

Introduction to Dynamic Programming

About me

- Carlos Gonzalez Oliver
- carlos@ozeki.io
- carlosoliver.co

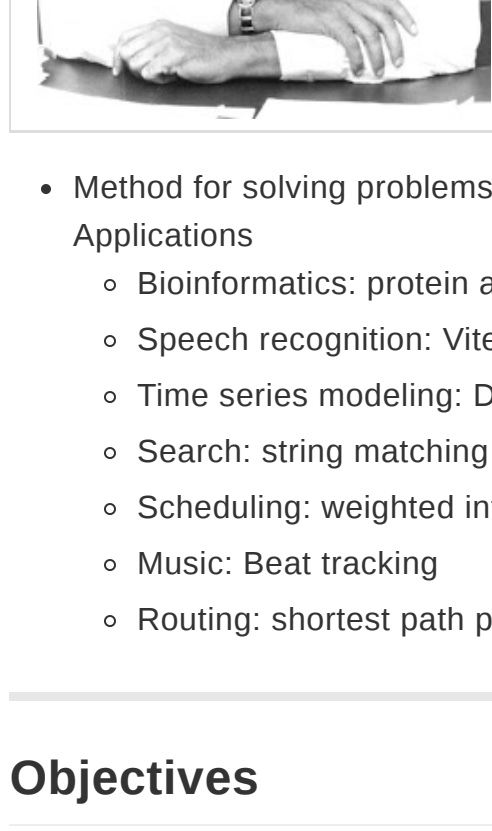
My interests:

- Structural Bioinformatics
- Graph algorithms
- Representation learning

Some questions I ask:

- How can we efficiently search through graph databases?
- What kinds of patterns can we discover in datasets of graphs?
- Can we model biological systems using efficient data structures to learn about how they function?

Dynamic Programming (DP)



- Roger Bellman, 1950s, working at RAND institute.
- Picked the name "Dynamic Programming" to please his boss.

- Method for solving problems by constructing the solution bottom-up.

- Applications
- Bioinformatics: protein and RNA folding, sequence alignment
 - Speech recognition: Viterbi's algorithm
 - Time series modeling: Dynamic time warping
 - Search: string matching
 - Scheduling: weighted interval
 - Music: Beat tracking
 - Routing: shortest path problems

Objectives

After this talk we should be able to:

- ☐ Recognize the ingredients needed to solve a problem with DP.
- ☐ Write down and execute some simple DP algorithms.
- ☐ Be able to implement a DP algorithm for a real-world problem (homework).

Basic Intuition

- What is:
 - $1+1+1+1+1+1=?$
- Now what is:
 - $1+1+1+1+1+1=?$

Second ingredient: Overlapping Substructures

The same subproblem's solution is used multiple times.

```
def fib(n):
    if n == 0 or n == 1:
        return 1
    else:
        return fib(n-1) + fib(n-2)
```

Call tree `fib(6)`:

Recursive solution is $O(2^n)$.

An example *without* overlapping subproblems.

Binary Search

```
def binary_search(A, left, right, query):
    if low > high:
        return None

    mid = (left + right) // 2
    if A[mid] == query:
        return 1
    elif A[mid] > query:
        return binary_search(A, left, mid-1, query)
    else:
        return binary_search(A, mid+1, right, query)
```

Call tree `binary_search(A=[15, 22, 32, 36, 41, 63, 75], left=0, right=4, query=75)`:

Case study: Weighted Interval Scheduling

- **Input:** n requests, labeled $\{1, \dots, n\}$. Each request has a start time s_i and an end time f_i , and a weight v_i .
- **Output:** a compatible subset S of $\{1, \dots, n\}$ that maximizes $\sum_{i \in S} v_i$.

S is compatible iff all pairs of intervals in S are non-overlapping.

- Uses: resource allocation for computer systems, optimizing course selection.

