

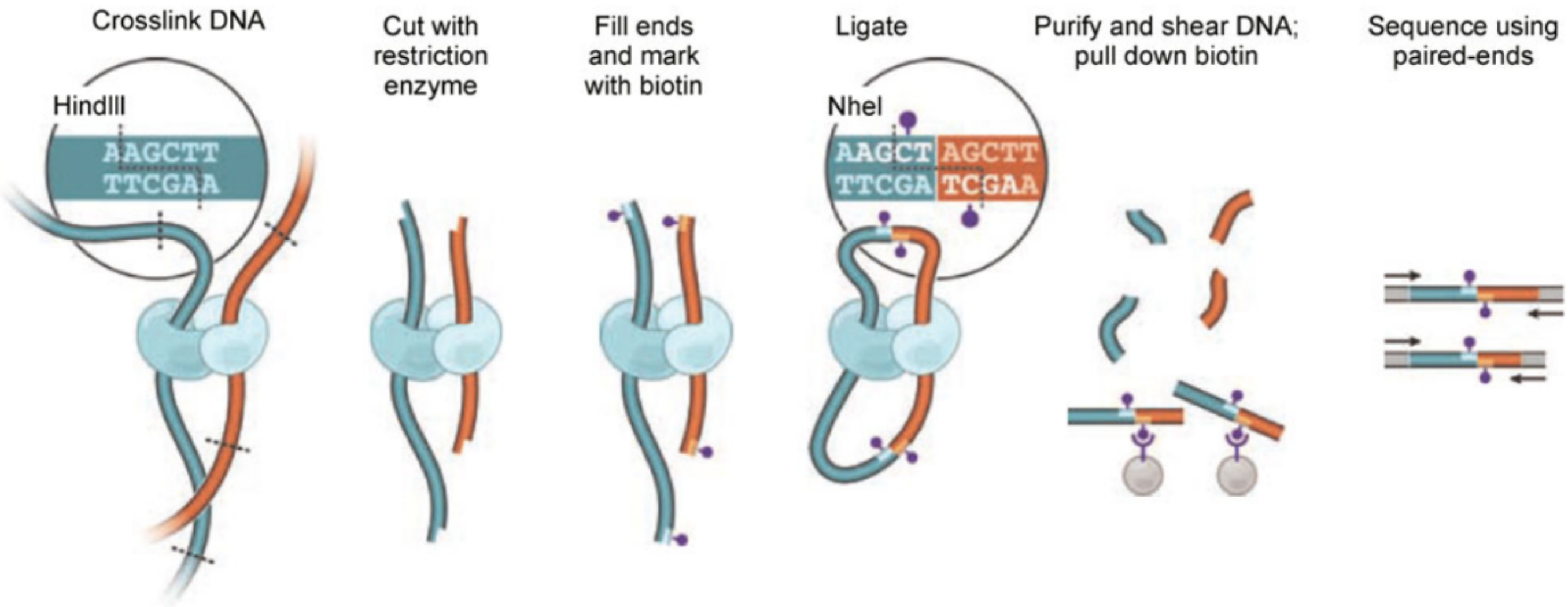
What we need to know about NGS in Hi-C

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Structural Genomics Group (CNAG-CRG)



