

Advanced Algorithms and Models for Computational Biology

Introduction to cell biology,
genomics, development, and
probability

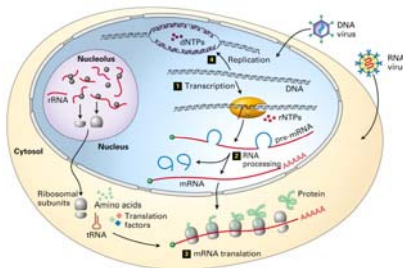
Eric Xing

Lecture 2, January 23, 2006

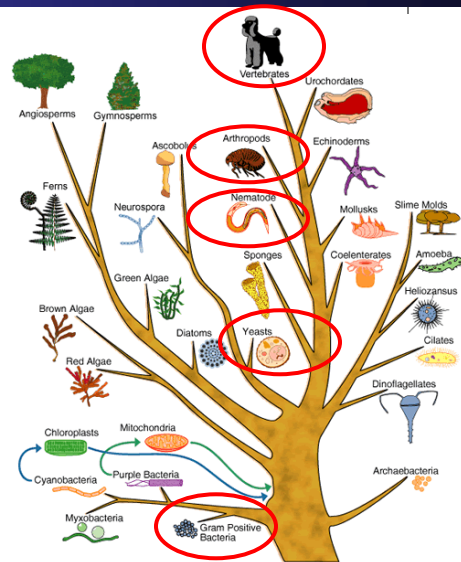
Reading: Chap. 1, DTM book



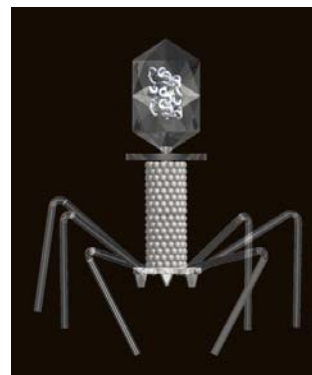
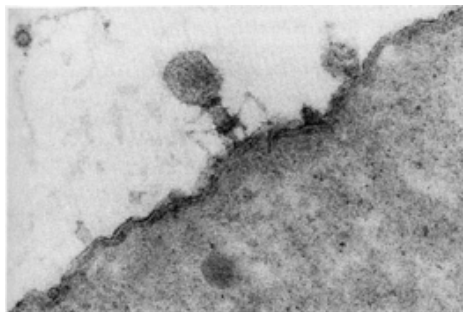
Introduction to cell biology,
functional genomics,
development, etc.



