CS 466
Introduction to Bioinformatics
Lecture 1

Mohammed El-Kebir

August 25, 2021

Course Staff

Instructor:

- Mohammed El-Kebir (melkebir)
- Office hours: Wednesdays, 3:30-4:30pm in Siebel 3216 / Zoom

Developing combinatorial algorithms to study all stages of cancer progression.

Zoom:

- https://go.cs.illinois.edu/CS466

TA:

- Leah Weber (leahlw2), office hours: Mondays, 4-5pm via Zoom
- Yuanyuan Qi (yq7), office hours: Fridays, 9-10am via Zoom

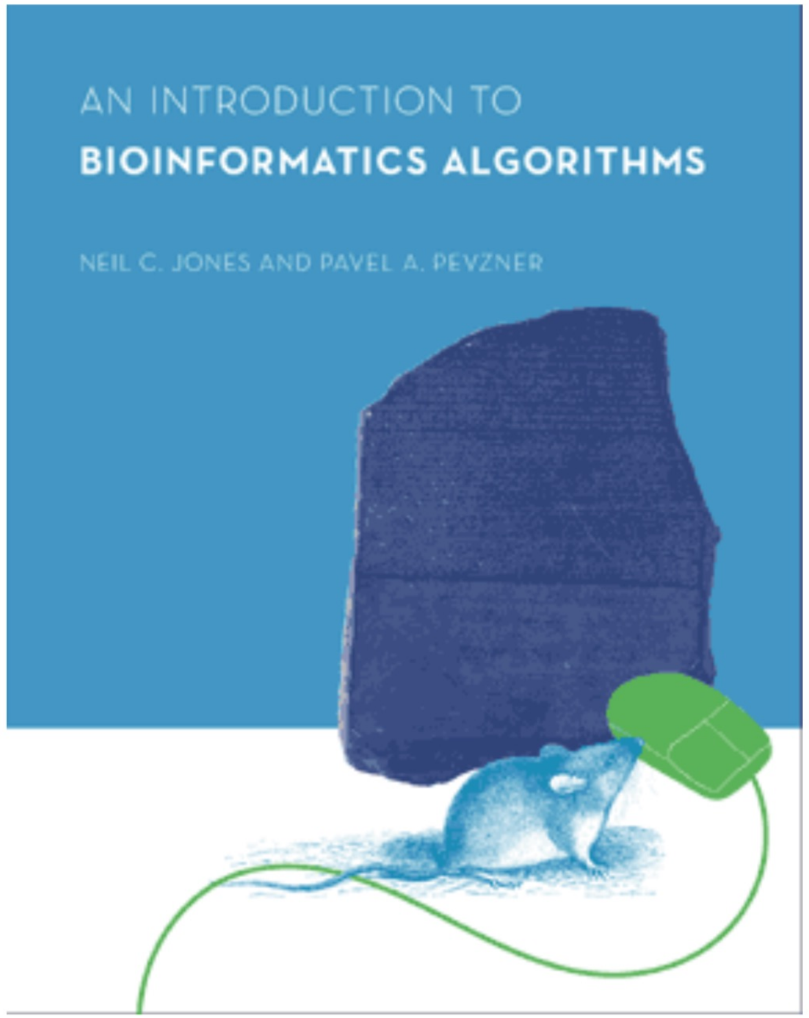
Course Organization

Course website:
https://www.el-kebir.net/teaching/CS466/Fall_2021/CS466.html

Syllabus:
- Prerequisites: CS 225 and its prerequisites
- Textbook

Grading:
- 5 written/programming assignments
- Midterm
- Final
- Research project
- Use Gradescope: 'X3KPBE'

Piazza: (please sign up)
- https://piazza.com/illinois/fall2021/cs466



Course Objectives

Learn:

- Learn underlying ideas of common algorithms in bioinformatics.
- Learn to translate a biological problem into a computational problem.
- Learn to read scientific papers, propose and conduct independent research.

Not learn:

- Will not learn to run popular bioinformatics packages.
- Will not learn how to program.

Homework Assignments

- 5 homework assignments
- Each homework assignment is a combination of written/programming exercises
- LaTeX highly recommended for homework assignments
- Python for programming exercises

Late policy:

- Students may use one 3-day extension in the semester for full credit
- Otherwise, late submission within 3 days 80%
- Otherwise, submission after 3 days 0%

Primer on Molecular Biology

Molecular Biology is the field of **biology** that studies the composition, structure and interactions of cellular **molecules** – such as nucleic acids and proteins – that carry out the **biological** processes essential for the cell's functions and maintenance.

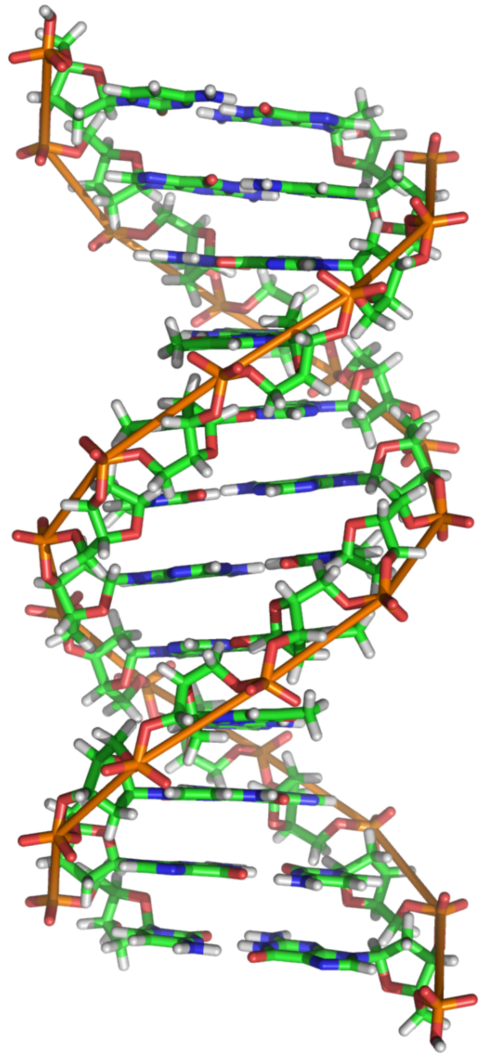
https://www.nature.com/subjects/molecular-biology

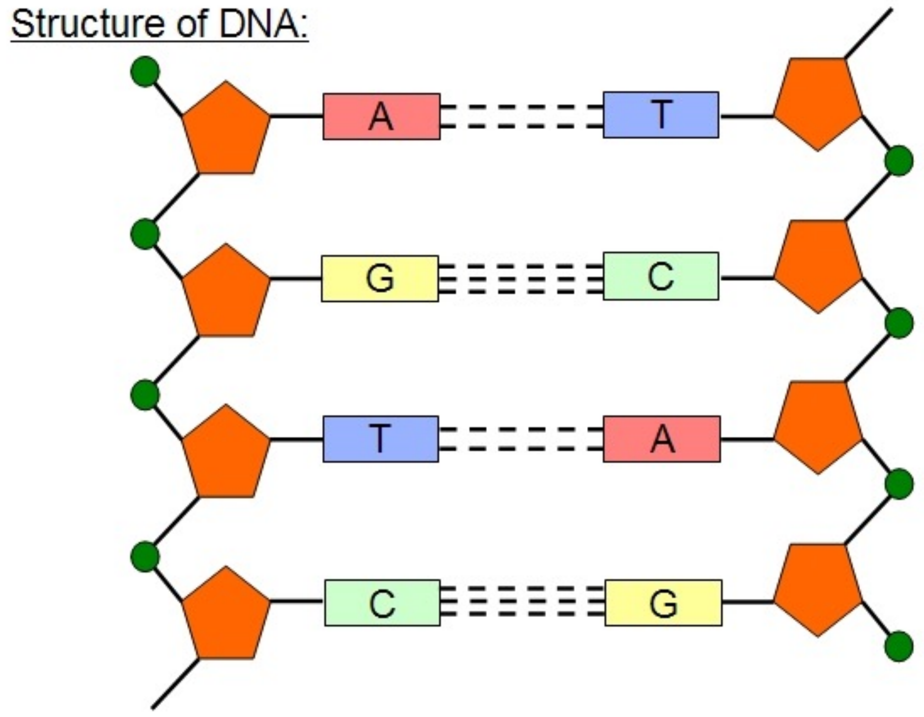
Cellular molecules:

1. DNA
2. RNA
3. Protein

DNA

Each strand composed of sequence of covalently bonded **nucleotides** (**bases**).





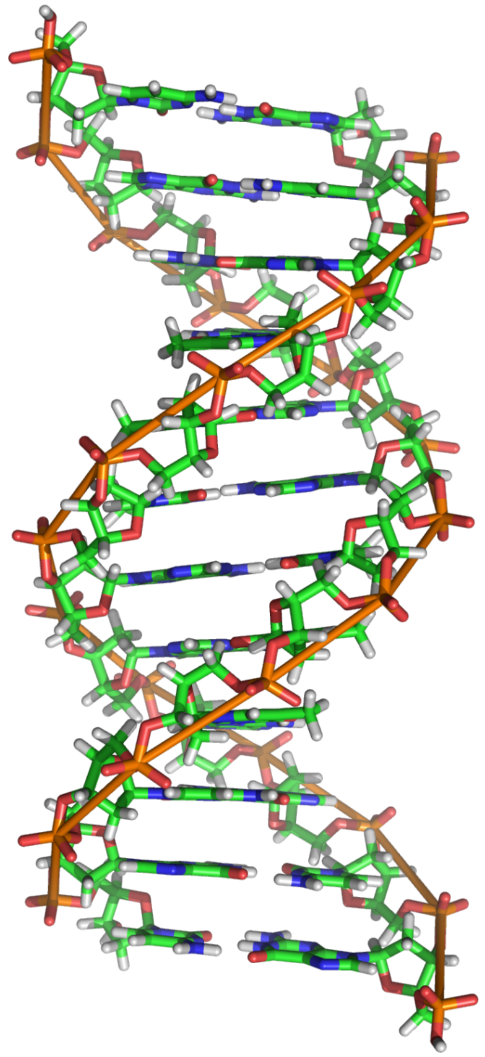
Four nucleotides:

A (adenine)
C (cytosine)
T (thymine)
G (guanine)

A ←→ T, C ←→G Watson-Crick base-pairing

DNA

Each strand composed of sequence of covalently bonded **nucleotides** (**bases**).



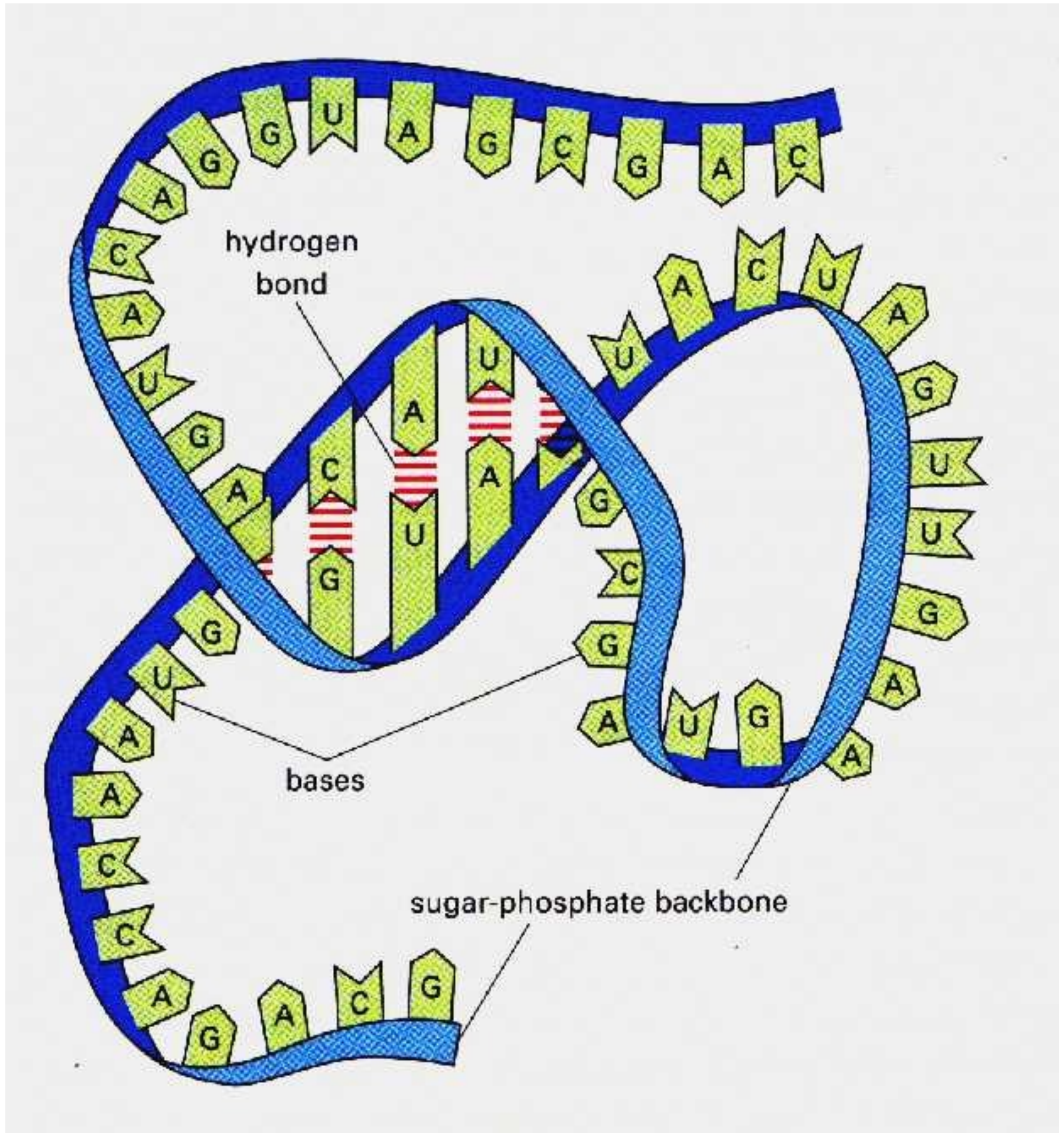
```
5’ ...ACGTGACTGAGGACCGTG... 3’
   ...||||||||||||||||||...
3’ ...TGCACTGACTCCTGGCAC... 5’
```

