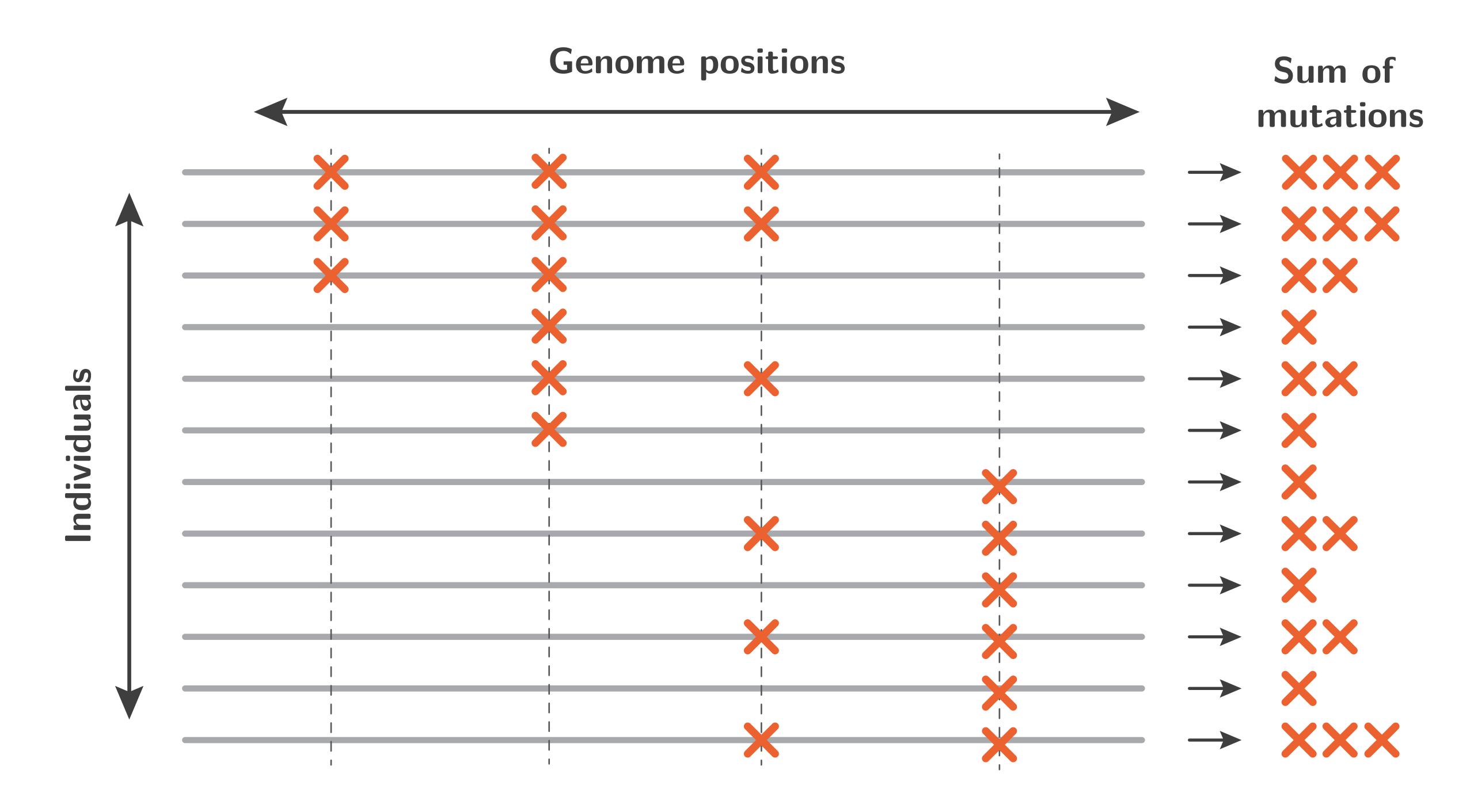
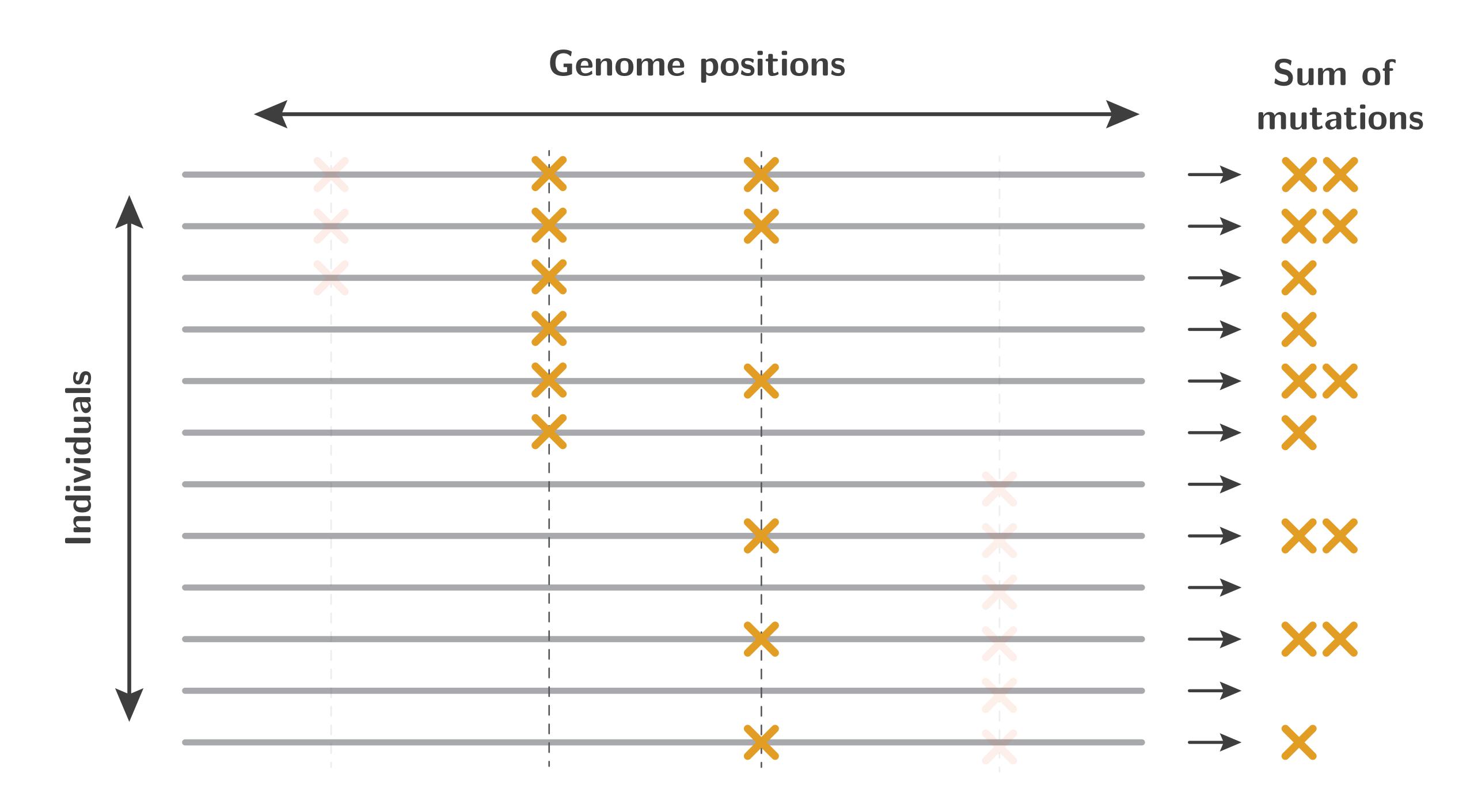
# Are deleterious mutation independent of one another?

