Paired Sequencing Reads

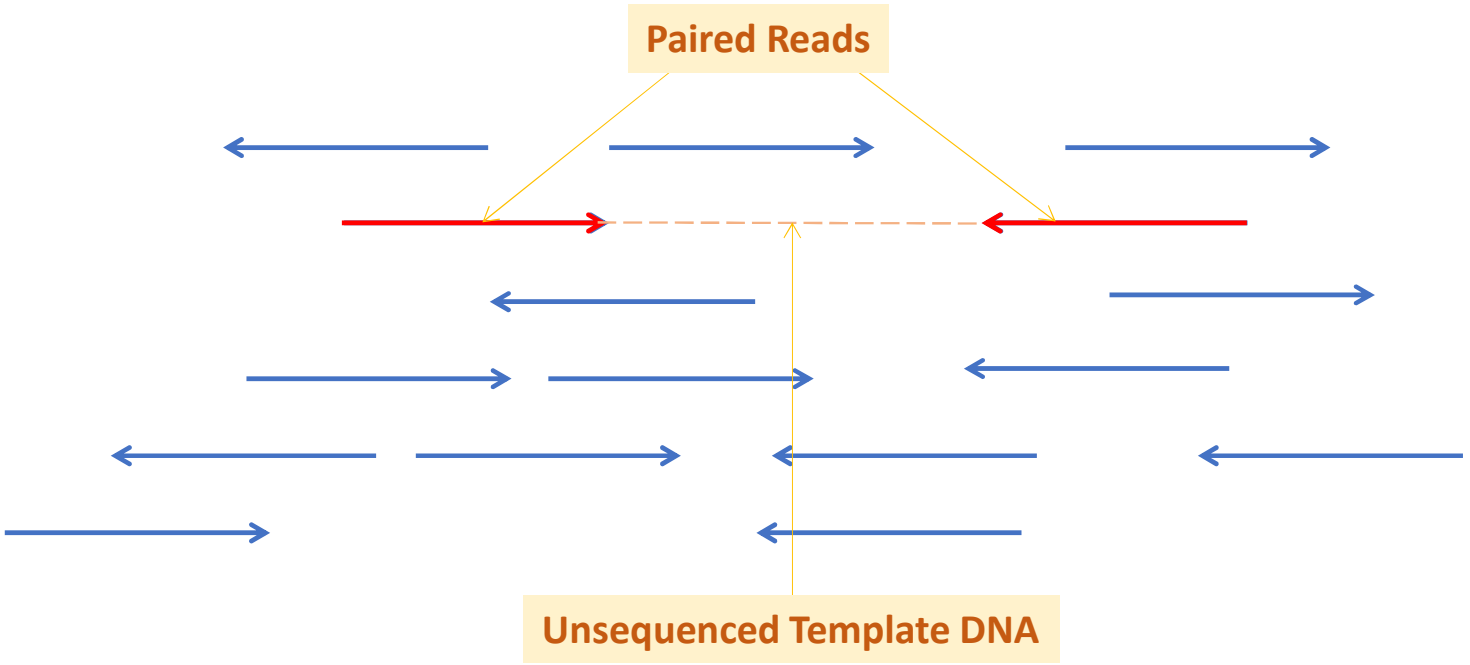
(Paired End and Mate Pair Sequencing)

Paired Sequencing Reads

Paired Sequencing Reads are created by sequencing DNA fragments from both ends.

Paired Sequencing Reads have been common from the early days of **Sanger Sequencing**.