Example:

False start: greedy approach

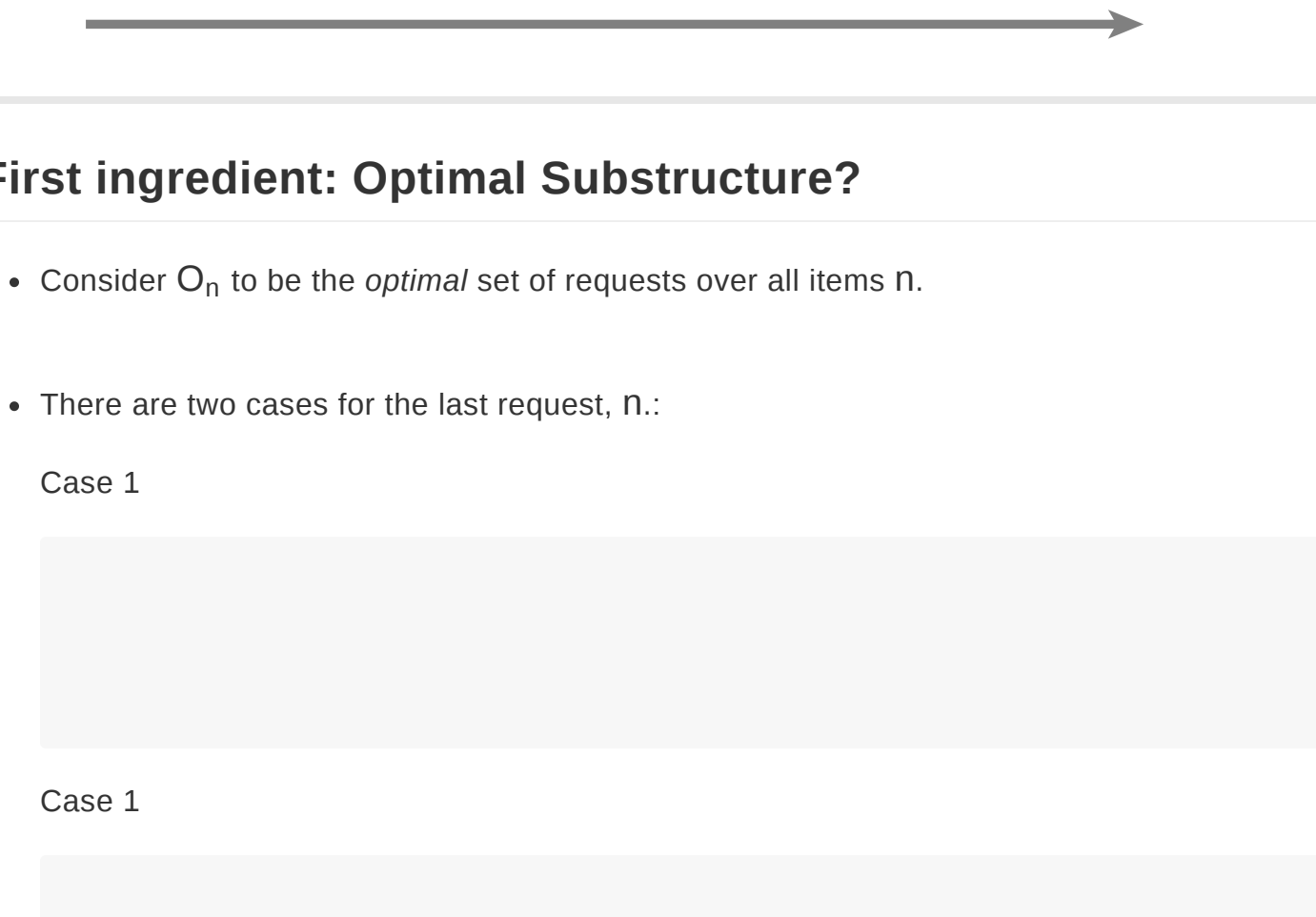
- From "previous" lectures we know the greedy approach to the unweighted IS problem gives the optimal solution (i.e. pick item with earliest ending time)

Counterexample:

A helper function

Let us sort all intervals by increasing finish time and let $P(j)$ return the latest interval i that is still compatible with j .

