A generalization of the ARG

Gustave EMPRIN

Laboratoire du CERMICS

JPS, 2018

PHD directors :

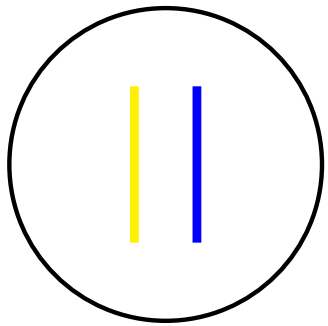
- Jean-Francois DELMAS (ENPC)
- Romain ABRAHAM (Orléans)

Outline

Outline

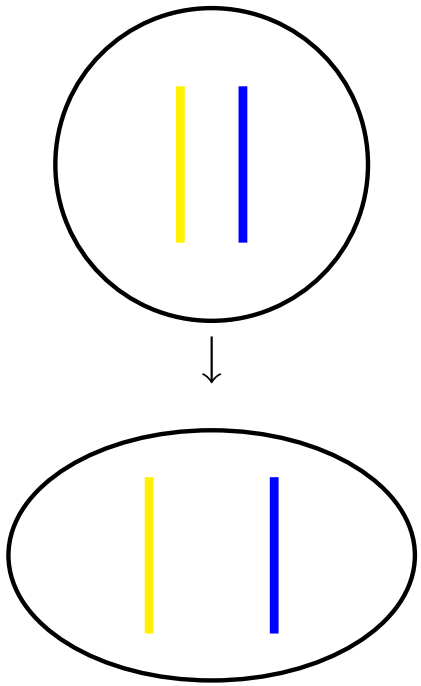
Recombination in genetics

Figure: On the left, we see the usual process for meiosis (the production of gamets).



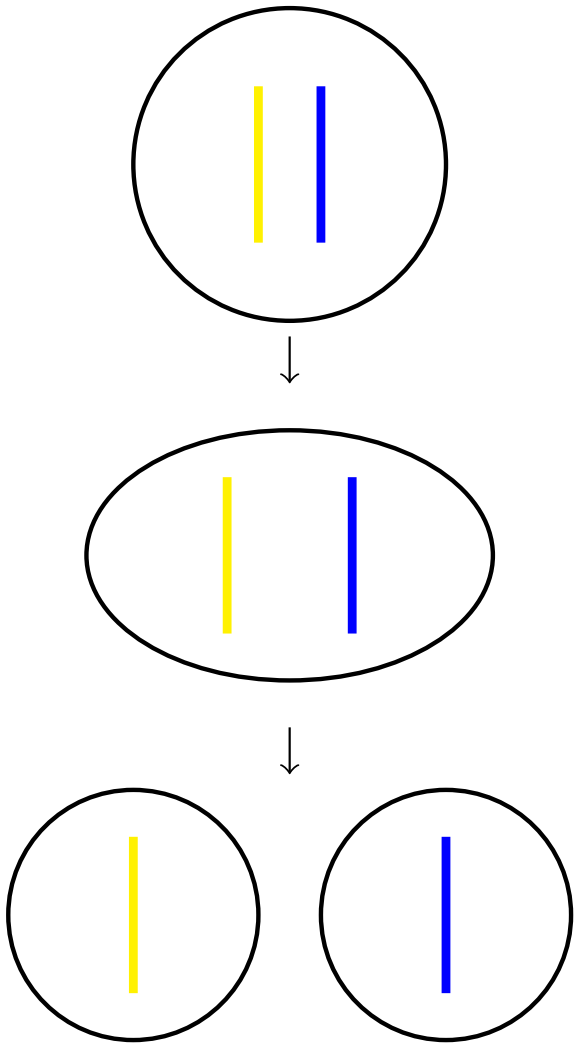
Recombination in genetics

Figure: On the left, we see the usual process for meiosis (the production of gamets).



