The Age of Things: Sticks Stones and the Universe
Fifth Lecture Notes
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4/24/2004

Potassium, Argon, DNA and Walking Upright

Thus far, we have considered events in human history or prehistory. Now we will go further back in time to when our ancestors first began to walk upright on two legs. Based on a combination of data from radioactive isotopes and molecular biology, it appears that fossils found in the last few years could be from the first animals to adopt this mode of locomotion.

1 The Hominids

Our peculiar form of bipedalism is one of the few traits that are unique to humans. Not even our closest living relatives, the great apes (chimpanzees, gorillas and orangutans), can walk about exactly in this way. Therefore, to find the origin of this trait, we must consult the fossils of those animals that are more closely related to us than to any other living animal. This group of animals is here called the **hominids**, but one should be aware that there is not universal agreement on the name of this group (some people call them hominines, for example).

The first hominids appeared after the ancestors of modern humans separated from the ancestors of the chimpanzees (By definition, hominids cannot exist before this). These early hominids should not have many uniquely human characteristics. However, over time, the hominids which are our direct ancestors acquired those traits which set us apart, and thus appeared more human-like with time (Of course, there were also other hominids, which acquired different traits but which left no descendants alive today). For example, preserved hominids have a range of brain sizes, earlier ones have brain sizes comparable to modern chimpanzees, while some (but not all) more recent ones have brains that are larger, all the way up to the sizes found modern humans.

This record of how hominid brain size changed over time provides a basis for exploring the mechanisms and processes responsible for these transformations. No similar record documents how our ancestors adopted an upright posture and full-time bipedalism. In all hominids with sufficient preservation, the spine, pelvis and legs already show modifications for walking on two legs in a nearly human-like way. Since even the hominids with roughly chimpanzee-sized brains had these traits (see figure 1), bipedal locomotion must have occurred before brain size increased. Bipedalism may even have been the first trait that hominids acquired after they diverged from the ancestors of chimpanzees. It is therefore for good reason that anthropologists are very interested in finding out exactly where, when and how bipedalism was first acquired by the hominids.

Thus far, no fossils have yet been found that clearly document the transition between classic human-like bipedalism and some other (probably arboreal) mode of locomotion. However, many expect that such fossils are going to be found very soon. This is because information in the DNA of humans and other apes provides a means to

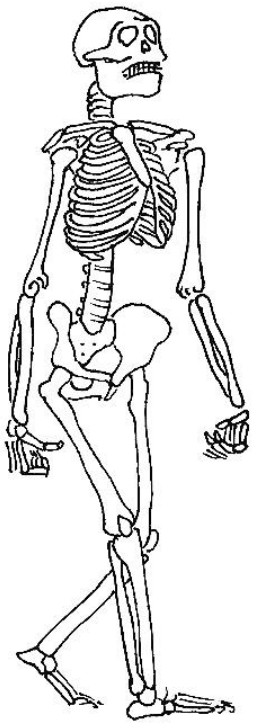


Figure 1: A reconstruction of the skeleton of the3-4 million year old hominid *Australopithecus afarensis*(redrawn from Conroy's *Reconstructing Human Origins*). This animal had a brain size comparable to modern chimpanzees, but already has features in its legs, pelvis and spine that indicate it could walk upright on two legs.

estimate when hominids began to walk upright, and fossils are now being discovered from the relevant time period.

2 Measuring the age of hominid fossils with rocks

The new fossils are older than any previously known hominid. The ages of these fossils are based on a radiometric technique using an unstable nucleus, like Carbon-14. In this case, the nucleus is Potassium-40, and it comes not from the sky, but from the earth.

