Dynamic Programming

Standard -Libraries

Arguments
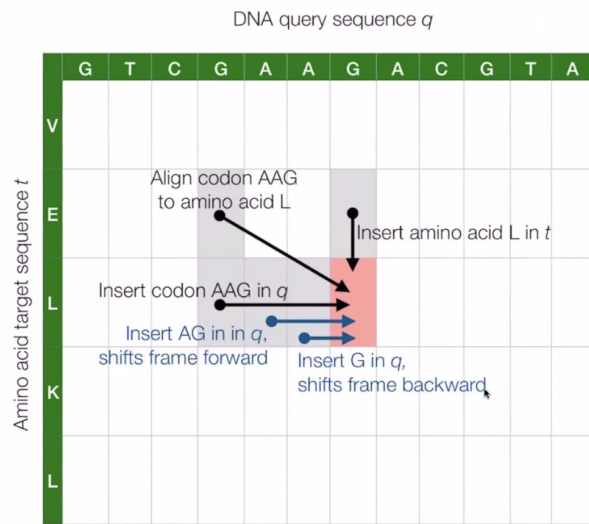- DNA } Input Files
- AA   }
- Gap Penalty
- BLOSUM
- Frameshift Penalty

DNA query sequence q

Amino acid target sequence t

Align codon AAG to amino acid L

Insert amino acid L in t

Insert codon AAG in q

Insert AG in in q, shifts frame forward

Insert G in q, shifts frame backward

\ remove insertion
/ add insertion

Tasks
- Main
  - I/o, Arguments
- Utilities
  - FASTA, Blosum, DNA Lookup
- DP
  - DP, Traceback
- Testcases
  - Documentation, Speed/Runtime assessment
    ↳ GitHub

Discuss if enough time and extend if possible
  Affine Gap Score
  Linear Space