Pair of strings from 4-character alphabet

```
5’ ...ACGTGACTGAGGACCGTG
      CGACTGAGACTGACTGGGT
      CTAGCTAGACTACGTTTTA
      TATATATATACGTCGTCGT
      ACTGATGACTAGATTACAG
      TGATTTTAAAAAATATT... 3’
```

Single string from 4-character alphabet

RNA



- **Single-stranded**
  - A (adenine)
  - C (cytosine)
  - U (uracil)
  - G (guanine)

- Can fold into **structures** due to base complementarity.

  A ←→ U, C ←→G

- Comes in many flavors:

  mRNA, rRNA, tRNA, tmRNA, snRNA, snoRNA, scaRNA, aRNA, asRNA, piwiRNA, etc.

Protein

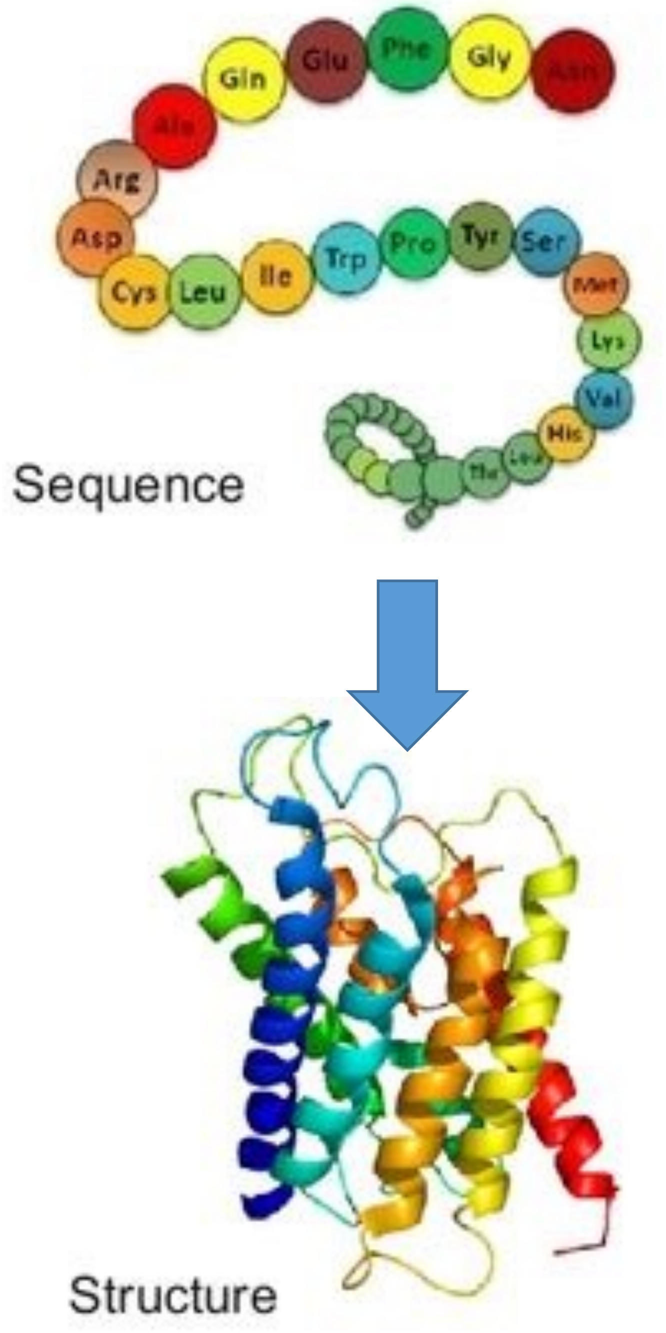
- String of amino acids: 20 letter alphabet

…DTIGDWNSPSFFGIQLVSSVHT
TLWYRENAFPVLGGFSWLSWFNW
HNMGYYYPVYHIGYPMIRCGTHL
VPMQFAFQSIARSFALVHWNAPM
VLKINPHERQDPVFWPCLYYSVD
IRSMHIGYPMIRCYQA…

Amino Acid	3-Letters	1-Letter
Alanine	Ala	A
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Cysteine	Cys	C
Glutamic acid	Glu	E
Glutamine	Gln	Q
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

Protein

- String of amino acids: 20 letter alphabet
- Folds into 3D structures to perform various functions in cells



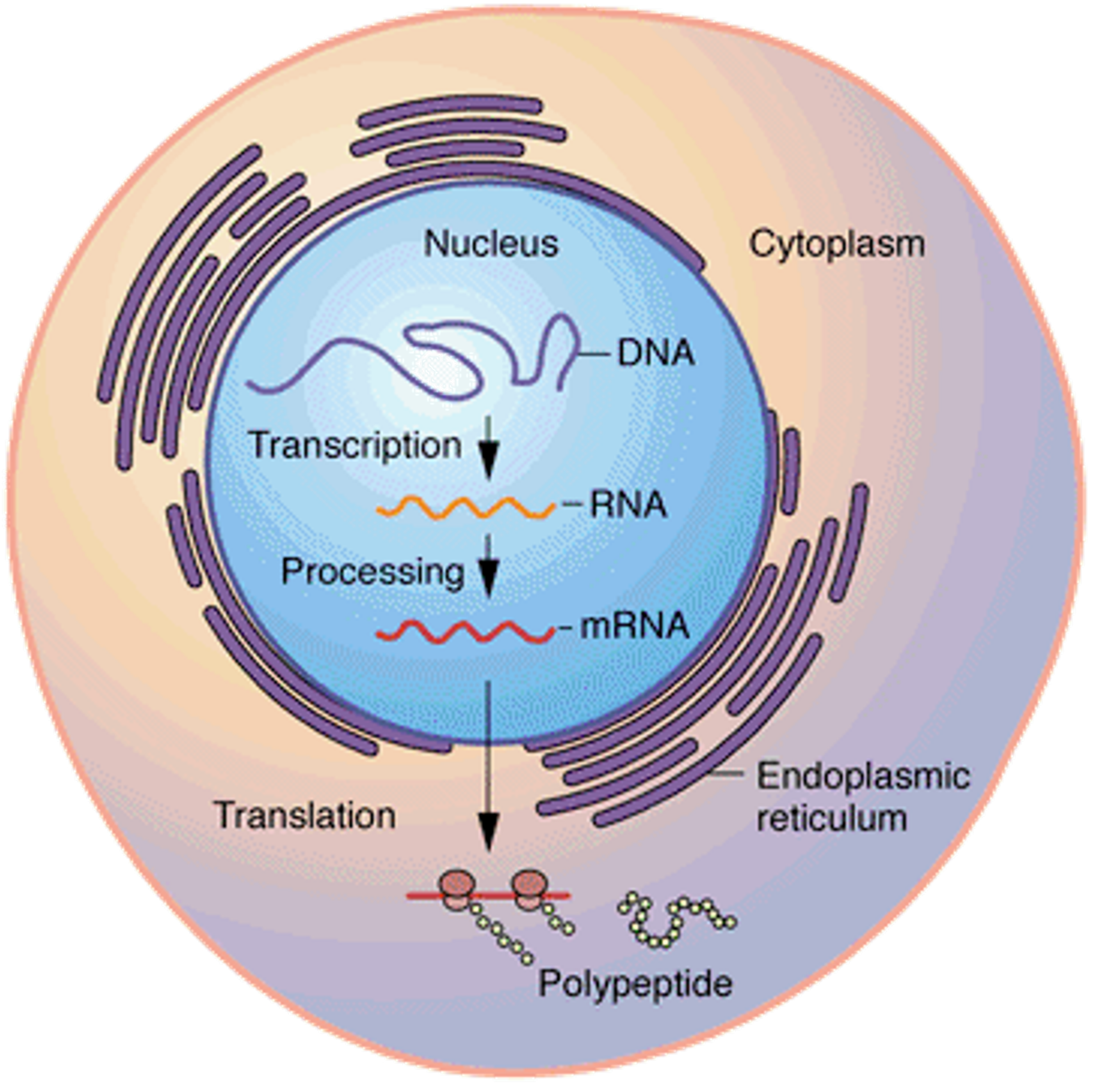
Primer on Molecular Biology

Three fundamental molecules:

1. **DNA**
   Information storage.

2. **RNA**
   Old view: Mostly a "messenger".
   New view: Performs many important functions.

3. **Protein**
   Perform most cellular functions (biochemistry, signaling, control, etc.)



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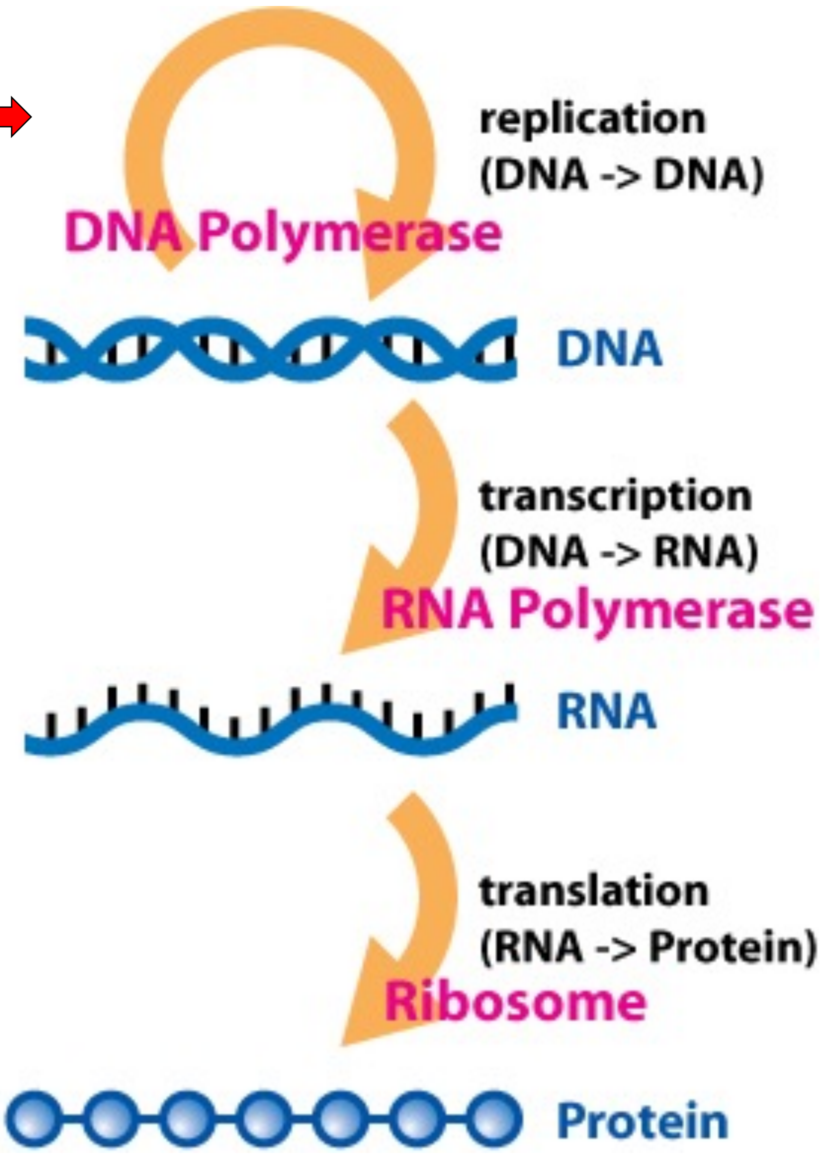
Central Dogma of Molecular Biology

