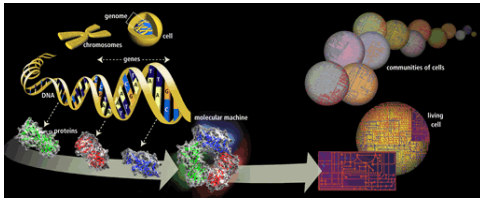


Molecular Biology Primer



Angela Brooks, Raymond Brown, Calvin Chen, Mike Daly, Hoa Dinh, Erinn Hama, Robert Hinman, Julio Ng, Michael Sneddon, Hoa Troung, Jerry Wang, Chei Fung Yung
Edited for Introduction to Bioinformatics (Autumn 2006) by Esa Pitkänen
<http://www.cs.helsinki.fi/mbl/courses/06-07/1b/>

Outline:

1. How molecular biology came about?
2. Similarities: What is life made of?
3. Differences: Variation in genomes

1. How Molecular Biology came about?

- Microscopic biology began in 1665
- Robert Hooke (1635-1703) discovered organisms are made up of cells
- Matthias Schleiden (1804-1881) and Theodor Schwann (1810-1882) further expanded the study of cells in 1830s



• Matthias Schleiden

• Theodor Schwann

Major events in the history of Molecular Biology 1800 - 1870

- **1865** Gregor Mendel discover the basic rules of heredity of garden pea.
 - An individual organism has two alternative heredity units for a given trait (**dominant trait** v.s. **recessive trait**)
- **1869** Johann Friedrich Miescher discovered DNA and named it nuclein.



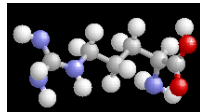
Mendel: The Father of Genetics



Johann Miescher

Major events in the history of Molecular Biology 1880 - 1900

- **1881** Edward Zacharias showed chromosomes are composed of nuclein.
- **1899** Richard Altmann renamed nuclein to nucleic acid.
- **By 1900**, chemical structures of all 20 amino acids had been identified



Major events in the history of Molecular Biology 1900-1911

- **1902** - Emil Hermann Fischer wins Nobel prize: showed amino acids are linked and form proteins
 - Postulated: protein properties are defined by amino acid composition and arrangement, which we nowadays know as fact
- **1911** – Thomas Hunt Morgan discovers genes on chromosomes are the discrete units of heredity
- **1911** Pheobus Aaron Theodore Lerene discovers RNA



Emil Fischer




Thomas Morgan


An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Major events in the history of Molecular Biology 1940 - 1950

- 1941 – George Beadle and Edward Tatum identify that genes make proteins




George Beadle



Edward Tatum

- 1950 – Edwin Chargaff find Cytosine complements Guanine and Adenine complements Thymine




Edwin Chargaff

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 7

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

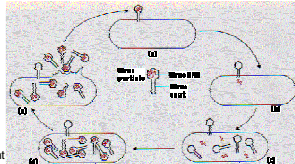
Major events in the history of Molecular Biology 1950 - 1952

- 1950s – Mahlon Bush Hoagland first to isolate tRNA



Mahlon Hoagland

- 1952 – Alfred Hershey and Martha Chase make genes from DNA




Hershey Chase Experiment

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 8

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info


Major events in the history of Molecular Biology 1952 - 1960

- 1952-1953 James D. Watson and Francis H. C. Crick deduced the double helical structure of DNA



James Watson and Francis Crick

- 1956 George Emil Palade showed the site of enzymes manufacturing in the cytoplasm is made on RNA organelles called ribosomes.



George Emil Palade

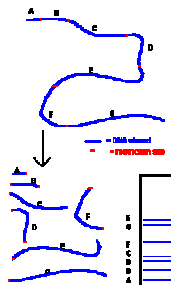
8.9.2006 Introduction to Bioinformatics (Autumn 2006) 9

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Major events in the history of Molecular Biology 1970

- 1970 Howard Temin and David Baltimore independently isolate the first restriction enzyme

- DNA can be cut into reproducible pieces with site-specific endonuclease called restriction enzymes;
 - the pieces can be linked to bacterial vectors and introduced into bacterial hosts. (gene cloning or recombinant DNA technology)




8.9.2006 Introduction to Bioinformatics (Autumn 2006) 10


An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Major events in the history of Molecular Biology 1970- 1977

- 1977 Phillip Sharp and Richard Roberts demonstrated that pre-mRNA is processed by the excision of introns and exons are spliced together.