Is the deleterious effects more (or less) than expected when deleterious mutation are in the same individual?

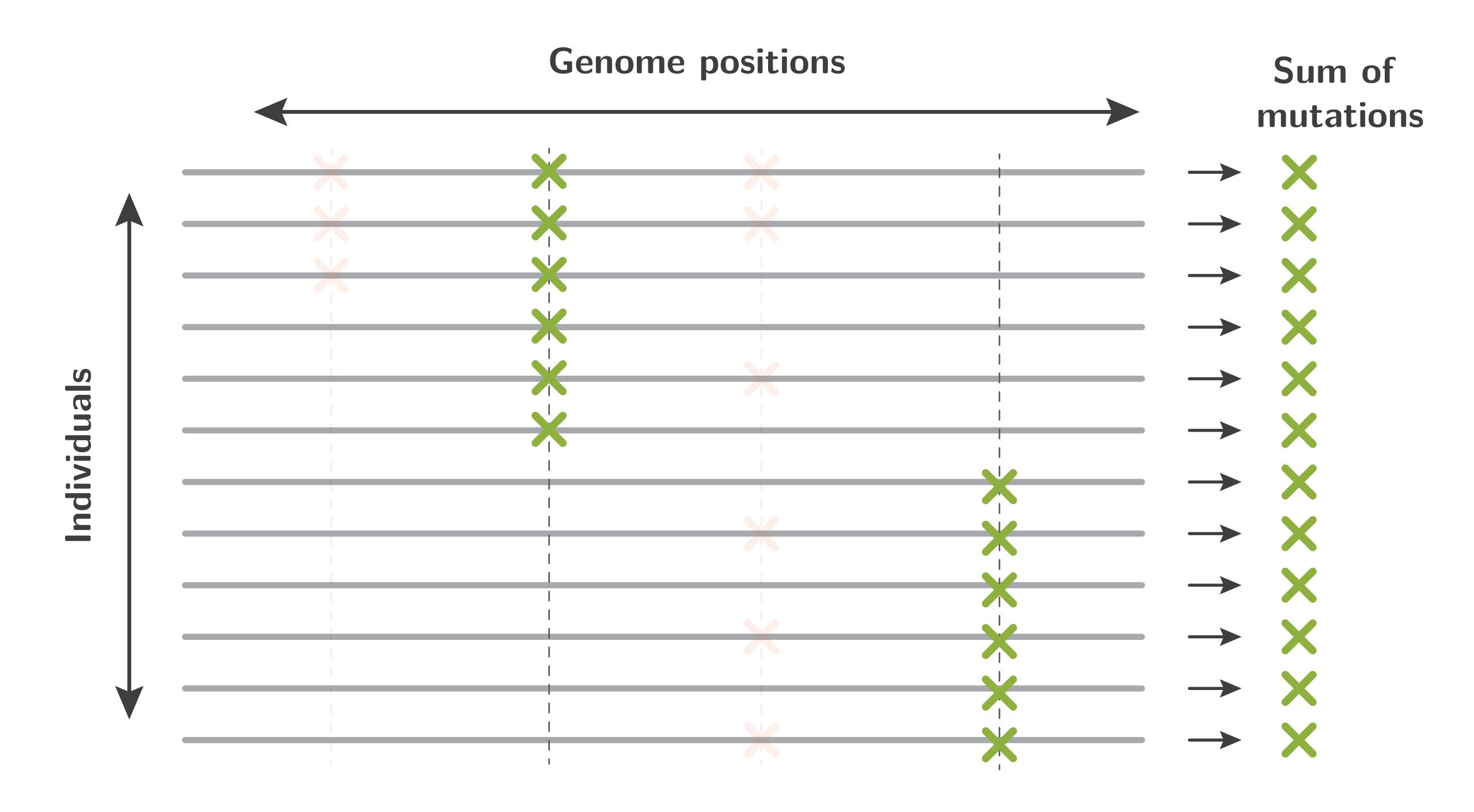
How to detect and quantify non-independence?