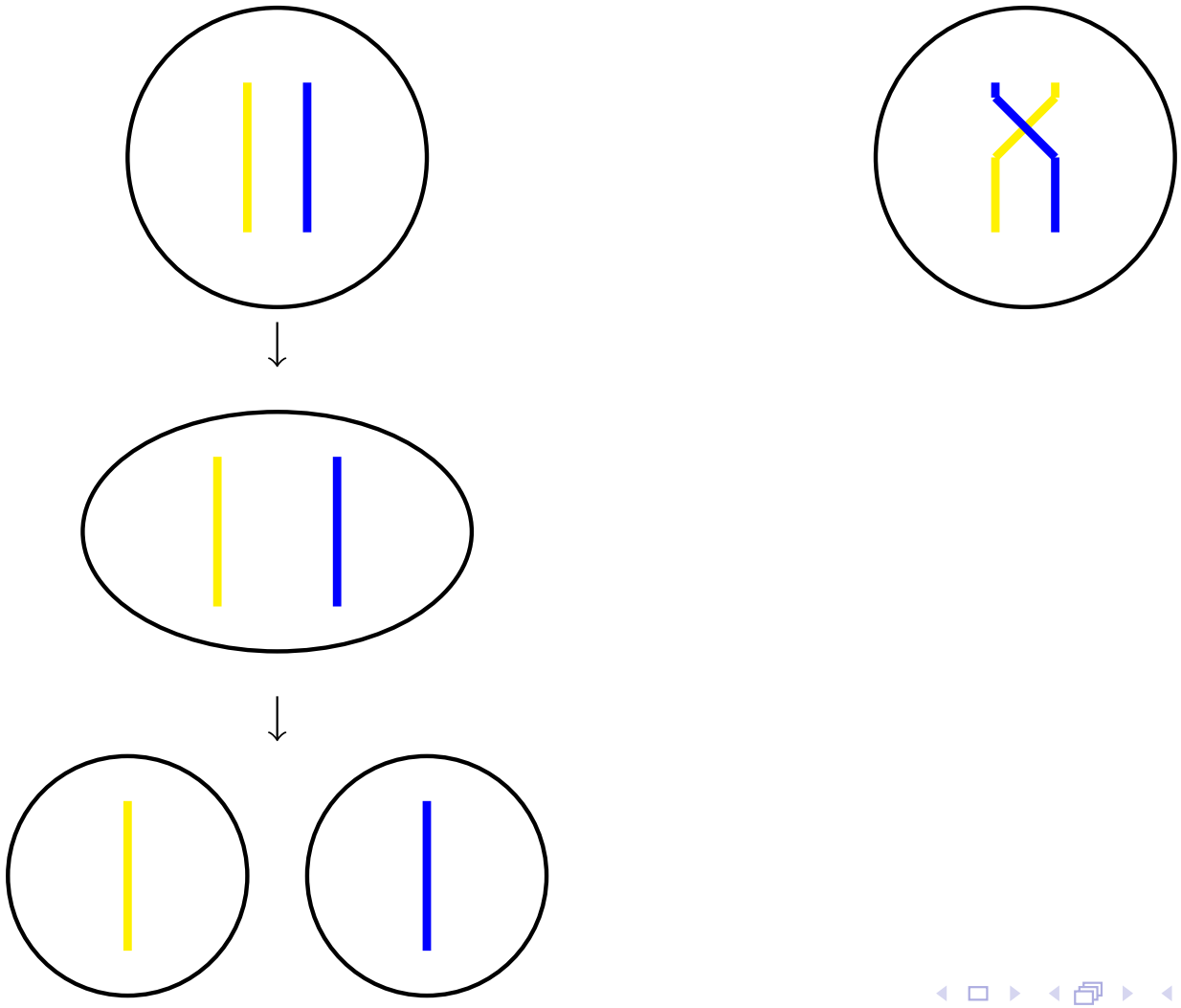
Recombination in genetics

Figure: On the left, we see the usual process for meiosis (the production of gamets).



