

Dynamic Programming

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Project

- Align two protein sequences using BLOSUM matrix
- Maximize alignment score and print out the optimal alignments

Two Homologous Sequences

- Glyma02g01040.1
MVSQRQRLARKRYKAEHPELFPKPEPTPPKDPEKKKKKKKNSAFKRKRPEP
KPGSRKRHPLRVPGMKPGESCFICKAMDHIAKLCPEKAWEKNIKICLRCRR
RGHRAKNCPEVLDGAKDAMYCYNCGENGHSLTQCPHPLQEGGTFKFAECF
VCNQRGHLKNCPCQNTHTGIYPKGGCCKICGGVTHLAKDCPDKGKSGSVAA
NRPADGWMRIEERP MGQVTKFVSGDDIEDDFMTDDIHSGDKKKPAKSTE
DHVKPKKKEGPKVVNF
- Glyma16g23370.1
QVKKHSHKHCRTCNRCEGFDHHCRLNLCVGRNYTAFLLMIFLLIKGG
TAIAIFIRCFVDRRGIEKELQRKLYVDFPRGVLATICVFLLLLTA YSSAALGQLF
FFHVVLIRKTNTHAIKSIIISLRKTYDYILAMKEENEAMELESFDDSDFSDES
DFDSPEKPTLMSGFLCKGNQGKKALLAAEKARERIMREKPMGEHNSLKPL
PLETKCGPLMNTYKNMDTEDFGSTSFIKGRNESPGRFSSPRRRRFSAGSPT
VFSSMMASPHHKYRSSFDLKLTVSRELETHISRQVLCVSKDDSEPSR

Discussion

- Input: two protein sequences; output: score and optimal alignment
- Subproblem
- Updating rule
- Algorithm
- Time and space complexity
- Implementation
- Evaluation
- Visualization of optimization process
- Challenges and solutions
- Task assignments