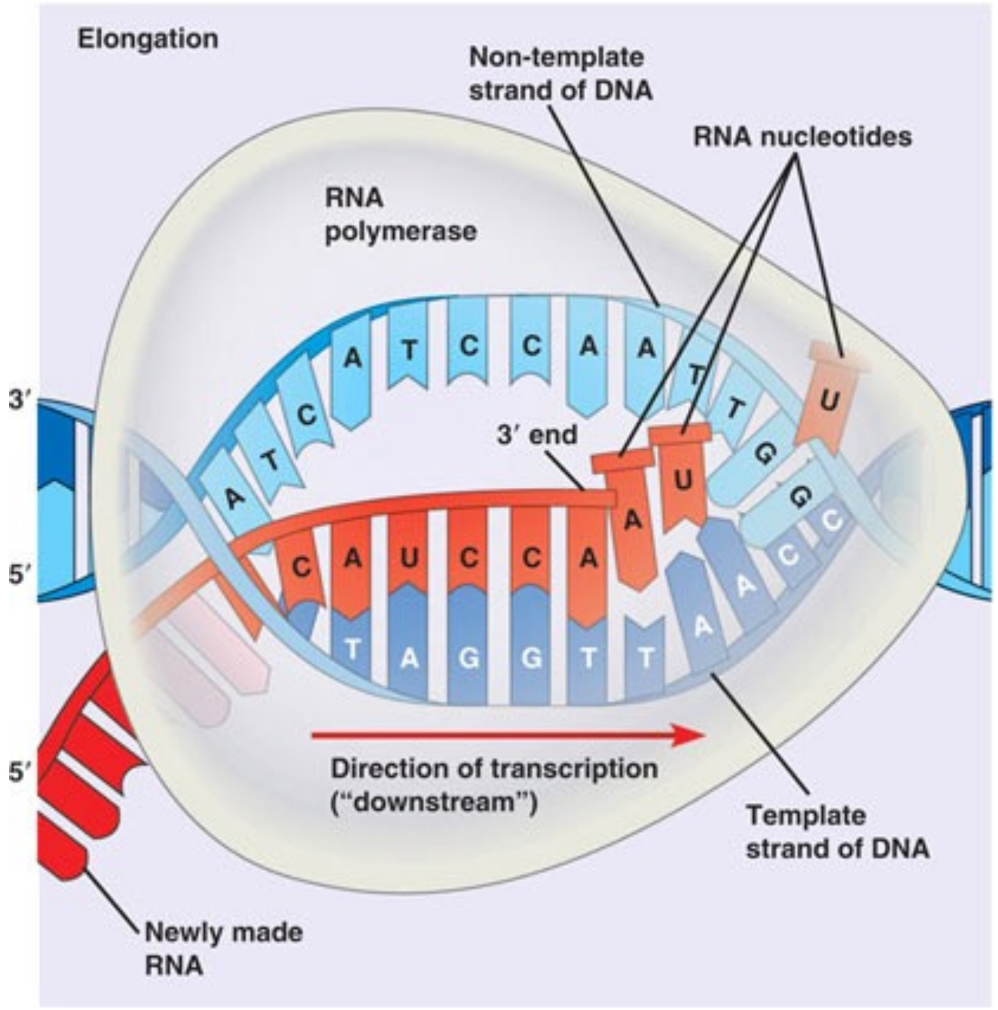
Start here



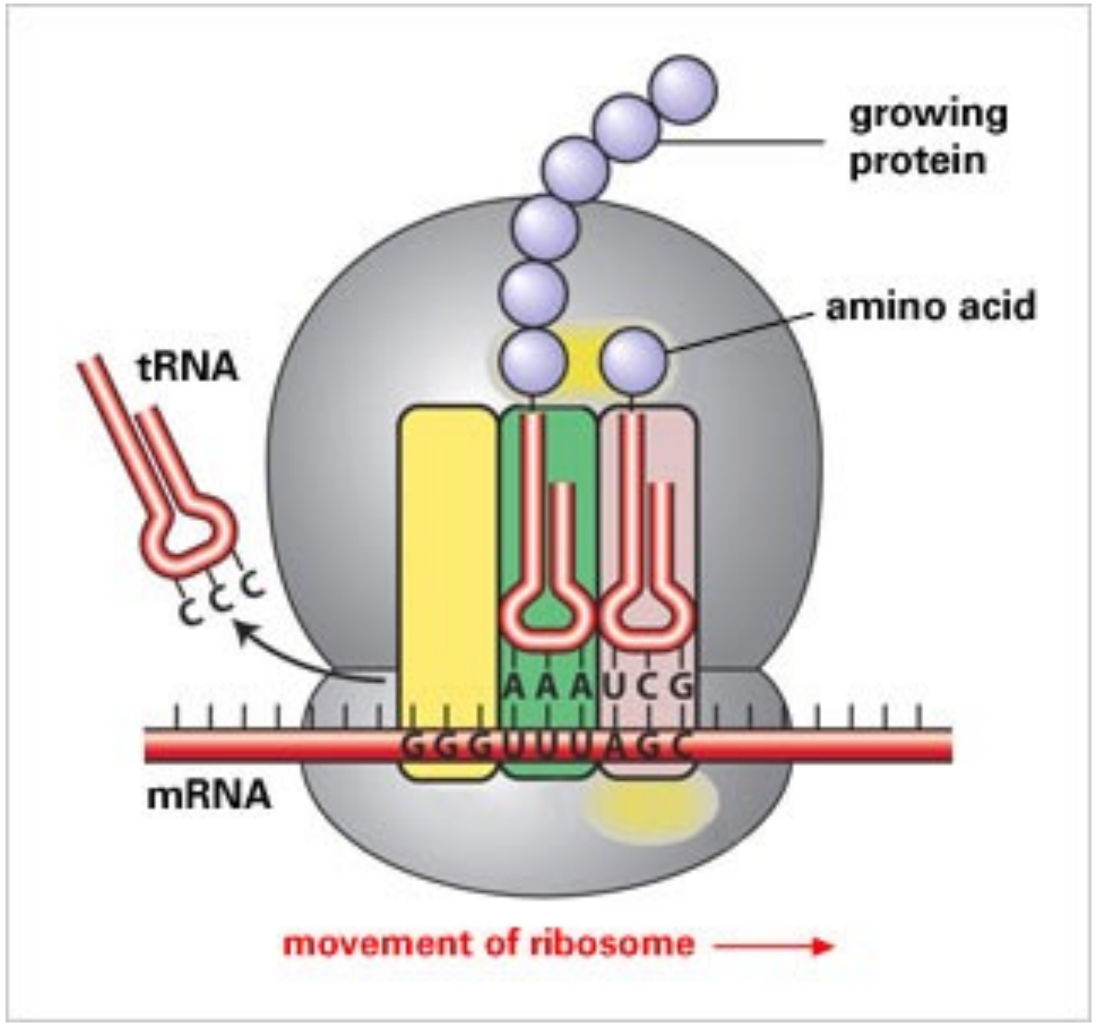
DNA → RNA → Protein:
The process by which cells "read" the genome

First proposed by Francis Crick in 1956.

Transcription and Translation

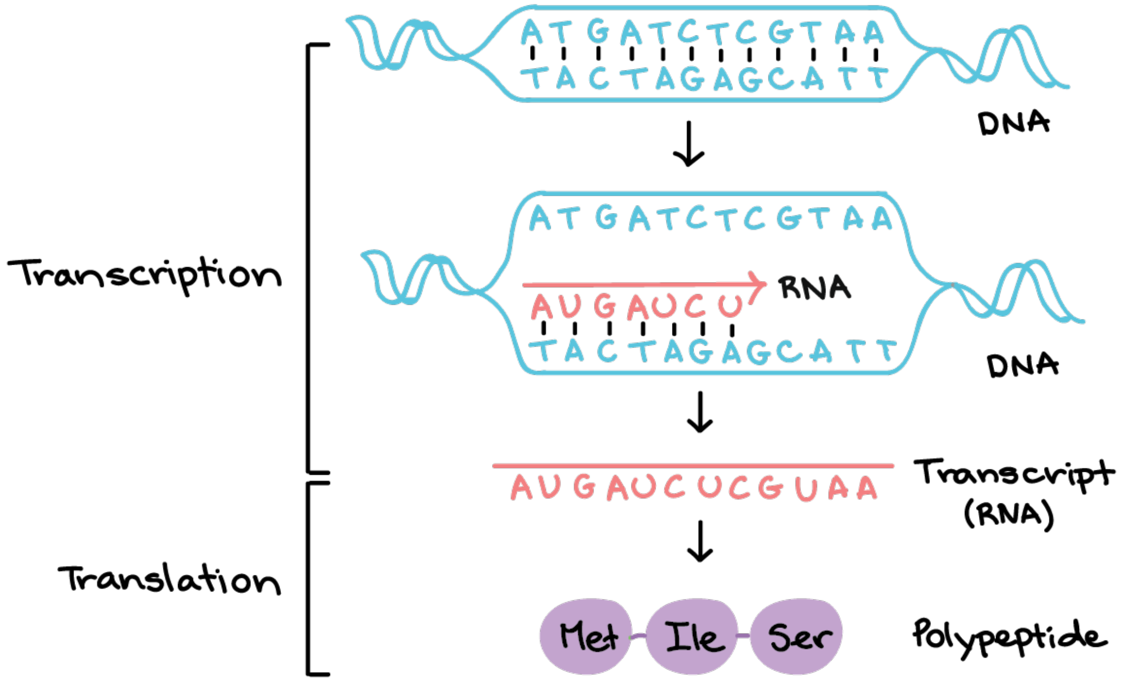


http://dna-rna.net/wp-content/uploads/2011/08/rna-transcription2.jpg

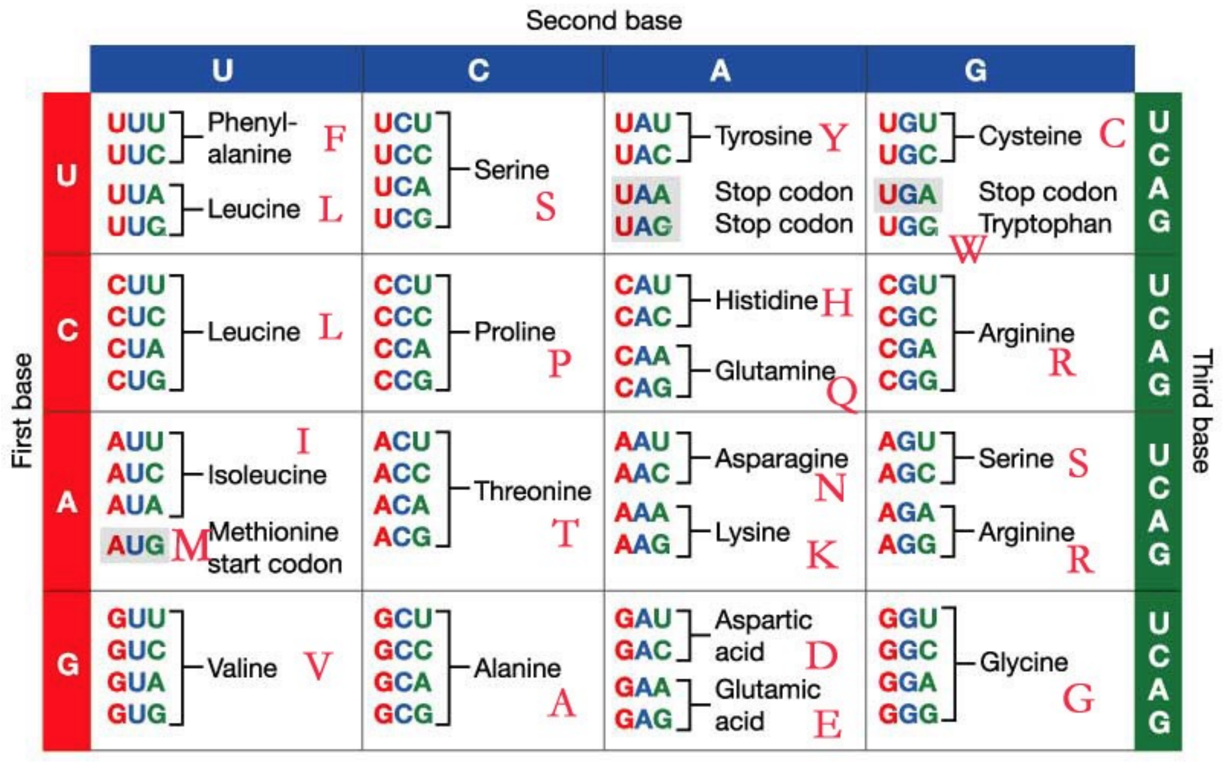


http://www.frontiers-in-genetics.org/en/pictures/translation_1.jpg

Transcription and Translation



https://www.khanacademy.org/science/biology/gene-expression-central-dogma/transcription-of-dna-into-rna/a/overview-of-transcription



