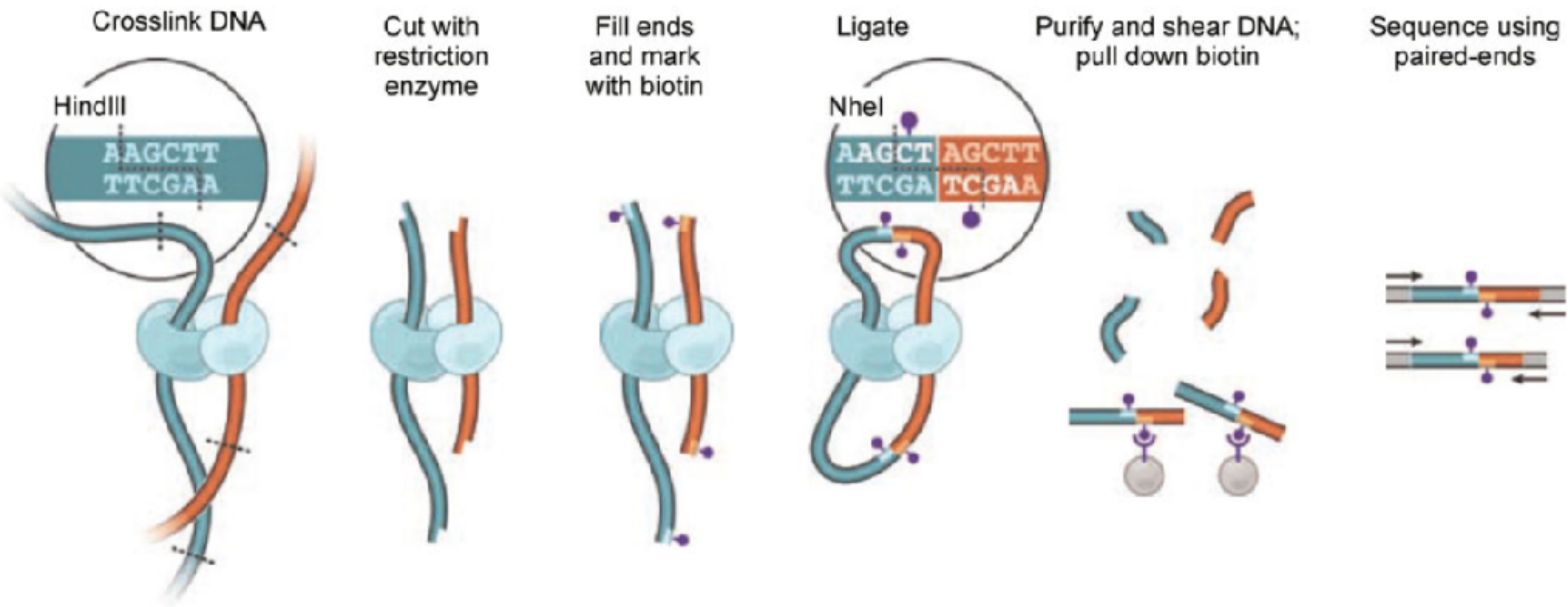


What we need to know about NGS in Hi-C

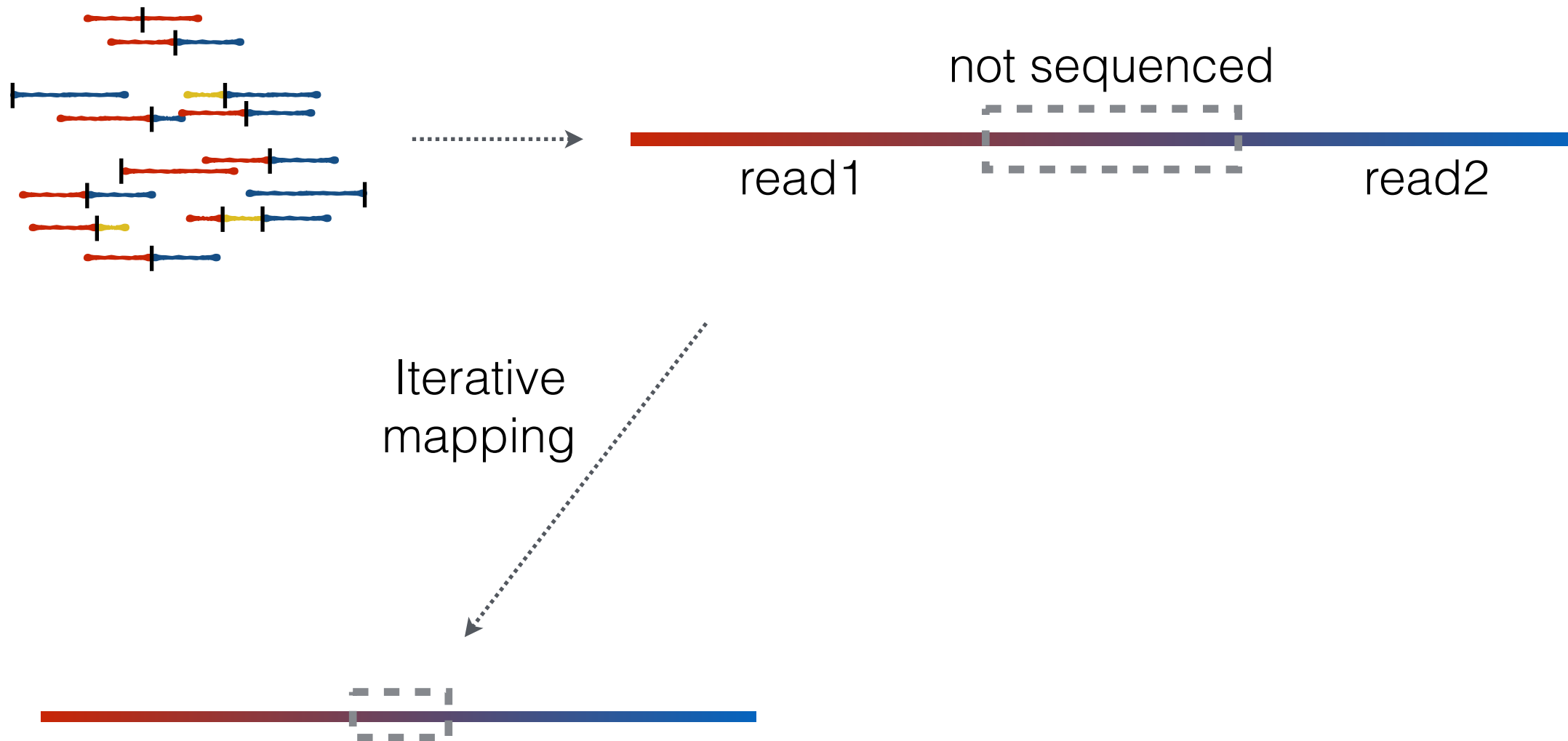
François Serra, Marco Di Stefano & Marc A. Marti-Renom
Structural Genomics Group (CNAG-CRG)



