
CS681: Advanced Topics in Computational Biology

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EA224

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CS681

- Class hours:
 - Wed 9:40 - 10:30; Fri 10:40 - 12:30
 - Class room: EE317
 - Office hour: Tue + Thu 13:00-14:00
 - Grading:
 - 1 project: 50%
 - Class participation: 10%
 - Paper presentation & summary report: 40%
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CS681

- Textbook: None
- Recommended Material
 - An Introduction to Bioinformatics Algorithms (Computational Molecular Biology), Neil Jones and Pavel Pevzner, MIT Press, 2004
 - 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
 - Scientific journals

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- This course is about **algorithms** in the field of bioinformatics / computational biology; mostly genomics:
 - What are the problems?
 - What algorithms are developed for what problem?
 - What is missing / needs advances in the field.
 - Possible research directions for graduate students.
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CS681: Assumptions

- You are assumed to know/understand
 - Advanced algorithms
 - Dynamic programming, greedy algorithms, graph theory
 - CS473 is required
 - CS573 is better
 - CS570 is recommended
 - Programming: C, C++, Java
 - You don't *have to* be a “biology expert” but MBG 101 or 110 would be beneficial
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INTRODUCTION, CONCEPTS AND TERMS

Bioinformatics & Computational Biology

- Bioinformatics: Development of methods based on computer science for problems in biology & medicine

- Sequence analysis (combinatorial and statistical/probabilistic methods)
- Graph theory
- Data mining

CS 481 and CS 681

- Database
- Statistics
- Image processing
- Visualization
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- Computational biology: Application of computational methods to address questions in biology & medicine

