Computers & Biotechnology

Introduction: A Graphic View of You!

Hunting for Genes

SNPs and Chips

Every Picture Tells a Story

Viewing Molecules and Proteins

Searching for Drugs

PROFILE

John McAlister: Computer Modeler

ACTIVITY

Molecular Puzzles

On the cover: Computers are helping us understand more about our world by showing us the shapes of molecules and the information contained in genes. This issue describes just a few of the computer modeling techniques and bioinformatic systems that provide a faster and more direct way of researching genetics and drugs. These techniques are also advancing many diverse fields of science, from agriculture to zoology. Today, all biotech research depends on computers. Who knows what tomorrow will bring?
Thirty years ago, students had it tough! They used manual typewriters and whiteout for term papers. They made copies with carbon paper instead of photocopiers. They used slide rules instead of calculators. If they had access to a computer, they used punchcards and programming language — there were no graphics. Video and computer games weren’t even science fiction yet. But now computers have completely changed the way you learn, work, and play!

Computers have also changed the way scientists conduct research. You can boil these changes down to two areas: handling enormous amounts of information and displaying this information in visual, graphic form. The same computer technology that makes realistic video games and special effects movies possible is now at work in physics, chemistry, biology, ecology, population studies, epidemiology, agriculture, forest management, archeology, anthropology, and more. This issue of Your World focuses on how computers help us study the world of genes, proteins, and molecules in search of better medicines and cures for diseases.

Your genes hold the secret to who you are. They play a major role in how you look, respond to your environment, get sick, age, and maybe even how you act. If we could get a complete computer “printout” of your genes, it would show everything you have in common with other living things, as well as everything that makes you unique. You could find out if you’re prone to a particular disease so you could get preventive treatments or cures. You could also learn which drugs might work best for you. To do such an analysis, though, we need to compare your genes to “standard” human genes and to variations of them. We also must understand the function of these gene variations and the different proteins they produce.

None of this would be possible without the enormous power of computers. First of all, we need computers to handle the huge amount of information stored in genes. The marriage of computers and genes is called bioinformatics.

We are also using computer modeling to learn more about how life functions at the molecular level. Sometimes the straightforward information about a gene’s DNA doesn’t provide enough clues about its function. But if scientists can see the shape of the protein the gene produces, they might say, “Ah, ha! We see how it might interact with other molecules of life.”

In this issue of Your World, you will learn about how computers have combined the fields of biology, genetics, and medicine to make our world more understandable, healthy, and safe.
A Genetic Gold Mine

In 1990, scientists began a united journey to explore the gold mine of information hidden in the human genome. “Genome” refers to all the DNA on all the chromosomes. Scientists called their effort the Human Genome Project. Their task would be hard enough if there were just one human genome. But there are billions, one for each person! And each person’s genome has three billion DNA bases. The result? An overwhelming number of massive sequences, each too large to comprehend.

Knowing sequences of bases in the genome is only half the story. The second half is finding useful information—genes—within the genome. We have about 100,000 genes, but they make up only about 10% of our genome.

To find and study genes, scientists first had to develop the new computers, programs, and data systems that have become known as bioinformatics. Computers allow us to store, organize, search, compare, and interpret enormous amounts of data. Without computers, genetic research would be like finding a needle in a haystack, or using a library without a catalog, or looking for specks of gold in “them thar hills.”

Data Mining

Scientists call the search for genes “data mining.” It is like digging for gold (a gene) among vast quantities of rock (the non-meaningful DNA that camouflages the gene). Instead of using pick axes, scientists use computer tools to sift through data.

PRIMER: GENES AND PROTEIN

Part of the secret of genes includes the tale of how genes make proteins. A gene is a unique sequence (order) of DNA bases. (We refer to the four chemical bases by the letters A, T, C, and G.) The sequence of bases in a gene determines the order of a chain of amino acids. Amino acids are small building block molecules that we break down from the proteins in the food we eat. Each three-letter genetic “word” codes for one of 23 different amino acids in our bodies. Once built, the amino acid chain folds, twists, and turns to form a protein with hills, valleys, and ridges. These shapes determine how the protein interacts with other proteins and molecules—and these interactions are the basis of many biological processes. A small change in the DNA sequence of a gene can substitute one amino acid for another in the protein, which may alter the way a protein folds. This change in shape can affect the way the protein functions, such as determining your eye color, your blood type, or whether you have a certain disease.
To complicate matters, all “words” in the genetic language are only three letters long. We could start reading in any of three positions:

1) gta ege get..
2) g tac gegeta...
3) gt acg ege tag...