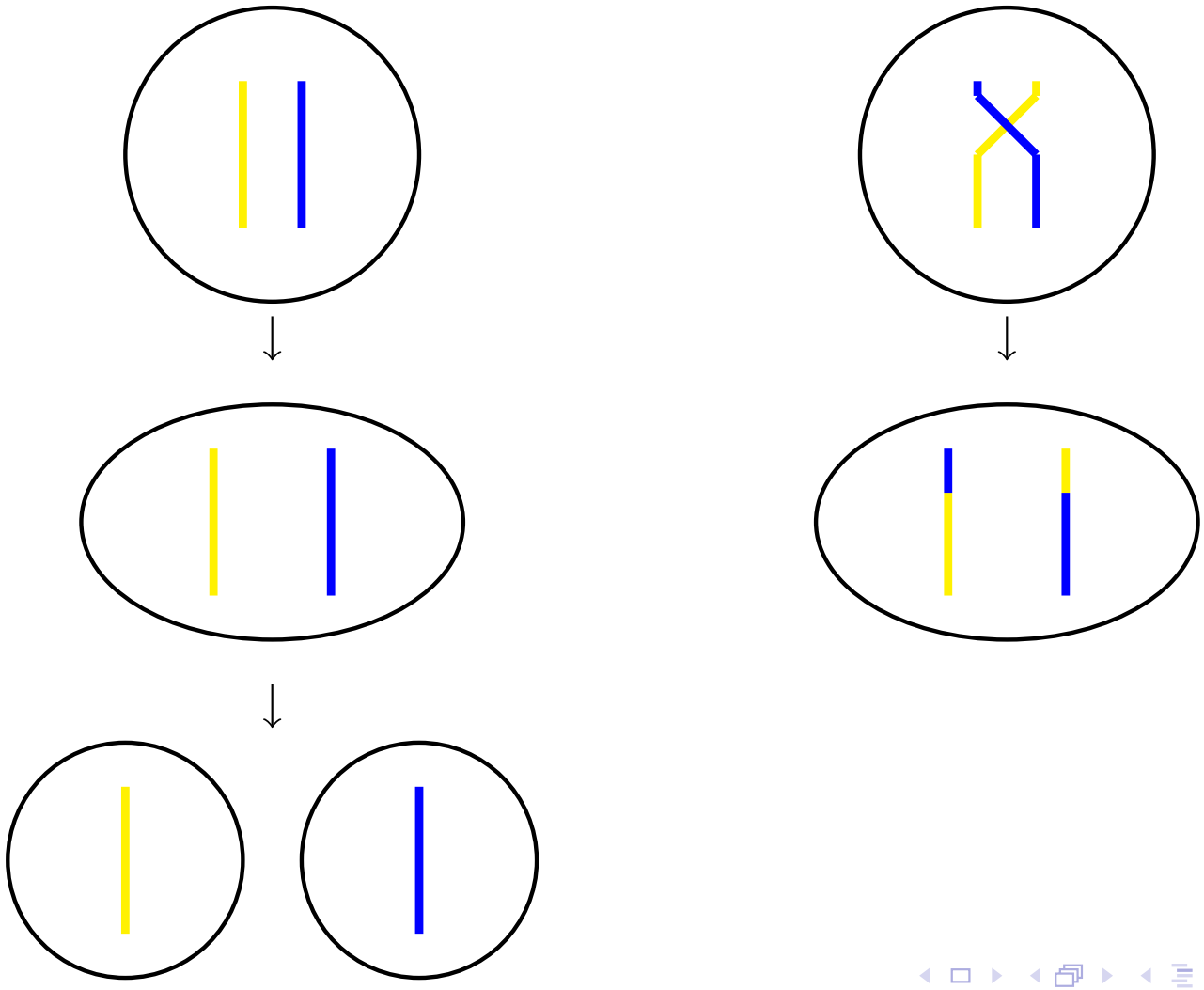
Recombination in genetics

Figure: On the left, we see the usual process for meiosis (the production of gamets). On the right,



