## Quiz

Jeremy Lin has created a time machine. Now, he knows exactly the price of $\$$ GME for the next $n$ days, which are $p_{1}, p_{2}, \cdots, p_{n}$.

Suppose Jeremy can only trade \$GME for at most $t$ times.
So, what is the best trading?

Let $w_{k, t}$ be the network at $k$-th day using $t$ trades.

$$
w_{k, t}=\max \left(w_{k-1, t}, \max _{j<k}\left(w_{j, t-1} \frac{p_{k}}{p_{j}}\right)\right) .
$$

This solution technically is wrong. What is the mistake?
I omitted initial cases.

## CSE 421

# Dynamic Programming <br> RNA, Sequence Alignment 

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## Announcement

- HW5 will be posted tonight. Sorry for the late.
- Swati OH is moved to Sunday (virtual). See website.
- Midterm is graded. Check your score on Canvas.
- Come to any OH for any grading mistakes.
- Come to my OH to get back the midterm (for in-person midterm)
- I will post the midterm solution tonight.


## Midterm

Here is the statistics

| percentile | Q1 | Q2 | Q3 | Q4 | Q5 | Total |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| $25 \%$ | $12(75 \%)$ | $17.5(72 \%)$ | $6.5(65 \%)$ | $3(20 \%)$ | $18(72 \%)$ | $66(73 \%)$ |
| $50 \%$ | $14(88 \%)$ | $21(87.5 \%)$ | $9(90 \%)$ | $8(53 \%)$ | $24(96 \%)$ | $72.8(81 \%)$ |
| $75 \%$ | $16(100 \%)$ | $21(87.5 \%)$ | $10(100 \%)$ | $14.5(97 \%)$ | $25(100 \%)$ | $80.8(90 \%)$ |

Q4 is the hardest one.
It is modified from some problem in a programming contest.
If you get >=50/90 in this midterm, you are on track for a 3.4 (depending on your homework)

## Midterm

- $n \cdot 2^{\log ^{2} n}$ is not $O\left(n^{3}\right)$.

Note that $n \cdot 2^{\log ^{2} n}=n^{1+\log n}$ which is not even polynomial.

- Some write $n^{\log _{2} 4}$. Please write $n^{2}$ instead.
- Don't write a large ambiguous paragraph to describe your algo. Use pseudo code instead. We will deduct point in final.
- MST takes $O(m \log n)$ or $O(m+n \log n)$, but not $O(n \log n)$.
- Q5, you don't need to do induction.


## Knapsack Problem

Given $n$ objects and a "knapsack."
Item $i$ weighs $w_{i}>0$ kilograms and has value $v_{i}>0$.


Knapsack has capacity of $W$ kilograms.
Goal: fill knapsack so as to maximize total value.

Ex: OPT is $\{3,4\}$ with value 40 .

|  | Item | Value | Weight |
| :---: | :---: | :---: | :---: |
|  | 1 | 1 | 1 |
| $W=11$ | 2 | 6 | 2 |
|  | 3 | 18 | 5 |
|  | 4 | 22 | 6 |
|  | 5 | 28 | 7 |

Greedy: repeatedly add item with maximum ratio $v_{i} / w_{i}$.
Ex: $\{5,2,1\}$ achieves only value $=35 \Rightarrow$ greedy not optimal.

## Stronger DP (Strengthening Hypothesis)

Let $O P T(i, w)=$ Max value of subsets of items $1, \ldots, i$ of weight $\leq w$
Case 1: OPT $(i, w)$ selects item $i$

- In this case, $\operatorname{OPT}(i, w)=v_{i}+O P T\left(i-1, w-w_{i}\right)$

Case 2: OPT( $i, w)$ does not select item $i$
Take best of the two

- In this case, $\operatorname{OPT}(i, w)=O P T(i-1, w)$.

Therefore,

$$
\operatorname{OPT}(i, w)= \begin{cases}0 & \text { If } i=0 \\ \operatorname{OPT}(i-1, w) & \text { If } w_{i}>w \\ \max \left(\operatorname{OPT}(i-1, w), v_{i}+\operatorname{OPT}\left(i-1, w-w_{i}\right)\right) & \text { o.w. }\end{cases}
$$

## RNA Secondary Structure

## RNA Secondary Structure

RNA: A String $B=b_{1} b_{2} \ldots b_{n}$ over alphabet $\{A, C, G, U\}$.
Secondary structure. RNA is single-stranded so it tends to loop back and form base pairs with itself. This structure is essential for understanding behavior of molecule.