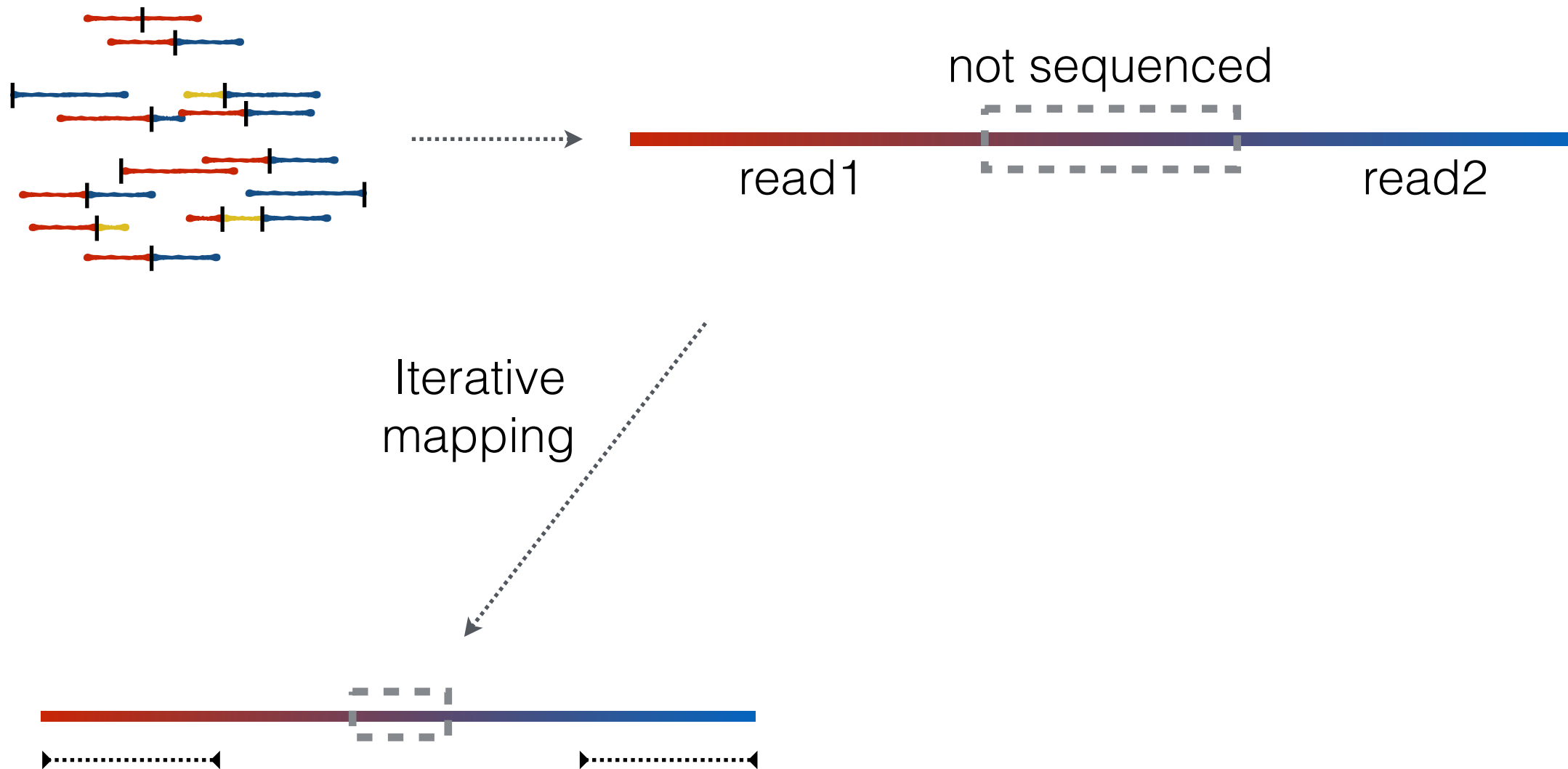
Hi-C experiment



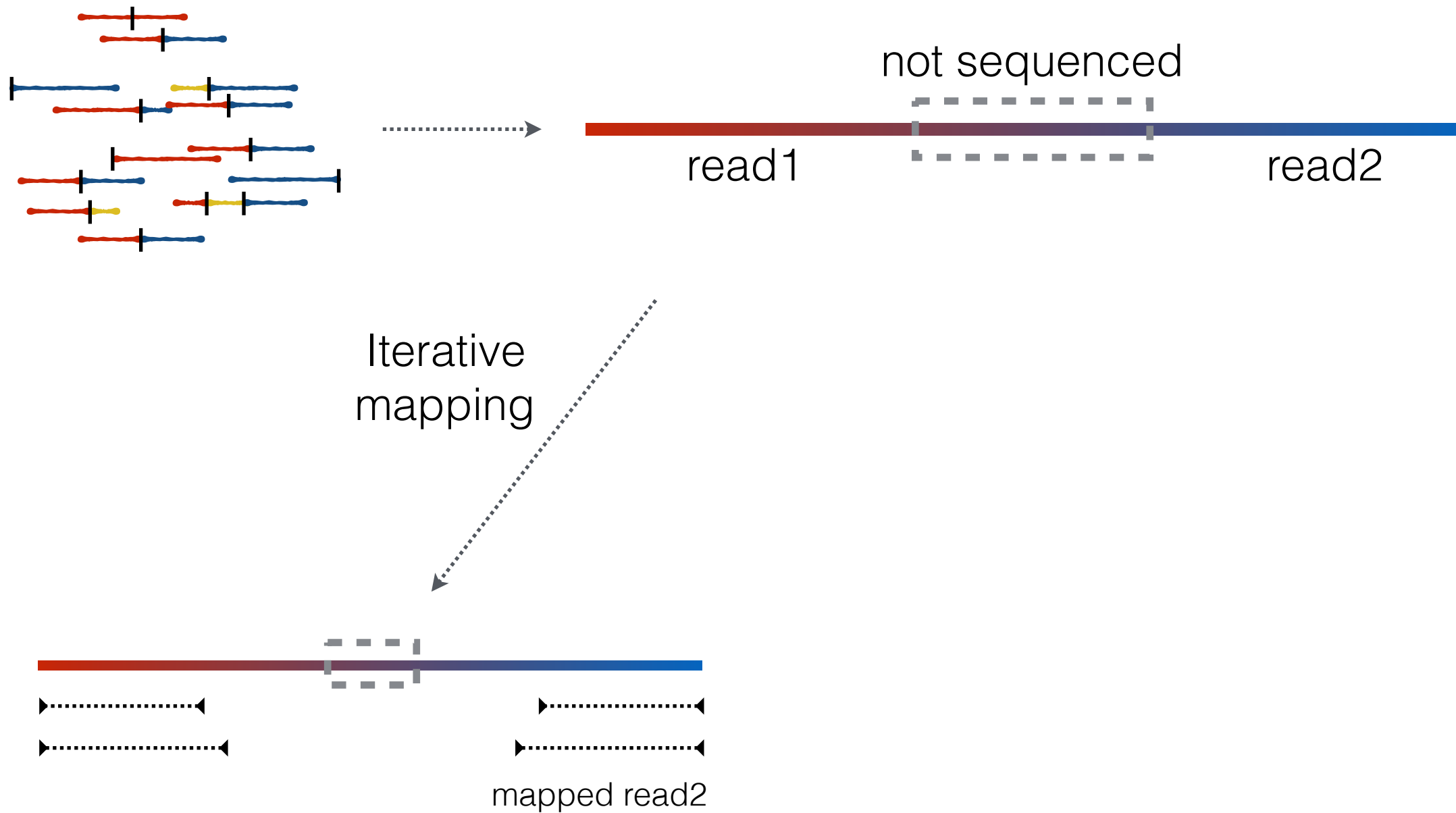
HiC mapping