Fortunately, we have some guideposts to help us “read” DNA. For example, the “rock” sections of DNA usually start with “GT” and end with “AG.” The computer ignores these stretches, clearing away some rock from the gold. Computers can identify signal sequences for the beginning or end of a gene, and look for clues about the function of a gene.

Working Backwards
Another gene-mining tool works backwards to the genes themselves. The living cell knows exactly how to separate gold from rock when making a protein. The cell extracts the DNA gold and translates it into messenger RNA (mRNA).

Scientists extract the mRNA and copy it back into a DNA sequence, called complementary DNA (cDNA), which corresponds to the gene. But it doesn’t have any rock, so it is easier to read. The computer can now search for the gene and pinpoint it in the genome.

Finding Similar Genes
We have about 100,000 genes, and each gene codes a unique protein. Thus, your body produces about 100,000 different proteins. But many of those proteins are similar and belong to a large family.

Within each family, related proteins perform similar functions, and their genes have similar sequences. Scientists are using information about similar sequences to find more members of a very important family that may help us treat diseases: receptors. Receptors on the cell’s surface receive messages, such as hormones, from outside and send the messages inside. There may be thousands of different receptors. One group of receptors interacts with about 60% of all our current drugs. So far scientists have identified about 250 members of this group, but they think there are about two thousand. Finding them will help us develop new drugs.

To hunt for them, scientists use a family profile. All the receptors in this group have seven amino acid segments that span the cell membrane. (These particular amino acids all like fat and don’t like water, so they stick into the fatty parts of the cell membrane!) A computer search for DNA sequences that produce similar seven-segment proteins can track down more members of this receptor group.

Let’s suppose the following “gene” lies buried in the DNA hillside:

```
gtacgcgctagctagctaagctagatgcatgdctagcttcagaggaaattaccccaaatggtggactacatgtcagtagcaaatggccctagc
```

These intermixed rocks make the task of sorting out words much harder! Now suppose we use only four letters instead of the 26 in our alphabet – as is the case with DNA:

```
glaczcgctagctagcgtagatcagtgdclagctccagaggaaattaccccaaatggtggactacatgtcagtagcaaatggccctagc
```

There are 5 billion people on earth, each having 3 billion bases. How many bases is that? 

\[(5 \times 10^9) \times (3 \times 10^9) = 15 \times 10^{18} = 15,000,000,000,000,000,000\]

Keeping track of this information is a task only computers can handle.
SNPs and Chips

A Snip of Individuality

Do you know your blood type? Whether you belong to the A, B, or O blood group depends on a tiny genetic variation you’ve inherited from your parents. The A blood group has this partial sequence: CGTGGTGACCCCTT. The O group has deleted one G base and has: CGTGGTACCCCTT. This genetic difference codes different proteins that then produce different antigens in your blood.

The ABO blood groups result from the most common type of genetic variation, single base changes. Scientists nickname this difference a SNP, pronounced “snip.” (The full name is single nucleotide polymorphism: “poly” means many; “morph” means shape; and “nucleotide” is a DNA base.)

Each SNP is a minute fraction of your genome, but it can make an enormous difference. It may determine whether you succumb to a disease or resist one. For example, a SNP in a gene called “apoE” can lead to Alzheimer’s disease. A certain rare SNP in a receptor gene makes people immune to HIV infection. SNPs may also explain why some people respond well to drugs, some do not, and others have negative side effects.

All in all, there may be three million SNPs buried in our genome. How can we find them all, much less understand their importance? Scientists are using computers to collect information about variations in the human genome and then match tiny variations with subtle differences in disease states and drug responses.

Such work will take a lot of time and effort, but scientists believe it will pay off. Drug companies may use SNP information to predict the effectiveness and side effects of a new drug – before costly clinical trials. Doctors may use it when prescribing drugs for patients, checking to see if a patient has a particular SNP that makes a drug unsafe or ineffective. We already have “contraindication” warnings on many drugs, but some people are still harmed by drugs. Bioinformatics could provide a more specific and accurate warning system for all of us.

Chips for Testing Genes

One tool to help scientists gather information about SNPs is the DNA chip. You may have seen the tiny circuits on a computer chip. Scientists use “photolithography” to create these circuits. They shine light through differently patterned masks and expose the chip to chemicals in those patterns to create different circuits. This process is similar to screen art: You use one stencil for yellow paint on white paper and another pattern for blue paint to create a design of yellow, blue, green, and white.