Ex: GUCGAUUGAGCGAAUGUAACAACGUGGCUACGGCGAGA


## RNA Secondary Structure (Formal)

Secondary structure. A set of pairs $S=\left\{\left(b_{i}, b_{j}\right)\right\}$ that satisfy:
[Matching]: $S$ is a matching.
[Valid]: each pair in $S$ is: $A-U, U-A, C-G$, or $G-C$.
[No sharp turns]: The ends of each pair are separated by at least 4 intervening bases. If $\left(b_{i}, b_{j}\right) \in S$, then $i<j-4$.
[Non-crossing] If $\left(b_{i}, b_{j}\right)$ and $\left(b_{k}, b_{l}\right)$ are two pairs in $S$, then we cannot have $i<k<j<l$.

Free energy: Usual hypothesis is that an RNA molecule will maximize total free energy

```
approximate by number of base pairs
```

Goal: Given an RNA molecule $B=b_{1} b_{2} \ldots b_{n}$, find a secondary structure $S$ that maximizes the number of base pairs.

## Secondary Structure (Examples)





## DP: First Attempt

First attempt. Let $O P T(n)=$ maximum number of base pairs in a secondary structure of the substring $b_{1} b_{2} \ldots b_{n}$.

Suppose $b_{n}$ is matched with $b_{t}$ in $\operatorname{OPT}(n)$.
What IH should we use?
match $b_{+}$and $b_{n}$


Difficulty: This naturally reduces to two subproblems

- Finding secondary structure in $b_{1}, \ldots, b_{t-1}$, i.e., OPT(t-1)
- Finding secondary structure in $b_{t+1}, \ldots, b_{n-1}$, ???


## DP: Second Attempt

Definition: OPT $(i, j)=$ maximum number of base pairs in a secondary structure of the substring $b_{i}, b_{i+1}, \ldots, b_{j}$

The most important part of a correct DP; It fixes IH
Case 1: If $j-i \leq 4$.

- $O P T(i, j)=0$ by no-sharp turns condition.

Case 2: Base $b_{j}$ is not involved in a pair.

- $\operatorname{OPT}(i, j)=O P T(i, j-1)$

Case 3: Base $b_{j}$ pairs with $b_{t}$ for some $i \leq t<j-4$

- non-crossing constraint decouples resulting sub-problems
- $\operatorname{OPT}(i, j)=\max _{i \leq t<j-4}\{1+O P T(i, t-1)+O P T(t+1, j-1)\}$


## Recursive Code

```
Let M[i,j]=empty for all i,j.
Compute-OPT(i,j) {
    if (j-i <= 4)
        return 0;
    if (M[i,j] is empty)
        M[i,j]=Compute-OPT(i,j-1)
        for t=i to j-5 do
            if (b
            M[i,j]=max(M[i,j], 1+Compute-OPT(i,t-1) +
                        Compute-OPT(t+1,j-1))
    return M[j]
}
```

Does this code terminate?

## Formal Induction

Let $O P T(i, j)=$ maximum number of base pairs in a secondary structure of the substring $b_{i}, b_{i+1}, \ldots, b_{j}$
Base Case: $\operatorname{OPT}(i, j)=0$ for all $i, j$ where $|j-i| \leq 4$.
IH: For some $\ell \geq 4$, Suppose we have computed $\operatorname{OPT}(i, j)$ for all $i, j$ where $|i-j| \leq \ell$.

IS: Goal: We find $O P T(i, j)$ for all $i, j$ where $|i-j|=\ell+1$. Fix $i, j$ such that $|i-j|=\ell+1$.
Case 1: Base $b_{j}$ is not involved in a pair.

- OPT $(i, j)=\operatorname{OPT}(i, j-1)$ [this we know by IH since $|i-(j-1)|=\ell]$

Case 2: Base $b_{j}$ pairs with $b_{t}$ for some $i \leq t<j-4$

- $O P T(i, j)=\max _{i \leq t<j-4}\{1+O P T(i, t-1)+O P T(t+1, j-1)\}$


## Bottom-up DP

```
for l = 1, 2, .., n-1
    for i = 1, 2, .., n-1
        j = i + \ell
        if (\ell<= 4)
            M[i,j]=0;
            else
\[
M[i, j]=M[i, j-1]
\]
            for t=i to j-5 do
            if (b
                M[i,j]=max(M[i,j], 1+ M[i,t-1] + M[t+1,j-1])
    return M[1, n]
}
```

Running Time: $O\left(n^{3}\right)$
(It is also okay to loop over $i, j$ or $j, i$ )

## Given n positive integers a1,...,an, decide whether the integers can be partitioned into

## 3 sets, such that each set has the same sum.

## Quiz Solution

Let $A(i, x, y, z)$ be true if and only if the numbers $a_{1}, a_{2}, \cdots, a_{i}$ can be partitioned into three sets whose sums are $x, y, z$.