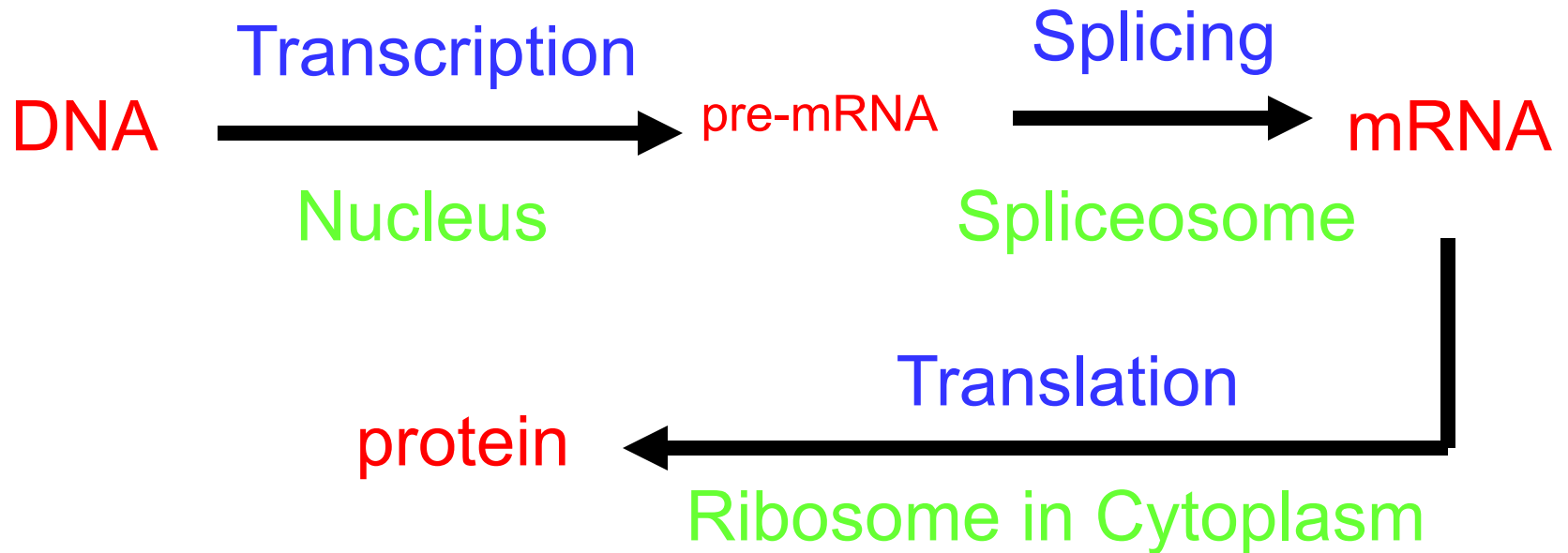
Concepts

- **Gene:** discrete units of hereditary information located on the chromosomes and consisting of DNA.
 - **Genetics:** study of inherited phenotypes
 - **Genotype:** The genetic makeup of an organism
 - **Phenotype:** the physical expressed traits of an organism
 - **Genome:** entire hereditary information of an organism
 - **Genomics:** analysis of the whole genome (that is, the DNA content for most organisms; RNA content for retroviruses)
 - **Transcriptome:** set of all RNA molecules
 - **Proteome:** set of all protein molecules
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All life depends on 3 critical molecules

- DNAs
 - Hold information on how cell works
 - RNAs
 - Act to transfer short pieces of information to different parts of cell
 - Provide templates to synthesize into protein
 - Proteins
 - Form enzymes that send signals to other cells and regulate gene activity
 - Form body's major components (e.g. hair, skin, etc.)
 - For a computer scientist, these are all strings derived from three alphabets.
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Central dogma of biology



- **Base Pairing Rule:** A and T or U is held together by 2 hydrogen bonds and G and C is held together by 3 hydrogen bonds.
- **Note:** Some RNA stays as RNA (ie tRNA, rRNA, miRNA, snoRNA, etc.).

Alphabets

DNA:

$$\Sigma = \{A, C, G, T\}$$

A pairs with T; G pairs with C

RNA:

$$\Sigma = \{A, C, G, U\}$$

A pairs with U; G pairs with C

Protein:

$$\Sigma = \{A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y\} \text{ and}$$

$$B = N \mid D$$

$$Z = Q \mid E$$

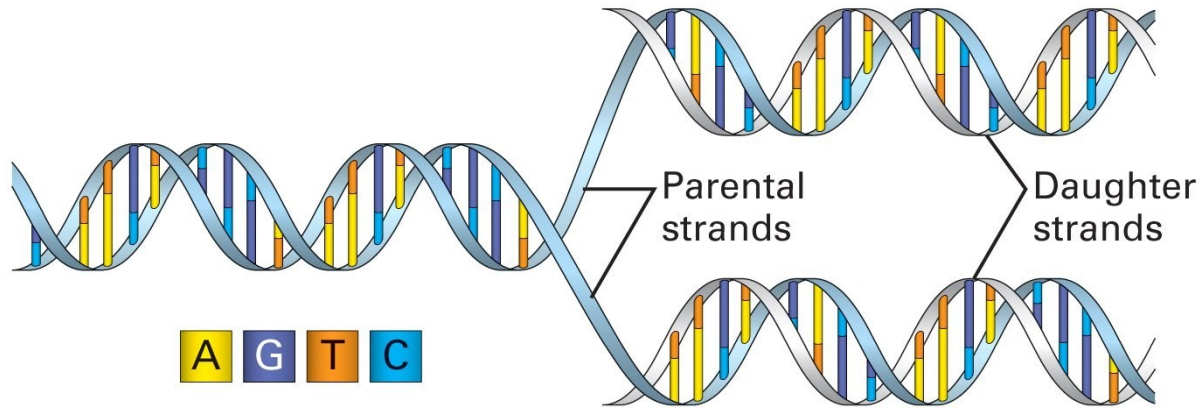
$$X = \text{any}$$

Cell Information: Instruction book of Life

- DNA, RNA, and Proteins are examples of strings written in either the four-letter nucleotide of DNA and RNA (A C G T/U)
- or the twenty-letter amino acid of proteins. Each amino acid is coded by 3 nucleotides called **codon**. (Leu, Arg, Met, etc.)

