Introduction to Genome Biology

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Bioconductor Short Course

Spring 2003

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Outline

- Cells, chromosomes, and cell division
- DNA structure and replication
- Proteins
- Central dogma: transcription, translation
- Microarrays
- Pathways

A brief history

1865	Genes are particulate factors
1903	Chromosomes are hereditary units
1910	Genes lie on chromosomes
1913	Chromosomes contain linear arrays of genes
1927	Mutations are physical changes in genes
1931	Recombination is caused by crossing over
1944	DNA is the genetic material
1945	A gene codes for a protein
1953	DNA is a double helix
1958	DNA replicates semiconservatively
1961	Genetic code is triplet
1977	DNA can be sequenced
1997	Genomes can be sequenced

Gregor Mendel (1823-1884)



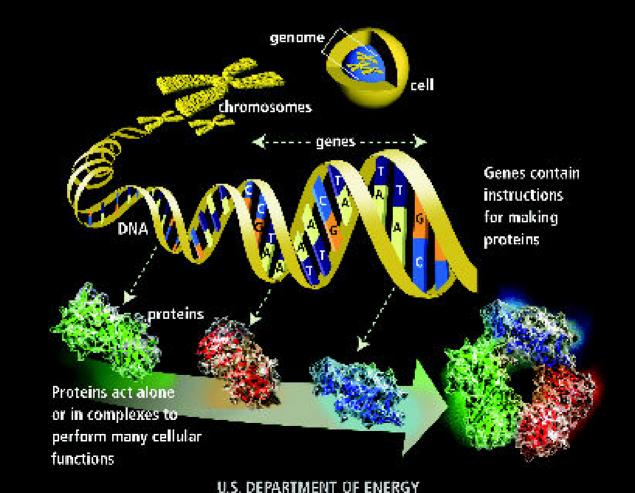
Thomas Hunt Morgan (1866-1945)

Francis Crick (1916-)

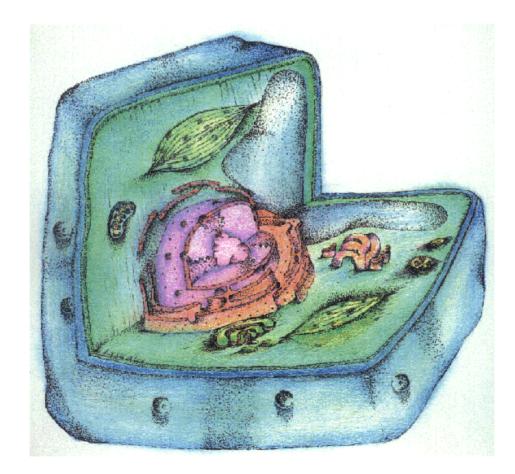


James D. Watson (1928-)

From chromosomes to proteins



Cells



Cells

- Cells: the fundamental working units of every living organism.
- Metazoa: multicellular organisms.
 E.g. humans: trillions of cells.
- Protozoa: unicellular organisms.
 E.g. yeast, bacteria.

Cells

- Each cell contains a complete copy of an organism's genome, or blueprint for all cellular structures and activities.
- Cells are of many different types (e.g. blood, skin, nerve cells), but all can be traced back to a single cell, the fertilized egg.

Cell composition

- 90% water.
- Of the remaining molecules, dry weight
 - 50% protein
 - 15% carbohydrate
 - 15% nucleic acid
 - 10% lipid
 - 10% miscellaneous.
- By element: 60% H, 25% O, 12%C, 5%N.

The genome

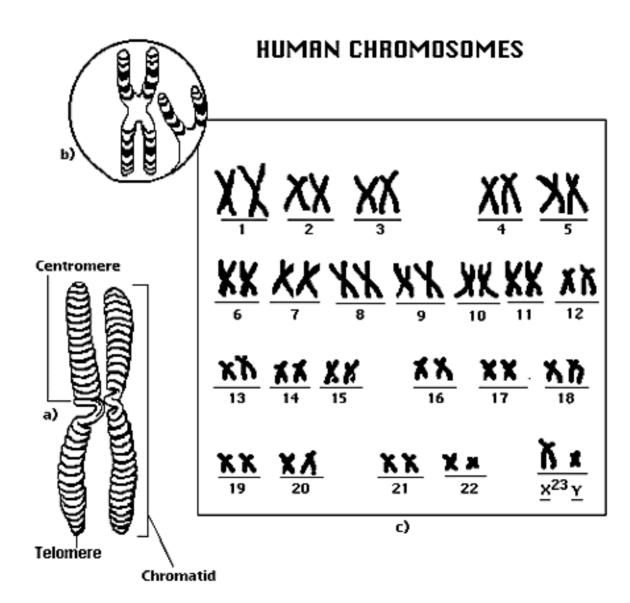
 The genome is distributed along chromosomes, which are made of compressed and entwined DNA.

 A (protein-coding) gene is a segment of chromosomal DNA that directs the synthesis of a protein.

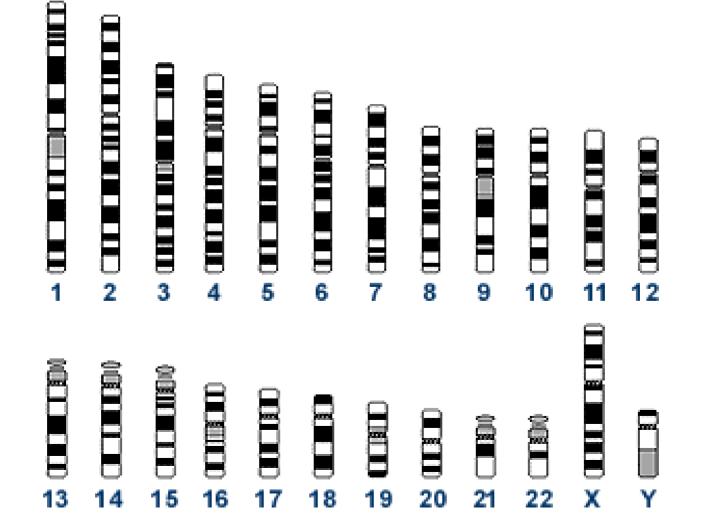
The human genome

- The human genome is distributed along 23 pairs of chromosomes
 - -22 autosomal pairs;
 - -the sex chromosome pair, XX for females and XY for males.
- In each pair, one chromosome is paternally inherited, the other maternally inherited (cf. meiosis).