2.1 Dating volcanic rocks with the Potassium-Argon method

Potassium-40 is an unstable variant of the element Potassium which has 19 protons and 21 neutrons (see figure 2). Like Carbon-14 it usually undergoes **beta decay**, in which a neutron converts into a proton, to form a nucleus of Calcium-40, with 20 protons and 20 neutrons. However, 10% of the time Potassium-40 decays in a somewhat different way; the nucleus captures an electron, and one of the protons converts into a neutron. This process produces Argon-40, with 18 protons and 22 neutrons. The production of Argon is what makes Potassium-40 so useful as a method

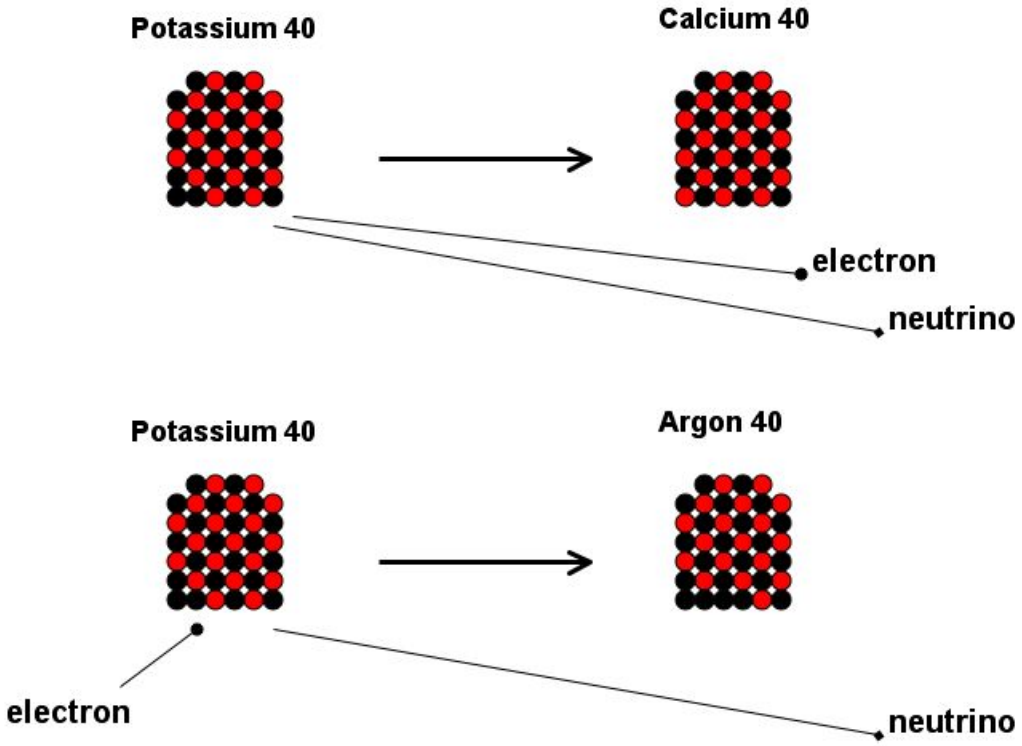


Figure 2: Potassium-40 can decay in two ways. 90% of the time it undergoes beta decay like Carbon-14, and a neutron (black circle) converts into a proton (red circle) to form Calcium-40. 10% of the time the nucleus captures an electron, a proton converts into a neutron, and the nucleus converts into Argon-40.

of measuring age, and is why it is usually called the **Potassium-Argon** (or K-Ar) method.

As with any other unstable nucleus, the amount of Potassium-40 in a sample decreases with time in a regular way with a well-defined half-life. The half-life of Potassium-40 is 1.25 billion years. Since it is so long-lived, Potassium-40 can be used to date objects that are much older than the time-range where Carbon-14 methods usually work. Indeed, the Potassium-40 found in the earth has been around since the earth formed 4.5 billion years ago.

As usual with a radiometric dating method, we calculate the age of the sample based on the fraction of the original amount of Potassium-40 that is still in the object. To compute this fraction, we need to know how much Potassium-40 the object has now and how much it had originally. The beauty of the Potassium-Argon system is that it allows us to measure both the current **and the original** Potassium-40 content of volcanic rocks.

The molten rocks produced by a volcano can possess Potassium and Calcium but they do not possess any Argon. Argon is what is called a noble gas. It does not chemically bond with other atoms to form compounds, and so it will diffuse

through the liquid rock and escape into the air. Therefore, when the volcanic rock first solidified it is (ideally) Argon-free.