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First ingredient: Optimal Substructure?

- Consider O_n to be the *optimal* set of requests over all items n .

- There are two cases for the last request, n :

Case 1

Case 1

Implication?

Optimal Substructure

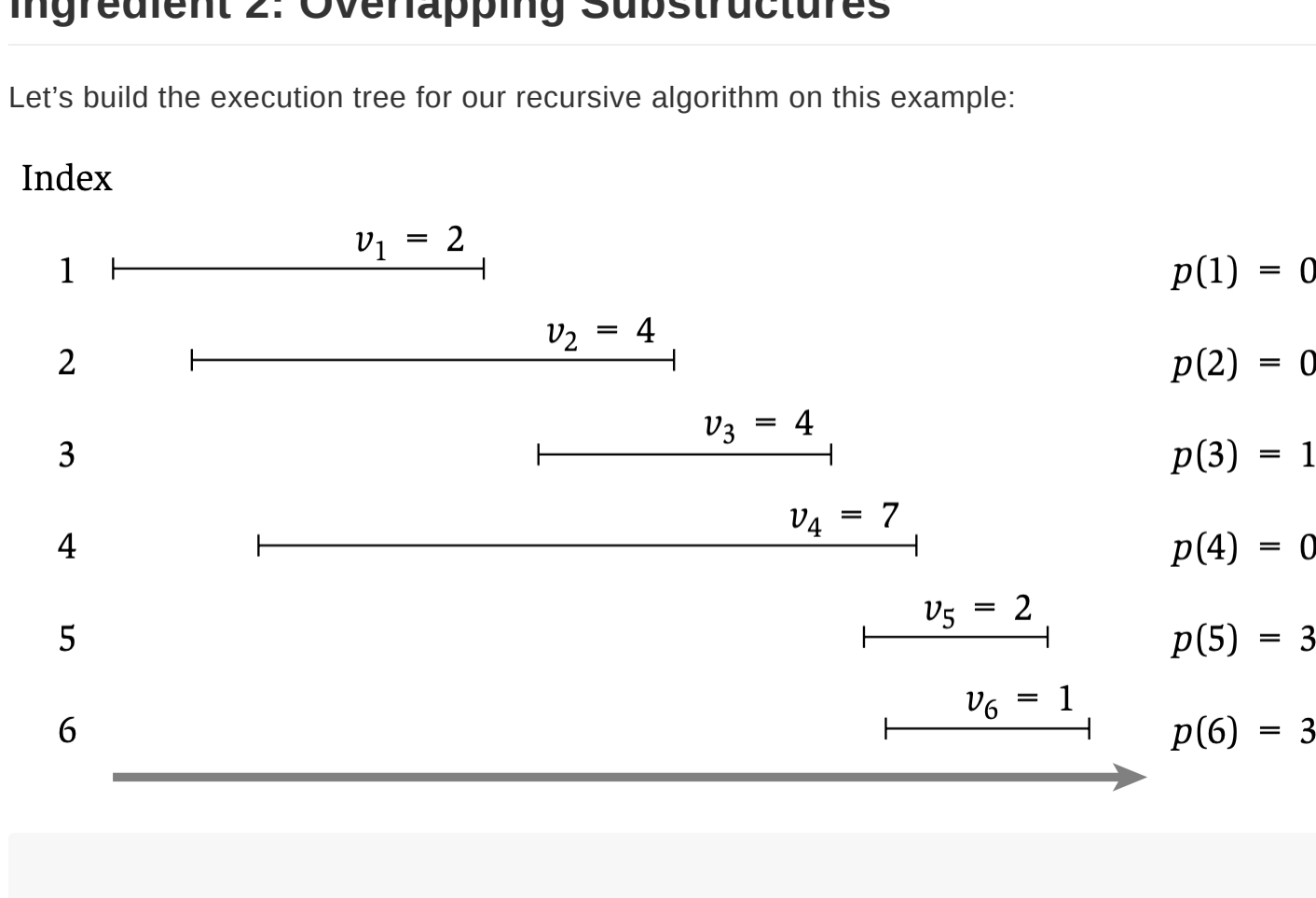
Let $OPT(j)$ be the total weight of the optimal over intervals up to j .

