CS4054
Bioinformatics

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Exercise 1

- Use global dynamic programming to align the following two sequences. -CAGCA , CG-CTA

- Find the alignment score, fill in the scoring matrix.

- Scoring function:
  - S(match) = 2,
  - S(mismatch) = -1,
 - S(gap, character) = -2

Exercise 2

- Given two DNA sequences to align TCCATCATCTGT and GCATTCTG

- You have a scoring scheme where
  - match gives you +1
  - mismatch gives you 0
  - gap opening costs −10

- Find the alignment, longest common subsequence and alignment score

Exercise 3

- Create Consider the following alignment:

- ACTG-TT-GACCTTACGA

- A-TGTATCGA--TCACTC

- Calculate the score of alignment shown above, using the following scoring rules: +1 for a match, -1 for a mismatch, -1 for a gap.

Exercise 4

- Find the longest path from source to sink
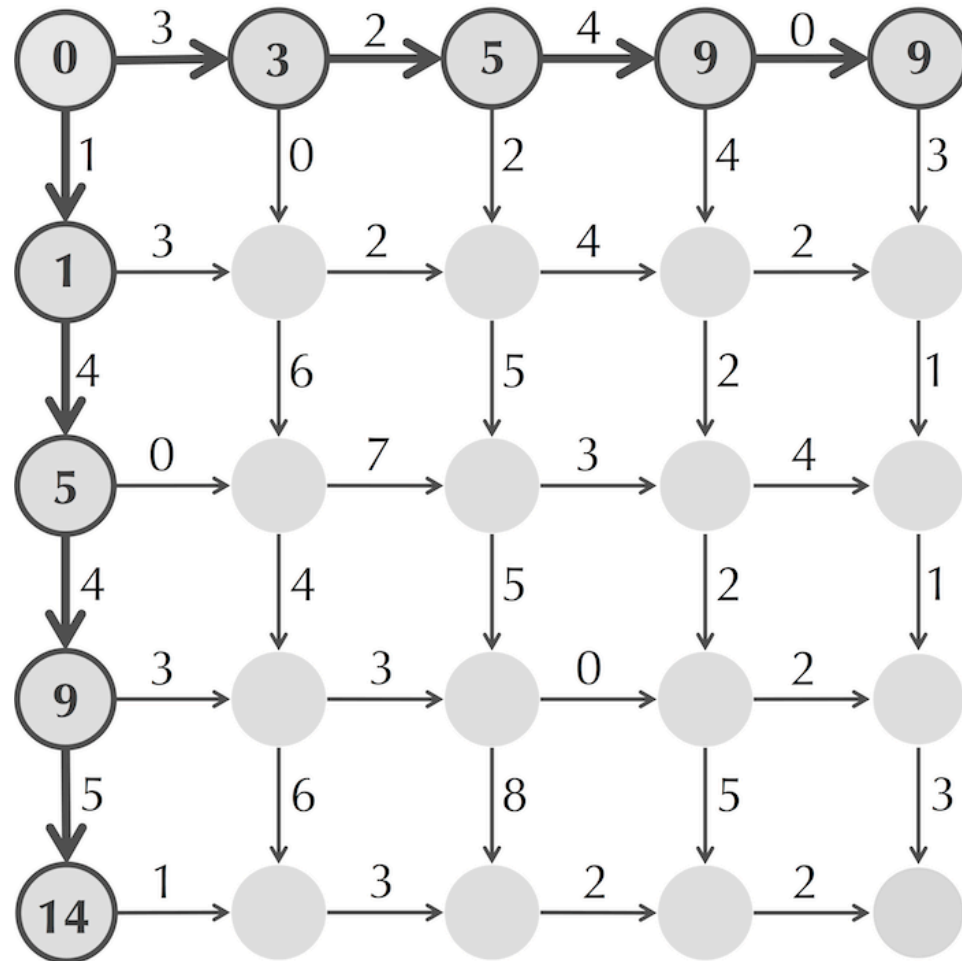
Exercise 5

- Find the shortest path from source to sink