Big Science

The Human Genome Project taught us as much about politics, power, and geneticists, as it did about human genetics.

In the weeks leading up to the publication of last month’s newsletter dedicated to The Failure of Genetics, I read, in chronological order, every article about the Human Genome Project published in the professional journals Science and Nature. It was like reading a murder mystery for the second time, knowing from the first page whodunit. I saw clues I didn’t see when I read those articles the first time a dozen years ago.

This review of the history of the Human Genome Project gives us a peek behind the curtain, showing how science really works. It provides a concrete example of how political and financial forces shape scientific research. It answers the questions, “If science is against the theory of evolution, why do so many academics defend it?” and “Is there really a conspiracy to teach a false theory?” But let’s save those questions for later.

Human Genome History

The Human Genome Project was controversial, but not for the reasons you might expect.

Of course, there were people who objected on religious grounds, saying that the structure of DNA is a secret only God should know, and could lead to terrible consequences if the information fell into the wrong hands. Since the professional journals tend not to be too concerned about religion, they didn’t address that issue—and neither will we. So few people seriously considered the moral implications in the professional scientific literature that it didn’t really rise to the level of controversy there.

The first controversy in the scientific literature was the controversy over whether it would be possible to fully decode the human genome.

The "job" is to map the chromosomes within 5 years and to decipher the full nucleotide sequence, all 3 billion base pairs, within 15 years—and at a total cost of no more than $3 billion. "If we go along the way NIH usually does, it could easily take 100 years to get the sequence," said Watson, who outlined NIH’s plans in San Diego last week at the Human Genome 1 meeting sponsored by Science. ¹

In 1989, Watson thought it was unrealistic to get the job done by 2004, and thought it might take until 2089 to do it. In fact, the job was essentially finished in 2001 for far less money. We know that now—but he didn’t at the time. So his concern was valid, and the controversy over whether it was technically possible was legitimate.

But there was another controversy centered around something called ‘Big Science’ in the professional literature (although the following quote doesn’t happen to use that term).

Nevertheless, it has been the idea of obtaining a complete readout of the sequence—all 3 billion bases of it—that unquestionably fueled the excitement. The gargantuan scale and cost of such an operation, which might consume 30,000 man-years of effort and $3 billion only seemed to make the prospect yet more exciting.

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James Watson told the NIH gathering that although he had qualified support for the proposal, "everyone else at Cold Spring Harbor was against it." These people are young, he explained. "They are scared that if sequencing

goes ahead there will be fewer funds available for their research." With a megaproject sucking up $3 billion, there is a real and valid fear that funds will be diverted from existing research.²

In 1986, young geneticists realized that only the most experienced scientists were likely to be assigned to the project, so they might lose their funding. Scientists working in fields other than genetics feared that research funding for other subjects might be reprogrammed to support the Human Genome Project.

**Money**

A dearly departed friend of mine, James L. Rieger, once told me the difference between a scientist and an engineer. I never forgot it.

When a scientist makes a great discovery, the first thing he thinks is, “Where can I publish it?”

When an engineer makes a great discovery, the first thing he thinks is, “How can I make a buck with it?”

It is generally believed that engineers are motivated by greed—but scientists are noble individuals motivated by the search for truth. That may have been true in 19th century Europe, when science was the hobby of wealthy men who financed their own research, and gathered in snobbish royal societies to discuss their discoveries. Those days of self-supporting science are gone. Today's science is financed by huge government grants, and there is cutthroat competition to get those grants.

We now know it did not take the feared 100 years to decode the human genome. In fact, it didn't even take the estimated 15 years. The job was done three years early, and under budget because private industry brought competition into play. Here is how it happened.