First base	Second base: U	C	A	G	Third base
U	UUU Phenyl-alanine F	UCU Serine S	UAU Tyrosine Y	UGU Cysteine C	U
U	UUC Phenyl-alanine F	UCC Serine S	UAC Tyrosine Y	UGC Cysteine C	C
U	UUA Leucine L	UCA Serine S	UAA Stop codon	UGA Stop codon	A
U	UUG Leucine L	UCG Serine S	UAG Stop codon	UGG Tryptophan W	G
C	CUU Leucine L	CCU Proline P	CAU Histidine H	CGU Arginine R	U
C	CUC Leucine L	CCC Proline P	CAC Histidine H	CGC Arginine R	C
C	CUA Leucine L	CCA Proline P	CAA Glutamine Q	CGA Arginine R	A
C	CUG Leucine L	CCG Proline P	CAG Glutamine Q	CGG Arginine R	G
A	AUU Isoleucine I	ACU Threonine T	AAU Asparagine N	AGU Serine S	U
A	AUC Isoleucine I	ACC Threonine T	AAC Asparagine N	AGC Serine S	C
A	AUA Isoleucine I	ACA Threonine T	AAA Lysine K	AGA Arginine R	A
A	AUG M Methionine start codon	ACG Threonine T	AAG Lysine K	AGG Arginine R	G
G	GUU Valine V	GCU Alanine A	GAU Aspartic acid D	GGU Glycine G	U
G	GUC Valine V	GCC Alanine A	GAC Aspartic acid D	GGC Glycine G	C
G	GUA Valine V	GCA Alanine A	GAA Glutamic acid E	GGA Glycine G	A
G	GUG Valine V	GCG Alanine A	GAG Glutamic acid E	GGG Glycine G	G

http://bioinfo.bisr.res.in/project/crat/pictures/codon.jpg

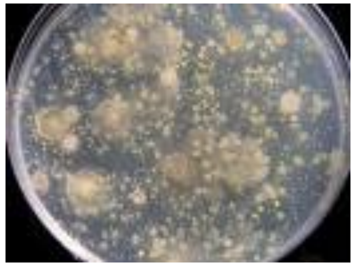
What is Computational Biology/Bioinformatics?

Computational biology and **bioinformatics** is an interdisciplinary field that develops and applies **computational methods** to analyze large collections of biological data, such as genetic sequences, cell populations or protein samples, to make new predictions or **discover new biology**.

https://www.nature.com/subjects/computational-biology-and-bioinformatics

Technology and Bioinformatics are Transforming Biology

Until late 20th Century



$\longrightarrow$ Hypothesis Generation and Validation

21th Century and Beyond

$\xrightarrow{\textbf{Algorithms}}$ Hypothesis Generation and Validation

High throughput technologies

A Deluge of Data

Log Scale

100,000,000

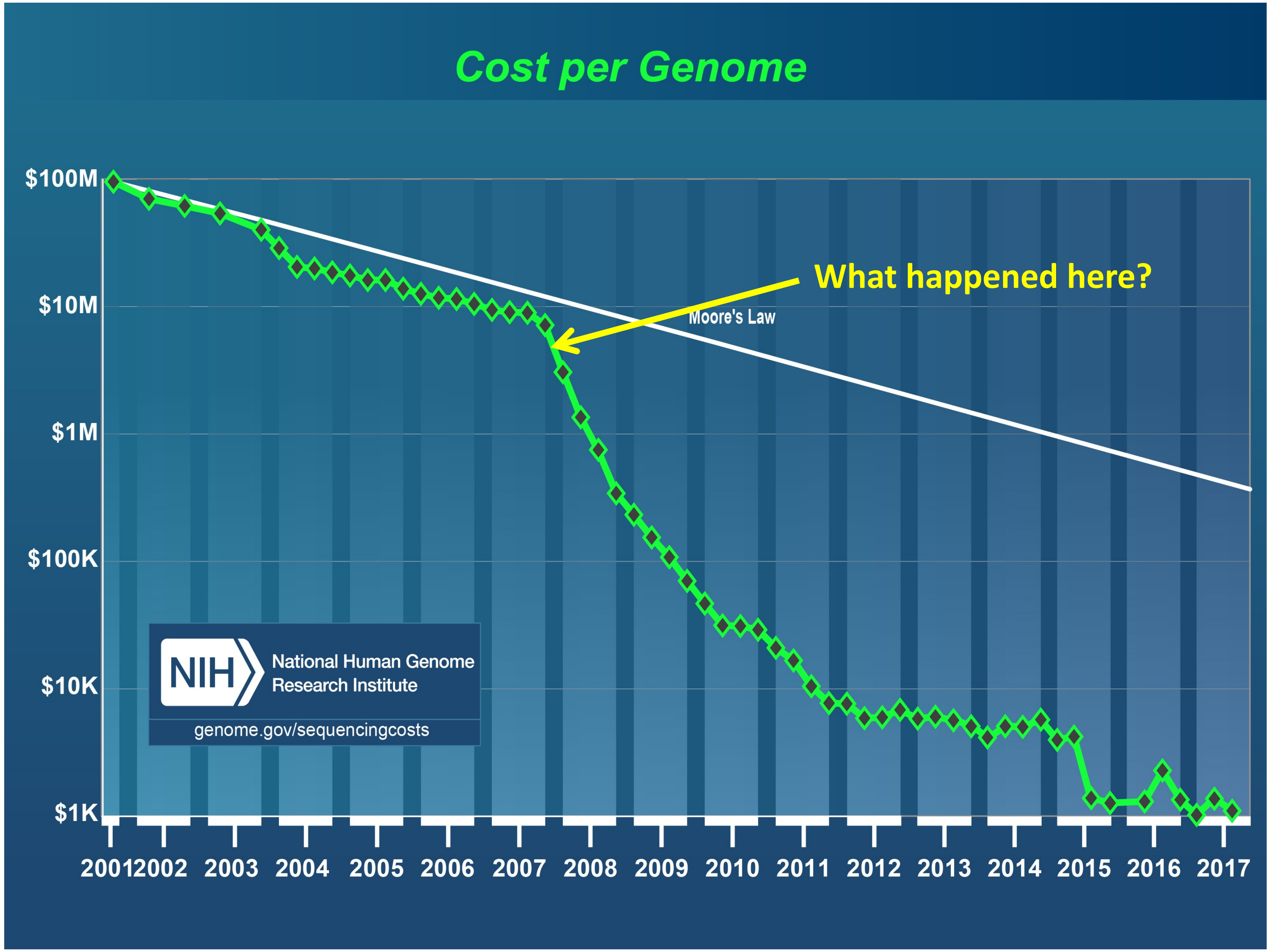
10,000,000

1,000,000

100,000

10,000

1,000



A Deluge of Data

1000 Genomes
A Deep Catalog of Human Genetic Variation

adsp
Alzheimer's Disease
Sequencing Project

1000 Plant
Genomes

T1K
Fish-T1K
Transcriptomes of 1000 Fishes

GENOME 10K

Autism
Genome
10K

100k
genomes
project

International
Cancer Genome
Consortium

HMP
NIH HUMAN
MICROBIOME
PROJECT

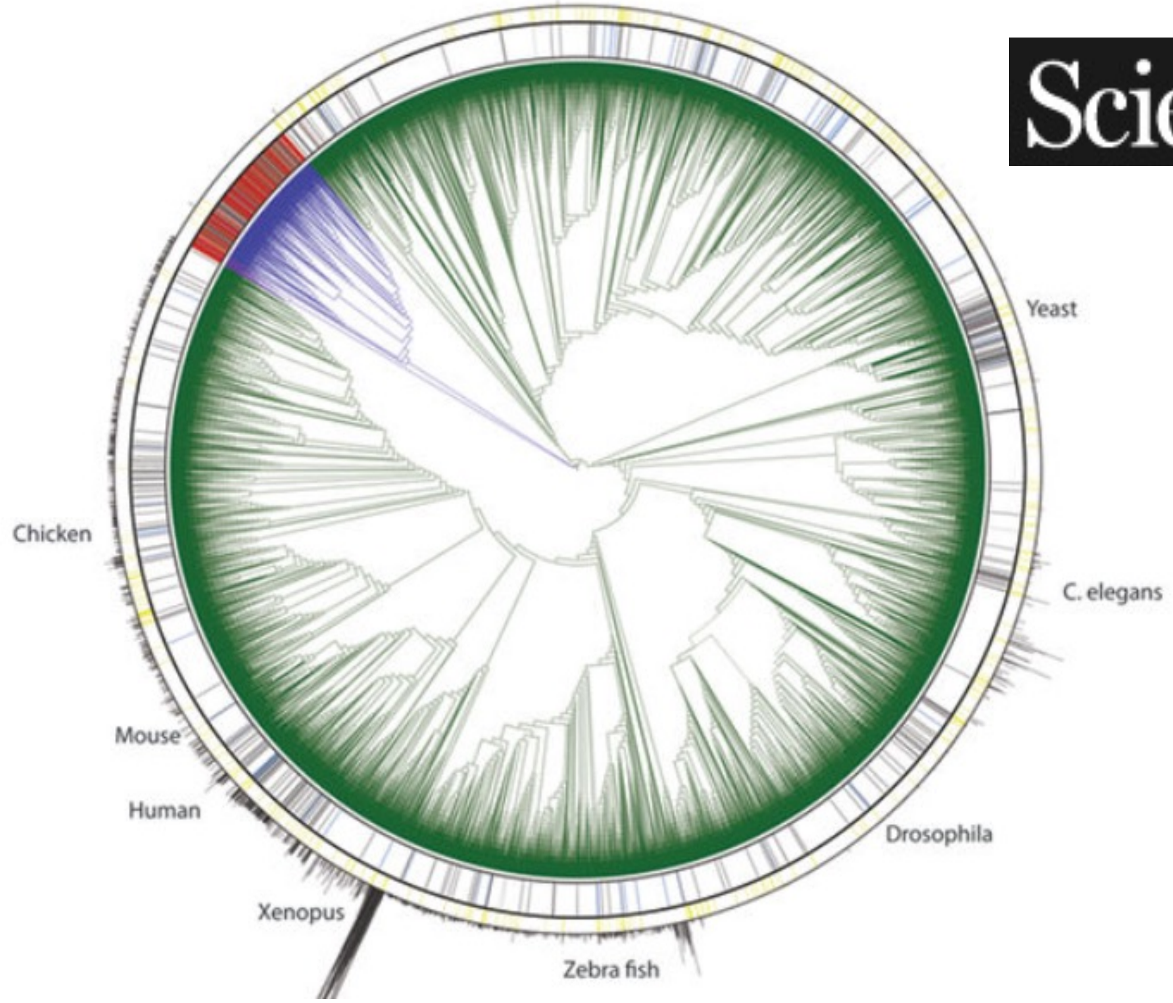
NIH
THE CANCER GENOME ATLAS
National Cancer Institute
National Human Genome Research Institute

A Deluge of Data

Biologists propose to sequence the DNA of all life on Earth

By Elizabeth Pennisi | Feb. 24, 2017 , 1:15 PM

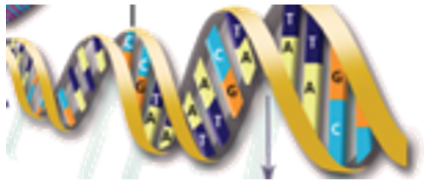
Science



Outer ring color scheme:
Red: Completed genome
Light Blue: Low resolution genome

Question: What does it mean that we can sequence a genome?

No technology exists that can sequence a complete (human) genome from end to end!



Genome
Millions -billions nucleotides

Next-generation DNA sequencing

… CATTCAGTAG …

… AGCCATTAG …

… GGTAGTTAG …

… GGTAAACTAG …

… TATAATTAG …

… CGTACCTAG …

10-100's million noisy ***reads***
Reads: 30-1000 nucleotides

Making sense of this data absolutely requires the use and development of **algorithms**!

Why Study Computational Biology?

Interdisciplinary

- Biology
- Computer Science
- Mathematics
- Statistics

= FUN!

Why choose just 1?