On the other hand, the newly solid rock does in general contain some amount of Potassium-40. As time goes on, some of the Potassium-40 decays into Argon-40. These Argon atoms cannot escape because the other atoms in the rock are locked into rigid crystal structures and the Argon atom cannot fit through the spaces between them. Argon-40 therefore begins to accumulate in the rock over time.

Say we have a volcanic rock and we find it contains 10 grams of Potassium-40 and 1 gram of Argon-40. Then 1 gram of Potassium-40 must have converted into Argon since the time the rock solidified. Since only 10% of the Potassium-40 atoms decay into Argon-40, we know a total of 10 grams of Potassium-40 have decayed in the rock. Thus the rock must have originally contained 20 grams of Potassium-40, of which 10 grams remain today. Therefore, one-half of the Potassium-40 atoms have decayed since the rock solidified, and the rock is one Potassium-40 half-life, or about 1 billion years, old.

(Note that even though the Calcium-40 content of the rock also increases over time, it is not as useful for measuring the age of the rock. Calcium does react chemically with other elements and does not escape from the molten rock, so the initial Calcium-40 content of a rock is not in general zero.)

Since we can deduce the original Potassium-40 content of the rock directly from the materials in the rock, and do not need to estimate it based on other sources of information, the Potassium-Argon system provides a somewhat "cleaner" age measurement than the Carbon-14 system. Nevertheless, there are still complications that must be kept in mind. For example, the rock could retain some "old" Argon-40 if it was not completely melted, in which case the derived age will be systematically off. We cannot deal with these issues in detail here, nor can we explore the practical aspects of obtaining Potassium-Argon dates, since we must see how we can use this method to measure the age of hominid fossils.

2.2 Volcanoes and fossils in East Africa

Potassium-Argon dating measures the age since molten volcanic rocks first solidified. Since bones do not last long in a lava flow, fossils are not usually found directly associated with such rocks. However, hominid fossils and volcanic rocks are found in associations that allow the age of the hominid remains to be be accurately measured, thanks to a geological feature called the East Africa Rift System.

The East African Rift System is a place where the earth's crust is being pulled apart. Since the rock of the earth's crust is brittle and cannot stretch, it fractures into blocks which slip past each other, forming a long series of valleys and depressions from Eritrea to Mozambique (see figure 3). Water pools into the bottom of these depressions, forming lakes, which attracts a variety of animals. Sediments also accumulate in the depressions, carried in by water or wind. These sediments can bury the remains of organisms and preserve them as fossils. The geological activity in and around the rift also produces volcanoes. Thus ash-falls and lava flows also cover various parts of this area. The rift system depressions are therefore filled with a mix of sedimentary and volcanic deposits.

