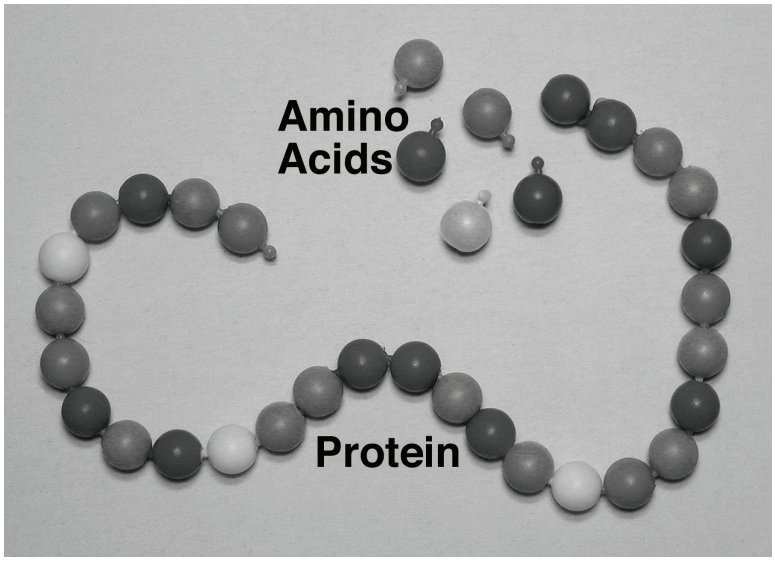
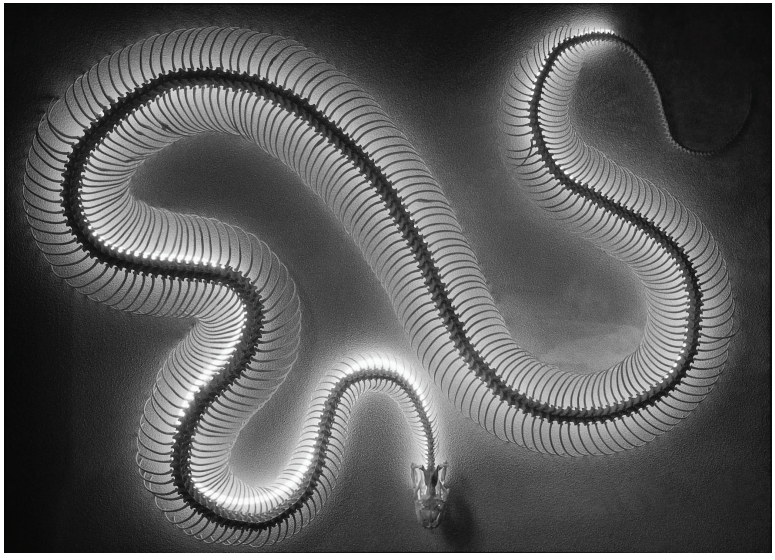
The Biology of Belief Illustration Guide

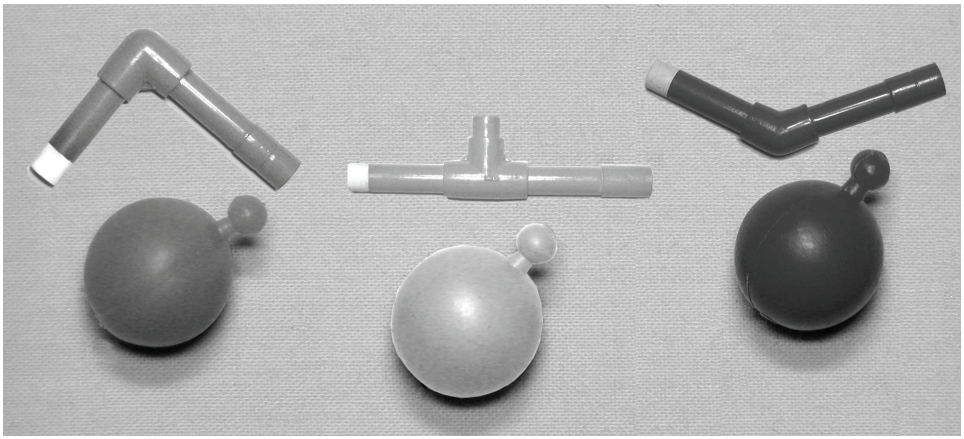
Chapter Two Illustrations



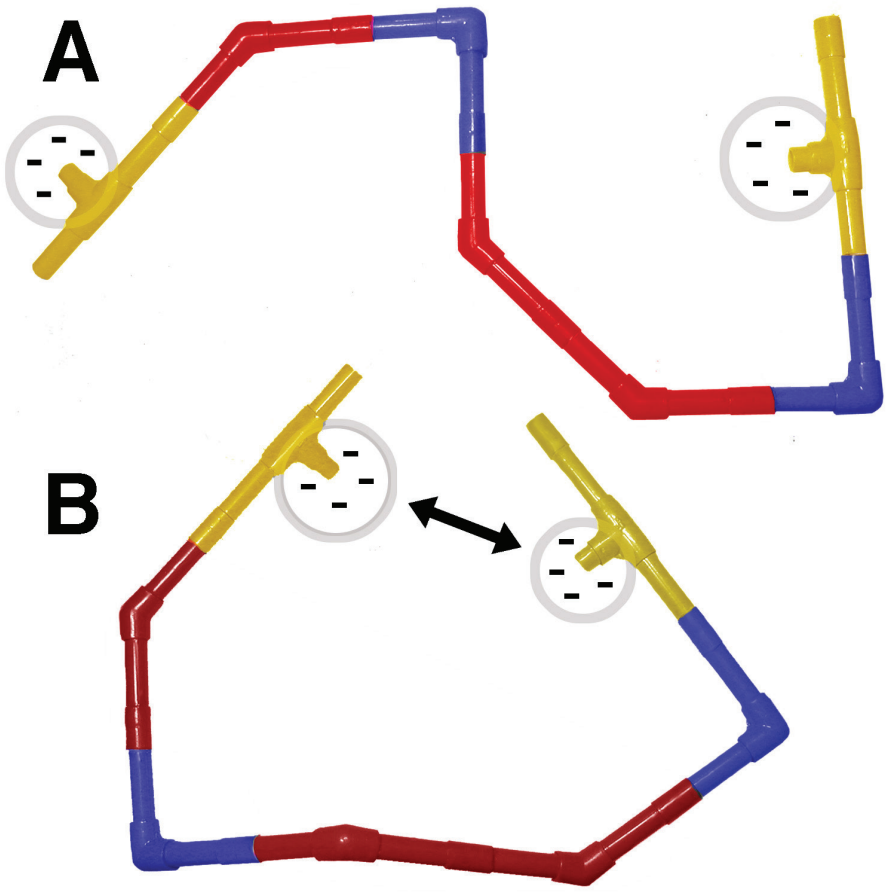
Amino Acid Necklace



Snake Backbone



Unlike uniformly shaped pop beads, each of the twenty amino acids comprising protein backbones has a unique shape (conformation). Consider the differences between the character of a "backbone" made from identically shaped pop beads and one assembled from the differently shaped pipe fittings illustrated above.