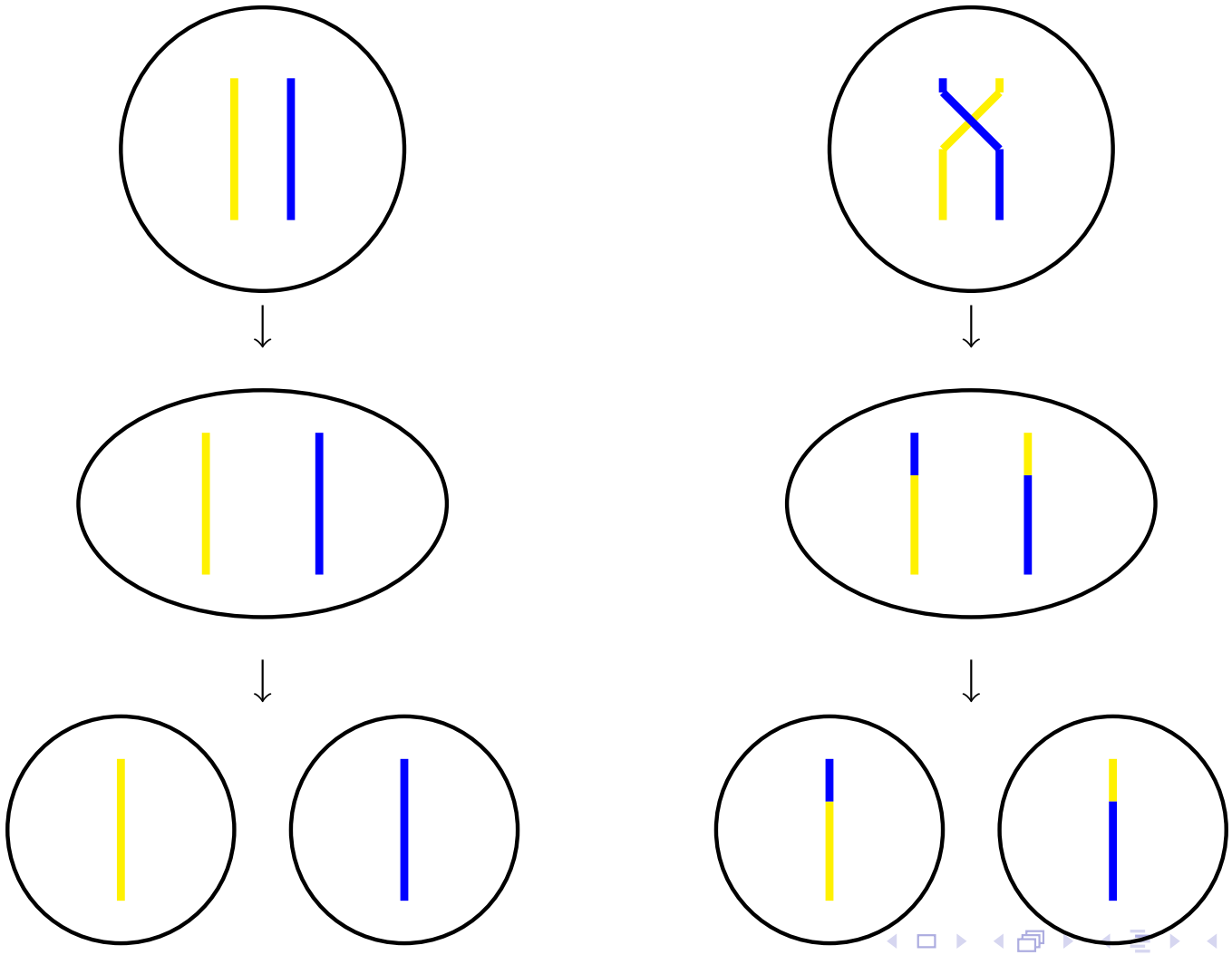
Recombination in genetics

Figure: On the left, we see the usual process for meiosis (the production of gamets). On the right, we see how recombination can happen during meiosis.



Recombination in genetics

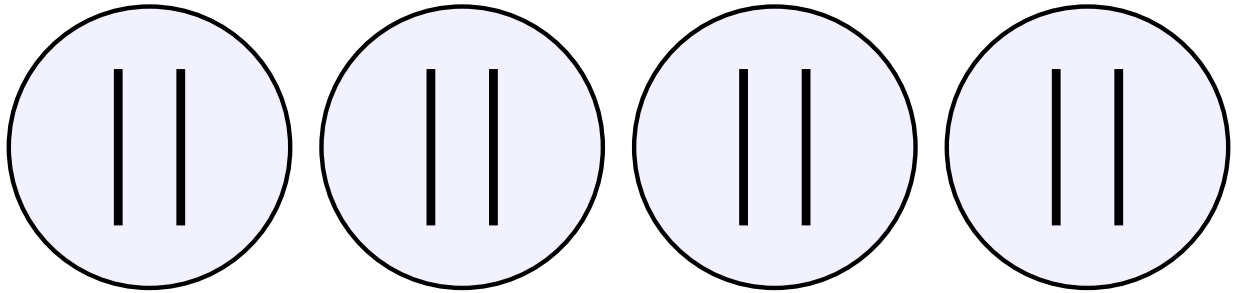
Figure: On the left, we see the usual process for meiosis (the production of gamets). On the right, we see how recombination can happen during meiosis.