The recent announcement by Perkin-Elmer of a new, fully automated sequencer (ABI PRISM 3700) permits a reevaluation of strategies for completing the human genome sequence. This instrument is a capillary-based sequencer that can process about 1000 samples per day with minimal hands-on operator time (about 15 min compared with about 8 hours for the same number of samples on ABI PRISM 377s). This reduction in operating labor, coupled with automation of sample purification and sequencing chemistry enabled by the sequencer's improved detection sensitivity, suggests that the tens of millions of sequencing reactions necessary to complete the human genome can be performed more quickly and at lower cost than previously anticipated. The Institute for Genomic Research (TIGR) and Perkin-Elmer have started a program to complete this task within 3 years using this new technology and a whole-genome shotgun strategy that obviates the need for a sequence-ready map before sequencing. We intend to form a new company to carry out this venture and develop a commercial business based on these efforts. The cost of the project is estimated to be between $200 million and $250 million, including the complete computational and laboratory infrastructure to develop the finished sequence and informatics tools to support access to it.

In fact, they did form this new company, and it sparked even more competition.

Many scientists were skeptical last May [1998] when DNA sequencer J. Craig Venter and his private backer—the Perkin-Elmer Corp. of Norwalk, Connecticut—said they were going to decode the entire human genome in just 3 years. At the time, the government-funded Human Genome Project wasn't due to deliver the goods until 2005. To some academics and government genome sequencers, Venter's pace seemed too fast to be credible. Then, in August, Incyte Pharmaceuticals Inc. of Palo Alto, California, joined the race. It said it was going after the entire human genome too, aiming to get just the genes in 2 years. Now, faced with growing private competition, the skeptics of rapid sequencing have become believers. In a radical change of plan, the chiefs of the U.S. genome project announced this week that they intend to match the private sector's pace and deliver comparable results just as fast.

The U.S. National Human Genome Research Institute (NHGRI) unveiled a 5-year plan this week that promises to produce a “working draft” of the human genome—including highly accurate sequences of most of the protein-coding regions—by 2001. The plan also promises to yield a polished, gold-standard version of the entire genome by 2003, 2 years ahead of the old schedule. If successful, this scheme will not only speed up the pace at government-funded labs but also, according to

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some of NHGRI's advisers, release data so rapidly that companies such as Perkin-Elmer and Incyte may not be able to get exclusive rights to all the DNA they hoped to patent. 4

Two private (profit-motivated) companies competed to get the job done, and the government tried to keep them from making a profit doing it. How noble of the government! ☺

Eventually, the race ended in a tie, sort of.

Beaming at each other, longtime rivals Francis Collins and J. Craig Venter shook hands in the East Room of the White House on 26 June [2000] as they declared joint victory—and announced an implicit truce—in their race to decipher the “book of life.” … What's more, the two former adversaries, who until recently have minced no words disparaging the other's work, said they hope to publish their work simultaneously in a peer-reviewed journal sometime this fall (see p. 2294).

This very public and very carefully orchestrated denouement—which required diplomatic skills akin to those behind the Camp David Peace Accord—brings to an end one of the most high-profile fights in recent biology, one that pitted a publicly funded consortium of scientists, led by Collins, against Venter's upstart company, Celera Genomics of Rockville, Maryland. With obvious relief, Collins and Venter agreed to forgo the barbs and share the credit for a biological tour de force that many scientists thought was impossible a mere 15 years ago. 5

This scientific advancement was made possible because private industry realized one way money could be made is by selling patented machines that decode DNA. Since then, many scientists have bought these machines and used them to decode the DNA of other living things. New genomes are published in the professional literature every few weeks now.

**Patented Human DNA**

The other financial motive was the possibility of patenting some parts of the human genome. That might shock, scare, and confuse you.


Don't worry. You won't be tested to see if your DNA contains a patented sequence, and have to pay royalties just to stay alive. They aren't going to insert patented DNA sequences into embryos to make super babies to sell on the open market.

There is an ethical and reasonable way to make money from patented DNA. One can not only patent a thing—one can also patent a process to make things.

Living things have natural defenses against disease. Their DNA manufactures chemical substances which fight infections. If one knows what DNA sequence produces the natural antibiotic against a particular disease, one can use that DNA in a laboratory to make that antibiotic, and convert it to a pill or liquid which can be sold for a profit. The profitable process of using a particular DNA sequence to produce a particular medicine can be patented (unless the government chooses not to grant the patent).

