INFORMATION, INTELLIGENCE & NETWORKS

Intracellular communications
For cells to be functional, the following nonmaterial entities are required:

- **A language** is required for any communications to occur as cells contain senders & receivers for communicating.
- **There are communication networks** just as we have for our telephone, television, and internet networks.
- **Without meaningful information it would be impossible for the cell to function.** This information, sent through the communication networks, is translated into a language that both the senders and receivers recognize.
- **An addressing system:**
  - The cellular system contains a ‘post office’ addressing arrangement for delivering information and materials. Kinesins, shown later in a video, are complex proteins that ‘walk’ along microtubules physically carrying packages to predetermined locations.

As all of these are nonmaterial entities they could not have been produced through materialistic evolution. Intelligence was required to produce this interrelated system, as random occurrences could not possibly produce them even given an astronomical amount of time.

And to rule out any possibility of random occurrence, they are **mutually defining** so that all of them must have arisen simultaneously!

DNA and protein
The material parts of the equation for life in our bodies are the DNA data storage devices in each cell, which have the capacity of 30 billion letters of information, and the protein, machines within the cells that do the physical work. Communication networks are systems for conveying meaningful data in a recognized language to the protein machines, just as two humans must know the same language to properly communicate.

In our approximately 100 trillion cells each nuclei contains 23 pair of chromosomes composed of DNA.¹

- DNA, in the form of a double helix, comprises chromosomes. The two outer ‘backbones’ must be comprised of all ‘right-handed’², chiral (ky-ral) sugar molecules.
- These molecules occur in equal numbers of ‘right-handed’
and ‘left-handed’ in nature, so fabricating the backbone by the random chance occurrence of billions of all ‘right-handed’ molecules appearing in nature would not be possible.

- To further rule out chance occurrence, the proteins in our bodies are actually machines composed of 400 to 30,000 amino acids. They will only function if formed using all ‘left-handed’ amino acids. There are about 500 amino acids in nature, but only 20 specific amino acids that make up the proteins in life.
  - They must all be in the exact right order.
  - Each section of protein coding DNA (a gene) has the ability to code for many different proteins.
  - Any given section of each genome can be doing multiple tasks simultaneously using overlapping codes.
  - This reveals that the genome is optimized to near perfection. Overlapping codes are nearly impossible to improve upon, as attempts to improve one of them will disrupt or destroy one or more of the others.
  - Random chance modifications and natural selection cannot achieve optimization in a highly complex organism. It would require an astronomical number of extremely rare beneficial mutations, plus a likewise astronomical number of trials and errors to achieve.

3-D micro-biological protein machines

DNA holds the instructions for building proteins, (3-dimensional micro-biological protein machines) in our body. Making them requires enzymes, which are themselves proteins, and proteins such as RNA polymerase (paˈlimərəs) and the ribosome (ribəˈsōm) described below, etc. are needed to fabricate all these. There are over 100,000 unique types, including ATP synthase (sinˈθās). These and many/most others are composed of multiple protein units. So, the bio-molecular ‘hardware’ required for life is actually a cascading order of irreducibly complex machines. (For simplification we call them proteins from now on.) Some important proteins are:

- ATP synthase: a rotary motor-generator that produces the ‘currency’ (nourishment) to sustain cells (the image at the right). In our mitochondria are hundreds of trillions of these motors.
- RNA polymerase: copies a section of the DNA’s genetic code (a gene). It must separate the double helix bonds, start and stop copying at exactly the right letter on the DNA, and produce a perfect error checked coded strand.
- Ribosome: processes the coded strand to produce the protein prescribed by its data (the image at the right).

A protein contains from about 400 to 30,000 (the protein titin in muscles) amino acids. All must be in the exact right order, and ‘left-hand’ orientated for the protein to function. Based on these molecular dictates, hardly one of the more than 100,000 protein types needed for life could have arisen by chance random mutations, let alone all; and thousands would have been simultaneously required for even the first simplest life form, a cell. Many even produce toxins if they are fabricated incorrectly.