If $i>0$, we have

$$
\begin{aligned}
& A(i, x, y, z) \\
& =A\left(i-1, x-a_{i}, y, z\right) \text { or } A\left(i-1, x, y-a_{i}, z\right) \text { or } A\left(i-1, x, y, z-a_{i}\right)
\end{aligned}
$$

If $i=0$, we have
$A(0, x, y, z)=$ True if $x=y=z=0$, False otherwise.

Sequence Alignment (Edit distance)

## Word Alignment

How similar are two strings? ocurrance occurrence
$\left.\begin{array}{lll|l|l|l|l|l|l}\hline 0 & c & u & r & r & a & n & c & e \\ \hline 0 & c & c & u & r & r & e & n & c\end{array}\right]$

| 0 | $c$ | - | $u$ | $r$ | $a$ | $n$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 0 | $c$ | $c$ | $u$ | $r$ | $r$ | $e$ |

$0 c-u r r-a n c e$
$0 c c u r r e$
0 mismatches, 3 gaps

## Edit Distance

Edit distance. [Levenshtein 1966, Needleman-Wunsch 1970]
Cost = \# of gaps + \#mismatches.
How to formalize the question.
Applications.

- Basis for Unix diff and Word correct in editors.
- Speech recognition.
- Computational biology.

| $C$ | $T$ | $G$ | $A$ | $C$ | $C$ | $T$ | $A$ | $C$ | $C$ | $T$ |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| $C$ | $C$ | $T$ | $G$ | $A$ | $C$ | $T$ | $A$ | $C$ | $A$ | $T$ |

Cost: 5


Cost: 3

## Sequence Alignment

Given two strings $x_{1}, \ldots, x_{m}$ and $y_{1}, \ldots, y_{n}$ find an alignment with minimum number of mismatch and gaps.

An alignment is a set of ordered pairs $\left(x_{i_{1}}, y_{j_{1}}\right),\left(x_{i_{2}}, y_{j_{2}}\right), \ldots$ such that $i_{1}<i_{2}<\cdots$ and $j_{1}<j_{2}<\cdots$

Example: ctaccg vs. tacAtg. Sol: We aligned
$x_{2}-y_{1}, x_{3}-y_{2}, x_{4}-y_{3}, x_{5}-y_{4}, x_{6}-y_{6}$.
So, the cost is 3 .

| $x_{1}$ | $x_{2}$ | $x_{3}$ | $x_{4}$ | $x_{5}$ |  | $x_{6}$ |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| $C$ | $T$ | $A$ | $C$ | $C$ | - | $G$ |
| - | $T$ | $A$ | $C$ | $A$ | $T$ | $G$ |
|  | $y_{1}$ | $y_{2}$ | $y_{3}$ | $y_{4}$ | $y_{5}$ | $y_{6}$ |

## DP for Sequence Alignment

Let $O P T(i, j)$ be min cost of aligning $x_{1}, \ldots, x_{i}$ and $y_{1}, \ldots, y_{j}$

Case 1: OPT matches $x_{i}, y_{j}$

- Then, pay mis-match cost if $x_{i} \neq y_{j}+$ min cost of aligning $x_{1}, \ldots, x_{i-1}$ and $y_{1}, \ldots, y_{j-1}$ i.e., $\operatorname{OPT}(i-1, j-1)$

Case 2: OPT leaves $x_{i}$ unmatched

- Then, pay gap cost for $x_{i}+O P T(i-1, j)$

Case 3: OPT leaves $y_{j}$ unmatched

- Then, pay gap cost for $y_{j}+O P T(i, j-1)$


## Bottom-up DP

```
Sequence-Alignment(m, n, x }\mp@subsup{x}{1}{}\mp@subsup{x}{2}{}\ldots\mp@subsup{x}{m}{},\mp@subsup{y}{1}{}\mp@subsup{y}{2}{}\ldots\mp@subsup{y}{n}{\prime})
    for i = 0 to m
        M[0, i] = i
    for j = 0 to n
        M[j, 0] = j
    for i = 1 to m
        for j = 1 to n
        M[i, j] = min( ( }\mp@subsup{\textrm{x}}{\textrm{i}}{=}=\mp@subsup{y}{j}{}\mathrm{ ? 0:1) + M[i-1, j-1],
                        1 + M[i-1, j],
                                1 + M[i, j-1])
    return M[m, n]
}
```