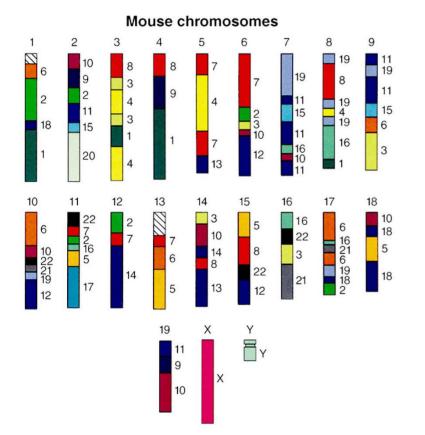
Chromosomes

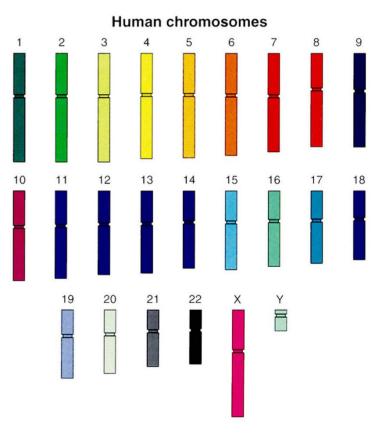


Chromosome banding patterns



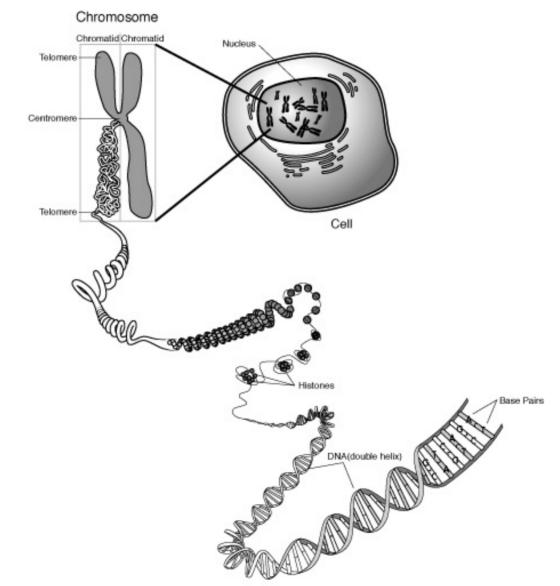
Of mice and men

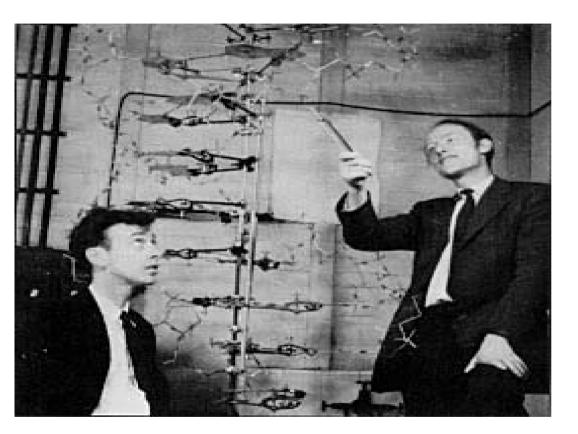




Courtesy Lisa Stubbs Oak Ridge National Laboratory

Chromosomes and DNA

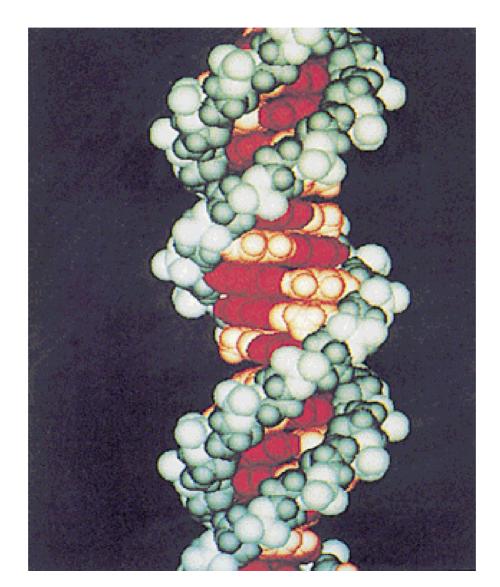


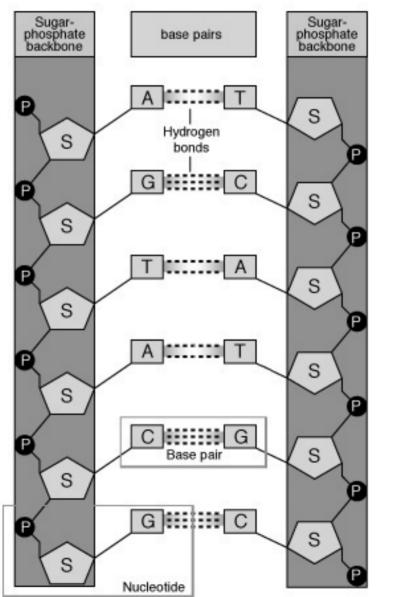


"We wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest."

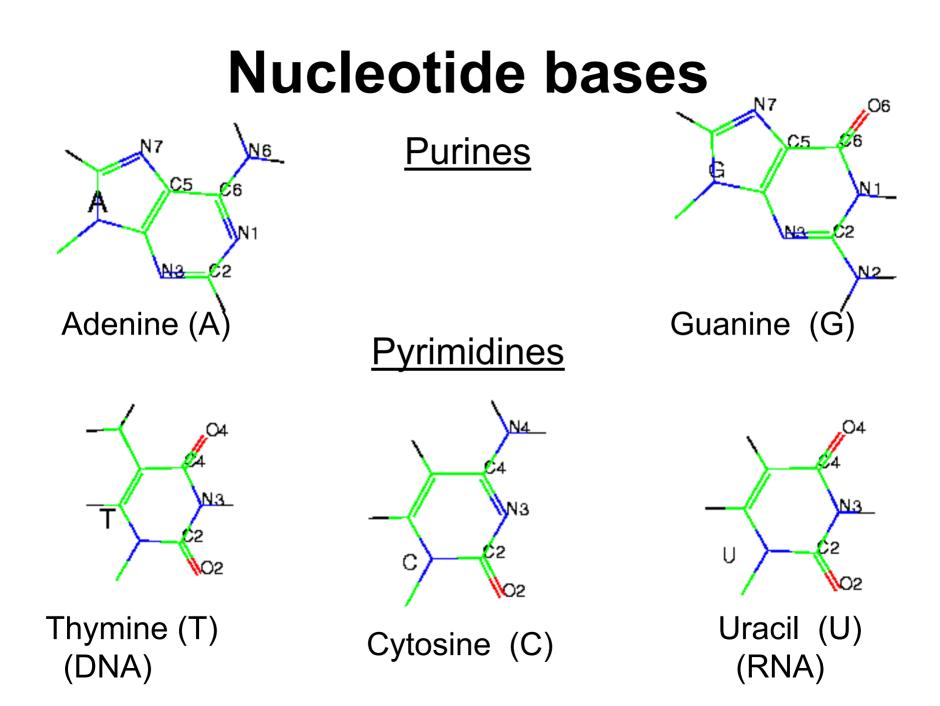
J.D. Watson & F. H. C. Crick. (1953). Molecular structure of Nucleic Acids. Nature. 171: 737-738.