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

DNA: The Code of Life



- The structure and the four genomic letters code for all living organisms
- Adenine, Guanine, Thymine, and Cytosine which pair A-T and C-G on complimentary strands.

DNA is organized into Chromosomes

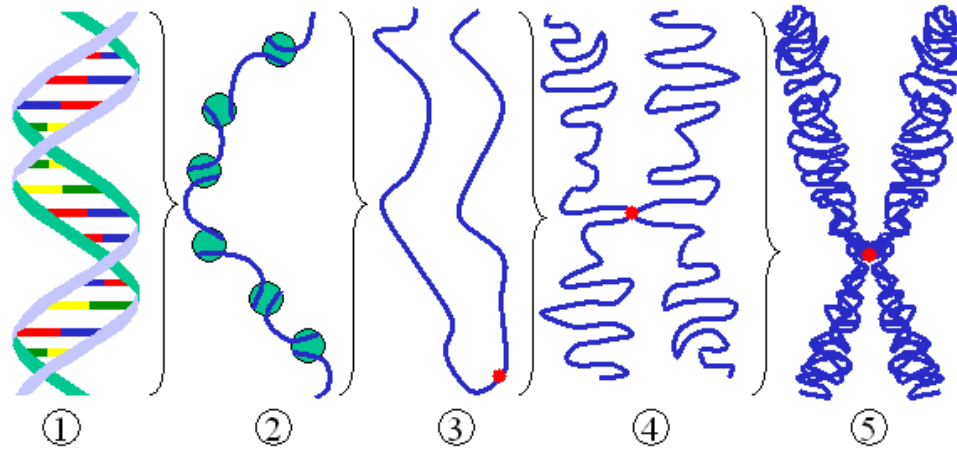
■ Chromosomes:

- Found in the nucleus of the cell which is made from a long strand of DNA, “packaged” by proteins called *histones*. Different organisms have a different number of chromosomes in their cells.
- Human genome has 23 pairs of chromosomes
 - 22 pairs of *autosomal* chromosomes (chr1 to chr22)
 - 1 pair of sex chromosomes (chrX+chrX or chrX+chrY)

■ Ploidy: number of sets of chromosomes

- Haploid (n): one of each chromosome
 - Sperm & egg cells; hydatidiform mole
- Diploid ($2n$): two of each chromosome
 - All other cells in mammals (human, chimp, cat, dog, etc.)
- Triploid ($3n$), Tetraploid ($4n$), etc.
 - Tetraploidy is common in plants

Genetic Information: Chromosomes



- ❑ (1) Double helix DNA strand.
- ❑ (2) Chromatin strand (**DNA** with **histones**)
- ❑ (3) Condensed chromatin during interphase with **centromere**.
- ❑ (4) Condensed chromatin during prophase
- ❑ (5) Chromosome during metaphase

