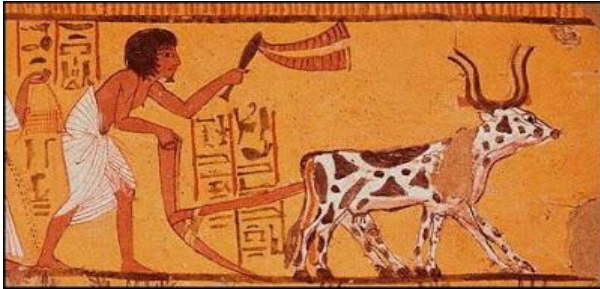
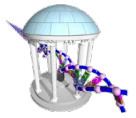
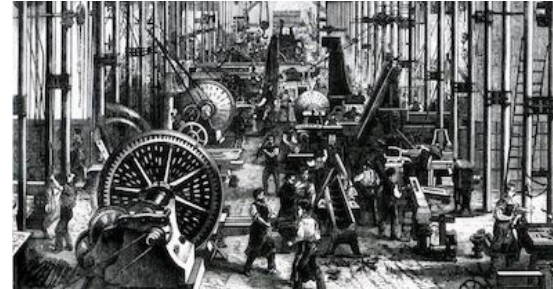


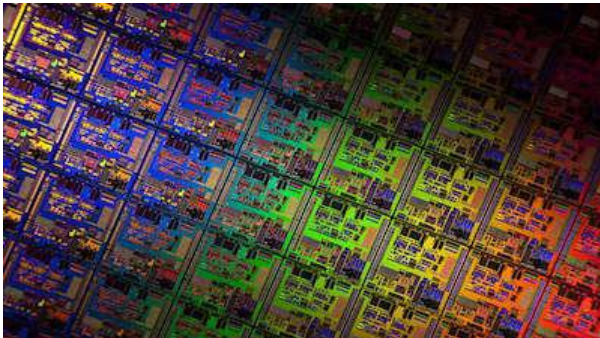
Comp 555 - BioAlgorithms - Spring 2022



Agrarian Revolution



Industrial Revolution



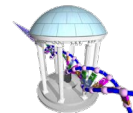
Electronics/Digital Revolution



Biotechnology Revolution

Welcome to the 4th Revolution!

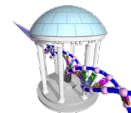
Comp 555's Intended Audience



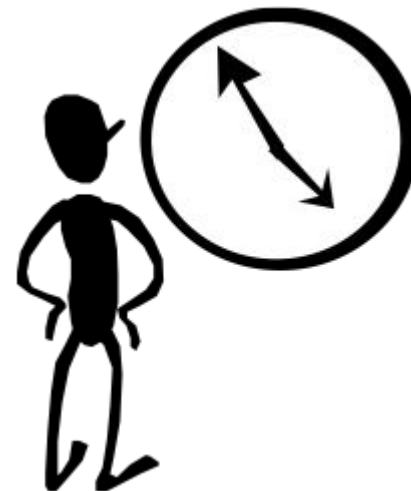
- Suitable for undergraduate and graduate students
- CS majors who want to learn bioinformatics
- Non CS majors from the statistics, biology, biostatistics, and general sciences who are interested in the algorithms with a focus on problems, and approaches used in bioinformatics.
- BCB/BBSP students



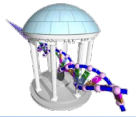
Why?



- **Benefits for Computer Scientists**
 - See CS fundamentals *applied* to real problems
 - What computer scientists can learn from biology
 - Robust, parallel, self-repairing, and energy efficient
- **Benefits for Biologist Multidisciplinary**
 - Help to close the CS-Bio "*language gap*"
 - Appreciate CS as more than just "coding"
 - What is a correct algorithm? An efficient one?
 - Approaches to algorithm "*design*"
- **Growth Potential**
 - Bioinformatics is a very marketable skill
 - Future of both CS and Biology



Logistics



- **Course Website:**
<https://csbio.unc.edu/mcmillan/index.py?run=Courses.Comp555S22>

Or just follow the links from
<https://csbio.unc.edu/mcmillan>

[Courses|Comp555] (and bookmark it)

- Syllabus is linked on the website
- Look there for announcements and zoom links.
- Include "COMP555" in subject line of all emails
- **Course grading:**
 - Many in-class exercises - 10 % (lowest 2 dropped)
 - 2 Problem Sets - 40 % (lowest dropped)
 - Midterm (mid march) - 25 %
 - Final - 25%

Logout as [mcmillan](#)

COMP 555 - Spring 2022

[Home](#) | [Courses](#) | [Publications](#) | [Data](#)

Announcements
Showing 1 of 1

- **January 11, First class meeting.** See you there

Course Description

Computational methods are being a revolution in the biological sciences. Computers are already nearly an indispensable requirement for understanding, analyzing, and interpreting biological systems. As a result, few new multi-disciplinary fields, bioinformatics and computational biology, have emerged. This course will explore the computational methods and algorithmic principles during the revolution. It will cover basic topics in molecular biology, genetics, and genomics. The course will address topics in computational theory and algorithms including computational evolution, bioinformatics, digital and network computation, signal processing, dynamic programming, combinatorial algorithms, the greedy algorithm, trees, graph algorithms, combinatorial optimization, algorithms for solving NP-complete problems drawn from contemporary biology. Examples biological topics include sequence alignment, motif finding, gene reconstruction, DNA sequencing, protein-protein interactions, phylogenies, and gene expression analysis.