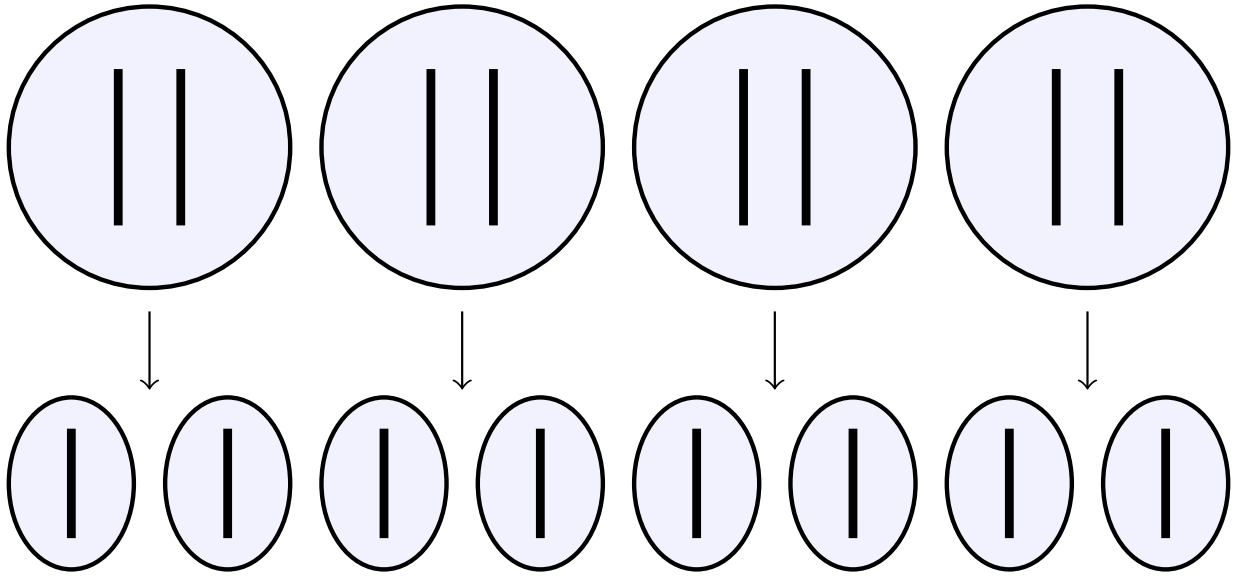


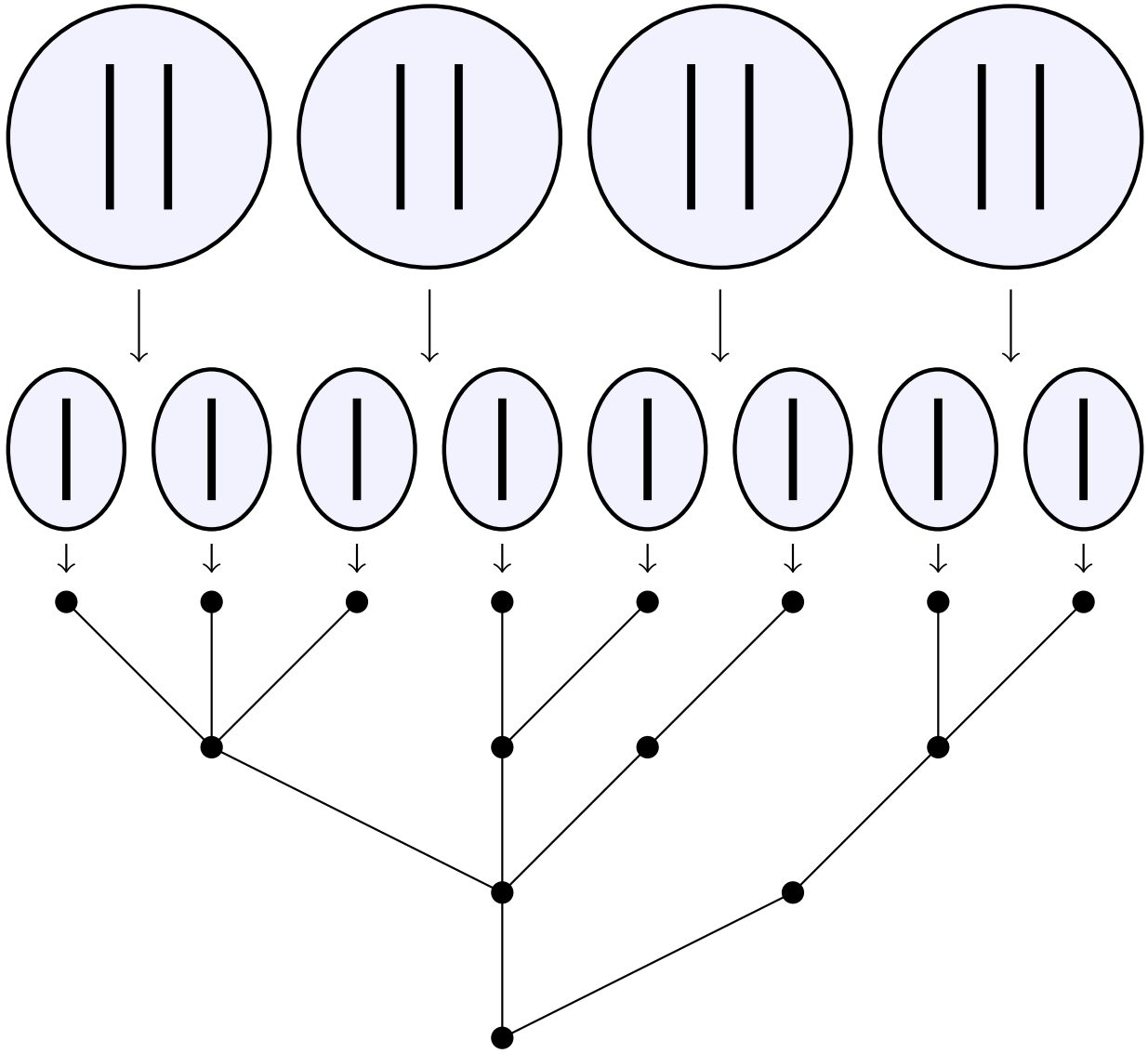
Outline

Change of population

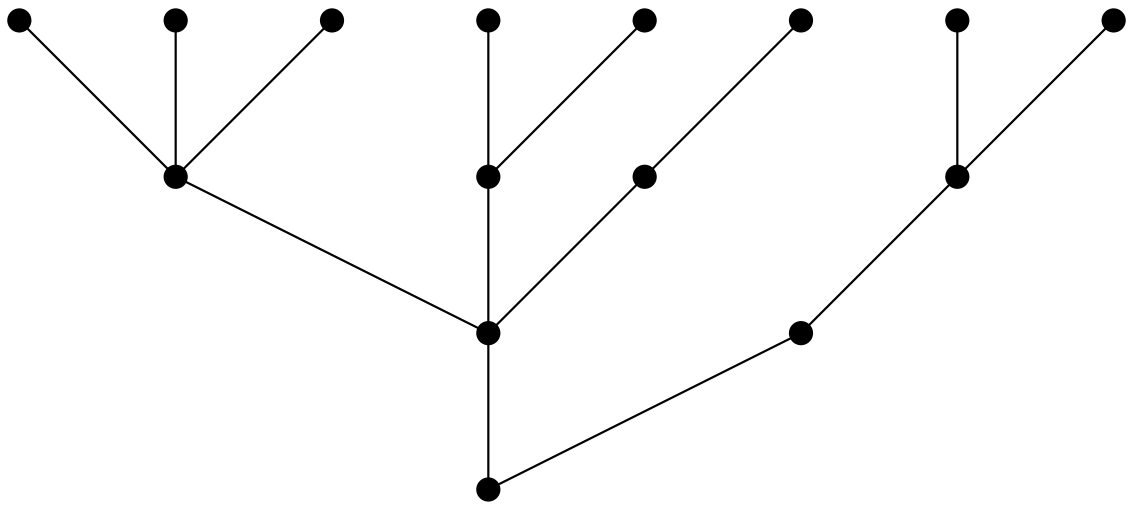
When individuals in the population have two parents, we will often have loops in the "genealogical tree". This means that the typical "genealogical tree" cannot be a tree.