In the past, biotech company scientists looking to develop new therapies for human diseases had to start with a protein already known to be a key player in the disorder, insulin in diabetes, say, or human growth factor in dwarfism. They would then clone the corresponding gene, and with it manufacture the protein to use in therapy. Now, HGS and other companies are mining large databases of human gene sequences, looking for previously unknown proteins that might have therapeutic value. Once promising genes are identified—often by their structural similarity to known molecules—company scientists screen the genes' protein products in cells and animals for medically useful effects. 6

So this is really no different from the standard pharmaceutical practice of analyzing the chemicals in traditional herbal remedies and synthesizing the same chemicals to put into pills. The process of using DNA sequences to produce the needed proteins is patentable.

**Questions Answered**

With this background, we can finally answer the questions we posed at the beginning of this essay. “If science is against the theory of evolution, why do so many academics defend it?” and “Is there really a conspiracy to teach a false theory?”

The answer to both questions is, “Big Science.” There’s no Vast Left Wing Conspiracy

coordinated by some shadowy figure, telling all the professors what to say. College professors are smart enough to know that they need funding, and need to be in the club to be respected and successful, and independently know what they need to teach to get that funding and stay in the club. It’s not a conspiracy—it’s just economics. Scientists have to get paid, and have to pay for their expensive equipment. To do that, you either have to produce a product or sell a story.

**Not Rocket Science**

Paleontology isn’t rocket science. In rocket science, sooner or later, you have to actually build the rocket. An eloquent presentation about how the rocket will work might convince sponsors to finance the project regardless of whether or not the theory is correct; but laws of nature aren’t swayed by a silver tongue. If the theory is wrong, the rocket won’t fly, no matter how convincing the argument, or how prestigious the alma mater of the presenter.

Paleontology can’t be put to the test. A fossil tooth may look like the teeth of other creatures; but that doesn’t really prove anything. A believable story isn’t necessarily true.

Paleontologists don’t produce a product, so they have to produce a story. New versions of the theory of evolution are produced all the time because nobody pays for the same story a second time. This month’s *Evolution in the News* column is a perfect example.

**Not Just Religion**

Yes, there is a religious component to the Theory of Evolution, too, which is well recognized. The Theory of Evolution is the creation myth of atheism. That can be a motivating factor for a particular scientist.

But if you are the head of a research department of a large university, the responsibility of paying the salaries of everyone in your department is a more compelling motivator. You need to come up with a story about a new possible human ancestor, or life on Mars, to get funding for your research. Furthermore, you need to protect your turf, as this month’s *Evolution in the News* column shows as well. You need to be the acknowledged leader in the field so that you get the grant—not your competitor.

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**Evolution in the News**

**Homo Naledi**

Homo naledi tells us more about paleontologists than evolution.

In this month’s feature article we tried to show that, in general, “Big Science” drives scientific research. In this column, we will give you a specific current example.

It was hard to miss all the publicity about *Homo naledi*, the new “human ancestor” discovered in South Africa. It was the subject of a Nova TV program, and on the cover of this month’s *National Geographic* magazine. In case you missed it (as hard as that is to believe) here’s our short version of the story.

Steven Tucker and Rick Hunter were exploring the Rising Star cave 30 miles northwest of Johannesburg, South Africa. They are both very skinny and managed to get through a very small passage, entering a chamber filled with bones. They took some photos and contacted Lee Berger, a paleoanthropologist who had previously asked cavers to keep an eye out for fossils.

Berger is famous for his previous discovery of *Australopithecus sediba*. *National Geographic* says this about that discovery:

Berger decided the skeletons were a new species of *australopithecine*, which he named *Australopithecus sediba*. But he also claimed they were “the Rosetta stone” to the origins of *Homo*. Though the doyens of paleoanthropology credited him with a “jaw-dropping” find, most dismissed his interpretation of it. *A. sediba* was too young, too weird, and not in the right place to be ancestral to *Homo*: It wasn’t one of us. In another sense, neither was Berger. Since then, prominent researchers have published papers on early *Homo* that didn’t even mention him or his find.

We must note in passing how fleeting fame is—but more important than that, note that Berger “wasn’t one of us.” Academic prejudice is fierce, as we have already stated, and as you will soon see again.

