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Dynamic programming records saves computation for reuse later.

- Programming: in the optimization sense ("Linear Programming")
- Dynamic: "... it's impossible to use [it] in a pejorative way." (Richard Bellman)
- Name designed to sound cool to RAND management and US Department of Defense
- A more descriptive term is look-up table



Richard Bellman

Start with a rod of integer length $n \dots$



... and cut it into several smaller pieces (of integer length).



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$$= 1$$
 $= 5$ $= 8$ $= 9$ $= 1 + 1 + 5 = 5 + 9 = 21$

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Now suppose each length has a different value:

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 $= 5$ $= 8$ $= 9$ $= 1 + 1 + 5 = 5 + 9 = 21$

How should we cut the rod into pieces?

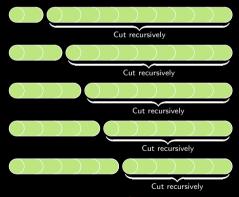
• 2^{n-1} possibilities for a rod of length n

First rod-cutting strategy (brute-force):

• For every possible cut, compute the value of the left part plus the value of optimally cutting the right part. Take the best cut.

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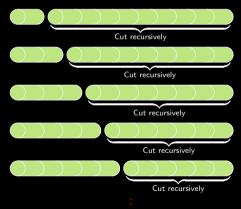
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First rod-cutting strategy (brute-force):

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Exponential recursion tree!

Second rod-cutting strategy (top-down):

- For every cut, compute value of left part and store it in a table
- Find value of optimal cut for right part in table
 - ► Compute it recursively if it doesn't exist yet

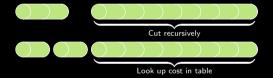
Second rod-cutting strategy (top-down):

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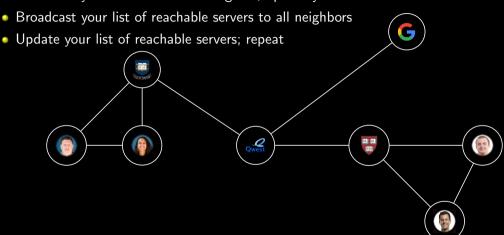


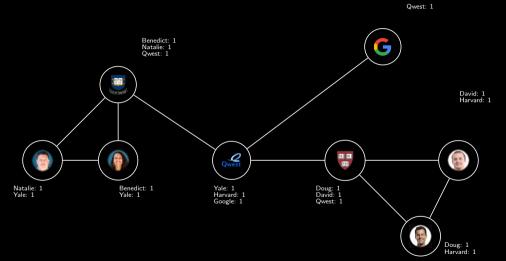
- Reduces computation from $O(2^n)$ to $O(n^2)$ (Why?)
- \bullet Requires an array of length n to store intermediate computations

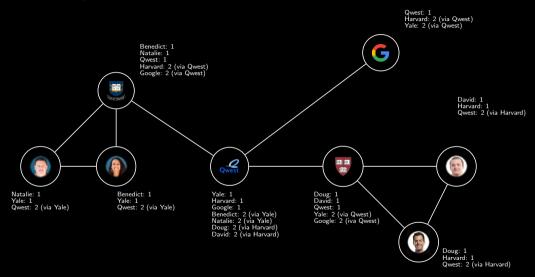
Thrid rod-cutting strategy (bottom-up):

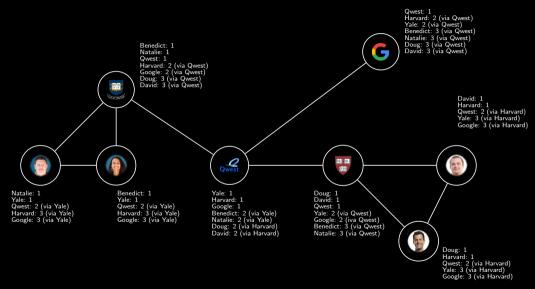
- Compute the value of a rod of length 1. Store it.
- Compute the value of a rod of length 2. You can only cut it into rods of length 1. The value of a rod of length 1 is already computed, so there is no recursion.
- Compute the value of successively longer rods up to length *n*. The optimal values of shorter rods are always computed first so there is no recursion.

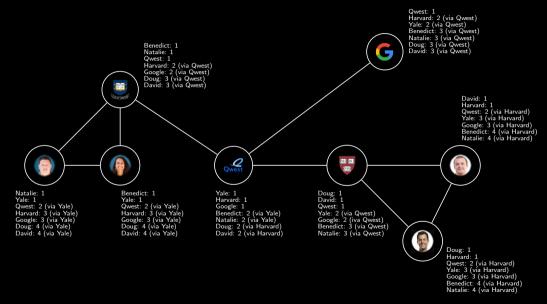
• Broadcast your existence to all neighors; update your list











Sequence Matching

- Human genes are coded by four bases: Adenine (A), Thymine (T), Guanine (G),
 Cytosine (C)
- DNA undergoes mutations with each copy:
 - ► Substitutions: replace one base with another
 - Deletions: some bases are dropped
- Suppose we isolate a gene in a new organism:

```
AACAGTTACC
```

Predict function by comparing to genes in know, organism:

```
e.g. T A A G G T C A
```

• How similar are A A C A G T T A C C and T A A G G T C A?

Sequence Matching

How similar are A A C A G T T A C C and T A A G G T C A?

