## CS481: Bioinformatics Algorithms

Can Alkan EA509 calkan@cs.bilkent.edu.tr

http://www.cs.bilkent.edu.tr/~calkan/teaching/cs481/

#### CS481

- Class hours:
  - Mon 10:40 12:30; Thu 9:40 10:30
- Class room: EB201
- Office hour: Tue + Thu 11:00-12:00
- TA: Fatma Kahveci (fatmaba@gmail.com)
- Grading:
  - 1 midterm: 25%
  - I final: 35%
  - Homeworks (theoretical & programming [C/C++]): 20%
  - Quizzes: 20%

#### CS481

- Textbook: An Introduction to Bioinformatics Algorithms (Computational Molecular Biology), Neil Jones and Pavel Pevzner, MIT Press, 2004
- Recommended Material
  - Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison, Cambridge University Press
  - Bioinformatics: The Machine Learning Approach, Second Edition, Pierre Baldi, Soren Brunak, MIT Press
  - Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biology, Dan Gusfield, Cambridge University Press
- (Most) of the course material is publicly available at: www.bioalgorithms.info

#### CS481

- This course is about algorithms in the field of bioinformatics:
  - □ What are the problems?
  - What algorithms are developed for what problem?
  - Algorithm design techniques
- This course is not about how to analyze biological data using available tools:
  - Recommended course: MBG 326: Introduction to Bioinformatics

#### CS481 and other courses

#### Includes elements from:

- CS201/202: data structures
- CS473: algorithms, dynamic programming, greedy algorithms, branch-and-bound, etc.
- CS476: complexity, context-free grammars, DFA/NFA
- CS464: hidden Markov models

#### CS481: Assumptions

You are assumed to know/understand

- Computer science basics (CS101/102 or CS111/112)
  - CS201/202 would be better
  - CS473 would be even better
- Data structures (trees, linked lists, queues, etc.)
- Elementary algorithms (sorting, hashing, etc.)
- Programming: C, C++
- You don't have to be a "biology expert": MBG 110 would be sufficient

#### Bioinformatics

 Development of methods based on computer science for problems in biology and medicine

- Sequence analysis (combinatorial and statistical/probabilistic methods)
   CS 481
- Graph theory
- Data mining
- Database
- Statistics
- Image processing
- Visualization
- ....

### **Bioinformatics:** Applications

#### Human disease

- Personalized Medicine
- Genomics: Genome analysis, gene discovery, regulatory elements, etc.
- Population genomics
- Evolutionary biology
- Proteomics: analysis of proteins, protein pathways, interactions
- Transcriptomics: analysis of the transcriptome (RNA sequences)

# Why would you learn these algorithms?

- Most developed for research within other fields that include string processing, clustering, textpattern search, etc.
- Bioinformatics (non-academic) jobs on the rise:
  - Genomics England, Genome Asia, etc.: 100,000 genome projects
  - DNAnexus, SevenBridges: genome analysis on the cloud.
    - SevenBridges has Ankara and Istanbul offices

#### **(VERY) BRIEF INTRODUCTION TO COMPLEXITY**

#### Tractable vs intractable

- Tractable algorithms: there exists a solution with O(f(n)) run time, where f(n) is polynomial
- P is the set of problems that are known to be solvable in polynomial time
- NP is the set of problems that are verifiable in polynomial time
  - NP: "non-deterministic polynomial"

## $P \subset NP$

#### NP-hard

- NP-hard: non-deterministic polynomial hard
  - Set of problems that are "at least as hard as the hardest problems in NP"
  - There are no known polynomial time optimal solutions
  - There may be polynomial-time approximate solutions