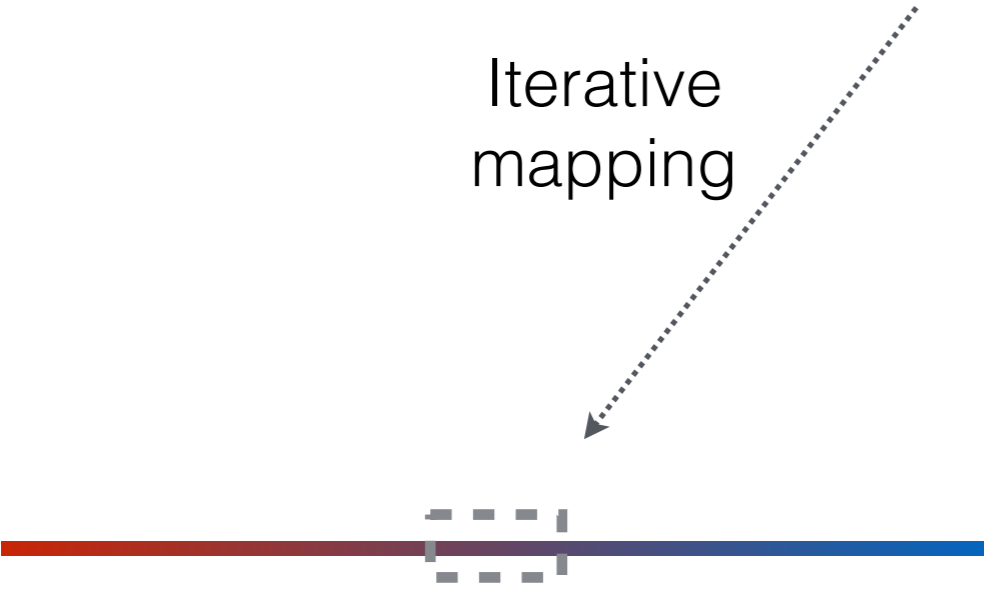
Hi-C experiment



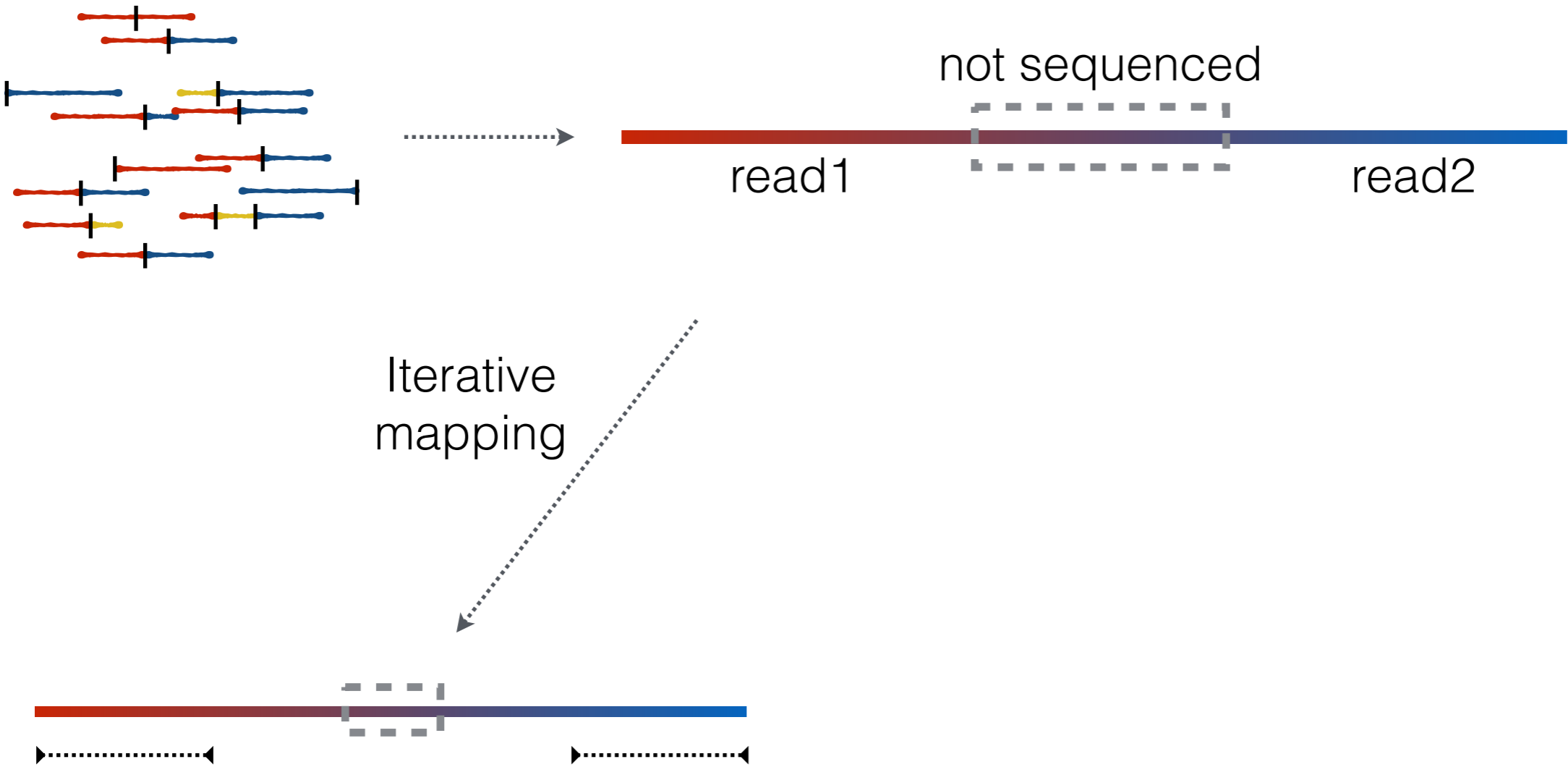
HiC mapping



Iterative mapping



HiC mapping



HiC mapping



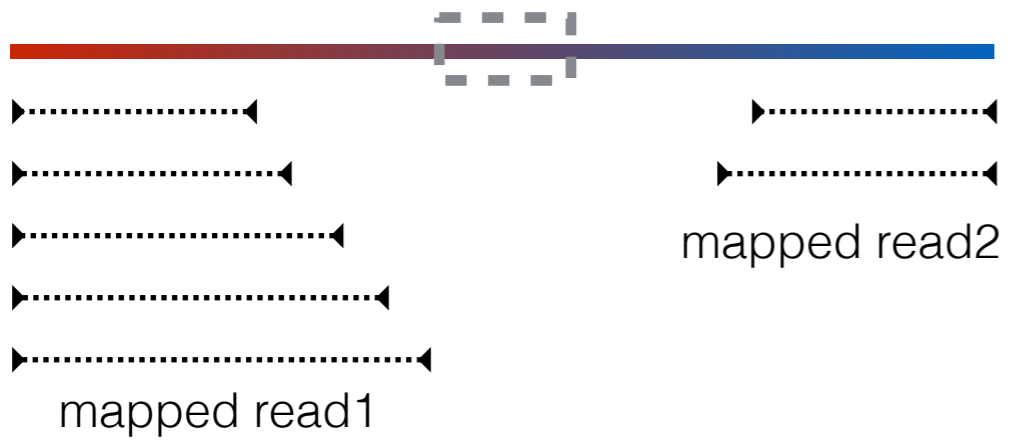