Best Jobs	Worst Jobs
1. Actuary	200. Newspaper reporter
2. Audiologist	199. Lumberjack
3. Mathematician	198. Enlisted Military Personnel
4. Statistician	197. Cook
5. Biomedical Engineer	196. Broadcaster
6. Data Scientist	195. Photojournalist
7. Dental Hygienist	194. Corrections Officer
8. Software Engineer	193. Taxi Driver
9. Occupational Therapist	192. Firefighter
10. Computer Systems Analyst	191. Mail Carrier

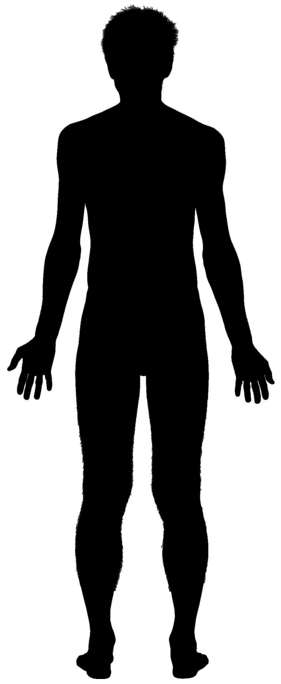
http://www.careercast.com/jobs-rated/jobs-rated-report-2015-ranking-top-200-jobs

Donald Knuth
Professor emeritus of Computer Science at Stanford University
Turing Award winner
"father of the analysis of algorithms."

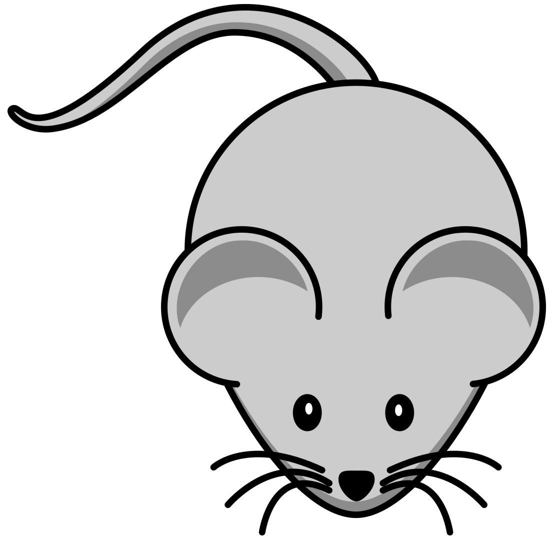
"I can't be as confident about computer science as I can about biology. Biology easily has 500 years of exciting problems to work on. It's at that level."

Course Topic #1: Sequence Alignment

Question: How do we compare two genes/genomes?



vs.



Human Genome:

…ACTCGACTGAGAGGATTTCGAGCATGA…

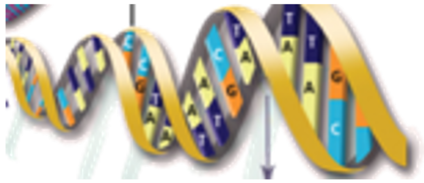
≈3.2 x 10^9 bp

Mouse Genome:

…ACTCAACTGAGATTCGAGCTTCAATGA…

≈2.8 x 10^9 bp

Course Topic #2: Genome Assembly



... CATTCAGTAG ...

... AGCCATTAG ...

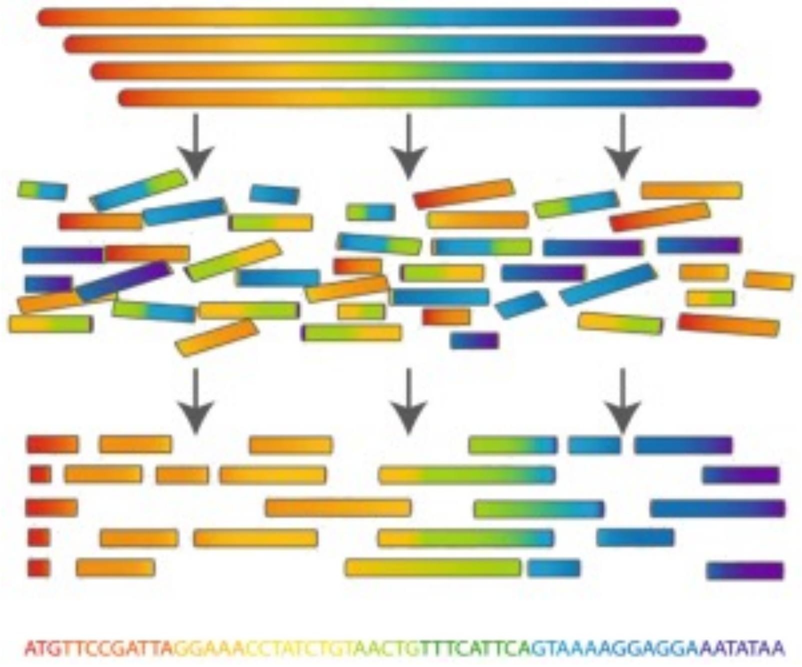
... GGTAGTTAG ...

... GGTAAACTAG ...

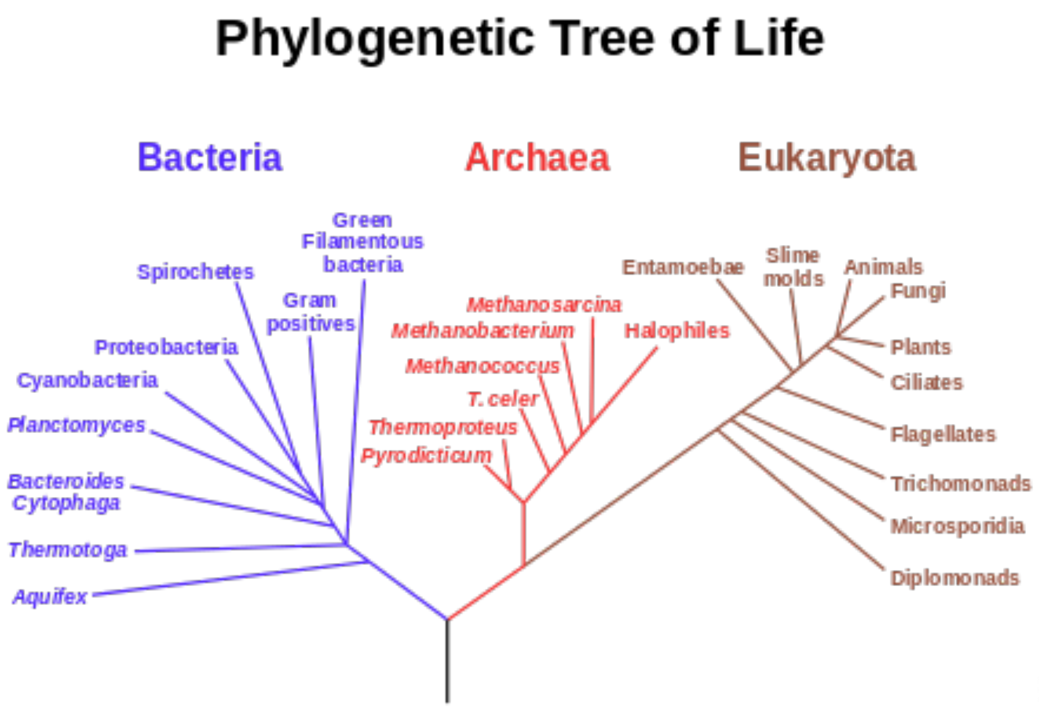
... TATAATTAG ...

... CGTACCTAG ...

Question: How do we put all the pieces back together?



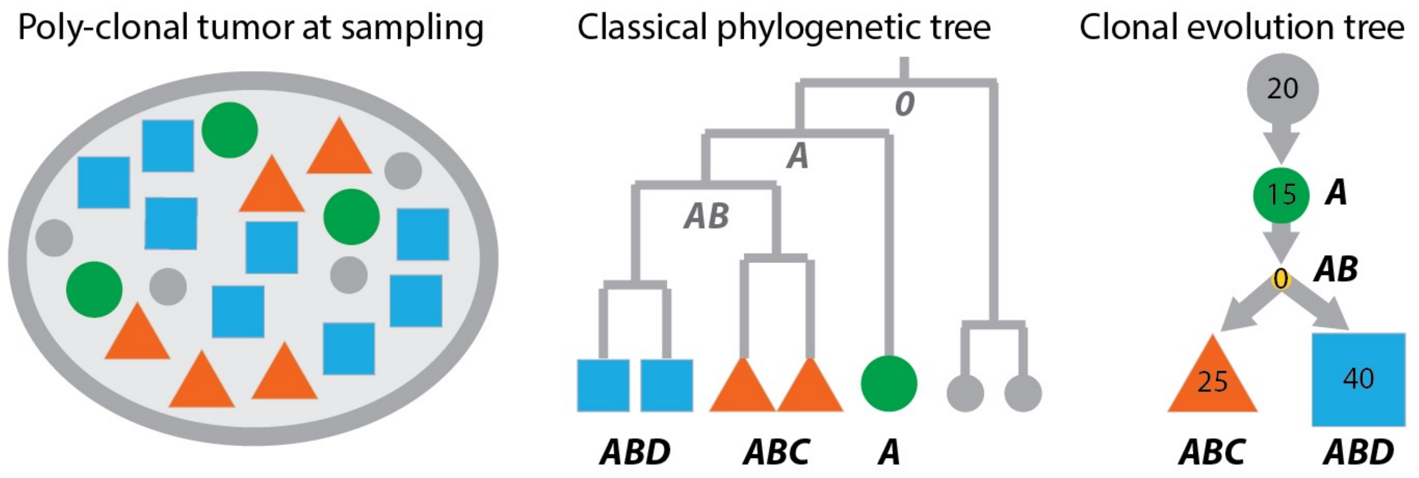
Course Topic #3: Phylogenetics



https://en.wikipedia.org/wiki/Phylogenetic_tree

Question: Can we reconstruct the evolutionary history of different species?

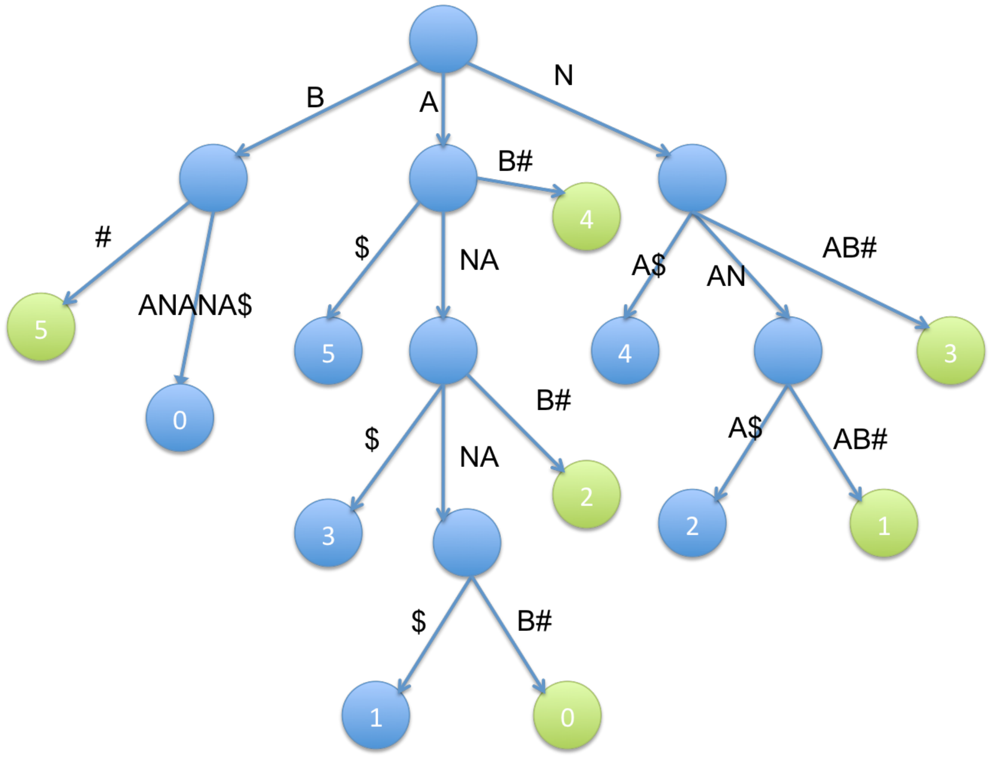
Question: Can we recover how a tumor has evolved overtime?



https://scientificbsides.wordpress.com/2014/06/09/inferring-tumour-evolution-2-comparison-to-classical-phylogenetics/

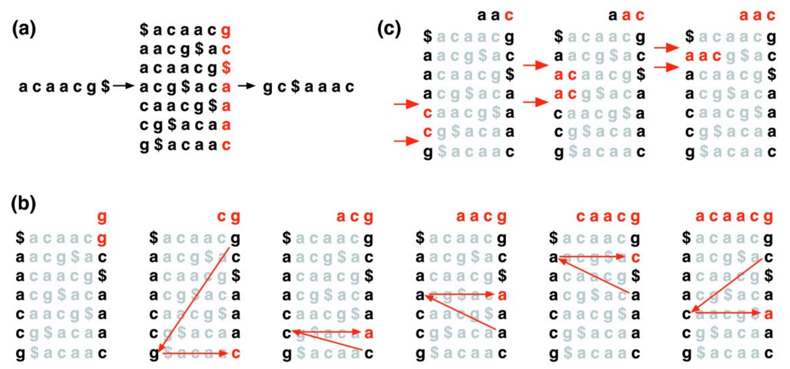
Course Topic #4: Pattern Matching

Question: How do we start to make sense of all these sequences?