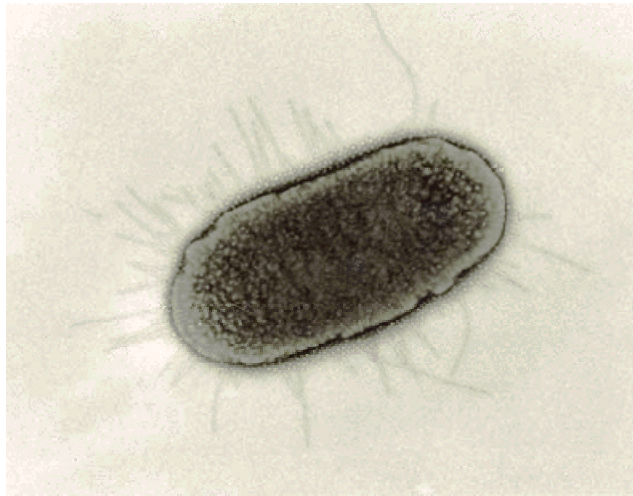
Model Organisms



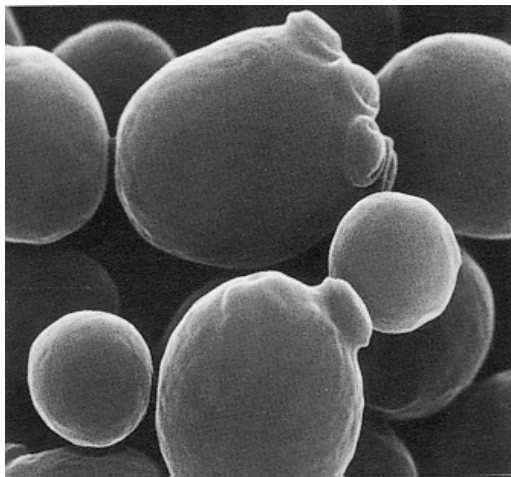
Bacterial Phage: T4



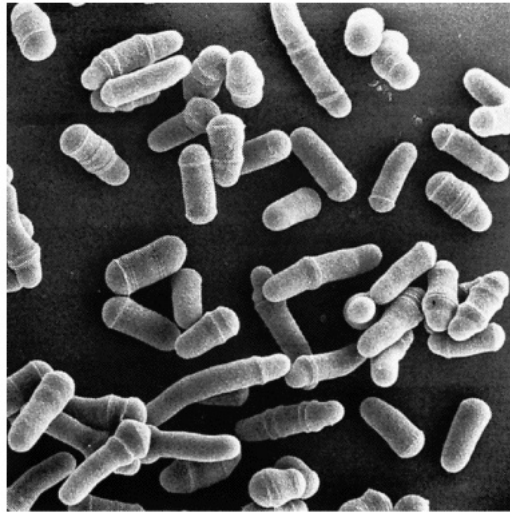
Bacteria: E. Coli



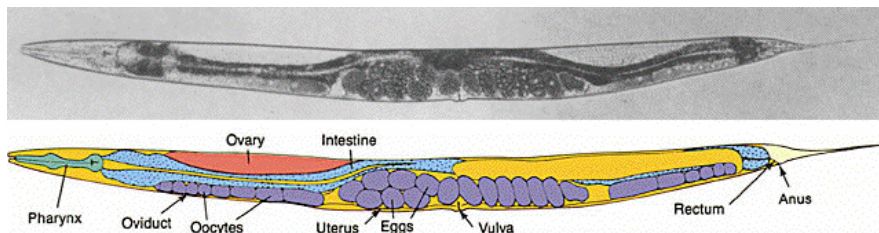
The Budding Yeast: *Saccharomyces cerevisiae*



The Fission Yeast: *Schizosaccharomyces pombe*



The Nematode: *Caenorhabditis elegans*



- SMALL: ~ 250 μm
- TRANSPARENT
- 959 CELLS
- 300 NEURONS
- SHORT GENERATION TIME
- SIMPLE GROWTH MEDIUM
- SELF- FERTILIZING HERMAPHRODITE
- RAPID ISOLATION AND CLONING OF MULTIPLE TYPES OF MUTANT ORGANISMS

The Fruit Fly: *Drosophila Melanogaster*



Normal



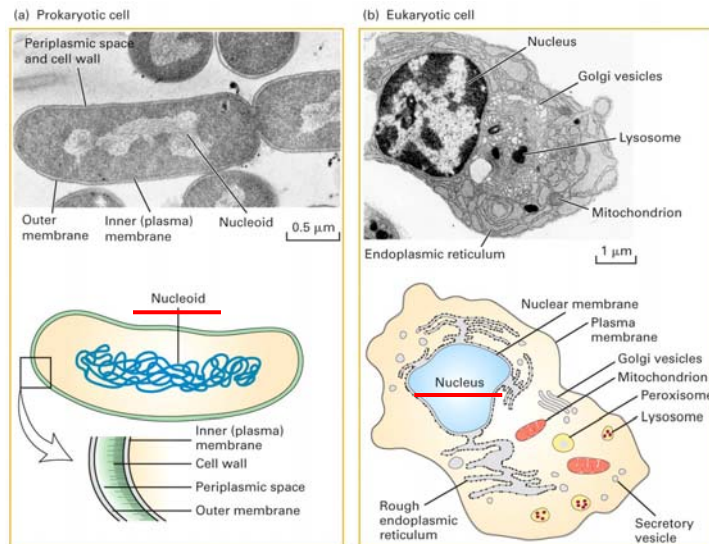
Ubx mutant

The Mouse



transgenic for human growth hormone

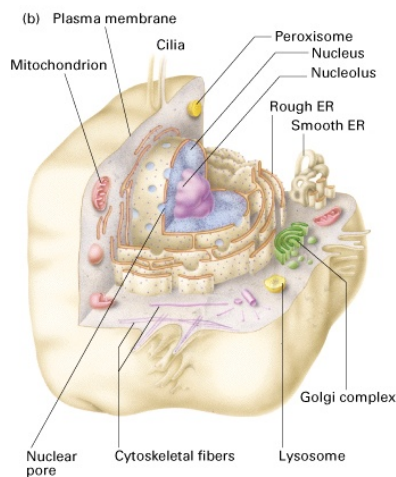
Prokaryotic and Eukaryotic Cells



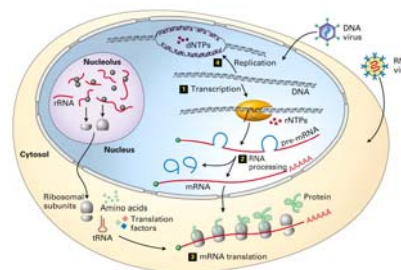
A Close Look of a Eukaryotic Cell



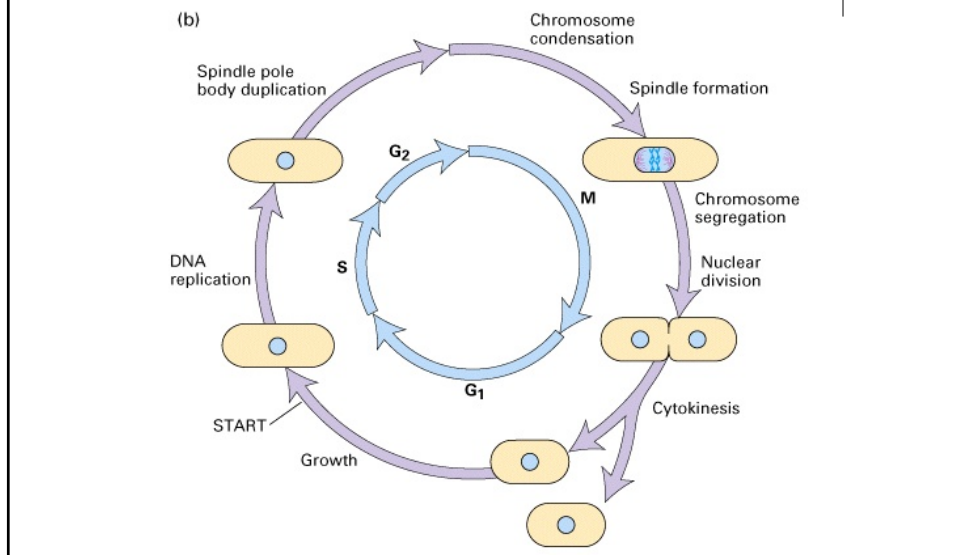
The structure:



The information flow:



Cell Cycle

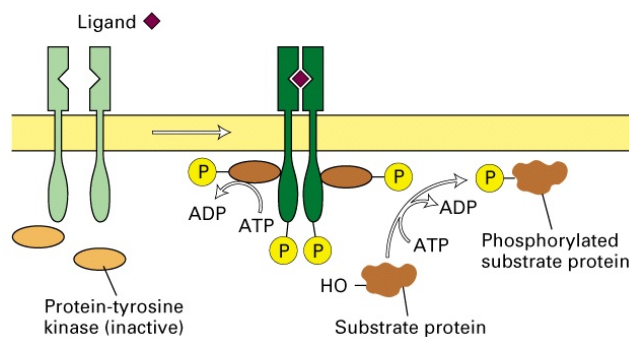


Signal Transduction

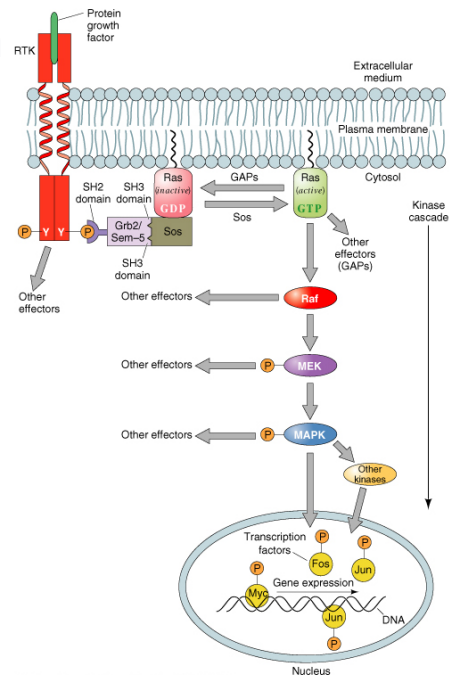


- A variety of plasma membrane receptor proteins bind extracellular signaling molecules and transmit signals across the membrane to the cell interior

(c) Tyrosine kinase-linked receptors (erythropoietin, interferons)

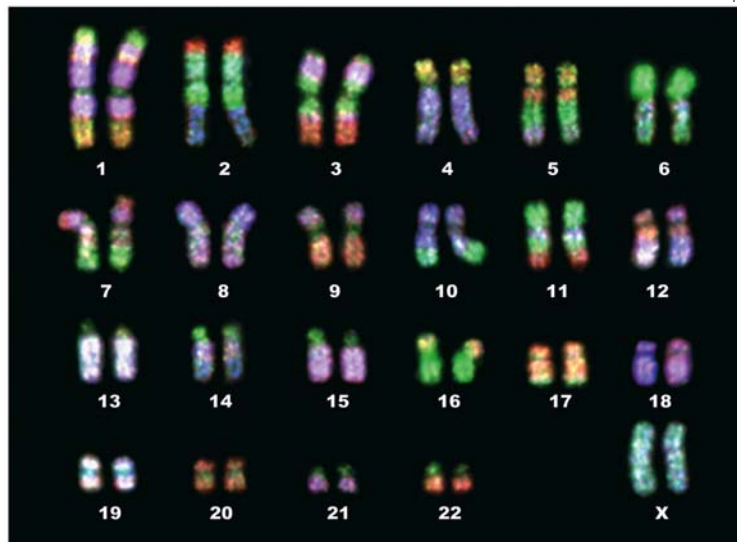


Signal Transduction Pathway

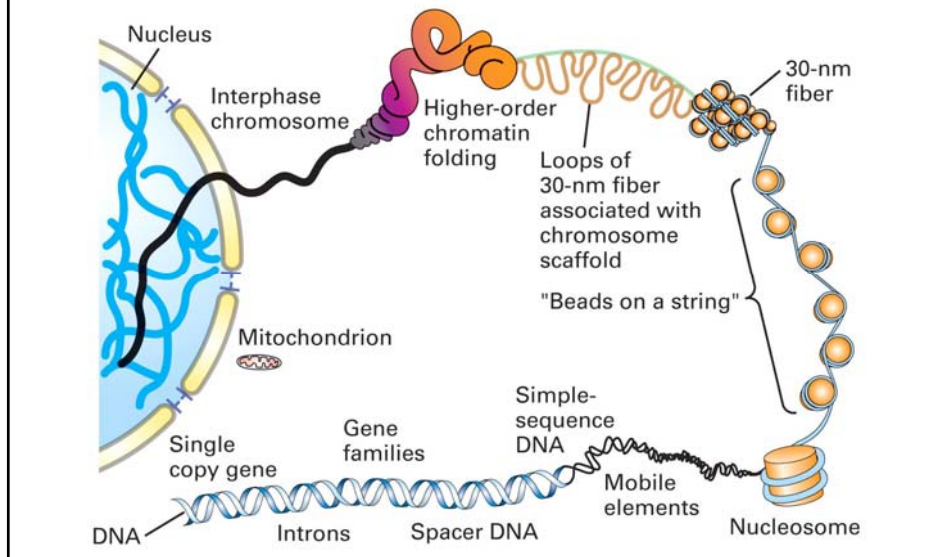


After Egan, S.E. and Weinberg, R.A. Nature 365, 782 (1993).
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Functional Genomics and X-omics