Iterative
mapping



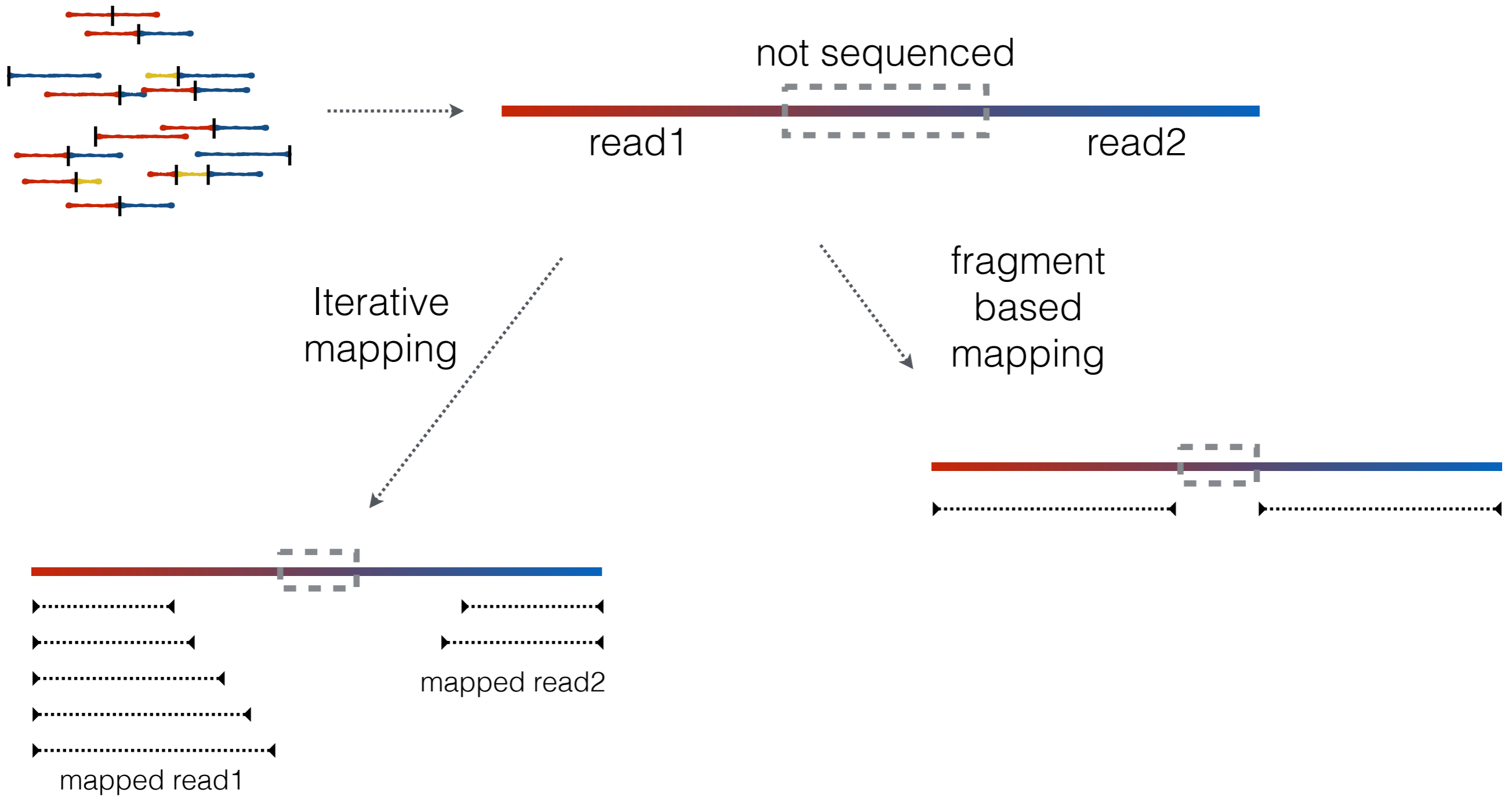
HiC mapping



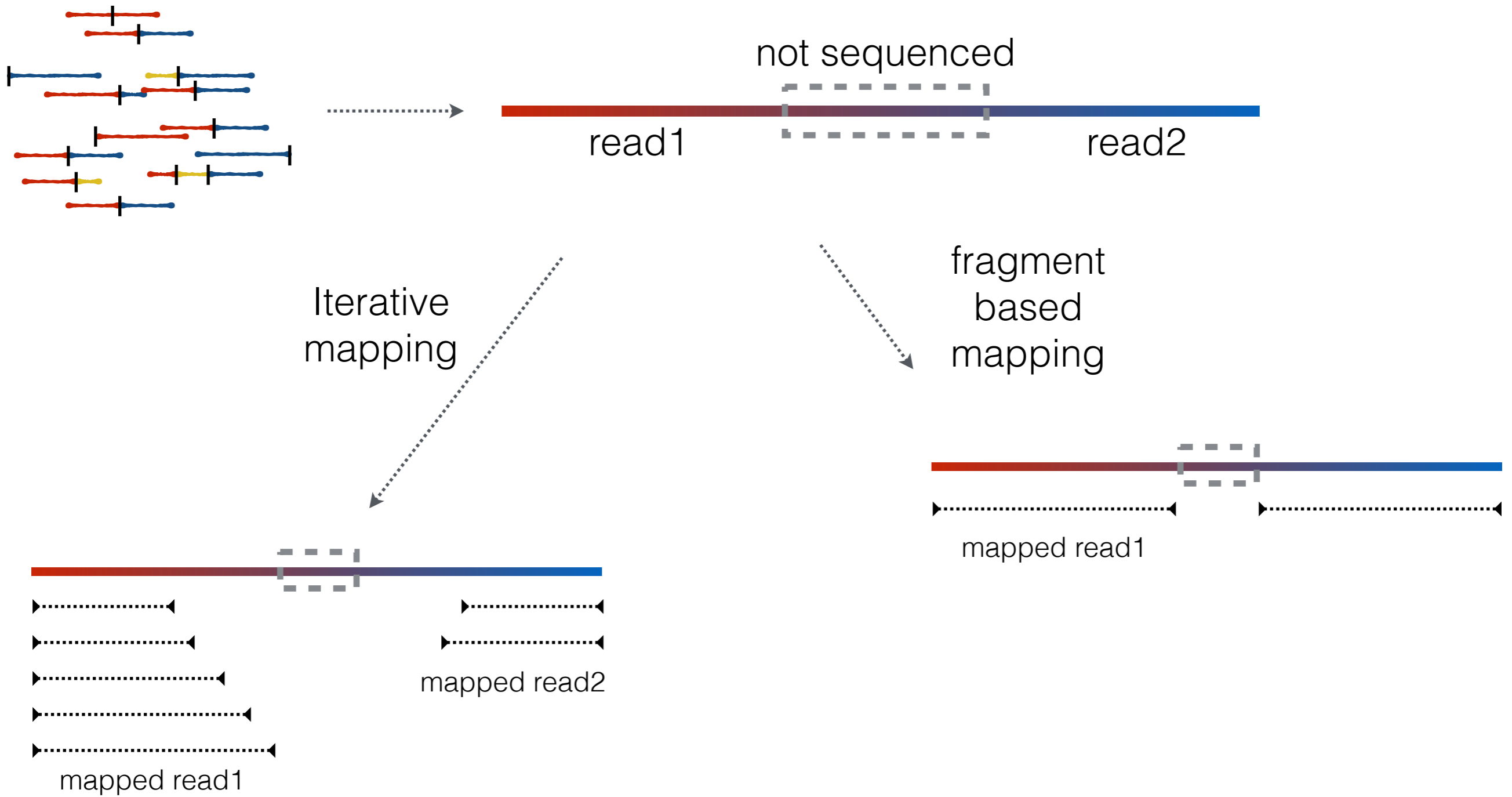
Iterative
mapping



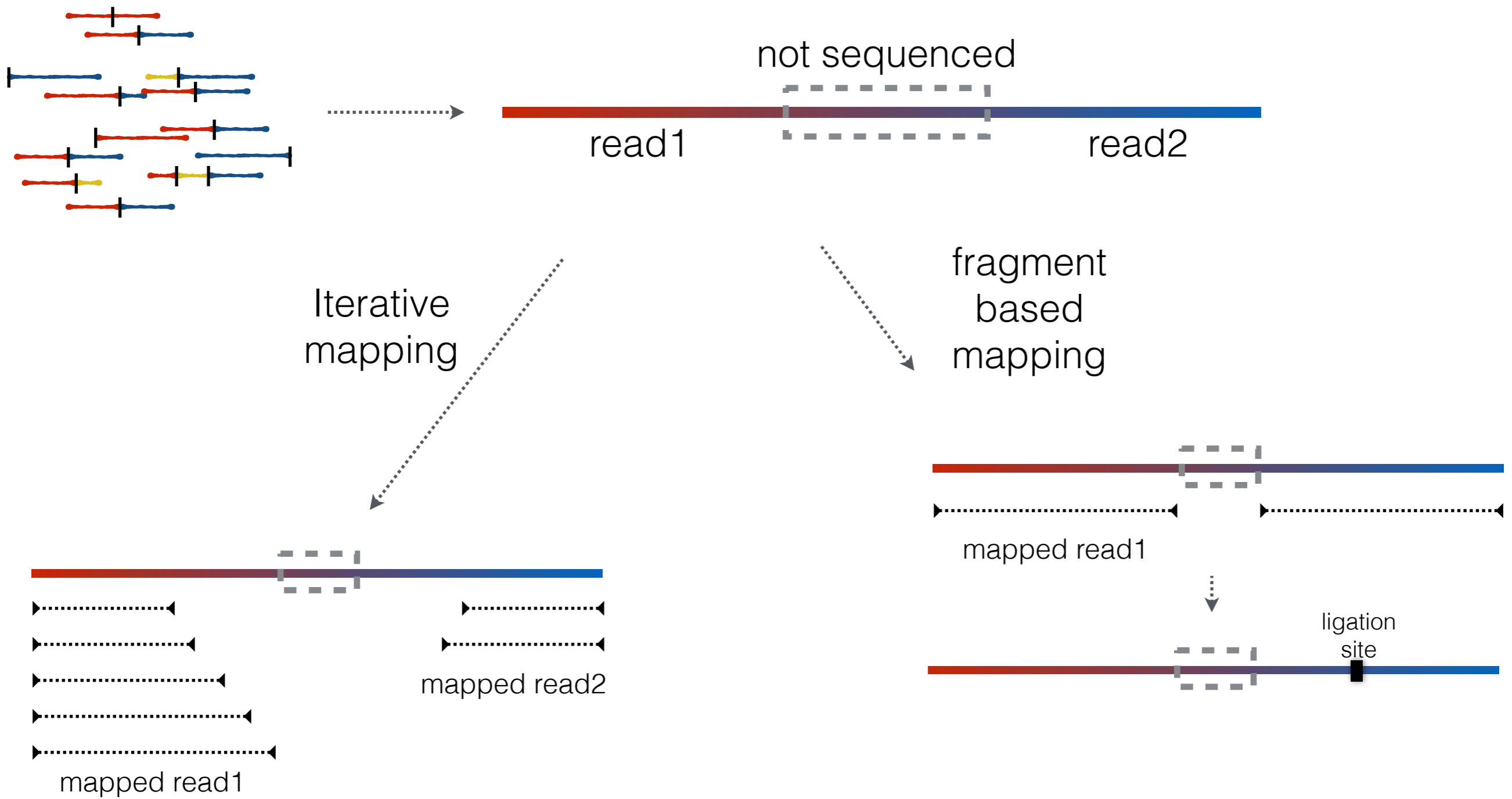
HiC mapping