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7 Nova, 16 November 2015, S42|E13 “Dawn of Humanity”
9 *ibid*. page 39
Berger hired a bunch of skinny people to go back into the cave and get the bones out. There turned out to be lots of bones!

There were some 1,550 specimens in all, representing at least 15 individuals. Skulls. Jaws. Ribs. Dozens of teeth. A nearly complete foot. A hand, virtually every bone intact, arranged as in life. Minuscule bones of the inner ear. Elderly adults. Juveniles. Infants, identified by their thimble-size vertebrae. Parts of the skeletons looked astonishingly modern. But others were just as astonishingly primitive—in some cases, even more apelike than the australopithecines. “We’ve found a most remarkable creature,” Berger said. His grin went nearly to his ears.

That’s a lot of fossils! But how do you make a buck with them? You could sell them, but you probably couldn’t get that much for them. You can get lots more money by selling the story.

He was paid by National Geographic, and we assume also from the Public Broadcasting System for the Nova program. National Geographic and PBS in turn made money by telling Berger’s story.

PBS is a taxpayer-funded, nonprofit corporation. But it costs lots of money to produce TV programs. They have to pay their employees every month. They need to produce stories which keep the government and the private sponsors happy. Nova keeps the money flowing.

National Geographic tried to sell magazines by printing “A NEW ANCESTOR SHAKES UP OUR FAMILY TREE” on the cover. A common refrain on the Nova program was, “We now know …” that something else previously believed about human evolution was wrong. PBS and National Geographic were telling a new and different story about human evolution. New stories sell better than old ones.

Despite the sensational claim on the cover of their magazine, the National Geographic article ended with these words:

When a major new find is made in human evolution—or even a minor new find—it’s common to claim it overturns all previous notions of our ancestry. Perhaps having learned from past mistakes, Berger doesn’t make such assertions for Homo naledi—at least not yet, with its place in time uncertain. He doesn’t claim he has found the earliest Homo, or that his fossils return the title of “Cradle of Humankind” from East to South Africa. The fossils do suggest, however, that both regions, and everywhere in between, may harbor clues to a story that is more complicated than the metaphor “human family tree” would suggest.

“What naledi says to me is that you may think the record is complete enough to make up stories, and it’s not,” said Stony Brook’s Fred Grine. Maybe early species of Homo emerged in South Africa and then moved up to East Africa. “Or maybe it’s the other way around.”

Berger himself thinks the right metaphor for human evolution, instead of a tree branching from a single root, is a braided stream: a river that divides into channels, only to merge again downstream. Similarly, the various hominin types that inhabited the landscapes of Africa must at some point have diverged from a common ancestor. But then farther down the river of time they may have coalesced again, so that we, at the river’s mouth, carry in us today a bit of East Africa, a bit of South Africa, and a whole lot of history we have no notion of whatsoever. Because one thing is for sure: If we learned about a completely new form of hominin only because a couple of cavers were skinny enough to fit through a crack in a well-explored South African cave, we really don’t have a clue what else might be out there.

Yes, they really don’t have a clue—but at least they have a story they can sell! And, as a bonus, they have set the stage for a sequel! The sequel will be “a story that is more complicated than the metaphor ‘human family tree’ would suggest.” Watch for it to appear in a magazine stand soon near you!

**Peer Reaction**

Let’s face it. National Geographic and Nova are nothing more than science tabloids. The only difference is that one is sold in grocery stores, and the other invades your home through your TV. They are just science gossip mongers. What do the real science journals say?

You might be surprised to learn that Science and Nature both paid very little attention to this truly remarkable discovery of such a large cache of undisturbed fossils. We believe this is because the fossils weren’t discovered by someone named Leakey, Johanson, or Tattersall. Berger isn’t a member of the club, so nothing he found can be of any importance (in their eyes).

Furthermore, the excavation was done by a bunch of skinny amateurs found on Facebook! That really angered the establishment paleontologists so much that they were reluctant to give Berger the credit he is due. Science began their review by saying,

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10 ibid. page 42
11 ibid. page 56
From the moment in 2013 when paleoanthropologist Lee Berger posted a plea on Facebook, Twitter, and LinkedIn for “tiny and small, specialised cavers and spelunkers with excellent archaeological, palaeontological and excavation skills,” some experts began grumbling that the excavation of a mysterious hominin in the Rising Star Cave in South Africa was more of a media circus than a serious scientific expedition. 12

Science didn’t like the way Berger assembled his team by using social media! How could anyone take anything produced by this media circus seriously?

