Patterns of Intelligence

Chapter 18

Patterns Of Intelligence

Before shifting gears, it might help to take a break from terminology and graphically see why randomness cannot have created the DNA of any species, much less all species. Later on we will do actual mathematical calculations which will be far more convincing. But for now, let's look at some bar charts.

A "histogram" is a bar chart that demonstrates how frequently something is found, such as in a document.

For example, if we made a "histogram" of how many times the different letters of the alphabet can be found in the individual words in a book in the English language, we would see one bar for each of the 26 letters of the alphabet.

For example, the word "quote" has the letters 'q', 'u', 'o', 't' and 'e' in it.

The height of one bar, for each letter, would represent how many times the letter was found in all of the words in the book. For example, we would count how many times the letter 'q' was found in all the words in the book, including the word "quote," for example. The taller the bar the more times the letter was found in the book.

To interpret the bar chart, as an example, if the bar for the letter 'a' was much taller than the bar representing the letter 'q' (which we would expect) then we would immediately know that the letter 'a' occurred far more often than the letter 'q' in the words in the book.

This kind of bar chart is called a "histogram."

Let us look at some examples of histograms to demonstrate the difference between intelligence and randomness.

For example, let us look at some of the "bits" of the compiled or object code of an actual computer program. A 'bit' is a 0 or 1. The compiled code or executable code of a computer program consists of nothing but '0's and '1's.

To see what I am talking about let us list a small segment of the compiled code of a computer program and then place a space between every 8 bits. This is a small section of the compiled code (I added spaces to make it easier to read):

```
01111101 00001110 00000100 00000010 00011111 00110111 ...
```

Note the first group of eight "bits": **01111101**. What if we went through the entire computer program and counted how many times the "**01111101**" sequence appeared? We could represent this count as the height of a bar on a histogram.

In fact, there are 256 possible ways that 8 "bits" (i.e. unique sequences of eight '0's and '1's) can be written. Each unique sequence is called a "permutation."

The 256 possible permutations are:

```
00000000 (the number 0 in binary)
00000001 (the number 1 in binary)
00000010 (the number 2 in binary)
00000011 (the number 3 in binary)
00000100 (the number 4 in binary)
... (to represent 5 through 253)
11111110 (the number 254 in binary)
11111111 (the number 255 in binary)
```

Let us count how many times each of these permutations occurs in a real computer program. What would this chart look like?

On the next page is an example of a histogram of a computer program written by Microsoft programmers. This histogram is of the compiled code of an old version of Microsoft Word®, where each bar represents how many times each of the 256 permutation of 8 '0's and '1's appears:
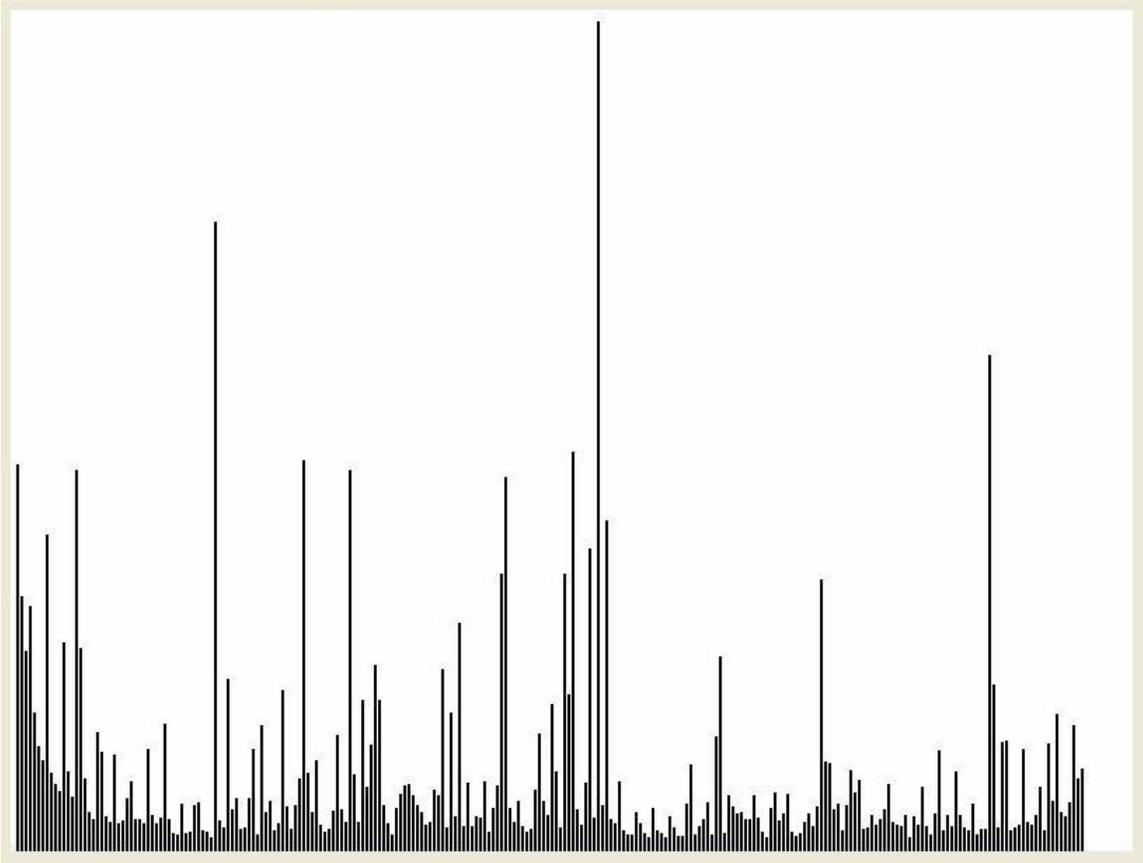
The endpoints of the histogram, 00000000 and 11111111, are not shown because they are so tall they would distort the height of all of the other bars and make the chart difficult to read.