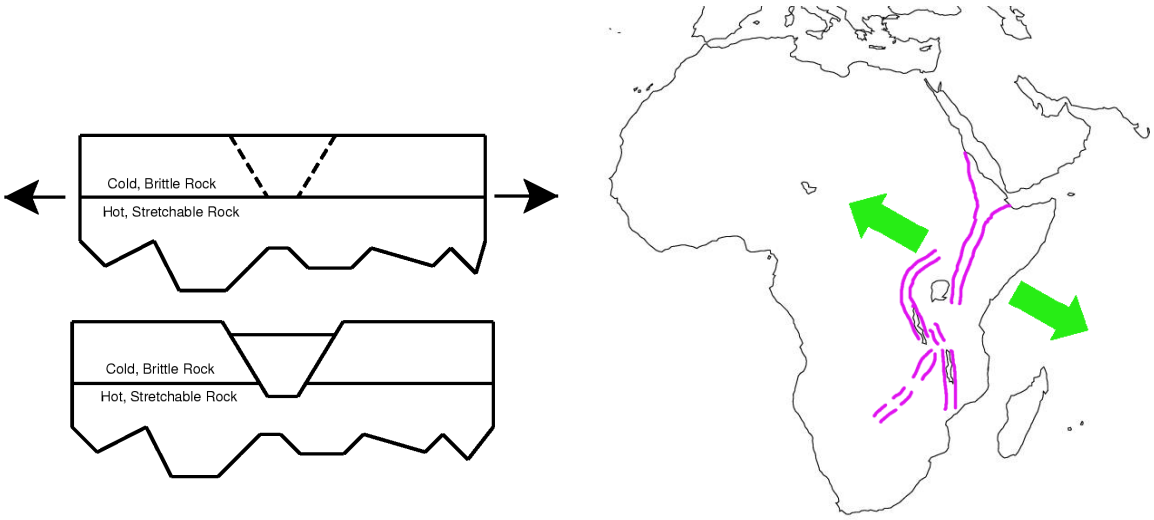


Figure 3: The East African Rift System. On the left we show a cartoon cross section of a rift system. The crust is being pulled apart. The lower layer stretches, but the upper layer breaks and a wedge slips down to form a depression. The right shows the East African Rift System itself, with the depression indicated by purple lines. The green arrows indicate the forces that acted on the crust of Africa to form these features.

In particular, the rift system contains fossil-bearing layers of sedimentary rock sandwiched between layers of volcanic rocks. The fossil-bearing layer must be younger than the volcanic deposit it sits on and older than the volcanic rocks on top of it, so dating the volcanic layers with the Potassium-Argon system provides tight constraints on age of the fossil-bearing layers as well. The age of the hominid remains from the East African Rift System are therefore well-established. Even hominids found outside East Africa benefit from the rift system age measurements, since they indicate when various animals that were found throughout Africa lived. When these animals are found at other locations, they can then be used to estimate the age of associated hominid remains (This is how some new hominid remains from Chad have been dated).

Until recently, all known hominid remains were from deposits less than about 4 million years old. However, in the last few years, several new hominid fossils have been found that date back to around 6 million years ago (see figure 4). Although these remains are fragmentary, they have generated a lot of excitement. Not only are these the oldest hominids yet discovered, but they also come from the time when molecular dating methods suggest hominids first acquired the ability to walk upright.

3 Estimating the age of bipedalism with molecules

Molecular dating techniques are a product of the relatively recent advances in molecular biology. The basic idea is that certain changes in our DNA occur at a fixed (or at least known) rate, and by comparing the DNA of various organisms, we can estimate when various things happened to their ancestors.