Nature, in an article with “Crowdsourcing” (but not Naledi) in the title, said,

John Hawks, a palaeoanthropologist at the University of Wisconsin–Madison who helped to coordinate the Rising Star dig and workshop, says that the team took flak for its unorthodox approach. “There’s a lot of the field that really believed we’re just a couple of cowboys who don’t know how things should be done,” he says. 13

Both journals were rather dismissive of the find, saying that they don’t mean anything without accurate dating.

We say no other Homo or Australopithecus has a more complete set of fossils. Naledi certainly is the most significant fossil find of the 21st century. These fossils tell us more about the physical characteristics of Homo naledi than Homo habilis or Homo erectus or Homo anything-else-except-sapiens.

But knowing what it looked like, or when it lived, doesn’t tell us anything about its ancestry. So, it doesn’t prove anything about human evolution. It merely gives evolutionists another character for their fairy tale.

What it does prove is how snobbish and close-minded the establishment paleontologists are. If you aren’t in the club, your discoveries don’t matter, no matter what they are.

Here is a diagram of Her Majesty’s family tree which we found on-line.  

Here is the caffeine cladogram from last month’s newsletter, rotated 90 degrees to make it easier for you to compare it to the Royal Family.

**No More Hints**

We have teased you long enough, hoping you will figure out for yourself why cladograms do not produce correct relationships. Here’s the proof.

Cladograms, like the one showing the relationship between coffee, tea, and cacao, are produced by a computer program. The way to test a computer program is to input data where the correct answer is known ahead of time to see if the program produces the correct output.

For example, to test a missile simulation program one has to fire a missile, track it with a radar, and use telemetry to send the missile’s guidance commands back to a ground station where they are recorded. Then the recorded guidance commands are used as the inputs to the missile simulation program to see what trajectory comes out. If the simulated trajectory doesn’t match the trajectory measured by the radar, then the simulation is wrong.

If you fed the genetic data from all the members of Britain’s Royal Family into the computer program used to produce the cladogram of plants above, it would not produce the correct family tree.

How can we be sure the program would not produce a correct genealogy for the British Royal Family? Because the algorithm is obviously flawed. The way the program is written, Queen Elizabeth would have to be the sister or cousin of Prince George, which is obviously incorrect.

How do we know that? The algorithm is clearly written using the false assumption that all living individuals are brothers, sisters, or cousins, and all their parents, grandparents, aunts, and uncles are deceased, unknown ancestors. There is no way the program could correctly tell us that Queen Elizabeth is the matriarch of the Royal Family because the algorithm is designed in such a way that it can’t produce the correct output no matter what the input is.

The program would compare the DNA of the 28 members of the Royal Family and determine which two members match most closely (using matching criteria which might not even be correct). It would then produce a mythical ancestor with a blend of the characteristics of the two closest matches. Then the program would repeat the process, comparing the 26 remaining living members plus the newly created mythical ancestor (a total of 27 individuals) to see which are the most similar, producing another mythical ancestor. The program would continue to loop through the ever decreasing data set, creating mythical ancestors of the two most similar individuals (real or imagined) until all the pairs have been established. The output would then be printed in the standard cladogram shape, not the unique shape of the Royal Family Tree.

Our hint last month was, “B2 has descendents D1, D2, and D3.” The cladogram program is written in such a way that the unknown ancestor always has two direct descendents. Queen Elizabeth has four direct descendents. That alone is proof the cladogram program can’t possibly produce a correct relationship tree for the Royal

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15 [http://www.britroyals.com/royalfamily.htm](http://www.britroyals.com/royalfamily.htm)
The thing to remember about computers is that they don't have any common sense. They just blindly perform the calculations, doing what they are told to do. It would never occur to a computer that some of the living individuals are parents or grandparents, or that a couple might have some number of children other than two. If the programmer told the computer that none of the data came from an ancestor, all the ancestors are unknown, and that all the unknown ancestors had exactly two children, the computer doesn't question that prejudicial assumption. It just fits the data into the structure assumed to be correct by the programmer using "optimal parsimony."

