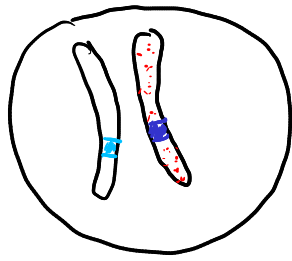
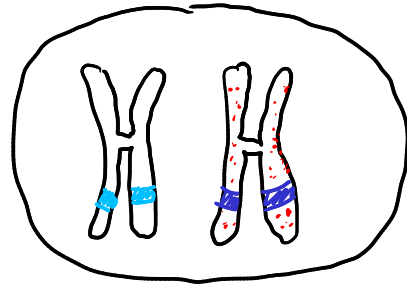


Simplified view of "copying" in biology:

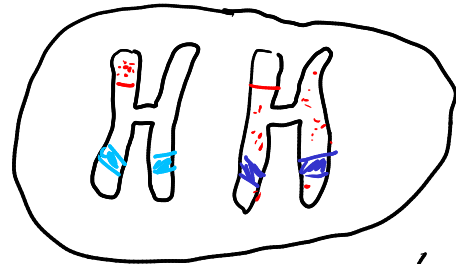
diploid = 2 copies of chromosomes



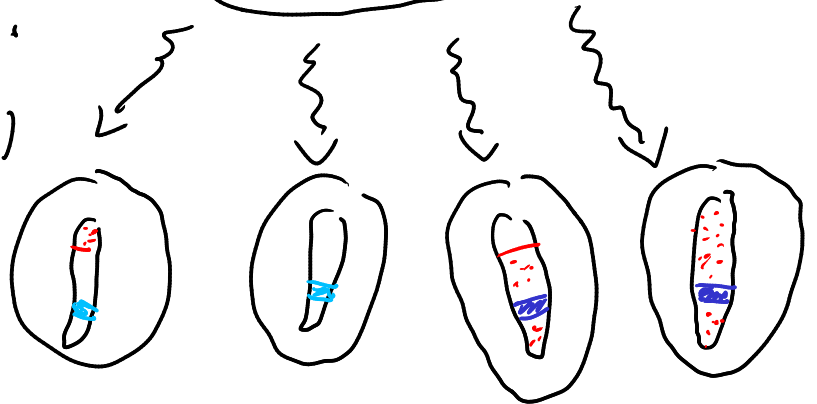
chromosome duplication



recombination



gametes (eggs or sperms)



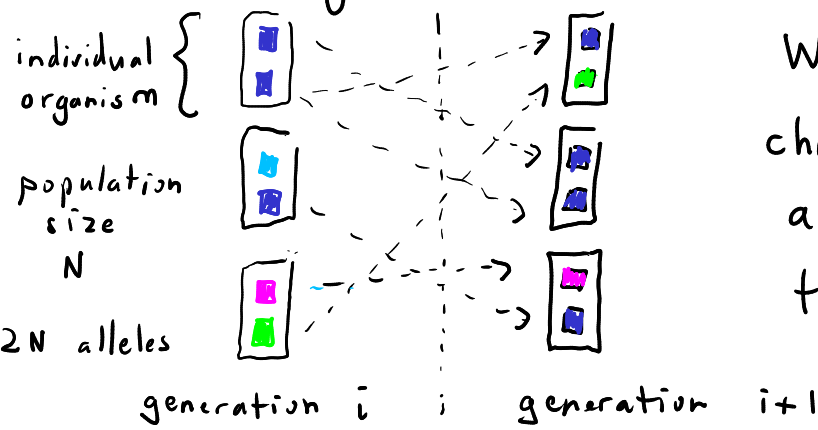
focus: one specific location on chromosome

≡ locus

⇒ exists in diff. variants (alleles)

abstract away complexity & focus on distribution of alleles at locus from

one generation to next:



Wright-Fisher model (WF):
choose "parent" of each allele randomly from the previous generation

reasons why this is dumb:

will fix

- completely random "mating"
(no male/female distinctions)
- self fertilization technically allowed

✓

✓

(unlikely as $N \rightarrow \infty$)

- fixed population size
from gen. to gen.

✓

- no mutations

✓

- no fitness differences

✓

- dominant vs. recessive

can be fixed

- generation time is fixed

✓

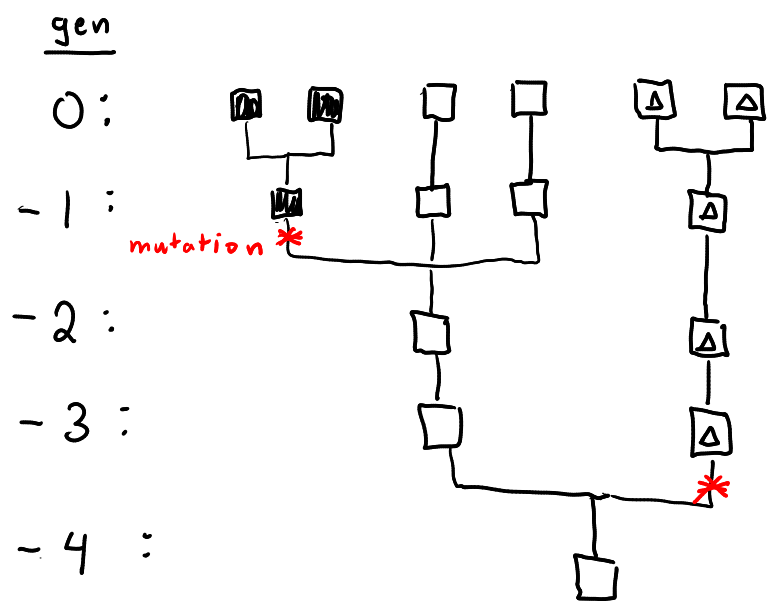
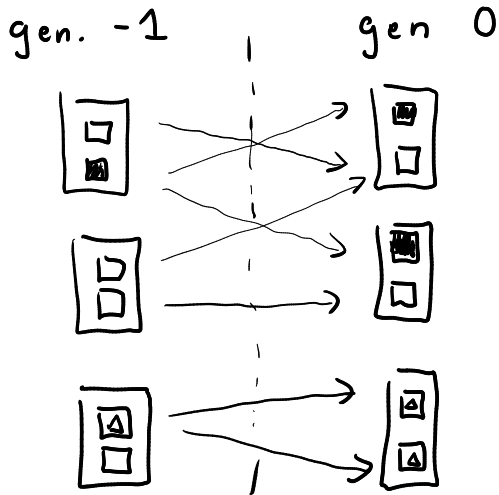
- no spatial effects

✓

First step: build family trees & look at math of these trees

⇒ coalescence theory

↳ merger of two lineages representing a shared parent



MRCA: most recent common ancestor for all alleles in curr. gen.