The protein backbones shown in A and B have the exact same amino acid (pipe fitting) sequence but reveal radically different conformations. Variations in the backbone's shape result from differential rotations at the junctions between adjacent pipe fittings. Like the pipe fittings illustrated above, the protein's differently shaped amino acids also rotate around their junctions (peptide bonds), allowing the backbone to wriggle like a snake. Proteins shape-shift, though they will generally prefer two or three specific conformations. Which of the two conformations, A or B, would our hypothetical protein prefer? The answer is related to the fact that the two terminal amino acids (pipe fittings) have regions of negative charges. Since like charges repel each other, the farther apart they are, the more stable the conformation. Conformation A would be preferred because the negative charges are farther apart than they are in B.

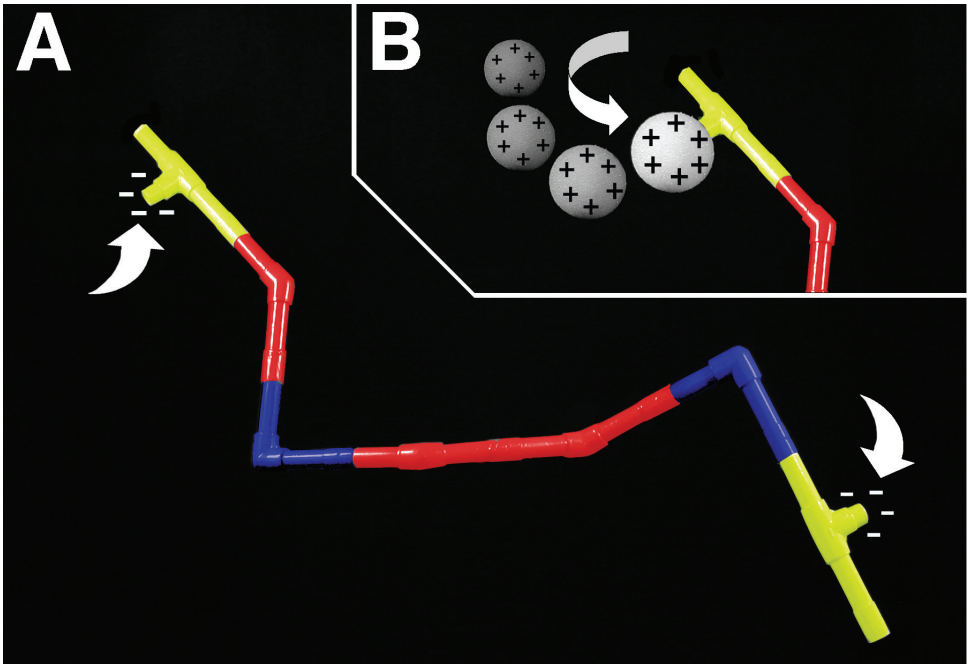


Figure A shows the preferred conformation of our hypothetical protein backbone. The repelling forces between the two negatively charged terminal amino acids (arrows) cause the backbone to extend so that the negative amino acids are as far apart as possible. Figure B shows a close-up of an end amino acid. A signal, in this case a molecule with a very positive electric charge (white sphere), is attracted to and binds with the negative site on the protein's terminal amino acid. In our particular scenario, the signal is more positive in charge than the amino acid is negative in charge. After the signal couples with the protein, there is an excess positive charge at this end of the backbone. Since positive and negative charges attract one another, the backbone's amino acids will rotate around their bonds so that positive and negative terminals will come closer together.