Scientists use this technology to make DNA chips for testing genetic variations in a sample. Instead of building up circuits, they build strings of DNA bases to create genetic probes. Computers design grids of thousands of probes for different genetic variations. Scientists expose the chip to the DNA and/or RNA from a cell. The chip captures any matching sequences in the sample. Beforehand, the genetic material was tagged with a fluorescent molecule. When scientists shine a visible light on the chip, the captured genetic sequences glow. A computer matches the glowing sites on the chip to the layout of genetic probes. Then it can provide a readout of the genetic variations found in the sample cell.

Scientists are using such tools to develop genetic “profiles” of diseases. A profile shows the pattern of genes that are active in a cell. Computers compare the profiles of normal and diseased cells so scientists can sort out the common genetic features of a disease.

These disease profiles may help us identify the genetic causes of a disease, diagnose complex diseases more accurately, and find new treatments or cures. Scientists will use these profiles to test thousands of potential drug molecules. They will test the gene profile after a diseased cell is treated with each drug candidate. If a molecule changes a disease profile to a healthy profile, it may make a good drug. The National Cancer Institute has profiled 60 types of cancer and screened 70,000 possible drug molecules against them. They are now searching databases to see if any of the molecules might be effective cancer fighters.
In 1995 an anthropologist was climbing the 20,700 foot Mt. Ampato in the Peruvian Andes Mountains when he found the frozen mummy of a teenage girl. This “Ice Maiden” had been sacrificed by Incan priests 500 years ago – perhaps to satisfy a mountain god. The icy temperature preserved her tissues so well that scientists could extract DNA from her cells. Anthropologists study people’s ethnic and cultural roots, so they hoped the Ice Maiden’s DNA could help explain the origins of the Incas.

Scientists focused on two DNA sequences, each about 450 bases long, from the mitochondria of her heart cells. (Mitochondria are the parts of the cell that produce energy.) Mitochondrial DNA is passed down only from the mother, so it is possible to trace family lines through the maternal DNA. Already, scientists had used bioinformatics to compare the mitochondrial DNA of Native Americans throughout North and South America. Using this analysis, anthropologists traced all these populations back to four original waves of Paleo-Indians who migrated from Asia into the Americas.

One of the Ice Maiden’s mitochondrial DNA sequences shows that she descended from one of these four waves, and it links her to the Ngobe of Panama. There are also similarities to genetic patterns found in Taiwan and Korea, which supports the theory that Paleo-Indians originally came from Asia. One sequence does not match any sequences found in any database so far.

Scientists do not yet have enough data on ancient populations to trace the source of the Ice Maiden’s family. But anthropologists have discovered three more frozen mummies in the Andes, so they will soon have more information about the Incas. Someday, scientists may use DNA comparisons to map the paths of early humans as we emerged from Africa and spread throughout the world.

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**First 20 Sequences of Four Genes**

<table>
<thead>
<tr>
<th>Gene 1</th>
<th>T G T C C A A A A T G T G A C A A A A C T G</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene 2</td>
<td>T G T C C A A A A T G T G A C A A A A C T G</td>
</tr>
<tr>
<td>Gene 3</td>
<td>G G C T G A T A T T G T G A C A C A C A C T G</td>
</tr>
<tr>
<td>Gene 4</td>
<td>T C G A A A A G A C G G G A T A A A A C C T</td>
</tr>
</tbody>
</table>

This diagram shows the first 20 base sequences from four genes. Notice the high percentage of positions that have the same bases. How many positions have the same bases in all four genes? In three genes? The similarity among the base sequences means they probably belong to a family of genes with common characteristics.
Scientists are now using models to understand the molecules of life. But molecules and proteins are much more difficult to model than planets and moons. Luckily, computers help us see these tiny structures.

Many biological functions are based on the interlocking shapes of molecules. For instance, antibodies recognize invading microorganisms by the shape of an antigen protein on the microbe, and they are said to fit together like a three-dimensional lock and key.

This lock and key analogy underlies many biochemical reactions, including those involving two types of proteins that are very important in disease and drug treatment: enzymes and receptors. Proteins have an “active site” where they bind smaller molecules to themselves, causing a chemical reaction. Part of the protein’s shape forms the lock, and part of the molecule forms a key that fits the lock. For many proteins, this lock is a deep cleft or pocket in its surface. Often, more than one kind of molecule has a key that fits the protein’s lock.