A Multi-resolution View of the Chromosome



DNA Content of Representative Types of Cells



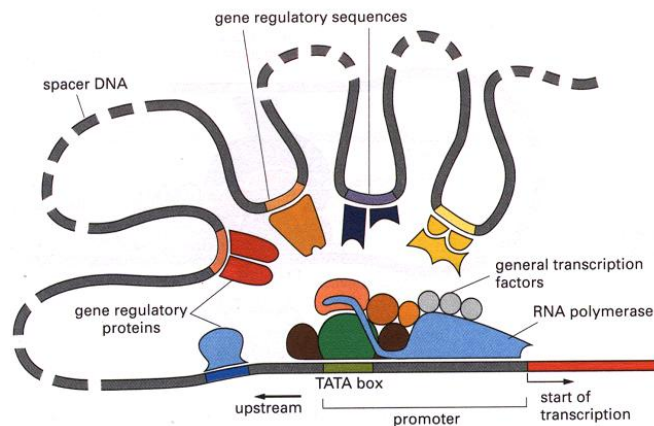
Organism	Number of base pairs (millions)	Number of encoded proteins	Number of chromosomes
<u>PROKARYOTIC</u>			
<i>Mycoplasma genitalum</i> (Bacterium)	0.58	470	1
<i>Helicobacter pylori</i> (Bacterium)	1.67	1590	1
<i>Haemophilus influenza</i> (Bacterium)	1.83	1743	1
<u>EUKARYOTIC</u>			
<i>Saccharomyces cerevisiae</i> (yeast)	12	5885	17
<i>Drosophila melanogaster</i> (insect)	165	13,601	4
<i>Caenorhabditis elegans</i> (worm)	97	19,099	6
<i>Homo sapiens</i> (human)	2900	30,000 TO 40,000	23
<i>Arabidopsis thaliana</i> (plant)	125	25,498	10

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.

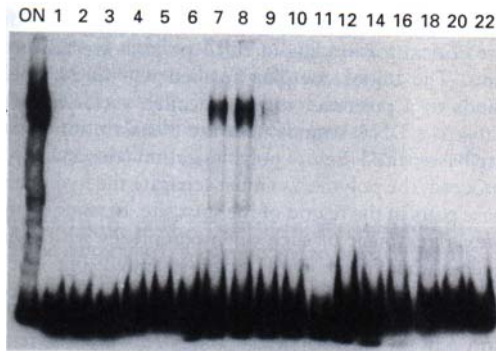
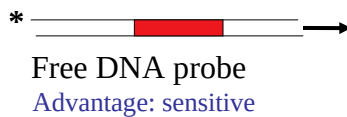
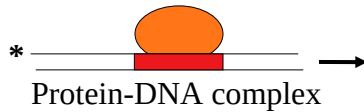
Regulatory Machinery of Gene Expression



Classical Analysis of Transcription Regulation Interactions



“Gel shift”: electrophoretic mobility shift assay
 (“EMSA”) for DNA-binding proteins

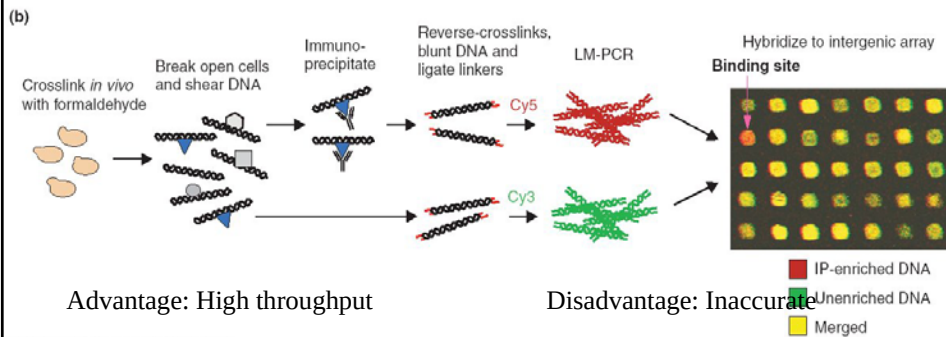


Disadvantage: requires stable complex;
 little “structural” information about which
 protein is binding

Modern Analysis of Transcription Regulation Interactions



- Genome-wide Location Analysis (ChIP-chip)



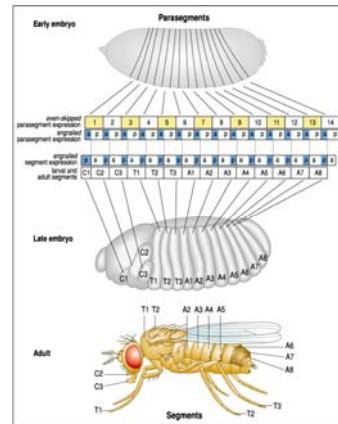


Gene Regulatory Functions in Development

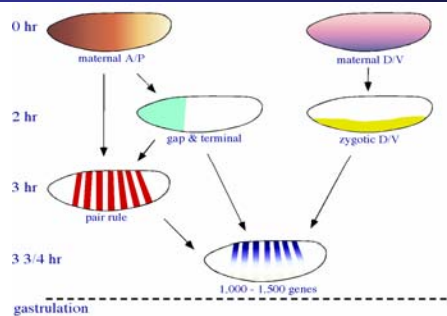


Figure 28.15 In each axis-determining system, localized products in the egg cause other maternal RNAs or proteins to be broadly localized at syncytial blastoderm, and zygotic RNAs are transcribed in bands at cellular blastoderm.