- A deoxyribonucleic acid or DNA molecule is a double-stranded polymer composed of four basic molecular units called nucleotides.
- Each nucleotide comprises
 - a phosphate group;
 - a deoxyribose sugar;
 - one of four nitrogen bases:
 - purines: adenine (A) and guanine (G),
 - pyrimidines: cytosine (C) and thymine (T).





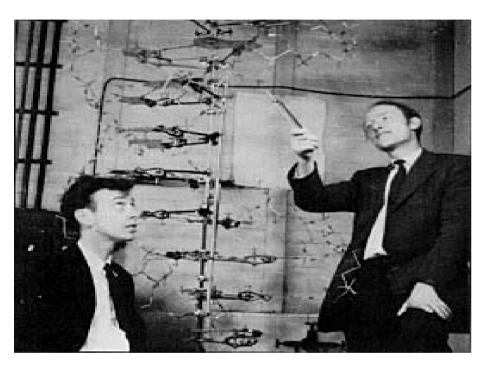




- Polynucleotide chains are directional molecules, with slightly different structures marking the two ends of the chains, the socalled 3' end and 5' end.
- The 3' and 5' notation refers to the numbering of carbon atoms in the sugar ring.
- The 3' end carries a sugar group and the 5' end carries a phosphate group.
- The two complementary strands of DNA are **antiparallel** (i.e, 5' end to 3' end directions for each strand are opposite)

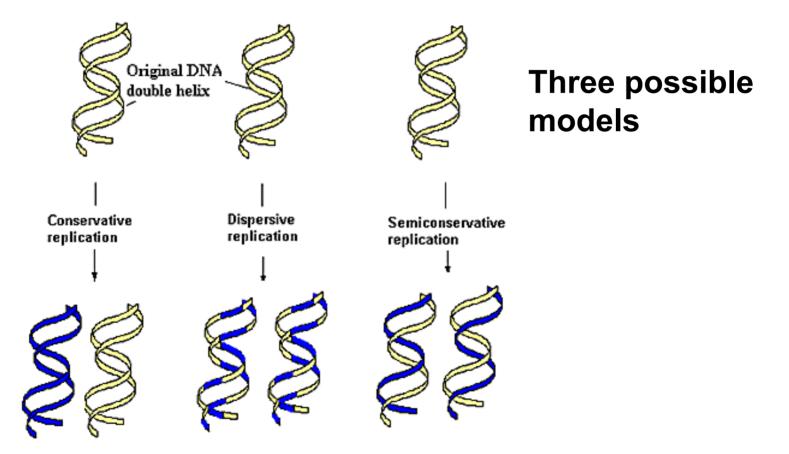
The human genome in numbers

- 23 pairs of chromosomes;
- 2 meters of DNA;
- 3,000,000,000 bp;
- 35 M (males 27M, females 44M);
- 30,000-40,000 genes.



"It has not escaped our notice that the specific pairing we have postulated immediately suggests a possible copying mechanism for the genetic material."

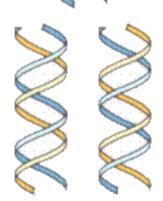
J.D. Watson & F. H. C. Crick. (1953). Molecular structure of Nucleic Acids. Nature. 171: 737-738.



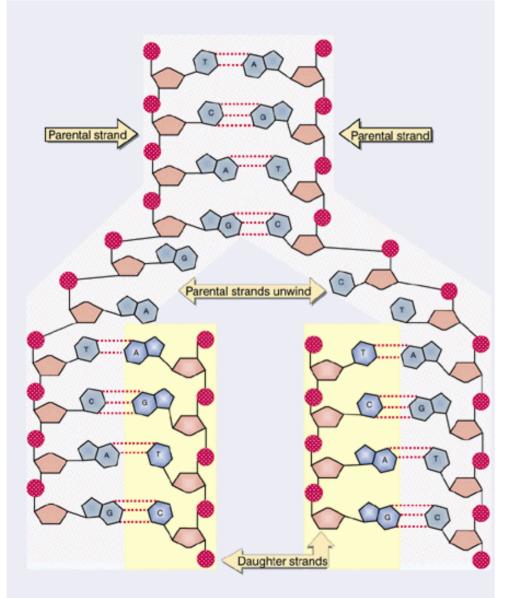
Semiconservative replication

Original DNA Helix

DNA helixes after one round of replication

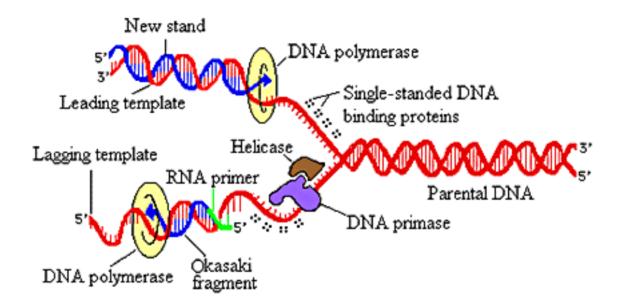


- In the replication of a double-stranded or duplex DNA molecule, **both** parental (i.e. original) DNA strands are copied.
- The parental DNA strand that is copied to form a new strand is called a **template**.
- When copying is finished, the two new duplexes each consist of one of the original strands plus its complementary copy - semiconservative replication.

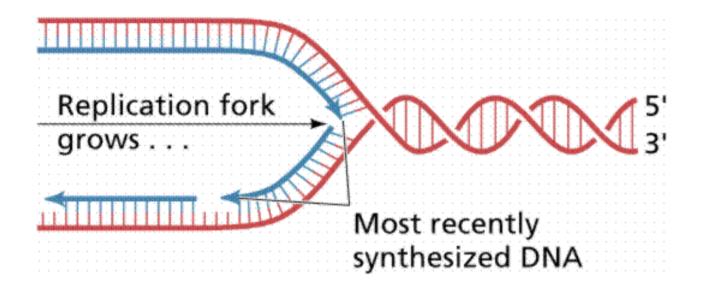


Base pairing provides the mechanism for DNA replication.

- Many enzymes are required to unwind the double helix and to synthesize a new strand of DNA.
- The unwound helix, with each strand being synthesized into a new double helix, is called the **replication fork**.
- DNA synthesis occurs in the 5' → 3' direction.



