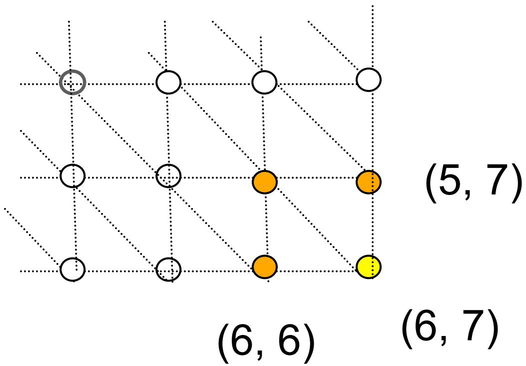
4. Sequence comparison

- How to predict gene/protein functions?
- Why gene/protein sequences may be similar?
- Measuring sequence similarity
- Aligning sequences is an optimization problem
- A sequence alignment as a path
- A path is optimal if all its sub-paths are optimal
- Alignment costs
- A recursive algorithm
- **Recursion can be avoided: an iterative version**
- How efficient is this algorithm?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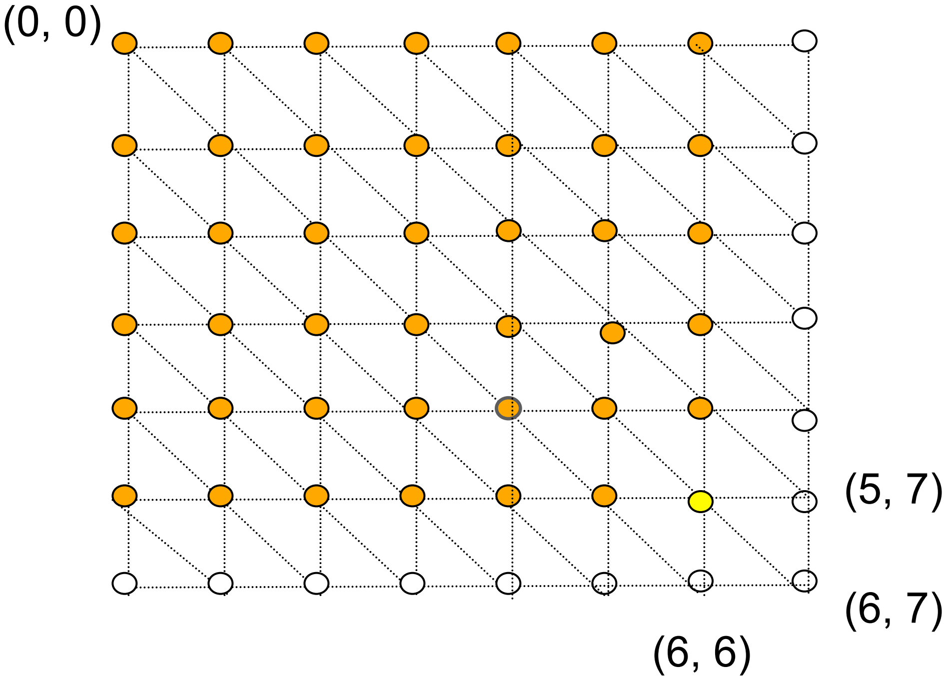
(6, 6)
(6, 7)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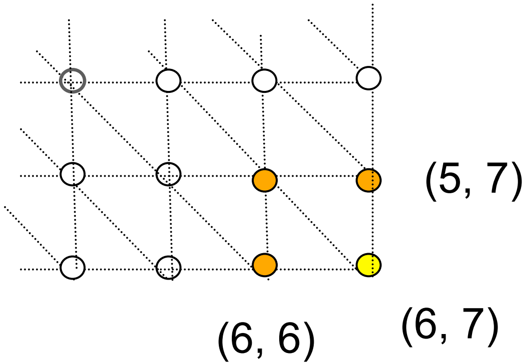
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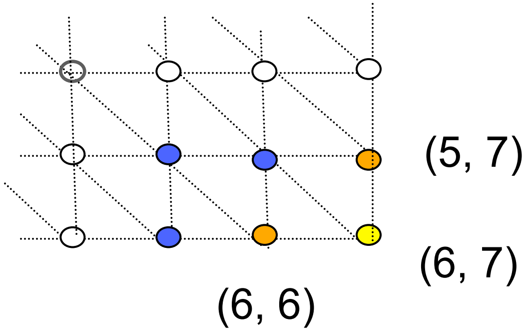