Phillip Sharp



Richard Roberts

- Joan Steitz determined that the 5' end of snRNA is partially complementary to the consensus sequence of 5' splice junctions.




Joan Steitz

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 11

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info


Major events in the history of Molecular Biology 1986 - 1995

- 1986 Leroy Hood: Developed automated sequencing mechanism



Leroy Hood

- 1986 Human Genome Initiative announced
- 1990 The 15 year Human Genome project is launched by congress
- 1995 Moderate-resolution maps of chromosomes 3, 11, 12, and 22 maps published (These maps provide the locations of "markers" on each chromosome to make locating genes easier)



8.9.2006 Introduction to Bioinformatics (Autumn 2006) 12

Major events in the history of Molecular Biology 1995-1996

- **1995** John Craig Venter: First bacterial genomes sequenced
- **1995** Automated fluorescent sequencing instruments and robotic operations
- **1996** First eukaryotic genome-yeast-sequenced



John Craig Venter

Major events in the history of Molecular Biology 1997 - 1999

- **1997** E. Coli sequenced
- **1998** PerkinsElmer, Inc.. Developed 96-capillary sequencer
- **1998** Complete sequence of the *Caenorhabditis elegans* genome
- **1999** First human chromosome (number 22) sequenced

Major events in the history of Molecular Biology 2000-2001

- **2000** Complete sequence of the euchromatic portion of the *Drosophila melanogaster* genome
- **2001** International Human Genome Sequencing: first draft of the sequence of the human genome published

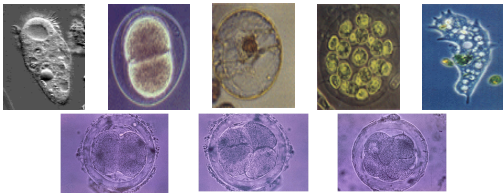


Major events in the history of Molecular Biology 2003- Present

- **April 2003** Human Genome Project Completed. Mouse genome is sequenced.
- **April 2004** Rat genome sequenced.



2. What is Life made of?



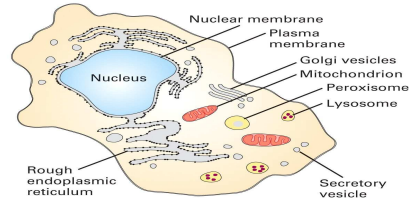
Cells

- **Fundamental working units** of every living system.
- Every organism is composed of one of two radically different types of cells:
 - **prokaryotic** cells or
 - **eukaryotic** cells.
- **Prokaryotes** and **Eukaryotes** are descended from the same primitive cell.
 - All prokaryotic and eukaryotic cells are the result of a total of 3.5 billion years of evolution.

Cells

- Chemical composition-by weight
 - 70% water
 - 7% small molecules
 - salts
 - Lipids
 - amino acids
 - nucleotides
 - 23% macromolecules
 - Proteins
 - Polysaccharides
 - lipids
- biochemical (metabolic) pathways
- translation of mRNA into proteins

Life begins with Cell

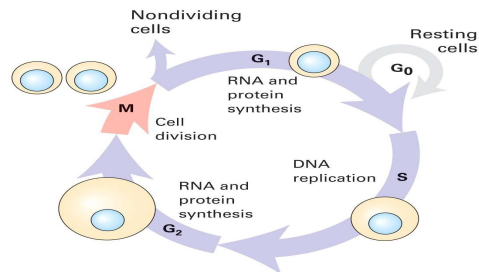


- A cell is a smallest structural unit of an organism that is capable of independent functioning
- All cells have some common features

Common features of organisms

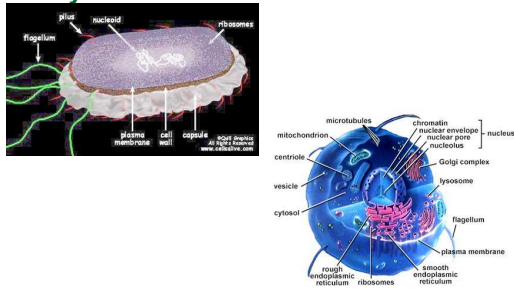
- Chemical energy is stored in ATP
- Genetic information is encoded by DNA
- Information is transcribed into RNA
- There is a common triplet genetic code
- Translation into proteins involves ribosomes
- Shared metabolic pathways
- Similar proteins among diverse groups of organisms

All Cells have common Cycles

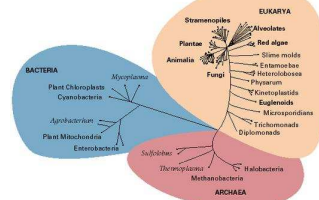


- Born, eat, replicate, and die

Two types of cells: Prokaryotes and Eukaryotes



Prokaryotes and Eukaryotes



- According to the most recent evidence, there are three main branches to the tree of life.
- Prokaryotes include Archaea ("ancient ones") and bacteria.
- Eukaryotes are kingdom Eukarya and includes plants, animals, fungi and certain algae.

