

BMI/CS 576 – Day 6

- Today
 - Assembly in practice
- Next week
 - Pairwise sequence alignment

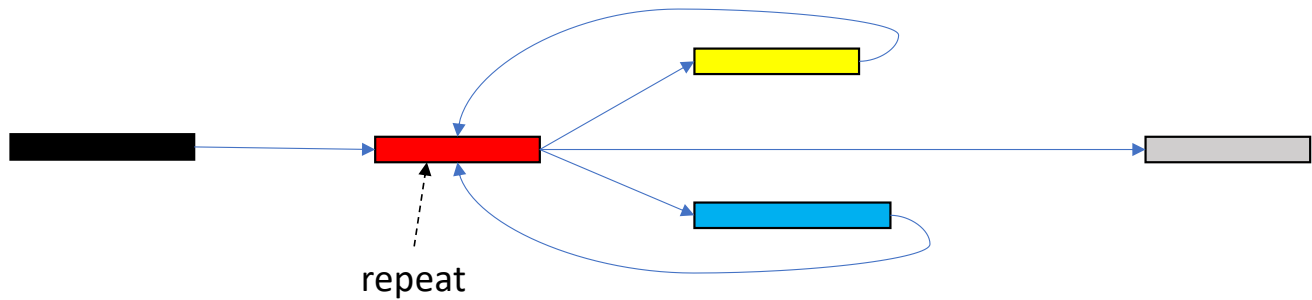
Purchase your Vocareum account

- Grace period expires after Sep 30
- Don't let this interrupt your coursework

Quiz: challenges in genome assembly

- Challenges
 - sequencing errors
 - uneven coverage of the genome by reads
 - repeats
- Things that make genome assembly easier
 - Paired-end reads
 - Long reads
 - High-quality reads

Paired-end reads help to order contigs



contigs:



possible full genome assemblies:

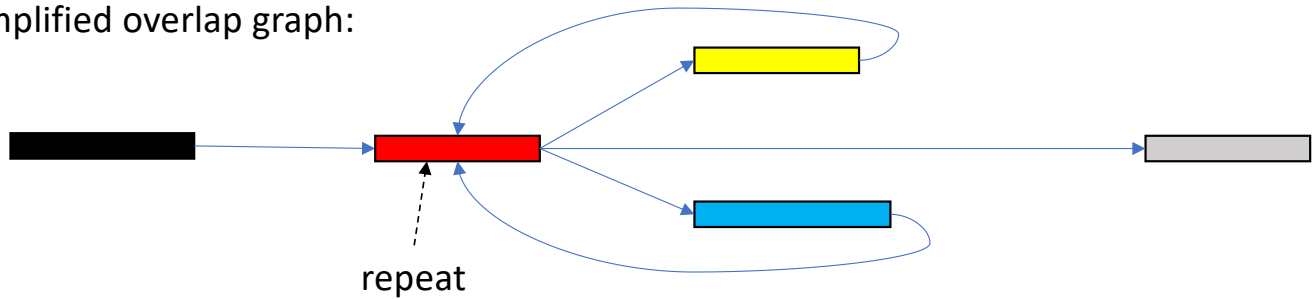


or



Repeats split assemblies into contigs

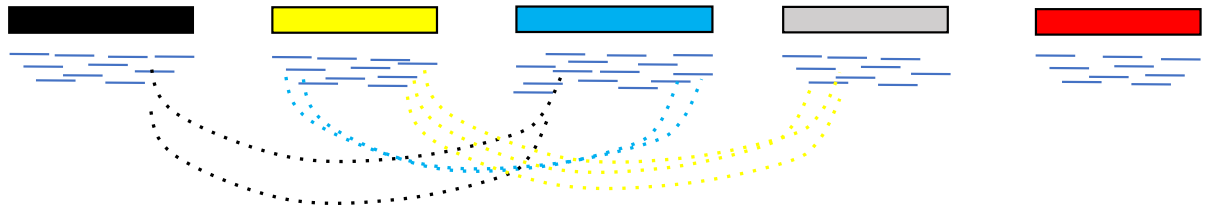
simplified overlap graph:



contigs:

reads:

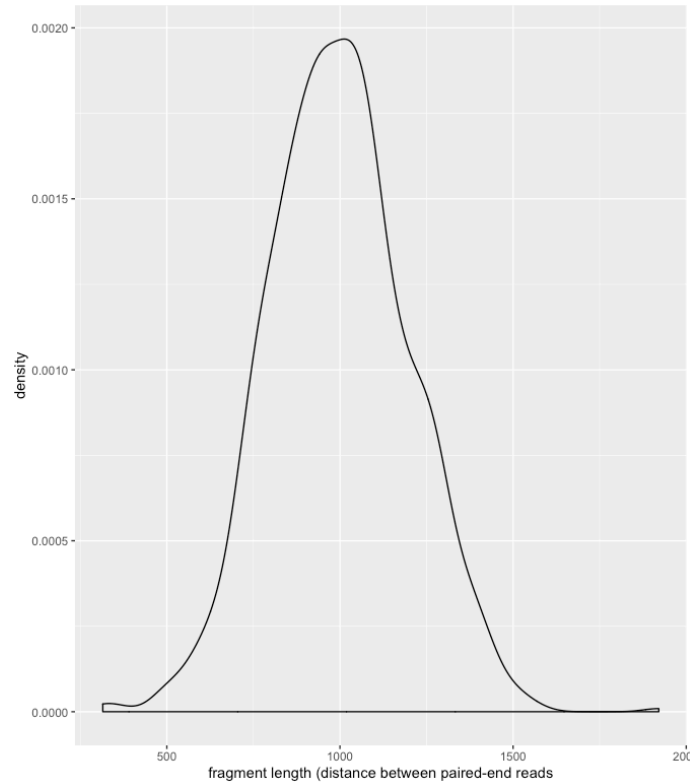
paired-end links:



Inferred genome assembly



Fragment length distributions

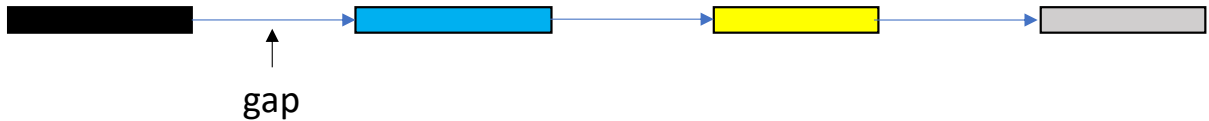


Fragment length distribution (range of fragment lengths) is controlled such that distance between paired-end reads can be estimated

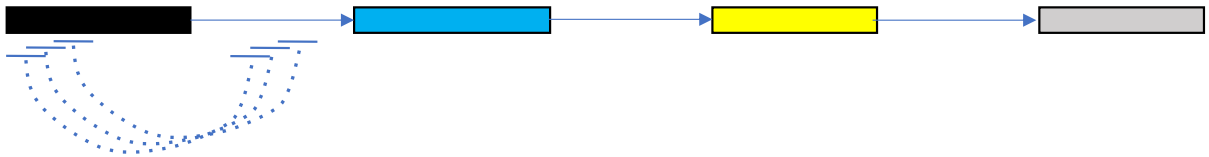
Gaps

Sometimes the repetitive sequences are complicated and you just get this:

Scaffold:



Paired-end reads can sometimes be used to fill in the gaps:



Sequence alignment

Brute force and dynamic
programming algorithms

Outline

- The space of global alignments
- Dynamic programming algorithms

Pairwise Alignment: Task Definition

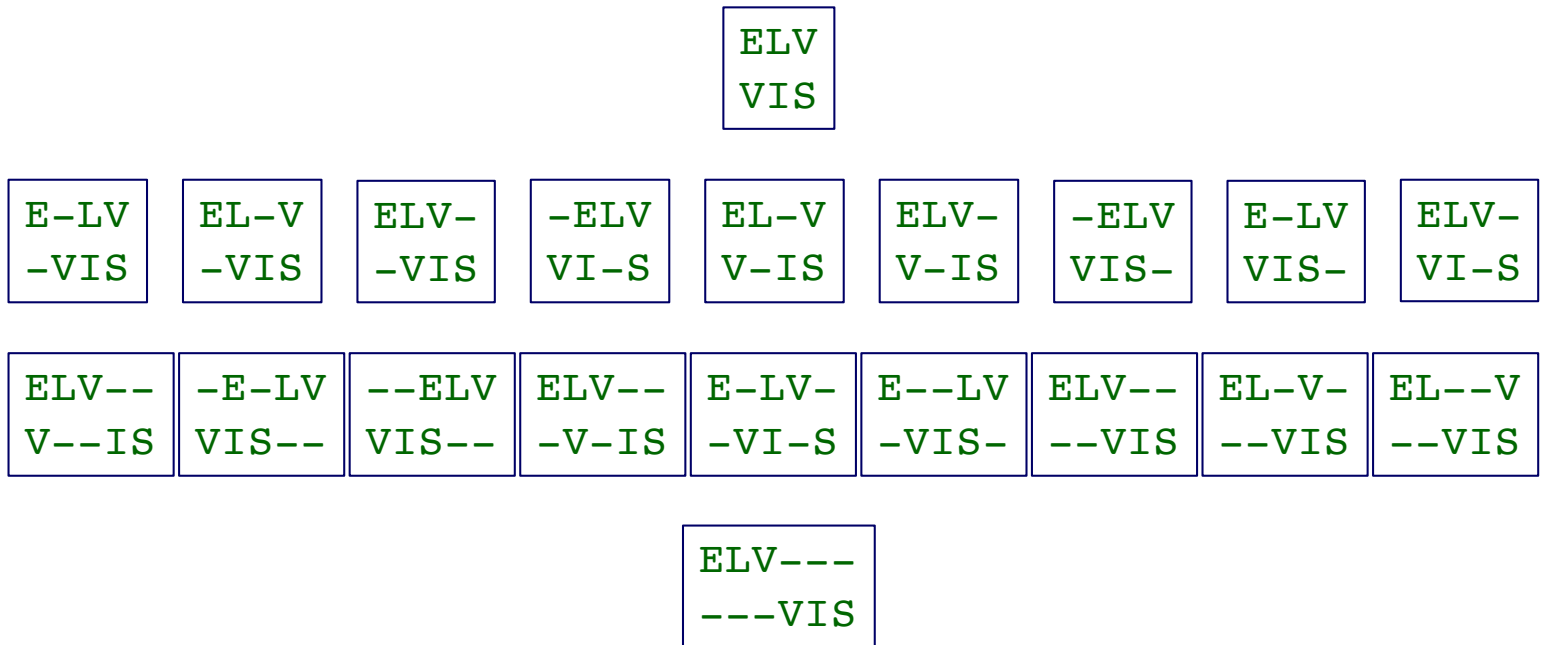
- Given
 - a pair of sequences (DNA or protein)
 - a method for scoring a candidate alignment
- Do
 - find an alignment for which the score is maximized

