***Slide 01***

Here we will consider, in overview, two types of **Paired Sequencing Reads** and how they are used to assist **Sequence Assembly**.

A **URL** is suggested at the end of this video for those who would like to know more about the way **Paired Sequencing Reads** are generated.

<>

***Slide 02***

**Sequencing Reads** are said to be **Paired** if they represent the sequence at either end of the same **Template**.

<>

The use of **Paired Sequencing Reads** has been common since the early days of **Sanger Sequencing**.

<>

***Slide 03***

The size of the **Template** from which **Paired Reads** originate is generally known, at least approximately.

The **Strand** of each **Paired Read** will also be known.

Therefore, **Paired Reads** must assemble, relative to each other, in an entirely predictable fashion.

<>

***Slide 04***

**Paired Reads** assembling in different **Contigs** of a **De Novo Assembly**, can be used to determine the **Order** and **Orientation** of those **Contigs**.

Essentially, whole **Contigs** can be assembled to form **Scaffolds** onto which further **Reads** can be mapped.

<>

***Slide 05***

The predictability of the assembly of **Paired Reads** can be used to assess the accuracy of their placement in a **Mapping** or **Resequencing** project.

A good idea of the size of the **Template** from which the **Reads** were generated will be available.

The **Orientation** of the **Two Reads** will be known.

If the **Reads** are assembled unexpectedly *too close together* or *too far apart* or *in unexpected orientation*, then it will be immediately apparent that something odd is indicated.

<>

***Slide 06***

**Paired Reads** that assemble unexpectedly close together might signal an **Insertion** in the **Template** relative to the **Reference Sequence**.

<>

***Slide 07***

**Paired Reads** that assemble unexpectedly far apart might signal a **Deletion** in the **Template** relative to the **Reference Sequence**.

<>

***Slide 08***

**Repeat Regions** represent a big problem in any sort of assembly.

<>

**Single Reads**, from a **Repeat Region**, might match convincingly in many instances of a **Repeat Family**.

<>

If **Reads** from within a **Repeat Region** could be **Paired** with **Reads** from outside that **Repeat Region**, the true match might be ascertained.

<>

***Slide 09***

There are two major categories of **Read Pair**.

**Paired Reads** generated by the process called **Paired End Sequencing** come from a relatively short **Template** of around **800 Base Pairs**.

**Paired End Sequencing Reads** are generated from the extreme ends of the **Template** and both face into the centre of the **Template**.

The main alternative strategy is called **Mate Pair Sequencing**.

**Mate Pair Sequencing** involves much longer **Templates** (**2,000** to **2,500 Base Pairs**).

**Mate Pair Sequencing Reads** represent regions ***NEAR*** the ends of the **Template** that face ***outwards*** from the **Template** centre.

If you wish, quite reasonably, to know of the processes employed to generate both these species of **Read Pair**, I recommend following the **URL** provided here for a very clear description.