Most of our existing drugs are molecules that interact with proteins, so having computers show us such shape interactions can help us develop more effective drugs. Scientists are keenly interested in creating models of the proteins involved in health problems ranging from diabetes to schizophrenia to migraines. These models can give us insights we could not get any other way.

**Modeling Proteins**

If scientists know the structure of the protein they want to study, they can crystallize it and take an X-ray image of it. The data from this image show the relative location of atoms in the protein, similar to distances on a road map: If you had all the distance measurements from every town in the country, a computer could construct a map of the country. In the same way, the computer can take the X-ray crystallography data, display the structure in various ways, and even rotate the views to reveal all the shape’s features. (For a simple example, see the different views of the caffeine molecule on page 10. A protein’s structure is more complicated, like a tangled ribbon of amino acid chains.) These rotating, 3-D views allow scientists to visualize how a small molecule might fit into a binding site on the protein.
Scientists are comparing proteins from different species as well as from humans. This comparison is possible because the genetic code is universal: it works the same for worms as for us. These comparisons are showing that evolution is conservative. That is, new species “recycle” genes from older species, so we have many genes that are almost identical to those in other species. These comparisons will help evolutionary biologists and anthropologists draw a more detailed family tree of the world.

This computer-generated image shows a molecule bound to neuraminidase, an enzyme that allows the influenza (flu) virus to reproduce and infect you. Scientists used this image to identify the cleft in the enzyme and to study the shape of the molecule that naturally binds to it. When this molecule binds, it breaks apart, allowing the virus to replicate. Using techniques discussed in the next article, scientists had the computer make models of other molecules that would fit into the cleft and not break apart. Next, they synthesized (made in the laboratory) several molecules that fit the bill and tested them. They used the most effective of these molecules in a new inhaler, which has been approved as a drug.

A New Flu Drug

Watson and Crick Model: James Watson and Francis Crick discovered the structure of the DNA molecule in 1953, but they could only represent it with mechanical parts. Today, computers can represent molecules more realistically.
Viewing the Caffeine Molecule

To see how computers can represent molecular shapes, consider these models of the relatively simple molecule, caffeine.

Caffeine 1
This two-dimensional image shows the relationship of atoms in the caffeine molecule. Atoms are represented by their first letter (C=carbon, H=hydrogen, N=nitrogen, O=oxygen). The chemical bonds between atoms are drawn as single, double, or triple lines to indicate the type of bond.

Caffeine 2
This model represents each atom as a ball and the connecting bonds as sticks. Different colors represent the atom types. (C=white, H=light green, O=red, N=blue.)

Caffeine 3
To simplify the display, the atoms and bonds are shown as tubes.

Caffeine 4
For a more realistic model, the computer represents the atoms as spheres with radii corresponding to atom size.

Caffeine 5&6
The computer rotates the image to reveal that most of the atoms of the molecule lie in one plane.

Caffeine 7
Do you want to see the molecule in three-dimensions? To fuse these images, follow the instructions for the neuraminidase protein on the previous page.
**Viewing Proteins**

Larger molecules, such as proteins, can be displayed in similar ways. Let’s take a look at the hexokinase protein, which binds to glucose (a sugar), and the hemoglobin molecule, which has four subunits that bind oxygen in your blood.

**Hexokinase 1**

This model represents the hexokinase protein as spheres. The amino acid chain cannot be distinguished, but you can see the deep cleft “lock” at the top center where the glucose “key” binds.

**Hexokinase 2**

This model represents the protein as a ribbon showing the chain of amino acids. We can follow the twists and turns of the protein’s folded form.

**Hemoglobin**

This image represents the four chains of a genetically modified hemoglobin molecule as ribbons. The atoms of the four heme groups that bind oxygen are shown as spheres with an iron atom in the middle.

From such computer images, scientists are learning about the interaction of specific shapes and how to design new molecules that might interact with these proteins.
Finding Similar Molecules

Suppose you know of a molecule that binds to a protein in a way that partially treats a disease. Perhaps, however, that molecule doesn’t make a good drug. (It may interact weakly, or can’t get into a cell, or has unwanted side effects, or also interacts with another protein in a harmful way.) Perhaps another molecule could bind to the same protein but work better. How do we find it? Traditionally, scientists tried to change the molecule’s structure to mimic other drugs – or they used the old hit-or-miss, trial-and-error method. Sometimes this works. But surely it also misses molecules.