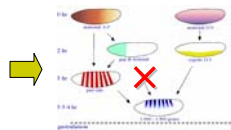
	Anterior system	Posterior system	Dorsal-ventral system
Egg	bicoid RNA is anterior	nanos RNA is posterior	Toll protein is ubiquitous; Spätzle protein (and therefore Toll) is activated ventrally
Products transcribed or activated by nurse or follicle cells	bicoid protein forms gradient	nanos protein is in posterior half	dorsal protein is ubiquitous; Spätzle protein is activated ventrally
Syncytial blastoderm	Maternal RNAs are translated	Maternal RNAs are translated	Maternal RNAs are translated
Cellular blastoderm	hunchback RNA fills anterior region	strips of Krüppel & giant RNA	dpp & zen RNA are dorsal
Zygotic RNAs are transcribed		krüppel & giant	hedgehog & engrailed RNA are ventral



Temporal-spatial Gene Regulation and Regulatory Artifacts

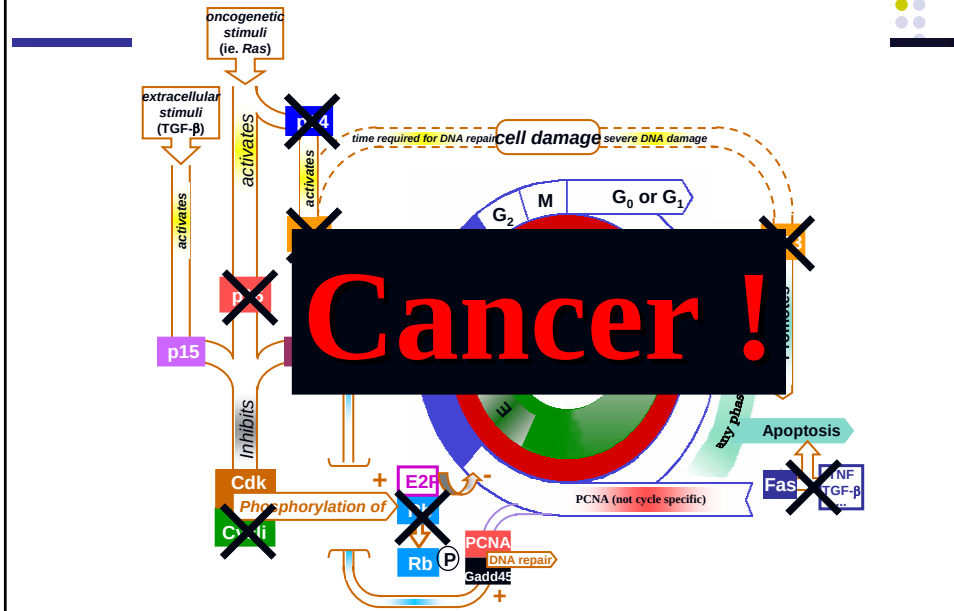


A normal fly

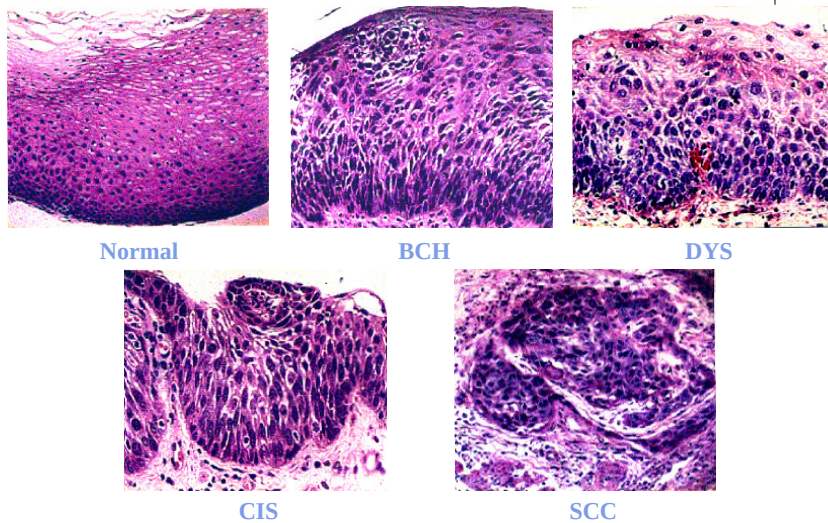


Hopeful monster?