Collaboration of Proteins at the Replication Fork

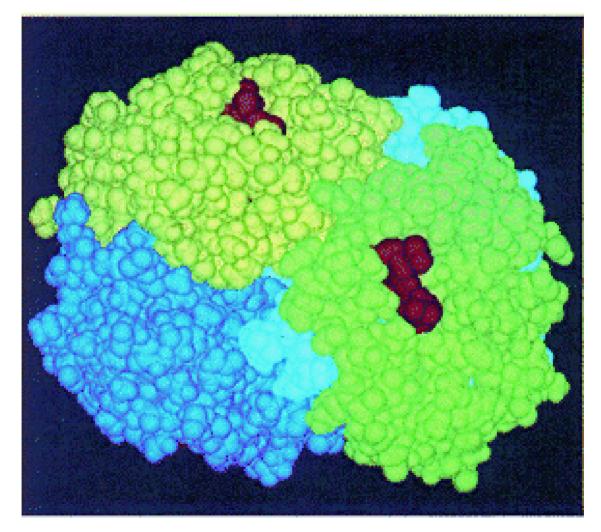


	$\boldsymbol{\lambda}$
and grows	5'
Okazaki fragments	3'
	X

Enzymes in DNA replication

- 1. **Topoisomerase**: removes supercoils and initiates duplex unwinding.
- 2. Helicase: unwinds duplex.
- **3. DNA polymerase**: synthesizes the new DNA strand; also performs proofreading.
- 4. Primase: attaches small RNA primer to singlestranded DNA to act as a substitute 3'OH for DNA polymerase to begin synthesizing from.
- 5. Ligase: catalyzes the formation of phosphodiester bonds.
- 6. Single-stranded binding proteins: maintain the stability of the replication fork.

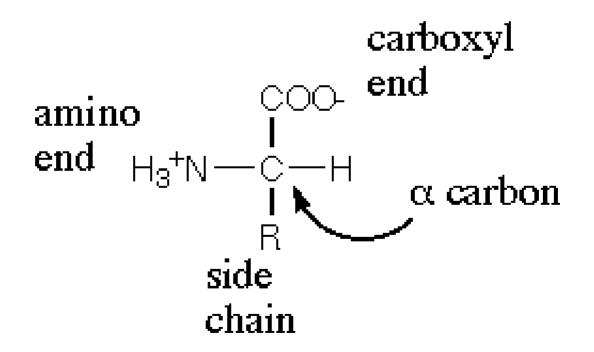
Proteins



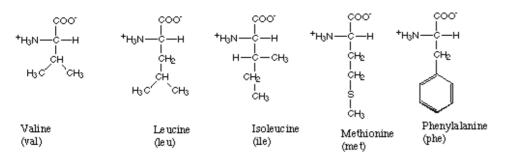
Proteins

- Proteins: large molecules composed of one or more chains of amino acids, polypeptides.
- Amino acids: class of 20 different organic compounds containing a basic amino group (-NH₂) and an acidic carboxyl group (-COOH).
- The order of the amino acids is determined by the base sequence of nucleotides in the gene coding for the protein.
- E.g. hormones, enzymes, antibodies.

Amino acids

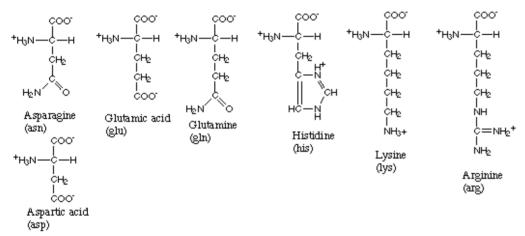


Amino acids with hydrophobic side groups

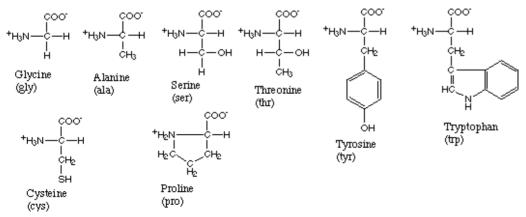


Amino acids

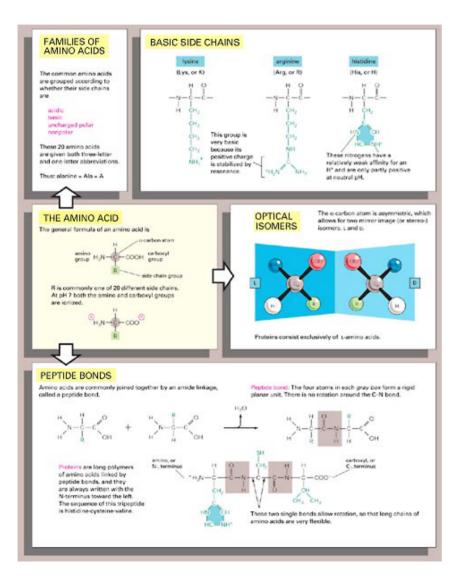
Amino acids with hydrophilic side groups