This course is suitable for both computer science and biology students at both undergraduate and graduate levels. Students who wish to take this course should have some programming experience in a modern programming language. Knowledge of data structures, algorithm design, and topology is helpful but not required. There will be 2 problem sets each with a short programming assignment. No late problem sets will be accepted, however, I will drop the score of the lowest when calculating the course grade. The grade will be computed as follows: the best 2 of 4 problem sets (each worth 10%), a midterm (worth 25%), 2 problem sets (each 25%), and one final exam (worth 25%). A syllabus for the offering of Comp555 can be downloaded from [here](#).

COVID-19 Considerations

Classes will be held both in face this semester as long as it is practical. All students must wear masks and maintain social distancing from each other and the instructor. Lecturers will be instructed on Zoom and should be used under the following conditions:

- If you experience any COVID-19 symptoms.
- If you have tested positive for COVID-19 in the previous 5 days prior to a class meeting.
- If you have been in close contact with anyone who has tested positive in the past 5 days and you have not yet been tested.

Should the instructor see positive or develop COVID-19 symptoms, he will attempt to teach remotely via zoom if possible. In any case, notification of whether or how the class will be held will be made via the "Announcements" section of the website a minimum of one hour before the start of class.

Other than will be held on Zoom, I will be the start of the semester. If any student is unable to attend an exam or problem set due to severe symptoms, exceptions to the class policies and public attendance exam times will be considered on a case-by-case basis, after notifying the instructor at least 24 hrs in advance. Please, be prepared to provide documentation. The safety of a successful semester relies on every person in our community taking responsible actions that include mask wearing, social spacing, frequent hand washing, and getting vaccinated.


Book, Course Information, and Prerequisites

This semester I will not be using a book. I will be teaching from my notes and I plan to add at least two modules of new material.

CREDIT POINTS:
 COURSE: 0014
 TYPE: TF 2 00 3 15
 URL: <https://www.csbio.unc.edu/mcmillan/From-Courses/Comp55522>
 Prerequisites: COMP 110, Math 301, or equivalent.

Course Instructor

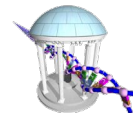
Instructor: Leonard McMillan
Office: 3011B
EMAIL: mcmillan@csbio.unc.edu
OFFICE HOURS: Wednesday 2pm-4pm



Schedule

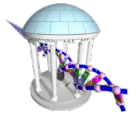
Date	Topic	Homework
January 11	Lectures 1: Introduction (online)	
January 13	Lectures 2: Genomics & Sequence Analysis (online)	
January 18	Lectures 3: Evolution & DNA Sequencing (online)	
January 20	Lectures 4: Protein Structure (DNA Sequencing) (online)	15-41
January 25	Lectures 5: Evolutionary Biology (Sequence Analysis) (online)	
January 27	Lectures 6: Family Trees & DNA Sequencing (online)	
February 01	Spring Vacation (online) (Spring Break)	
February 03	Lectures 7: Assembly & Sequence Analysis (online)	
February 08	Lectures 8: Protein Structure (Sequence Analysis) (online)	15-40, 15-41, 15-4
February 10	Lectures 9: Protein Structure (Protein Sequencing) (online)	
February 15	Lectures 10: Computational Protein Sequencing (online)	
February 17	Lectures 11: DNA Analysis and Sequencing (online)	
February 19	Lectures 12: DNA Analysis and Sequencing (online)	15-40, 15-41, 15-4
February 22	Lectures 13: Midterm (20% of course)	
February 24	Lectures 14: Introduction to Bioinformatics (online)	
February 26	Lectures 15: Introduction to Bioinformatics (online)	

First Exercise



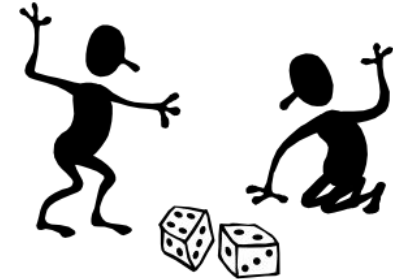
<https://forms.gle/RRzwd1uitpbcvHzHA>

Bioinformatics = Biology + Information



- **What is information?**

- Information: that which resolves uncertainty
- Computer scientists measure information in “bits”
- Information = $-\log_2(\text{probability})$
 - A coin is tossed and lands heads. How many bits?
 - A 7 is rolled on a pair of dice. How many bits?
 - A 3 is rolled? How many bits?
- Information systems need mechanisms for
 - Storing information (memory)
 - Processing information (logic)
 - Transporting information (networks/connectivity)



6 out of 36 possible rolls are “7”s.
Thus, a roll of 7 conveys:

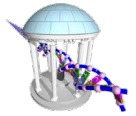
$$-\log_2(6/36) = 2.58 \text{ bits}$$

- **Computer science *is* about information**
- **What about biological systems?**
Are they information systems?