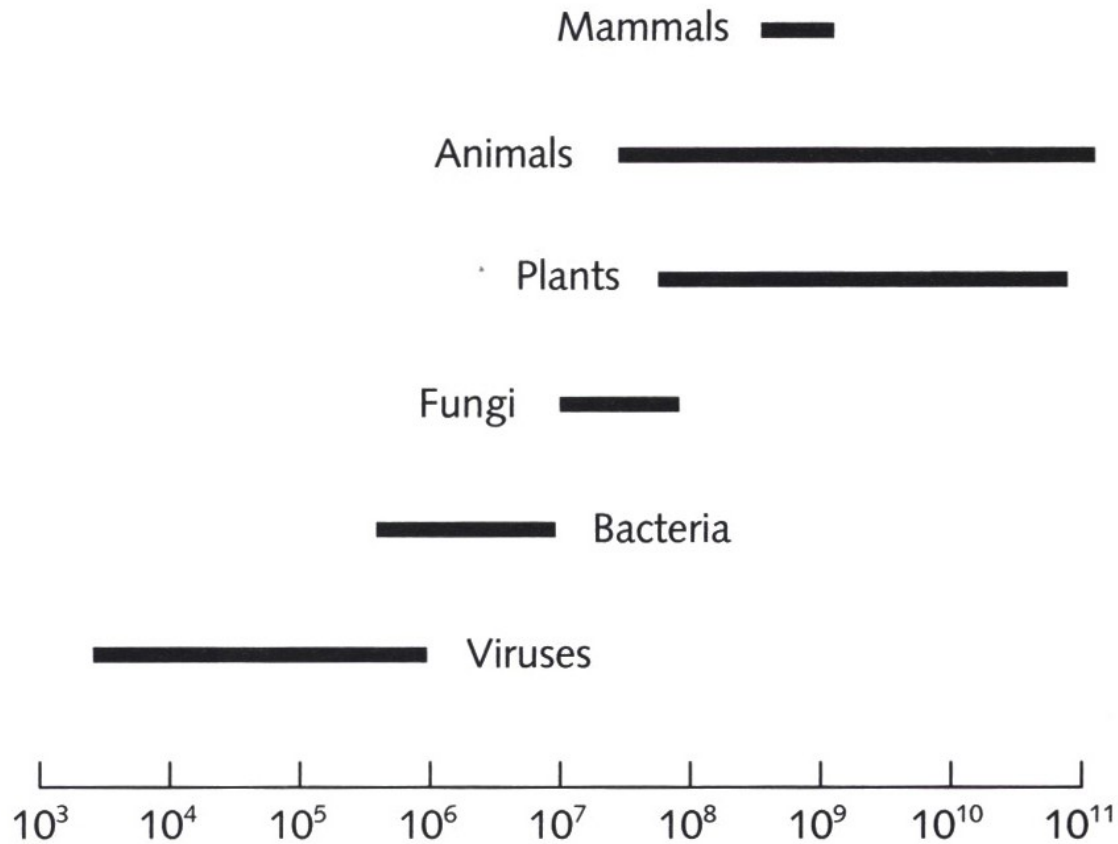
Euchromatin: Lightly packed DNA; gene rich, often active

Heterochromatin: Tightly packed DNA; usually repetitive; structural functions

Genomes

- Definition (again): the entire collection of hereditary material
 - Most organisms: DNA content
 - Retroviruses (like HIV, influenza): RNA content
- Eukaryotes can have 2-3 genomes:
 - Nuclear (default)
 - Mitochondrial
 - Plastid
- Libraries & instruction sets for the cells
- Identical in most cells, except the immune system cells
- Germline DNA: material that may be transmitted to the child (germ cell)
 - Germ cell: cells that give rise to gametes (sperm/egg)
- Somatic DNA: material in cells other than germ cells & gametes
 - Changes in somatic cells do not transmit to offspring

How big are genomes?



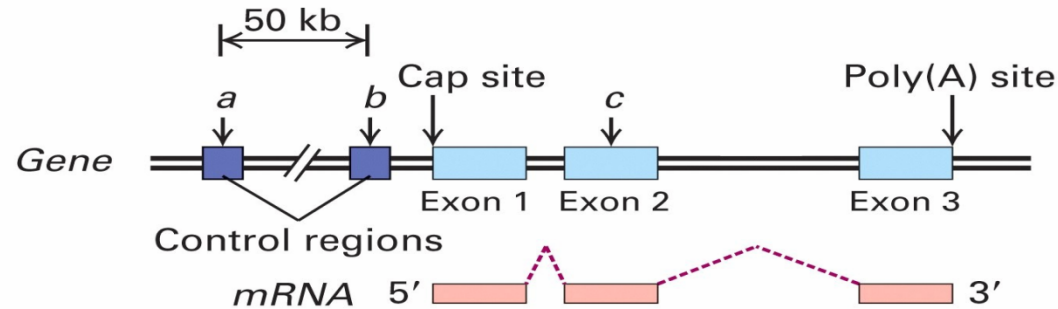
How big are genomes?