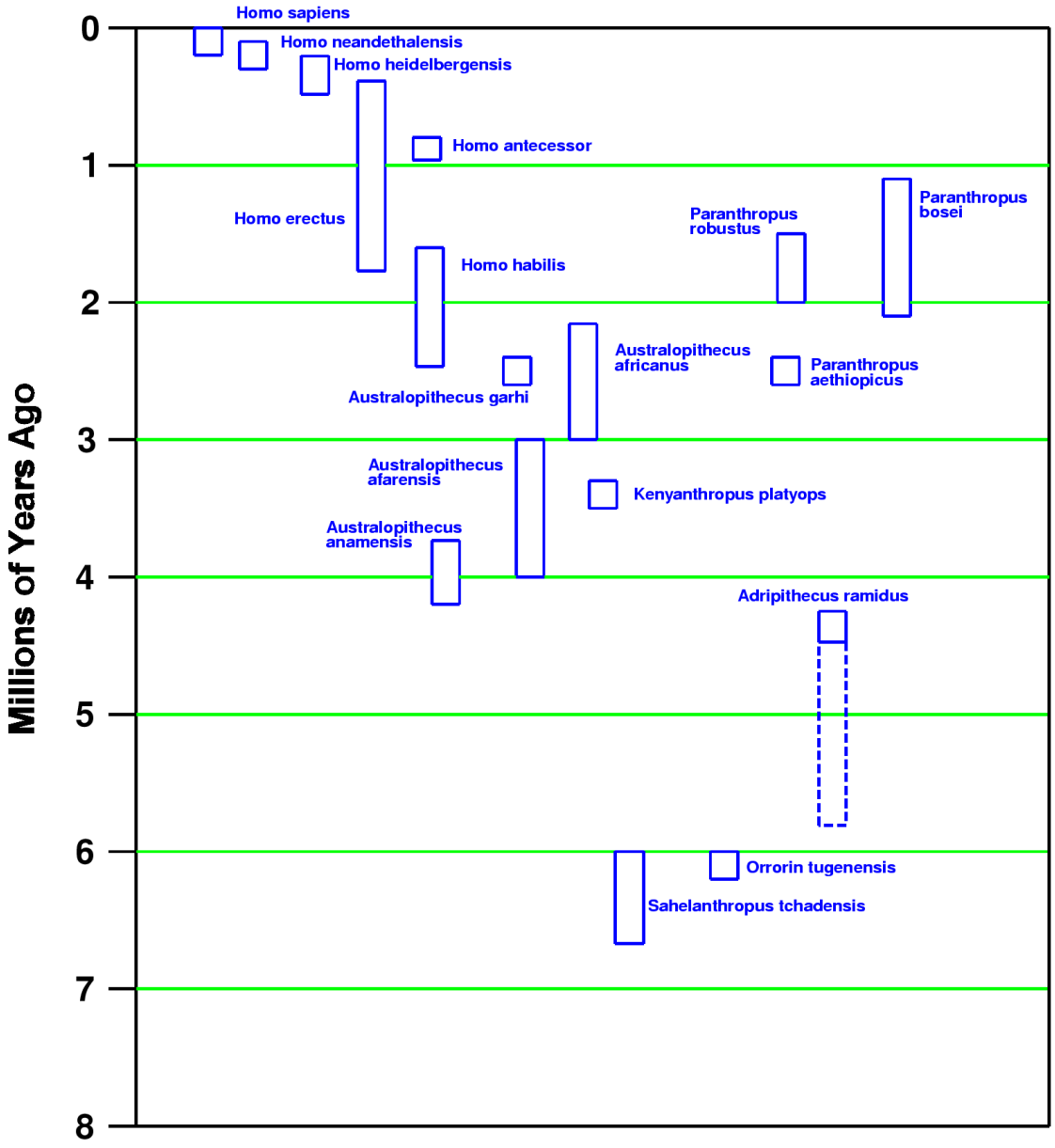


Figure 4: Dates of various different types of Hominids, based on a figure by Bernard Wood in *Nature* Vol 418 (2002), page 134. Bars indicate the range of time the various types of hominids probably lived. The recently discovered hominids *Adripithecus, Orrorin, and Sahelanthropus* are significantly older than the previously known hominids, and probably come from the time when the ancestors of humans first began to walk upright.

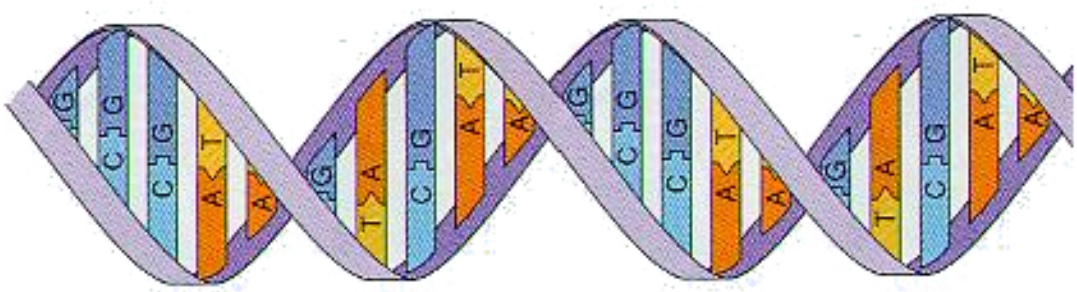


Figure 5: A diagram of a DNA molecule. The famous double helix consists of two strands, connected by a series of base pairs formed by two nucleotides, which are marked with the letters A, T , C and G.

3.1 DNA and the diversity of life

DNA, or deoxyribonucleic acid, are large molecules found in (nearly) every cell of every organism and contain the instructions which indicate how the cells should work and interact in order to produce a functional creature. These ladder-like molecules consist of two spiral strands connected together by a sequence of **base pairs**, which are made up of two **nucleotides**, one attached on each strand (see figure 5). There are four different nucleotides found in DNA: Adenine, Thymine, Cytosine and Guanine, which are usually represented by the letters A, T, C and G, respectively. An A on one strand always pairs with a T on the other and C always pairs with G, so the two strands complement each other. It is the sequence of nucleotides along the strands that encodes information (These sequences are often depicted as a string of letters corresponding to the nucleotides on one strand, such as ACTTGCT). For example, various parts of the sequence provide instructions for making different proteins, while other parts determine the circumstances when these proteins should be made.