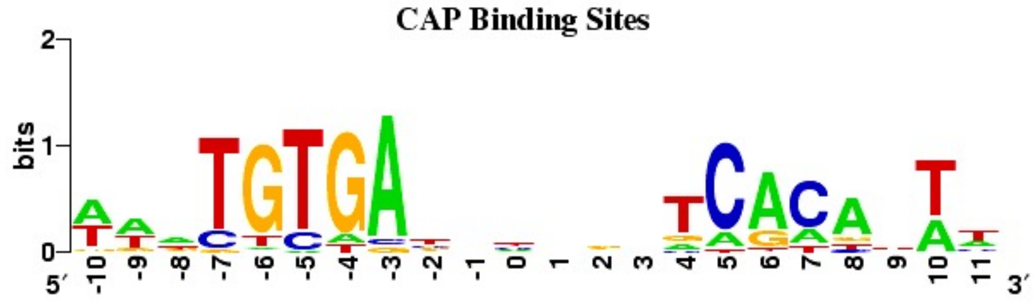
Suffix Trees

Burrows Wheeler Transform



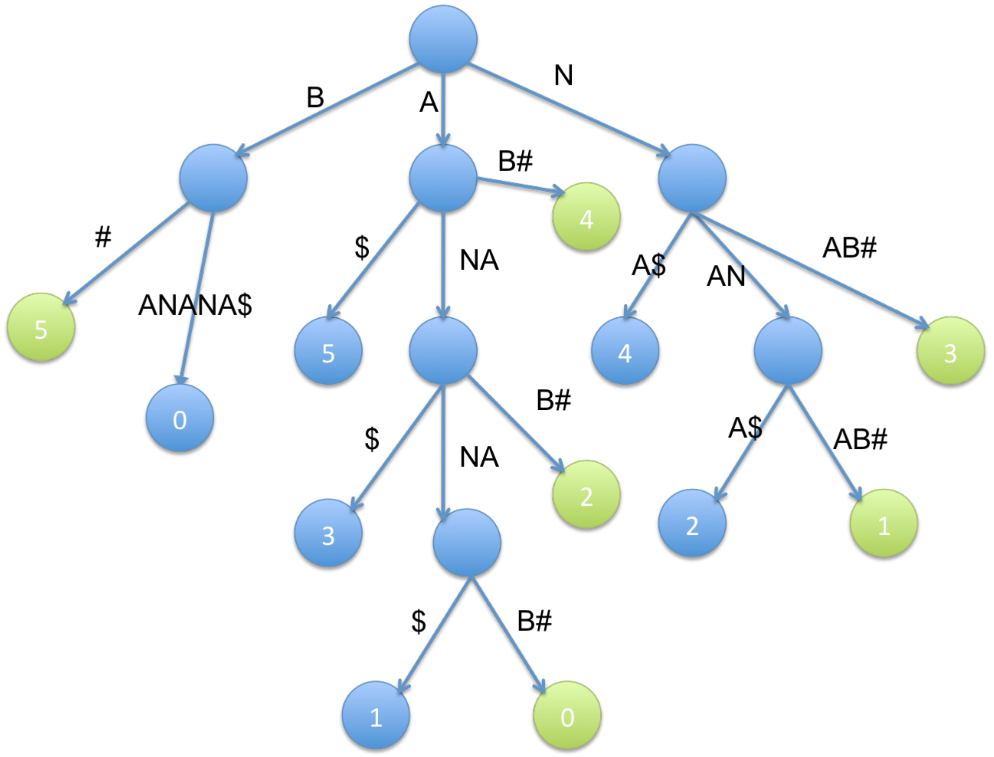
http://www.genomebiology.com/2009/10/3/R25/figure/F1?highres=y

Motif Finding



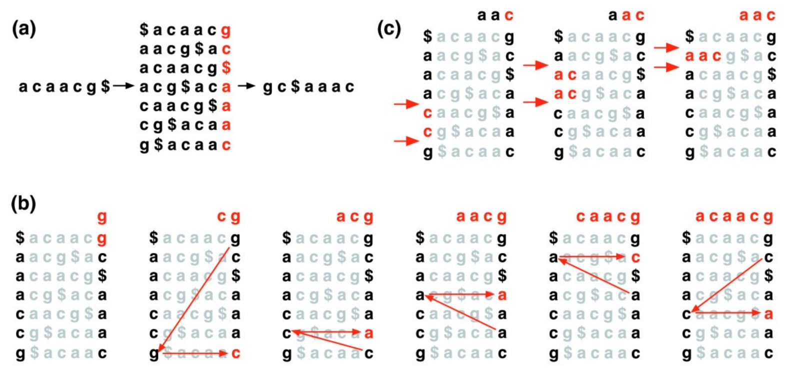
Course Topic #4: Pattern Matching

Question: How do we start to make sense of all these sequences?



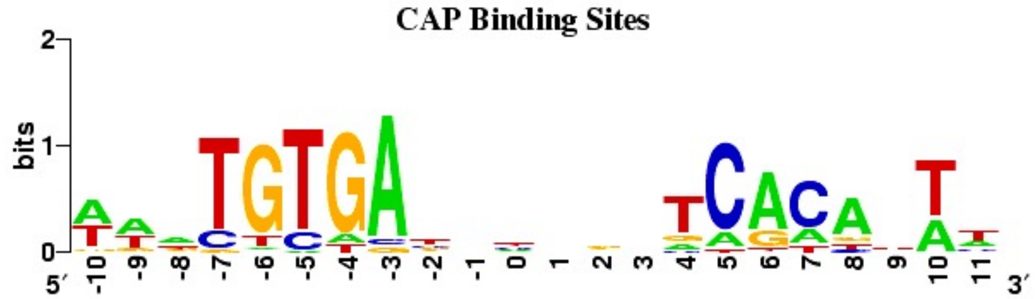
Suffix Trees

Burrows Wheeler Transform

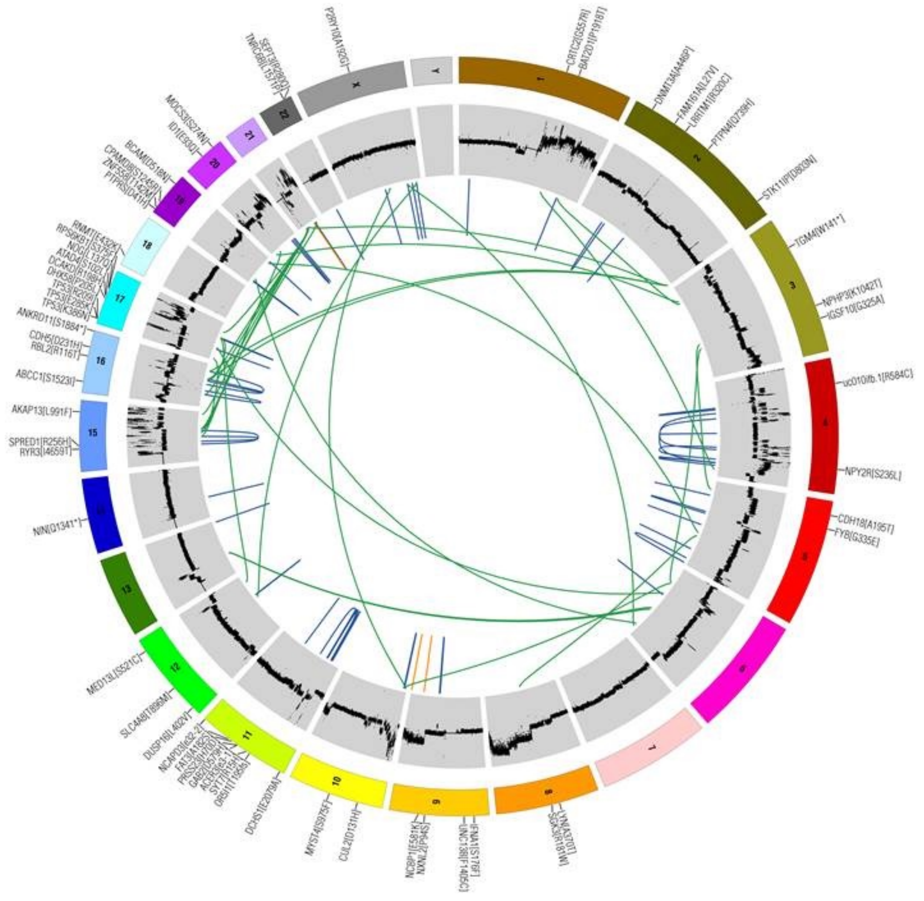


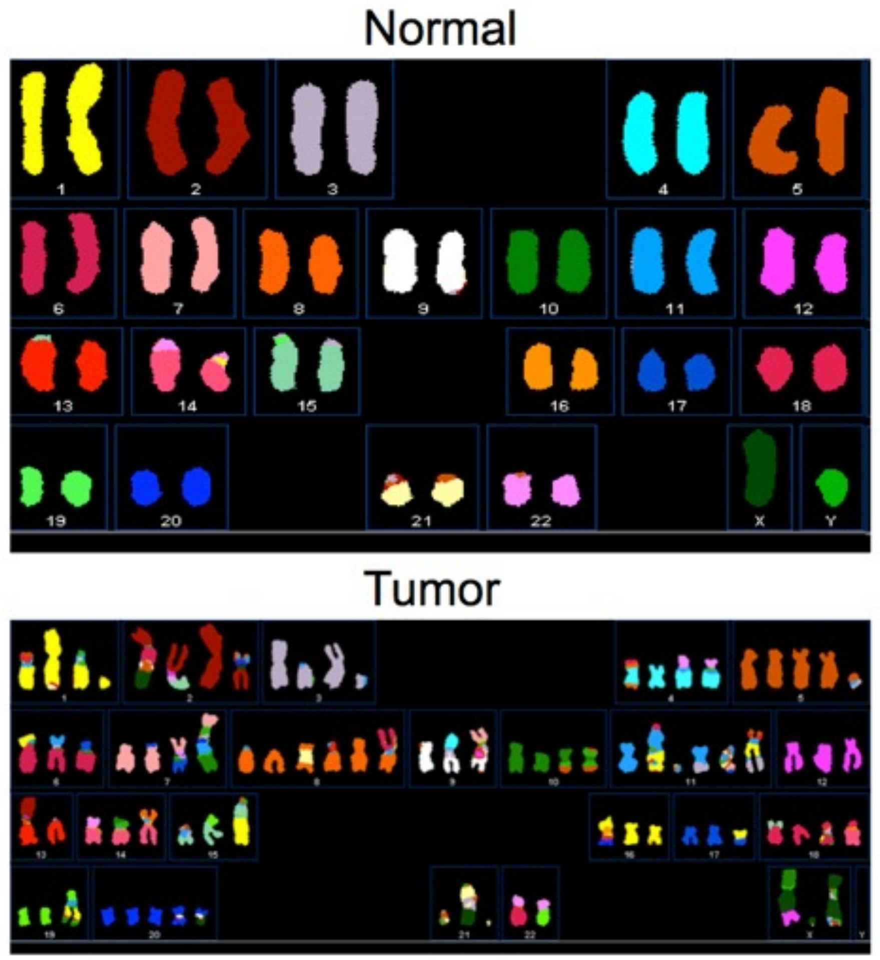
http://www.genomebiology.com/2009/10/3/R25/figure/F1?highres=y

Motif Finding



Course Topic #5: Cancer Genomics





Question: How can we analyze available data to determine what drives tumor growth and how to treat or prevent it?