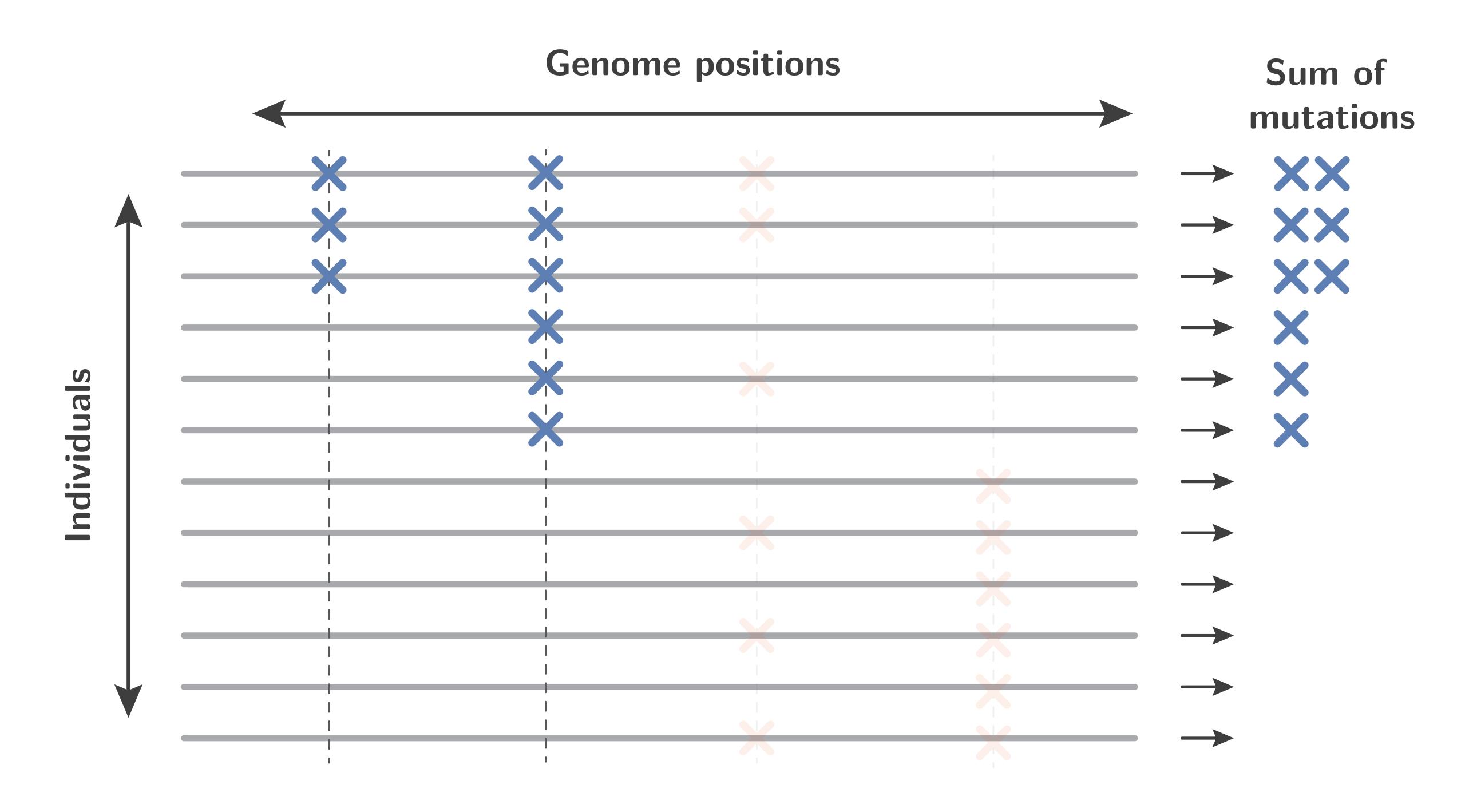
## Polymorphism dataset.