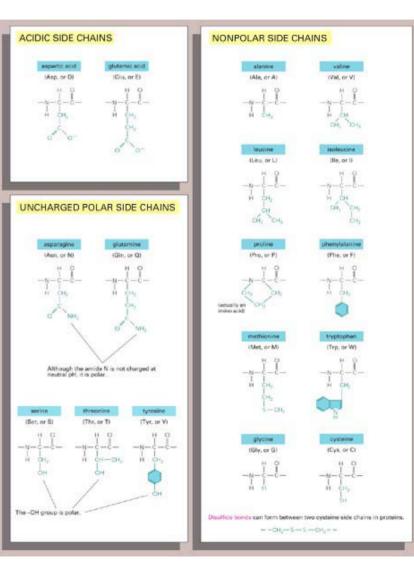


Amino acids that are in between

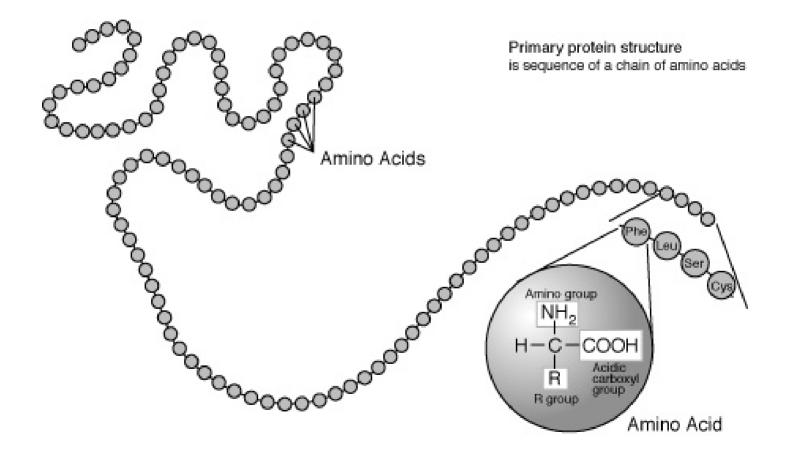


Amino acids

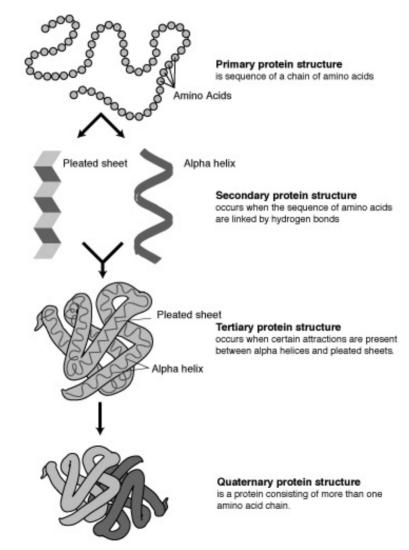




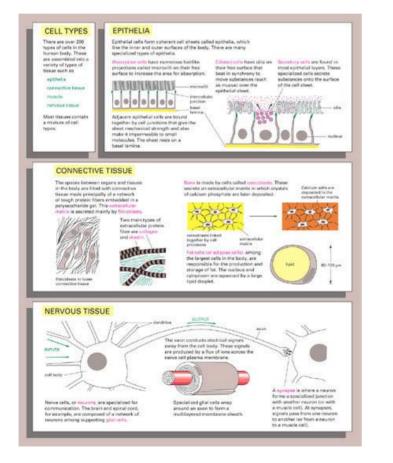
Proteins



Proteins



Cell types



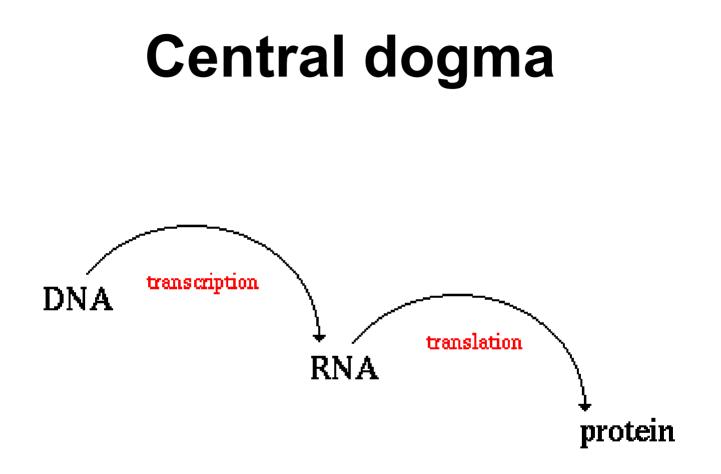


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internative

Differential expression

- Each cell contains a complete copy of the organism's genome.
- Cells are of many different types and states E.g. blood, nerve, and skin cells, dividing cells, cancerous cells, etc.
- What makes the cells different?
- Differential gene expression, i.e., when, where, and how much each gene is expressed.
- On average, 40% of our genes are expressed at any given time.



Central dogma

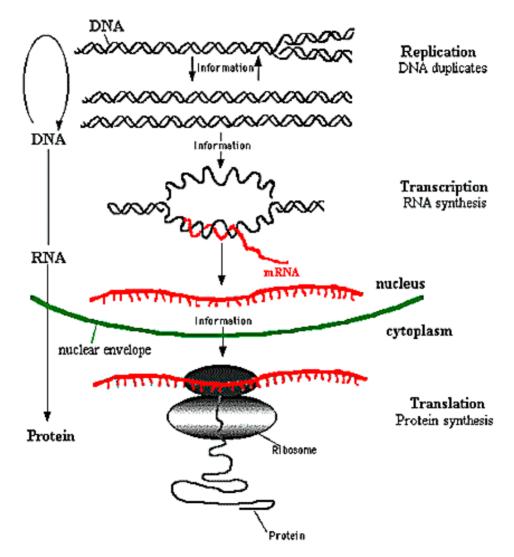
The **expression** of the genetic information stored in the DNA molecule occurs in two stages:

- (i) transcription, during which DNA is transcribed into mRNA;
- (ii) translation, during which mRNA is translated to produce a protein.

DNA → mRNA → protein

Other important aspects of regulation: methylation, alternative splicing, etc.

Central dogma



The Central Dogma of Molecular Biology

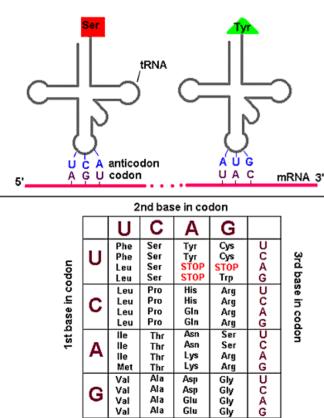
RNA

- A ribonucleic acid or RNA molecule is a nucleic acid similar to DNA, but
 - single-stranded;
 - ribose sugar rather than deoxyribose sugar;
 - uracil (U) replaces thymine (T) as one of the bases.
- RNA plays an important role in protein synthesis and other chemical activities of the cell.
- Several classes of RNA molecules, including messenger RNA (mRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), and other small RNAs.

The genetic code

- **DNA:** sequence of **four** different nucleotides.
- **Proteins:** sequence of **twenty** different amino acids.
- The correspondence between DNA's fourletter alphabet and a protein's twenty-letter alphabet is specified by the genetic code, which relates nucleotide triplets or codons to amino acids.

The genetic code



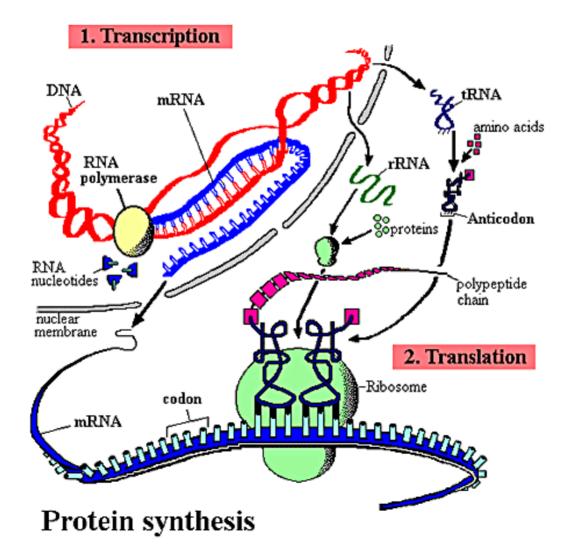
The Genetic Code

Start codon: initiation of translation (AUG, Met). **Stop codons**: termination of translation.

Mapping between codons and amino acids is **many-to-one**: 64 codons but only 20 a.a..

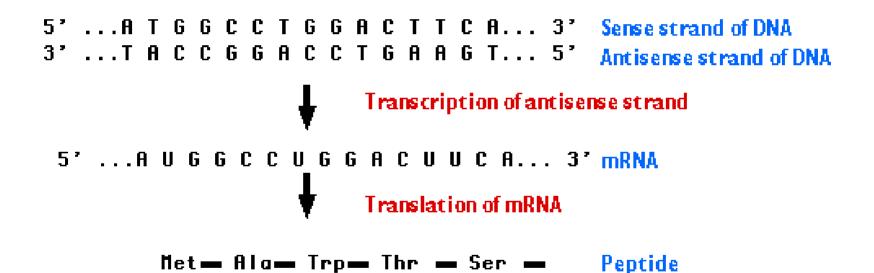
Third base in codon is often redundant, e.g., stop codons.