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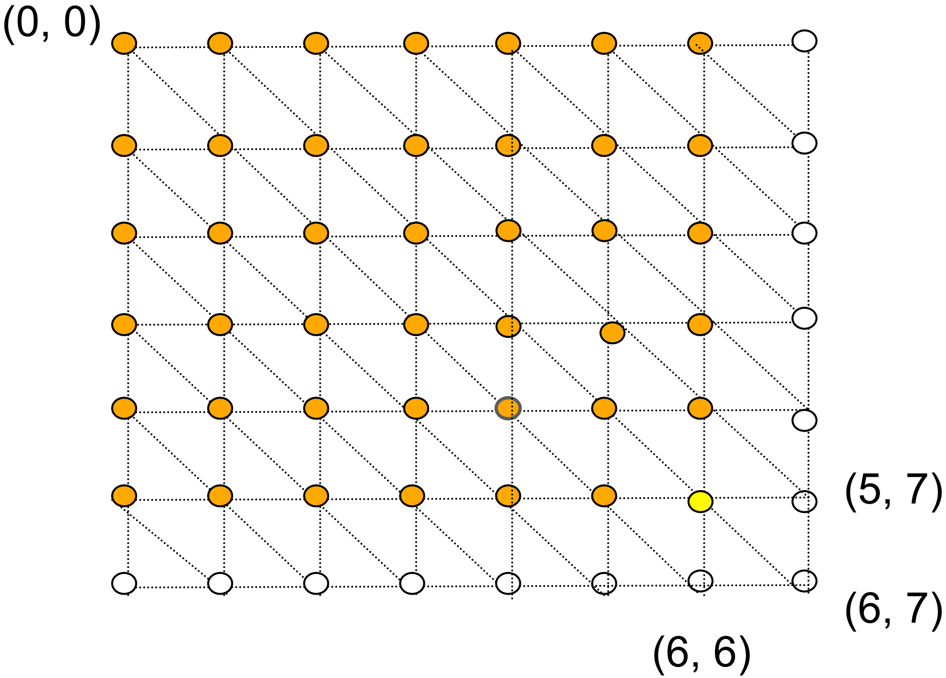
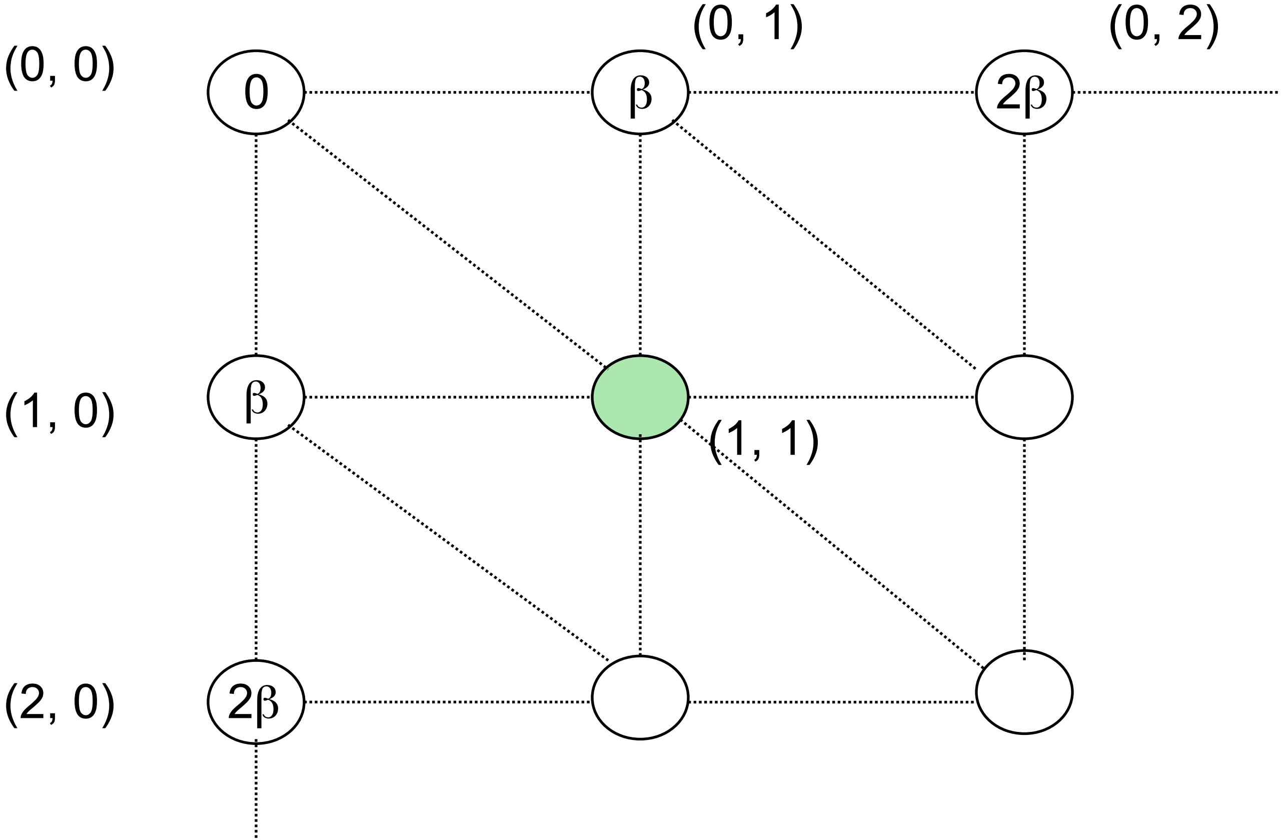
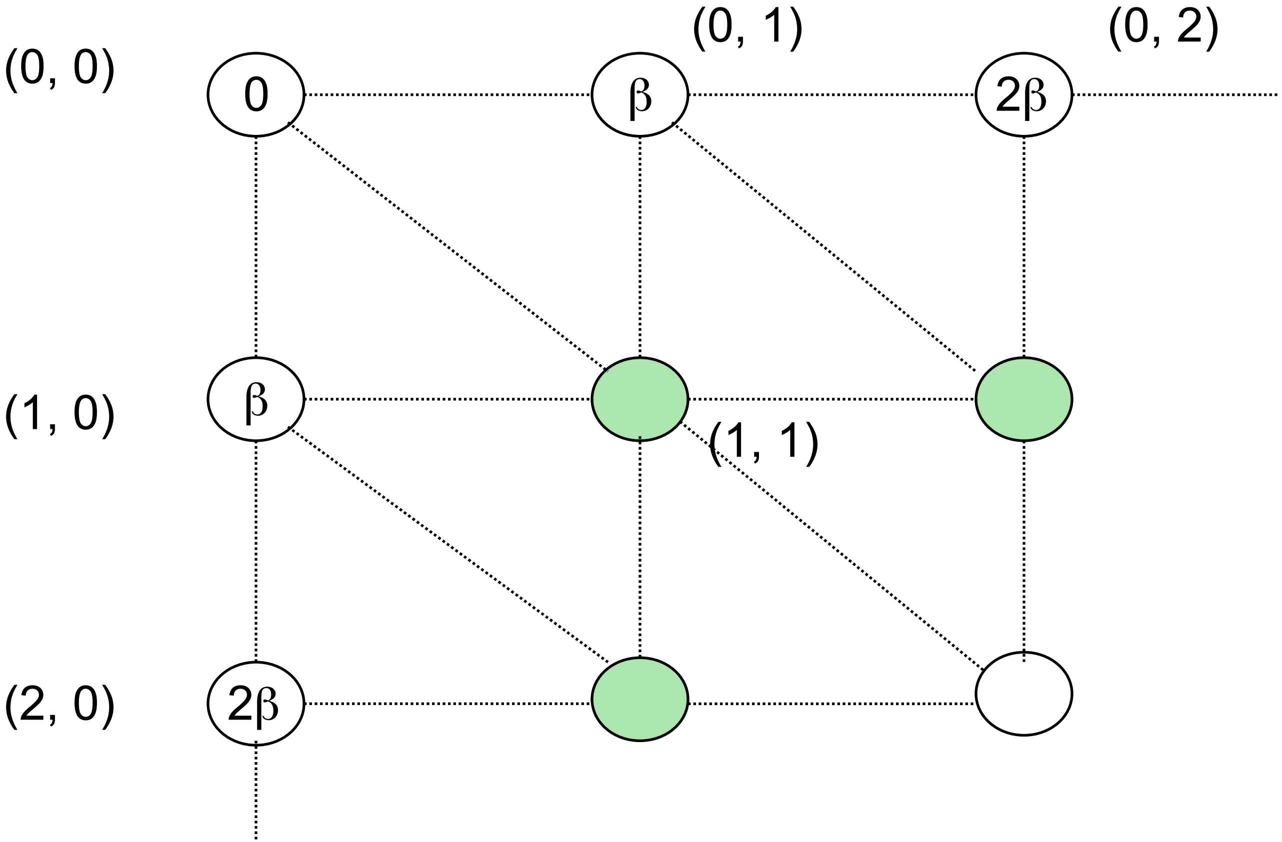
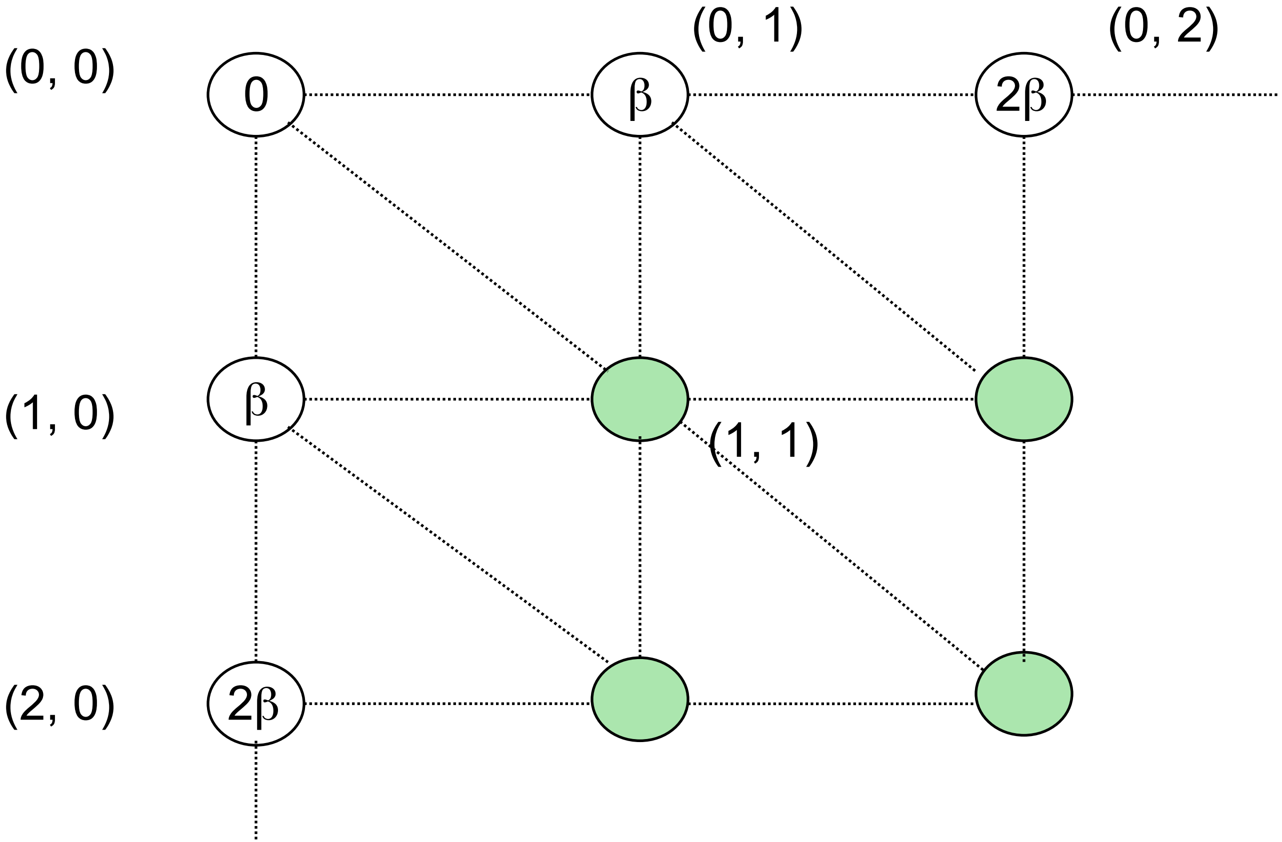

