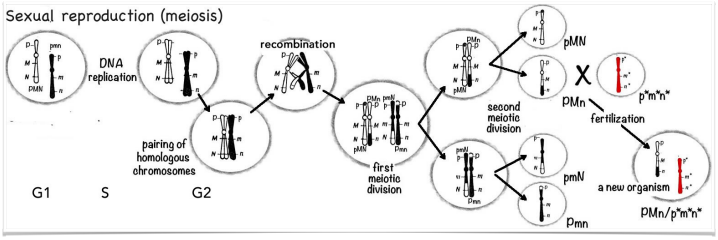
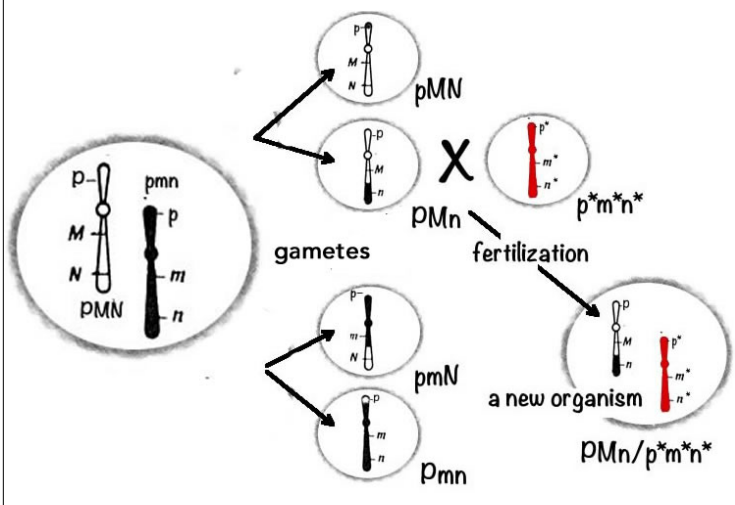
coreBio II - genetics: Monday 12 Feb 2018

email aidan: aiba2640@colorado.edu hand in questions!

reviewing meiosis





mechanism of synaptonemal complex formation
(veronica's question from last time)

Modeling meiotic chromosome pairing: nuclear envelope attachment, telomere-led active random motion, and anomalous diffusion

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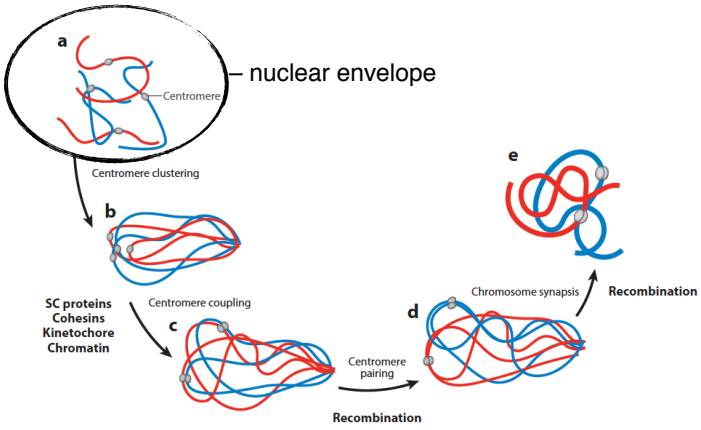
Keywords: diffusion, homologous pairing, computer simulation, meiosis, telomere, homologous chromosome, nuclear envelope attachment

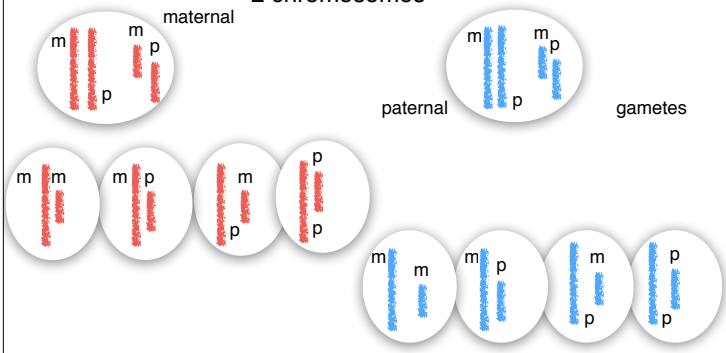
Abstract

The recognition and pairing of homologous chromosomes during meiosis is a complex physical and molecular process involving a combination of polymer dynamics and molecular recognition events. Two highly conserved features of meiotic chromosome behavior are the attachment of telomeres to the nuclear envelope and the active random motion of telomeres driven by their interaction with cytoskeletal motor proteins. Both of these features have been proposed to facilitate the process of homolog pairing, but exactly what role these features play in meiosis remains poorly understood. Here we investigate the roles of active motion and nuclear envelope tethering using a Brownian dynamics simulation in which meiotic chromosomes are represented by a Rouse polymer model subjected to tethering and active forces at the telomeres. We find that tethering telomeres to the nuclear envelope slows down pairing relative to the rates achieved by unattached chromosomes, but that randomly directed active forces applied to the telomeres speed up pairing dramatically in a manner that depends