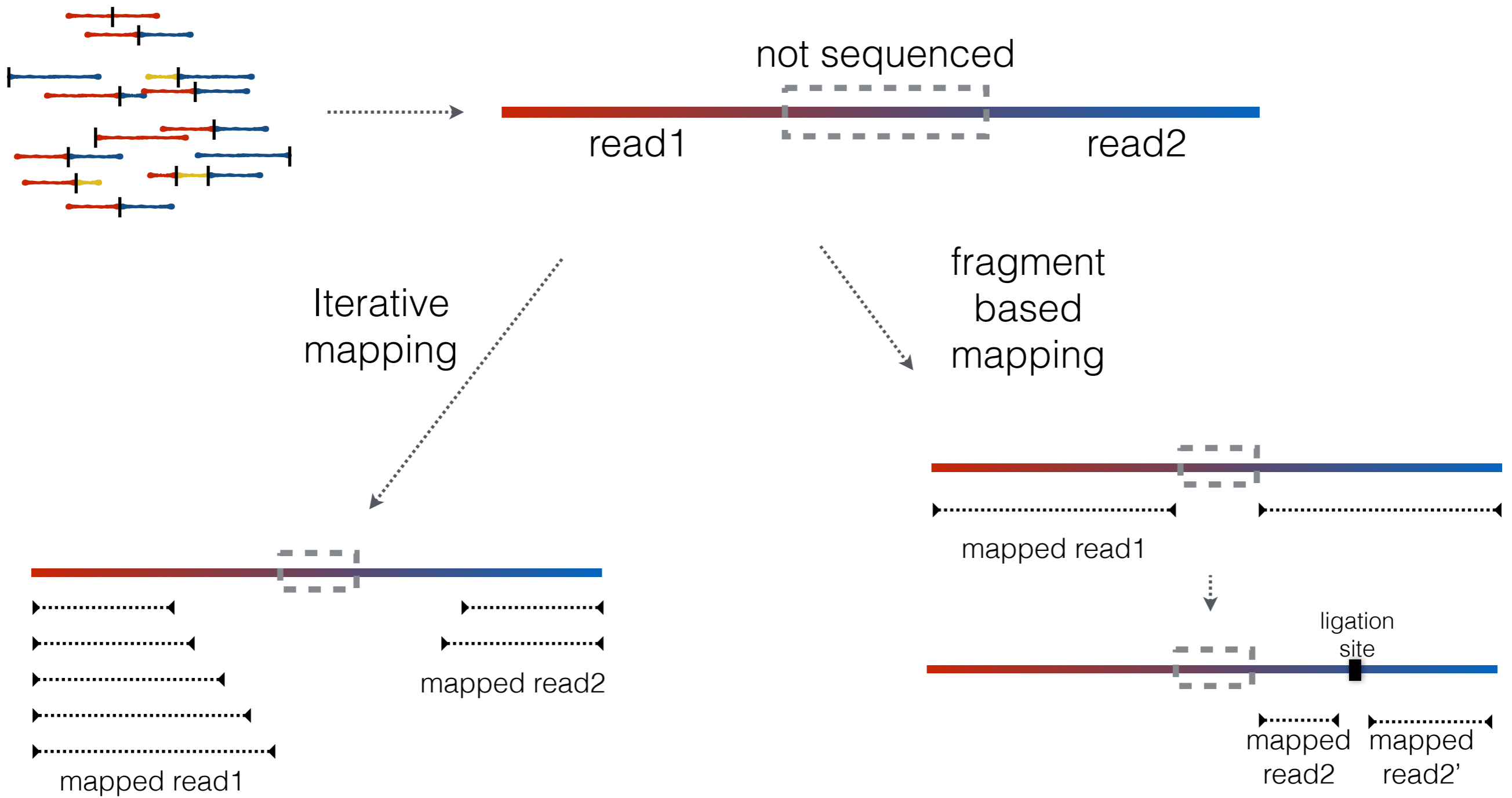
HiC mapping



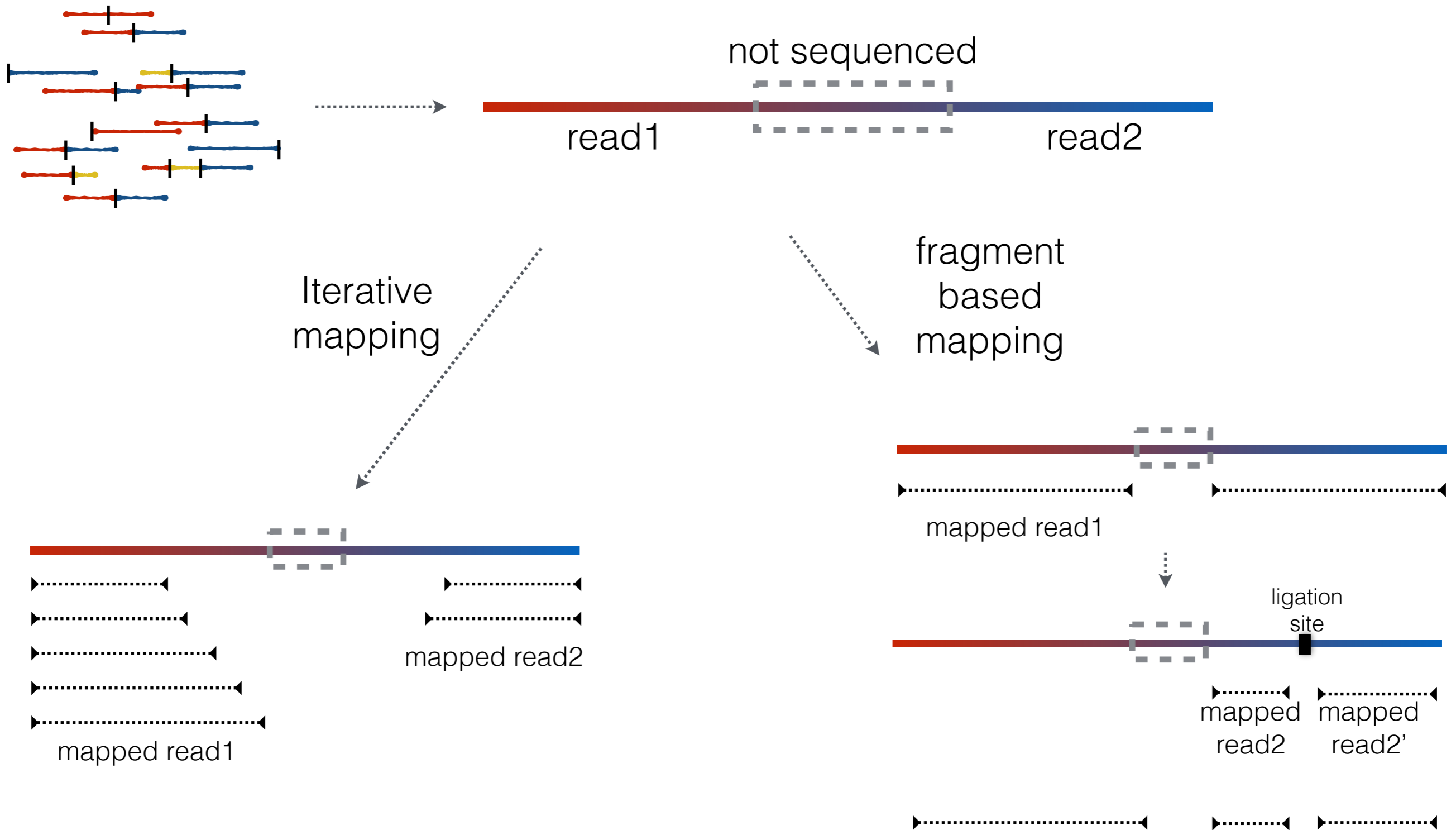
HiC mapping



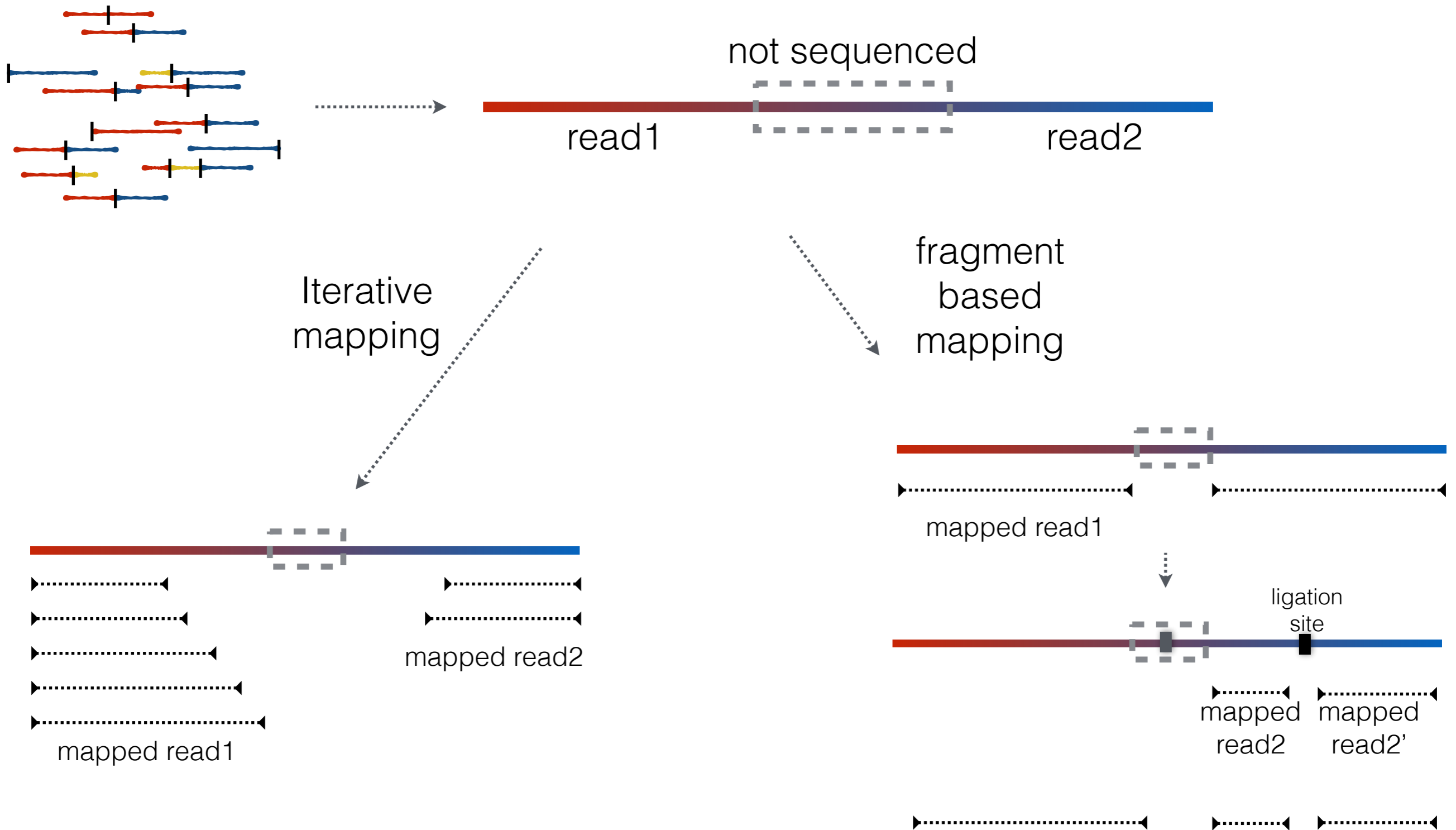
HiC mapping



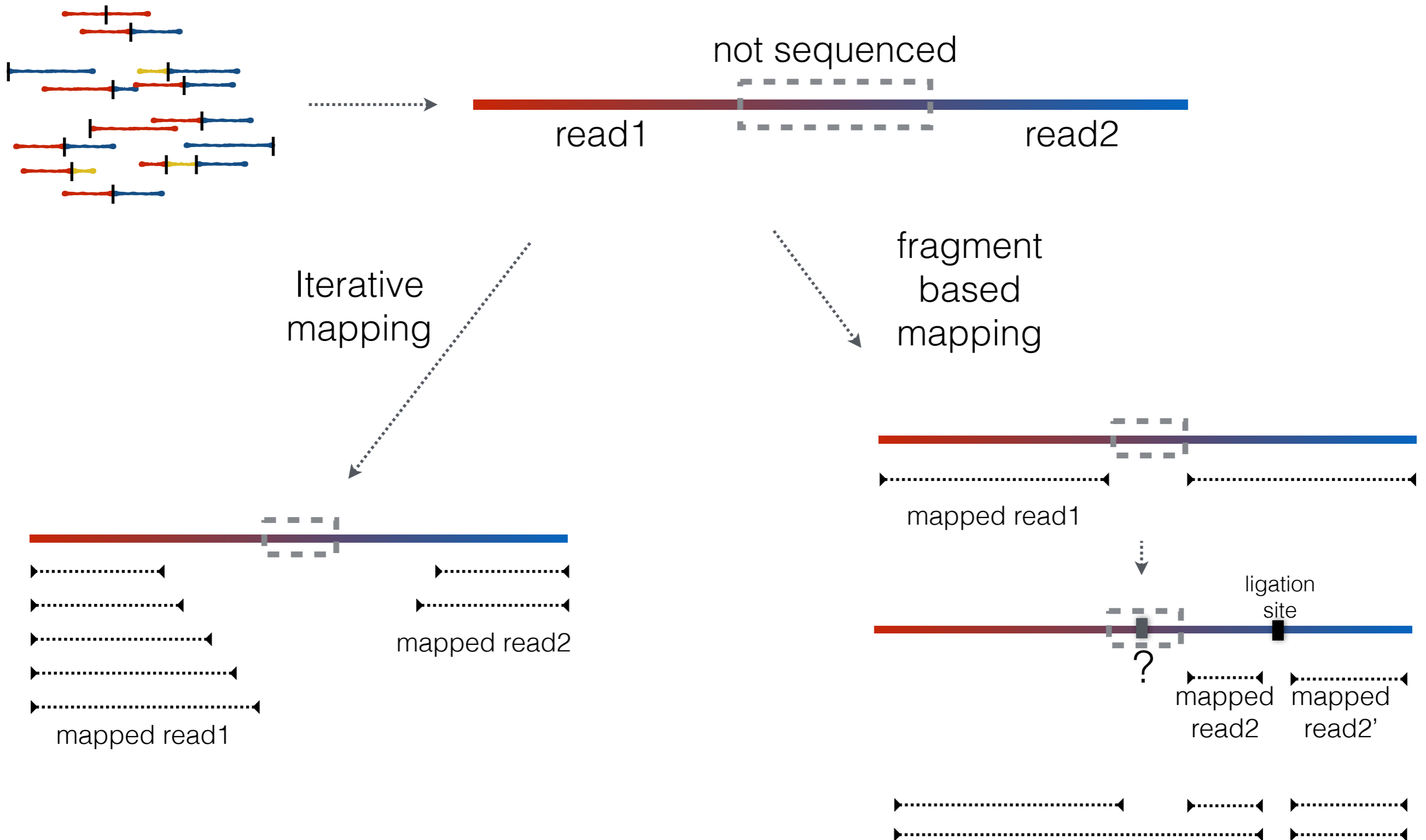