(0, 0)
(5, 7)
(6, 7)
(6, 6)

An iterative algorithm in two phases

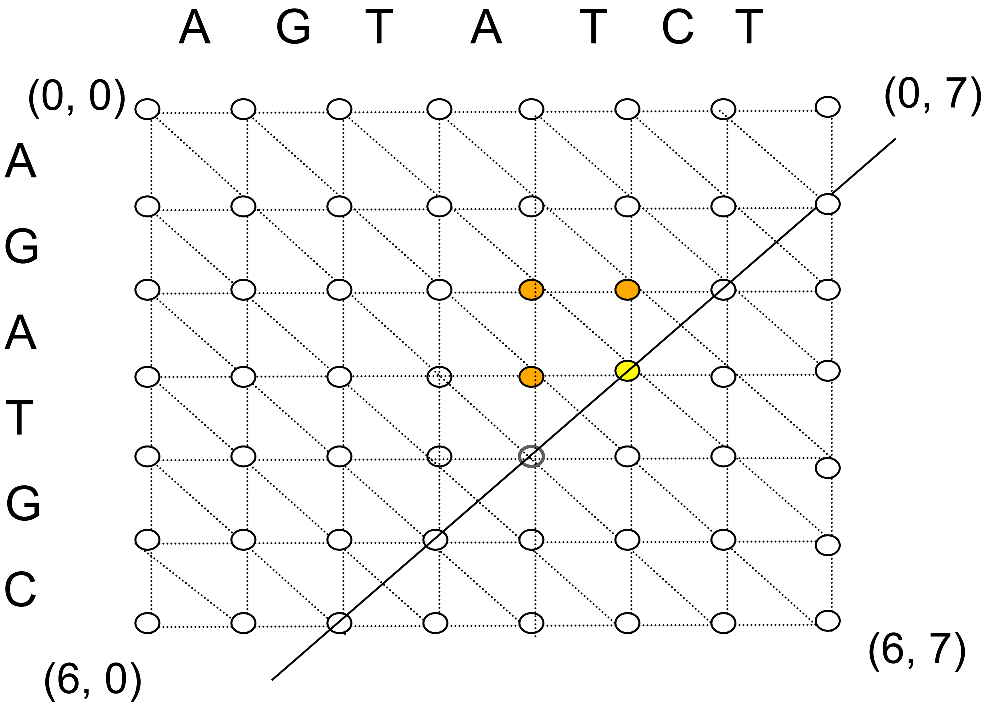
- First phase
  - Compute the cost of the optimal path ending on each node [I, J] starting from node [0, 0] until node [N, M]
  - and store them in a matrix


(0, 0)
0
(0, 1)
β
(0, 2)
2β
(1, 0)
β
(1, 1)
(2, 0)
2β


(0, 0)
0
(0, 1)
β
(0, 2)
2β
(1, 0)
β
(1, 1)
(2, 0)
2β


(0, 0)
(0, 1)
(0, 2)
(1, 0)
(1, 1)
(2, 0)
0
β
2β
β
2β

Parallelization is possible

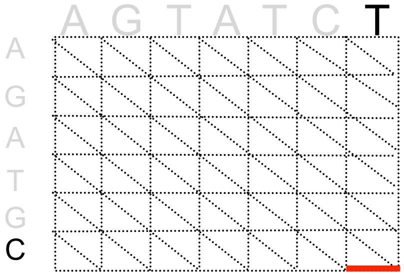


An iterative algorithm in two phases

- First phase
  - Compute the cost of the optimal path ending on each node [I, J] starting from node [0, 0] until node [N, M]
  - and store them in a matrix
- Second phase
  - Compute the optimal paths backwards, from node [N, M] to node [0, 0], using the precomputed costs in the matrix

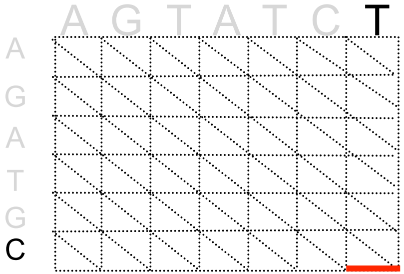
—
T

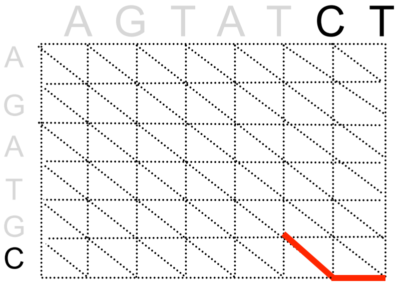
(a)



—
T

(a)



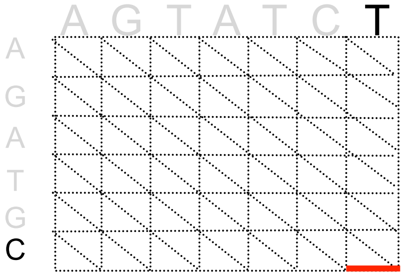


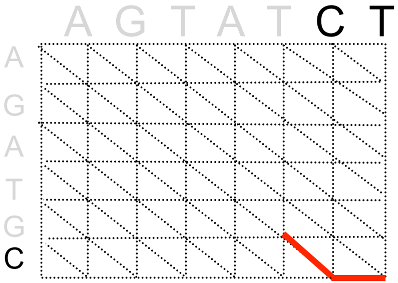
(b)

C —
C T

—
T

(a)





(b)

C —
C T

G C —
T C T

(c)