One way to expand the search is to teach a computer to analyze complicated shapes. We humans recognize shapes very quickly. We immediately know the difference between a cat and a dog. But can a computer tell the difference? Both animals have a head, two eyes, a nose, a body, four legs, and a tail. How could a computer distinguish two breeds of dogs – a task that is closer to the problems of drug discovery? Here are some methods scientists have developed.

Ping Pong Ball

Let’s pretend you want to analyze a particular dog’s shape. You can use a ping pong ball as a probe and roll it over the entire surface of the dog. At each point on the surface, a computer records the exact location of the ball on a three-dimensional grid. The entire set of coordinates (X, Y, Z) of the ball in the grid represents the dog’s shape.

In the same way, a computer traces a molecule in a three-dimensional grid, measures the location of a small probe molecule when it bumps up against the larger molecule and records the coordinates. This is one method called “quantitative structure activity relationship” or QSAR. We can use it to record the shape of several molecules that we know “lock” to a certain protein and then ask the computer to search for a “key” feature that all those molecules share.
Then scientists can search for other molecules with the same feature. Scientists used a QSAR approach in developing the new antibacterial drug norfloxacin, the Alzheimer's treatment donepezil (Aricept™), and the migraine drug zolmitriptan (Zomig™).

### The Animal's Den
Another approach allows us to guess the shape of the protein's binding site by examining the molecules that bind to it. What shapes do these molecules have in common? What can that tell us about the protein's “lock” (binding site)? Scientists call this approach the “pharmacore” method, and it is like trying to define the shape of a den by examining the animals that fit in it. If they are all long and thin, the den is probably narrow and deep. Once you have modeled the shape of the protein's “den” (or “lock”), you can look for molecules that have a “key” that would fit it. These molecules may all have quite different chemical properties, but they share a similar “key” for the same protein.

### Finding Different Molecules
The ping pong ball and animal's den approach only get us so far in our search for new molecules, though. Suppose you want to find molecules that are different from those you have studied? Perhaps none of the known molecules interacts in just the right way with a protein involved in a deadly disease. In that case, you may want to combine different molecules together to make new compounds. This method, called “combinatorial chemistry,” allows scientists to synthesize millions of new compounds. It is like choosing all possible combinations from a Chinese restaurant menu: an entry from column A combined with each meat option from column B; the second entry from A combined with each option from B, and so on. If each column had ten thousand options, there are 100 million (10⁴ x 10⁴) possible combinations. Maybe one of them is just the new drug you want to find...

Now the trick is to screen those compounds to see if any interact with the disease protein. But there are so many compounds to test – even using the robots that are now common in labs! And many compounds have almost identical shapes and biological activity. Scientists would like to test only those with significantly different shapes and – probably – different activities. Computers are helping weed out the similar shapes, so scientists can concentrate on representatives from different families of shapes. Then, if they find one promising molecule, they can study its other family members. Alternatively, they can use these methods to look for molecules with shapes similar to one they know, in order to develop variations on a successful drug theme. That’s how new alternatives to the antidepressant drug fluoxetine (Prozac®) were created; scientists looked for molecules with similar “keys” to that which allows the drug molecule to interact with chemicals in our brains.

### Virtual Libraries
Computerized “virtual libraries” store the shapes of larger molecular fragments. Computers then “cook up” all the possible shape combinations in the Chinese menu columns and point out those “meals” that are similar and different. Once scientists identify molecules of interest, they can synthesize and test them. Alternatively, the computer can model the molecule’s structure and superimpose it on the protein to see if it fits.

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**Fragments**
The most common way to sort molecules is to break them into fragments, like breaking the shape of a dog down into nose, tail, ears, legs, etc. Then, a computer represents the pattern of those fragments as “bit strings.” For each possible fragment, it assigns a “1” or a “0” to show if the fragment is present to create a string like this: 00010011101010. Then the computer compares millions of bit streams. Molecules with similar strings may have similar shapes and binding properties, so computers can sort molecules into families. Scientists can use these families either to concentrate on differently shaped molecules or to isolate members of one family.

**Virtual Libraries**
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**Fragments:** The molecule on the top row is broken down into some of the possible overlapping fragments, which are shown in the second row. The third row shows a bit string where these fragments are represented as a “1.” The “H” (hydrogen) atom doesn’t affect the activity of the molecule, so H₂CCH, CH₂CH₂, and CH₃C all produce the same fragment, C-C.
Every morning John McAlister tucks his tie into his shirt, puts his computer in his backpack, and rides his motorcycle to work. He started riding motorcycles as a graduate student when it was the only transportation he could afford. Now he takes one on cross country camping and backpacking trips with his sons, looking for freedom and adventure. John finds the same sense of adventure and beauty in science. Ever since he was inspired by his high school science teachers, John has enjoyed the “excitement of discovery that science is all about.”