DNA Instability

As DNA carries the entire code for the construction and functioning of an organism, it must remain free of inadvertent changes. However, it is quite unstable. If ‘unrepaired’ no organism would survive its embryo stage as an estimated one million breaks per day occur in the DNA within each cell.2 With about 100 trillion cells in our bodies, each cell has to repair about $10^{14} \times 10^6$ breaks or, $100,000,000,000,000,000,000,000$ breaks per day. Therefore in each cell an assemblage of proteins (enzymes) is required to work continuously to keep the DNA in tact.

This is a real, ‘chicken-and-egg’ challenge for the evolution model. DNA needs a huge compliment of these repair enzymes to be maintained as each repairs a different type of damage. They are coded
in the DNA, yet the DNA in the chromosomes requires them. They would be severely affected by DNA changes, and mutations are often catastrophic. Therefore, as evolution takes millions of years, and life cannot exist without them, how could they have originated by the process of mutations over time?

Information: fundamental to intra-cellular life

The problem is not just stored data, but also communication networks interfacing with machinery. Within the cell are proteins that divide cells, reproduce chromosomes, read the code on a section of DNA (a gene), and fabricate proteins that the code describes. In these operations, multiple information systems direct elaborate machines (proteins) to accomplish these and thousands of other tasks.

**Replication of chromosomes (DNA) (Image on right)**

- Proteins called RNA polymerases open both strands of the DNA helix by breaking the hydrogen bonds.
- One moves along each strand, duplicating it by adding letters (bases) to complete the open bases of the original ‘parent’, thus forming two ‘daughters’.
- Transfer RNA (tRNA) molecules are instructed to bring the exact bases needed at each location at the rate of about 1000 per second.
- A major complication is that the upper (lagging) strand is the reverse of the bottom, and cannot add bases directly. Okazaki fragments must be built up and inserted requiring added proteins.

**Protein fabrication**

**Transcription** is the first process (copying the DNA code)

- The RNA polymerase copies one strand onto a molecular ribbon, a messenger RNA (mRNA),
- It must attach to an exact location on the gene at one specific base pair, a DNA code letter,
- Again as in attaching, it must terminate on an exact base pair on the gene. If it does not the resulting protein will not work. (And, if just one code letter is incorrect it also will not work.)
- The code is a sequence of one of the four bases, the amino acids (G, C, A, T) on the mRNA,
- The mRNA is then checked as it exits the nucleus through one of 2000 nuclear pore complexes (NPC) each made of at least 256 proteins, and each can conduct 1000 translocations / second.
- It is then exported out of the nucleus by importins, carrier molecules that recognize and transport cargo containing a nuclear localization signal (NLS) into and out of the nucleus.

**Translation** is the second process (fabricating the protein)

- The mRNA, now in the cytoplasm outside the nucleus, is guided to a ribosome, which engulfs it and processes its code, like an audiotape being fed through a reel-to-reel tape player, to fabricate a protein specified by the code. (Image far right)
- Again, transfer RNA molecules bring amino acids to fabricate the new protein to the ribosome. Each is programmed to transfer one of the 20 specific amino acids in the exact needed sequence.
- As the mRNA is processed through the ribosome, tRNA units match a three-letter code (a codon) with the three-letter code on the mRNA to reduce fabrication errors to near zero.
- The specified amino acid attached to the tRNA is delivered to the growing protein.
- Then, other molecules called chaperones surround the fabricated protein because of its fragility, and carry it to a chaperonin that receives instructions to fold it to the exact shape for this particular machine. (These transcription, translation, and folding process is shown in the images above.)
o Now the fabricated protein, through the bi-
molecular communication system, is sent to the
location to do the task that it was fabricated for.