Prokaryotes and Eukaryotes, continued

Prokaryotes	Eukaryotes
Single cell	Single or multi cell
No nucleus	Nucleus
No organelles	Organelles
One piece of circular DNA	Chromosomes
No mRNA post transcriptional modification	Exons/Introns splicing

Signaling Pathways: Control Gene Activity

- Instead of having brains, cells make decision through complex networks (or pathways) of chemical reactions
 - Synthesize new materials
 - Break other materials down for spare parts
 - Signal to eat or die

Cells Information and Machinery

- Cells store all information to replicate itself
 - Human genome is around 3 billions base pair long
 - Almost every cell in human body contains same set of genes
 - But not all genes are used or expressed by those cells
- Machinery:
 - Collect and manufacture components
 - Carry out replication
 - Kick-start its new offspring
 (A cell is like a car factory)

Overview of organizations of life

- **Nucleus = library**
- **Chromosomes = bookshelves**
- **Genes = books**
- Almost every cell in an organism contains the same libraries and the same sets of books.
- Books represent all the information (DNA) that every cell in the body needs so it can grow and carry out its various functions.

Terminology

- The **genome** is an organism's complete set of DNA.
 - a bacteria contains about 600,000 DNA base pairs
 - human and mouse genomes have some 3 billion.
- Human genome has 24 distinct chromosomes.
 - Each chromosome contains many **genes**.
- **Gene**
 - basic physical and functional units of heredity.
 - specific sequences of DNA bases that encode instructions on how to make **proteins**.
- **Proteins**
 - Make up the cellular structure and function
 - large, complex molecules made up of smaller subunits called **amino acids**.

All Life depends on 3 critical molecules

- **DNAs (Deoxyribonucleic acid)**
 - Hold information on how cell works
- **RNAs (Ribonucleic acid)**
 - 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.)

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

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 complementary strands.

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 31

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

DNA, continued

- DNA has a double helix structure which is composed of
 - sugar molecule
 - phosphate group
 - and a base (A,C,G,T)
- By convention, we read DNA strings in direction of transcription: from 5' end to 3' end
 5' ATTTAGGCC 3'
 3' TAAATCCGG 5'

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 32

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

DNA is packed into chromosomes

- Double helix DNA strand.
- Chromatin strand (DNA with **histones**)
- Condensed chromatin during interphase with **centromere**.
- Condensed chromatin during prophase
- Chromosome during metaphase

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 33

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Human chromosomes

- Somatic cells in humans have 2 pairs of 22 chromosomes + XX (female) or XY (male) = total of 46 chromosomes
- Germline cells have 22 chromosomes + either X or Y = total of 23 chromosomes

Karyogram of human male using Giemsa staining (<http://en.wikipedia.org/wiki/Karyotype>)

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 34

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Length of DNA and number of chromosomes

Organism	#base pairs	#chromosomes (germline)
Prokaryotic		
Escherichia coli (bacterium)	4x10 ⁶	1
Eukaryotic		
Saccharomyces cerevisia (yeast)	1.35x10 ⁷	17
Drosophila melanogaster (insect)	1.65x10 ⁸	4
Homo sapiens (human)	2.9x10 ⁹	23
Zea mays (corn)	5.0x10 ⁹	10

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 35

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Human Genome Composition

Class	Length	Copy Number in Human Genome	Fraction of Human Genome, %
Protein-coding genes			
Solitary genes	Variable	1	~1% (0.8) ^a
Duplicated or diverged genes in gene families	Variable	2–1000	~1% (0.8) ^a
Tandemly repeated genes encoding rDNA, rRNA, and histones	Variable	20–300	0.3
Repetitious DNA			
Simple-sequence DNA	1–500 bp	Variable	3
Interspersed repeats			
DNA transposons	2–3 kb	300,000	3
LTR retrotransposons	4–11 kb	440,000	8
Non-LTR retrotransposons			
LINEs	6–8 kb	840,000	21
SINEs	100–500 bp	1,600,000	13
Processed pseudogenes	Variable	1–100	~0.4
Unclassified spacer DNA	Variable	n.a. ^b	~23

^aComplete transcript sets, including introns.
^bProtein-coding genes. The total number of human protein-coding genes is estimated to be 30,000–35,000, but this number is based on current methods for identifying genes in the human genome sequence and may be an underestimate. See Appendix 10-1.