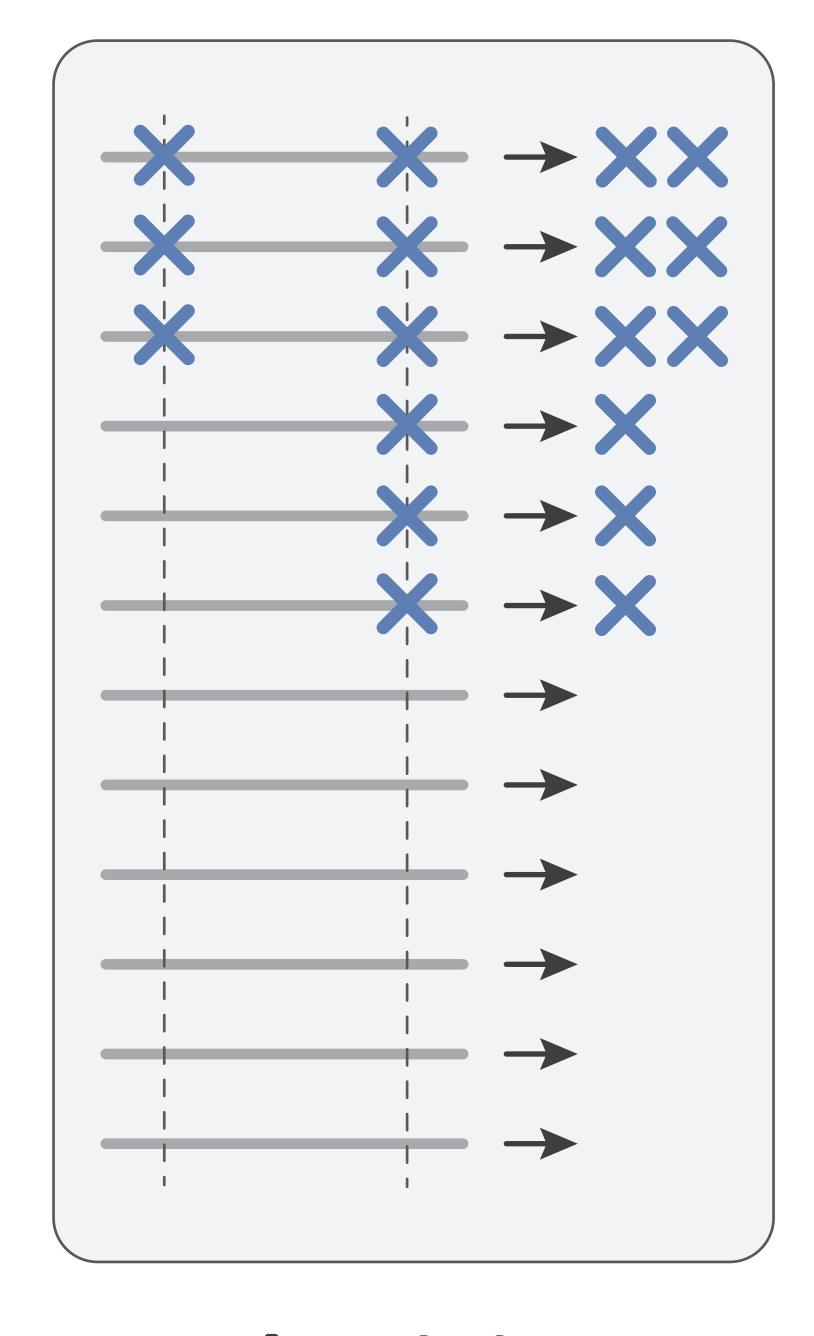
## Independent mutations.