#### NP-Complete

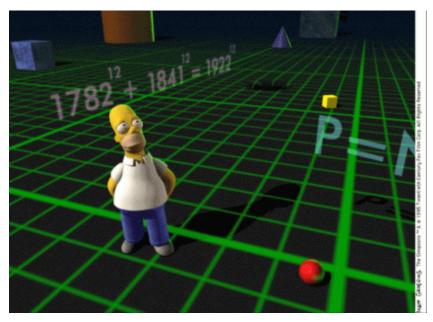
- A decision problem C is in NPC if :
  - C is in NP
  - Every problem in NP is reducible to C in polynomial time
  - That means: if you could solve any NPC problem in polynomial time, then you can solve all of them in polynomial time
    - Decision problems: outputs "yes" or "no"

#### NP-intermediate

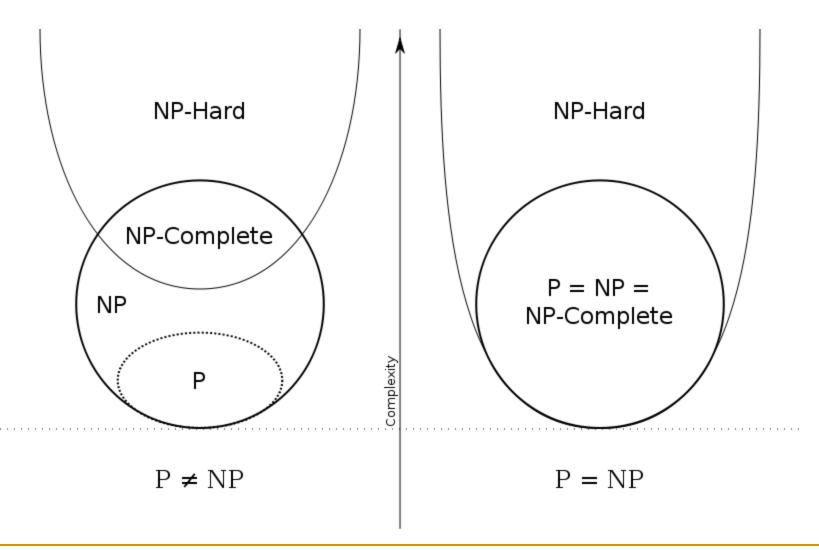
Problems that are in NP; but not in either NPC or NP-hard

#### P vs. NP

- We do not know whether P=NP or P≠NP
  - Principal unsolved problem in computer science
  - It is believed that P≠NP



#### P vs. NP vs. NPC vs. NP-hard



#### Examples

#### **P**:

- Sorting numbers, searching numbers, pairwise sequence alignment, etc.
- NP-complete:
  - Subset-sum, traveling salesman, etc.
- NP-intermediate:
  - □ Factorization, graph isomorphism, etc.

#### Historical reference

- The notion of NP-Completeness: Stephen Cook and Leonid Levin independently in 1971
  - First NP-Complete problem to be identified: Boolean satisfiability problem (SAT)
    - Cook-Levin theorem
- More NPC problems: Richard Karp, 1972
  - "21 NPC Problems"
- Now there are thousands....

#### ALGORITHM DESIGN TECHNIQUES

### Sample problem: Change

- Input: An amount of money M, in cents
- Output: Smallest number of coins that adds up to M
  - Quarters (25c): q
  - Dimes (10c): d
  - Nickels (5c): n
  - Pennies (1c): p
  - Or, in general, c<sub>1</sub>, c<sub>2</sub>, ..., c<sub>d</sub> (*d* possible denominations)

Exhaustive search / brute force

## Examine every possible alternative to find a solution

```
BRUTEFORCECHANGE(M, \mathbf{c}, d)
    smallestNumberOfCoins \leftarrow \infty
1
    for each (i_1, ..., i_d) from (0, ..., 0) to (M/c_1, ..., M/c_d)
2
         valueOfCoins \leftarrow \sum_{k=1}^{d} i_k c_k
3
         if valueOfCoins = M
4
              numberOfCoins \leftarrow \sum_{k=1}^{d} i_k
5
              if numberOfCoins < smallestNumberOfCoins
6
7
                    smallestNumberOfCoins \leftarrow numberOfCoins
8
                    bestChange \leftarrow (i_1, i_2, \ldots, i_d)
9
    return (bestChange)
```