mechanism of synaptonemal complex formation
(veronica's question)



2 chromosomes



calculate (draw) the number of different zygotes

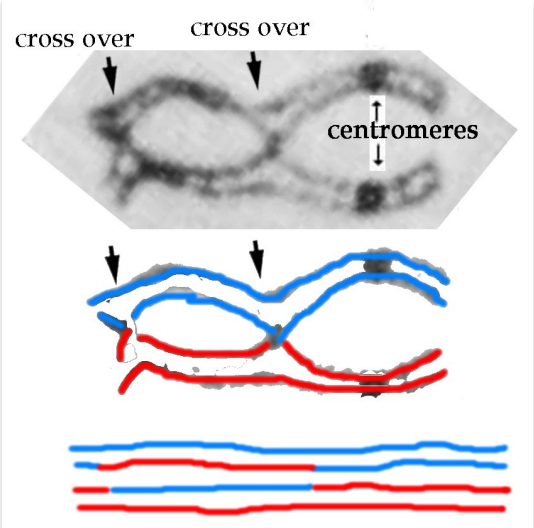
What happens if there are 4 or 23 distinct chromosomes

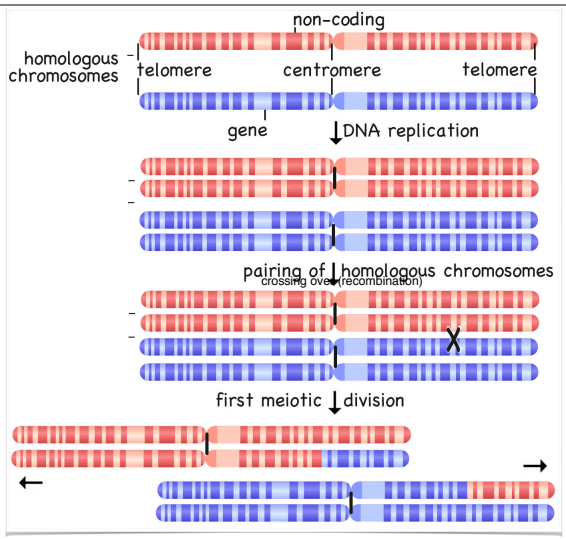
for 4 chromosomes: how many gametes

how many (genetically) different zygotes (new organisms)

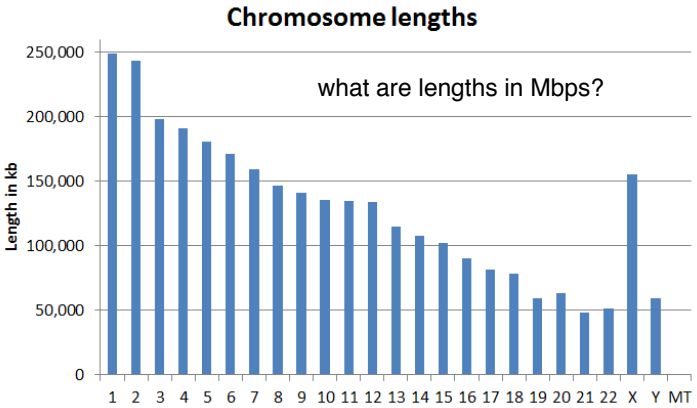
How does the number of alleles of a gene in a population impact your calculations.