HiC mapping



HiC mapping

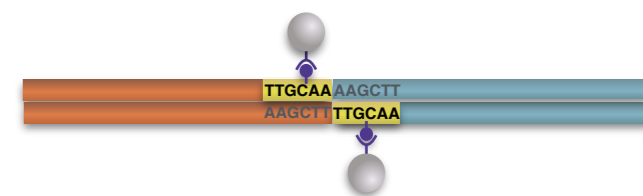
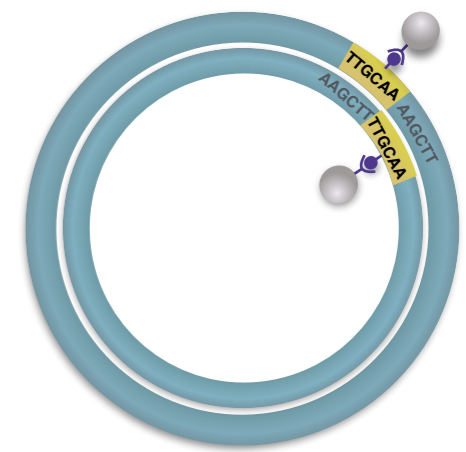
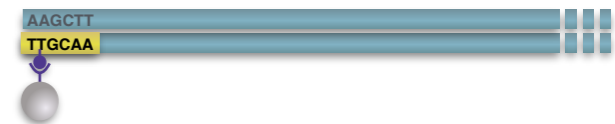


HiC mapping



How much do we map?