Note the variety of bar sizes in the above chart. Some bars are very, very short and others are very tall. It looks somewhat like a mountain range. This is a sign that it was written by **intelligent** people (I have a son who works for Microsoft so I better add that the people at Microsoft are very intelligent). Note also that every possible permutation is represented by a bar (i.e. there are no empty slots where there was no permutation found).

Another Example of a Histogram

Let us look at another histogram of a document written by human beings. In this case it is a book called "War and Peace" by Leo Tolstoy.

It is too complicated to explain how I converted a book into a bar chart, because it was a multi-step process, but let's look at the bar chart anyway:
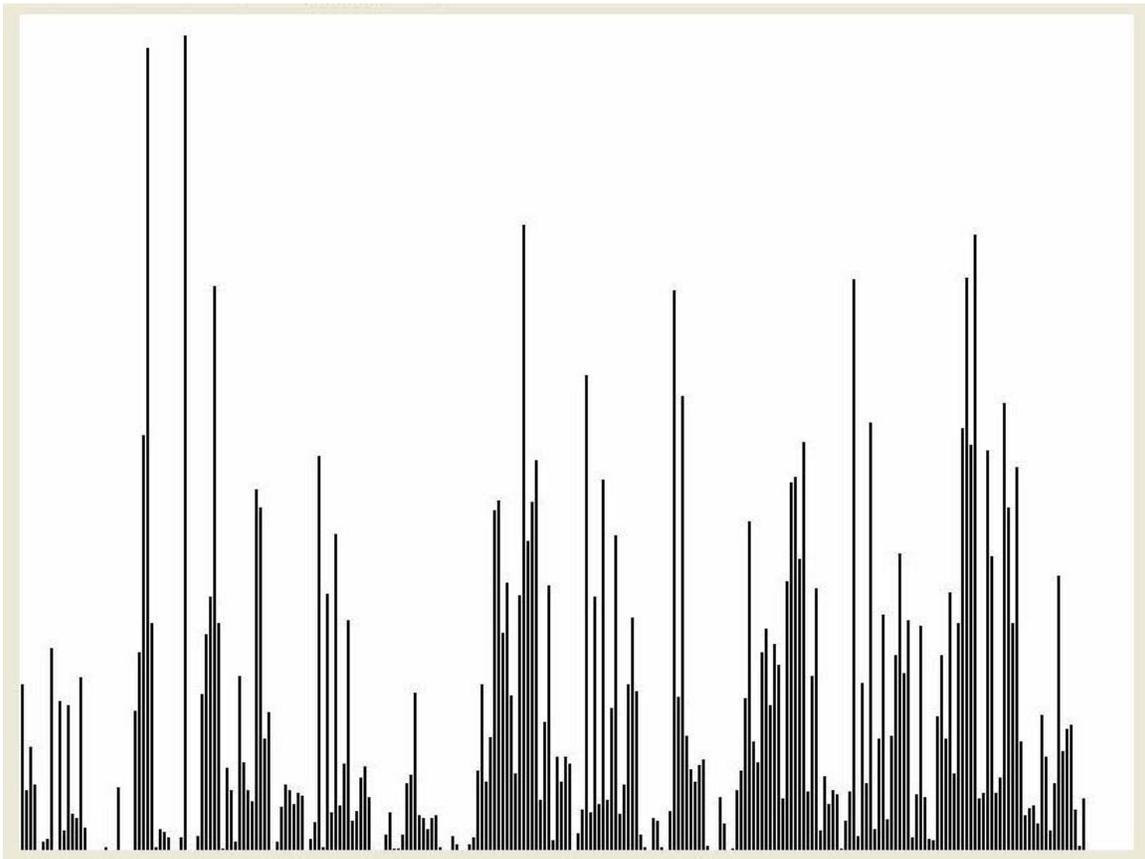
This looks significantly different than the computer program, but again you see the tall mountains and small valleys. In this case you also see some empty spaces where there is no bar, meaning there were no examples of some permutations of punctuation, letters and numbers. This makes sense if you think about it (e.g. think about how many times you would see the sequence of letters: ZZAB or MNNC in a history book).