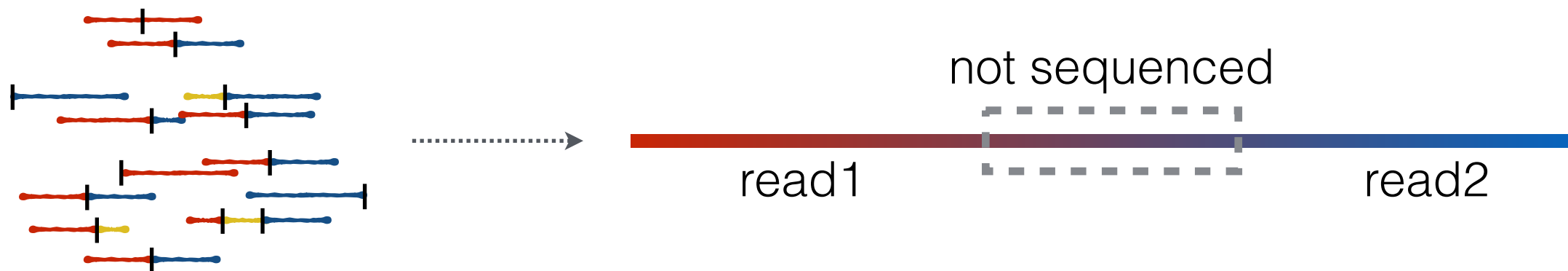
HiC mapping



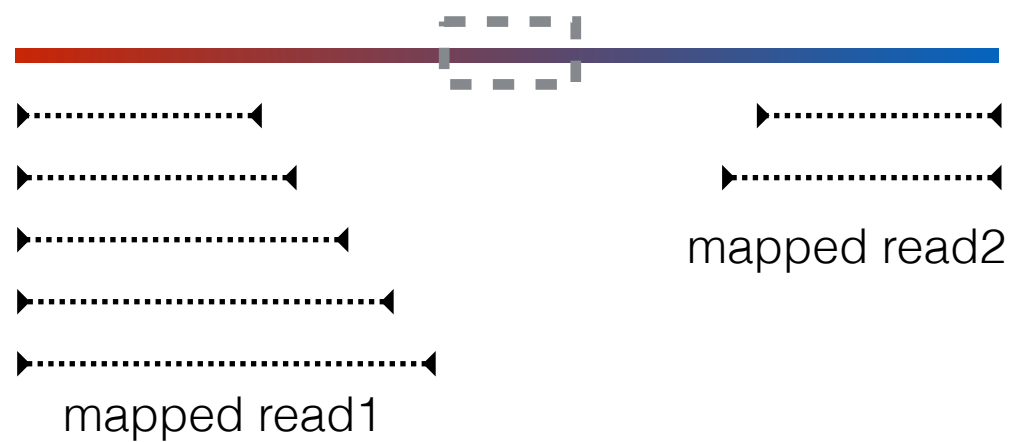
HiC mapping



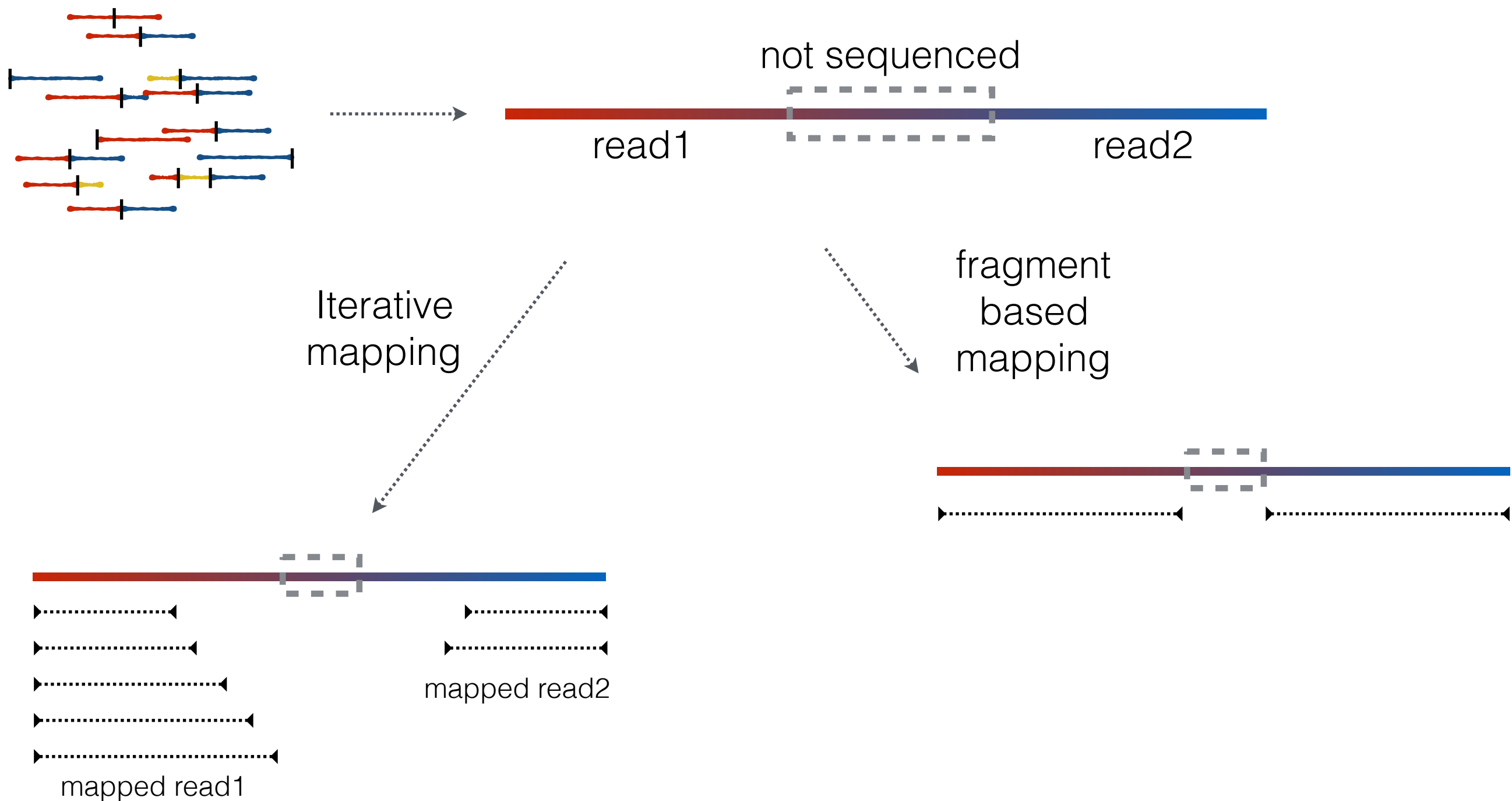