Now add recombination (crossing over)

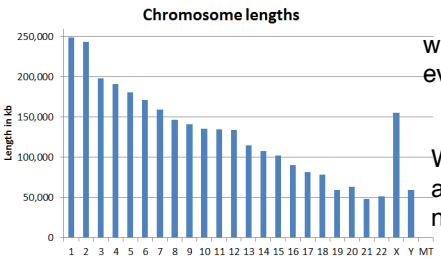




1 cM = 1% chance of a crossing over event.
two sites 50 Mbps apart = probability on crossing over ~50%

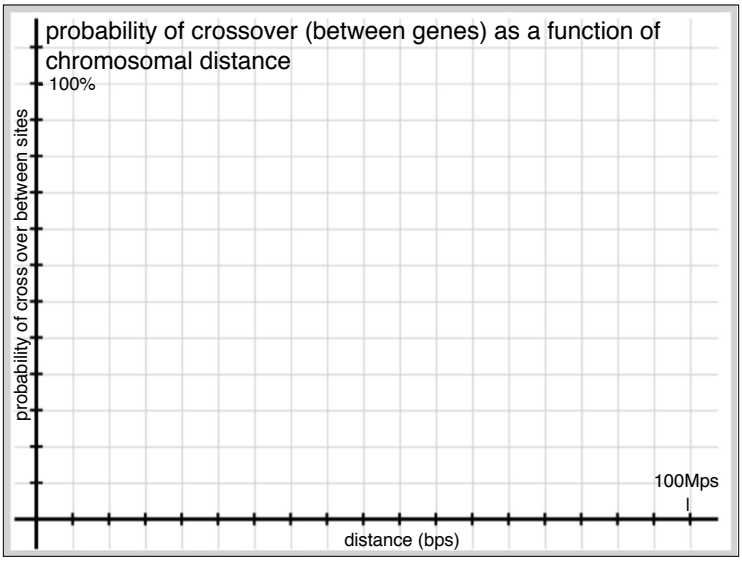


calculate (average) number of crossover events

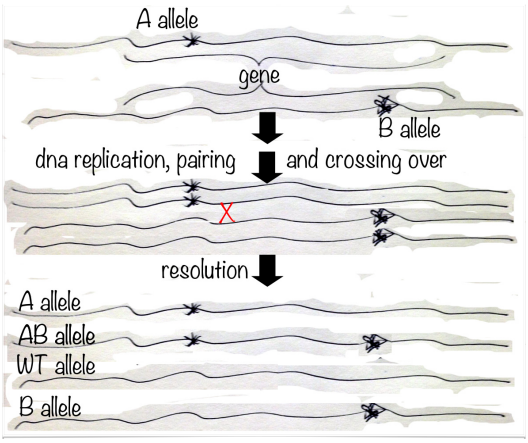


what percent of cross over events are “invisible”?

What is the probability that a specific chromosome has no cross-over events?



cross over to generate new allele (rarity) - why?



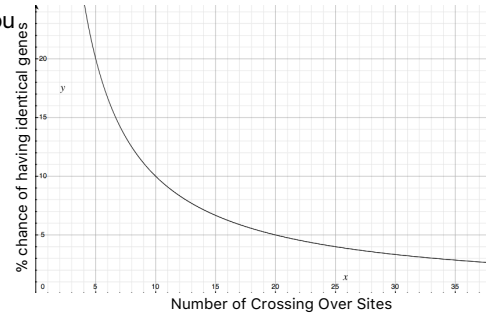
Aidan: why is there crossing over any way?

Questions to Consider

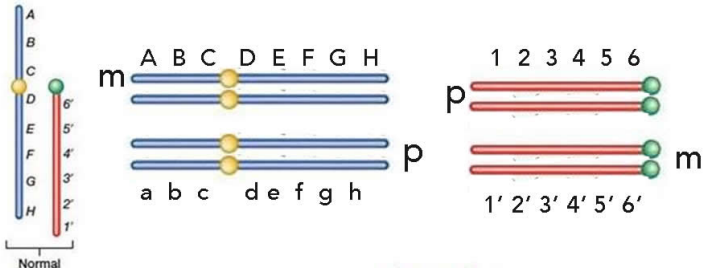
- What is the purpose of chromosome rearmament if genetic information is not gained or lost?
- When cutting: What are the odds of cutting between section 1 and 6 versus cutting between section 1 and 2
- After Trading: What % of same genes do you have after you traded?