A Histogram From Mother Nature

Now let us look at a bar chart taken from a section of actual human DNA. Let us see if Mother Nature is smart!! Because there are four different kinds of nucleotides (A, C, G, and T) on DNA, we need to group them together before we count them.

Human DNA consists of about 3.2 billion "rungs" or pairs of nucleotides. A "rung" will simply be referred to as a "nucleotide" because we only care about the nucleotide on one side of the rung.

On a DNA strand, a "quad" will be defined to be four consecutive nucleotides. Thus, ACCG, TTAC, GGGG, AGGT, etc. are possible "quads."

For example, to generate the next chart, let us look at this actual sequence of human DNA taken from the sample:

GTGCCCCACAACACCCCTGTGGGTAAGAATGTCACTCATTTCAT

One way to analyze it would be to break up this string into the following "quads":

GTGC CCCA CAAC ACCC CTGT GGGT AAGA ATGT CACT CATT TCAT

There are other ways to count "quads," but this is the easiest way to explain.

As the computer program goes through looking at the DNA, it counts how many times it finds the "GTGC" quad and how many times it finds the "CCCA" quad, and so on.

Once the final counts are accumulated, the counts are represented by the height of a vertical line, meaning we will create a histogram. For example, one of the vertical lines below represents how many times the computer program found "GTGC."

There are 256 possible ways to represent four consecutive nucleotides so there will be 256 bars in the chart. In the chart on the next page, for each possible quad there is a vertical line (a "bar"). The height of this line is the result of how many times each quad can be found when analyzing real human DNA.

The chart below is a histogram created by analyzing more than 11,000,000 consecutive quads of actual human DNA taken from chromosome 5. This means more than 44,000,000 **real human nucleotides** were analyzed and are represented in this graph:
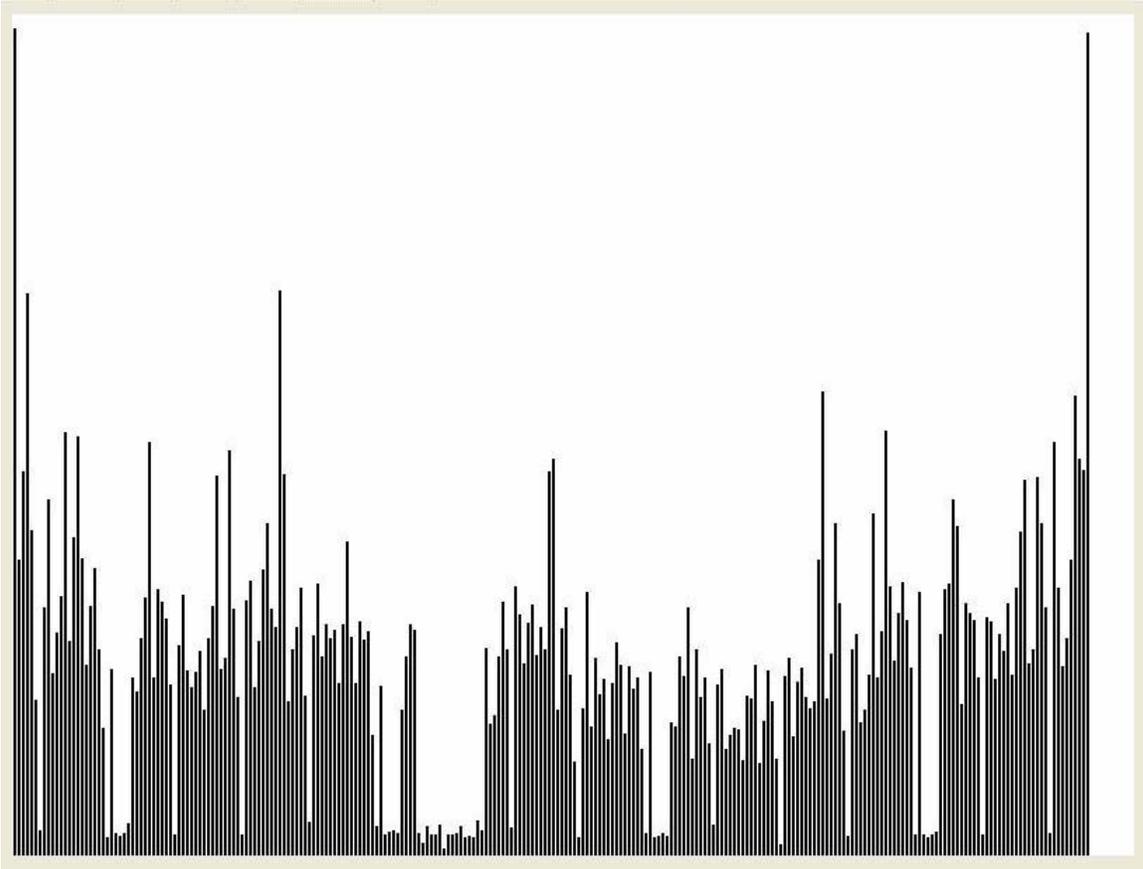
I want to emphasize that this is not a bar chart of the entire DNA, it is only a bar chart from a section of chromosome 5. My computer is not powerful enough to deal with a complete human DNA strand.