This leads us to consider the population (twice as big) of the chromosomes, since they have only a parent.



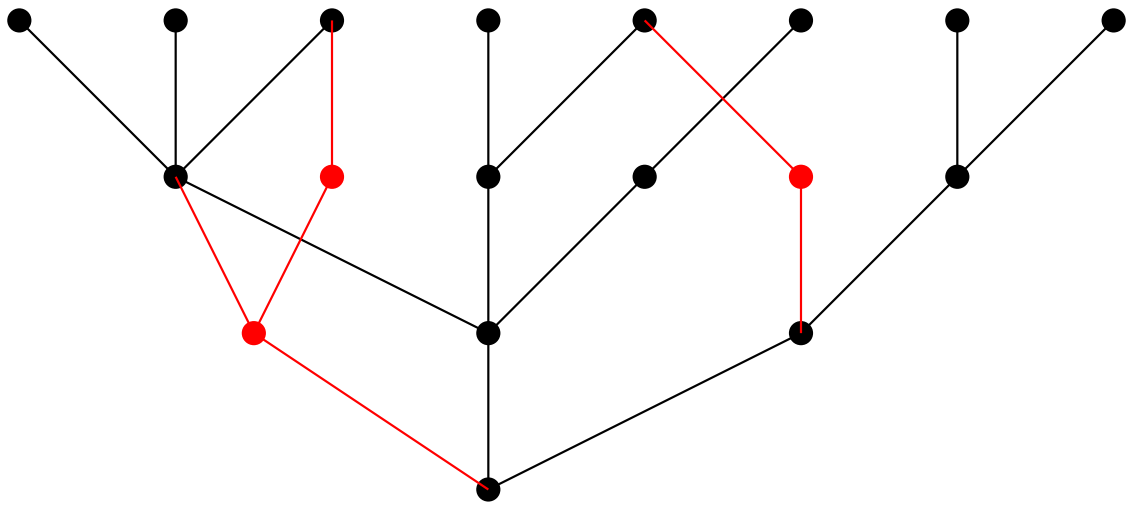




When adding reconbination events to the ancestry, we obtain the Ancestral Recombination Graph, that contains all the contributions to the genome of the N individuals.