This process uses a whole series of proteins to
translate between two completely unrelated languages,
the linear code of mRNA and opened DNA, to the three-
dimensional code of proteins. So, we’ve added a layer of
complexity to the language, and we will see in the next section that DNA has 4-dimensions of
communication. There certainly appears to be intelligence required for this process.
Even the simplest first cell would have required this, but how would all this have arisen by chance?

GENOME COMPLEXITY, REDUNDANCY, AND JUNK DNA

The multi-dimensional complexity of the genome
As mentioned above, there is another level of complexity. The genome, which consists of coded
sections on each chromosome, is actually a one, two, three and four-dimensional unit:

o The First Dimension is when DNA is stretched out to allow copying to take place. Along with
mRNA, it is a one-dimensional coded string of base pairs.

o The Second Dimension is the multiplicity of proteins that can be fabricated from only a part of
one gene. The human body has over 100,000 different proteins, and Smithsonian.com (2015)
estimates about 19,000 genes. The Encyclopedia of DNA Elements project (ENCODE) found
that each part of a gene can be used in many different proteins, these parts are spliced
together to form the more than 100,000 distinct proteins. Also, different cells can produce
different proteins, and they can be different at different times! Cells ‘know’ what, when, and
under what conditions to produce them. Certainly this process is intelligently controlled.

o The Third Dimension is the 3-D structure of DNA (the chromosomes) in the nucleus. Here,
genes are ordered and clustered according to need. Genes normally used together end up next
to each other when the chromosomes are folded, and are also close to a nuclear pore or a
transcription area. Therefore, something in the first dimension code controls the 3-D folding.

o The Fourth Dimension is that this three-dimensional structure is changing over time. As
different cell types need access to different genes on different chromosomes at different times,
the genome is constantly unwrapping, wrapping, and then unwrapping different sections to
expose the appropriate genes. 4

This perfectly directed symphony of a complex, interleaved, four-dimensional system with data
compression and flexibility again could hardly have been created by mutation and natural selection.
The genome far exceeds the complexity of the largest computer operating systems in the world today.

Codon redundancy
Our mathematics operates in a base-10 system (0-9), and computers in a base-2 system (0-1).
The genome, with its four bases of Guanine, Cytosine, and Adenine, Thymine, operates on a base-4
system. (In RNA the Thymine is replaced by Uracil.) The ribosome attaches each amino acid to the
growing protein by matching a three-letter code (a codon) on the tRNA that brings the amino acid to
the ribosome, to the complementary codon on the mRNA. complimentary matches are A-U and G-C.

Three positions of four letters allows for 4 x 4 x 4 = 64 combinations. But, there are only 20
different amino acids that fabricate protein, so some can be given multiple codon combinations.
Alanine for example is assigned GCA, GCC, GCG, and GCU so that a mutation in the last letter will
produce the same amino acid. That way at least some mutations in protein coding regions of the
genome will have little or no effect.
‘Junk DNA’ (non-protein coding)

Non-protein coding DNA, which makes up about 98% of the genome, was initially called ‘junk DNA’ by evolutionary biologists who claimed it was garbage (junk) left over from evolutionary mistakes and therefore didn’t have any function. However:

- The ENCODE project mentioned above proved that that all or almost all of it is functional.
- Instead of containing codes to fabricate proteins, it fabricates RNA, cellular workhorses that often affect protein production down the line. It also controls many different functions in the cell.
- Randomly a letter of code in ‘junk DNA’ is used on average in six different RNA transcriptions, which means that statistically nearly 100% of the letters are functional.
- It’s like having a variety of colored balls in a bag in relatively equal numbers. If you blindly pull out a particular color six times, you will probably end up pulling out balls of most colors.
- The ‘Junk DNA’ is effectively an RNA computer as it can be transcribed to: regulatory noncoding RNAs (i.e. tRNAs, rRNAs), origins of DNA replication, centromeres, telomeres, and scaffold attachment regions (SARs). It also controls the cell by regulating genes, serving as gene promoters/enhancers, protein splicing, controlling protein switches, etc.
- According to evolutionary biologist, J.S. Mattick: “The failure to recognize the full implications of this . . . may well go down as one of the biggest mistakes in the history of molecular biology.”
- Virologist Nessa Carey says in her book: “It's the 'junk DNA' that is running the whole show.”