The brute force algorithm

```
best_alignment = null
for each possible alignment, a, of the sequences:
    if score(a) > score(best_alignment):
        best_alignment = a
return best_alignment
```

The Space of Global Alignments

the possible global alignments for **ELV** and **VIS**



Number of Possible Alignments

- given sequences of length m and n
- assume we don't count as distinct $\begin{array}{c} \text{C-} \\ \text{-G} \end{array}$ and $\begin{array}{c} \text{-C} \\ \text{G-} \end{array}$
- we can have as few as 0 and as many as $\min\{m, n\}$ aligned pairs
- therefore the number of possible alignments is given by

$$\sum_{k=0}^{\min\{m, n\}} \binom{n}{k} \binom{m}{k} = \binom{n+m}{n}$$

Number of Possible Alignments

- there are
$$\binom{2n}{n} = \frac{(2n)!}{(n!)^2} \approx \frac{2^{2n}}{\sqrt{\pi n}}$$

possible global alignments for 2 sequences of length n

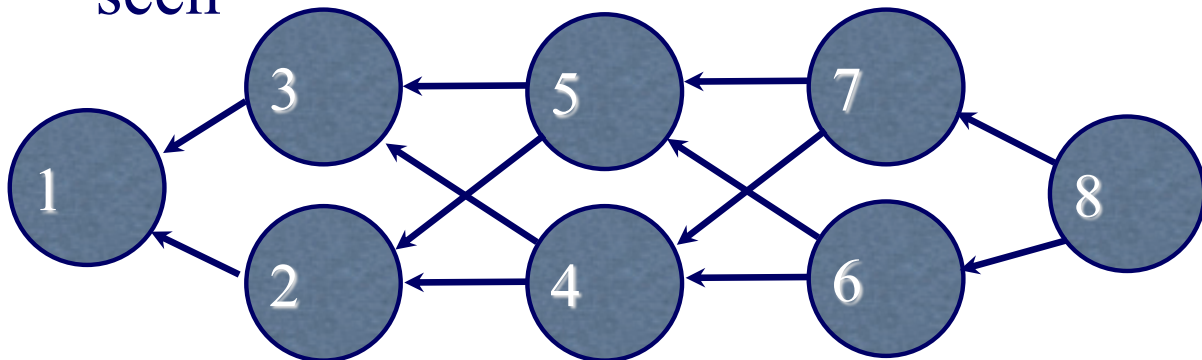
- e.g. two sequences of length 100 have $\approx 10^{59}$ possible alignments
- but we can use *dynamic programming* to find an optimal alignment efficiently

Dynamic Programming

- Algorithmic technique for optimization problems that have two properties:
 - *Optimal substructure*: Optimal solution can be computed from optimal solutions to subproblems
 - *Overlapping subproblems*: Subproblems overlap such that the total number of distinct subproblems to be solved is relatively small