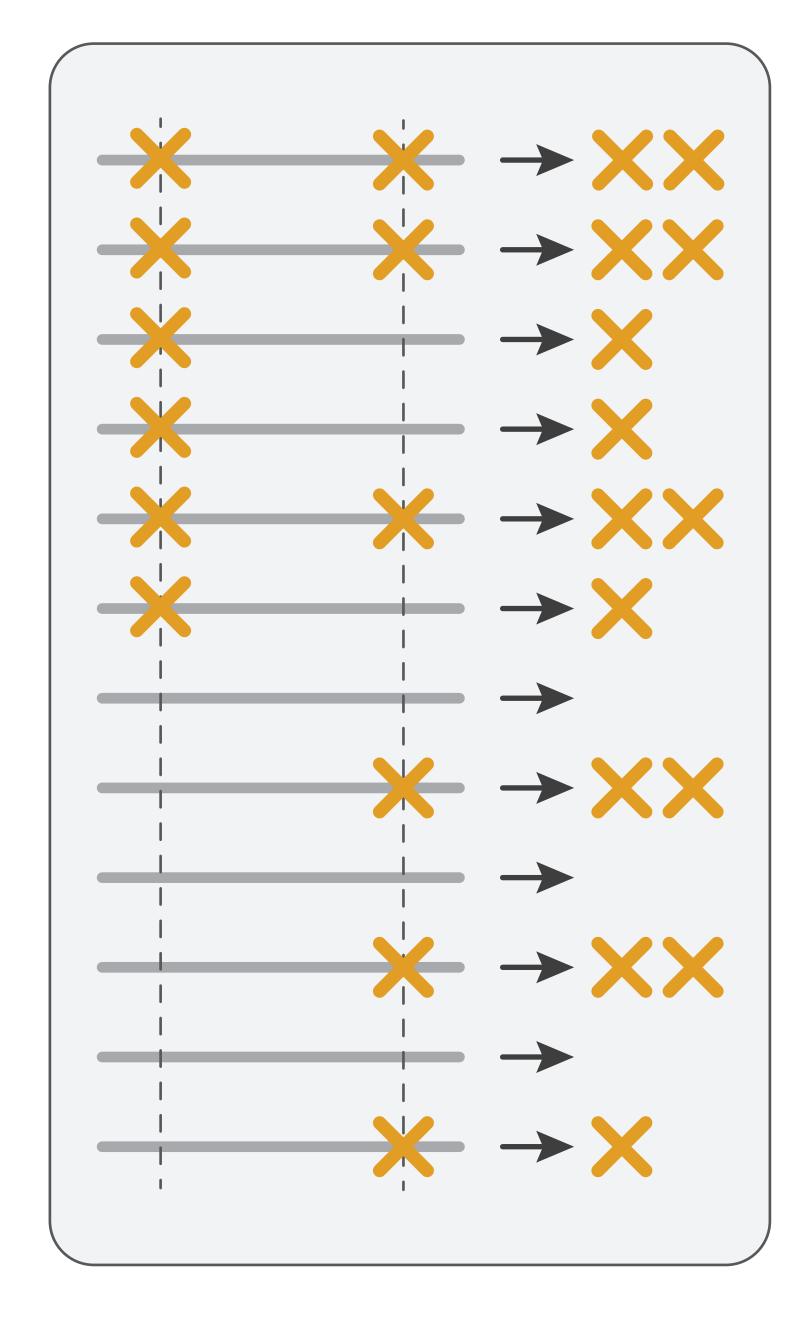


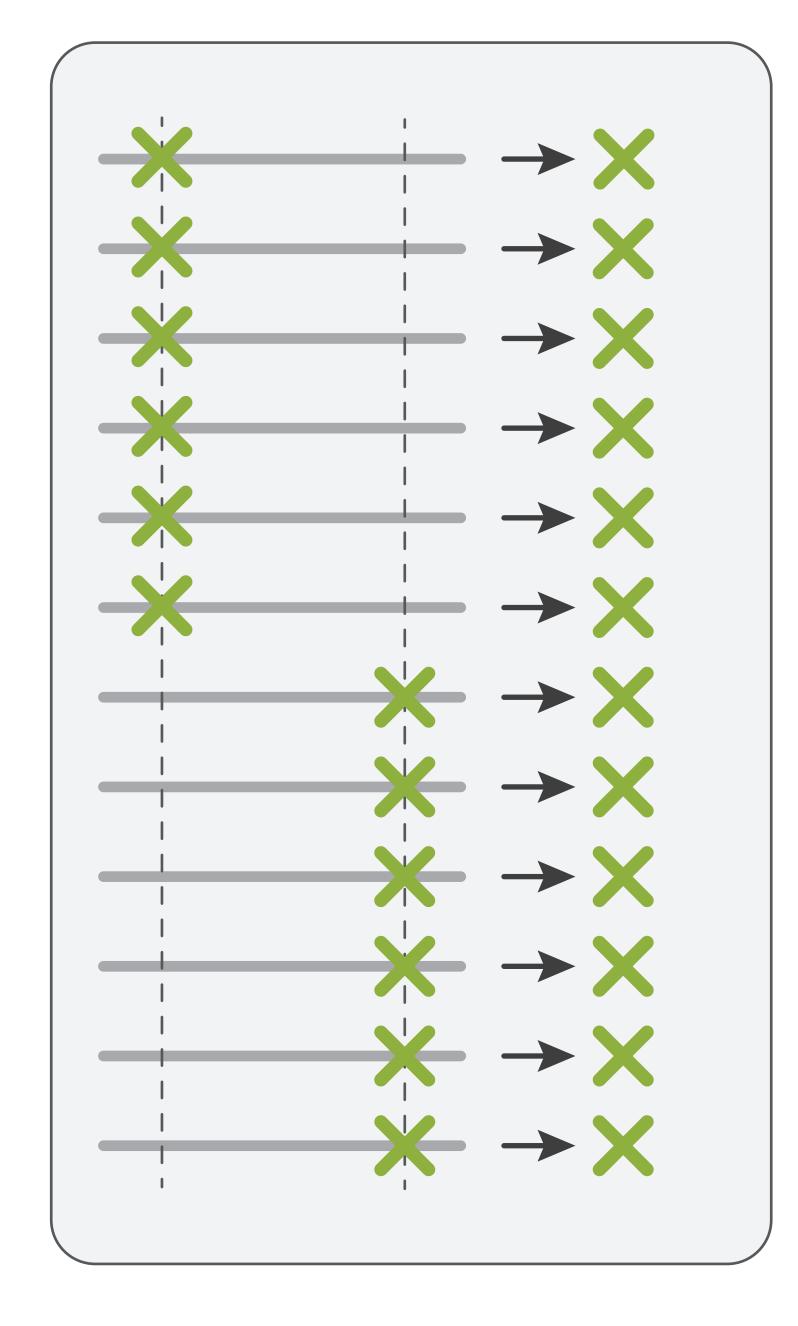
## Repulsive mutations, synergistic epistasis.



Associative mutations, antagonistic epistasis.