The DNA in any organism is inherited from its parents and passed on to its offspring. Over the generations this DNA changes or **mutates** in various ways, either due to errors in transmission or to damage to the molecules themselves. These mutations can change how the cells of the organism function and also alter the characteristics of the organism. Over time, these changes can accumulate such that two descendants of a single organism eventually appear very different. Indeed all of the various forms of life on earth can be understood as the descendants of a single organism, with the diversity of life today being the result of huge numbers of mutations over billions of years.

3.2 Measuring relationships with DNA

Since mutations accumulate over many generations, two organisms which share a recent common ancestor should not have had the time to accumulate as many differences as two organisms with a more ancient ancestor. Thus, one can attempt to work out the kinship relations between various creatures based on how many traits they have in common. The resulting "family history" of these creatures can then provide insight into the patterns and processes behind the variations found in the organisms.

It is possible and often useful to use the physical characteristics of the organisms

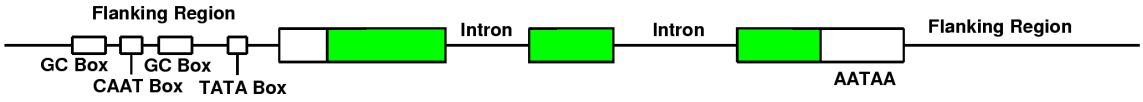


Figure 6: The general structure of a gene, a piece of DNA that contains instructions for making a protein (Based on a figure in Li's *Molecular Genetics*). Only the green (gray) shaded regions contain the information for making the protein. In between these regions are the introns that are ignored when the protein is made. There are also flanking regions, which contain various characteristic sequences that allow the machinery in the cell to identify where the useful information is located.

as a basis for evaluating the relationships between them. However, when possible, using the DNA sequences of the creatures has distinct advantages. For one, changes in the DNA sequence are much easier to quantify than changes in physical traits. For example, it is not obvious if bipedal locomotion in humans should be considered one "trait", or several separate modifications to the spine, pelvis and legs. One the other hand, any change in the DNA can be reckoned as the addition, removal, movement or replacement of a countable number of base-pairs.

Furthermore, changes in the physical characteristics of an organism are often constrained by complex interactions environment. For example, if a mutation caused an rabbit to have a white coat instead of a dark coat, then what happens to that rabbit and its offspring depends on where they live. If the rabbit lived in a forest, it would probably be killed and eaten by predators and few or none of its offspring would survive. However, if it lived in the arctic, it would do quite well and may contribute more offspring to the next generation than we might otherwise expect. While these interactions with the environment are very interesting, they indicate that the changes which are passed on through the generations occur at different rates in different situations. This will also be true for the mutations in the DNA sequence which are responsible for the changes the physical characteristics of the organism. However, there are DNA mutations which have no impact on the creature's structure or function. We expect that these mutations will exhibit a more regular behavior in time and space.

3.3 "Silent" Mutations and the passage of time

Even though we still do not know all of the information encoded in the DNA, we do know that there are many parts of the DNA sequence that do not appear to encode any useful information. These regions can be identified because for a segment of DNA to be useful, it must have certain recognizable characteristics.

For example, a **gene** is a piece of DNA that contains instructions for making a particular protein (or ribonucleic acid), which performs some specified function in the cell. In order for the cellular machinery to "read" the instructions and make the protein, it must know where on the DNA to look. Every gene is therefore surrounded **flanking regions**, which contain certain characteristic nucleotide sequences like CAAT and TATA that indicate where the useful information is located (see figure 6). Using these sequences, the DNA that is informative for making proteins can be identified.