As an undergraduate John studied chemistry and mathematics at Tarleton State College in Texas. After graduating in 1971, he entered a Ph.D. program at the University of Wisconsin and almost became a synthetic organic chemist. But the biochemistry department had X-ray crystallography equipment, and John started analyzing the structure of molecules and proteins. Growing bacterial cell cultures from which to isolate the materials left a lot of idle time. John used it wondering whether mathematics and computers could predict the structures the molecules would assume. There were no such programs at the time, so John started writing his own.

At that time, X-ray crystallography data consisted of large tables with numbers. Graphing this raw data meant tediously drawing lines on plastic sheets and then stacking them up to give a sense of the three dimensional structure. Mechanical models (such as the one shown with Watson and Crick on page 9) were constructed by matching parts to the molecule image on the stacked sheets. Again, John thought there must be a better way.

Assembling parts from different companies, John built one of the first molecular graphic systems in the world. He wrote the software to teach the computer how to display the numerical data as an image.

In 1980 John moved to Washington University in St. Louis to write software for a computer graphics system to be given to 16 university biochemistry departments. This work led to a job as principal programmer at a new local company, Tripos, Inc., which was starting to develop modeling hardware and software. He often worked a programmer’s typical 24 hour day to get the programs right. Eventually John became a manager so that, as he puts it, he could “monitor who touched his code.”

Today, many of those programs are still used as the basis of high tech software. John is now president of Tripos, which has become one of the world’s premier suppliers of molecular graphics software to the biotechnology industry. John likes managing a scientific company and finding the resources to help creative people achieve their ideas. As for the future of molecular modeling and analysis, John believes people are just beginning to understand the power of visualizing and mathematically analyzing the information extracted from molecular data and the relationship among numbers.

Most of all, John hopes that students of today will share the excitement of discovery on new scientific frontiers and appreciate that “science is a beautiful way to understand the world.”
How good are you at hunting for genes and matching keys to locks? Here are a few activities to test your skills.

**Gene Hunting**
The sequence of letters on the bottom right contains a gene starting with ATATTAG and ending with CCTTAT. Can you find it? What strategies might help you find the sequence? Once you’ve found the beginning and end of the gene, you can sequence the entire gene!

**Gene Probing**
A gene probe can quickly find a matching part of a DNA sequence. Trace the “probe” at the right of the page, including the separating lines, and then cut out the tracing. This probe matches part of the sequence shown on the diagonal. Each shape on the probe must fit exactly into its counterpart in the sequence, since complementary DNA base pairs fit together like puzzle pieces. Time how long it takes you to find the probe’s match.

- 5 seconds = genius gene finder;
- 10 seconds = average gene finder;
- >15 seconds = you need a computer!

**Molecular Modeling**
Use ping pong balls, Styrofoam balls, or similar round objects and some glue to construct a three dimensional model of the caffeine shown on page 10 of this issue.

Rotate the model to match the computer generated viewpoints.
- What can you learn from seeing the model in three dimensions?
- Caffeine interacts with certain proteins/receptors in your body.
- How would you describe the “key” shape of the caffeine molecule?
- What does the shape of this key tell you about the “lock” (binding cleft) in the protein/receptor?
Dear Students and Teachers:

We are delighted to provide you with this copy of Your World. The issue highlights the convergence of two important areas of technology and illustrates how they enable new discoveries, products, and services. This is the fifteenth Your World issue published over the past eight years on various topics in biotechnology.

This issue is an important milestone because it marks the movement of Your World’s publication from the Pennsylvania Biotechnology Association (PBA) to a new home within the Biotechnology Institute. The Biotechnology Institute has been formed by the Biotechnology Industry Organization and PBA to create a new national institute focused on biotechnology education. The Institute will continue publishing Your World for an expanded national and international audience and will introduce other biotechnology education initiatives.

For more information on the Institute, to look at or order previous issues, or to let us know your thoughts, please visit our web site at www.biotechinstitute.org. The next issue of Your World will address Biotechnology and AIDS.

The Biotechnology Institute thanks our founding sponsors, whose generous support has launched the Institute and made this issue of Your World possible.

Sincerely,

Jeff Davidson
Director of Bioscience Education
Biotechnology Institute