CSE 326: Data Structures
The Algorhythmics

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Today's Outline

- Greedy
- Divide & Conquer
- Dynamic Programming

Greedy Algorithms

Repeat until problem is solved:

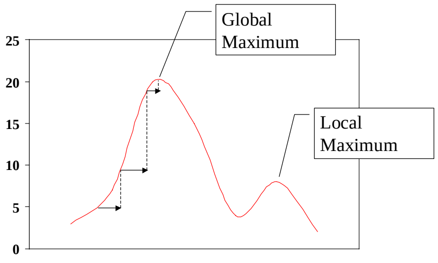
- Consider possible next steps
- Choose best-looking alternative and commit to it

Greedy algorithms are normally fast and simple.

Sometimes appropriate as a *heuristic* solution or to approximate the optimal solution.

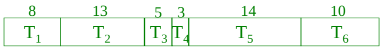
Greed in Action

Hill-Climbing



Scheduling Problem

- Given:
  - a group of tasks $\{T_1, \ldots, T_n\}$
  - each with a duration $\{d_1, \ldots, d_n\}$
  - a single processor without interrupts
- Select an order for the tasks that minimizes average completion time



Average time to completion:

Greedy Solution

Divide & Conquer

- Divide problem into multiple smaller parts
- Solve smaller parts
  - Solve base cases directly
  - Otherwise, solve subproblems recursively
- Merge solutions together (Conquer!)

Often leads to elegant and simple recursive implementations.

Divide & Conquer in Action

Memoizing/ Dynamic Programming

- Define problem in terms of smaller subproblems
- Solve and record solution for base cases
- Build solutions for subproblems up from solutions to smaller subproblems

Can improve runtime of divide & conquer algorithms that have shared subproblems with *optimal substructure*.

Usually involves a table of subproblem solutions.

Dynamic Programming in Action

- Sequence Alignment
- Fibonacci numbers
- *All* pairs shortest path
- Optimal Binary Search Tree
- Matrix multiplication

Fibonacci Numbers

```
F(n) = F(n - 1) + F(n - 2)
F(0) = 1      F(1) = 1
```

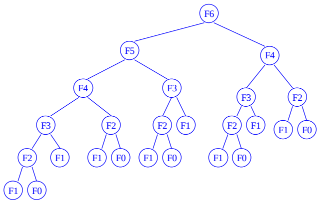
Fibonacci Numbers

`F(n) = F(n - 1) + F(n - 2)`

`F(0) = 1      F(1) = 1`

Divide & Conquer

```
int fib(int n) {
  if (n <= 1)
    return 1;
  else
    return fib(n - 1) +
           fib(n - 2);
}
```



Runtime:

Fibonacci Numbers

`F(n) = F(n - 1) + F(n - 2)`

`F(0) = 1      F(1) = 1`

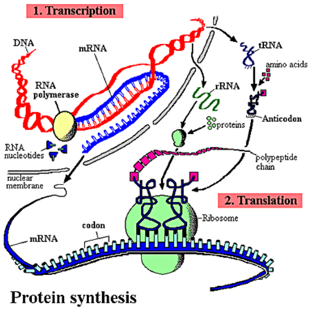
Memoized

```
int fib(int n) {
  // Create an array however your favorite language allows
  int fibs[n];

  if (n <= 1)
    return 1;

  if (fibs[n] == 0)
    fibs[n] = fib(n - 1) +
              fib(n - 2);

  return fibs[n];
}
```

Runtime:

Sequence Alignment

Biology 101:



Protein synthesis

DNA Sequence

- String using letters (nucleotides): A,C,G,T

  For example: ACGGGCATTATCGTA

- DNA can mutate!

  Change a letter: ACGGGCAT → ACGTGCAT

  Insert a letter: ACGGGCAT → ACGGGCAAT

  Delete a letter: ACGGGCAT → ACGGGAT

- A few mutations makes sequences “different”, but “similar”
- Similar sequences often have similar functions

What is Sequence Alignment?

- Use underscores (_) or wildcards to match up 2 sequences
- The “best alignment” of 2 sequences is an alignment which minimizes the number of “underscores”
- For example: `ACCCGTTT` and `TCCCTTT`

Best alignment: `A_CCCGTTT`

(3 underscores) `_TCCC_TTT`

Solutions

Naïve solution

- Try all possible alignments
- Running time: exponential

Dynamic Programming Solution

- Create a table
- Table(x,y): best alignment for first x letters of string 1, and first y letters of string 2
- Running time: polynomial

Example Alignment

Match ACCGTTAG with ACTGTTAA

(1) match ‘G’ with ‘_’: 1 + *align*(ACCGTTA,ACTGTTAA)

(2) match ‘A’ with ‘_’: 1 + *align*(ACCGTTAG,ACTGTTA)

- Suppose we have already determined the best alignment for:
  - First x letters of string1 with first y-1 letters of string2
  - First x-1 letters of string1 with first y-1 letters of string2
  - First x-1 letters of string1 with first y letters of string2

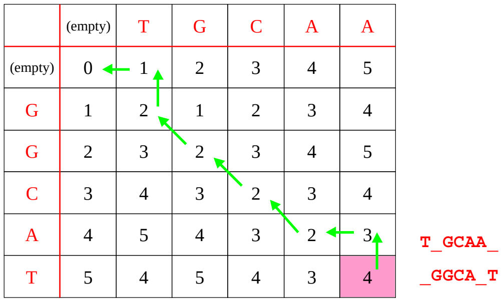
If (string1[x] == string2[y]) then TABLE[x,y] = TABLE[x-1,y-1]

Else TABLE[x,y] = *min*(1+TABLE[x,y-1], 1+TABLE[x-1,y])

Example GGCAT and TGCAA

	(empty)	T	G	C	A	A
(empty)						
G						
G						
C						
A						
T						

Example GGCAT and TGCAA



	(empty)	T	G	C	A	A
(empty)	0	1	2	3	4	5
G	1	2	1	2	3	4
G	2	3	2	3	4	5
C	3	4	3	2	3	4
A	4	5	4	3	2	3
T	5	4	5	4	3	4

T_GCAA_

_GGCA_T

Pseudocode (bottom-up)

```
int align(String X, String Y, TABLE[1..x,1..y]) {
        int i,j;
        // Initialize top row and leftmost column
        for (i=1; i<=x, ++i) TABLE[i,1] = i;
        for (j=1; j<=y; ++j) TABLE[1,j] = j;

        for (i=2; i<=x, ++i) {
                for (j=2; j<=y; ++j) {
                        if (X[i] == Y[j])
                                TABLE[i,j] = TABLE[i-1,j-1]
                        else
                                TABLE[i,j] = min(TABLE[i-1,j],
                                                    TABLE[i,j-1])+1
                }
        }
        return TABLE[x,y];
}
```

runtime:

Pseudocode (top-down)

```
int align(String X,String Y,TABLE[1..x,1..y])
{
     Compute TABLE[x-1,y-1] if necessary
     Compute TABLE[x-1,y] if necessary
     Compute TABLE[x,y-1] if necessary
     if (X[x] == Y[y])
          TABLE[x,y] = TABLE[x-1,y-1];
     else
          TABLE[x,y] = min(TABLE[x-1,y],
                           TABLE[x,y-1]) + 1;
     return TABLE[x,y];
}
```

Dynamic Programming Wrap-Up

- Re-use expensive computations
- Store optimal solutions to sub-problems in table
- Use optimal solutions to sub-problems to determine optimal solution to slightly larger problem