HiC mapping



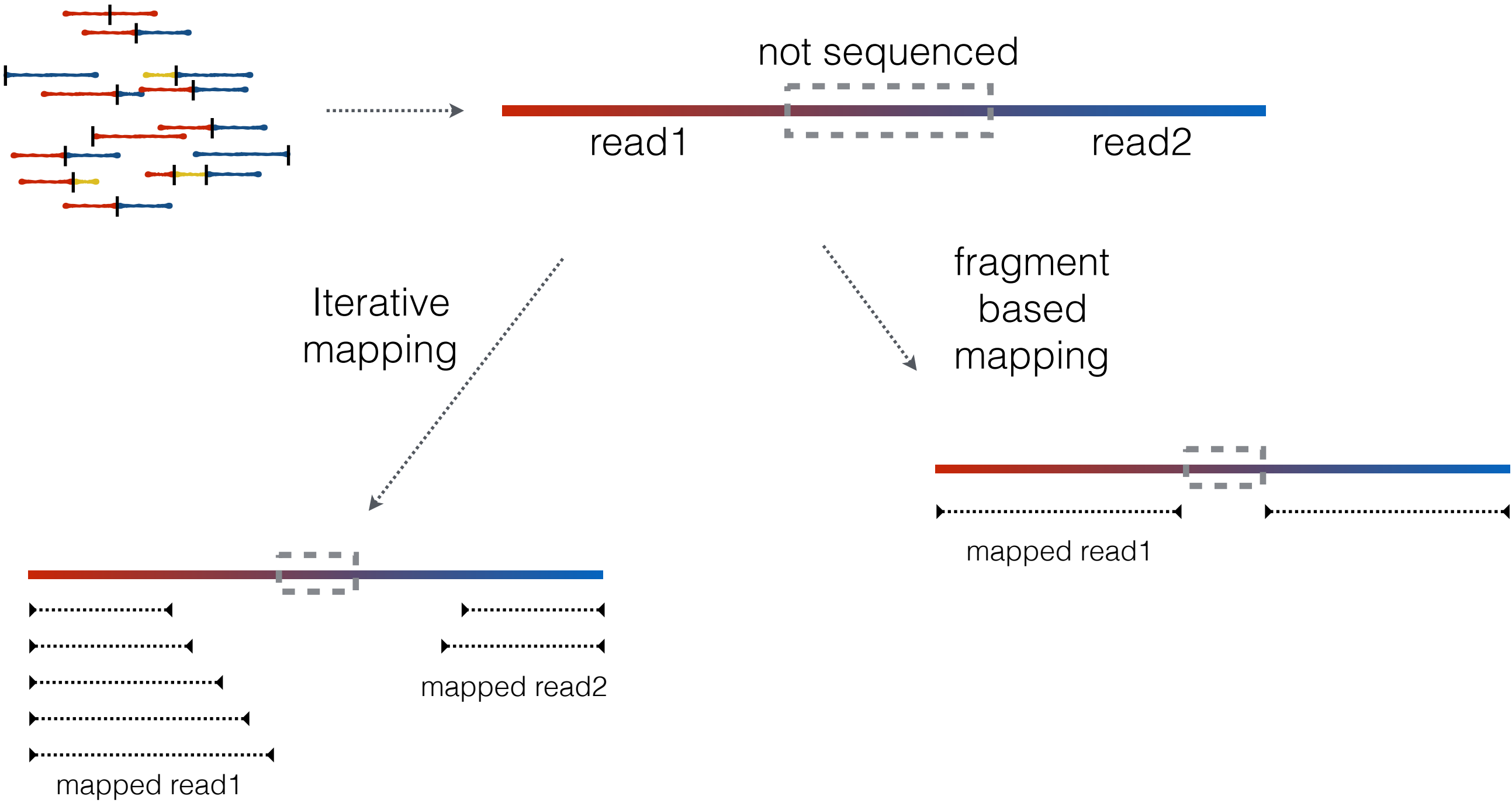
Iterative
mapping



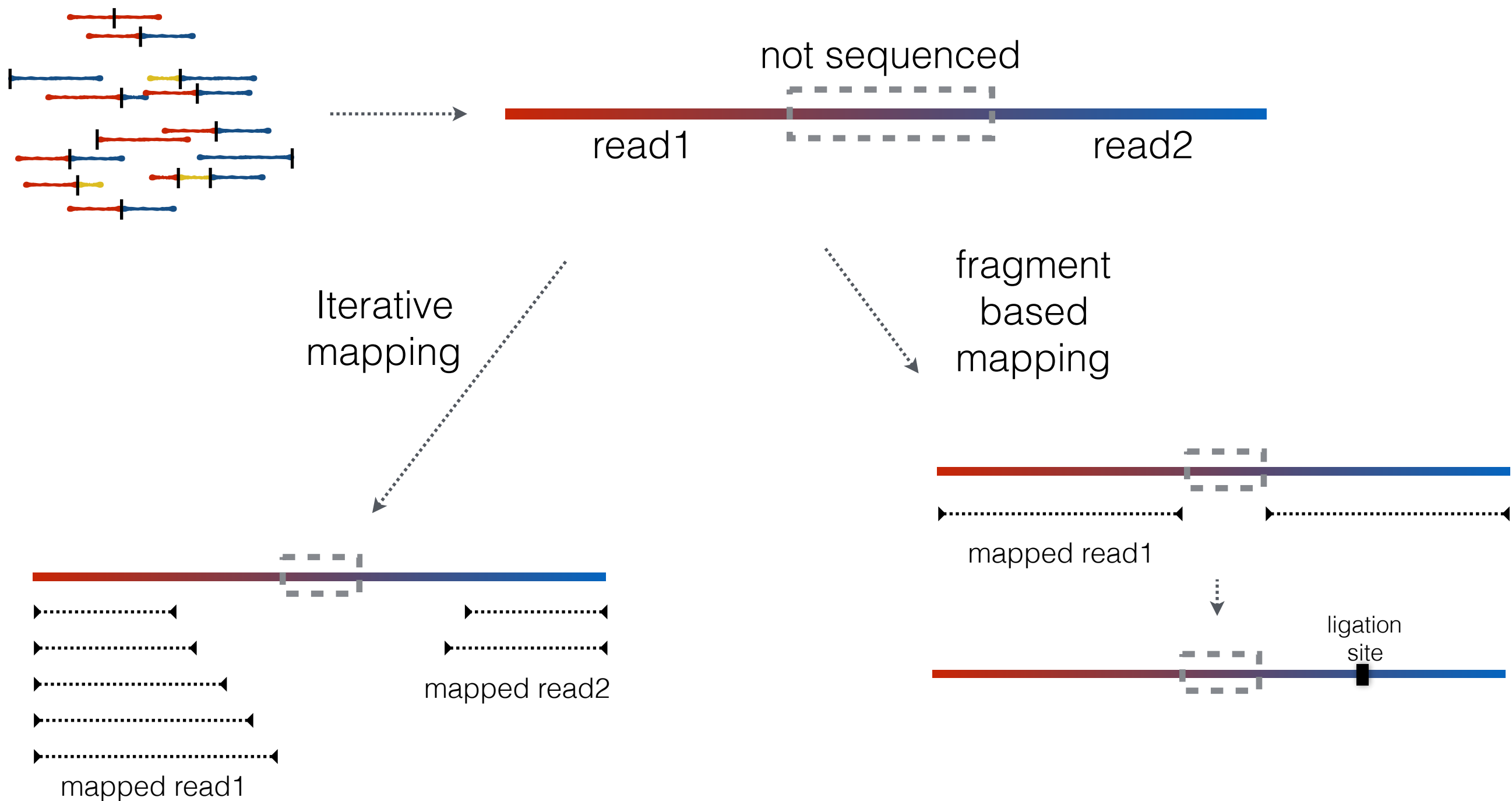
HiC mapping