We can now write an expression for computing $OPT(j)$:

```
compute_OPT(j):
```

Ingredient 2: Overlapping Substructures

Let's build the execution tree for our recursive algorithm on this example:



Runtime:

Ingredients

- ☒ Optimal Substructure
- ☒ Overlapping Subproblems

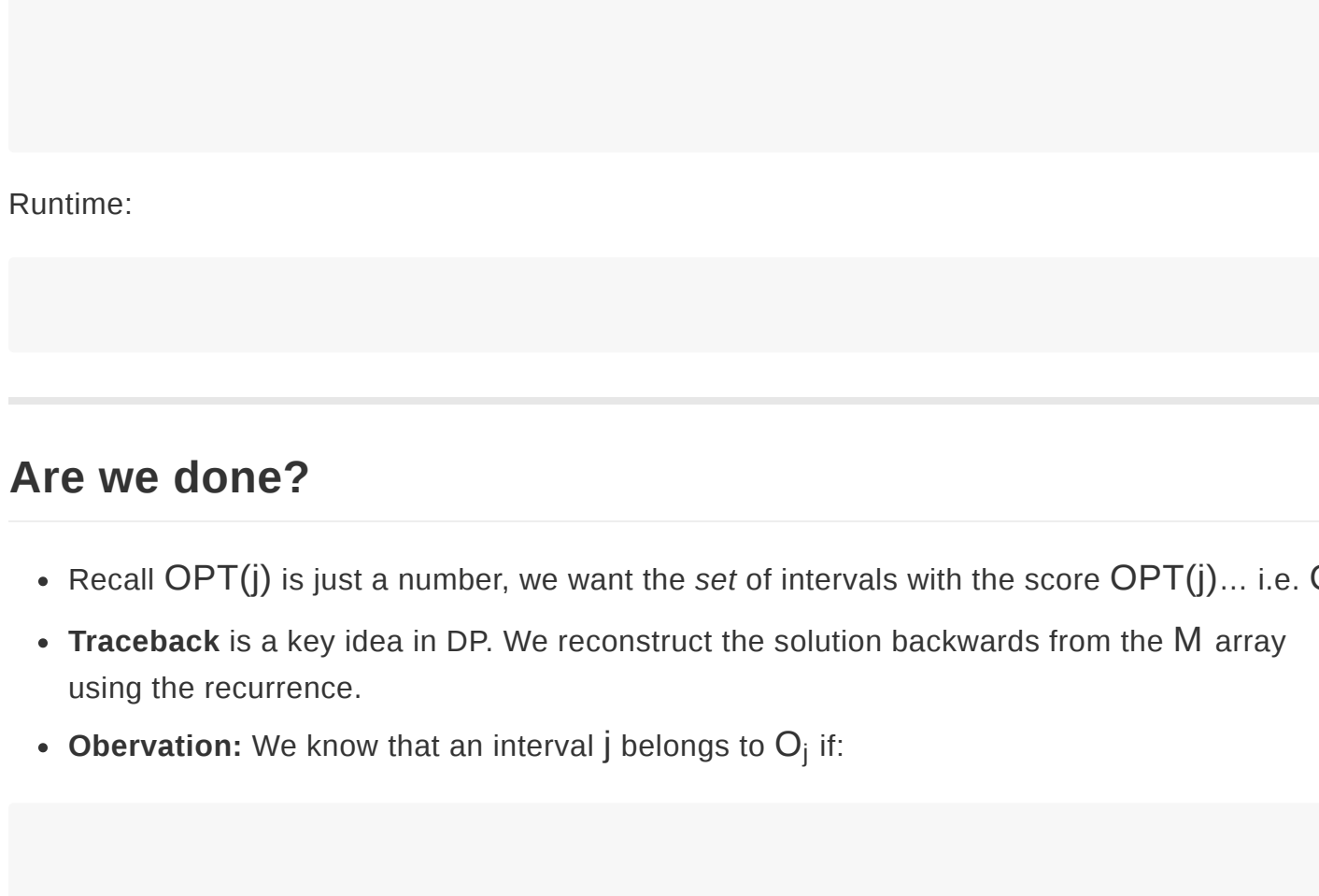
First algorithm

Now we can write down a recursive algorithm that gives us the maximum weight over $1, \dots, n$.