SOURCE: E. S. Lander et al., 2001, Nature 409:860.

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 36

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

RNA

- RNA is similar to DNA chemically. It is usually only a single strand. T(hyamine) is replaced by U(racil)
- Several types of RNA exist for different functions in the cell.

A.

B.

tRNA linear and 3D view: <http://www.cgl.ucsf.edu/home/glasfeld/tutorial/tma/trna.gif>

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 37

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

DNA, RNA, and the Flow of Information

"The central dogma"

Replication

DNA can replicate.

Information coded in the sequence of base pairs in DNA is passed to molecules of RNA.

Information in RNA is passed to proteins. It never passes from proteins to nucleic acids.

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 38

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Overview of DNA to RNA to Protein

- A gene is expressed in two steps
 - 1) Transcription: RNA synthesis
 - 2) Translation: Protein synthesis

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 39

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Proteins

- Proteins are polypeptides (strings of amino acid residues)
- Represented using strings of letters from an alphabet of 20: A E G L V ... W K K L A G
- Typical length 50...1000 residues

Urease enzyme from Helicobacter pylori

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 40

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

How DNA/RNA codes for protein?

- DNA alphabet contains four letters but must specify protein, or polypeptide sequence of 20 letters.
- Dinucleotides are not enough: $4^2 = 16$ possible dinucleotides
- Trinucleotides (triplets) allow $4^3 = 64$ possible trinucleotides
- Triples are also called *codons*

		Second letter				
		U	C	A	G	
First letter	U	UUU Phenylalanine	UUC Tyrosine	UUA Tyrosine	UUG Cysteine	U
	C	CUU Leucine	CCU Proline	CAU Histidine	CCG Arginine	C
	A	AUU Isoleucine	AUC Methionine start codon	AUA Methionine start codon	AUG Methionine start codon	A
	G	GUU Valine	GCC Alanine	GAU Aspartic acid	GGU Glycine	G
		UUA Stop codon	UUG Stop codon	UAG Stop codon	UGG Tryptophan	

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 41

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

How DNA/RNA codes for protein?

- Three of the possible triplets specify "stop translation"
- Translation usually starts at triplet AUG (this also codes for methionine)
- Most amino acids may be specified by more than triplet
- How to find a gene? Look for start and stop codons (not that easy though)

		Second letter				
		U	C	A	G	
First letter	U	UUU Phenylalanine	UUC Tyrosine	UUA Tyrosine	UUG Cysteine	U
	C	CUU Leucine	CCU Proline	CAU Histidine	CCG Arginine	C
	A	AUU Isoleucine	AUC Methionine start codon	AUA Methionine start codon	AUG Methionine start codon	A
	G	GUU Valine	GCC Alanine	GAU Aspartic acid	GGU Glycine	G
		UUA Stop codon	UUG Stop codon	UAG Stop codon	UGG Tryptophan	

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 42

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Proteins: Workhorses of the Cell

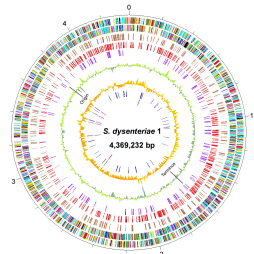
- 20 different amino acids
 - different chemical properties cause the protein chains to fold up into specific three-dimensional structures that define their particular functions in the cell.
- Proteins do all **essential work** for the cell
 - build cellular structures
 - digest nutrients
 - execute metabolic functions
 - Mediate information flow within a cell and among cellular communities.
- Proteins work together with other proteins or nucleic acids as "molecular machines"
 - structures that fit together and function in highly specific, lock-and-key ways.