There are only 2 ways
to roll a “3”, (1,2) or (2,1)
Thus, a roll of “3” conveys:

$$-\log_2(2/36) = 4.17 \text{ bits}$$

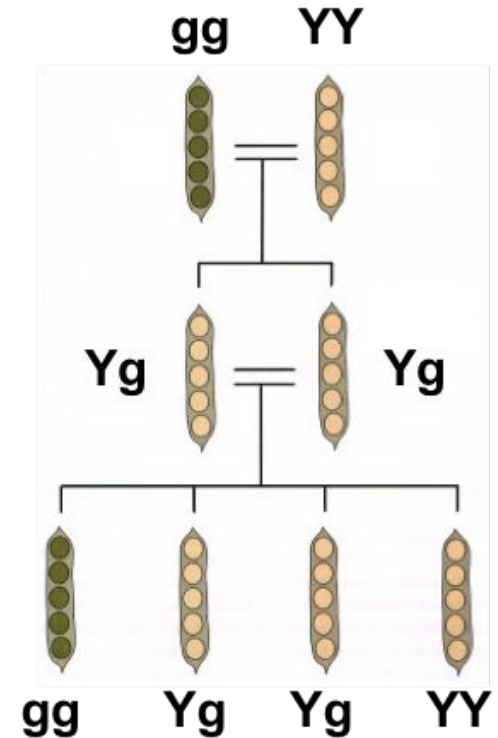
Information in Biological Systems



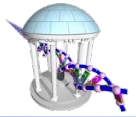
- Information is somehow passed between successive generations of plants and animals
- Distinguishable traits are inherited (phenotypes)
- Latent (recessive) traits can be masked by dominant traits, yet reappear in later generations
- Laws of Heredity
- Basis for Genetics



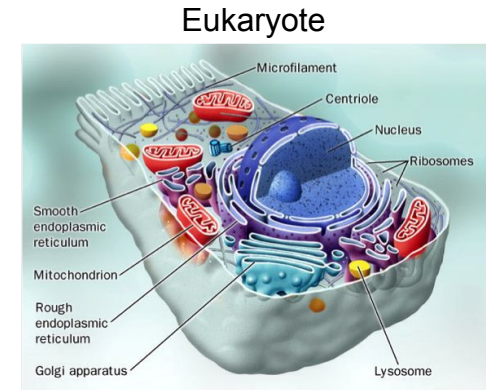
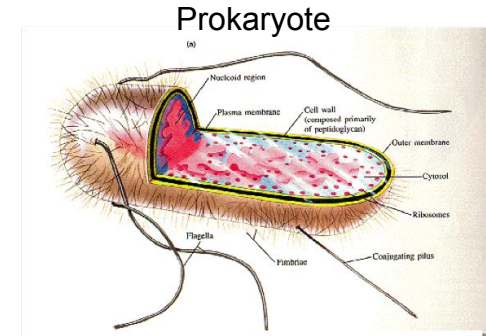
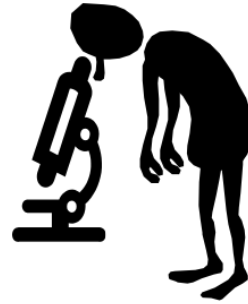
Gregor Mendel
1822-1884



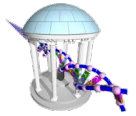
Where is “Biological” Information?



- Enter the Age of Microbiology
- Cells: the smallest structural unit of a living organism capable of functioning independently
- Cell composition by weight
 - 70% water
 - 7% small molecules
salts, amino acids, nucleotides, lipids (fats, oils, waxes)
 - 23% larger polymers
proteins, polysaccharides
- Two cell types
 - Prokaryotes: bacteria (no nucleus)
 - Eukaryotes: yeast, plants, and animals (with nucleus)



Looking for the Source of Heredity

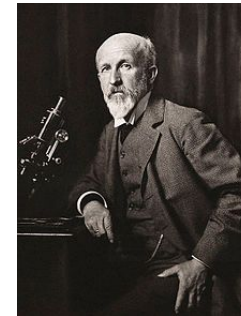


- In 1879 Walther Fleming, a German anatomist, discovered threadlike structures clearly visible during cell division. He called this material chromatin, which was later renamed chromosomes
- Zoologists Oskar Hertwig and Hermann Fol first observed the process of fertilization in detail in the early 1880s. In 1881, Edward Zacharias showed that chromosomes contained nucleic acids. In 1884, Hertwig wrote:

"nucleic acid is the substance that is responsible not only for fertilization but also for the transmission of hereditary characteristics."



Fleming

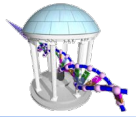


Hertwig



Fol

Early 20th Century Genetics

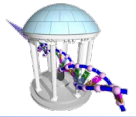


- In 1908, Thomas Hunt Morgan and Alfred H. Sturtevant showed that genes (a new name for inheritable traits) were located on chromosomes. Experimenting with *Drosophila* (fruit flies) they found sex chromosomes, sex-linked traits, and crossing-over. They were able to associate mutations to specific chromosomal regions, thus mapping gene locations.
- By the 1930's biochemists knew that the nucleic acid present in chromosomes was DeoxyriboNucleic Acid, DNA. They also knew that chromosomes contained proteins in addition to DNA. DNA appeared to be long repetitive chains, and therefore, it seemed unlikely to carry information. Proteins, however, looked more interesting and were generally assumed to contain genetic materials. DNA was considered as just some sort of “glue”.



