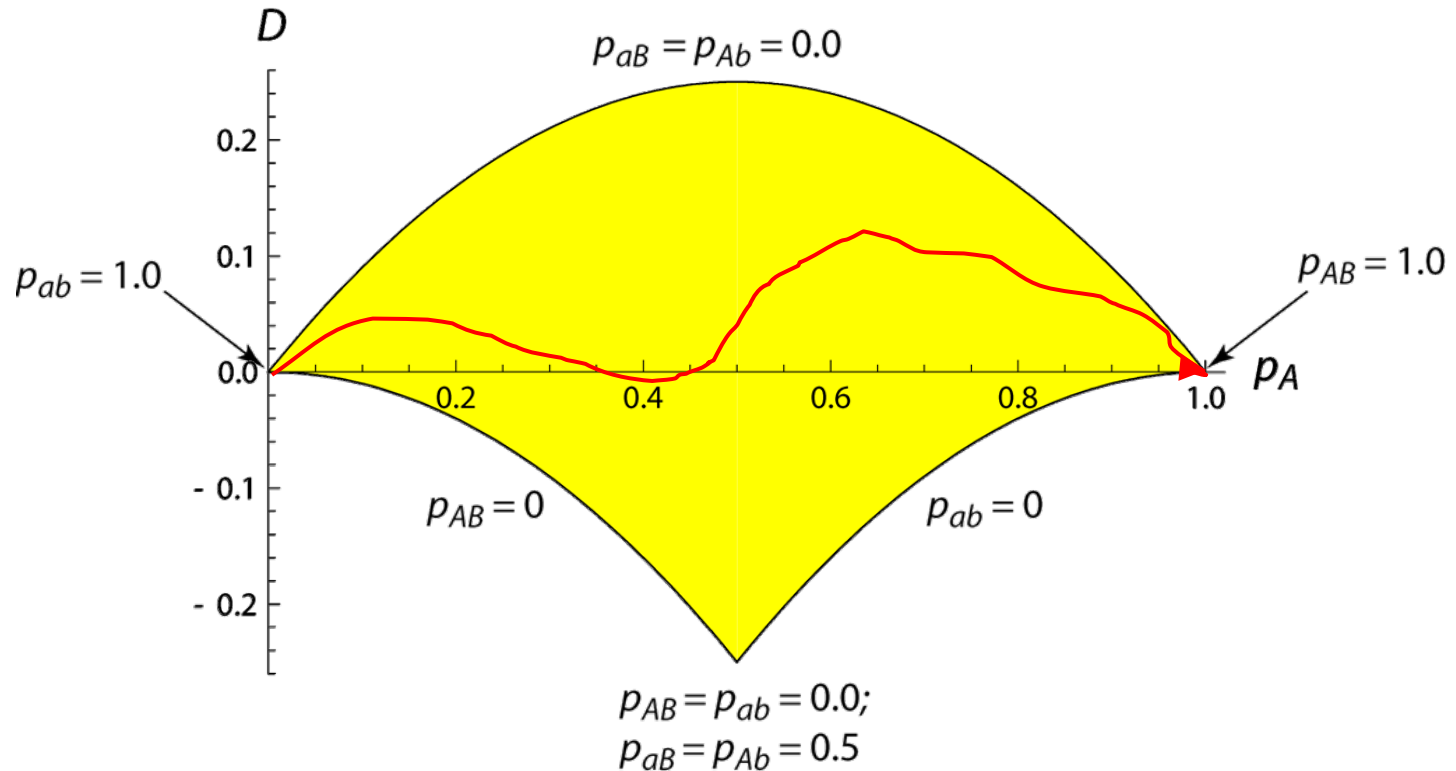


Genotype Frequency Space



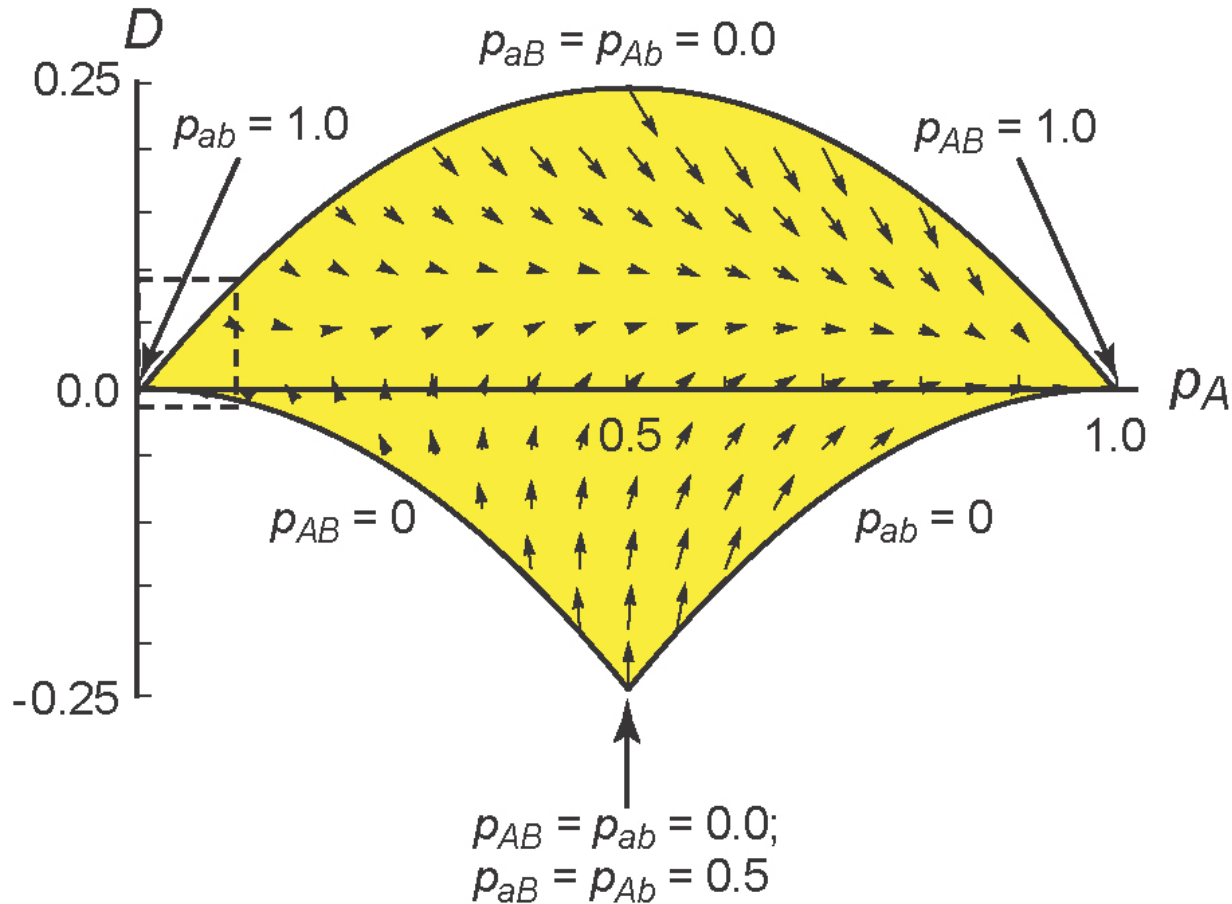
Allele Frequency/LD Space

$p_A \times D$ – space