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 43

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

3. Where does the variation in genomes come from?

- Prokaryotes are typically haploid: they have a single (circular) chromosome
- DNA is usually inherited vertically (parent to daughter)
- Inheritance is clonal
 - Descendants are faithful copies of an ancestral DNA
 - Variation is introduced via mutations, transposable elements, and horizontal transfer of DNA



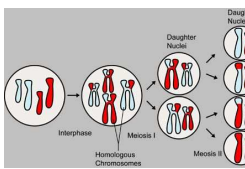
Chromosome map of *S. dysenteriae*, the nine rings describe different properties of the genome http://www.mgc.ac.cn/SNIBASE/circular_Sd197.htm

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 44

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Mitosis and meiosis

- Sexual organisms are usually diploid
 - Germline cells (gametes) contain N chromosomes
 - Somatic (body) cells have 2N chromosomes
- Meiosis: reduction of chromosome number from 2N to N during reproductive cycle
 - One chromosome doubling is followed by two cell divisions
- Mitosis: growth and development of the organism
 - One chromosome doubling is followed by one cell division



Major events in meiosis
<http://en.wikipedia.org/wiki/Meiosis>
<http://www.ncbi.nlm.nih.gov/About/Primer>

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 45

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Recombination and variation

- Allele is a viable DNA coding occupying a given locus (position in the genome)
- In recombination, alleles from parents become shuffled in offspring individuals via chromosomal crossover over
- Allele combinations in offspring are usually different from combinations found in parents
- Recombination errors lead into additional variations

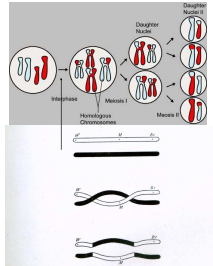


Fig. 63. Scheme to illustrate double crossing over.
 Chromosomal crossover as described by T. H. Morgan in 1916

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 46

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Recombination frequency and linked genes

- Genetic marker: some DNA sequence of interest (e.g., gene or a part of a gene)
- Recombination is more likely to separate two distant markers than two close ones
- Linked markers: "tend" to be inherited together
- Marker distances measured in centimorgans: 1 centimorgan corresponds to 1% chance that two markers are separated in recombination

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 47

An Introduction to Bioinformatics Algorithms www.bioalgorithms.info

Recombination and longer time scales

Conserved synteny

Chromosome i, species B
 9_{2B} 9_{1B} 9_{3B}

Chromosome j, species C
 9_{1C} 9_{2C} 9_{3C}

Syntenic blocks and segments

Chromosome i, species B
 9_{3B} 9_{4B} 9_{1B} 9_{2B} 9_{3B}

Chromosome j, species C
 9_{4C} 9_{5C} 9_{1C} 9_{2C} 9_{3C}

syntenic block: 9_{3B} 9_{4B} 9_{1B} 9_{2B} 9_{3B}
 syntenic segment: 9_{1C} 9_{2C} 9_{3C}

- Assume that species B and C are descendants of A
- Conserved synteny: group of genes linked in both B and C
- Conserved segment: conserved synteny with same gene order
- Syntenic segment: group of markers (!) linked in both B and C
- Syntenic block: set of syntenic segments which may contain set inversions and duplications

8.9.2006 Introduction to Bioinformatics (Autumn 2006) 48

Biological string manipulation

- Errors get introduced to DNA during replication
 - Deletion: removal of one or more contiguous bases (substring)
 - Insertion: insertion of a substring
 - Segmental duplication: insertion of a copy of a DNA region into a different location
 - Inversion: reversal of substring
 - Translocation: removal and insertion of a substring
 - Point mutation: substitution of a base

References

- Richard C. Deonier, Simon Tavaré and Michael S. Waterman. *Computational Genome Analysis, An Introduction*. Springer, 2005.
- Daniel Sam, "Greedy Algorithm" presentation.
- Glenn Tesler, "Genome Rearrangements in Mammalian Evolution: Lessons from Human and Mouse Genomes" presentation.
- Ernst Mayr, "What evolution is".
- Neil C. Jones, Pavel A. Pevzner, "An Introduction to Bioinformatics Algorithms".
- Alberts, Bruce, Alexander Johnson, Julian Lewis, Martin Raff, Keith Roberts, Peter Walter. *Molecular Biology of the Cell*. New York: Garland Science. 2002.
- Mount, Ellis, Barbara A. List. *Milestones in Science & Technology*. Phoenix: The Oryx Press. 1994.
- Voet, Donald, Judith Voet, Charlotte Pratt. *Fundamentals of Biochemistry*. New Jersey: John Wiley & Sons, Inc. 2002.
- Campbell, Neil. *Biology, Third Edition*. The Benjamin/Cummings Publishing Company, Inc., 1993.
- Snustad, Peter and Simmons, Michael. *Principles of Genetics*. John Wiley & Sons, Inc, 2003.