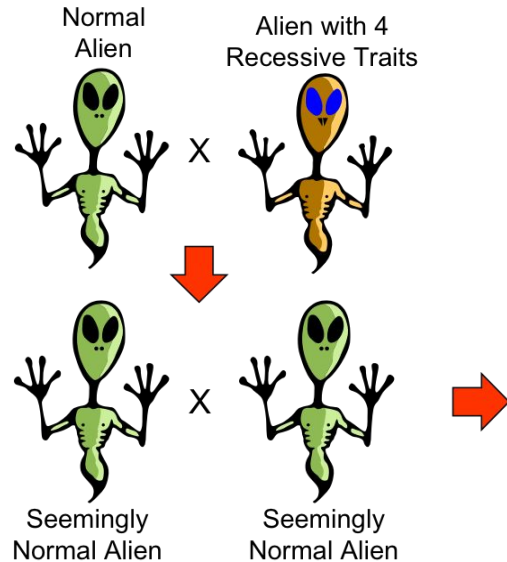
Morgan





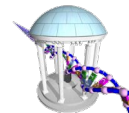
Inferring Genetic Maps

Even without knowing the mechanisms of how heredity information is represented, clever scientists (Morgan) were able to “map” genes...



Normal	201	Short-fingered	9
Brown	64	Brown, blue-eyed, & triangle nosed	6
Blue-eyed	58	Triangle-nosed	5
Short fingered & triangle-nosed	54	Short-fingered & Brown	5
Short fingered, triangle-nosed, & brown	21	Brown, short fingered, triangle-nosed, & blue-eyed	4
Short fingered, triangle-nosed, & blue-eyed	20	Short-fingered & blue-eyed	4
Brown & blue-eyed	19	Triangle-nosed & brown	1
Blue-eyed & triangle-nosed	12	Brown, short fingered, & blue-eyed	1

Steps to Infer a Genetic Map



- **Verify Mendelian ratios**

- Brown $(64 + 21 + 19 + 6 + 5 + 4 + 1 + 1) / 484 = 0.250$
- Blue-eyes $(58 + 20 + 19 + 12 + 6 + 4 + 4 + 1) / 484 = 0.256$
- Triangle-nose $(54 + 21 + 20 + 12 + 6 + 5 + 4 + 1) / 484 = 0.254$
- Short-finger $(54 + 21 + 20 + 9 + 5 + 4 + 4 + 1) / 484 = 0.244$

- **Test pairwise linkages**

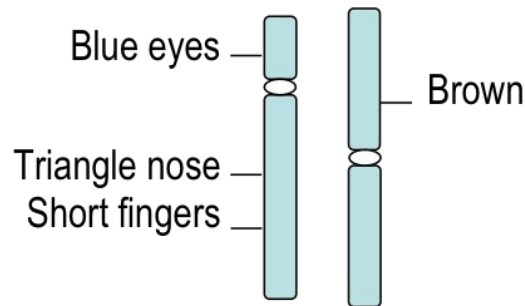
(we expect $1/4 \times 1/4 \times 484 \approx 30$ if independent)

- Short-finger & triangle-nose $54 + 21 + 20 + 4 = 99$
- Triangle nose & brown $21 + 6 + 4 + 1 = 32$
- Short-finger & brown $21 + 5 + 4 + 1 = 31$
- Blue-eyes & triangle-nose $20 + 12 + 6 + 4 = 42$
- Short-finger & blue-eyes $20 + 4 + 4 + 1 = 29$
- Brown & blue-eyes $19 + 6 + 4 + 1 = 30$

- **Indicates**

- Short-fingers & triangle-nose are closely linked
- Blue-eyes & triangle-nose are probably linked
- Short-finger & blue-eyes appear independent, thus the triangle nose gene should lie between them
- Brown gene is likely to be on another chromosome

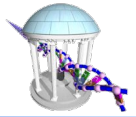
3x more than
I'd expect by
chance



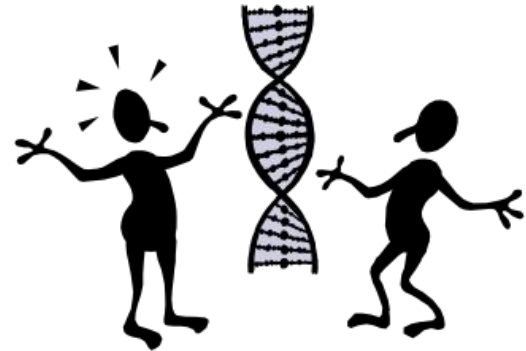
Morgan came up with even more clever techniques that were able to precisely locate the relative positions of genes on chromosomes. Even today chromosomal gene positions are measured in units of centiMorgans



DNA's Central Role

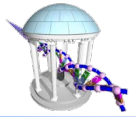


- In 1944, Oswald Avery showed that one of those “nucleic acids”, DNA, not proteins, carries hereditary information.
- In the late 1940's and early 50's Linus Pauling and associates develop methods for simultaneously determining the structure and chemical makeup of crystallized proteins and other large molecules.
- In 1952, James Watson and Francis Crick, are able to determine the structure and chemical makeup of DNA, using X-ray crystallography data collected by Rosalind Franklin and Maurice Wilkins.