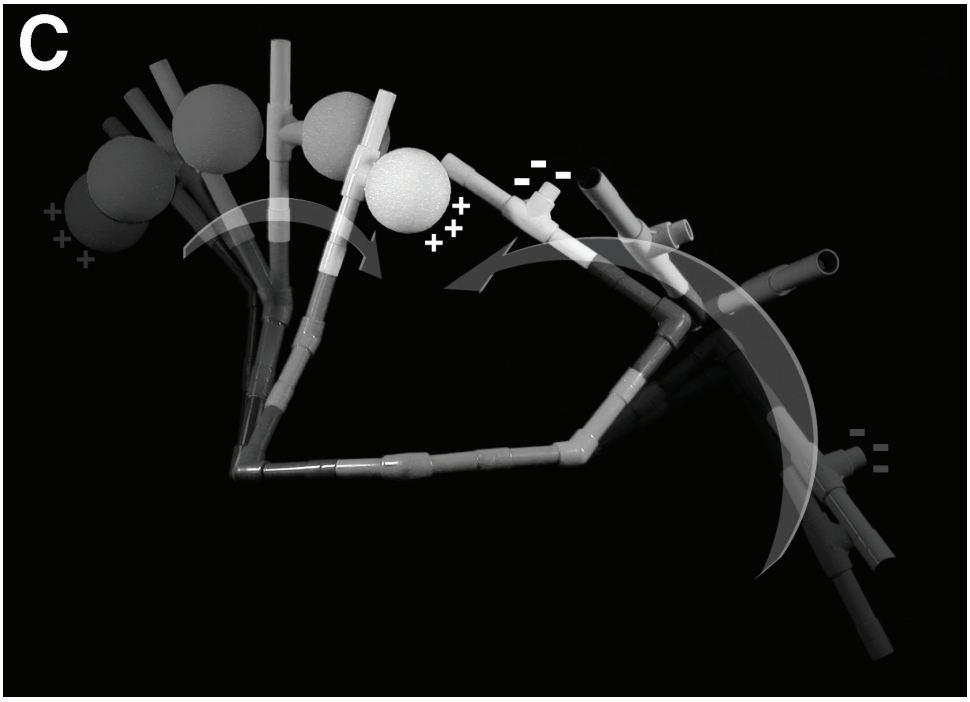
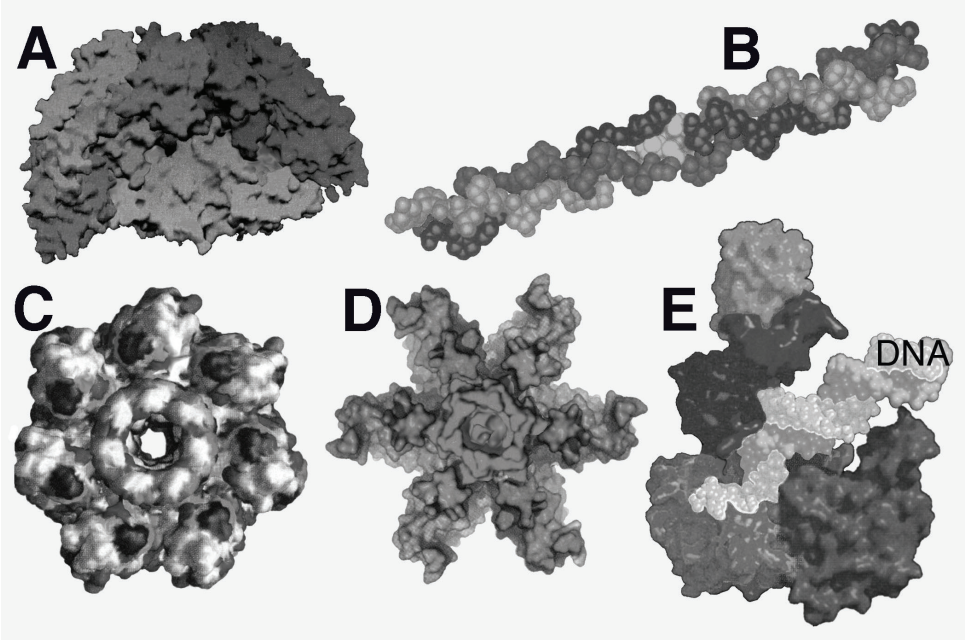
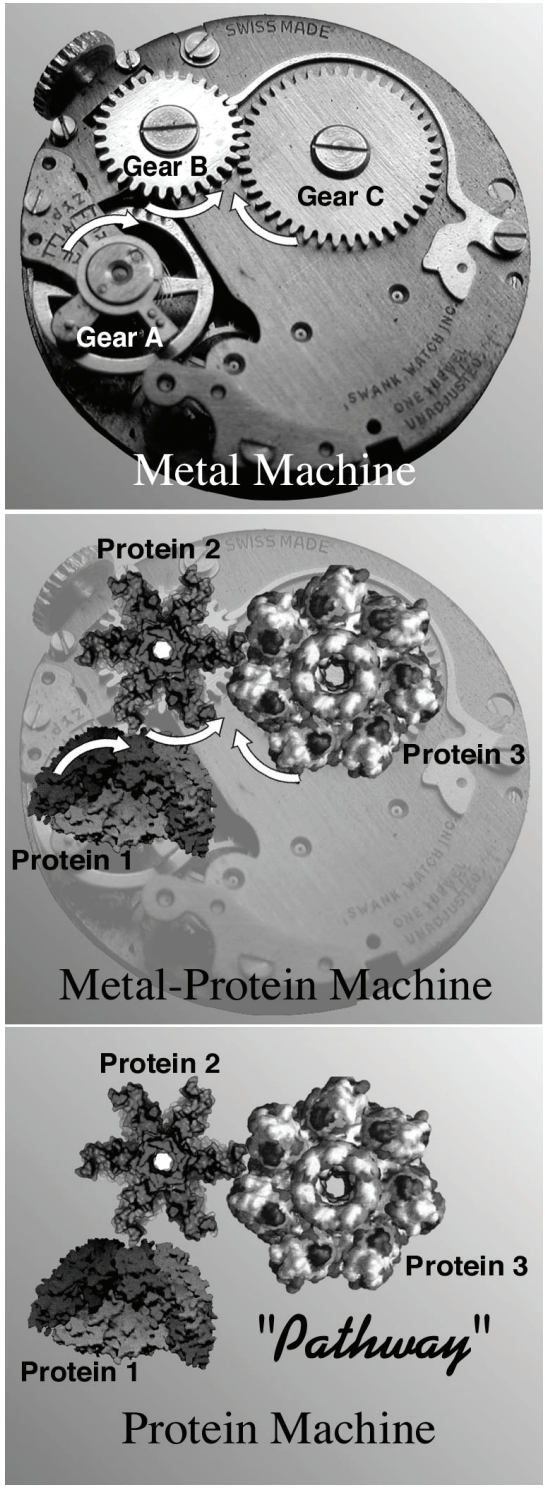


Figure C shows the protein changing from conformation A to conformation B. Changing conformations generates movement and the movement is harnessed to do work, providing for such functions as digestion, respiration, and muscle contraction. When the signal molecule detaches, the protein returns to its preferred extended conformation. This is how signal-generated protein movements provide for life.

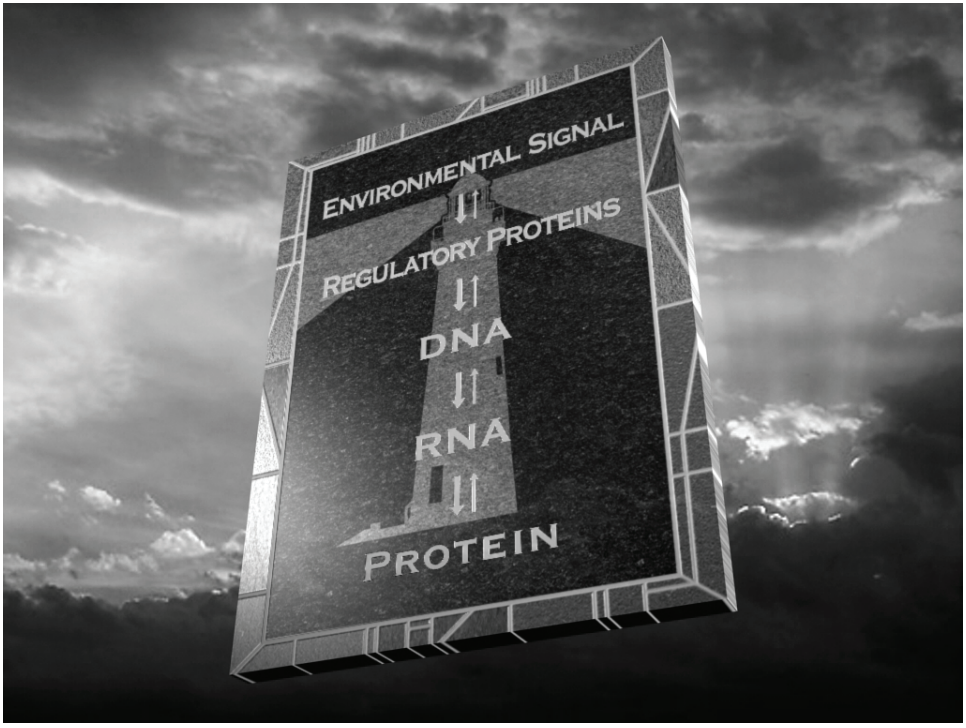


Protein Menagerie. Illustrated above are five different examples of protein molecules. Each protein possesses a precise three-dimensional conformation that is the same for each copy of itself in every cell. A) Enzyme that digests hydrogen atoms; B) Woven filament of collagen protein; C) Channel, a membrane-bound protein with hollow central pore; D) Protein subunit of "capsule" that encloses a virus; E) DNA synthesizing enzyme with attached helical DNA molecule.

