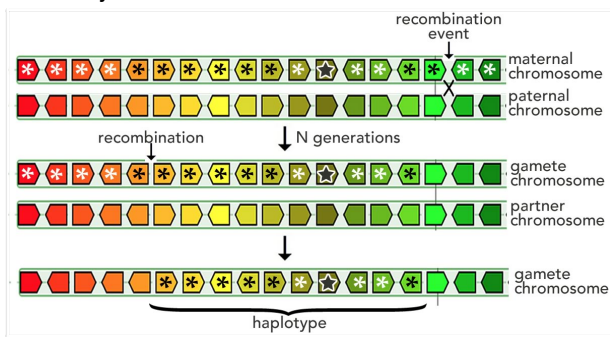


evolutionary effects: disconnecting alleles



What happens if there is strong positive / negative selection on
☆ how does it effect neighboring alleles?

evolutionary effects: disconnect alleles



we can estimate time that region was inherited by looking at
the combination of alleles interited together.

Now consider mutation rate

Article | [OPEN](#)

Differences between germline and somatic mutation rates in humans and mice

Brandon Milholland, Xiao Dong, Lei Zhang, Xiaoxiao Hao, Youxin Suh & Jan Vijg 

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[Ageing](#) [Genomics](#) [Mutation](#)

in human: germline mutation rate (males) $\sim 3 \times 10^{-11}$ per bp
Somatic mutation rate $\sim 3 \times 10^{-9}$ per bp
haploid human genome $\sim 3 \times 10^9$ bps

both mutation rates are higher in mouse

Genetics

Fathers pass on four times as many new genetic mutations as mothers – study

The figures mean that a child born to 30-year-old parents would, on average, inherit 11 new mutations from the mother, but 45 from the father.

why, exactly?

Questions (you should be able) to answer:

212. Graph, as a function of distance, the likelihood that recombination will disconnect a selected (whether positively or negatively) allele from alleles in surrounding genes.
213. Why might a crossing over event inhibit nearby crossing over events?
214. How can you use the size of a conserved genomic region to estimate time of isolation of a population?
215. What are the benefits of recombination in terms of environmental adaptation?

Questions to ponder:

- How does the size of haplotype regions reflect the reproductive history of a population?
- How does the presence of a deleterious allele influence the selective pressures on an organism? How might it open up (over generational) time, new evolutionary possibilities?