HUMAN / CHIMP GENETIC ‘SIMILARITY’

The similarity of human and chimp DNA myth defies

Evolutionary biologists in the effort to demonstrate primate evolution by showing similarity had claimed that the DNA was 99% identical. Again, only looking at the protein coding DNA was their downfall. There is actually only 70% similarity with entire human gene families not in chimps. And there should be considerable similarity as we are physically very similar.

“In fact there are about 35 million single-letter differences that had to arise (half in each species), spread through the respective populations, and become fixed . . . in those few (thousand) generations. Likewise, tens of thousands of chromosomal rearrangements had to occur, spread, and fix, as well as tens of millions of base pairs of insertions and deletions.”

Human chromosome 2 fusion myth

Dr. Jeffrey Tompkins, Ph.D. in Genetics from Clemson University, states:

“... the chromosome end-capping (telomere). ... protect the ends of linear chromosomes ... A cluster of these telomere sequences in the middle of human chromosome 2 has, in part, led evolutionists to postulate that it was produced by the fusion of two smaller ape-like chromosomes ... [I]t has become evident that telomere repeats were not unique to the ends of chromosomes. Therefore this author developed software that enables the scanning of whole chromosomes for internal telomere content. ... Surprisingly, the entire human genome contains ... 0.19 to 0.25% intact telomere sequences. ... chromosome 2 (the supposed fusion product) contains over 91,000 (0.23%) intact internal telomere sequences. Fewer than 300 ... attributed to the so-called fusion site.”

“It’s now known this particular ITS [Interstitial Telomere Sequence] is ... a second genetic switch called a promoter. Telomeres are ... void of genes, so it would be impossible for a telomere fusion to provide the proper DNA sequences. ... ITSs show strong evidence of design. ... The presence of ITSs affects gene expression by changing the ... (three-dimensional) properties of the DNA.”

BUILDUP OF DETRIMENTAL MUTATIONS

Genetic entropy

There is a profound problem with the genomes of all organisms, which is that they are all degrading due to the accumulation of detrimental mutations. In an average human, about three new
mutations are formed every time a cell divides. By the time we are sixty, we have up to 40,000 mutations per skin cell, with the total in our body numbering in the trillions.

An even bigger problem threatening humanity and all organisms is genetic entropy. Offspring inherit a fraction of our mutations, which continues on with each generation adding more mutations.

“The average mutation rate of 1 in 85 million nucleotides or genetic code letter during sperm or egg production may sound low. However, the human genetic code is 6 billion [single] letters long. This mutation rate adds up to dozens of mutations per generation . . .”

Natural selection cannot solve this problem, it can only slow it down by preventing reproduction in the ‘unfit’ (eugenics, covered later in ‘ETHICAL IMPLICATIONS’). Most of the rest with detrimental mutations will pass them on. There are now over 188,000 (August release 2016.2) disease-causing mutations in the Human Genome Mutation Database, with over 10,000 more discovered each year.

Organisms are devolving rather than evolving due to over 1000 detrimental mutations to only one that is beneficial. This degradation of the genome is the complete opposite of evolution.

Genetic correlation to biblical timescale

A research report by Jacob A. Tennesen et al. published in Science in 2012 concluded that,

“The resulting demographic model . . . strongly supports a recent, dramatic acceleration of population growth. The maximum-likelihood time for accelerated growth was 5115 years ago.”

The chart to the right is from another paper, which validated that the live spans of Noah’s descendants decrease exponentially as genetic entropy would predict. The time frame equates to a time beginning at Noah’s birth about 4900 years ago, with the beginning of the population acceleration about 600 years later. The author noted regarding the accelerated population growth that,

“Amazingly, this recent explosion of human genome variation, mostly associated with genetic entropy, [mutations] also fits the same pattern of human life expectancy rapidly declining after the Flood as recorded in the Bible. . . The results of these genetic studies fit perfectly with the predictions of a young-earth creation timeframe . . .”