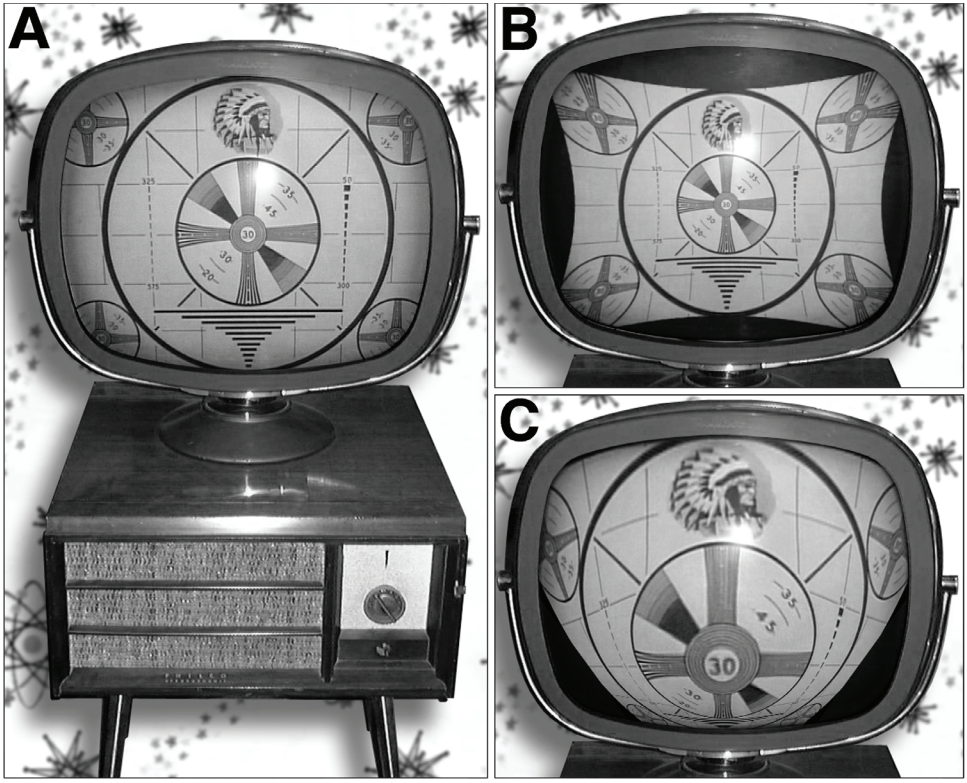


Protein Machine

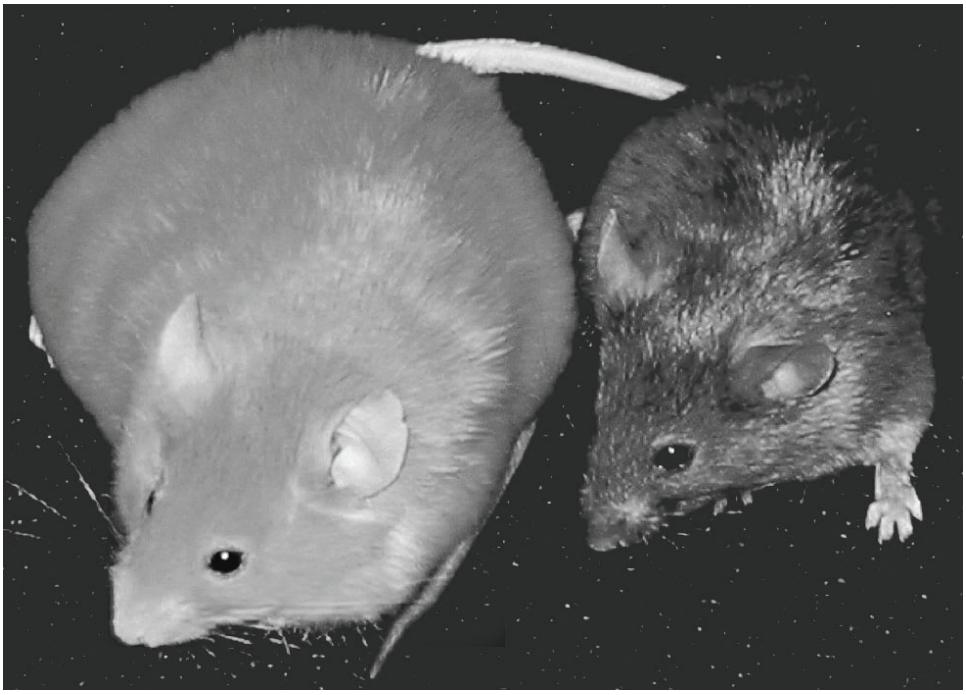
The Central Dogma. The dogma, also referred to as the Primacy of DNA, defines the flow of information in biological organisms. As indicated by the arrows, the flow is only in one direction, from DNA to RNA and then to protein. The DNA represents the cell's long-term memory, passed from generation to generation. RNA, an unstable copy of the DNA molecule, is the active memory that is used by the cell as a physical template in synthesizing proteins. Proteins are the molecular building blocks that provide for the cell's structure and behavior. DNA is implicated as the "source" that controls the character of the cell's proteins, hence the concept of DNA's primacy that literally means "first cause."



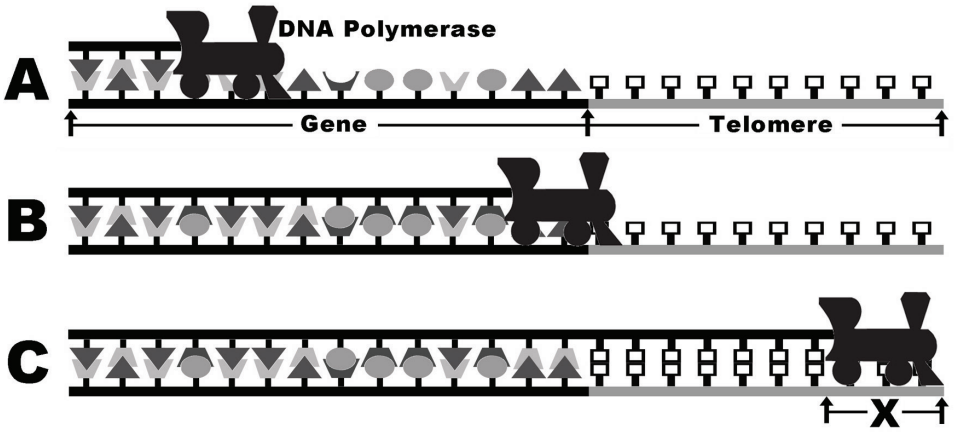
Primacy of Environment. The new science reveals that the information that controls biology starts with environmental signals that, in turn, control the activity of regulatory proteins on the DNA. Regulatory proteins direct the activity of genes. The DNA, RNA, and protein functions are the same as described in the Primacy of DNA chart. Note: the flow of information is no longer unidirectional. In the 1960s, Howard Temin challenged the Central Dogma with experiments that revealed RNA could go against the predicted flow of information and rewrite the DNA program. Originally ridiculed for his "heresy," Temin later won a Nobel Prize for describing reverse transcriptase, the molecular mechanism by which RNA can rewrite the genetic code. Reverse transcriptase is now notorious, for it is used by the AIDS virus's RNA to commandeer the infected cell's DNA. It is also now known that epigenetic changes in the DNA molecule, such as adding or removing methyl chemical groups, influence the binding of regulatory proteins. Proteins must also be able to buck the predicted flow of information, since protein antibodies in immune cells are involved with changing the DNA in the cells that synthesize them. The size of the arrows indicating information flow are intentionally not the same. There are tight restrictions on the reverse flow of information, a design that would prevent radical changes to the cell's genome.