Beginning of Molecular Biology!

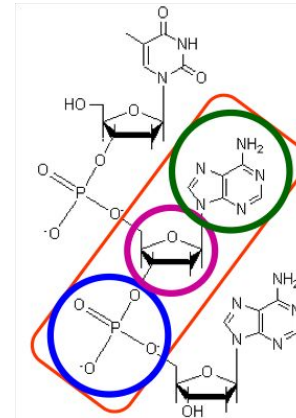
More on DNA



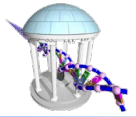
- The *information* stored in DNA organizes inanimate molecules into living organisms and orchestrates their lifelong function
- A long “complementary” chain of nucleotides



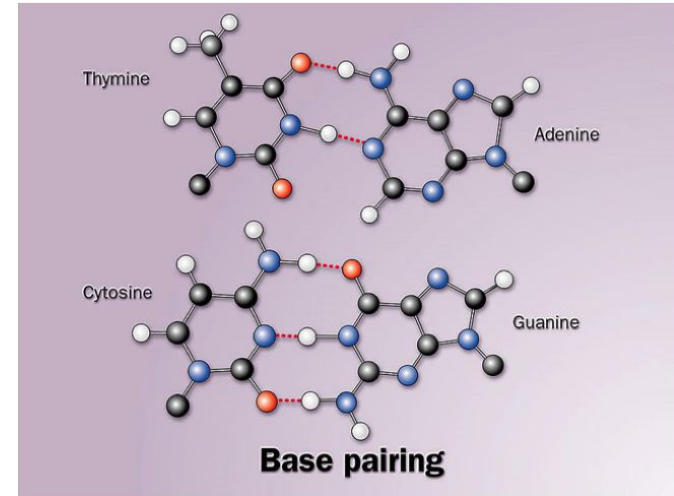
- Each nucleotide has 3 components
 - A **phosphate** group
 - A **ribose sugar**
 - One of four **nitrogenous bases**
- The information resides in the sequence of bases



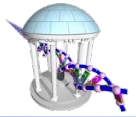
DNA Components



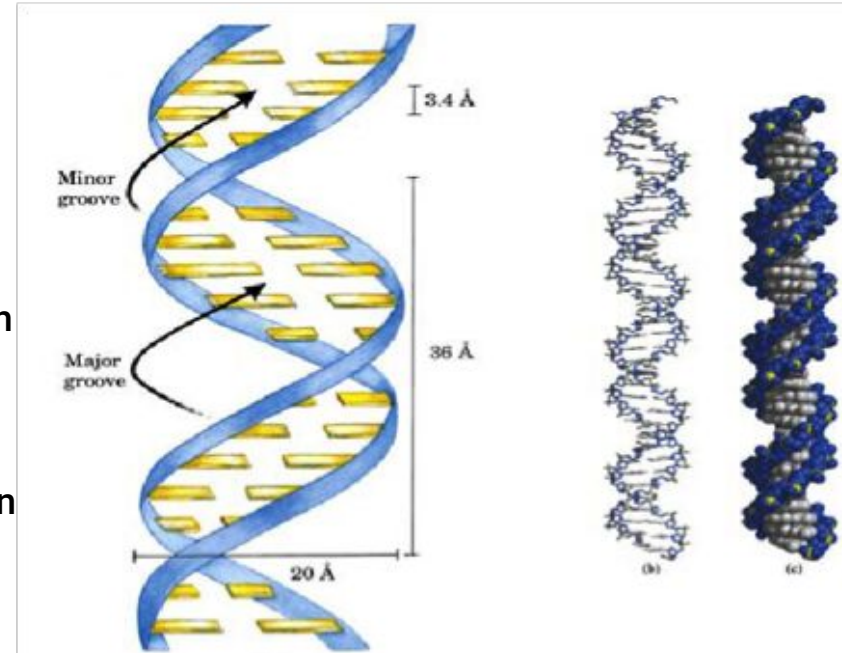
- DNA is used by all living organisms
- Differences in nitrogenous bases code sequences that distinguish
 - Plants from animals
 - Species
 - Individuals
- A complete DNA sequence for an organism is called its “genome”
- Code sequences are composed of 4 bases (Adenine, Cytosine, Guanine, Thymine)
- Each base binds with another specific base (Thymine with Adenine and Cytosine with Guanine)
- A DNA molecule is comprised of primary sequence and a redundant “complementary” copy that aids self replication (each acts like a template for the other sequence)



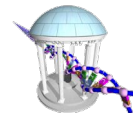
DNA Schematic



- Many more details are required to give a complete picture of DNA
 - Complementary strands are antiparallel and, thus, oriented
 - Not a simple twist, but has a major and minor grooves which are recognized by interacting with proteins
- Rather than keep track of all the details we will often consider DNA as a string of nucleotides
5' . . .ACGGATAGCATGGA . . .3'
- By convention DNA sequences are always ordered in the 5'-to-3' direction. Not coincidentally, this is also the order in which they are synthesized using an important class of molecules call polymerases.

