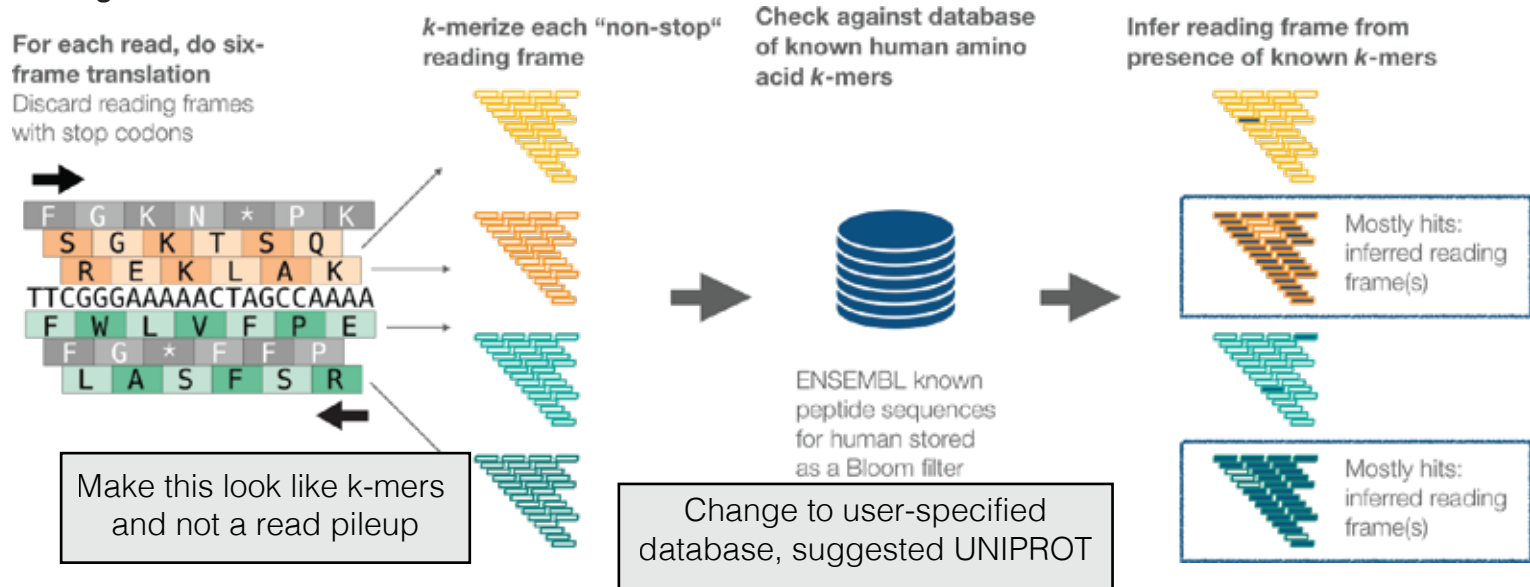


A oolong translate



B

ATGGAAATGTAACATGCATTATATGTGGACAACCCACCATGAA
GAAGAAATGATGTTCTGTGATGTGTGACAGAGTCTGCTG6ATT

Translation in forward direction:

frame +1
LYVDSPTGKK*CVHCVVEVAG ✗ Stop codon

frame +2
YHWTFP*RRNDVL*CV*QRSLD ✗ Stop codon

frame +3
ICQPHREEDHFCVDCGRWI → 53% of 7-mers matched known peptides

Translation in reverse direction:

frame -1
NPATSVTHTEHFFRVGLSTV → 6% of 7-mers matched known peptides

frame -2
IQRPLSHTSQNIISSHWGPFI → 0% of 7-mers matched known peptides

frame -3
SSDLCHTERTSFLRGGVVI* ✗ Stop codon

✓ Accepted reading frame

C

>AB0111133:HKVJ305X:1:2362:27895:31454 2:N:8:TTTACAGCTG+TCATTACATCAT
CTC0076ATGAGGCCAGATGCAAGAGACCAACAGAGGACAGGAGGATCTCAGGAAAACTTTGCTTGGATCCTTGGCAAGACAGATTCTC

>AB0111133:HKVJ305X:1:2362:27895:31454 2:N:8:TTTACAGCTG+TCATTACATCAT translation_frame: -1 jaccard: 1.0
ENLVFGKQFQKIFPCLLGLLALFAGLEDR

>AB0111133:HKVJ305X:1:2362:27895:31454 2:N:8:TTTACAGCTG+TCATTACATCAT translation_frame: -2 jaccard: 0.5185185185185185
KILSLAKDSAGFFLNFSSASCLSLASSTE

UCSC Genome Browser on Human Dec. 2013 (GRCh38/hg38) Assembly



D