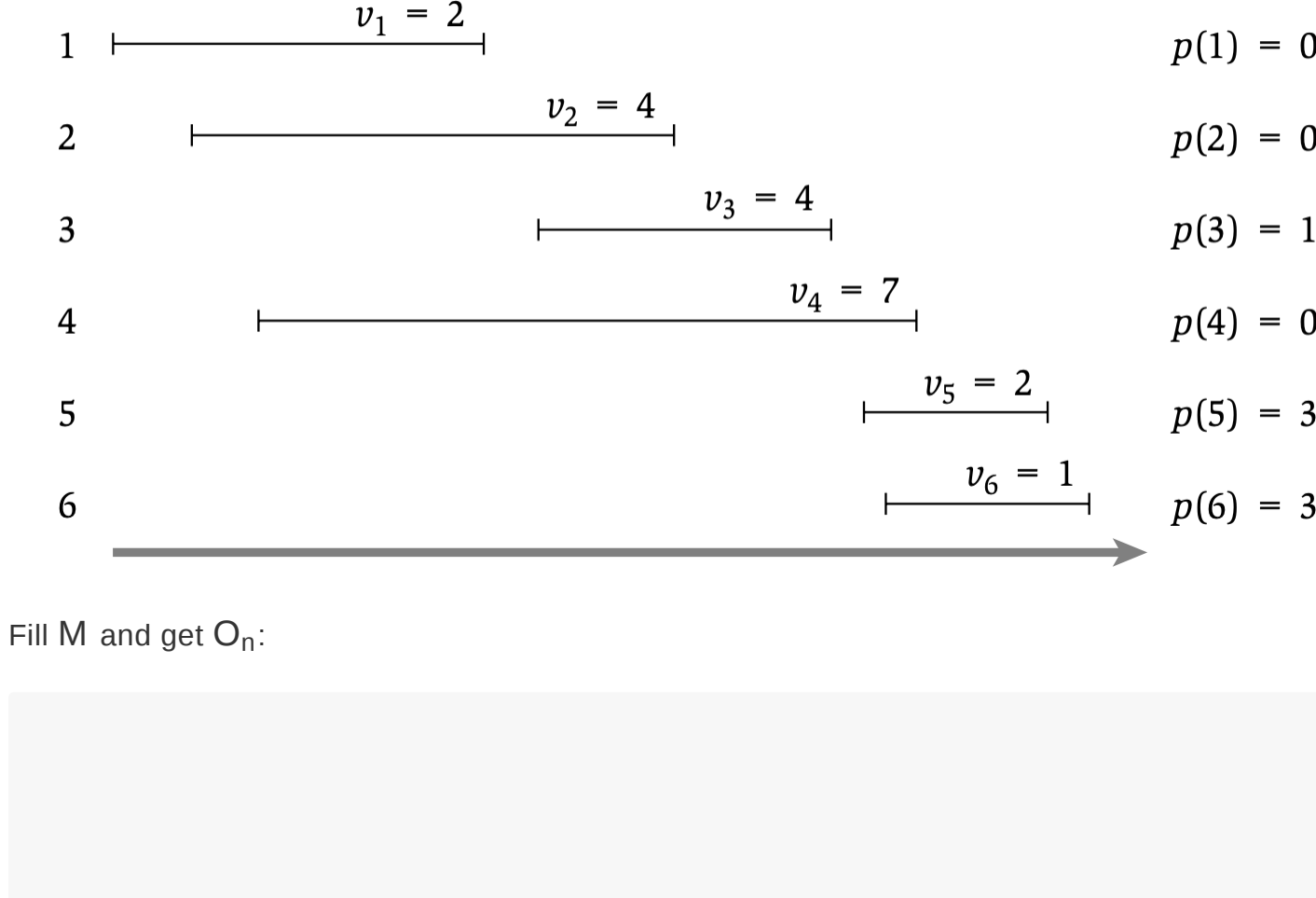
```
compute_OPT(j):
```

Ingredient 2: Overlapping Substructures

Let's build the execution