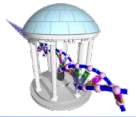


Biological Computing Machines



- **DNA is an “Operating System” with “programs”**
 - Collect raw materials and convert chemicals to energy
 - Perform specialized functions (neurons, muscle, retinal cones)
 - Protect and repair itself
 - Replicate itself, or duplicate an entire organism
- **How are these “programs” encoded?**
- **What biological machinery “executes” this program?**
- **How is the program’s execution sequenced?**





Genes are the Programs

- Specific subsequences of DNA bases determine specific functions (programs) of a cell, these subsequences are the modern definition of “genes”
- Genes are distributed throughout a genome
- Not all DNA sequence sections contain genes
- Genes might not be entirely contiguous within the DNA sequence
- Genes can be either active or inactive
- Genes provide instructions for assembling proteins, which are the machinery of life
- How are these instructions encoded?
- What is the output of these programs?



key:

Protein Generators:

-hok/sok system

- Holin

- beta galactosidase

Promoters:

- constitutive promoter

- inducible promoter

-repressible promoter

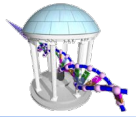
-signal peptide

-inverter

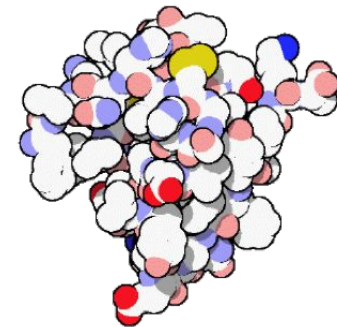
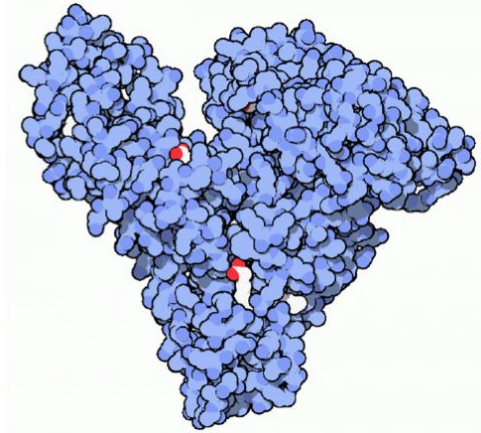
-RBS

-terminator

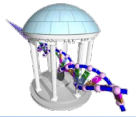
What are Proteins?



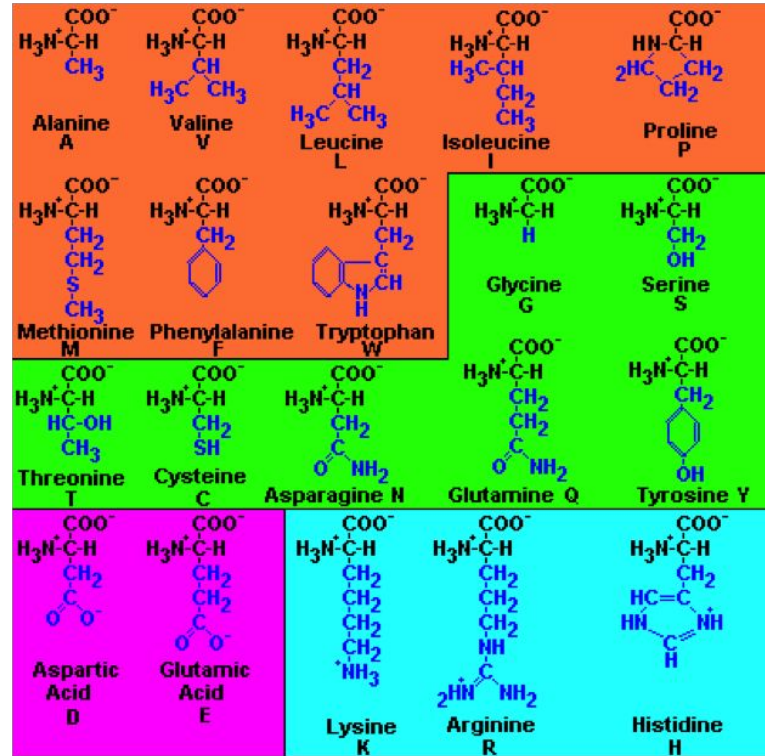
- Proteins are incredibly diverse and composed of another type of sequence (amino acid peptides)
- Some are building materials, like collagen which provides structural support and rigidity
- Some make other things happen-- like enzymes (pepsin) which act as catalysts that hasten critical reactions without taking part in them
- Some proteins deliver cargo, i.e. transport small molecules and minerals to where they are needed within an organism (hemoglobin)
- Some are used for signaling and intercellular communication (insulin)
- Others absorb photons to enable vision (rhodopsin)
- Proteins are assembled from simple molecules, called amino acids.



Amino Acids

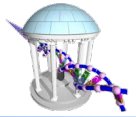


- 20 main ingredients of proteins
- Varying side chain is shown in **dark blue**
- **Orange** indicates non-polar and Hydrophobic, the remainder are polar or hydrophilic
- **Magenta** indicates acidic
- **Cyan** indicates a base



A hydrophobic amino acid avoids water whereas a hydrophilic amino acid is attached to water. This influences the shapes that proteins fold into.