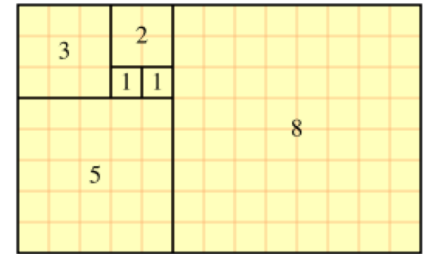
Dynamic Programming

- Break problem into overlapping subproblems
- use *memoization*: remember solutions to subproblems that we have already seen

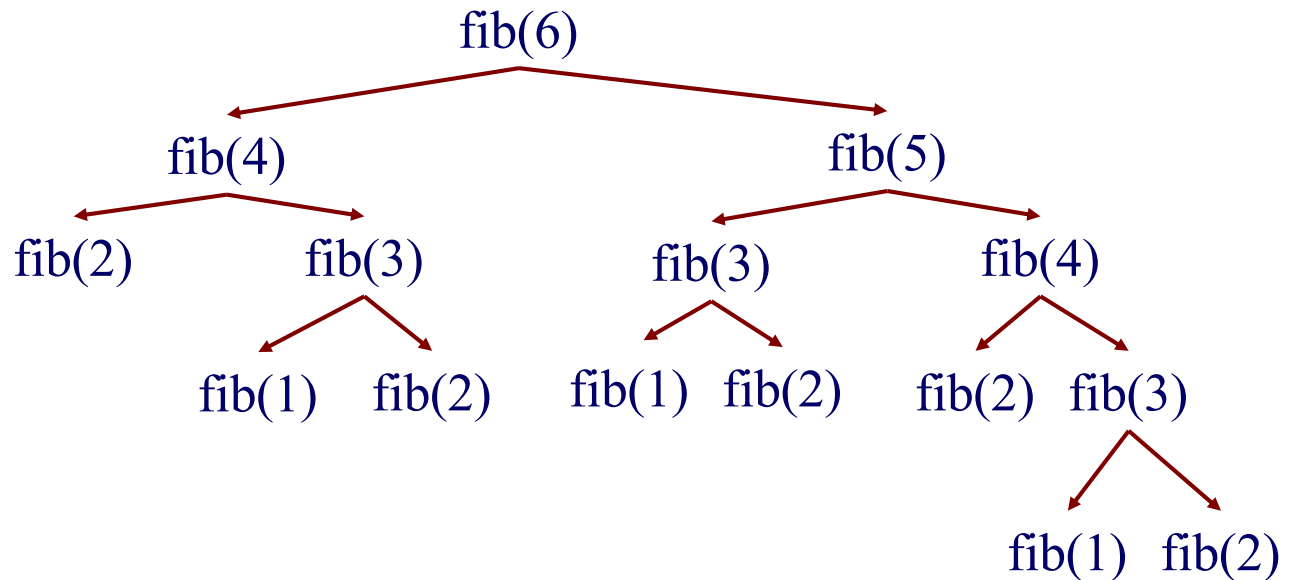


Fibonacci example

- 1,1,2,3,5,8,13,21,...
- $fib(n) = fib(n - 2) + fib(n - 1)$
- Could implement as a simple recursive function
- However, complexity of simple recursive function is exponential in n



Recursive Fibonacci call stack



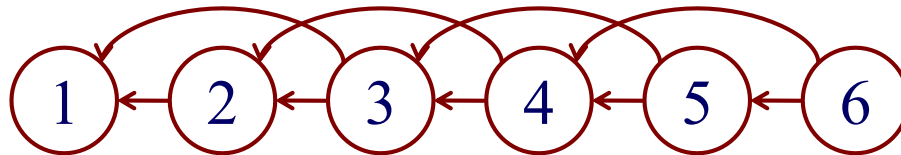
15 calls – only 6 unique calls

Fibonacci dynamic programming

- Two approaches
 1. *Memoization*: Store results from previous calls of function in a table (top down approach)
 2. Solve subproblems from smallest to largest, storing results in table (bottom up approach)
- Both require evaluating all $(n-1)$ subproblems only once: $O(n)$

Dynamic Programming Graphs

- Dynamic programming algorithms can be represented by a directed acyclic graph
 - Each subproblem is a vertex
 - Direct dependencies between subproblems are edges



graph for fib(6)

Why “Dynamic Programming”?

- Coined by Richard Bellman in 1950 while working at RAND
- Government officials were overseeing RAND, disliked research and mathematics
- “programming”: planning, decision making (optimization)
- “dynamic”: multistage, time varying
- “It was something not even a Congressman could object to. So I used it as an umbrella for my activities”

Summary

- The space of possible alignments is huge!
- Brute force algorithms are infeasible
- Dynamic programming will offer a solution
- Two properties of dynamic programming problems
 - Optimal substructure
 - Overlapping subproblems