In another report, Mothers pass mitochondrial DNA (mtDNA) to their offspring, so any mutated mtDNA leaves a genetic trail through the female lineage. Thus, everyone alive today carries a unique ancestral maternal sequence. Dr. Nathaniel Jeanson, a PhD in Cell and Developmental Biology from Harvard, downloaded mtDNA sequences from Human Mitochondrial Genome Database (HMGD), and then arranged the most similar sequences closest together. The result is a tree-like diagram with three major nodes of ancestry (the green arrows in the image), and 115 mtDNA differences between those individuals and todays. Factoring in the established number of generations per mutation using a divergence calculation (differences = mutation rate*time*2), correlates with the date of the worldwide flood. This fits Genesis 6:18, which conveys that all humans who exist today descended from the three wives of Noah’s three sons.

In addition, our current lifespan was proclaimed by God in the Bible. Wikipedia (also confirmed by Guinness World Records) states: “This is a list of the 100 verified oldest people. The oldest verified person on record was French woman Jeanne Calment (1875–1997), who lived to the age of 122 years 164 days.” After Calment, the next 99 range from 119 down to 114 years. Genesis 6:3, which records life beginning about 100 years before the worldwide flood (over 4000 years ago) states: “Then the LORD said, "My Spirit will not put up with humans for such a long time, for they are only mortal flesh. In the future, their normal lifespan will be no more than 120 years."

Now, over 4000 years later, after great health and medical advances, God’s command is still true!
SUMMARY

- Neither DNA backbones comprised of billions of all right-handed sugar molecules, nor proteins comprised of thousands of all left-handed amino acids, could have arisen by random chance.
- Each section of protein coding DNA has the ability to code for many different proteins. Any given section of each genome has more than one message, which can control overlapping codes. This is extreme optimization, nearly impossible to improve upon.
- A huge assemblage of special proteins (enzymes) is required to work continuously to repair the approximately 100 million, trillion DNA breaks that are occurring in our bodies each day.
- In order for the simplest cell to function, an enormous amount of data, incredible communication networks, and thousands of complex proteins are simultaneously required.
- DNA is a one, two, three, and four-dimensional communication system with data compression.
- The base-4 codon redundancy is yet another optimization.
- All the above had to come about without evolution as they’re prior to the first life, the cell.
- ‘Junk DNA’, a blunder by evolutionary biologists claiming it “junk” from evolutionary mistakes to support evolutionary model is now known ~100% functional, a vastly complicated RNA computer.
- A 99% human/chimp DNA similarity was claimed by evolutionary biologists to support primate evolution. However, it is closer to 70% with about 35 million single-letter differences.
- Recent data shows human chromosome 2 is not the fusion of two ape-like ones. Rather the ITSs are genetic switches, promoters that affect gene expression. They are strong evidence of design.
- The accumulating of harmful mutations is being passed down from generation to generation, corrupting the genomes of all organisms. In effect we are de-evolving, rather than evolving.
- Recent research found a dramatic acceleration of population growth around 5115 years ago. This equates amazingly well to the worldwide flood after which life on earth was reestablished.
- The pattern of human life expectancy decline after the flood, due to genetic entropy from mutations that began after man sinned, fits perfectly with the predictions of a young-earth creation timescale.
- mtDNA genetic ancestry dates back to three nodes, relatable to the three wives of Noah’s sons.
- The number of mtDNA variances from the three nodes to now places them at the time of the flood.
- >4000 years ago God ruled 120-year future lives. With modern health & medicine is still 120 years!

BIBLIOGRAPHY

4. Creation Ministries International, Ref 1, pp. 60-62
8. Creation Ministries International, Ref 1, p. 37
11. science.opposingviews.com/mutation-dna-molecule-passed-offspring-2346.html