Gene Regulation and Carcinogenesis



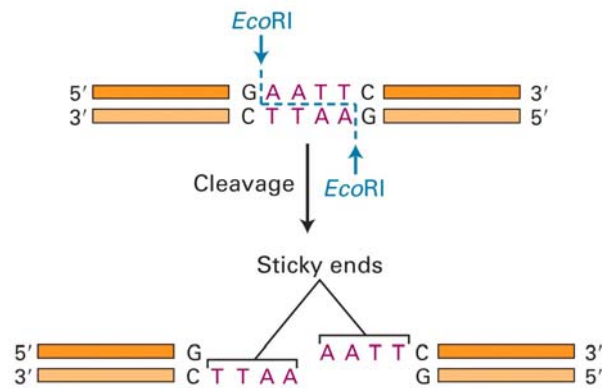
The Pathogenesis of Cancer



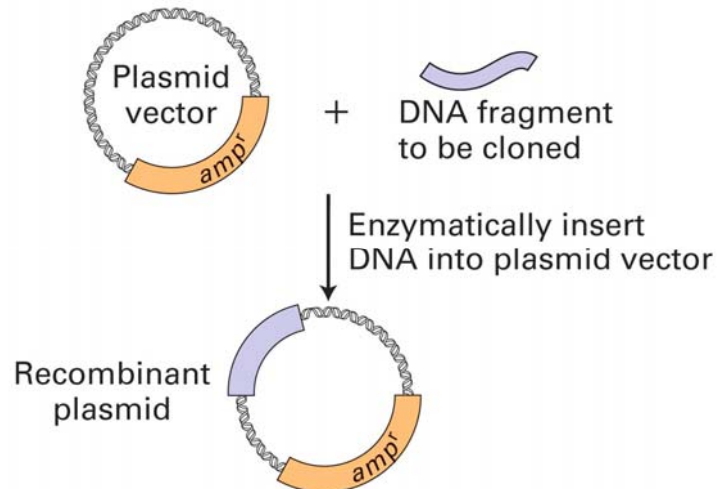
Genetic Engineering: Manipulating the Genome



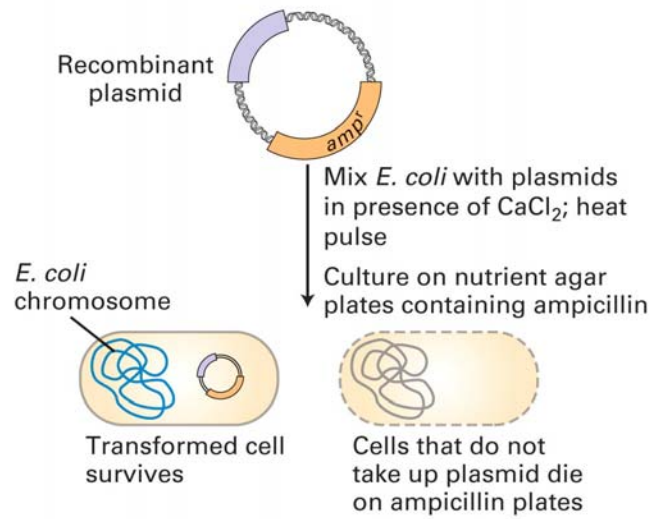
- **Restriction Enzymes**, naturally occurring in bacteria, that cut DNA at very specific places.



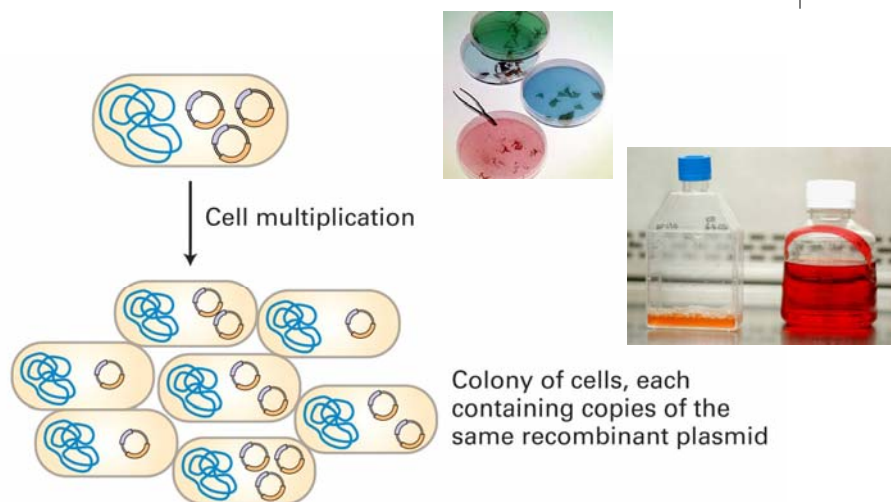
Recombinant DNA



Transformation



Formation of Cell Colony

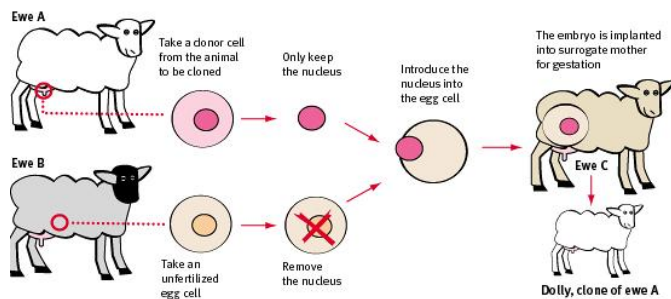


How was Dolly cloned?



- Dolly is an exact genetic replica of another sheep.