Analysis: $\Theta(m n)$ time and space.
Computational biology: $m=n=1,000,000.1000$ billions ops OK, but 1TB array?

$$
M[i, j]=\min \left(\quad\left(x_{i}=y_{j} ? 0: 1\right)+M[i-1, j-1]\right.
$$

## |nOUCtiOn $\begin{aligned} & 1+\mathrm{m}[\mathrm{i}-1, j] \text {, } \\ & 1+\mathrm{m}[\mathrm{i}, \mathrm{j}-1])\end{aligned}$

What is the order of induction? (i.e. why there is no loop?) We can do induction on $i+j$.
(Alternatively, we can induct on the "step" of the algorithm)


## Optimizing Memory

We just need to use the last (row) of computed values.

```
```

Sequence-Alignment ( $m, n, x_{1} x_{2} \ldots x_{m}, y_{1} y_{2} \ldots y_{n}$ ) \{

```
```

Sequence-Alignment ( $m, n, x_{1} x_{2} \ldots x_{m}, y_{1} y_{2} \ldots y_{n}$ ) \{
for $i=0$ to $m$
for $i=0$ to $m$
$\mathrm{m}[0, \mathrm{i}]=\mathrm{i}$
$\mathrm{m}[0, \mathrm{i}]=\mathrm{i}$
for $\mathrm{j}=0$ to n
for $\mathrm{j}=0$ to n
$\mathrm{M}[\mathrm{j}, 0]=\mathrm{j}$
$\mathrm{M}[\mathrm{j}, 0]=\mathrm{j}$
for $i=1$ to $m$
for $i=1$ to $m$
for $j=1$ to $n$
for $j=1$ to $n$
$M[i, j]=\min \left(\quad\left(x_{i}=y_{j} ? 0: 1\right)+M[i-1, j-1]\right.$,
$M[i, j]=\min \left(\quad\left(x_{i}=y_{j} ? 0: 1\right)+M[i-1, j-1]\right.$,
$1+M[i-1, j]$,
$1+M[i, j-1])$
$1+M[i-1, j]$,
$1+M[i, j-1])$
$1+M[i-1, j]$,
$1+M[i, j-1])$
$1+M[i-1, j]$,
$1+M[i, j-1])$
return $\mathrm{M}[\mathrm{m}, \mathrm{n}]$
return $\mathrm{M}[\mathrm{m}, \mathrm{n}]$
\}

```
```

\}

```
```



Just need $i-1, i$ rows to compute M[i,j]

## DP with $O(m+n)$ memory

- Keep an Old array containing values of the last row
- Fill out the new values in a New array
- Copy new to old at the end of the loop


```
    for i = 0 to m
        O[i] = i
    for i = 1 to m
        N[0]=i
        for j = 1 to n
            N[j] = min( ( }\mp@subsup{\textrm{x}}{\textrm{i}}{=}=\mp@subsup{y}{j}{}?0:1)+O[j-1]
                                    1+O[j],}M[i-1, j
                                    1 +N[j-1]) ఒM[i, j-1]
        for j = 1 to n
            O[j]=N[j]
    return N[n]
}
```

$$
M[i, j]=\min \left(\quad\left(x_{i}=y_{j} ? 0: 1\right)+M[i-1, j-1]\right.
$$

## Shortest Path $\quad \begin{aligned} & 1+M[i-1, j] \text {, } \\ & 1+M[i, j-1])\end{aligned}$

Edit distance is the distance between $(0,0)$ and $(m, n)$ of the following graph.

- All horizontal edges has cost 1 .
- All vertical edges has cost 1 .
- The cost of edges from $(i-1, j-1)$ to $(i, j)$ is $1_{x_{i} \neq y_{j}}$

The graph is a DAG.
Question: How to recover the alignment (or how to find the shortest path) without using $m n$ space?


Figure 6.17 A graph-based picture of sequence alignment.

## How to recover the alignment?

Idea 1: Suffices to find the point a shortest path pass on the middle row.