- 80-90% each end => 64-81% intersection
- 1% multiple contacts
- many of these will be lost in the filtering...



Dynabeads with streptavidin

TTGCAA

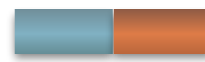
Restriction enzyme (RE) site

TTGCATCGAA

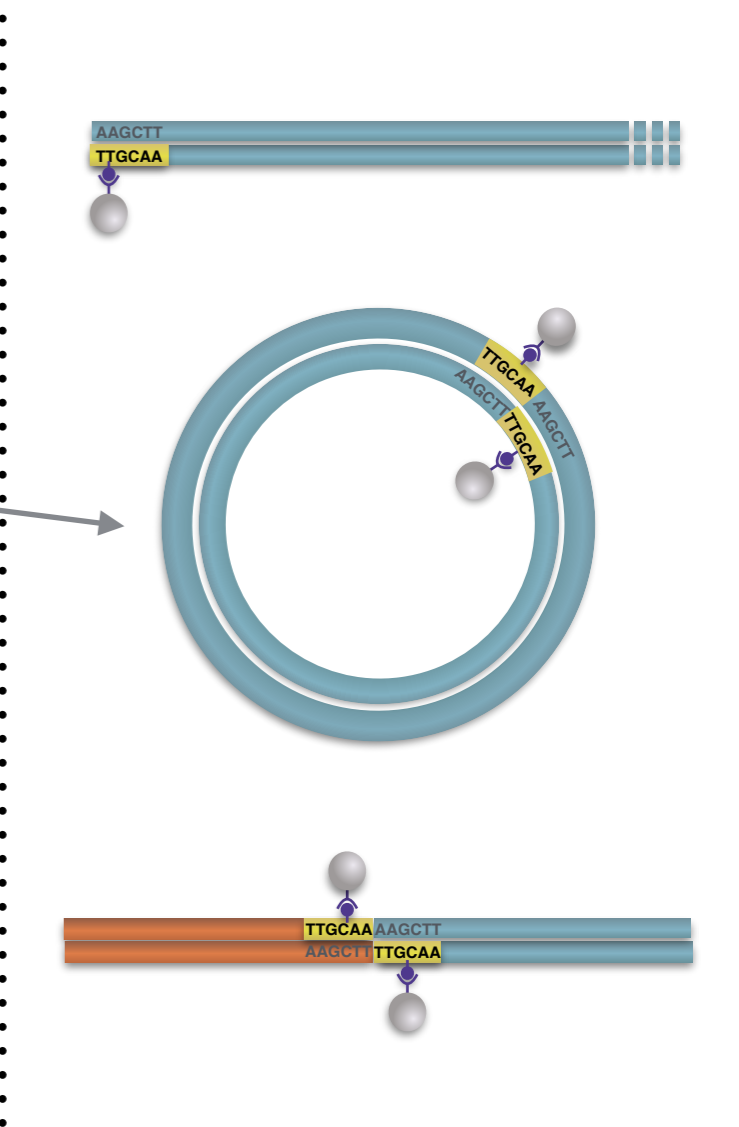
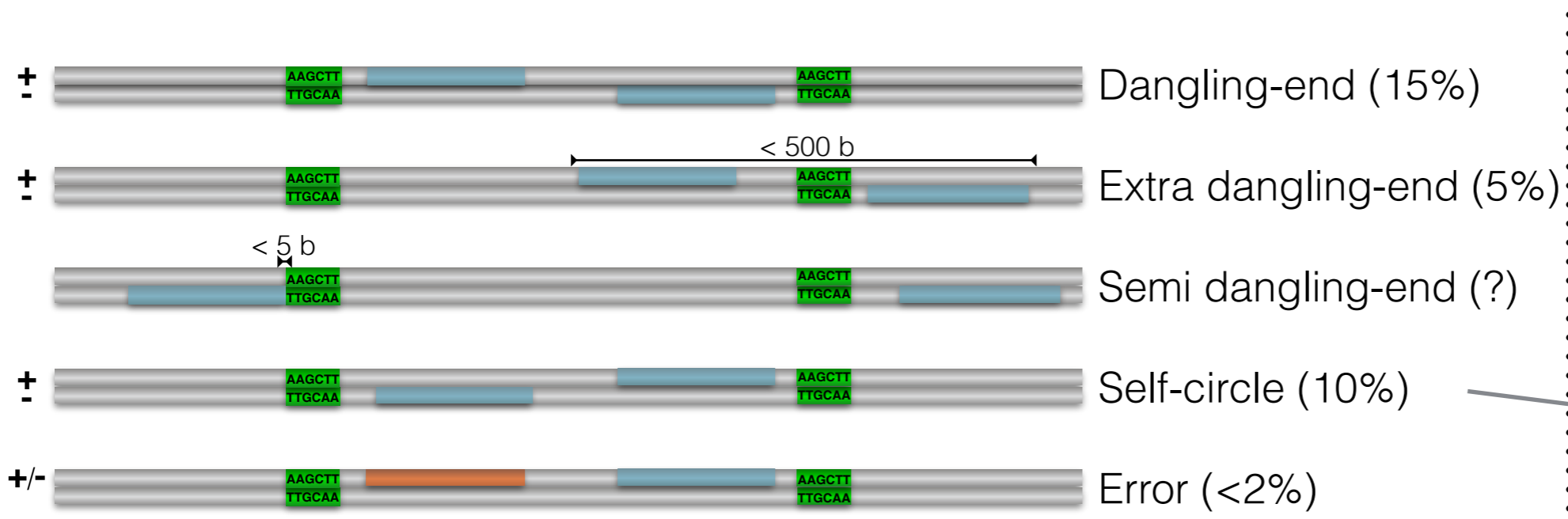
RE ligation site, repaired nucleotides in yellow (new cytosins are byotiniated)