In humans and other animals, only a small fraction of the DNA contains information for making proteins. While some portion of the remaining DNA certainly has some function (for example, certain DNA sequences may regulate when various genes are read), a large amount of this material can be altered without have any noticeable affect on the cell or the organism. In fact, some of this DNA can be identified as "broken genes", that is, genes with various alterations to them and their flanking regions which makes these DNA sequences impossible to read, and thus prevents them from having any useful function.

In addition to the various non-coding regions between the genes, there are segments of DNA within the genes themselves that do not provide information about the nature of the final protein (these are the introns shown in figure 6). Even the informative regions of the genes contain redundancies that allow certain transformations to occur without altering the resulting protein. Therefore, there is a lot of DNA that can mutate without having any impact on the health or appearance of the organism.

Mutations in this "excess" DNA have no impact on how the organism interacts with its environment, so the probability that the mutation gets passed on is unaffected by the specific circumstances of where and how the creature lived. Therefore, the rate at which these mutations accumulate over the generations is determined entirely by how often the mutations themselves occur. Since the molecular machinery responsible for copying and repairing DNA is almost identical in all animals, we may hope that the mutation rate will be the same for all animals, and the accumulated number of mutations can be used to estimate the passage of time.

4 Patterns in the mutations of humans and apes

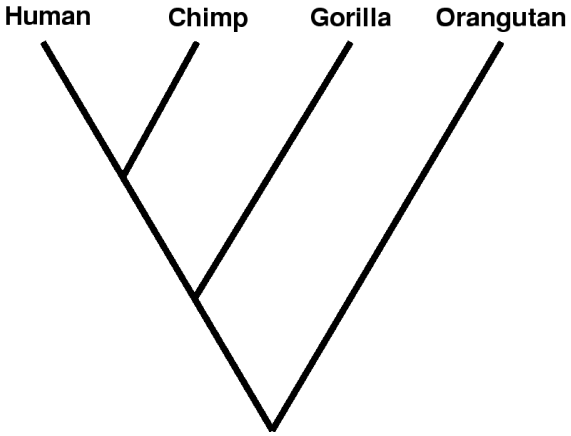
The DNA of humans and other primates have been studied for many years in order to determine if the mutation rate in non-coding regions could really be a constant in time. Recently, Feng-Chi Chen and Wen-Hsiung Li have produced a very nice paper on this subject (see the reference section for the details on the paper).

These researchers took DNA from a human, a chimpanzee, a gorilla, and an orangutan, and they obtained the sequences of 53 non-coding regions, with a total of 24,234 base-pairs. They then looked for a specific type of mutation which are called point substitution mutations. These are mutations where a single base-pair is replaced with another base-pair, for example when the sequence ACTG changes into ACCG. These sorts of changes are very easy to quantify. For any pair of animals, we can calculate the fraction of nucleotides are the different in the two sequences. The results of these measurements are given in the following table:

	Chimp	Gorilla	Orangutan
Human	1.24%	1.62%	3.08%
Chimp		1.63%	3.12%
Gorilla			3.09%

Thus, for example, the Human and Chimpanzee sequences have different nucleotides in 1.24% of the 24,234 positions. The differences beteween these animals are rather small indeed.

We can use these data to deduce the relationships between these animals. Recall that animals with a more recent common ancestor will have less time to accumulate distinct mutations. Since the human and the chimpanzee have the smallest number of differences, these two animals must have the most recent common ancestor. The gorilla has less differences from humans or chimps than the orangutan, therefore the gorilla has a more recent common ancestor with chimps and humans than the orangutan does. All this suggest the following family tree for these animals.



With this chart, we can now see whether these animals have been accumulating mutations at the same rate. The tree clearly shows that the ancestors of the human, chimpanzee and gorilla all have had the same amount of time to accumulate mutations that distinguish them from the orangutan. If these animals all accumulated mutations at the same rate, they should have the same percentage differences between them and the orangutan. Indeed all three animals have about a 3.1% difference from the orangutan. Furthermore, the chimps and humans both are about 1.6% different from the gorilla, which is also consistent with these two animals accumulating the mutations at the same rate. Therefore, in these primates at least, it does appear that these animals have all been accumulating mutations at a single, consistent rate.