In this epigenetic analogy, the test pattern on the screen represents the genetic code (program). While the TV's controls can change the appearance of the pattern (B and C), they do not change the original pattern of the broadcast (i.e., the gene). Epigenetic control modifies the read-out of a gene without changing the DNA code.



Agouti Sisters. One-year-old female genetically identical agouti mice. Maternal methyl donor supplementation shifts coat color of the offspring from yellow to brown and reduces the incidence of obesity, diabetes, and cancer. (Photo courtesy of Randy Jirtle)



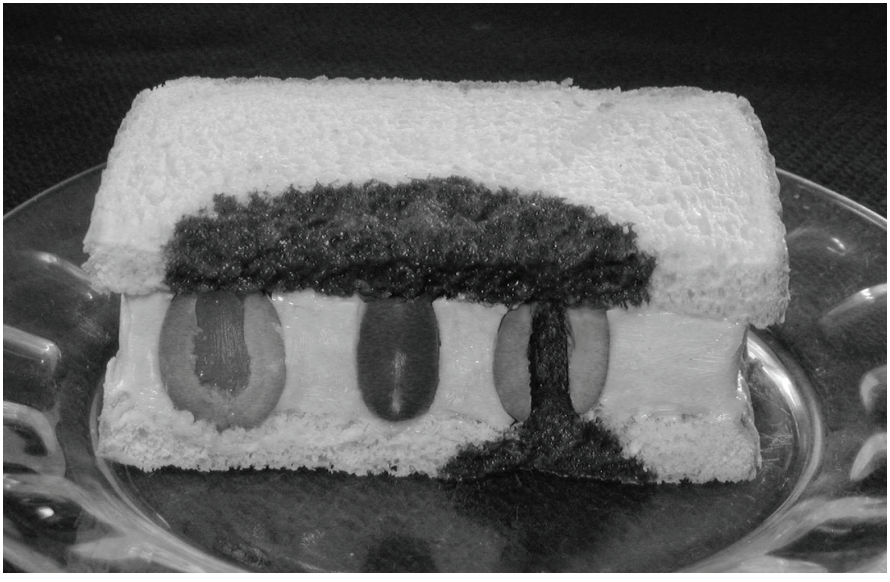
Replication of DNA. Before DNA is copied, the double helix is split into two separate helical strands. In figure A, DNA polymerase, an enzyme that copies the DNA, is represented by the train engine. The polymerase enzyme travels down the length of a single strand of DNA. The gene-coding section of the DNA strand, represented by the black "train track," has a sequence of bases that code for the protein. The telomere section of the DNA, represented by the gray portion of the "train track," has a sequence of noncoding DNA (white "boxes"). As the polymerase moves down the DNA, it assembles a complementary DNA strand in its wake. In figure B, the length of the new complementary DNA strand is longer as the polymerase copies more of the original strand. In figure C, the polymerase reaches the end of the DNA strand ("track"). The new complementary DNA molecule is complete. However, it is shorter than the original DNA template because the polymerase enzyme cannot copy the section of DNA on which it sits (X). Each time the DNA is copied, the new DNA strand is shorter than the previous version. After a number of cell divisions, the telomere extension is eliminated and the polymerase begins to clip off pieces of DNA that contain the protein's code. Proteins synthesized from a shortened DNA code are defective and can cause the cell to become dysfunctional.

Chapter Three Illustrations

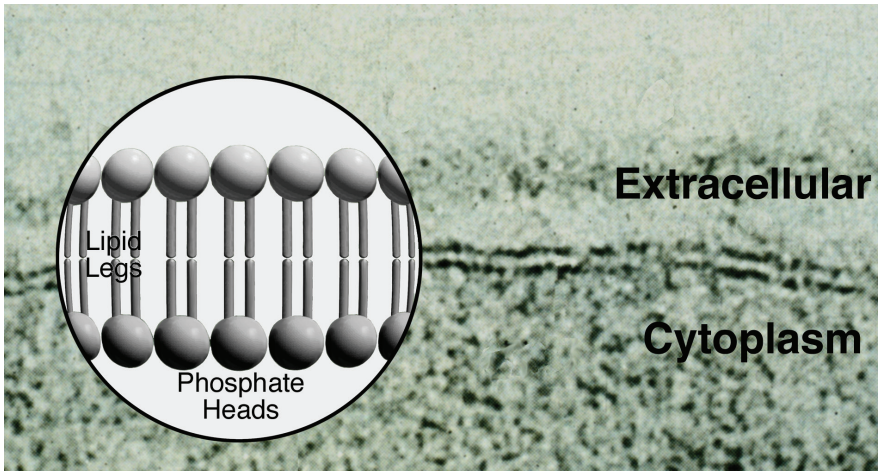
Bread and Butter Sandwich—Step 1

Bread and Butter Sandwich—Step 2

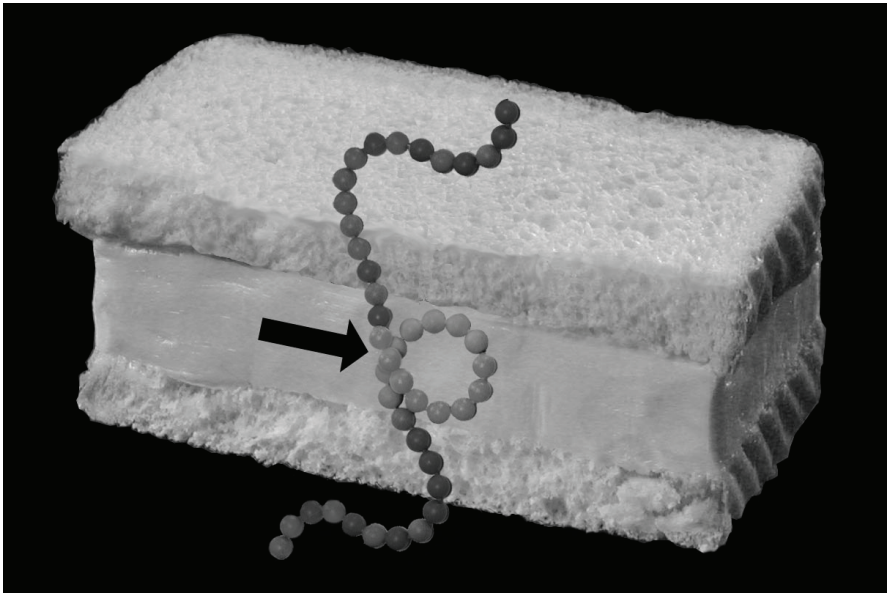
Bread and Butter with Olives Sandwich—Step 1