Genetic Diversity

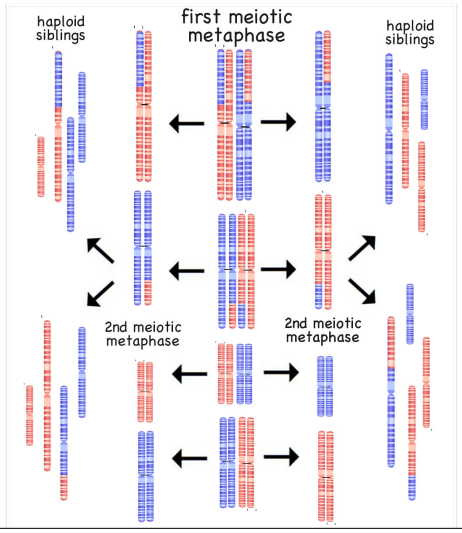
- 83% chance that you have a different genome than what you started out with from just crossing over



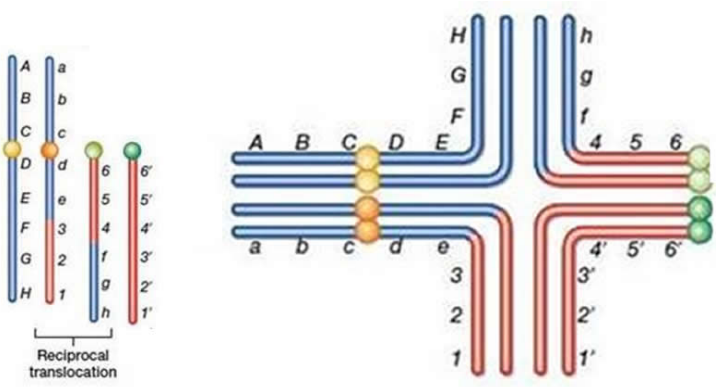
crossing over… normal chromosomes

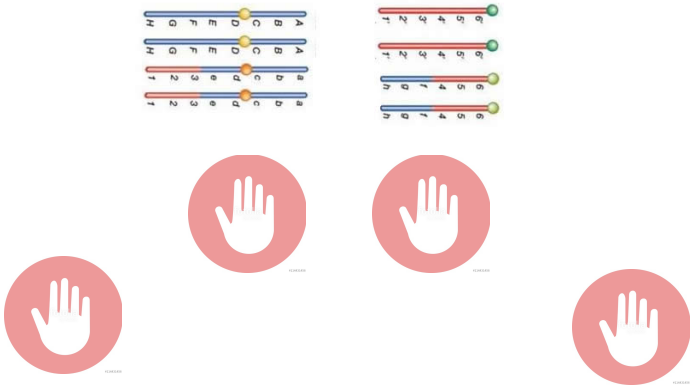


generation of variation

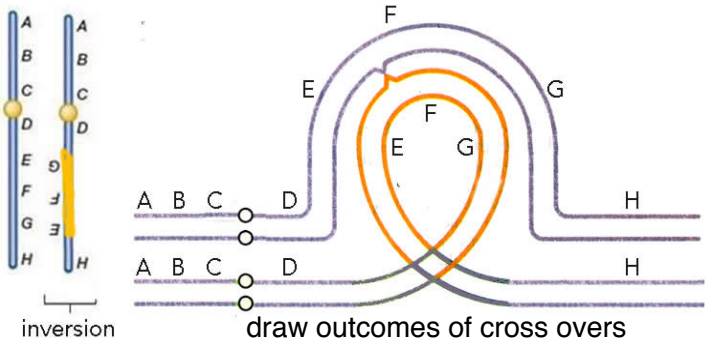


reciprocal translocation





inversion



evolutionary effects: disconnect alleles

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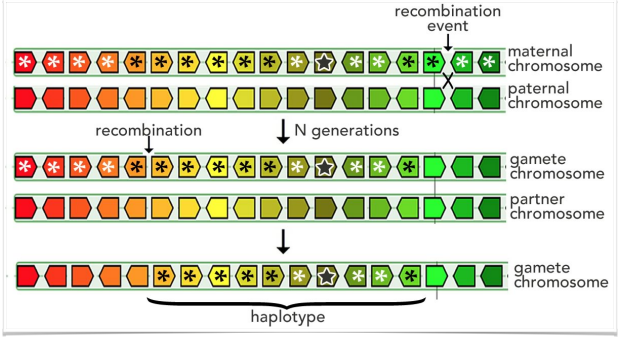

Now consider mutation rate

Article | OPEN

Differences between germline and somatic mutation rates in humans and mice

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

Nature Communications 8, Article number: 15183 (2017) doi:10.1038/ncomms15183 Download Citation

Ageing Genomics Mutation

Received: 21 July 2016 Accepted: 08 March 2017 Published online: 09 May 2017

in human: germline mutation rate (males) ~3 x 10^{-11} per bp
Somatic mutation rate ~3 x 10^{-9} per bp
haploid human genome ~3 x 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) toanswer:

212. Graph, as a function of distance, the likelihood that recombination will disconnect a selected (whether positively of 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?