#### Greedy algorithms:

 Choose the "most attractive" alternative at each iteration
 USCHANGE(M)

BETTERCHANGE
$$(M, \mathbf{c}, d)$$
  
1  $r \leftarrow M$   
2 for  $k \leftarrow 1$  to  $d$   
3  $i_k \leftarrow r/c_k$ 

- 4  $r \leftarrow r c_k \cdot i_k$
- 5 return  $(i_1, i_2, ..., i_d)$

- $\begin{array}{cccc} 1 & r \leftarrow M \\ 2 & q \leftarrow r/25 \\ 3 & r \leftarrow r 25 \cdot q \end{array}$
- 4  $d \leftarrow r/10$
- 5  $r \leftarrow r 10 \cdot d$
- 6  $n \leftarrow r/5$
- 7  $r \leftarrow r 5 \cdot n$
- 8  $p \leftarrow r$
- 9 return (q, d, n, p)

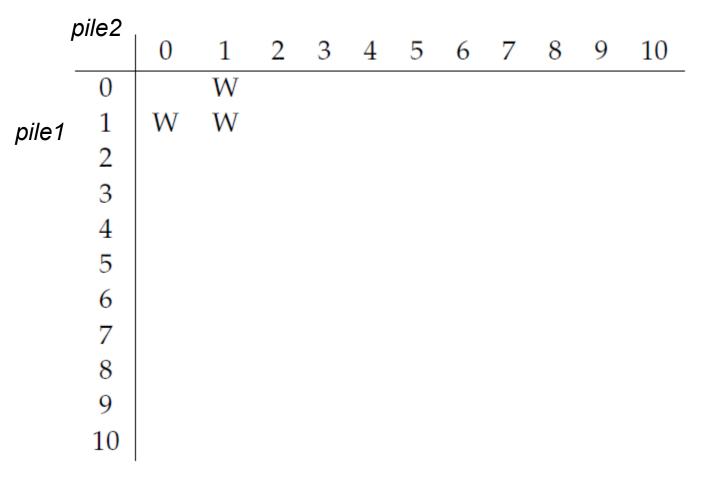
#### Dynamic Programming:

- Break problems into subproblems; solve subproblems; merge solutions of subproblems to solve the real problem
- Keep track of computations to avoid recomputing values that you already solved
- Dynamic programming table

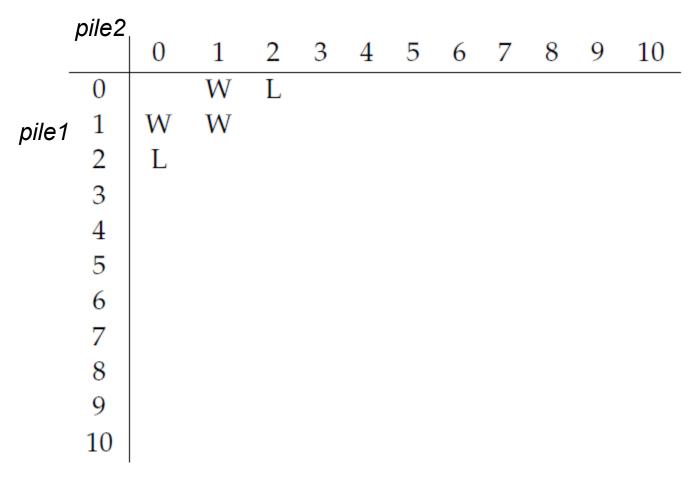
#### DP example: Rocks game

- Two players
- Two piles of rocks with p<sub>1</sub> rocks in pile 1, and p<sub>2</sub> rocks in pile 2
- In turn, each player picks:
  - One rock from either pile 1 or pile 2; OR
  - One rock from pile 1 and one rock from pile2
- The player that picks the last rock wins