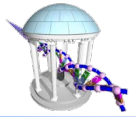


Encoding Protein Assembly

- Each DNA base can be one of 4 values (G,C,A,T)
- Proteins are polymer chains of amino acids ranging in length from tens to millions
- There are 20 amino acids
- How do you encode variable length chains of 20 amino acids using only 4 bases?
- Do you need other codings?
- Clearly, we can't encode 20 different amino acids using only one base. How many encodings are possible using a pair of bases? How many with three?



Codons



- Triplets of nucleotide bases determine the amino acid sequence of a protein
- All genes begin with a particular code, AUG, for the amino acid Methionine
- Three codes are used to indicate STOP, and thus end the transcription process for the gene
- Most amino acids have redundant encodings

		Second Letter				Third Letter
		U	C	A	G	
U	U	UUU phe	UCU ser	UAU tyr	UGU cys	
	U	UUC	UCC ser	UAC tyr	UGC cys	
	U	UUA leu	UCA ser	UAA stop	UGA stop	
	U	UUG leu	UCG ser	UAG stop	UGG trp	
C	U	CUU leu	CCU pro	CAU his	CGU arg	
	U	CUC leu	CCC pro	CAC his	CGC arg	
	U	CUA leu	CCA pro	CAA gln	CGA arg	
	U	CUG leu	CCG pro	CAG gln	CGG arg	
A	U	AUU ile	ACU thr	AAU asn	AGU ser	
	U	AUC ile	ACC thr	AAC asp	AGC ser	
	U	AUA ile	ACA thr	AAA lys	AGA arg	
	U	AUG met	ACG thr	AAG lys	AGG arg	
G	U	GUU val	GCU ala	GAU asp	GGU gly	
	U	GUC val	GCC ala	GAC asp	GGC gly	
	U	GUA val	GCA ala	GAA asp	GGA gly	
	U	GUG val	GCG ala	GAG asp	GGG gly	

Legend: ■ Initiation (AUG) ■ Termination (UAA, UAG, UGA)

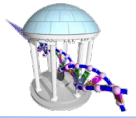


Why are there Us in this table?

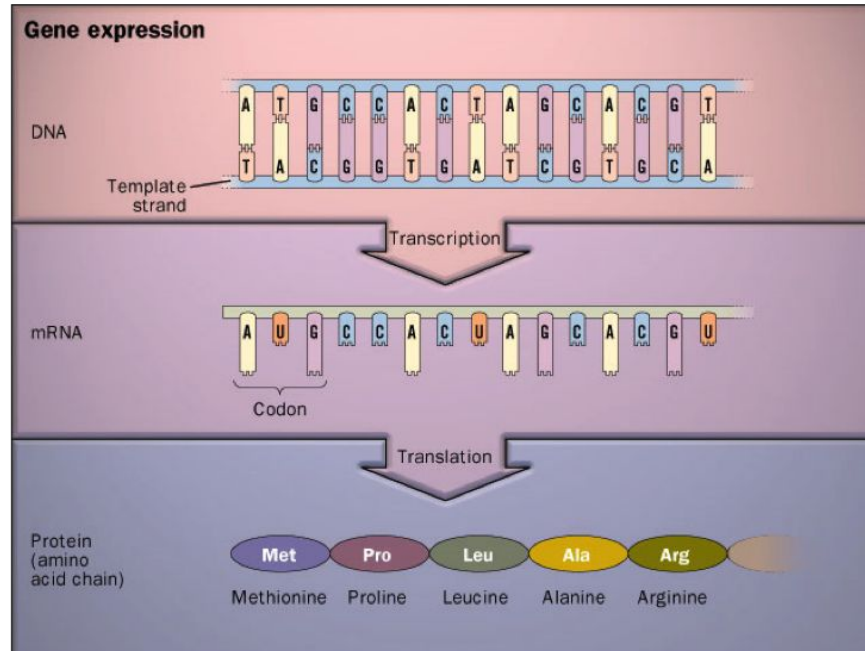
Before a DNA sequence is translated into a protein, a copy is first made. This copy is made from RNA. In RNA, the nucleotide "Uracil" replaces "Thymine". Uracil and Thymine are both chemically and structurally very similar.



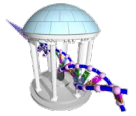
From Genes to Proteins



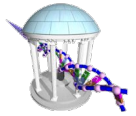
The central dogma of molecular biology is that information encoded by the bases of DNA are transcribed by RNA and then converted (translated) into proteins.



Is the Code Perfect?



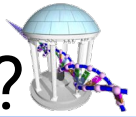
- Proteins are generally unaffected by small variations in their code sequence, particularly changes to a small number of bases (error-correction)
- Minor variations in genes, called alleles, are responsible for many individual variations (blood-type, hair color, etc.)
- Errors in *translation* (the substitution for one amino acid for the one encoded by the gene), occur at roughly 0.1% of all residues. This means that a single large protein will have at least one incorrect amino acid somewhere! Many of these will still function, in part because the substituted residue will often be adequate. Still, is a bit curious that this level of error is acceptable.
- In eukaryotes (humans, plants) gene sequences are not contiguous. They are broken into codon carrying segments called **exons** separated by seemingly meaningless base sequences called introns



How Big is a Genome?