Course Topics

1. Sequence alignment
   'How do we compare two genes/genomes?'

2. Genome assembly
   'How do we put all the pieces back together?'

3. Phylogenetics
   'What is the evolutionary history of different sequences?'

4. Pattern matching
   'How do we start to make sense out of all these sequences?'

5. Cancer genomics
   'How do we identify what drives tumor growth and how to treat/prevent it?'

Course Topics

1. Sequence alignment
   Dynamic programming: edit distance

2. Genome assembly
   Graphs: de Bruijn graph, Eulerian and Hamiltonian paths

3. Phylogenetics
   Trees and distances: distance matrices, neighbor joining, hierarchical clustering.
   Phylogenies: Sankoff/Fitch algorithms, perfect phylogeny and compatibility

4. Pattern matching
   Suffix trees/arrays. Burrows-Wheeler transform, Hidden Markov Models (HMMs)

5. Cancer genomics
   Cancer phylogenies: Integer linear optimization and graph algorithms

Problem != Algorithm

Problem Π with instance X and solution set $\Pi(X)$:

- Decision problem:
  - Is $\Pi(X) = \emptyset$?
- Optimization problem:
  - Find $y^* \in \Pi(X)$ s.t. $f(y^*)$ is optimum.
- Counting problem:
  - Compute $|\Pi(X)|$.
- Sampling problem:
  - Sample uniformly from $\Pi(X)$.
- Enumeration problem:
  - Enumerate all solutions in $\Pi(X)$

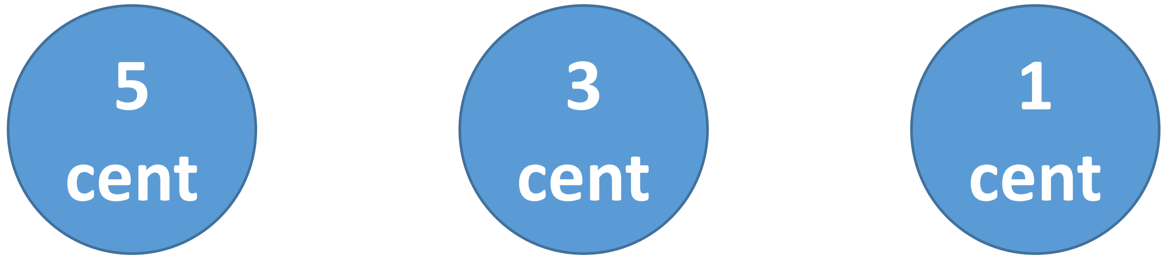
Algorithms:

Set of instructions for solving problem.

- Exact
- Heuristic

The Change Problem

- Suppose we have three coins:



- What is the minimum number of coins needed to make change for ***M*** cents?

The Change Problem

- Suppose we have three coins:

$\mathbf{c} = ($ **5 cent** , **3 cent** , **1 cent** $)$

- What is the minimum number of coins needed to make change for ***M*** cents?

Change Problem: Given amount $M \in \mathbb{N} \setminus \{0\}$ and coins $\mathbf{c} = (c_1, \dots, c_n) \in \mathbb{N}^n$ s.t. $c_n = 1$ and $c_i \geq c_{i+1}$ for all $i \in [n-1] = \{1, \dots, n-1\}$, find $\mathbf{d} = (d_1, \dots, d_n) \in \mathbb{N}^n$ s.t. (i) $M = \sum_{i=1}^{n} c_i d_i$ and (ii) $\sum_{i=1}^{n} d_i$ is minimum

Idea #1: Choose largest coin possible

```
GreedyChange($M, c_1, \ldots, c_n$)
1. for $i \leftarrow 1$ to $n$
2.     $d_i \leftarrow \lfloor M/c_i \rfloor$
3.     $M \leftarrow M - d_i c_i$
```

Idea #1: Choose largest coin possible

```
GreedyChange($M, c_1, \ldots, c_n$)
1. for $i \leftarrow 1$ to $n$
2.     $d_i \leftarrow \lfloor M/c_i \rfloor$
3.     $M \leftarrow M - d_i c_i$
```

Is this a good algorithm? Two properties of a good algorithm:

Idea #1: Choose largest coin possible

```
GreedyChange($M, c_1, \ldots, c_n$)
1. for $i \leftarrow 1$ to $n$
2.     $d_i \leftarrow \lfloor M/c_i \rfloor$
3.     $M \leftarrow M - d_i c_i$
```

Is this a good algorithm? Two properties of a good algorithm:

Correctness: gives the correct output for any input.

- Works for $\mathbf{c} = (5, 3, 1)$ and $M = 8$.
- But what about $\mathbf{c} = (5, 4, 1)$ and $M = 8$?

Efficient: *running time* of the algorithm does not increase too rapidly with input size.

Idea #2: When in doubt, apply brute force...

Change Problem: Given amount $M \in \mathbb{N} \setminus \{0\}$ and coins $\mathbf{c} = (c_1, \dots, c_n) \in \mathbb{N}^n$ s.t. $c_n = 1$ and $c_i \geq c_{i+1}$ for all $i \in [n-1] = \{1, \dots, n-1\}$, find $\mathbf{d} = (d_1, \dots, d_n) \in \mathbb{N}^n$ s.t. (i) $M = \sum_{i=1}^{n} c_i d_i$ and (ii) $\sum_{i=1}^{n} d_i$ is minimum

$\mathbf{c} = ($ **5 cent** , **4 cent** , **1 cent** $)$

Correct? yes
Efficient? no

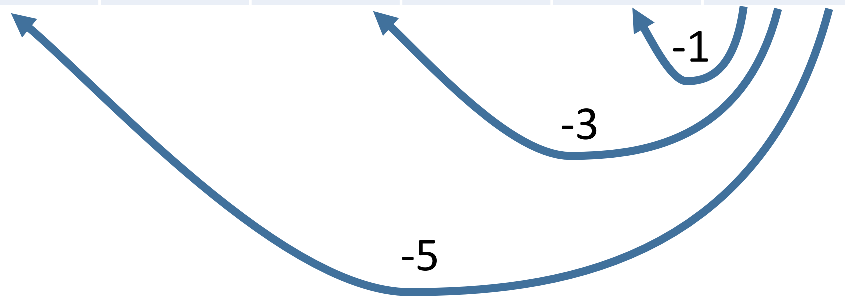
- Check all possible solutions:
  - 11 = 5 + 5 + 1
  - 11 = 5 + 4 + 1 + 1
  - 11 = 5 + 1 + 1 + 1 + 1 + 1 + 1
  - 11 = 4 + 4 + 1 + 1 + 1
  - …

```
ExhaustiveChange($M, c_1, \dots, c_n$)
1. for $(d_1, \dots, d_n) \in \{0, \dots, \lfloor M/c_1 \rfloor\} \times \dots \times \{0, \dots, \lfloor M/c_n \rfloor\}$
2.     if $\sum_{i=1}^{n} c_i d_i = M$
3.         return $(d_1, \dots, d_n)$
```

Idea #3: Recursion

$\mathbf{c} = ($ **5 cent** , **3 cent** , **1 cent** $)$

Value	1	2	3	4	5	6	7	8	9	10	11
Min # coins	?	?	?	?	?	?	?	?	?	?	?



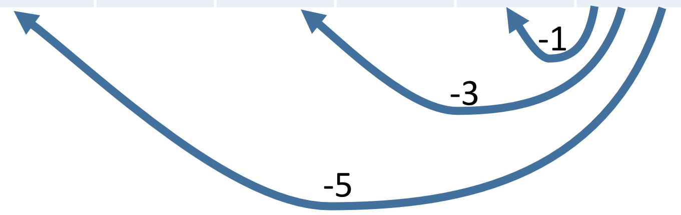
Optimal substructure:

Optimal solution is obtained from optimal solutions of subproblems

Idea #3: Recursion

$\mathbf{c} = (5, 3, 1)$

Value	1	2	3	4	5	6	7	8	9	10	11
Min # coins	?	?	?	?	?	?	?	?	?	?	?



- This example can be expressed using a recurrence relation
- Let minNumCoins(*M*) be the minimum number of coins to make change for *M* cents

$$\text{minNumCoins}(M) = \min \begin{cases} \text{minNumCoins}(M-1)+1, \\ \text{minNumCoins}(M-3)+1, \\ \text{minNumCoins}(M-5)+1. \end{cases}$$

Idea #3: Recursion

Change Problem: Given amount $M \in \mathbb{N} \setminus \{0\}$ and coins $\mathbf{c} = (c_1, \dots, c_n) \in \mathbb{N}^n$ s.t. $c_n = 1$ and $c_i \geq c_{i+1}$ for all $i \in [n-1] = \{1, \dots, n-1\}$, find $\mathbf{d} = (d_1, \dots, d_n) \in \mathbb{N}^n$ s.t. (i) $M = \sum_{i=1}^{n} c_i d_i$ and (ii) $\sum_{i=1}^{n} d_i$ is minimum

$$\text{minNumCoins}(M) = \min \begin{cases} \text{minNumCoins}(M - c_1) + 1, \\ \text{minNumCoins}(M - c_2) + 1, \\ \dots \\ \text{minNumCoins}(M - c_n) + 1. \end{cases}$$

Idea #3: Recursion

Given coins $\mathbf{c} = (1, 3, 7)$ and amount $M = 77$, find $\mathbf{d} = (d_1, \ldots, d_n) \in \mathbb{N}^n$ such that: (i) $M = \sum_{i=1}^{n} c_i d_i$ and (ii) $\sum_{i=1}^{n} d_i$ is minimum.

$$\text{minNumCoins}(77) = \min \begin{cases} \text{minNumCoins}(77-1)+1, \\ \text{minNumCoins}(77-3)+1, \\ \text{minNumCoins}(77-7)+1, \end{cases}$$

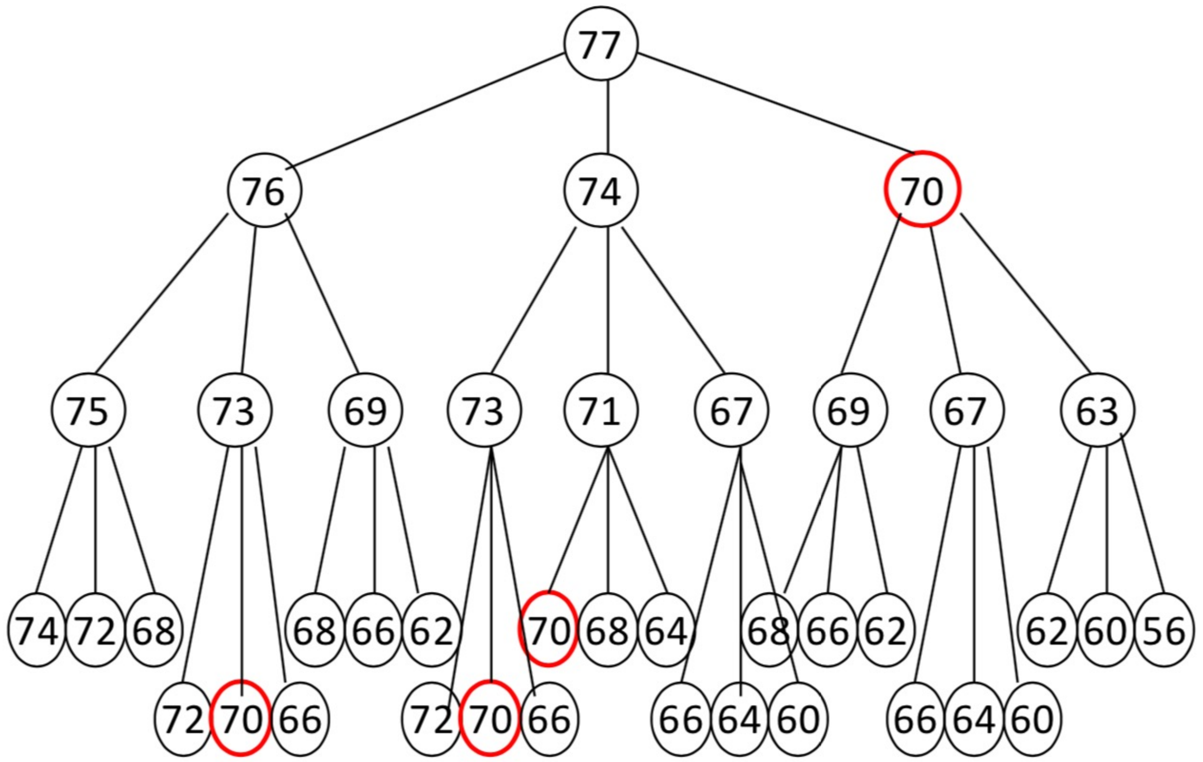
$$\text{minNumCoins}(76) = \min \begin{cases} \text{minNumCoins}(76-1)+1, \\ \text{minNumCoins}(76-3)+1, \\ \text{minNumCoins}(76-7)+1, \end{cases}$$

$$\vdots$$

$$\text{minNumCoins}(7) = 1$$
$$\text{minNumCoins}(3) = 1$$
$$\text{minNumCoins}(1) = 1$$

