Comparison of long-read alignment tools

### Unicycler-align
- **Minimap alignment**
- **Common k-mers**
- **Alignment seed**
- **Line tracing**
- **K-mer selection**
- **SeqAn alignment**

Minimap efficiently finds approximate alignments between contigs and reads. These alignments are local (not semi-global) and only provide start/end coordinates (not a base-by-base alignment).

Unicycler-align uses this alignment to identify relevant regions of the read and contig for use in subsequent steps. This example shows a read which aligns to a long contig, overlapping past the contig end.

### Commands:
- `bwa mem contig.fasta read.fastq`
- `bwa index contig.fasta`
- `unicycler_align --ref contig.fasta`

Unicycler-align scores each common k-mer based on its neighbouring points. Nearby points that lie on or near the diagonal to the point contribute positively to the score, while nearby points away from the diagonal detract from the score.

Starting with this point, Unicycler-align then traces the line outward in each direction. The line is made up of discreet segments, and the angle of each is selected with a hill climbing algorithm to maximise the proximity of the line to common k-mers.

As Unicycler-align performs semi-global alignment, the line tracing proceeds until a sequence end is reached, even in regions where the alignment is weak.

### BWA-MEM (v0.7.15-r1140)
- **Minimap alignment**
- **Common k-mers**
- **Alignment seed**
- **Line tracing**
- **K-mer selection**
- **SeqAn alignment**

BWA-MEM finds the same alignment line as Unicycler-align, though there are small gaps on both ends. It also reports a secondary alignment in the repetitive region. While this alignment is genuine, it is spurious when looking for the read’s single best alignment to the contig.

### Commands:
- `bwa mem -D contig.fasta`
- `bwa index contig.fasta`

BWA-MEM finds the same alignment line as Unicycler-align, though there are small gaps on both ends. It also reports a secondary alignment in the repetitive region.

### BLAST (megablast, v2.6.0+)
- **Minimap alignment**
- **Common k-mers**
- **Alignment seed**
- **Line tracing**
- **K-mer selection**
- **SeqAn alignment**

BLAST extends the primary alignment line further than BWA-MEM, leaving only a small gap at the start of the read. It also reports additional alignments in the repetitive region.

### Commands:
- `makeblastdb -dbtype nucl -in contig.fasta`
- `makeblastdb -dbtype nucl -in contig.fasta`
- `blastn -db contig.fasta -query read.fastq`

BLAST extends the primary alignment line further than BWA-MEM, leaving only a small gap at the start of the read. It also reports additional alignments in the repetitive region.

### LAST (v843)
- **Minimap alignment**
- **Common k-mers**
- **Alignment seed**
- **Line tracing**
- **K-mer selection**
- **SeqAn alignment**

LAST follows the main alignment line, though it is split into two parts at read position 490. This results in a large end gap for the main alignment. LAST also reports many smaller alignments in the repetitive region.

### Commands:
- `lastdb -Q1 contig_db read.fastq`
- `lastdb -R01 contig_db contig.fasta`

LAST follows the main alignment line, though it is split into two parts at read position 490. This results in a large end gap for the main alignment. LAST also reports many smaller alignments in the repetitive region.

### BLASR (v5.3.f8bfa9c)
- **Minimap alignment**
- **Common k-mers**
- **Alignment seed**
- **Line tracing**
- **K-mer selection**
- **SeqAn alignment**

BLASR finds a single alignment without an end gap, but the repetitive region causes a major deviation from the true alignment line. This results in an incorrect read position at the point of overlap.

### Commands:
- `blasr read.fasta contig.fasta`

BLASR finds a single alignment without an end gap, but the repetitive region causes a major deviation from the true alignment line. This results in an incorrect read position at the point of overlap.

### GraphMap (v0.5.1)
- **Minimap alignment**
- **Common k-mers**
- **Alignment seed**
- **Line tracing**
- **K-mer selection**
- **SeqAn alignment**

GraphMap performs true semi-global alignment, leaving no end gaps, but its alignment deviates in the repetitive region. Like BLASR, it gives an incorrect read position at the point of overlap.