PBG 200A Notes

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- Hitch-hiking effect
  - We expect to see a loss of heterozygosity as we move along the genome toward the selected allele
  - Example in Malaria parasite - plasmodium falciparum - resistance to anti-Malaria drugs
  - Use the width of non-heterozygous regions to give us information on the strength of selection - faster sweeping doesn't allow for much recombination.
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$$t_s = \frac{4}{s}\log(2N_e) \tag{1}$$

$$p_{\text{NR}} = \prod_{t=1}^{t_s}(1 - r(1 - x_t)) \approx \exp\left[-r\sum_{t=1}^{t_s}(1 - x_t)\right] \tag{2}$$

but

$$\overline{(1 - x_t)} = \frac{1}{t_s}\sum_{t=1}^{t_s}(1 - x_t) = 0.5 \tag{3}$$

so

$$p_{\text{NR}} = \exp\left[-rt_s\overline{(1 - x_t)}\right] \tag{4}$$

$$= \exp[-rt_s/2] \tag{5}$$

  - With probability $\pi = p_{\text{NR}}^2 \times 0 + (1 - p_{\text{NR}}^2)4N\mu = (1 - \exp[-rt_s])4N\mu$.
  - Look at how far along the genome we need to see a 50% return in heterozygosity.
- Interaction between selected alleles and recombination
  - Suppose AB and ab have high fitness, but Ab and aB have low fitness. Then recombination is a detriment to fitness. Recombination is general is breaking up the high fitness haplotypes for lower fitness haplotypes. Selection and Recombination are in opposition.
- Inverted genes
  - Can cause "supergenes."