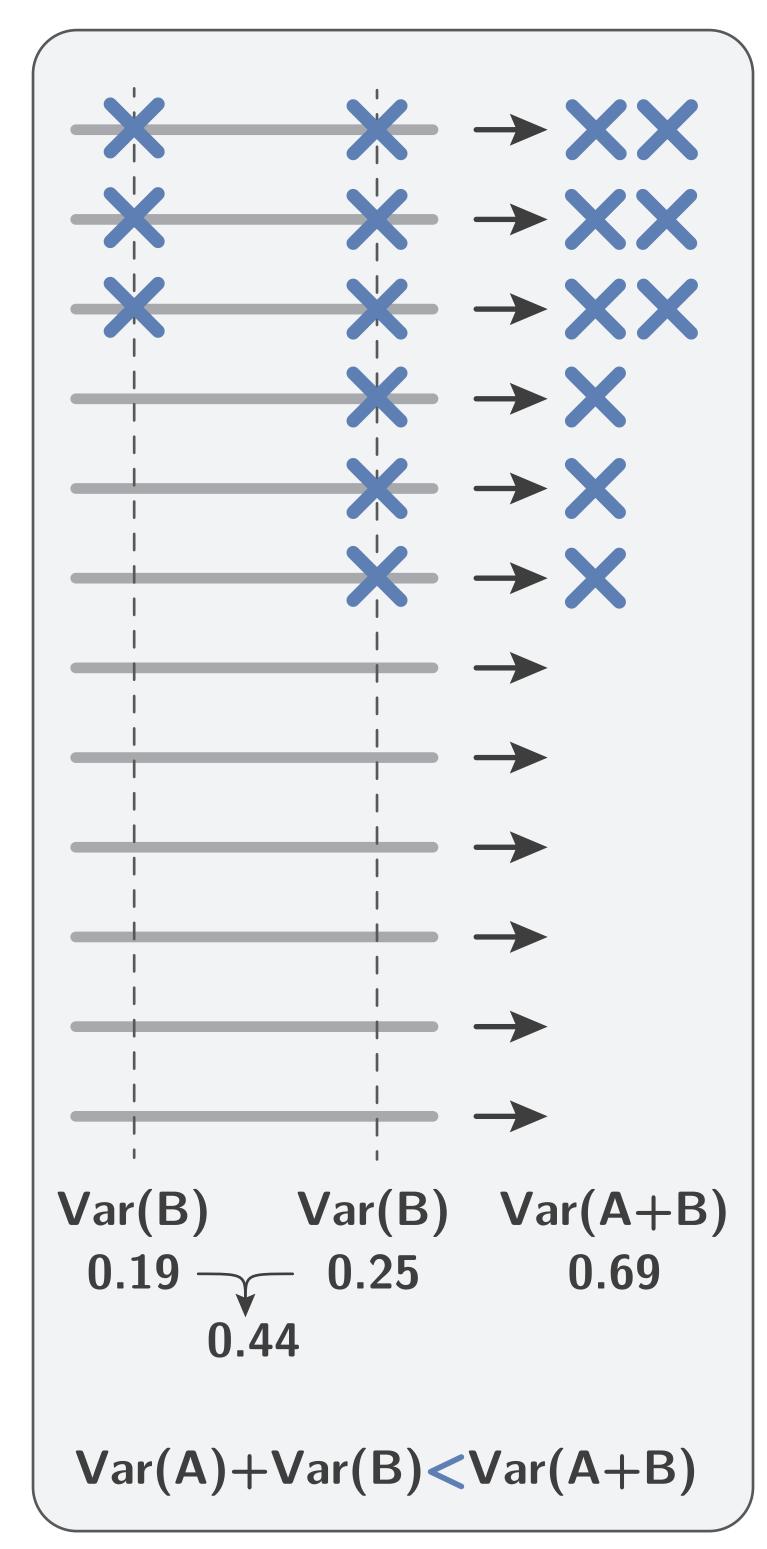
Association

Antagonistic epistasis

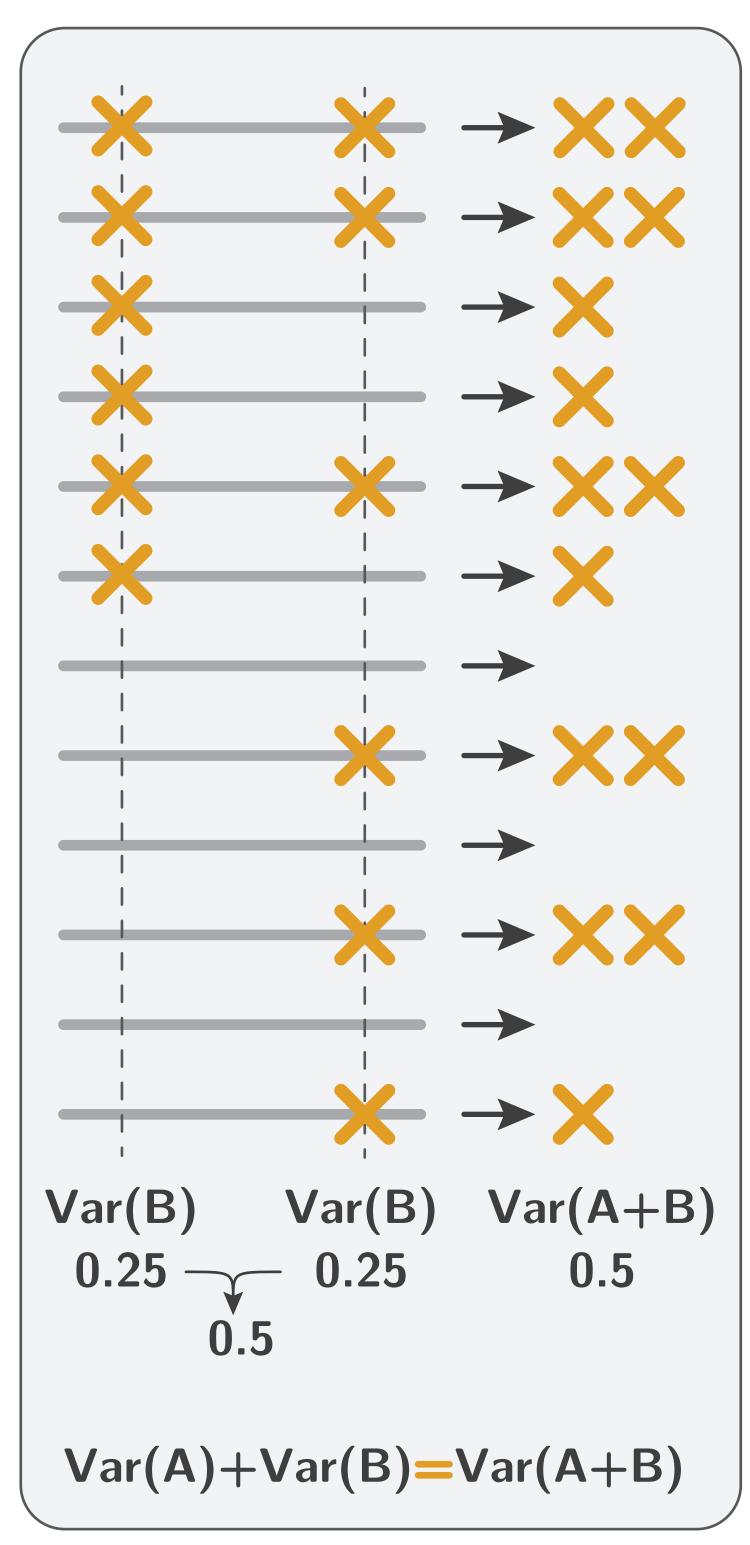
Independence

Repulsion

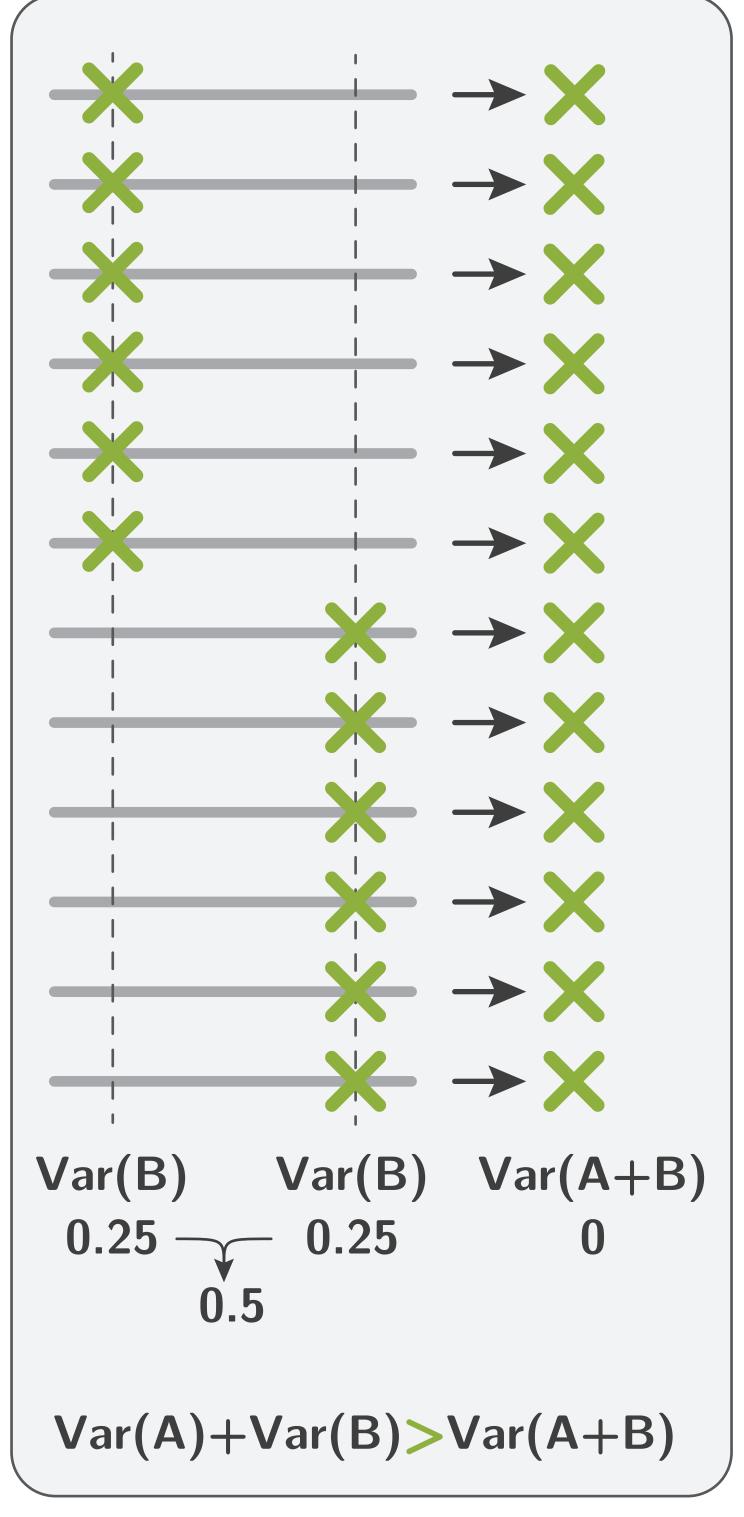