tree for our recursive algorithm on this example:



Full Example



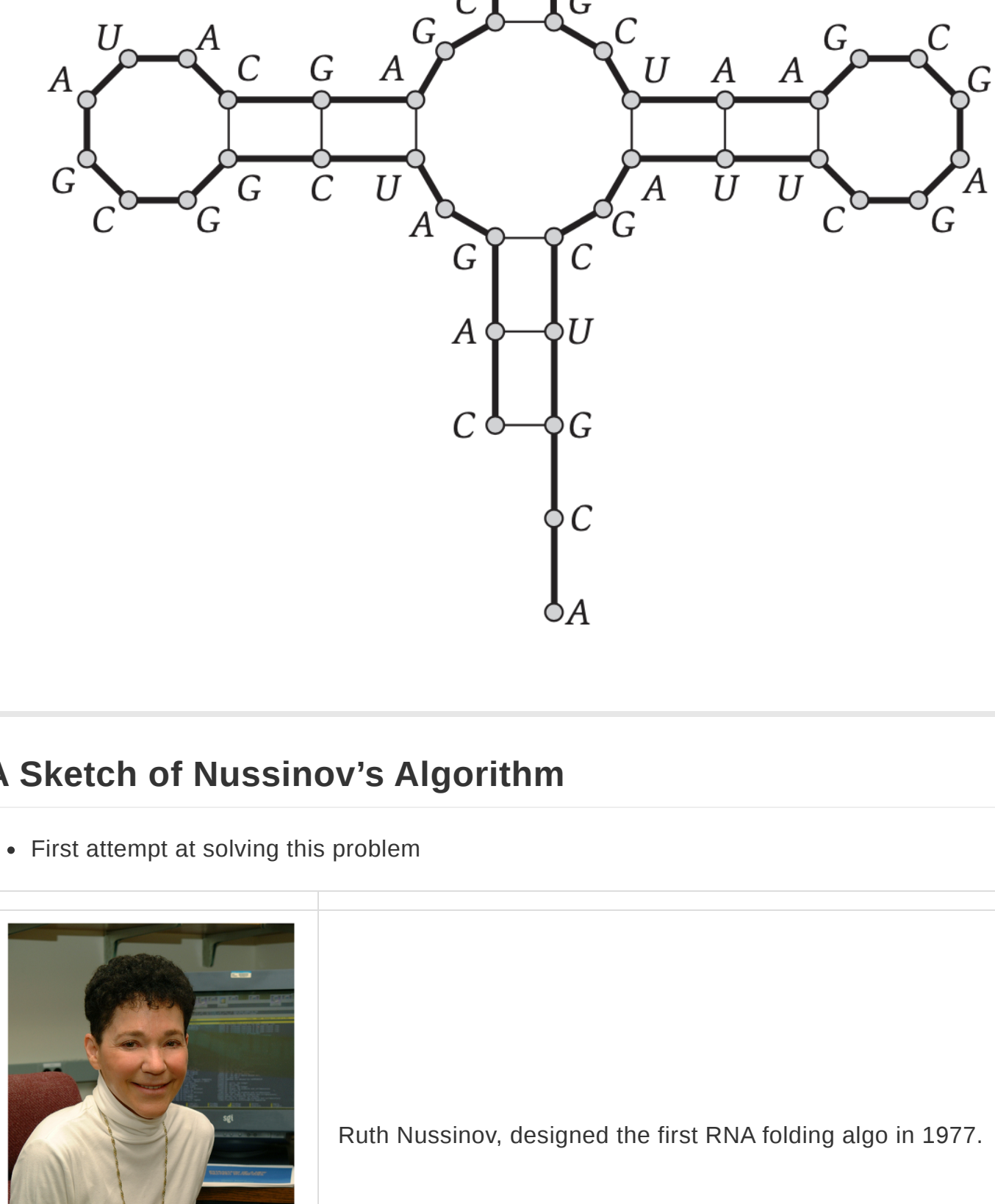
Fill M and get O_n :