Note that in this bar chart, of actual human DNA, you also see tall bars and short bars. It also looks like a mountain range. Note that there are no empty slots.

The endpoints (AAAA and TTTT) are shown and are the most common quads and are about equal in height.

This bar chart looks very different than the bar chart of the computer program above. While it is true that human DNA does contain some "computer programs" or more correctly: "algorithms," the algorithms, genes, etc. on human DNA are doing something much different, and much, much more sophisticated, than any computer program ever written by human beings!!

Notice that this histogram also looks like a mountain range with many very deep valleys and many very tall peaks. One difference in this bar chart is that many more of the bars have a near "average" height.

The third highest quad is ATTT which occurs 117,256 times. The smallest quad, the very small bar slightly to the left of center, is CGCG which occurs only 1,565 times (out of the more than 11,000,000 quads which were analyzed).

See if you can find the four tall bars which have very, very short bars on both sides of them, meaning they stick-out like a "sore thumb." This is a very interesting phenomenon and is a **very, very strong indication of intelligent design**.

See if you can find the eleven very short bars which are surrounded by multiple tall bars on both sides. This is also an interesting phenomenon and is also a **very, very strong indication of intelligent design**.

For those who understand this terminology:
Average Size of Bar: 40,233.76
Standard Deviation: 25,505.06
Standard Deviation as percent of Average Size: 63.39%

The term "standard deviation" is a way to measure how much variety there is in the height of the bars. A perfectly flat bar chart, where the height of every bar was the same, would have a "standard deviation" of zero (i.e. 0.00).

The number I want to emphasize is 63.39%, which is the ratio of the "standard deviation" as a percentage of "average size." Even without seeing the bar chart itself, a statistician, knowing only the 63.39%, would know that there was a lot of variety in the bar heights.

SIMULATING EVOLUTION

What if we tried to simulate evolution? What would a bar chart look like if the DNA were randomly generated by a computer (i.e. to represent evolution)? In other words, suppose we used a random number generator to represent evolution (instead of using Mother Nature) to generate a segment of DNA the same size as the above chart? What would that histogram look like?

