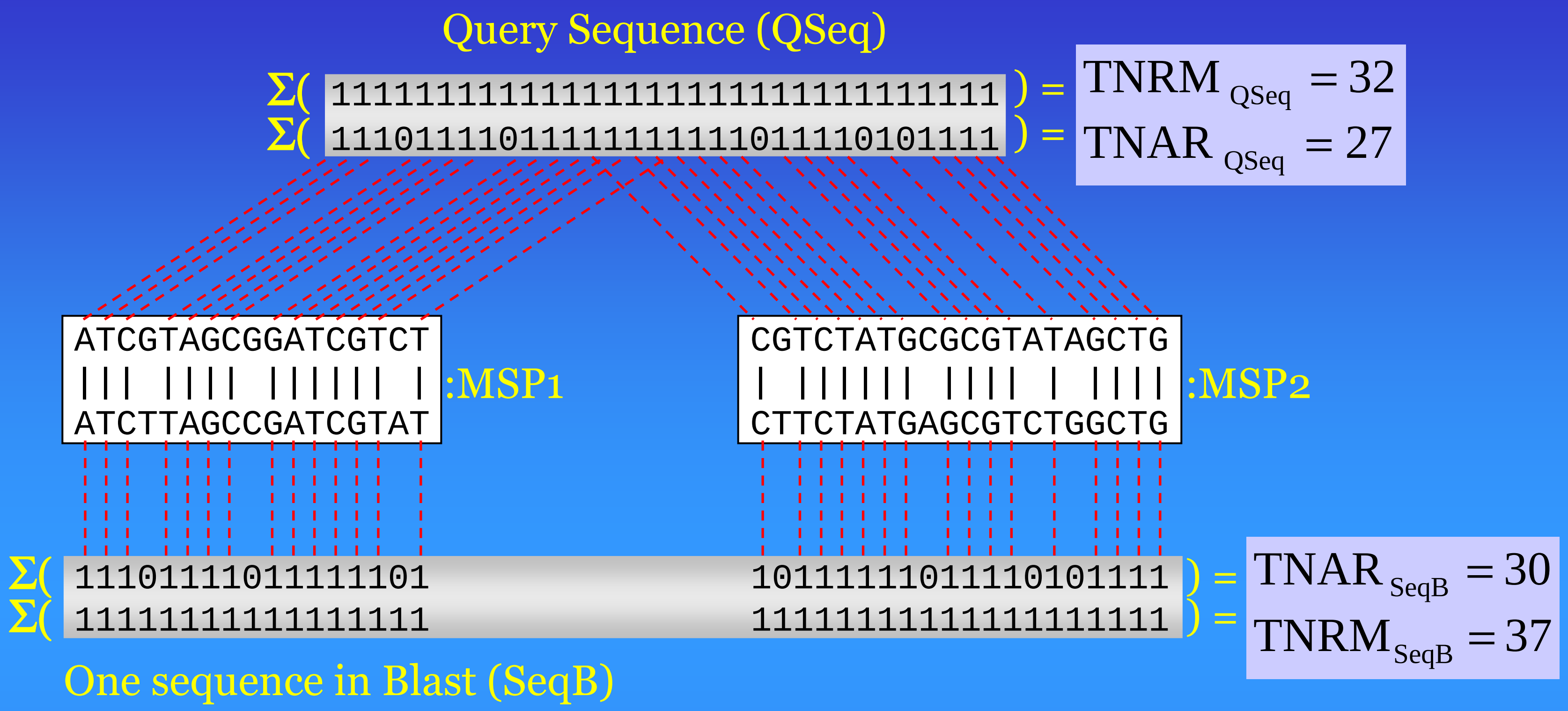


Query Sequence (QSeq)

$$\Sigma(\ 11111111111111111111111111111111\ ) = \mathrm{TNRM}_{\mathrm{QSeq}} = 32$$

$$\Sigma(\ 11101111011111111111011110101111\ ) = \mathrm{TNAR}_{\mathrm{QSeq}} = 27$$

```
ATCGTAGCGGATCGTCT
||| |||| |||||| |
ATCTTAGCCGATCGTAT
```