- How many mutations to change first sequence into second?
- How (un)likely is each mutation

Edit Distance: minimum cost to convert one string into another.

Each change (mutation) has an associated cost:

Gap 2 Mismatch 1 Match 0

Example matchings:

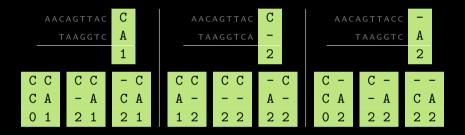
A A C A G T T A C C
T A A G G T C A - -

A A C A G T T A C C
T A - A G G T - C A
1 0 2 0 0 1 0 2 0 1

Edit Distance

Brute-force recursive solution:

Start at end of sequence and work backwards



- Recurse until we have all possible matches, then find minimum
- Three children per node $\Rightarrow O(3^n)$ matching cost
- We need to do better!

Edit Distance

Dynamic Programming recursive solution

• Consider a pair of characters in the middle:

- What is the cost of matching from this pair of Gs to the end?
 - Cost of matching Gs (0) + lowest cost of matching T T A C C to T C A.
 - ▶ Brute force solution computes *all possible* costs
- Idea: For each pair of characters, keep track of best match up to end

Idea: For each pair of characters, keep track of best match to end

	A	A	C	A	G	T	T	A	C	С	-
Т											16↓
A											14↓
A											12↓
G											10↓
G											8↓
Т											6↓
С											4↓
A											2↓
-	20→	18→	16→	14→	12→	10→	8→	6→	$4 \rightarrow$	2->	0

Initialization:

- Cost of zero-length match (lower right) is zero
- Inserting a gap (move right or down in table) costs two

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		n pan or	Characters, i	nccp traci		DCSt Illate	ii to ciid

	A	A	C	A	G	T	T	A	C	C	-
T											16↓
A											14↓
A											12↓
G											10↓
G											8↓
T											6↓
С											4↓
A										1	2↓
-	20→	18→	16→	14→	12→	10→	8→	6→	4→	2->	0

Iteration:

- Work back from lower right
- Cost of cell cost[i][j] is

Idea: For each pair of characters, keep track of best match to end

	A	A	C	A	G	T	T	A	C	C	_
T											16↓
A											14↓
A											12↓
G											10↓
G											8↓
T											6↓
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A									3 🔪	1 📐	2↓
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- 10	lea.	For each	n nair of c	characters. I	keen traci	\leftarrow	hest matcl	h to enc
	ica.	l oi caci	i pan or c	cilai acters,	nccp traci	\ O1	DCSL IIIatci	II to cire

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	A	A	C	A	G	T	T	A	C	C	-
T	7	6	6	7↓	9	8	9 📐	11↓	13	14↓	16↓
A	8	6	5	5	7	8	8	9	11	12↓	14↓
A	10	8	6→	4	5	6	7	7	9	10↓	12↓
G	12	10	8	6	4	4	5	6	7	8↓	10↓
G	13→	11>	9→	$7 \rightarrow$	5	4	3	4	5	6↓	8↓
T	15	13	11>	9→	7→	5	3 🔪	2	3	4↓	6↓
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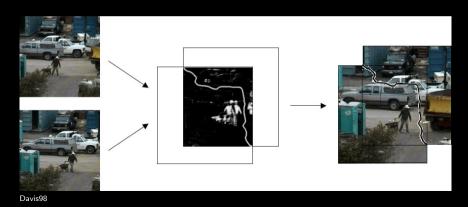
	Α	A	C	A	G	T	T	A	С	C	-
Т	7	6 📐	6 📐	7↓	9 🔪	8 📐	9 🔪	11↓	13 📐	14↓	16↓
Α	8 🔪	6	5 📐	5 📐	7 📐	8 📐	8 📐	9 📐	11	12↓	14↓
A	10 📐	8 📐	$6 \rightarrow$	4	5 📐	6 📐	7 📐	7 📐	9 📐	10↓	12↓
G	12	10 📐	8 📐	6 📐	4	4 📐	5 🔪	6 📐	7	8↓	10↓
G	13→	11→	9→	7→	5 📐	4	3 🔪	4 📐	5 🔪	6↓	8↓
Т	15 🔪	13 📐	11→	9→	7→	5 📐	3 🔪	2 📐	3 📐	4↓	6↓
С	16→	$14 \rightarrow$	12	11	9 🔪	7 📐	5 🔪	3→	1	2 📐	4↓
Α	18 🔪	16	14→	12	10→	8→	6→	4 📐	3 🔪	1	2↓
-	20→	18→	16→	14→	12→	10→	8→	6→	$4 \rightarrow$	2->	0

Recovering the best alignment:

- Final cost is in cell cost [0] [0]
- Follow arrows to reconstruct string
- ullet ightarrow aligns letter in the current column with a gap
- ullet \downarrow aligns letter in the current row with a gap
- \(\square\) matches letters in current row and column with each other
- Total running time: O(mn)!

Some More Examples

- Image Compositing
 - ► Given a set of overlapping images, what is the best way to stitch them?
 - ► Cut the images along an "invisible" seam, and splice them together.
 - ▶ The optimal seam can be found through dynamic programming.
 - ★ Even better: shortest path



Some More Examples

- Seam carving (see demo)
 - ▶ Shrink an image by finding one row or column of pixels to remove
 - ► The seam doesn't have to be straight—it can wiggle
 - ▶ Use dynamic programming to find the best set of pixels to remove