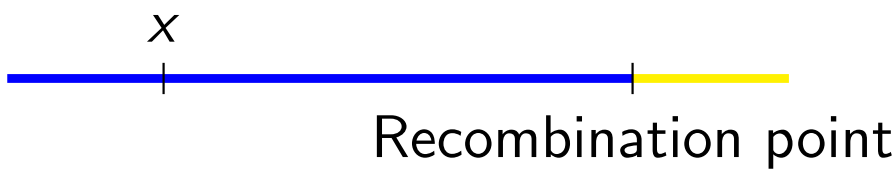


When adding reconbination events to the ancestry, we obtain the Ancestral Recombination Graph, that contains all the contributions to the genome of the N individuals.

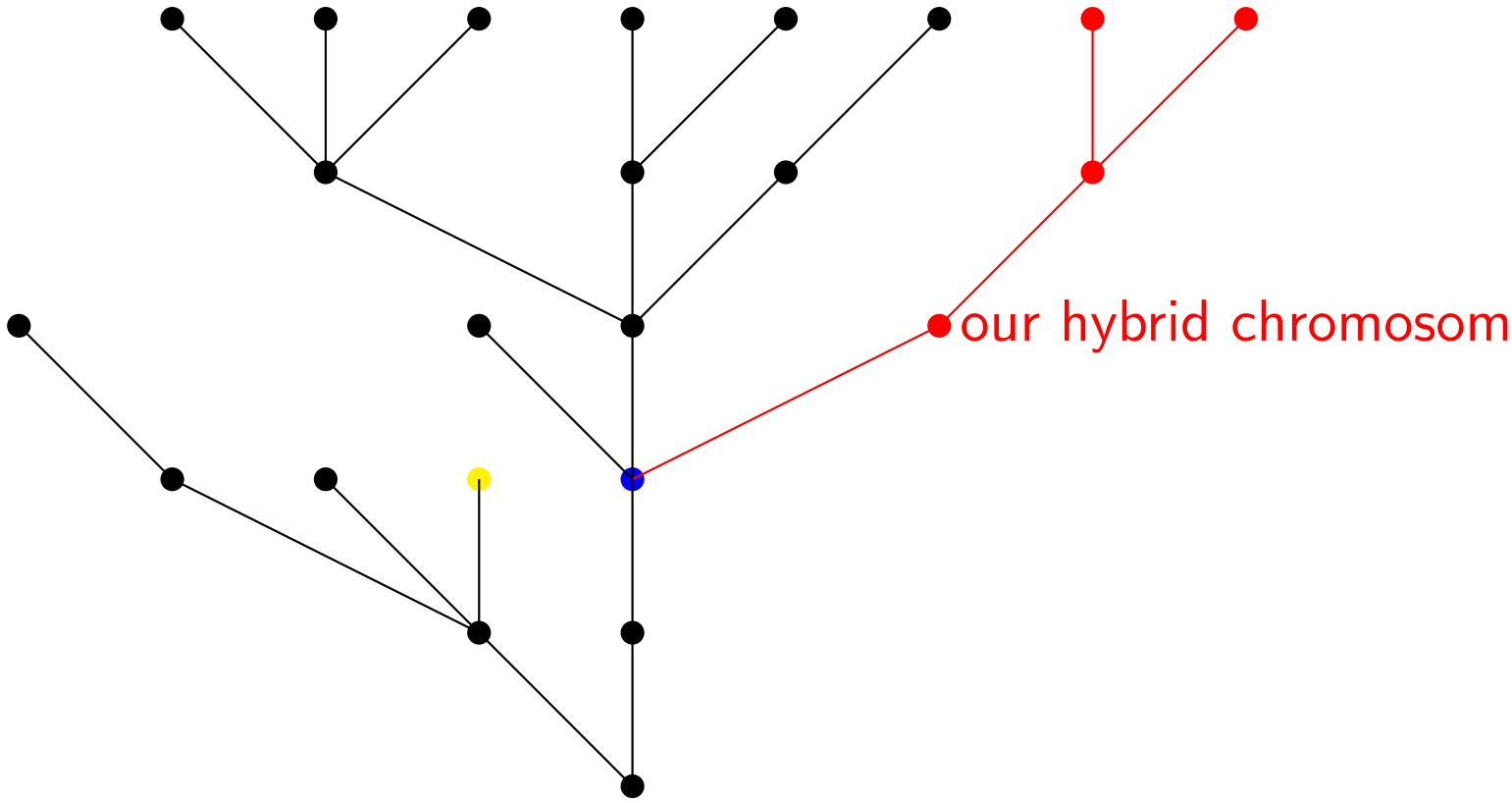


Outline

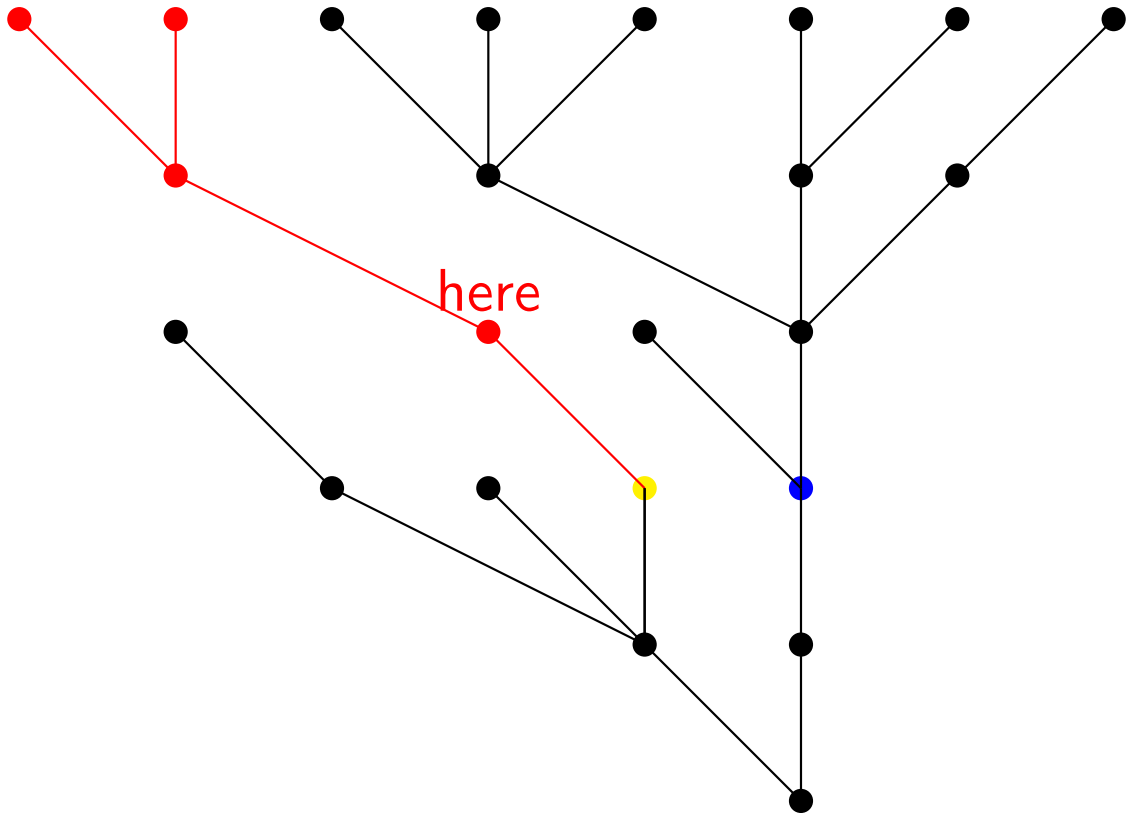
To extend the ARG, let look at the effect of a recombination event on the whole population (past, present, future). To keep our tree structure, we draw the genealogical tree for a specific locus x on the chromosome.



Example with x before the recombination point.



Now, with x after the recombination point.



Outline

Using the description of a recombination as a jump of ancestor, we can define a random process indexed by our parameter x :

- each individual (vertex) has a Poisson process
- at every tick of its Poisson, the individual choses himself a new ancestor uniformly on the previous generation

Characteristics of the process

- The trees cannot have a lower bound
- We don't know if changes way down the tree can typically affect the tree near the present (we hope they don't)
- Is there a locus for which the genealogical tree doesn't have the usual properties (abnormally high number of ascendents, non-connexity...)?

Study of the process (done under the invariant laws)

- Invariant laws
- Definition for the continuous-tree version of the processus
- Control of the depth of the most recent common ancestor (mrca)
- Control of the number of ancestors in a generation
- Regularity of the trajectories (càdlàg)
  - Defition of a distance on the space of trees rooted at $-\infty$

Prospects

- Ergodicity
- Definition/convergence in law for more general initial distributions

For Further Reading

- Richard Durrett. *Probability models for DNA sequence evolution.* Springer Science & Business Media, 2008.
- J. F. C. Kingman. *The coalescent. Stochastic Processes and their Applications,* 13(3):235-248, September 1982.
- Mikhail Gromov. *Metric structures for Riemannian and non-Riemannian spaces.* Springer Science & Business Media, 2007.
- Romain Abraham, Jean-Francois Delmas, Patrick Hoscheit, and others. *A note on the Gromov-Hausdorff-Prokhorov distance between (locally) compact metric measure spaces.* Electron. J. Probab, 18(14):1-21, 2013.

Thank you for your attention.