:MSP1

```
CGTCTATGCGCGTATAGCTG
| |||||| |||| | ||||
CTTCTATGAGCGTCTGGCTG
```

:MSP2

$$\Sigma(\ 11101111011111101 \quad 10111111011110101111\ ) = \mathrm{TNAR}_{\mathrm{SeqB}} = 30$$

$$\Sigma(\ 11111111111111111 \quad 11111111111111111111\ ) = \mathrm{TNRM}_{\mathrm{SeqB}} = 37$$

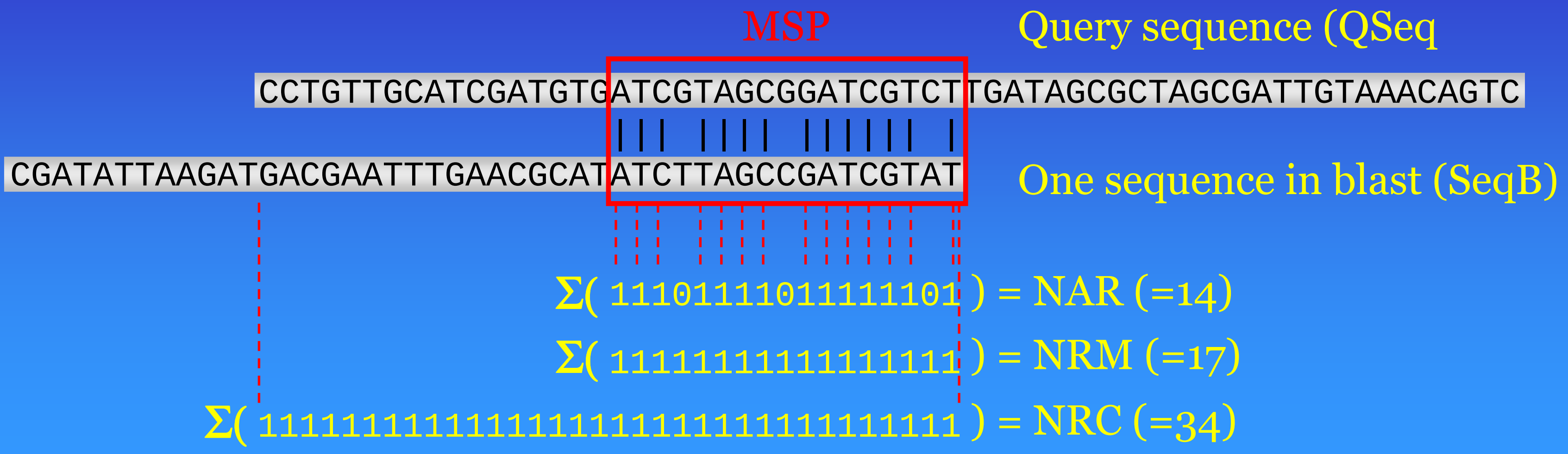
One sequence in Blast (SeqB)

$$\mathrm{GID}_{\mathrm{SeqB}} = \frac{\mathrm{TNAR}_{\mathrm{SeqB}}}{\mathrm{TNRM}_{\mathrm{SeqB}}} \times 100 = \frac{30}{37} \times 100 = 81.1\%$$

TNAR: Total Number of Aligned Residue

TNRM: Total Number of Residue in MSP (*Maximum Segment Pair*)

GID: Global Percent Identity



MSP

Query sequence (QSeq

```
                           CCTGTTGCATCGATGTGATCGTAGCGGATCGTCTTGATAGCGCTAGCGATTGTAAACAGTC
                                             ||| |||| |||||| |
CGATATTAAGATGACGAATTTGAACGCATATCTTAGCCGATCGTAT
```

One sequence in blast (SeqB)

Σ(11101111011111101) = NAR (=14)

Σ(11111111111111111) = NRM (=17)

Σ(1111111111111111111111111111111111) = NRC (=34)

$$pCover = \frac{NAR}{NRC} \times 100 = \frac{14}{34} \times 100 = 41.2\%$$

NAR: Number of aligned residue in MSP (*Maximum Segment Pair*)

NRM: Number of residue in MSP

NRC: Number of residue in coverage

pCover: Percent coverage between the 2 sequences.