2. The making of Dolly



Definitions



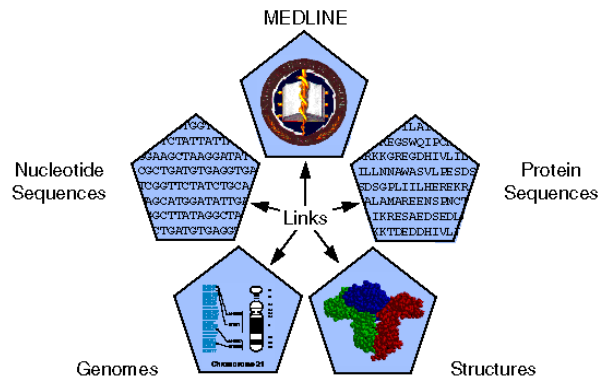
- **Recombinant DNA:** Two or more segments of DNA that have been combined by humans into a sequence that does not exist in nature.
- **Cloning:** Making an exact genetic copy. A **clone** is one of the exact genetic copies.
- **Cloning vector:** Self-replicating agents that serve as vehicles to transfer and replicate genetic material.

Software and Databases

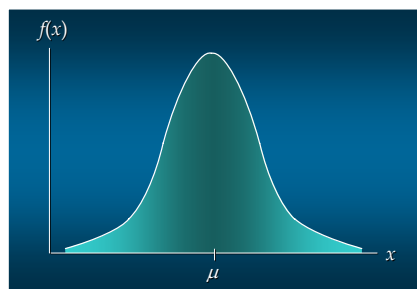
- NCBI/NLM Databases Genbank, PubMed, PDB

- DNA
- Protein
- Protein 3D
- Literature

Entrez



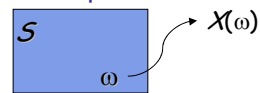
Introduction to Probability



Basic Probability Theory Concepts



- A **sample space** $\mathcal{S}$ is the set of all possible outcomes of a conceptual or physical, repeatable experiment. ($\mathcal{S}$ can be finite or infinite.)
 - E.g., $\mathcal{S}$ may be the set of all possible nucleotides of a DNA site: $\mathcal{S} \equiv \{A, T, C, G\}$
- A **random variable** is a function that associates a unique numerical value (a token) with every outcome of an experiment. (The value of the r.v. will vary from trial to trial as the experiment is repeated)
 - E.g., seeing an "A" at a site $\Rightarrow X=1$, o/w $X=0$.
 - This describes the true or false outcome a **random event**.
 - Can we describe richer outcomes in the same way? (i.e., $X=1, 2, 3, 4$, for being A, C, G, T) --- think about what would happen if we take expectation of X .
- Unit-Base Random vector
 - $X_i = [X_{iA}, X_{iT}, X_{iG}, X_{iC}]^T$, $X_i = [0, 0, 1, 0]^T \Rightarrow$ seeing a "G" at site i



Basic Prob. Theory Concepts, ctd



- (In the discrete case), a probability distribution P on $\mathcal{S}$ (and hence on the domain of X) is an assignment of a non-negative real number $P(s)$ to each $s \in \mathcal{S}$ (or each valid value of x) such that $\sum_{s \in \mathcal{S}} P(s) = 1$. ($0 \leq P(s) \leq 1$)
 - intuitively, $P(s)$ corresponds to the **frequency** (or the likelihood) of getting s in the experiments, if repeated many times
 - call $\theta_s = P(s)$ the **parameters** in a discrete probability distribution
- A probability distribution on a sample space is sometimes called a **probability model**, in particular if several different distributions are under consideration
 - write models as M_1, M_2 , probabilities as $P(X|M_1), P(X|M_2)$
 - e.g., M_1 may be the appropriate prob. dist. if X is from "splice site", M_2 is for the "background".
 - M is usually a two-tuple of {dist. family, dist. parameters}

Discrete Distributions



- Bernoulli distribution: $\text{Ber}(p)$

$$P(x) = \begin{cases} 1-p & \text{for } x=0 \\ p & \text{for } x=1 \end{cases} \Rightarrow P(x) = p^x (1-p)^{1-x}$$

- Multinomial distribution: $\text{Mult}(1, \theta)$

- Multinomial (indicator) variable: $X = \begin{bmatrix} X_A \\ X_C \\ X_G \\ X_T \end{bmatrix}$, where $X_j = [0,1]$, and $\sum_{j \in \{A,C,G,T\}} X_j = 1$
 $X_j = 1$ w.p. θ_j , $\sum_{j \in \{A,C,G,T\}} \theta_j = 1$.

$$p(X(j)) = P(\{X_j = 1, \text{ where } j \text{ index the observed nucleotide}\}) \\ = \theta_j = \theta_A^{x_A} \times \theta_C^{x_C} \times \theta_G^{x_G} \times \theta_T^{x_T} = \prod_k \theta_k^{x_k} = \theta^x$$

- Multinomial distribution: $\text{Mult}(n, \theta)$

- Count variable: $X = \begin{bmatrix} x_1 \\ \vdots \\ x_k \end{bmatrix}$, where $\sum_j x_j = n$

$$p(x) = \frac{n!}{x_1! x_2! \dots x_k!} \theta_1^{x_1} \theta_2^{x_2} \dots \theta_k^{x_k} = \frac{n!}{x_1! x_2! \dots x_k!} \theta^x$$