Recap

- Dynamic Programming works well when we have a problem structure such that:
 - Combining sub-problems solves the whole problem
 - Sub-problems overlap
- We can often reduce runtime complexity from exponential to polynomial or linear.

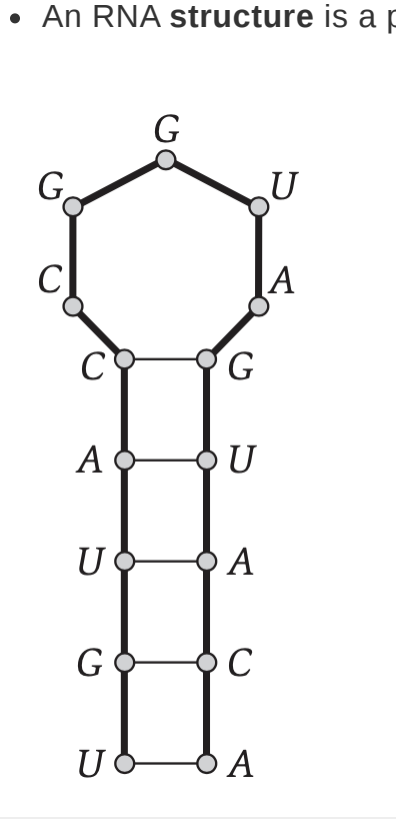
General interest: RNA folding

- RNA molecules are essential to all living organisms.
- Knowing the sequence is easy but not so informative, knowing the structure is hard but tells us a lot about the molecule's function.