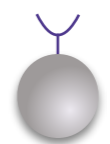






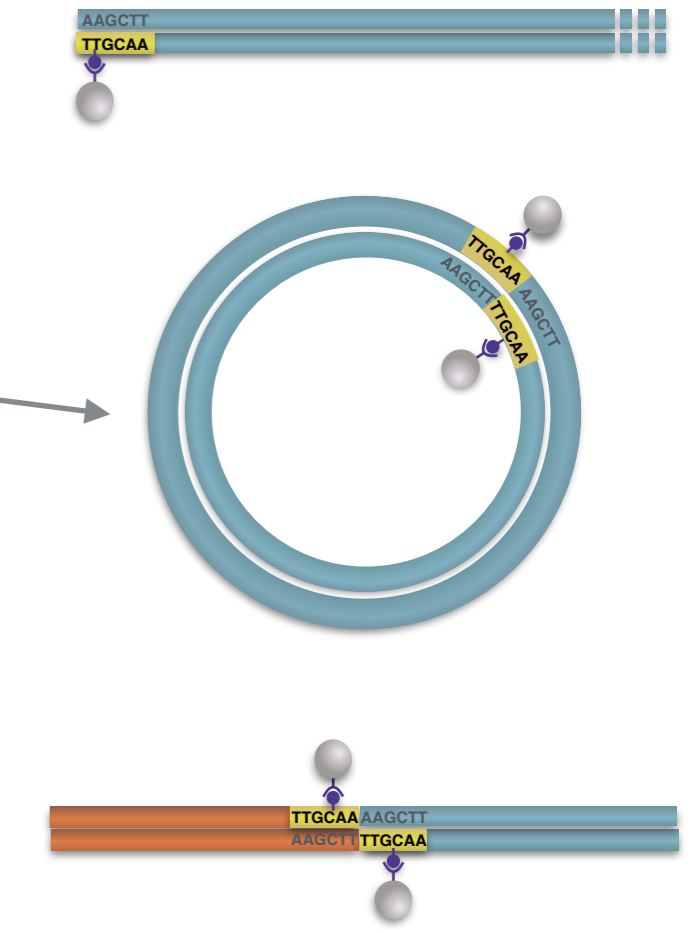
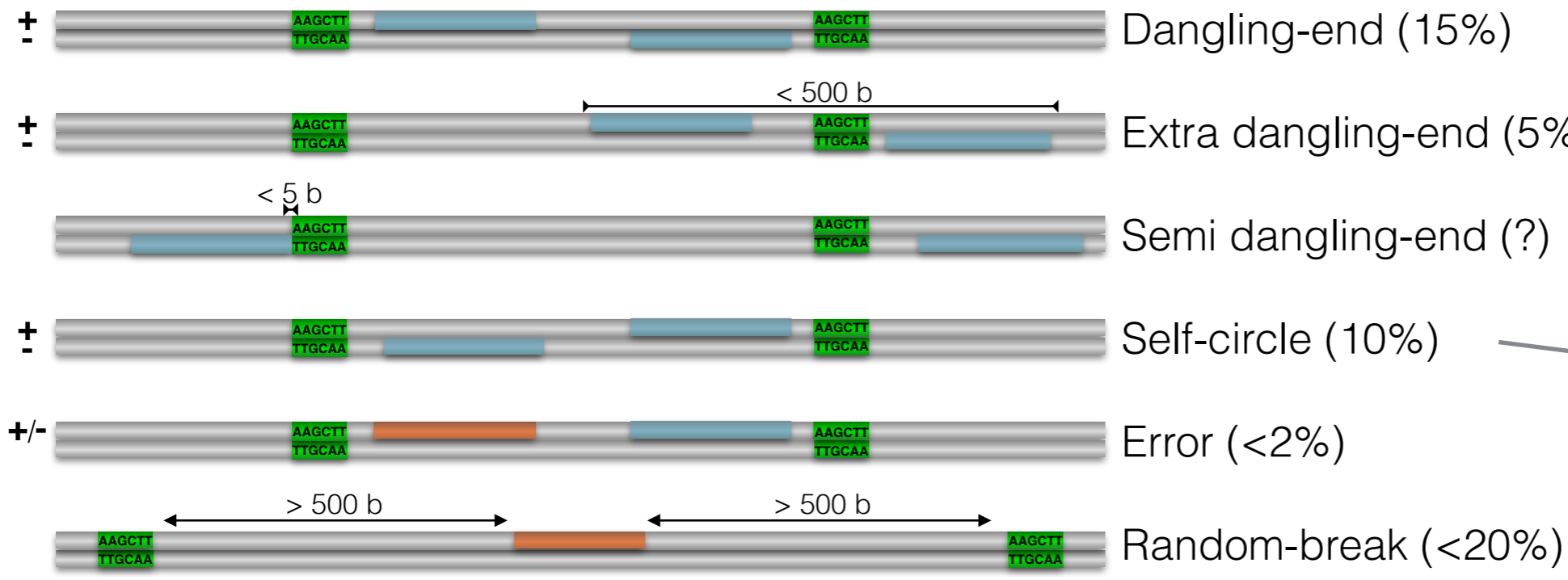
Genomic single strand regions

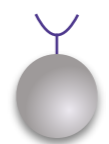



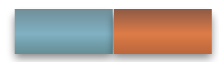


read fragments from Hi-C



-  Dynabeads with streptavidin
-  **TTGCAA** Restriction enzyme (RE) site
-  **TTGCATCGAA** RE ligation site, repaired nucleotides in yellow (new cytosins are biotinylated)
-  Genomic single strand regions
-  read fragments from Hi-C



- 
 Dynabeads with streptavidin
- 
 Restriction enzyme (RE) site
- 
 RE ligation site, repaired nucleotides in yellow (new cytosins are biotinylated)
- 
 Genomic single strand regions
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 read fragments from Hi-C