Bread and Butter with Olives Sandwich—Step 2

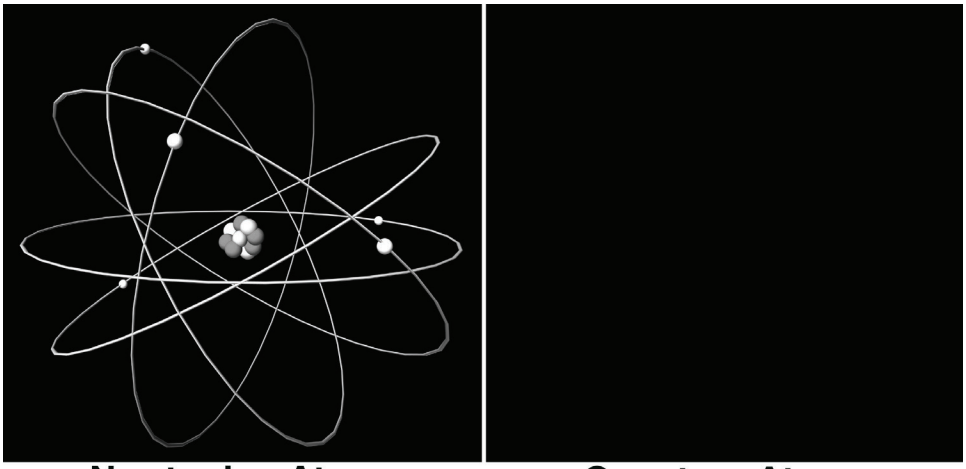


Electron micrograph showing the cell membrane at the surface of a human cell. The dark-light-dark layering of the cell membrane is due to the ordering of the barrier's phospholipid molecules (inset). The lighter center of the membrane, the equivalent of the butter in our sandwich, represents the hydrophobic zone formed by the nonpolar legs of the phospholipids. The dark layers above and below the central lipid zone, the equivalent of the bread slices, represent the molecule's water-loving phosphate heads.

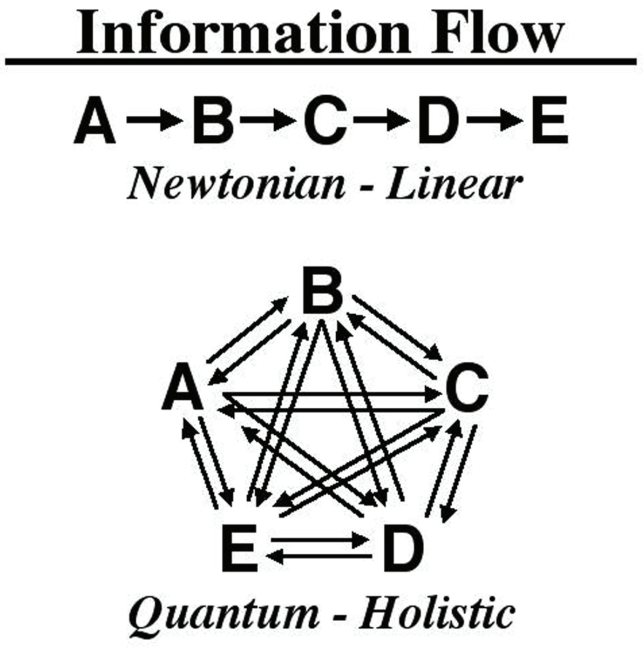


Hydrophobic amino acids seeking stability by finding an oil-loving environment like the membrane's lipid core. (See arrow above.)

