

Input reads

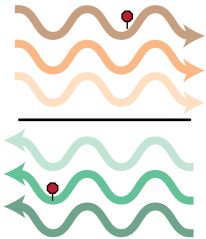
For each read, do
six-frame translation

Discard reading frames
with stop codons

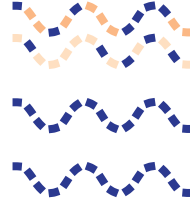
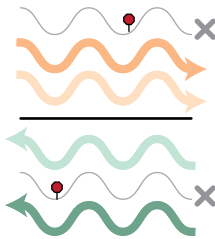
Decompose into
amino acid k -mers

Check k -mer presence
in reference proteome

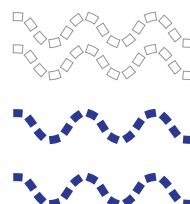
Use reading
frames with k -mer
match to proteome



Translated protein
sequences



Reference
proteome



Accepted reading frames