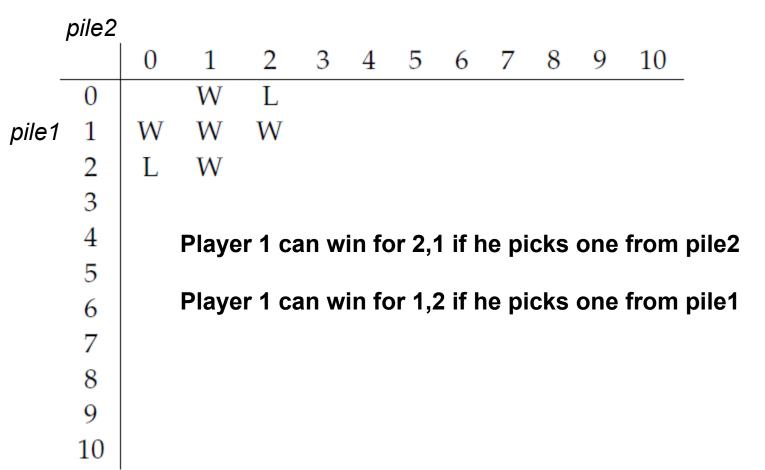
- Problem:  $p_1 = p_2 = 10$
- Solve more general problem of p<sub>1</sub> = n and p<sub>2</sub>
   = m
- It's hard to directly calculate for n=5 and m=6; we need to solve smaller problems



Initialize; obvious win for Player 1 for 1,0; 0,1 and 1,1



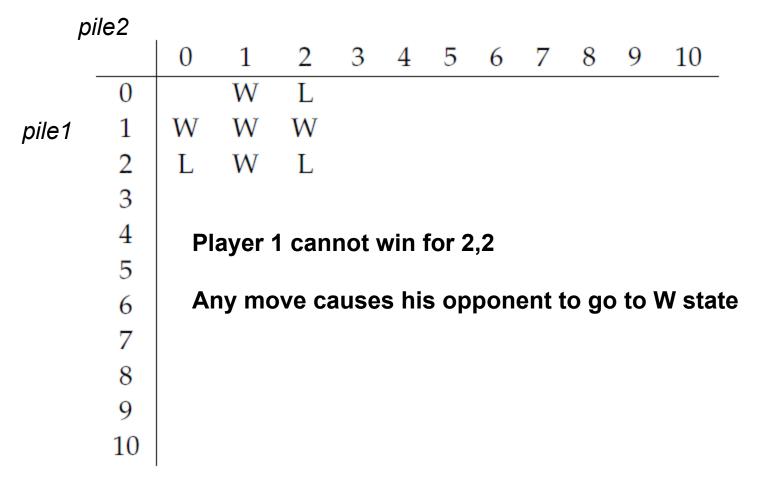
Player 1 cannot win for 2,0 and 0,2



pile1

Player 1 can win for 2,1 if he picks one from pile2

Player 1 can win for 1,2 if he picks one from pile1



#### DP "moves"

When you are at position (i,j)

Go to:

Pick from pile 1: (i-1, j)

Pick from pile 2: (i, j-1)

Pick from both piles 1 and 2: (i-1, j-1)

#### DP final table

	0	1	2	3	4	5	6	7	8	9	10
0		W	L	W	L	W	L	W	L	W	L
1	W	W	W	W	W	W	W	W	W	W	W
2	L	W	L	W	L	W	L	W	L	W	L
3	W	W	W	W	W	W	W	W	W	W	W
4	L	W	L	W	L	W	L	W	L	W	L
5	W	W	W	W	W	W	W	W	W	W	W
6	L	W	L	W	L	W	L	W	L	W	L
7	W	W	W	W	W	W	W	W	W	W	W
8	L	W	L	W	L	W	L	W	L	W	L
9	W	W	W	W	W	W	W	W	W	W	W
10	L	W	L	W	L	W	L	W	L	W	L

Also keep track of the choices you need to make to achieve W and L states: *traceback table* 

#### Divide and conquer:

- Split, solve, merge
  - Mergesort

#### Machine learning:

Analyze previously available solutions, calculate statistics, apply most likely solution

#### Randomized algorithms:

Pick a solution randomly, test if it works. If not, pick another random solution