Idea #3: Recursion

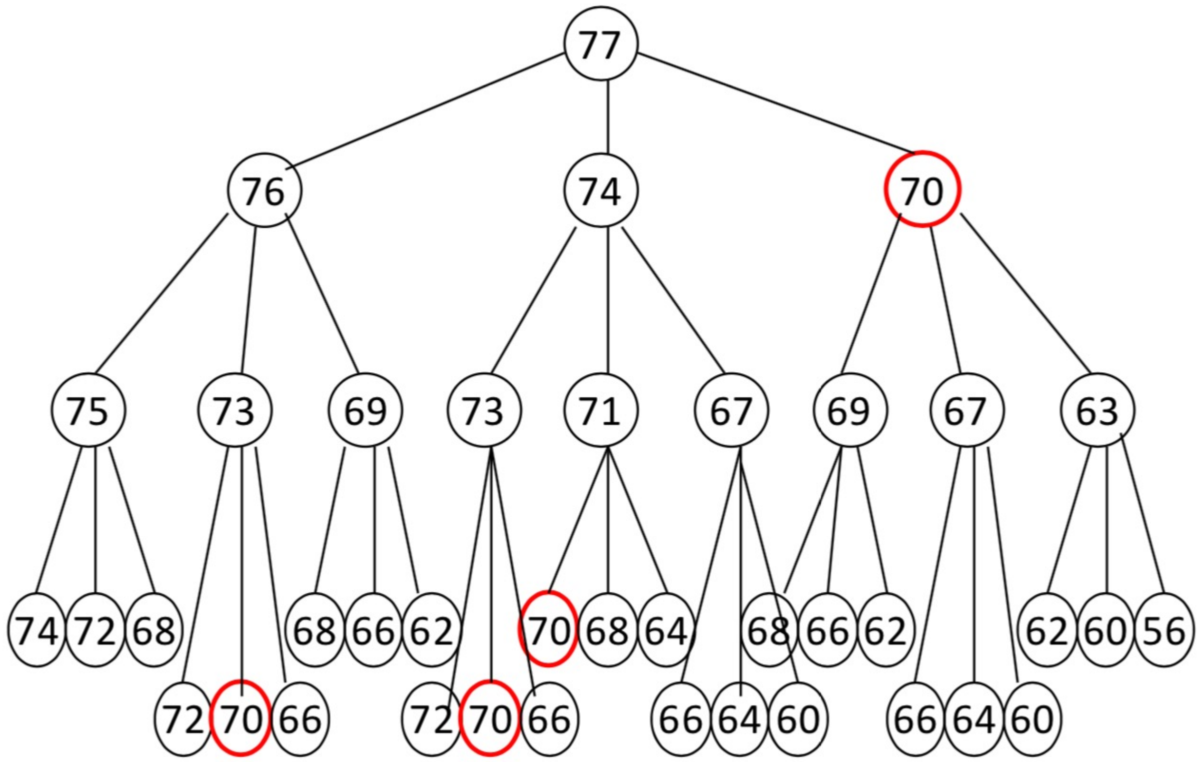
```
RecursiveChange($M, c_1, \ldots, c_n$)
1. if $M = 0$
2.     return 0
3. bestNumCoins ← ∞
4. for $i$ ← 1 to $n$
5.     if $M \geq c_i$
6.         numCoins ← RecursiveChange($M - c_i, c_1, \ldots, c_n$)
7.         if numCoins + 1 < bestNumCoins
8.             bestNumCoins ← numCoins + 1
9. return bestNumCoins
```



Correct but inefficient:
Same subproblem is solved many times!

Idea #3: Recursion

```
RecursiveChange($M, c_1, \dots, c_n$)
1. if $M = 0$
2.     return 0
3. bestNumCoins ← $\infty$
4. for $i$ ← 1 to $n$
5.     if $M \geq c_i$
6.         numCoins ← RecursiveChange($M - c_i, c_1, \dots, c_n$)
7.         if numCoins + 1 < bestNumCoins
8.             bestNumCoins ← numCoins + 1
9. return bestNumCoins
```



Correct but inefficient:
Same subproblem is solved many times!

Solutions:
- Remember previously computed values: memoization
  - Bottom up computation: dynamic programming

Idea #4: Solve recurrence with dynamic programming

Fill in table “bottom up”: from smallest to largest.

$\mathbf{c} = ($ 5 , 3 , 1 $)$

Value	1	2	3	4	5	6	7	8	9	10	11
Min # coins	**1**		**1**		**1**						

$$\text{minNumCoins}(M) = \min \begin{cases} \text{minNumCoins}(M-1)+1, \\ \text{minNumCoins}(M-3)+1, \\ \text{minNumCoins}(M-5)+1. \end{cases}$$

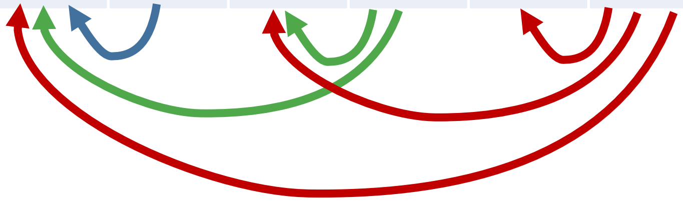
Only one coin is needed to make change for the values 1, 3 and 5

Idea #4: Solve recurrence with dynamic programming

Fill in table "bottom up": from smallest to largest.

$\mathbf{c} = (\, 5 \, , \, 3 \, , \, 1 \,)$

Value	1	2	3	4	5	6	7	8	9	10	11
Min # coins	1	2	1	2	1	2					



$$\text{minNumCoins}(M) = \min \begin{cases} \text{minNumCoins}(M-1)+1, \\ \text{minNumCoins}(M-3)+1, \\ \text{minNumCoins}(M-5)+1. \end{cases}$$

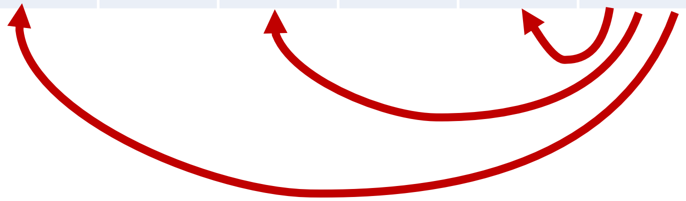
Two coins are needed to make change for the values 2, 4 and 6

Idea #4: Solve recurrence with dynamic programming

Fill in table “bottom up”: from smallest to largest.

$\mathbf{c} = ($ 5 , 3 , 1 $)$

Value	1	2	3	4	5	6	7	8	9	10	11
Min # coins	**1**	**2**	**1**	**2**	**1**	**2**	**3**				



$$\text{minNumCoins}(M) = \min \begin{cases} \text{minNumCoins}(M-1)+1, \\ \text{minNumCoins}(M-3)+1, \\ \text{minNumCoins}(M-5)+1. \end{cases}$$

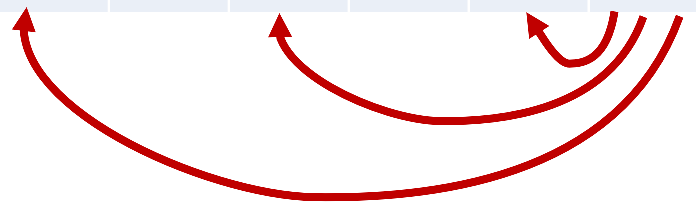
Three coins are needed to make change for the value 7

Idea #4: Solve recurrence with dynamic programming

Fill in table "bottom up": from smallest to largest.

c = (5 , 3 , 1)

Value	1	2	3	4	5	6	7	8	9	10	11
Min # coins	1	2	1	2	1	2	3	2			



$$\text{minNumCoins}(M) = \min \begin{cases} \text{minNumCoins}(M-1)+1, \\ \text{minNumCoins}(M-3)+1, \\ \text{minNumCoins}(M-5)+1. \end{cases}$$

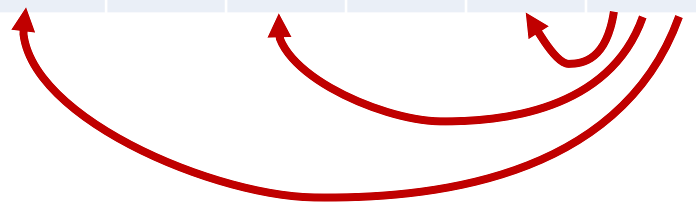
Optimal substructure: Optimal solution obtained from optimal subsolutions

Idea #4: Solve recurrence with dynamic programming

Fill in table “bottom up”: from smallest to largest.

$\mathbf{c} = (5, 3, 1)$

Value	1	2	3	4	5	6	7	8	9	10	11
Min # coins	**1**	**2**	**1**	**2**	**1**	**2**	**3**	**2**	**3**	**2**	**3**



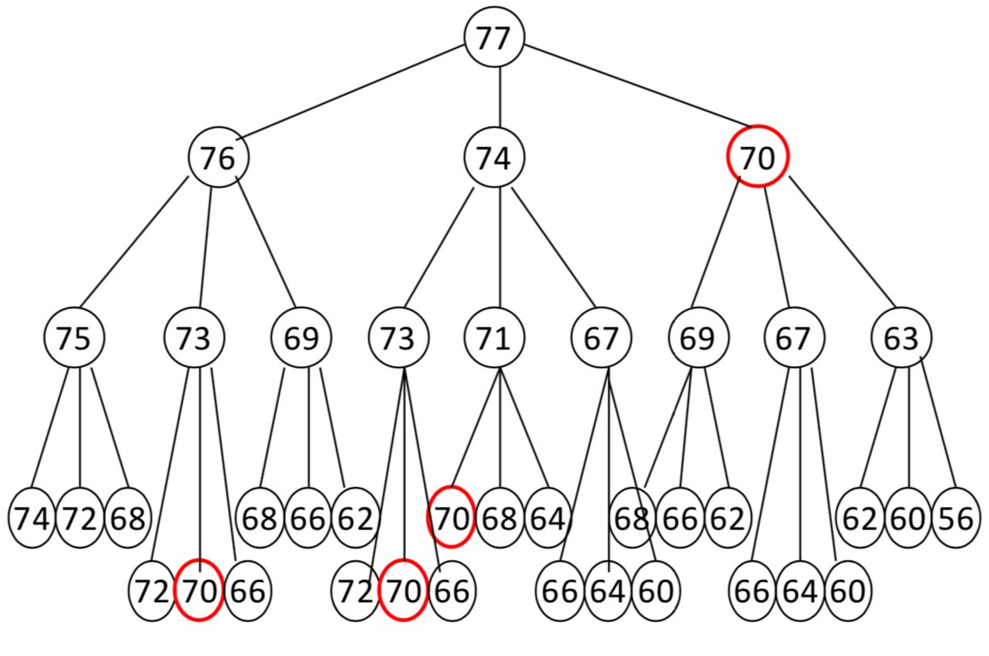
$$\text{minNumCoins}(M) = \min \begin{cases} \text{minNumCoins}(M-1)+1, \\ \text{minNumCoins}(M-3)+1, \\ \text{minNumCoins}(M-5)+1. \end{cases}$$

Optimal substructure: Optimal solution obtained from optimal subsolutions

Idea #4: Solve recurrence with dynamic programming

Change Problem: Given amount $M \in \mathbb{N} \setminus \{0\}$ and coins $\mathbf{c} = (c_1, \dots, c_n) \in \mathbb{N}^n$ s.t. $c_n = 1$ and $c_i \geq c_{i+1}$ for all $i \in [n-1] = \{1, \dots, n-1\}$, find $\mathbf{d} = (d_1, \dots, d_n) \in \mathbb{N}^n$ s.t. (i) $M = \sum_{i=1}^{n} c_i d_i$ and (ii) $\sum_{i=1}^{n} d_i$ is minimum

```
DPChange($M, c_1, \dots, c_n$)
1. for $m$ ← 1 to $M$
2.     minNumCoins[$m$] ← ∞
3. for $i$ ← 1 to $n$
4.     minNumCoins[$c_i$] ← 1
5. for $m$ ← 1 to $M$
6.     for $i$ ← 1 to $n$
7.         if $m > c_i$
8.             minNumCoins[$m$] ← min(1 + minNumCoins[$m - c_i$], minNumCoins[$m$])
9. return minNumCoins[$M$]
```



Correct? yes
Efficient? yes

Different algorithm techniques

Change Problem: Given amount $M \in \mathbb{N} \setminus \{0\}$ and coins $\mathbf{c} = (c_1, \dots, c_n) \in \mathbb{N}^n$ s.t. $c_n = 1$ and $c_i \geq c_{i+1}$ for all $i \in [n-1] = \{1, \dots, n-1\}$, find $\mathbf{d} = (d_1, \dots, d_n) \in \mathbb{N}^n$ s.t. (i) $M = \sum_{i=1}^{n} c_i d_i$ and (ii) $\sum_{i=1}^{n} d_i$ is minimum

Technique	Correct?	Efficient?
Greedy algorithm [GreedyChange]	no	yes
Exhaustive enumeration [ExhaustiveChange]	yes	no
Recursive algorithm [RecursiveChange]	yes	no
Dynamic programming [DPChange]	yes	yes

Summary

- DNA, RNA and proteins are sequences
  - Central dogma of molecular biology: DNA -> RNA -> protein
- Problem != algorithm
- Different algorithm techniques
  - Greedy
  - Exhaustive search/brute force
  - Recursive algorithm
  - Dynamic programming algorithm
- Reading:
  - "Biology for Computer Scientists" by Lawrence Hunter (http://www.el-kebir.net/teaching/CS466/Hunter_BIO_CS.pdf)
  - Jones and Pevzner: Chapters 2.1, 2.3, 2.4, 6.2

Sources

- CS 362 by Layla Oesper (Carleton College)
- CS 1810 by Ben Raphael (Brown/Princeton University)
- An Introduction to Bioinformatics Algorithms book (Jones and Pevzner)