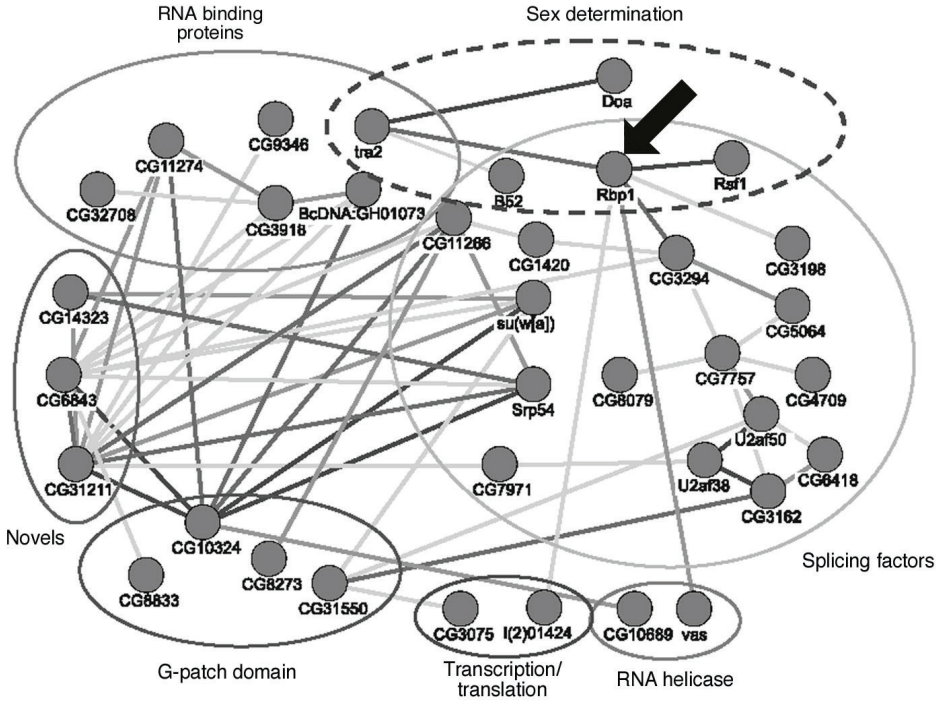
Chapter Four Illustrations



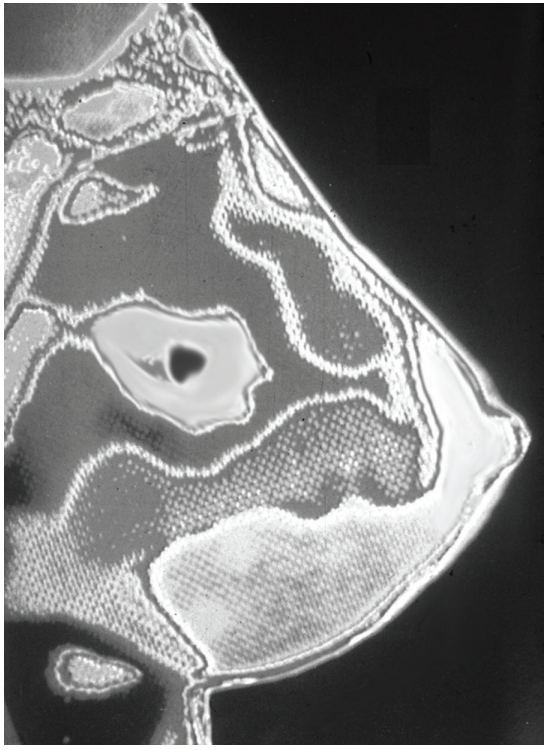
Newtonian Atom vs Quantum Atom



How information flows: Newtonian vs Quantum

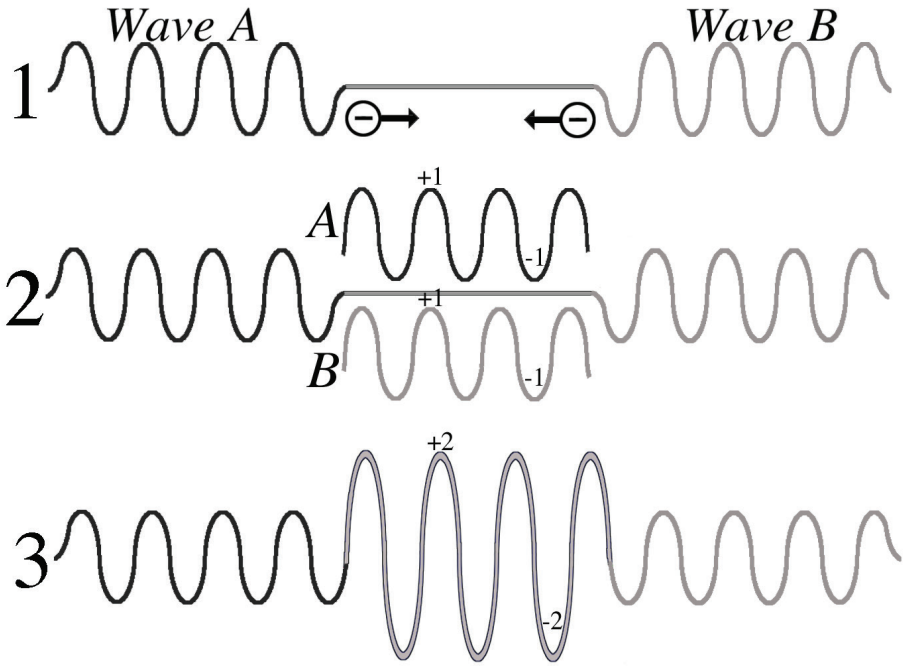


Map of interactions among a very small set of the cellular proteins (shaded and numbered circles) found in a Drosophila (fruit fly) cell. Most of the proteins are associated with the synthesis and metabolism of RNA molecules. Proteins enclosed within ovals are grouped according to specific pathway functions. Connecting lines indicate protein-protein interactions. Protein interconnections among the different pathways reveal how interfering with one protein may produce profound "side effects" upon other related pathways. More widespread "side effects" may be generated when a common protein is utilized in completely different functions. For example, the same RBP1 protein (arrow) is used in RNA metabolism as well as in pathways associated with sex determination. Reprinted with permission from Science 302:1727-1736. Copyright 2003 AAAS.

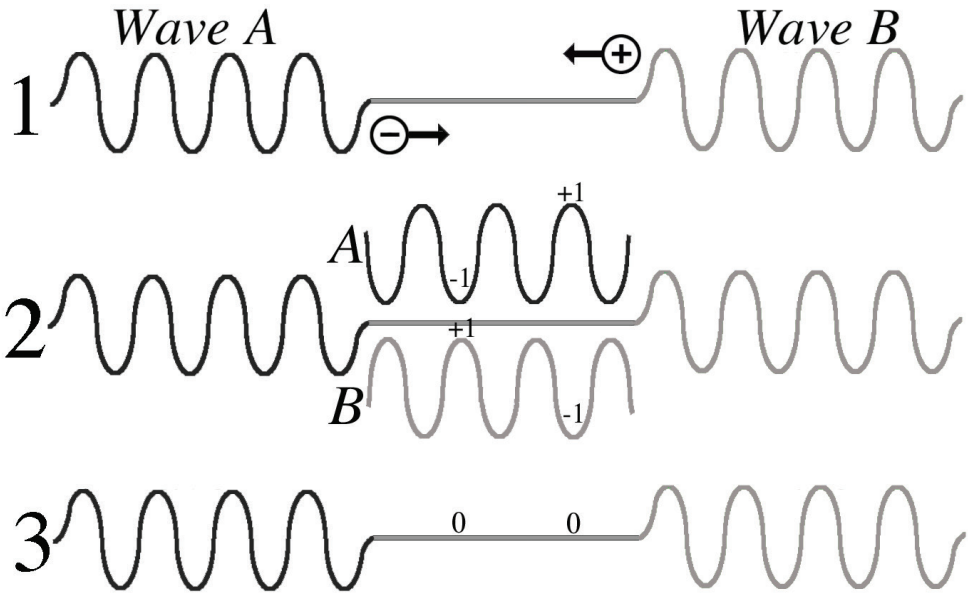


Mammogram. Note the above illustration is not a photograph of a breast, it is an electronic image created from scanning the radiant energy characteristics of the organ's cells and tissues. Differentials in the energy spectra enable radiologists to distinguish between healthy and diseased tissues (the black spot in the center).

