samtools

github.com/jo-mc/disbamer

Displaying a read, from a bam file, with the reference in a bash shell terminal.

Get read

Extract fields
• Region
• Cigar
• sequence

Extract REF

Create view
• annotate
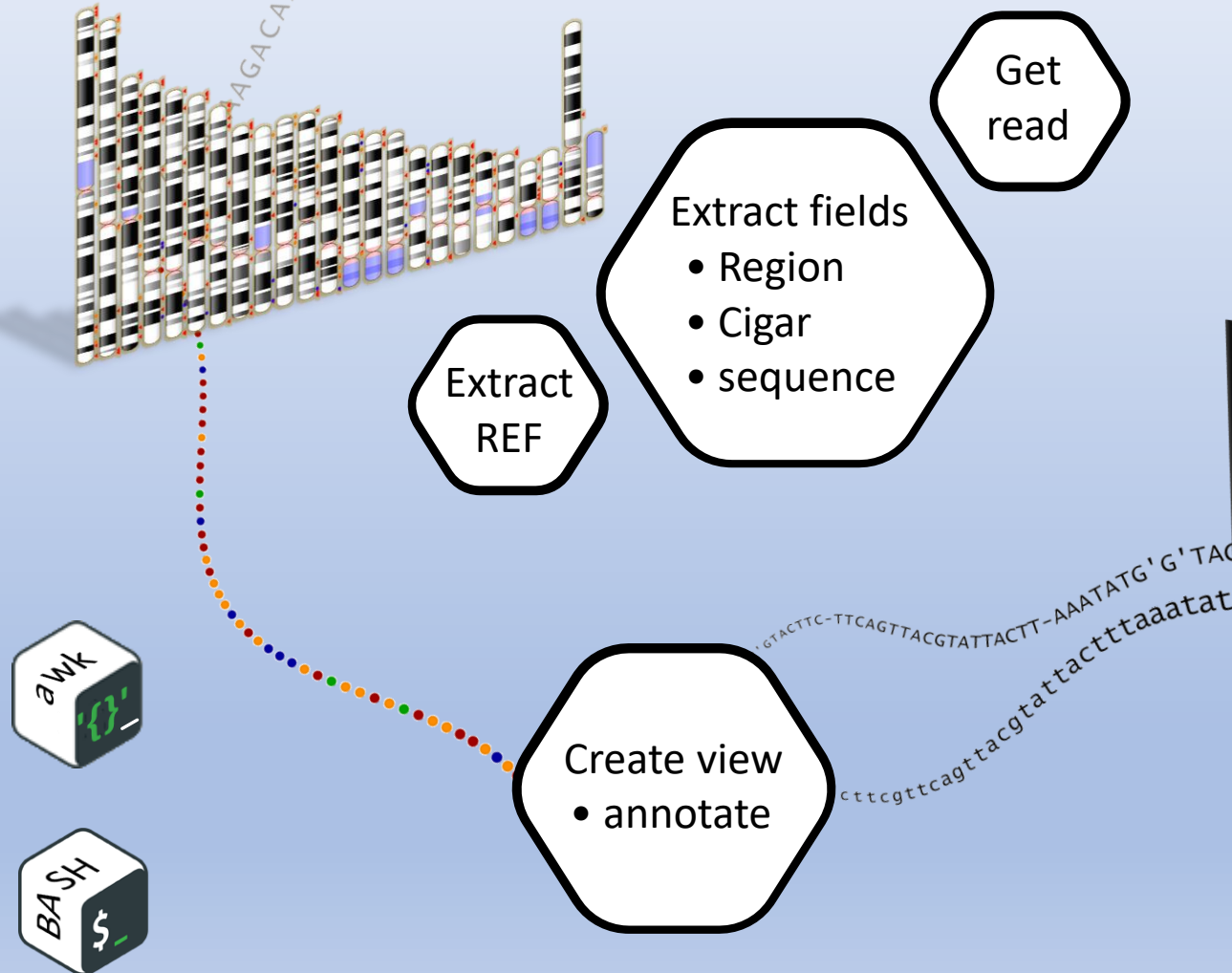
```
D I S B A M E R
--------g-e-n-o-m-i-c---v-i-e-w------ (xviewread.awk)
Legend:  line 1: aligned seq. line 2: reference seq. line 3: indicator

      |50        |60,,,       |70      |80      |90      |100     |110    |120
1 CTTGTGCAGGTTAGTT'C'ACATATGTATACATGTGCCATG-TGATGCATTGAACCCACTAACAAATCATCTAGCATTAGGTAT
2 cttgtgcaggttagtt'+'acatatgtatacatgtgccatgctggtgcgctgaacccactaactcgtcatctagcattaggtat
3 ...............'+'.........................-..x...xx...........xxx.................
      |50        |60,,,       |70      |80      |90      |100     |110    |120

Inserts: 151, Deletes: 272, Matches: 5382. (using M-I-D cigars only)
Read Length (less clipping): 5533  Reference Length: 5656   Miss matches : 223.
```

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awk

BASH

The University of Adelaide

DNA