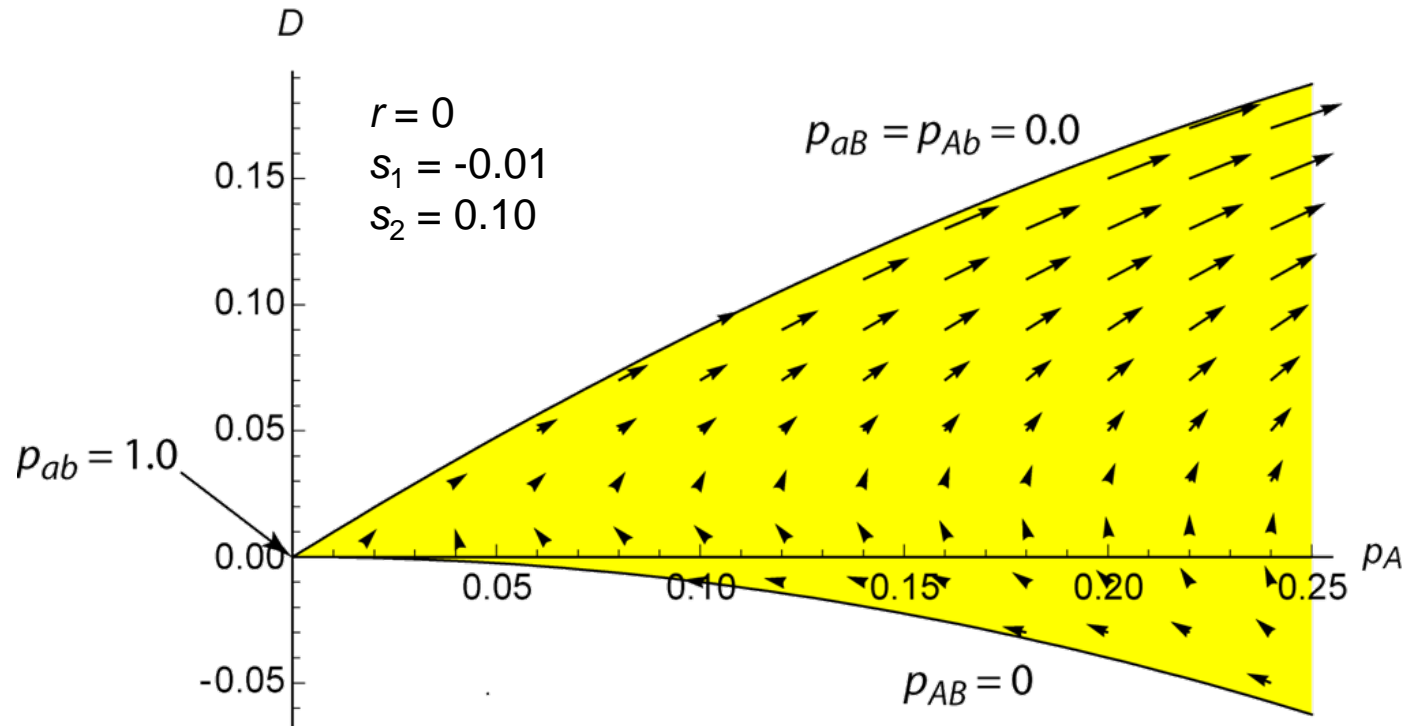
In general, how do recombination, mutation and selection determine what trajectory an evolving populations will follow?