Protein synthesis



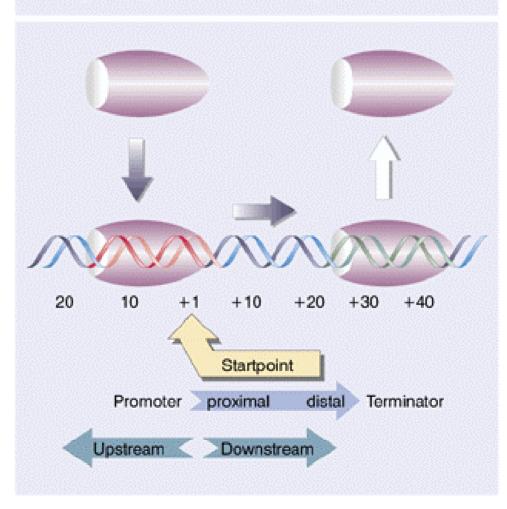
- Analogous to DNA replication: several steps and many enzymes.
- **RNA polymerase** synthesizes an RNA strand complementary to one of the two DNA strands.
- The RNA polymerase recruits **rNTPs** (ribonucleotide triphosphate) in the same way that DNA polymerase recruits dNTPs (deoxunucleotide triphospate).
- However, synthesis is single stranded and only proceeds in the 5' to 3' direction of mRNA (no Okazaki fragments).

- The strand being transcribed is called the template or antisense strand; it contains anticodons.
- The other strand is called the sense or coding strand; it contains codons.
- The RNA strand newly synthesized from and complementary to the template contains the same information as the coding strand.



- Promoter. Unidirectional sequence upstream of the coding region (i.e., at 5' end on sense strand) that tells the RNA polymerase both where to start and on which strand to continue synthesis. E.g. TATA box.
- Terminator. Regulatory DNA region signaling end of transcription, at 3' end .
- Transcription factor. A protein needed to initiate the transcription of a gene, binds either to specific DNA sequences (e.g. promoters) or to other transcription factors.

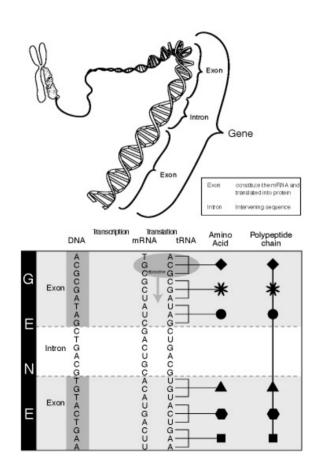
Figure 9.2 Overview: a transcription unit is a sequence of DNA transcribed into a single RNA, starting at the promoter and ending at the terminator.



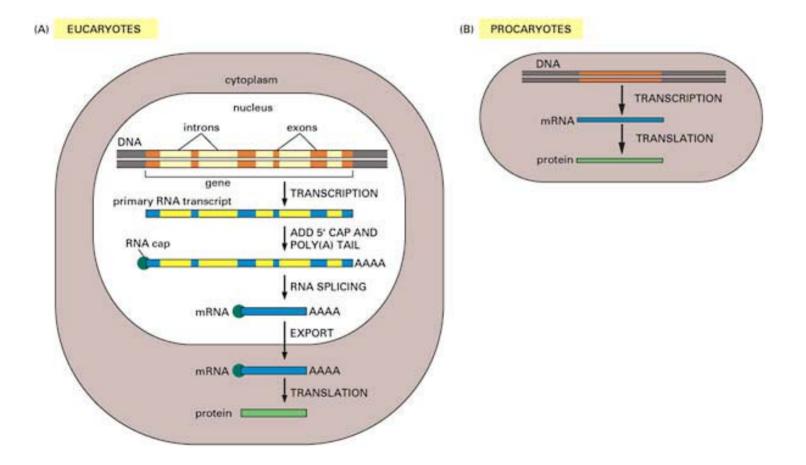
Exons and introns

- Genes comprise only about 2% of the human genome.
- The rest consists of **non-coding** regions
 - chromosomal structural integrity,
 - cell division (e.g. centromere)
 - regulatory regions: regulating when, where, and in what quantity proteins are made.
- The terms **exon** and **intron** refer to coding (translated into a protein) and non-coding DNA, respectively.

Exons and introns



Splicing



Translation

Ribosome:

- cellular factory responsible for protein synthesis;
- a large subunit and a small subunit;
- structural RNA and about 80 different proteins.
- transfer RNA (tRNA):
 - adaptor molecule, between mRNA and protein;
 - specific **anticodon** and **acceptor site**;
 - specific charger protein, can only bind to that particular tRNA and attach the correct amino acid to the acceptor site.

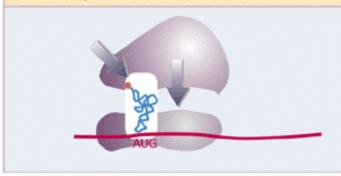
Translation

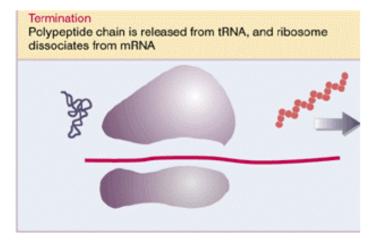
- Initiation
 - Start codon AUG, which codes for methionine, Met.
 - Not every protein necessarily starts with methionine. Often this first amino acid will be removed in post-translational processing of the protein.
- Termination:
 - stop codon (UAA, UAG, UGA),
 - ribosome breaks into its large and small subunits, releasing the new protein and the mRNA.

Translation



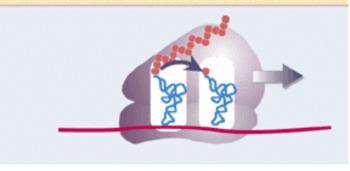
30S subunit on mRNA binding site is joined by 50S subunit and aminoacyl-tRNA binds