4.1 So, when did hominids begin to walk upright?

Given that the mutation rates in the great apes do exhibit a certain regularity, we can now estimate when our ancestors first began to walk upright. Since humans walk upright but chimpanzees and other primates do not, our ancestors must have acquired this ability something after they diverged from the ancestors of the chimpanzees. If we can estimate when this divergence occurred, we can know that bipedalism developed more recently than this.

There is no way yet to calculate from first principles the amount of time it would take to accumulate the 1.24% difference in the DNA sequences between humans and chimpanzees. However, since this difference is two-fifths of the 3.1% difference between the orangutan and any of the other apes, we can estimate that the divergence of the human and chimpanzee lines is two-fifths as old as the divergence of the orangutans from the other apes.

Fortunately, there is evidence of the timing of the divergence of orangutans based on fossil and geological data. A fossil animal named *Sivapithecus* shares several

striking facial characteristics with the orangutan, which suggests that *Sivapithecus* is closely related to the unique ancestors of orangutans (the other apes do not have these features). Since *Sivapithecus* fossils are found in deposits dated to about 12 million years ago, this means the orangutan divergence must be more than 12 million years old. Another fossil animal named *Proconsul*, on the other hand, has features which are shared by all of the great apes (for example, it lacks a tail), but it has no features which are unique to any particular one of the living apes. Thus, this creature probably existed before any of the living apes' lines diverged from one another. Since this creature is found in deposits from 20 million years ago, the orangutan divergence should not be more than 20 million years old. Therefore, the ancestors of the orangutans probably first diverged from the ancestors of the other apes about 16 million years ago (give or take a few million years).

If the orangutan line diverged about 16 million years ago, then our ancestors diverged from the ancestors of chimpanzees about $2/5 * 16$, or about 6.5 million years ago. Other people have used similar methods to calculate the probable age of this split, using other fossils to convert DNA differences into real years, and have obtained basic the same result. The molecular evidence therefore does appear to indicate that hominids appeared (as distinct from the ancestors of the chimpanzees) around 6 or 7 million years ago, and acquired the ability to walk upright relatively soon after this (hominids were already bipedal 4.5 million years ago). Now that hominids have finally been found from this time period, we should soon be able to see if these estimates are correct. If they are, then additional, more complete specimens should document how our ancestors began to walk upright. If they do not, then we will have to re-evaluate our relationships with the other apes. In either case, the near future of this subject should be very interesting.

For these primates, the analysis of the DNA differences is relatively straightforward. The divergences between the animals considered are small and so is the number of animals involved. Next time, we will discuss a more complicated situation with more animals, larger differences between the DNA sequences, and mutation rates that probably vary from animal to animal. Specifically, we will consider when and how mammals diversified during the end of the age of Dinosaurs.

5 References

For information on Human evolution at a popular level, try

- Ian Tattersal and Jeffrey Schwartz *Extinct Humans* (Westview Press 2000)

For more details, try

- Glenn C Conroy *Reconstructing Human origins* (W.W. Norton 1997)

And for an overview of the recent discoveries, see the news article on page 133 of the journal *Nature* Volume 418 (2002).

For Potassium Argon Dating, see the relevant chapter in

- Taylor and Aitken *Chronometric Dating in Archaeology* (Plenum Press 1997)

A nice treatment can also be found in

- Brian J Skinner and Stephen C Porter *The Dynamic Earth, 2nd Ed* (John Wiley and Sons, 1992).

For the basics of genetics, a good place to start is

- Larry Gonick and Mark Wheeler *The Cartoon Guide to Genetics* (Perennial Press, 1991)

Some books on reconstructing relationships from genetic data at the college level, see

- Wen-Hsiung Li *Molecular Evolution* (Sinauer 1997)
- M Nei and S Kumar *Molecular Evolution and Phylogenetics* (Oxford U Press 2000)

For the details of the genetic analysis cited in this talk, see Chen and Li "Genomic Divergences between Humans and Other Hominids...." in the *American Journal of Human Genetics* Vol 68 (2001) pp 444-456.