Synergistic epistasis



Association Antagonistic epistasis



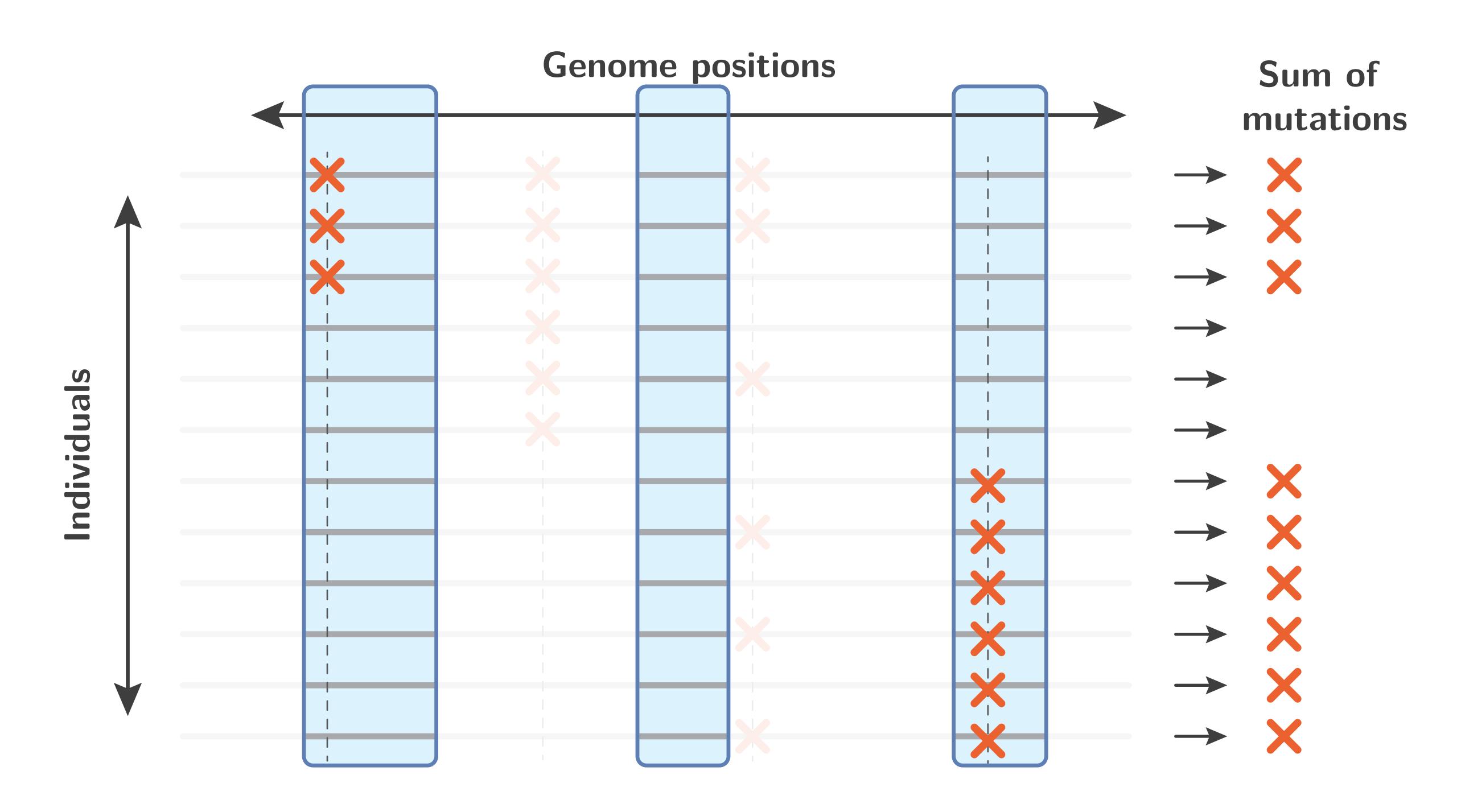
Independence



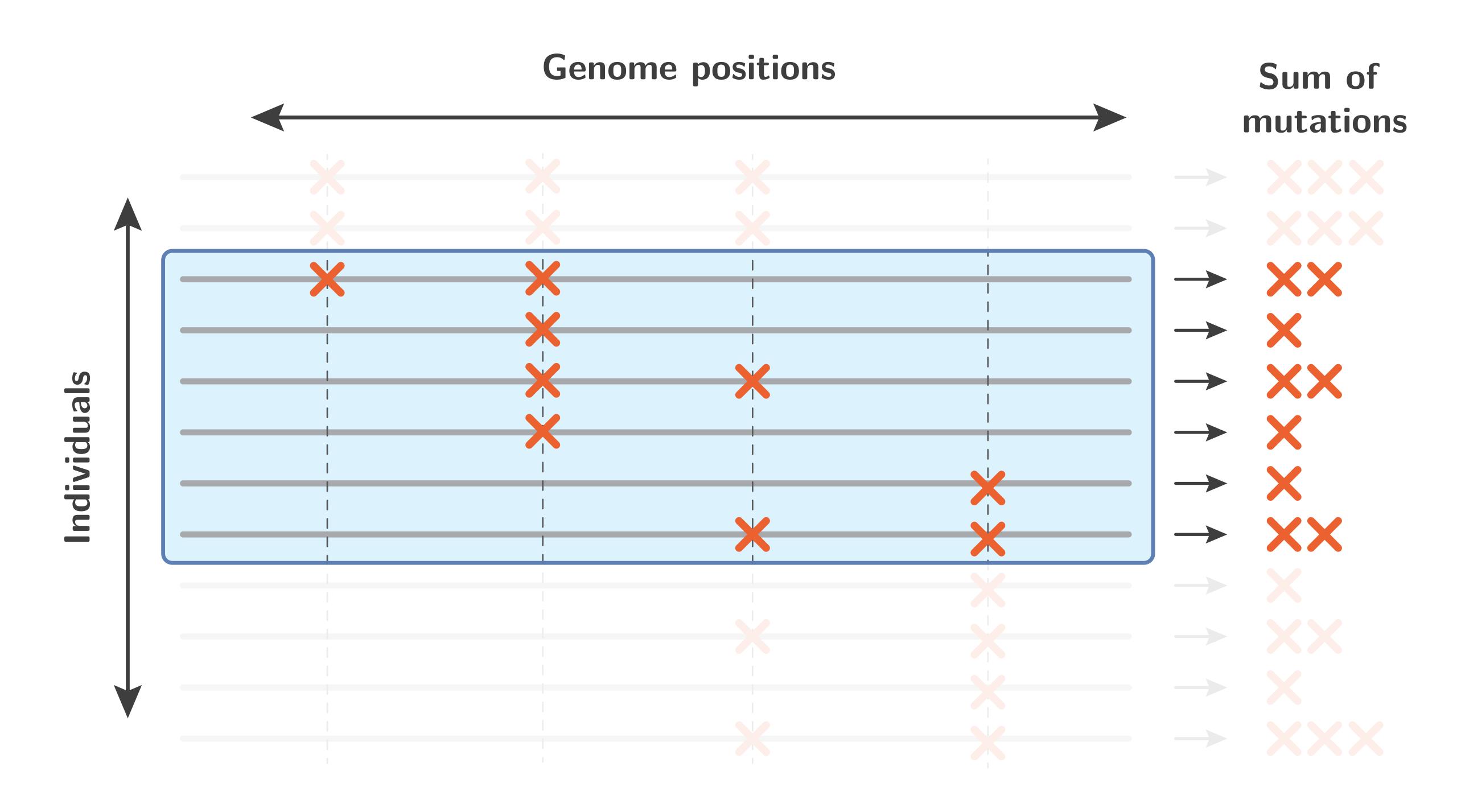
Repulsion Synergistic epistasis

In which part of the genome?

In which population?



Filtering out polymorphism.



Filtering out individuals.

# Let's do this!