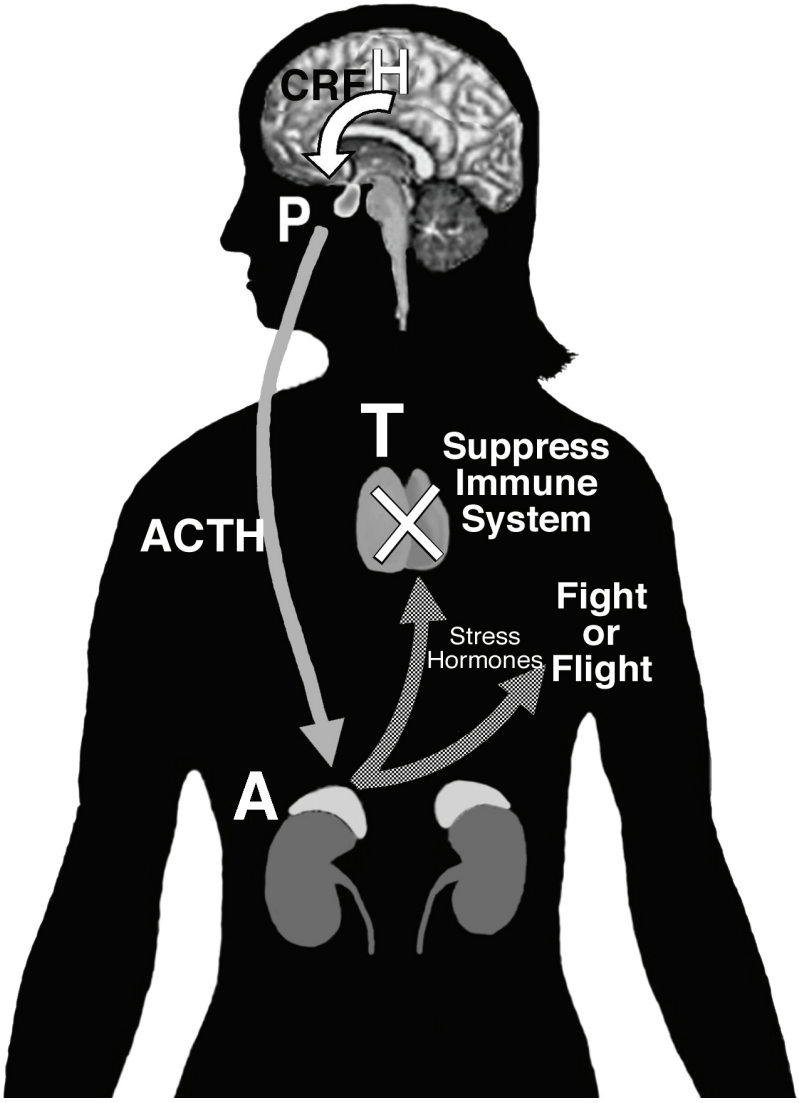
Ripples in water



Constructive Interference. In 1 above, two sets of ripples are moving across the surface of water toward each other. As illustrated, both wave A and B are moving toward each other with their ripples in phase, in this case both waves are going up and down at the same time. Their cycle patterns are aligned. The waves merge together at the interface where two ripples meet. To illustrate the consequence of this merger, the waves are drawn with one above the other in figure 2. Where the amplitude of A is +1, the amplitude of B is also +1. Add the two together, and the resulting amplitude of the composite wave at that point is +2. Likewise, where A is -1 so is B; together the total amplitude will be -2. The resulting higher amplitude composite wave is illustrated in 3.



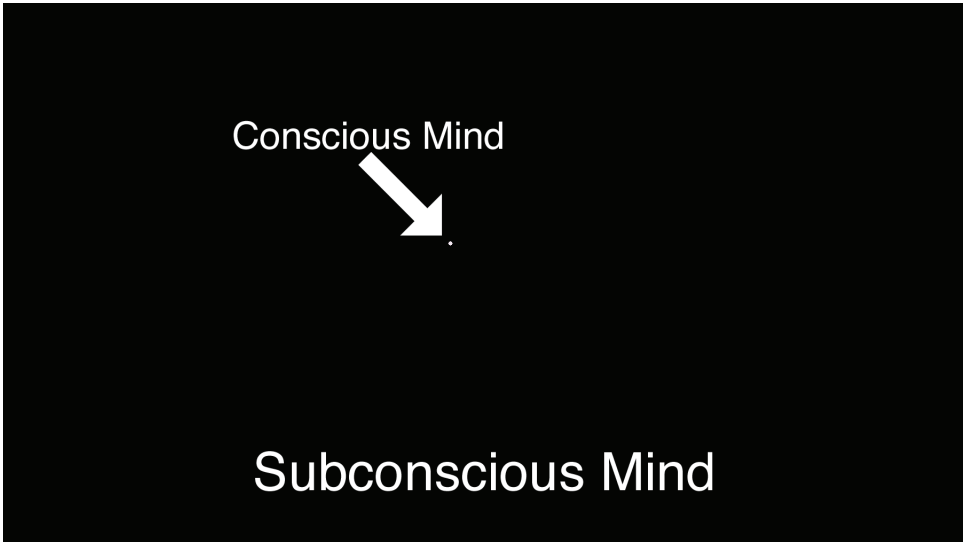
Destructive Interference. In figure 1, the ripples derived from the first pebble, labeled as Wave A, are moving from left to right. Wave B, moving right to left, represents the ripples from a second pebble dropped shortly after the first. Since the pebbles did not hit the water at the same time, the waves will not be aligned when they merge at the interface; they will be "out of phase." In the illustration, Wave A is leading with a negative amplitude, and Wave B is leading with a positive amplitude. Where they meet in figure 2, the waves are mirror images of each other; the high amplitude (+1) of one wave is aligned with the low amplitude (-1) of the other, and vice versa. As shown in 3, the amplitude values of each wave cancel each other out, so that the composite wave having 0 amplitude is no wave at all . . . it's flat!


CRF
H
P
T
Suppress
Immune
System
ACTH
Fight
or
Flight
Stress
Hormones
A

HPA axis

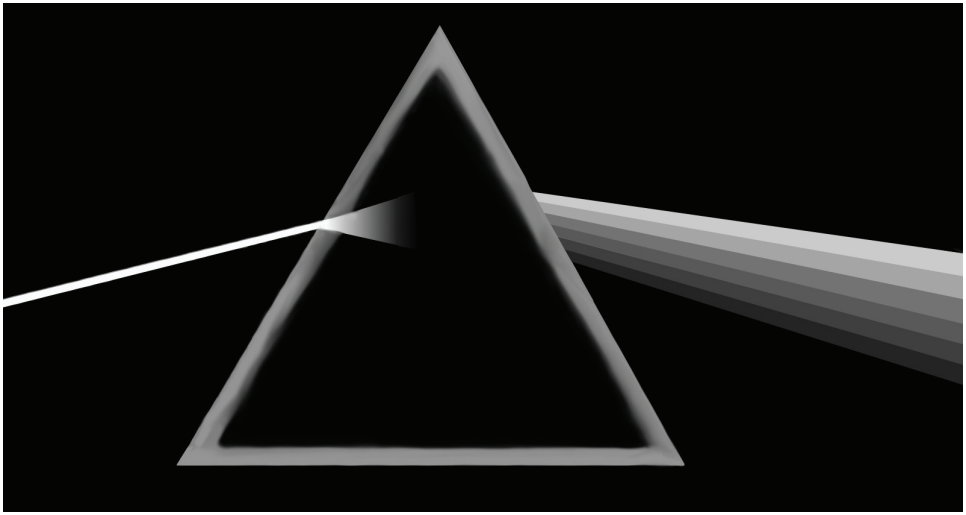
Chapter Seven Illustrations

Visualizing the information-processing powers of the conscious and subconscious minds. Consider that the image of Machu Picchu above is comprised of 20 million pixel dots, each representing a BIT of information received by the nervous system. The powerful subconscious mind processes all this information in one second. How much of that incoming information enters the conscious mind?



In the above picture, the dot represents the total amount of information that is processed by the conscious mind in that same second. (Actually the dot is 10X more than enters consciousness. I had to enlarge it because it was barely visible.)

Epilogue Illustrations



Prism