Since the cladogram program doesn't produce the correct answer when we know what the correct answer is, why should we believe it produces the correct answer when we don't know what the correct answer is?

**Deep Green**

The Deep Green project used genetic data to produce a cladogram that "rewrote" the evolutionary history of flowering plants.

For plant taxonomists, the new data strike a blow to the foundation of their discipline ... because many plants presumed by their appearance to be closely related—such as the water lily and the lotus—are in fact quite different genetically. ... Moreover, Mishler says, the brown, red, and green plants each arose independently from a common single-celled ancestor and thus deserve their own kingdoms. Overall, he claims, at least half the [accepted] Linnaean classifications are wrong.

Since the cladogram didn't produce the accepted answer, other evolutionists said,

In response to the article "Deep Green rewrites evolutionary history of plants" by Kathryn S. Brown ... The new cladistic analyses of plant evolutionary relationships deserve to be reported, but it is vital that all realize that every cladogram is a hypothesis and, perhaps more important, that such hypotheses depend on both the algorithm used to generate the hypotheses ... and on the character matrix used as the basis of the analysis ... . The character matrices are themselves evolving rapidly and are affected by additions of new characters, such as new gene sequences, and by the selection and definition of morphological-structural characters. Thus, the phylogeny presented as the basis for a radical shift in our understanding of green plant relationships is a transitory hypothesis that likely will be replaced by other different hypotheses.

**Binary Evolution**

You were probably taught a simplified, incorrect story about how evolution occurs. Most people were taught that a new species arises when one breeding pair had a mutant offspring that was more suited for survival. The descendants of that mutant offspring (that is, the new species) thrived, driving the normal offspring (the old species) to extinction. Creationists try to debunk this oversimplified, incorrect explanation of evolution by saying, "If man evolved from monkeys, why are there still monkeys?" The evolutionists turn this false argument back on the creationists by saying that creationists don't really understand how evolution works.

Humans did not evolve from monkeys. Humans are more closely related to modern apes than to monkeys, but we didn't evolve from apes, either. Humans share a common ancestor with modern African apes, like gorillas and chimpanzees. Scientists believe this common ancestor existed 5 to 8 million years ago. Shortly thereafter, the species diverged into two separate lineages. One of these lineages ultimately evolved into gorillas and chimps, and the other evolved into early human ancestors called hominids.

How do evolutionists come to this conclusion? Obviously, if the new species drives the old species to extinction immediately, then the number of different living species can't increase. That is, the old species is simply replaced by new species, so the number of living species would remain the same. Evolutionists need to explain how the first living species evolved into the innumerable species living today.

Evolutionists are forced to believe that the new species doesn't drive the old species to extinction immediately. The old species has to hang around long enough to beget another new species, too, and then the old species goes extinct.

**References**


18 http://www.pbs.org/wgbh/evolution/library/faq/cat02.html
But why couldn’t the old species, like Queen Elizabeth (begging Your pardon, Your Majesty) have four descendants? Why just two descendants? Or, why can’t the old species have Elizabethan longevity and still be living today, along with multiple descendents?

The answer to these questions goes back to gene dilution and Darwin’s basic assumption of survival of the fittest, which is equivalent to extinction of the less fit.

**Gene Dilution**

If the new species isn’t sufficiently better to drive the old species to extinction, the novel mutation will rapidly disappear from the gene pool because of gene dilution.

The first parent with the mutant gene (mutant allele, for the nit-pickers) has only a 50-50 chance of passing that mutant gene to its child because half of a child’s genes come from the normal parent, and the other half come from the mutant parent. Therefore, only half of the children in the first generation are capable of passing the gene along. Statistically, only half of their children will get the new gene, so 1/4 of the second generation will have the mutant gene, and 1/8 of the third generation will have it—unless natural selection biases the percentages.