Why?
Divide and Conquer!


```
Find \(\left(\mathbf{i}_{1}, \dot{j}_{1}, \mathbf{i}_{2}, \dot{j}_{2}\right)\{/ /\) Due to spacing, ignored boundary cases
    Let \(k=\left\lfloor\left(i_{1}+i_{2}\right) / 2\right\rfloor\)
    Compute \(d_{\left(i_{1}, j_{1}\right) \rightarrow\left(k, j_{2}\right)}\) for all \(j\) via Sequence-Alignment.
    Compute \(d_{(k, j) \rightarrow\left(i_{2}, j_{2}\right)}\) for all \(j\) via similar algo run backward.
    Let \(\boldsymbol{j}=\operatorname{argmin}_{j} \boldsymbol{d}_{\left(\boldsymbol{i}_{1}, \boldsymbol{j}_{1}\right) \rightarrow\left(\boldsymbol{k}, \boldsymbol{j}_{2}\right)}+\boldsymbol{d}_{\left(\boldsymbol{k}, \boldsymbol{j}_{2}\right) \rightarrow\left(\boldsymbol{i}_{2}, \boldsymbol{j}_{2}\right)}\)
    \(p_{1}=\operatorname{Find}\left(i_{1}, j_{1}, k, j\right)\)
    \(p_{2}=\operatorname{Find}\left(k, j, i_{2}, j_{2}\right)\)
    return \(p_{1}, p_{2}\)
\}

\section*{Lesson}

Advantage of a bottom-up DP:
It is much easier to optimize the space.

By the way, edit distance
- can be computed in \(O(s \times \min (m, n))\) if edit distance \(\leq s\)
- can be computed in \(O\left(\frac{n^{2}}{\log ^{2} n}\right)(1980)\).
- can be approximated by log factor in \(O\left(n^{1+\varepsilon}\right)(\sim 2010)\).
- cannot be solved in \(O\left(n^{2-\delta}\right)\) exactly (2015).
- can be approximated by \(\mathrm{O}(1)\) factor in \(O\left(n^{2-2 / 7}\right)(\sim 2018)\).
- can be approximated by \(O(1)\) factor in \(O\left(n^{1+\epsilon}\right)(\sim 2020)\).

\section*{Longest Path in a DAG}

\section*{Longest Path in a DAG}

Goal: Given a DAG G, find the longest path.

Recall: A directed graph \(G\) is a DAG if it has no cycle.

This problem is NP-hard for general directed graphs:
- It has the Hamiltonian Path as a special case


\section*{DP for Longest Path in a DAG}

Q: What is the right ordering?
Remember, we have to use that G is a DAG, ideally in defining the ordering

We saw that every DAG has a topological sorting
So, let's use that as an ordering.


\section*{DP for Longest Path in a DAG}

Suppose we have labelled the vertices such that \((i, j)\) is a directed edge only if \(i<j\).


Let \(O P T(j)=\) length of the longest path ending at \(j\) Suppose OPT(j) is \(\left(i_{1}, i_{2}\right),\left(i_{2}, i_{3}\right), \ldots,\left(i_{k-1}, i_{k}\right),\left(i_{k}, j\right)\), then Obs 1: \(i_{1} \leq i_{2} \leq \cdots \leq i_{k} \leq j\).
Obs 2: \(\left(i_{1}, i_{2}\right),\left(i_{2}, i_{3}\right), \ldots,\left(i_{k-1}, i_{k}\right)\) is the longest path ending at \(i_{k}\).
\[
O P T(j)=1+O P T\left(i_{k}\right) .
\]

\section*{DP for Longest Path in a DAG}

Suppose we have labelled the vertices such that \((i, j)\) is a directed edge only if \(i<j\).

Let \(O P T(j)=\) length of the longest path ending at \(j\)
\[
O P T(j)= \begin{cases}0 & \text { If } j \text { is a source } \\ 1+\max _{i:(i, j) \text { an edge }} O P T(i) & \text { o.w. }\end{cases}
\]

\section*{Outputting the Longest Path}
```

Let G be a DAG given with a topological sorting: For all edges
(i,j) we have i<j.
Initialize Parent[j]=-1 for all j.
Compute-OPT(j) {
if (in-degree(j)==0)
return 0
if (M[j]==empty)
M[j]=0;
for all edges (i,j)
if (M[j] < 1+Compute-orr(i)) we used to compute OPT(j)
M[j]=1+Compute-opr(i)
Parent[j]=i
return M[j]
}
Let M[k] be the maximum of M[1],···,M[n]
While (Parent[k]!=-1)
Print k
k=Parent[k]

```
```