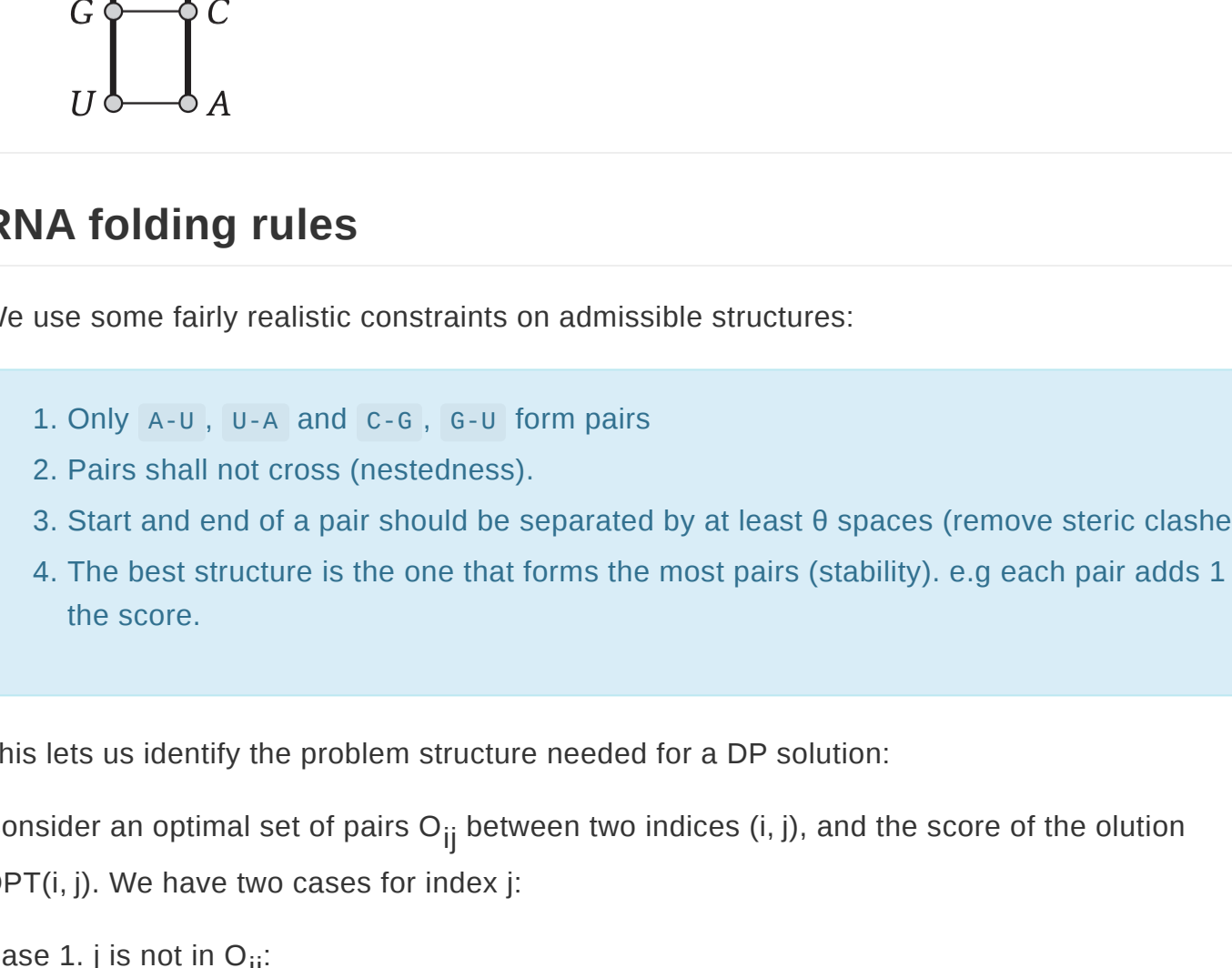
A Sketch of Nussinov's Algorithm

- First attempt at solving this problem



Ruth Nussinov, designed the first RNA folding algo in 1977.

- In CS terms, an RNA is a string on a 4-letter alphabet.
- An RNA **structure** is a pair of indices over the string with certain constraints.



RNA folding rules

We use some fairly realistic constraints on admissible structures:

1. Only $A-U$, $U-A$ and $G-C$, $C-G$ form pairs
2. Pairs shall not cross (nestedness).
3. Start and end of a pair should be separated by at least 0 spaces (remove steric clashes).
4. The best structure is the one that forms the most pairs (stability). e.g. each pair adds 1 to the score.

This lets us identify the problem structure needed for a DP solution:

Consider an optimal set of pairs O_{ij} between two indices (i, j) , and the score of the solution $OPT(i, j)$. We have two cases for index j :

Case 1. j is not in O_{ij} :

Note we introduce a new variable \rightarrow 2 dimensional DP.

Case 2. j is in O_{ij} :

Ingredients?

- ☐ Optimal substructures
- ☐ Overlapping subproblems

From this we can build our recurrence that fills the table up to $OPT(1, L)$.

Bonus Questions: What is the runtime for filling the table?

If you want an exercise sheet to learn how to implement this send me an email
carlos@ozeki.io.