Basic Prob. Theory Concepts, ctd



- A **continuous random variable** X can assume any value in an interval on the real line or in a region in a high dimensional space
 - X usually corresponds to a real-valued measurements of some property, e.g., length, position, ...
 - It is not possible to talk about the probability of the random variable assuming a particular value --- $P(x) = 0$
 - Instead, we talk about the probability of the random variable assuming a value within a given interval, or half interval
 - $P(X \in [x_1, x_2])$, $P(X < x) = P(X \in [-\infty, x])$
- The probability of the random variable assuming a value within some given interval from x_1 to x_2 is defined to be the area under the graph of the probability density function between x_1 and x_2 .
 - Probability mass: $P(X \in [x_1, x_2]) = \int_{x_1}^{x_2} p(x) dx$, note that $\int_{-\infty}^{+\infty} p(x) dx = 1$.
 - Cumulative distribution function (CDF): $P(x) = P(X < x) = \int_{-\infty}^x p(x') dx'$
 - Probability density function (PDF): $p(x) = \frac{d}{dx} P(x)$

Continuous Distributions

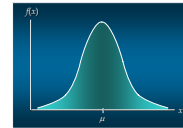


- Uniform Probability Density Function

$$p(x) = \begin{cases} 1/(b-a) & \text{for } a \leq x \leq b \\ 0 & \text{elsewhere} \end{cases}$$

- Normal Probability Density Function

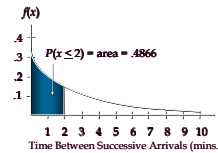
$$p(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-(x-\mu)^2/2\sigma^2}$$



- The distribution is symmetric, and is often illustrated as a bell-shaped curve.
- Two parameters, μ (mean) and σ (standard deviation), determine the location and shape of the distribution.
- The highest point on the normal curve is at the mean, which is also the median and mode.
- The mean can be any numerical value: negative, zero, or positive.

- Exponential Probability Distribution

$$\text{density: } p(x) = \frac{1}{\mu} e^{-x/\mu}, \quad \text{CDF: } P(x \leq x_0) = 1 - e^{-x_0/\mu}$$



Statistical Characterizations



- Expectation:** the center of mass, mean value, first moment):

$$E(X) = \begin{cases} \sum_{i \in S} x_i p(x_i) & \text{discrete} \\ \int_{-\infty}^{\infty} x p(x) dx & \text{continuous} \end{cases}$$

- Sample mean:

$$\mu = \frac{1}{N} \sum_{i=1}^N x_i$$

- Variance:** the spreadness, second moment:

$$Var(X) = \begin{cases} \sum_{x \in S} [x - E(X)]^2 p(x_i) & \text{discrete} \\ \int_{-\infty}^{\infty} [x - E(X)]^2 p(x) dx & \text{continuous} \end{cases}$$

- Sample variance

$$\sigma^2 = \frac{1}{N-1} \sum_{i=1}^N (x_i - \mu)^2$$

Basic Prob. Theory Concepts, ctd



- Joint probability:

- For events E (i.e. $X=x$) and H (say, $Y=y$), the probability of both events are true:

$$P(E \text{ and } H) := P(x, y)$$

- Conditional probability

- The probability of E is true given outcome of H

$$P(E \text{ and } H) := P(x | y)$$

- Marginal probability

- The probability of E is true regardless of the outcome of H

$$P(E) := P(x) = \sum_x P(x, y)$$

- Putting everything together:

$$P(x | y) = P(x, y) / P(y)$$

Independence and Conditional Independence



- Recall that for events E (i.e. $X=x$) and H (say, $Y=y$), the conditional probability of E given H , written as $P(E|H)$, is

$$P(E \text{ and } H) / P(H)$$

(= the probability of both E and H are true, given H is true)

- E and H are (statistically) independent if

$$P(E) = P(E|H)$$

(i.e., prob. E is true doesn't depend on whether H is true); or equivalently

$$P(E \text{ and } H) = P(E)P(H).$$

- E and F are *conditionally* independent given H if

$$P(E|H, F) = P(E|H)$$

or equivalently

$$P(E, F|H) = P(E|H)P(F|H)$$

Representing multivariate dist.



- Joint probability dist. on multiple variables:

$$P(X_1, X_2, X_3, X_4, X_5, X_6) \\ = P(X_1)P(X_2 | X_1)P(X_3 | X_1, X_2)P(X_4 | X_1, X_2, X_3)P(X_5 | X_1, X_2, X_3, X_4)P(X_6 | X_1, X_2, X_3, X_4, X_5)$$

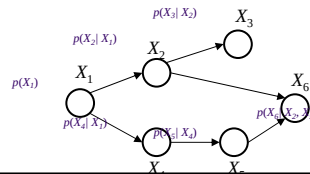
- If X_i 's are independent: ($P(X_i | \cdot) = P(X_i)$)

$$P(X_1, X_2, X_3, X_4, X_5, X_6) \\ = P(X_1)P(X_2)P(X_3)P(X_4)P(X_5)P(X_6) = \prod_i P(X_i)$$

- If X_i 's are conditionally independent, the joint can be factored to simpler products, e.g.,

$$P(X_1, X_2, X_3, X_4, X_5, X_6) = P(X_1) P(X_2 | X_1) P(X_3 | X_2) P(X_4 | X_1) P(X_5 | X_4) P(X_6 | X_2, X_5)$$

- The **Graphical Model** representation



The Bayesian Theory



- The Bayesian Theory: (e.g., for data D and model M)

$$P(M|D) = P(D|M)P(M)/P(D)$$

- the **posterior** equals to the **likelihood** times the **prior**, up to a constant.
- This allows us to capture uncertainty about the model in a principled way