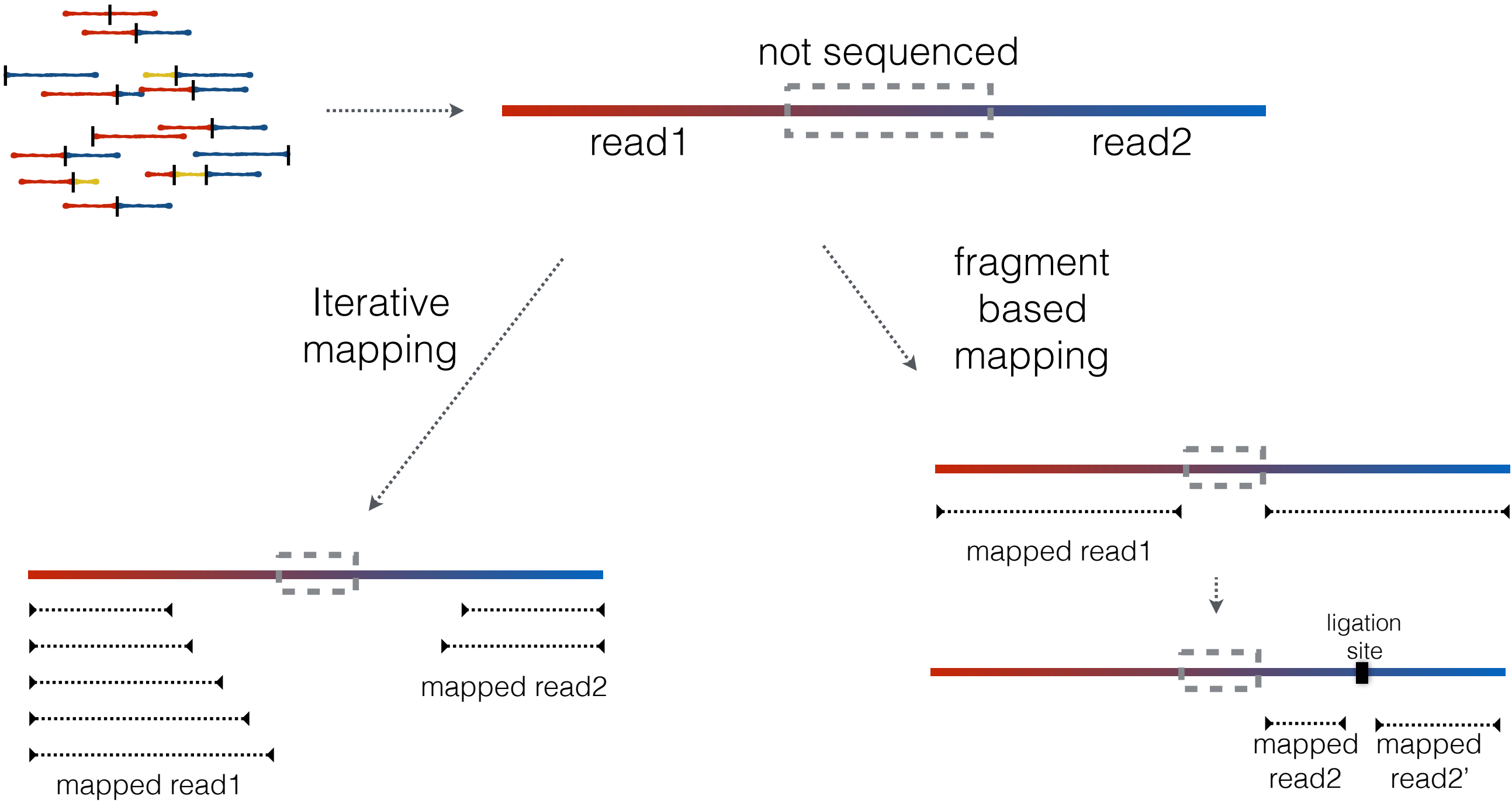
HiC mapping



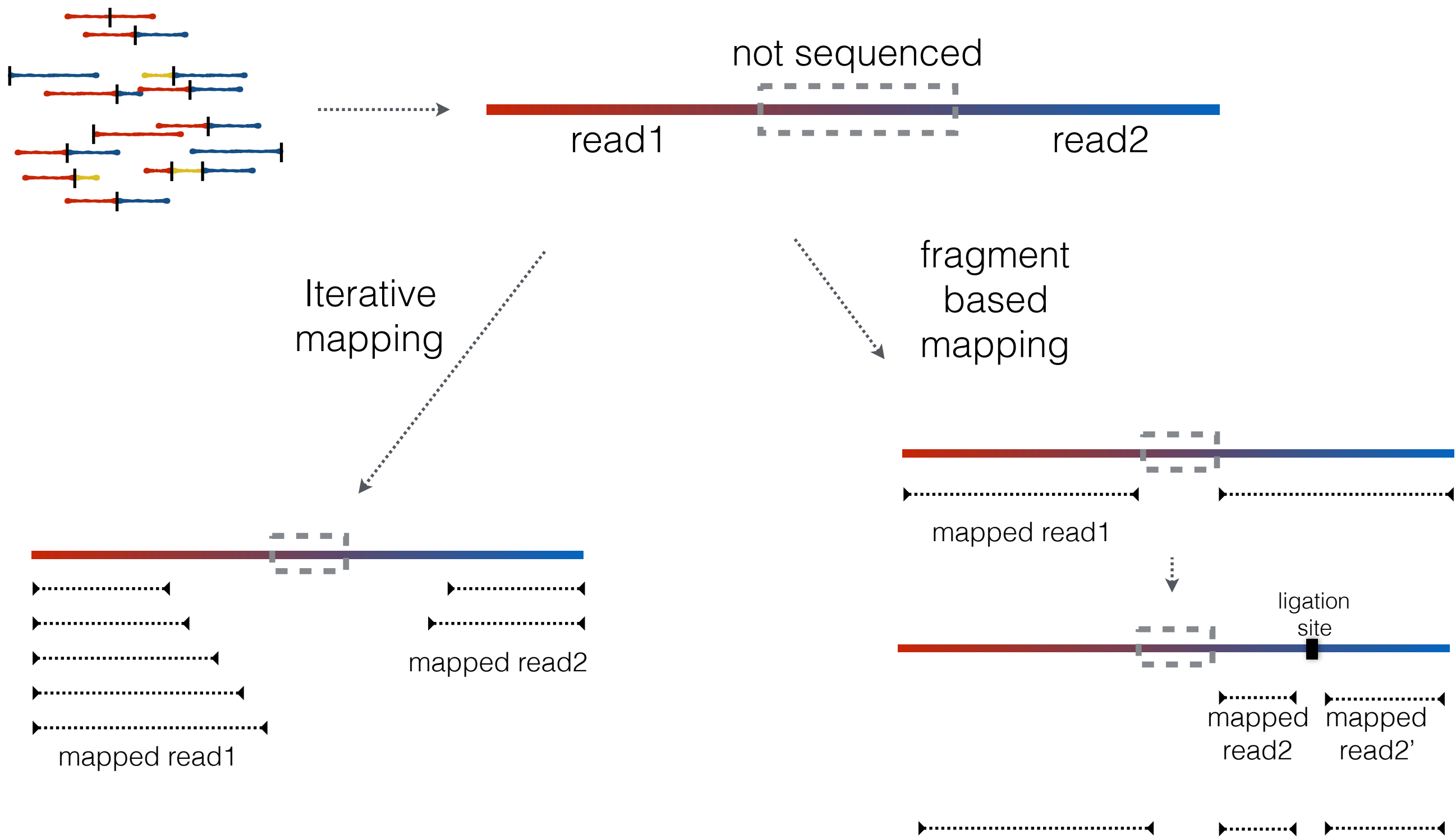
HiC mapping