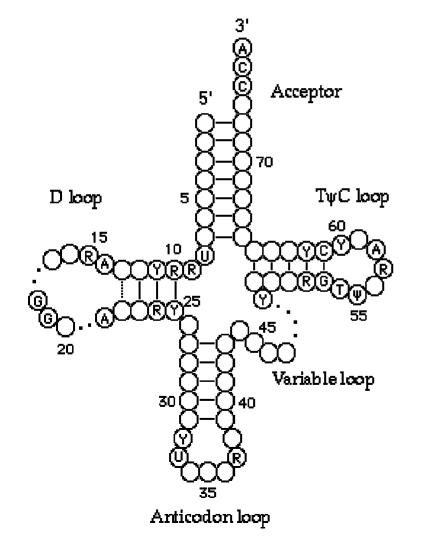


Elongation

Ribosome moves along mRNA and length of protein chain extends by transfer from peptidyl-tRNA to aminoacyl-tRNA



tRNA

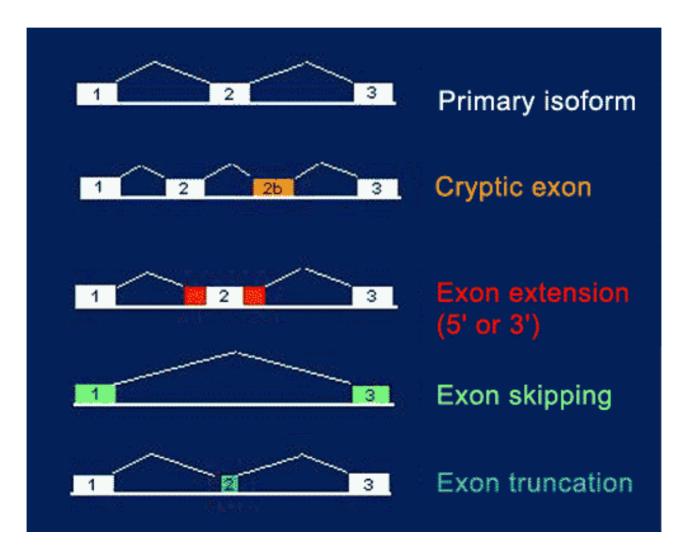


- The tRNA has an anticodon on its mRNA-binding end that is complementary to the codon on the mRNA.
- Each tRNA only binds the appropriate amino acid for its anticodon.

Alternative splicing

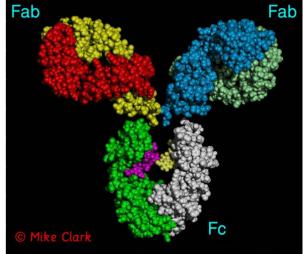
- There are more than 1,000,000 different human antibodies. How is this possible with only ~30,000 genes?
- Alternative splicing refers to the different ways of combining a gene's exons. This can produce different forms of a protein for the same gene.
- Alternative pre-mRNA splicing is an important mechanism for regulating gene expression in higher eukaryotes.
- E.g. in humans, it is estimated that approximately 30% of the genes are subject to alternative splicing.

Alternative splicing



Immunoglobulin

- B cells produce antibody molecules called immunoglobulins (Ig) which fall in five broad classes.
- Diversity of Ig molecules
 - DNA sequence: recombination, mutation.
 - mRNA sequence: alternative splicing.
 - Protein structure: post-translational proteolysis, glycosylation.

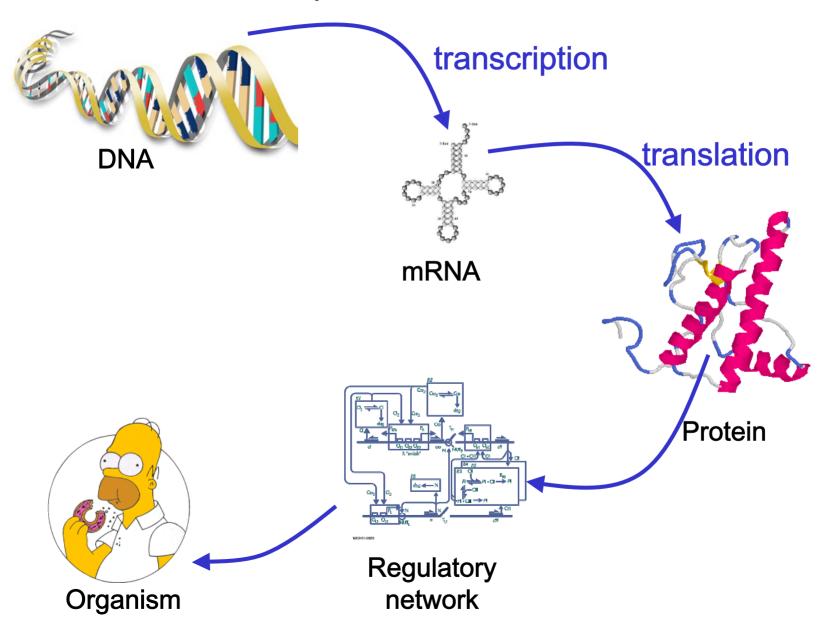


lgG1

Post-translational processing

- Folding.
- Cleavage by a proteolytic (protein-cutting) enzyme.
- Alteration of amino acid residues
 - phosphorylation, e.g. of a tyrosine residue.
 - glycosylation, carbohydrates covalently attached to asparagine residue.
 - methylation, e.g. of arginine.
- Lipid conjugation.

Transcription and translation



Control of Gene Expression

- there is strong evidence that the DNA content of most cells in a multi-cell organism is identical
- different cell types synthesize different sets of proteins at different times

Gene expression





Control of Gene Expression

- there are at least six ways to control protein expression
 - 1. control when and how often a gene is transcribed
 - 2. control how the transcript is spliced
 - 3. select which mRNA's are exported from the nucleus
 - 4. control translation

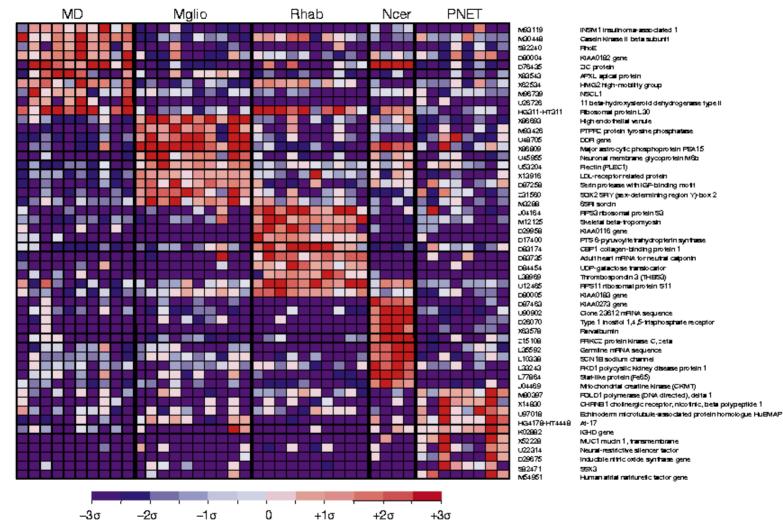
Controlling Expression

- 5. selectively destabilize mRNAs in the cytoplasm
- control protein activity (degradation, inactivate, isolate), post-translational modifications
- for most genes transcriptional control is the most important

Gene Expression

 for many diseases specific patterns of gene expression (mRNA expression) have been associated with the different phenotypes

Class discovery



Different Tumors have different patterns of expression

Fig. from Pomeroy et al. Nature 415 (2002)