Well, on the next page we will see:
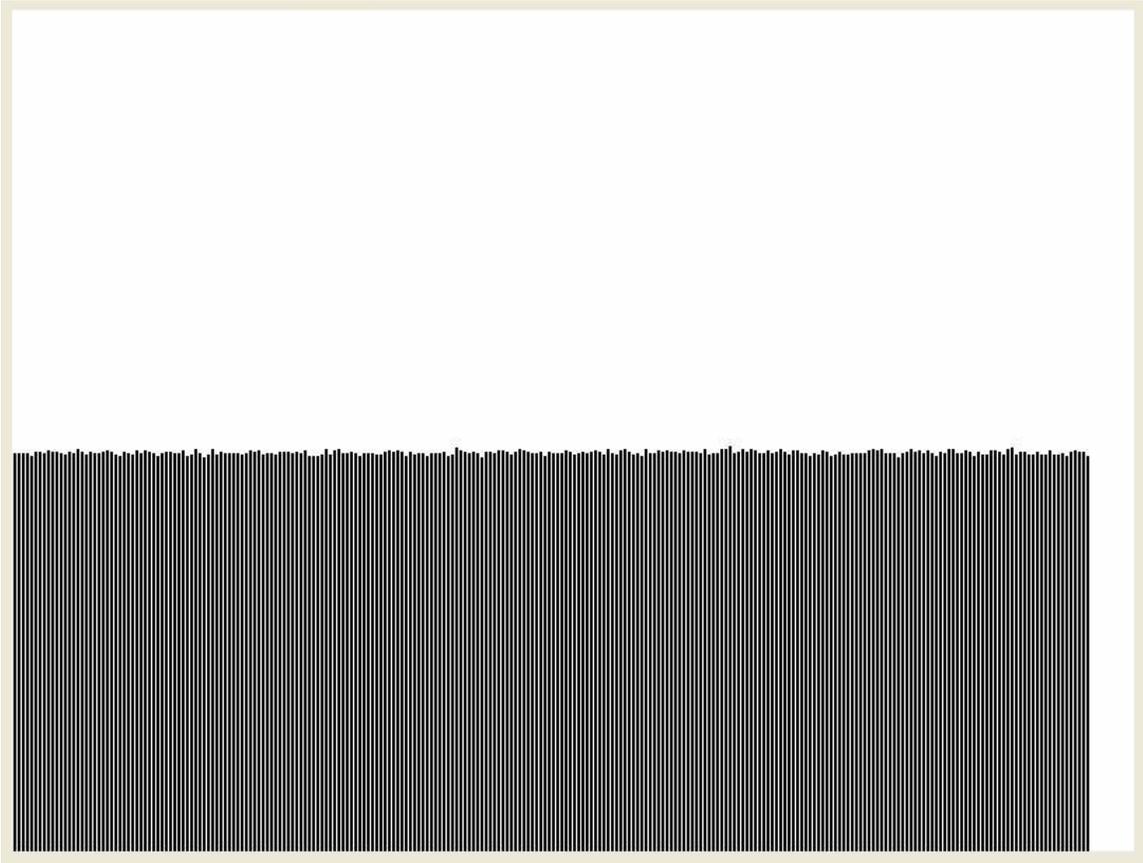
Notice that this histogram is flatter than a pancake - **literally**!! It is even flatter than the state of Kansas, which itself is flatter than a pancake!! There is nothing even remotely resembling a valley or a mountain peak. The standard deviation looks like it should be zero!! It almost is (as a percent of the average size).

For those who understand this terminology:
Average Size of Bar: 40,233.76 (same as above, by design)
Standard Deviation: 204.06
Standard Deviation as percent of Average Size: *0.51%*

Note that the standard deviation as a percentage of average size is only 0.51%. Compare this to the 63.39% from actual DNA!!!! That is an indication of how flat the chart is!!

There is literally more than 100 times more variety in real DNA than in computer simulated DNA (based on the ratio of standard deviation to average size)!! You can also see this just by looking at the charts.

But there are other problems in using randomness. Here is a breakdown of the percentage of times the four different types of nucleotides are found in the real DNA sample:

A = 30.74%
C = 19.28%
G = 19.24%
T = 30.74%

Here are the percentages using randomly generated nucleotides:

A = 24.999%
C = 25.019%
G = 24.996%
T = 24.986%

All four of these numbers are almost exactly 25.000%. This is exactly what you would expect from a random number generator.

My point is that this ratio is not going to create intelligent human DNA.

But even the vast differences in the above bar charts totally fail to demonstrate just how massively different real human DNA is compared to randomly generated DNA!!

The reason is that the difference between the above bar charts does not even begin to remotely demonstrate the vast, vast, vast difference in the intelligence built into human DNA (e.g. the morphing of the embryo, to be discussed later) versus the mindless nonsense of the randomly generated DNA!!

Try to learn something from a book which was entirely written by a random letter and space generator!! Try to hop in an airplane (and fly away) which was designed by randomly generated architecture drawings!!

It is possible to play with the assumptions above and make randomly generated bar charts that look like mountain ranges and which have high standard deviations, but doing this will *not* solve the intelligence issue. It won't create a functional computer program, for example.

Nor will it have the massive differences between bars which are right next to each other, like we saw with the real DNA.

Randomness can never generate intelligence no matter what assumptions you make and no matter what your bar chart looks like.