Recombination + Two Fitness Maxima

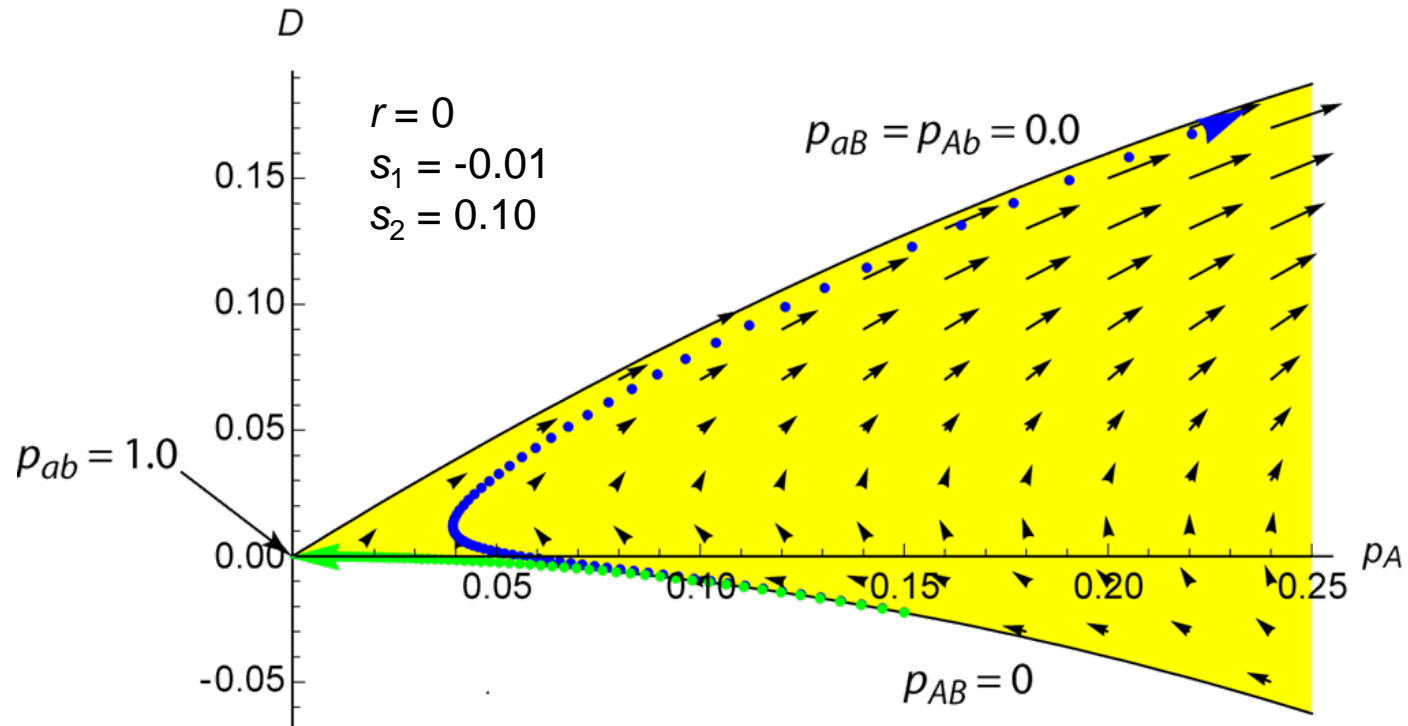


$r = 0$
 $s_1 = -0.01$
 $s_2 = 0.10$

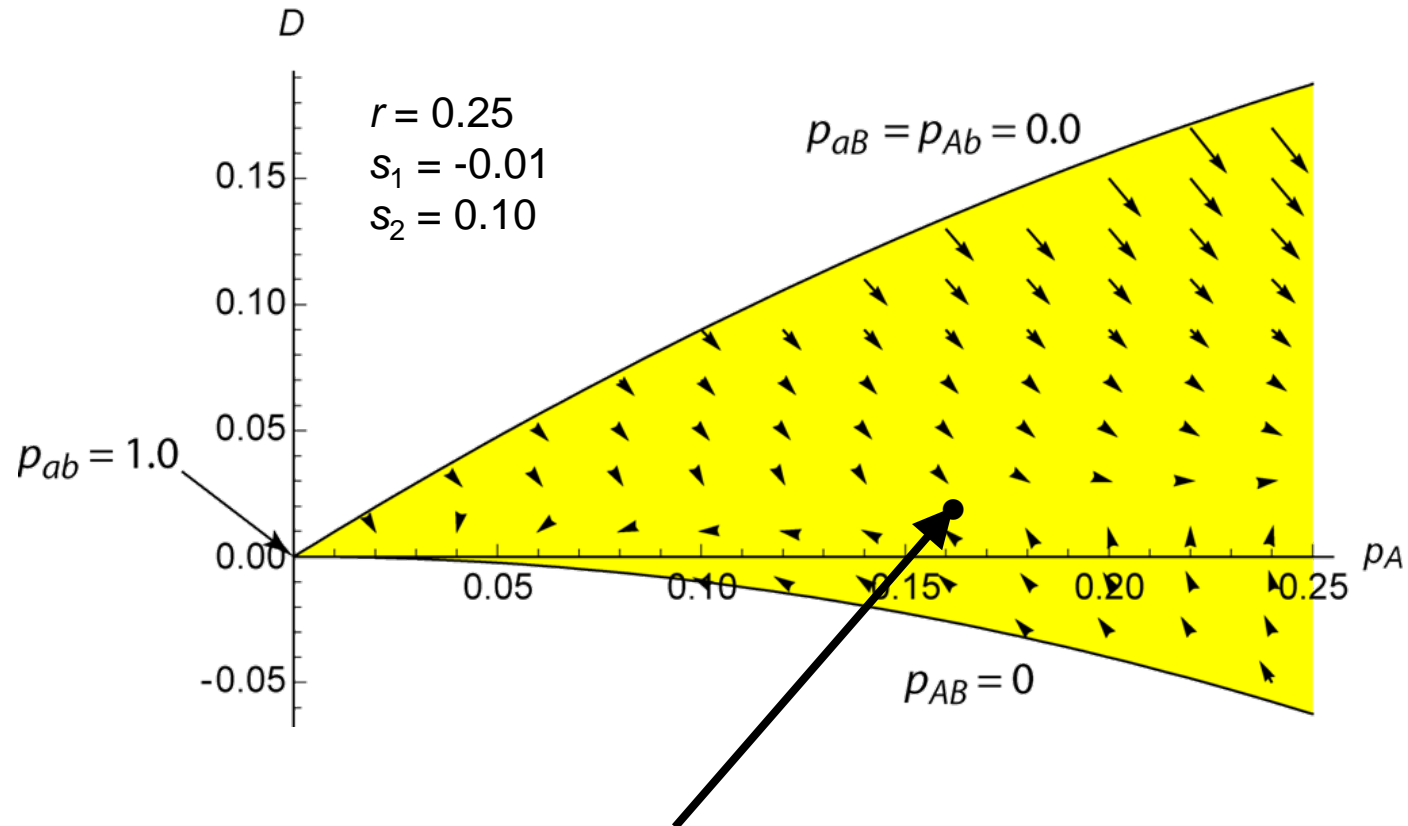
Recombination + Two Fitness Maxima



Recombination + Two Fitness Maxima

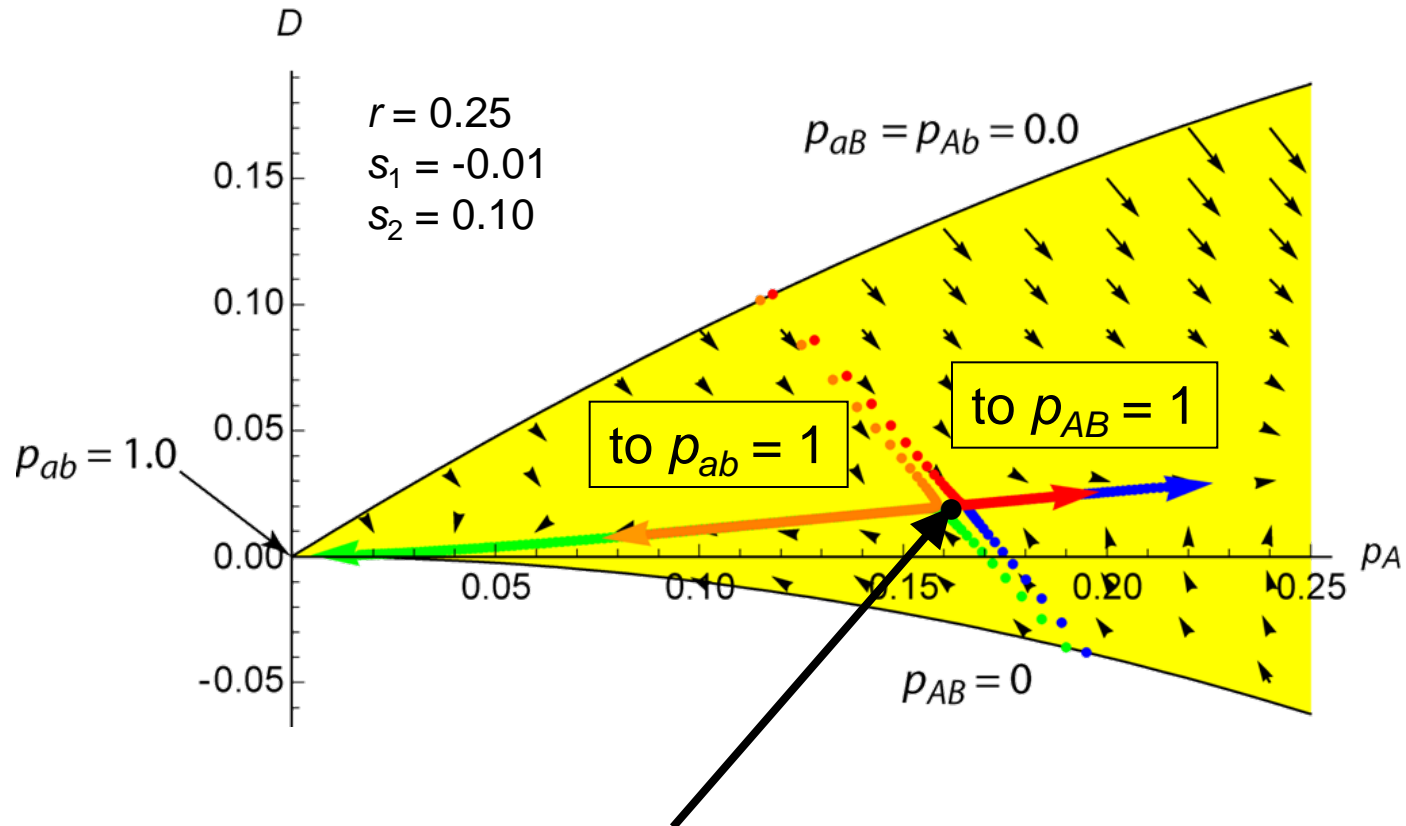


Recombination + Two Fitness Maxima



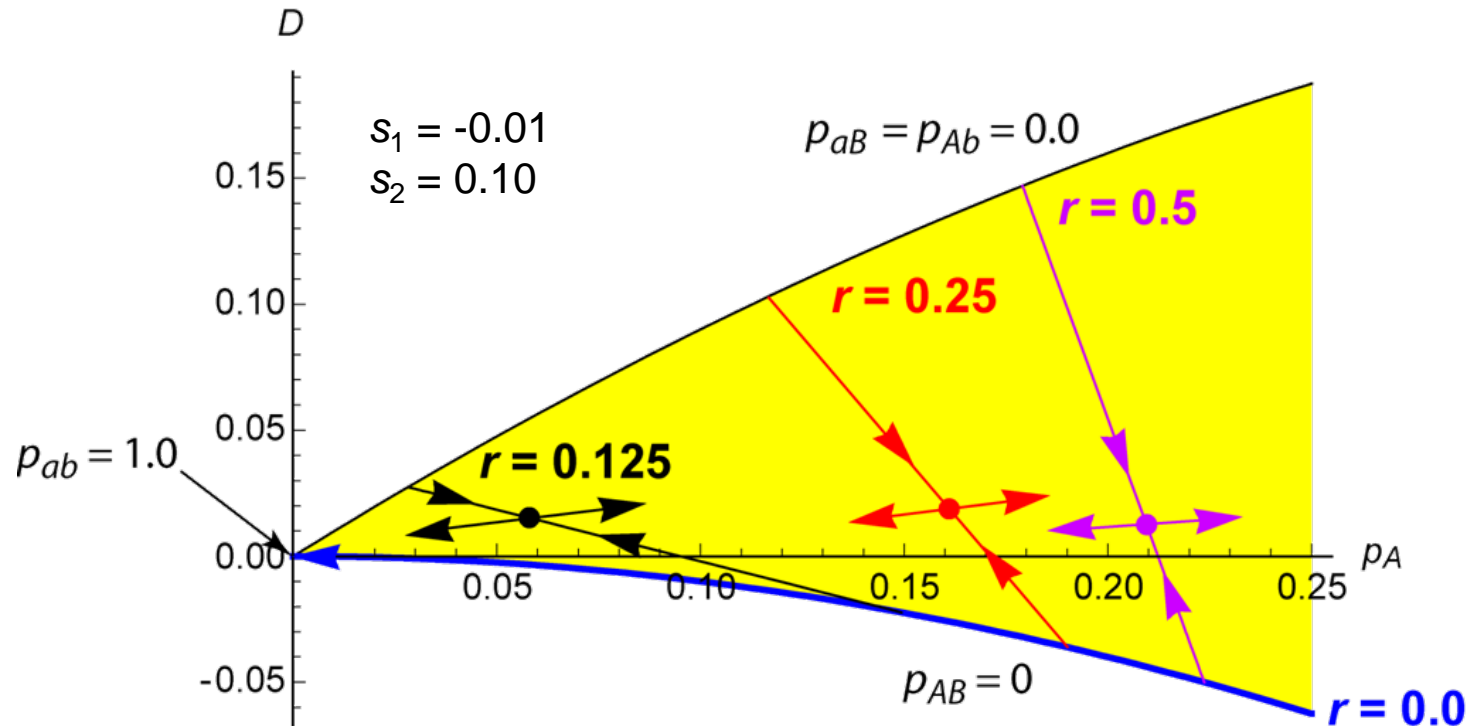
Saddle fixed-point emerges when $r > s_2/(1 + s_2)$; see also Crow and Kimura (1965).

Recombination + Two Fitness Maxima



Saddle fixed-point emerges when $r > s_2/(1 + s_2)$; see also Crow and Kimura (1965).

Recombination + Two Fitness Maxima



Can analytically locate the fixed points and approximate the corresponding boundaries between basins of attraction as a function of selection and recombination.

Whither the Fitness Landscape?

- Although the fitness function isn't continuous, subject to SSWM assumptions it is predictive. Why? Because it's a potential function, and the local gradient defines the direction an evolving population is likely to move.
- Is there a potential function over $p_A \times D$ - space? No. In point of fact our vector field $(\Delta p_A, \Delta D)$ corresponds to no potential function. (Formally, $\partial(\Delta p_A)/\partial D \neq \partial(\Delta D)/\partial p_A$.)
- Interestingly, violating SSWM appears to also render the fitness landscape less predictively useful because the fate of any lineage now depends on the fitnesses of whoever else is cosegregating.
- Speculate: Predictive population landscapes do not exist.

Acknowledgements

- Richard Watson
- Suzanne Sindi



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Biology