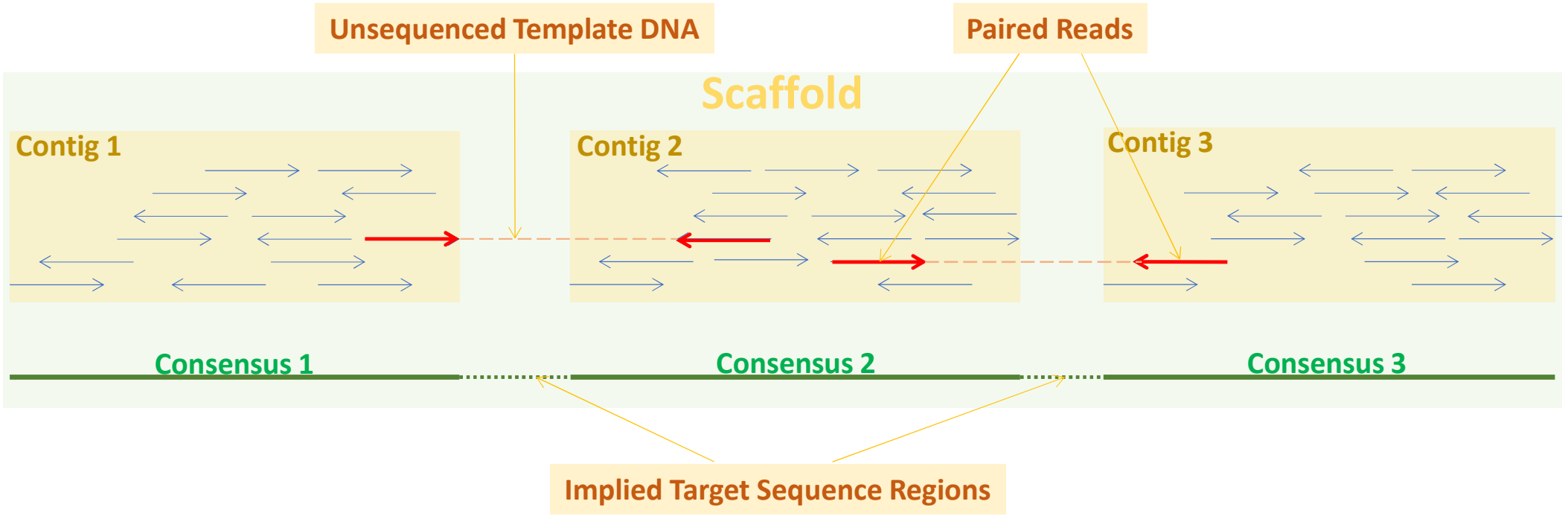
Paired Sequencing Reads



Paired Sequencing Reads must assemble predictable relative to each other.

Paired Sequencing Reads

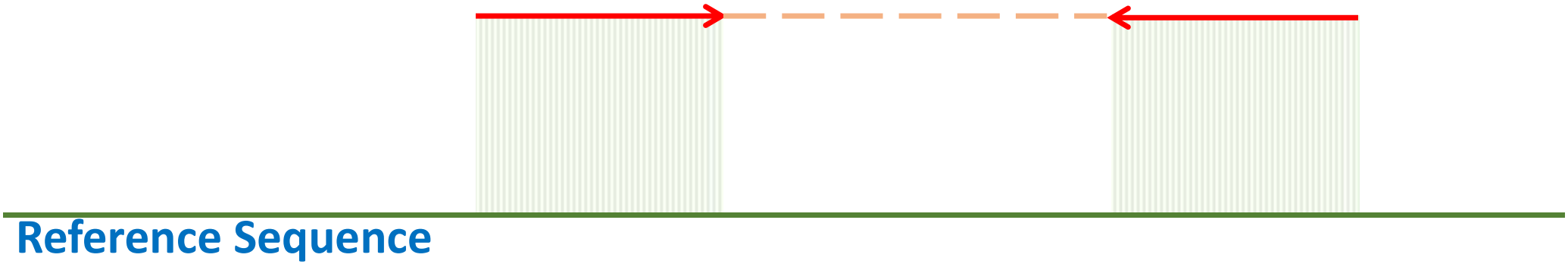
For "De Novo Assembly", this enables combining Contigs to form Scaffolds.



Paired Reads that assemble in separate **Contigs** indicate **Order** and **Orientation**.

Paired Sequencing Reads

With a **Reference Sequence** (“**Resequencing**” or “**Mapping**”), **Paired Reads** have a number of uses, including:



Assessing the accuracy of an assembly from the predictable assembly of the **Paired Reads**.