- The human genome is roughly 3 billion bases
- A typical gene is roughly 3000 bases
- The largest known human gene (dystrophin) has 2.4 million bases
- The estimated number of human genes is roughly 30K
- The genome is nearly identical for every human (99.9%)
- Human DNA is 98% identical to chimpanzee DNA.
- The functions are unknown for more than 50% of discovered genes.
- Genes appear to be concentrated in random areas along the genome, with vast expanses of noncoding DNA between.

Is a Bigger Genome a better one? More Advanced?



- The genome size of a species is relatively constant
- Large variations can occur across species lines
- Not strictly correlated with organism complexity
- Genome lengths can vary as much as 100 fold between similar species
- Length and variability are more of an indications of a phylum's susceptibility to mutation



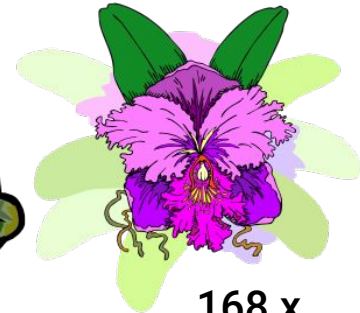
670 Bbp



118 Bbp



13 Bbp



168 x

Amoeba (*Amoeba dubia*) ~ 670 Bbp

Salamander (120.60pg, *Necturus lewisi*, Gulf coast waterdog) ~118 Bbase pairs

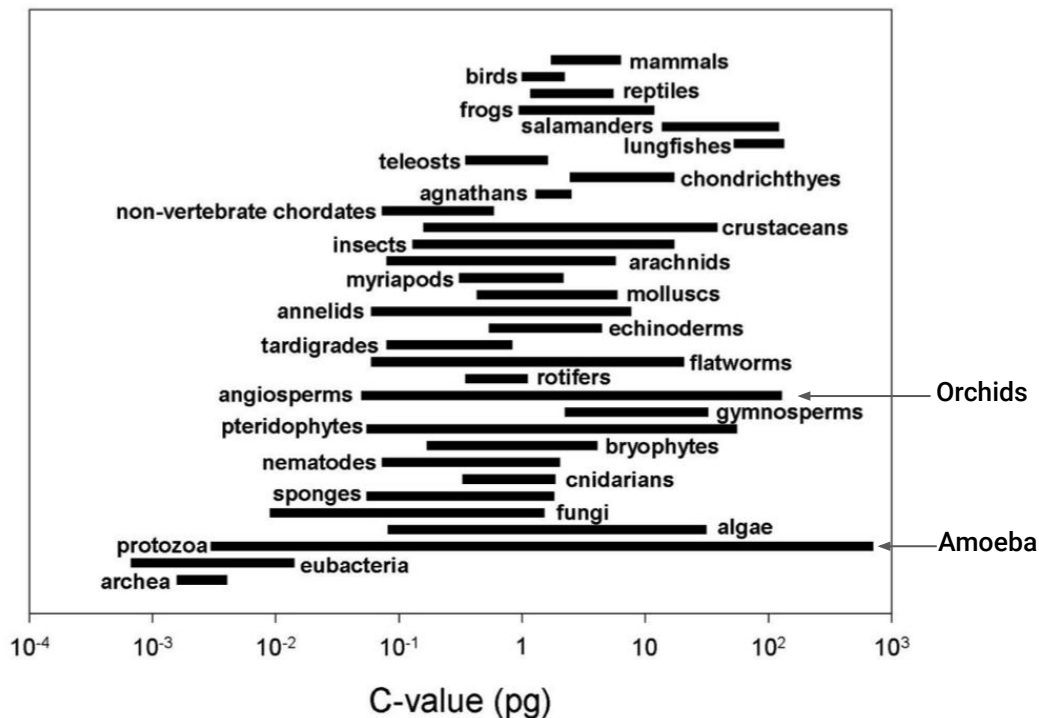
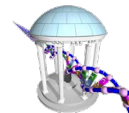
Frog (13.40pg, *Ceratophrys ornata* (8n), Ornate horned frog) ~13 Bbase pairs

Marbled Lungfish (130pg) ~ 130 Bbp

Orchids (angiosperms) have the the largest variation within a species

(strains that can interbreed and generate fertile progeny) with a range that varies at least 168-fold.

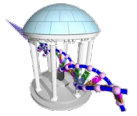
Genome Variation



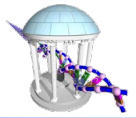
Length and variability are more of an indications of a phylum's susceptibility to mutations than its complexity

(C-value = the Amount of DNA in an unreplicated gametic nucleus. It is measures in pico Grams, and 1pg = 978M base pairs.)

Summary



- Information resolves uncertainty
- Heredity provides evidence that information is passed on by biological systems
- Biological information is stored as DNA
- Genes are segments of DNA sequence that encode assembly instructions for proteins
- The central dogma of molecular biology is that DNA sequences are transcribed by RNA polymerases into mRNAs that are then translated by ribosomes into proteins.
- A genome's length is not a good indicator of its information content



Next Time

- Examine DNA sequences
- Look for Patterns
- Data-driven hypotheses