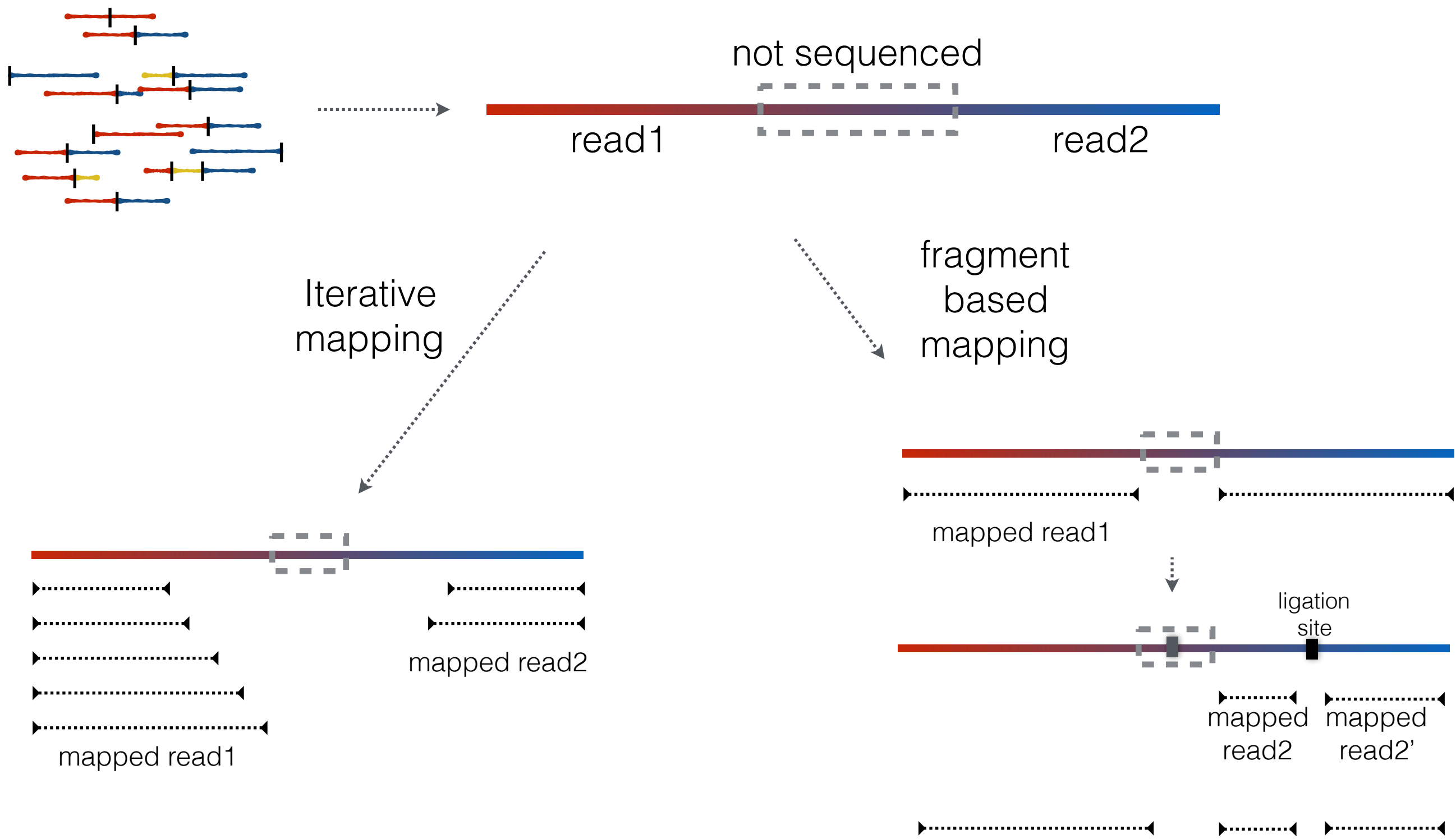
HiC mapping



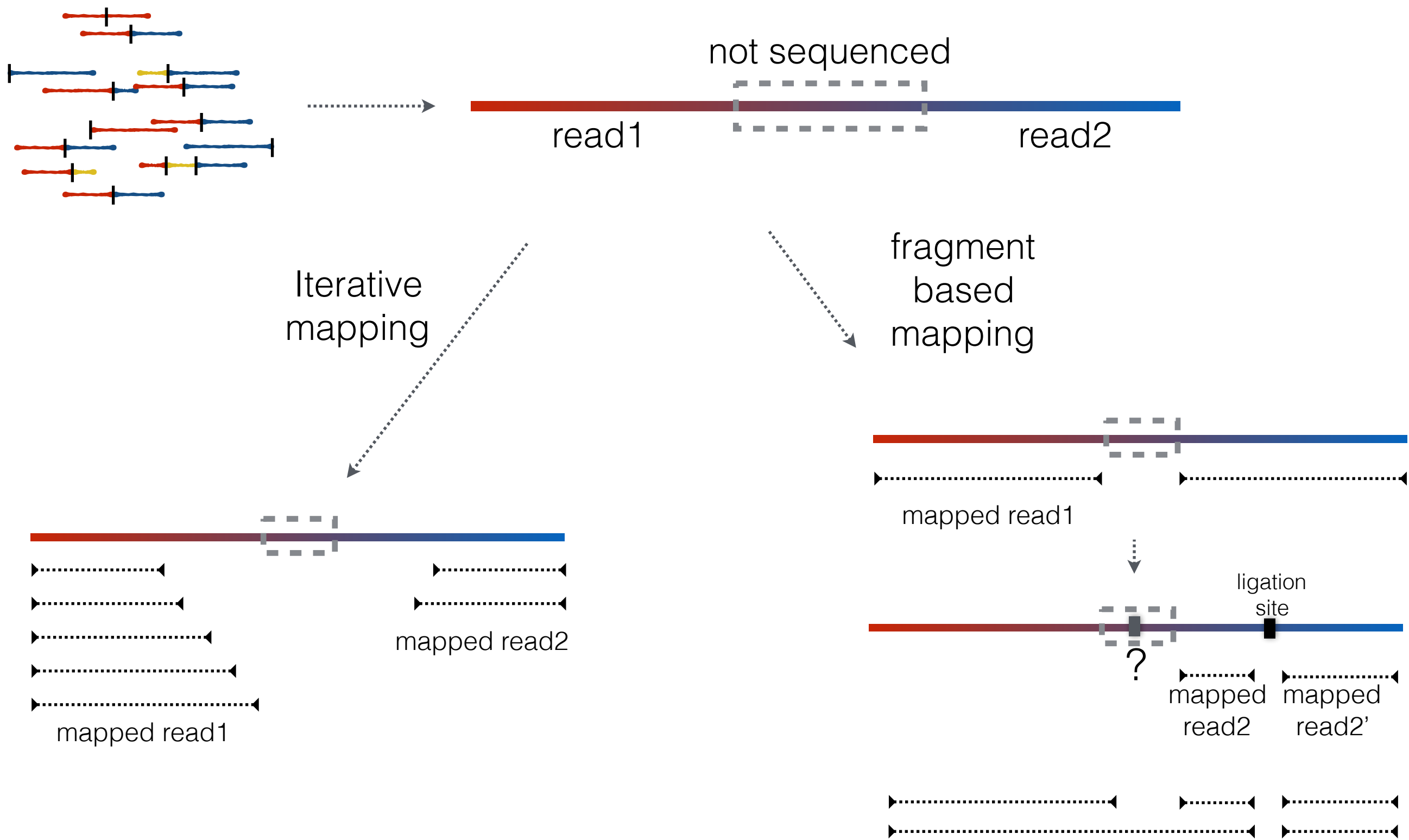
HiC mapping



HiC mapping

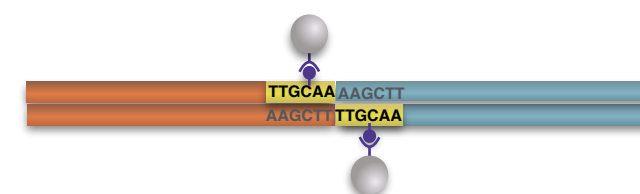
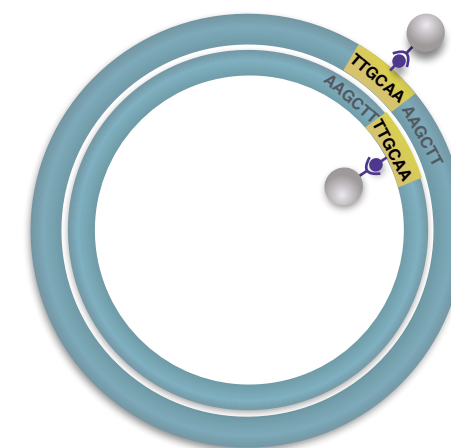


HiC mapping



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

TTGCA**TCGAA**

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



Genomic single strand regions



read fragments from Hi-C