Paired Sequencing Reads

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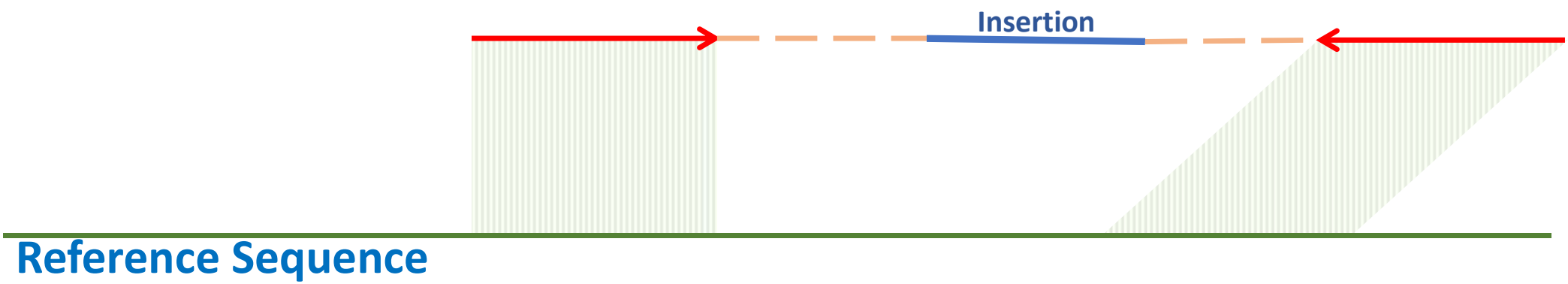
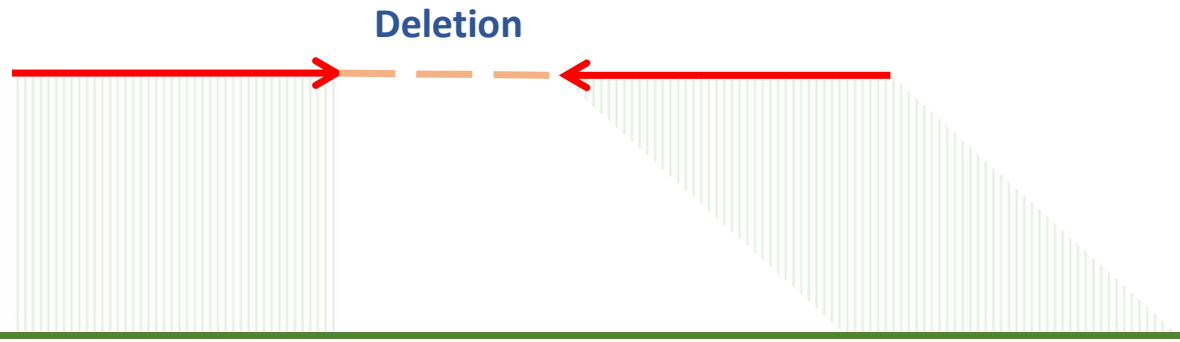


Detection of **Insertions** (assuming the **Template** size is fairly accurately known).

Paired Sequencing Reads

With a **Reference Sequence** (“**Resequencing**” or “**Mapping**”), **Paired Reads** have a number of uses, including:



Detection of **Deletions** (assuming the **Template** size is fairly accurately known).

Paired Sequencing Reads

With a **Reference Sequence** ("**Resequencing**" or "**Mapping**"), **Paired Reads** have a number of uses, including:

Resolving ambiguous assembly issues caused by repeat regions.

A single read might match several similar repeat regions.

If paired with a read outside the repeat, the correct match might be ascertained.

Paired Sequencing Reads

Paired Sequencing Reads fall into two main categories.

Paired End Sequencing:

Short template (**~800 bp**)

Reads point inwards from the ends of the template

Mate Pair Sequencing:

Longer template (**2,000 – 2,500 bp**)

Reads point outwards from near the ends of the template

For further details, try this excellent video