| Organism | Genome Size (Bases) | Estimated Genes |
|---|---------------------|-----------------|
| Human (<i>Homo sapiens</i>) | 3 billion | 20,000 |
| Laboratory mouse (<i>M. musculus</i>) | 2.6 billion | 20,000 |
| Mustard weed (<i>A. thaliana</i>) | 100 million | 18,000 |
| Roundworm (<i>C. elegans</i>) | 97 million | 16,000 |
| Fruit fly (<i>D. melanogaster</i>) | 137 million | 12,000 |
| Yeast (<i>S. cerevisiae</i>) | 12.1 million | 5,000 |
| Bacterium (<i>E. coli</i>) | 4.6 million | 3,200 |
| Human immunodeficiency virus (HIV) | 9700 | 9 |

Genome “table of contents”

- Genes (~35%; but only 1% are coding exons)
 - Protein coding
 - Non-coding (ncRNA only)
 - Pseudogenes: genes that lost their expression ability:
 - Evolutionary loss
 - Processed pseudogenes
 - Repeats (~50%)
 - Transposable elements: sequence that can copy/paste themselves. Typically of virus origin.
 - Satellites (short tandem repeats [STR]; variable number of tandem repeats [VNTR])
 - Segmental duplications (5%)
 - Include genes and other repeat elements within
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Genes



- Subsequences of DNA that are transcribed into RNA
 - Some encode for proteins, some do not
- Regulatory regions: up to 50 kb upstream of +1 site
- Exons: protein coding and untranslated regions (UTR)
 - 1 to 178 exons per gene (mean 8.8)
 - 8 bp to 17 kb per exon (mean 145 bp)
- Introns: sequence between exons; spliced out before translation
 - average 1 kb – 50 kb per intron
- Gene size: Largest – 2.4 Mb (Dystrophin). Mean – 27 kb.

Genes can be switched on/off

- In an adult multicellular organism, there is a wide variety of cell types seen in the adult. eg, muscle, nerve and blood cells.
 - The different cell types contain the *same* DNA.
 - This **differentiation** arises because different cell types express different genes.
 - Type of gene regulation mechanisms:
 - Promoters, enhancers, methylation, RNAi, etc.
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Pseudogenes

- “Dead” genes that lost their coding ability
 - Evolutionary process:
 - Mutations cause:
 - Early stop codons
 - Loss of promoter / enhancer sequence
 - Processed pseudogenes:
 - A real gene is transcribed to mRNA, introns are spliced out, then reverse transcribed into cDNA
 - This cDNA is then reintegrated into the nuclear genome
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Repeats

- Transposons (mobile elements): generally of viral origin, integrated into genomes millions of years ago
 - Can copy/paste; most are fixed, some are still active
 - Retrotransposon: intermediate step that involves transcription (RNA)
 - DNA transposon: no intermediate step
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Retrotransposons

- LTR: long terminal repeat
- Non-LTR:
 - LINEs: Long Interspersed Nucleotide Elements
 - L1 (~6 kbp full length, ~900 bp trimmed version): Approximately 17% of human genome
 - They encode genes to copy themselves
 - SINEs: Short Interspersed Nucleotide Elements
 - *Alu* repeats (~300 bp full length): Approximately 1 million copies = ~10% of the genome
 - They use cell's machinery to replicate
 - Many subfamilies; *AluY* being the most active, *AluJ* most ancient

Satellites

- **Microsatellites (STR=short tandem repeats) 1-10 bp**
 - Used in population genetics, paternity tests and forensics
- **Minisatellites (VNTR=variable number of tandem repeats): 10-60 bp**
- **Other satellites**
 - Alpha satellites: centromeric/pericentromeric, 171bp in humans
 - Beta satellites: centromeric (some), 68 bp in humans
 - Satellite I (25-68 bp), II (5bp), III (5 bp)

Segmental duplications

- Low-copy repeats, >1 kbp & > 90% sequence identity between copies
 - Covers ~5% of the human genome
 - Both tandem and interspersed in humans, about half inter chromosomal duplications
 - Tandem in mice, no inter chromosomal duplications
 - Gene rich
 - Provides elasticity to the genome:
 - More prone to rearrangements (and causal)
 - Gene innovation through duplication: Ohno, 1970
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Gene innovation through duplication