DNA Microarrays

- the data obtained from microarray experiments is a measure of the abundance of a nucleic acid
- usually they are used for detecting mRNA levels
- some of the issues mentioned previously can affect the observed abundance of mRNA

Low values of mRNA

- the gene may be deleted
- the gene may be being repressed
- the gene may no longer be enhanced
- the gene may be methylated
- the mRNA may be kept in the nucleus

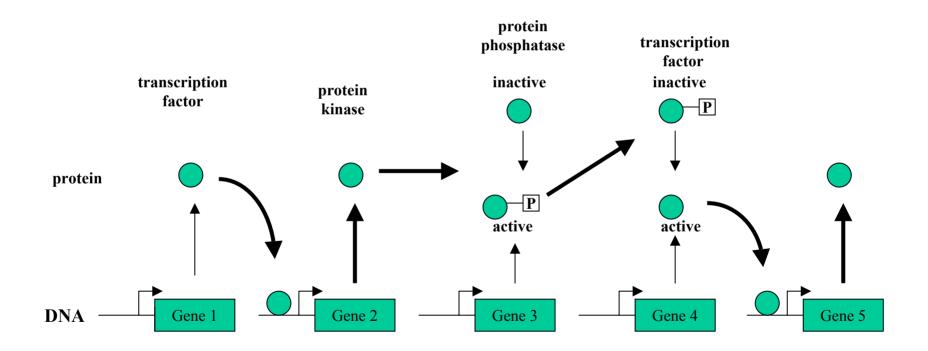
High Levels of mRNA

- the gene may be part of an amplicon
- the gene may no longer be being repressed
- the gene may be being enhanced

Other Issues

- was the right sequence applied to the chip?
- alternative splicing: which one are we measuring?
- cross-hybridization genes with similar sequences may hybridize

An example of the interactions between some genes (adapted from Wagner 2001)



Downstream Consequences

- many genes fall into the class of genes called transcription factors
- while most genes are transcribed by RNA polymerase II it cannot initiate transcription itself in eukaryotic cells
- transcription factors identify and then bind to specific sites in the DNA
- the TFs then guide and activate RNA polymerase

Downstream Consequences

- TFs tend not to be specific for one gene
- disregulation (or over or under production) of a TF can have large effects on gene expression
- for example ESR1 (estrogen receptor 1) is a transcription factor
- it affects production of cyclin d1 (CCND1)

Downstream Consequences

- CCND1 forms a complex with CDK4 and/or CDK6
- this complex inactivates the repressor function of pRb (retinoblastoma protein) which regulates cell proliferation
- and so on....

Functional genomics

 The various genome projects have yielded the complete DNA sequences of many organisms.

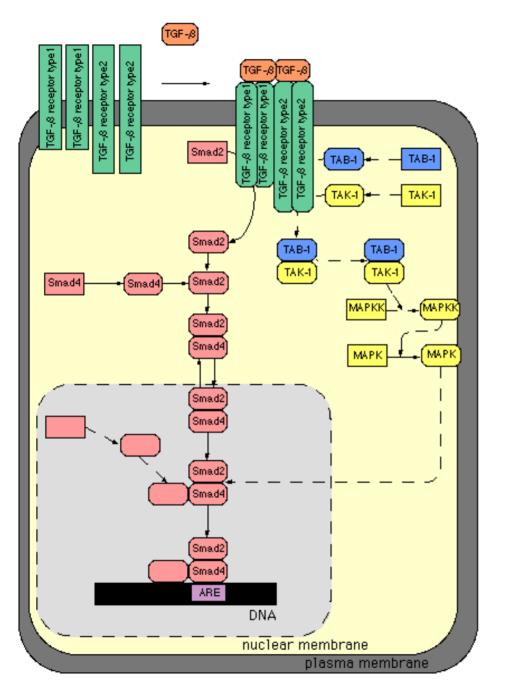
> E.g. human, mouse, yeast, fruitfly, etc. Human: 3 billion base-pairs, 30-40 thousand genes.

 Challenge: go from sequence to function, i.e., define the role of each gene and understand how the genome functions as a whole.

Pathways

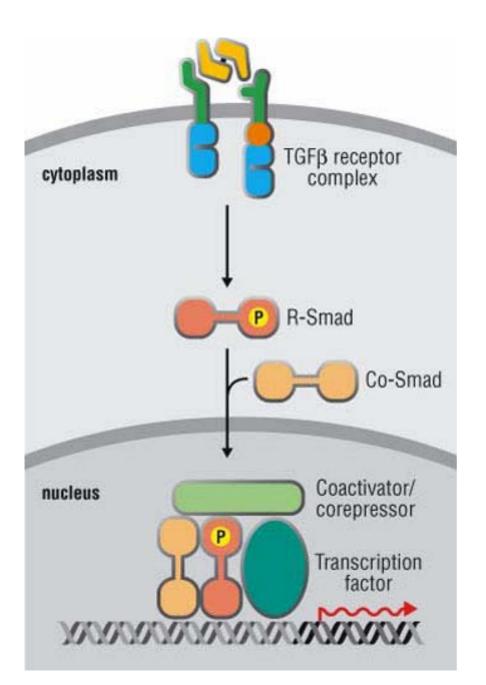
- The complete genome sequence doesn't tell us much about how the organism functions as a biological system.
- We need to study how different gene products interact to produce various components.
- Most important activities are not the result of a single molecule but depend on the coordinated effects of multiple molecules.

- Transforming Growth Factor beta, TGF-β, plays an essential role in the control of development and morphogenesis in multicellular organisms.
- The basic pathway provides a simple route for signals to pass from the extracellular environment to the nucleus, involving only four types of molecules.



Four types of molecules

- TGF- β
- TGF- β type I receptors
- TGF- β type II receptors
- SMADS, a family of signal transducers and transcriptional activators.



 Extracellular TGF-β ligands transmit their signals to the cell's interior by binding to type II receptors, which form heterodimers with type I receptors.

• The receptors in turn activate the SMAD transcription factors.

- Phosphorylated and receptor-activated SMADs (R-SMADs) form heterodimers with common SMADs (co-SMADs) and translocate to the nucleus.
- In the nucleus, SMADs activate or inhibit the transcription of target genes, in collaboration with other factors.

Pathways

- <u>http://www.grt.kyushu-u.ac.jp/spad/</u>
- There are many open questions regarding the relationship between gene expression levels (e.g. mRNA levels) and pathways.
- It is not clear to what extent microarray gene expression data will be informative.

WWW resources

Access Excellence

http://www.accessexcellence.com/AB/GG/

- Genes VII
 <u>http://www.oup.co.uk/best.textbooks/biochemistry/genesvii/</u>
- Human Genome Project Education Resources
 http://www.ornl.gov/hgmis/education/education.html
- Kimball's Biology Pages

http://www.ultranet.com/~jkimball/BiologyPages/

MIT Biology Hypertextbook

http://esg-www.mit.edu:8001/