If the new gene doesn’t provide a sufficient survival advantage, the odds are that after several generations a very small percentage of the population will have the gene. That, coupled with the fact that more creatures are born than reach reproductive age, makes it statistically likely that all the individuals with the new gene will sooner or later be eliminated from the population.

On the other hand, if the new gene provides a great survival advantage, all the individuals without the gene will quickly go extinct.

For the Theory of Evolution to work, the mutation has to fall into the Goldilocks Zone, where the mutation has enough survival advantage to drive the original species to extinction, but doesn’t cause the original species to go extinct before mutating into a second time, and doesn’t drive that second mutation to extinction either. (The second mutation has to fall in the Goldilocks Zone, too.)

That’s why the cladogram algorithm is based on the assumption that each species mutates twice before going extinct.

(We are just telling you what the assumption is and why that assumption is made. Don’t ask us to defend the evolutionary assumption! ☺)

Cladograms produce nice, neat, impressive-looking evolutionary relationships—but the results are often nonsense! The independent evolution of caffeine and results of Deep Green are just two examples in this month’s newsletter. Last month, the genetic analysis of the octopus genome was another example. The octopus geneome brings us to this month’s second Email column.

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**Email**

**Remodeling the Octopus**

*Can one remodel something that doesn’t exist?*

Jeffery had this interesting comment on last month’s *Evolution in the News*.

From the Octopus Evolution section of the latest newsletter:

"Our analysis suggests that substantial expansion of a handful of gene families, along with extensive remodeling [Jeff’s emphasis] of genome linkage and repetitive content, played a critical role in the evolution of cephalopod morphological innovations, including their large and complex nervous systems."

My question to the evolutionists would be, "If something is being, or has been REModeled, doesn’t it require it first be modeled? Especially since, as you say "their large and complex [Jeff’s emphasis] nervous systems." Isn’t that basically the same as design? Don’t all models require that first they be designed?

Apparently, they weren’t constantly keeping in mind that all living things have only the appearance [Jeff’s emphasis] of design. :-)

Evolutionists assume that everything evolved from something else. Therefore, its genome had to be the result of some change to a previous genome. Some part of the genome had to be duplicated, or deleted, or switched around somehow, or inherited from some other creature. It’s just the way they think. It never seems to occur to them to ask where the genome they are remodeling came from. It’s like the old joke about the woman who said, “It’s turtles all the way down!”

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19 https://en.wikipedia.org/wiki/Turtles_all_the_way_down
Dr. Ben Carson’s
Creation vs. Evolution Video
https://www.youtube.com/watch?v=YPqq6fr2CF4

Creation the Signature of God

This month’s web site review looks at a video found on YouTube where Dr. Ben Carson presents his views regarding the theory of evolution. This video comes from a presentation he made in 2011. Since he is currently running for President of the United States, his views on various topics have been in the news and have attracted a lot of attention.

Dr. Carson covers many of the hot topics of the creation vs. evolution debate in this video. Not surprisingly, this brain surgeon chose to entitle his remarks “The Frontal Lobe.” Throughout his talk he stresses the fact that the human brain really is a wonder of creation.

In his beginning remarks, Dr. Carson talks about his experience of being invited to be the commencement speaker at Emory University. Some biology professors objected to this because they knew he did not believe in evolution and started a petition complaining about Dr. Carson’s views of creation. He then tells how difficult it is for anyone in academia to advance to higher positions because of the bias of the politically correct belief that creation and belief in God should not be taught in schools and universities.

Next Dr. Carson talks about some of his experiences debating with evolutionists and atheists about creation and faith and science. As is often the case, when creation arguments cannot be refuted then evolutionists resort to name calling.

The fossil record, missing links, dating methods, Darwin’s theory of natural selection and the Big Bang theory are all discussed in the video.

While watching the video on your computer, you will find links to additional videos found on YouTube that cover the material discussed by Dr. Carson.

At the end of the presentation, when Dr. Carson answers some questions from the audience, you learn that he is planning on writing a book called The Organ of Species (in contrast to Darwin’s The Origin of Species) which will describe the organs of the human body and how they refute evolution. He plans on making this book easy to read and not too technical for people to understand.