CREATION RESEARCH SOCIETY

QUARTERLY

Volume 62 Spring 2026 Number 4

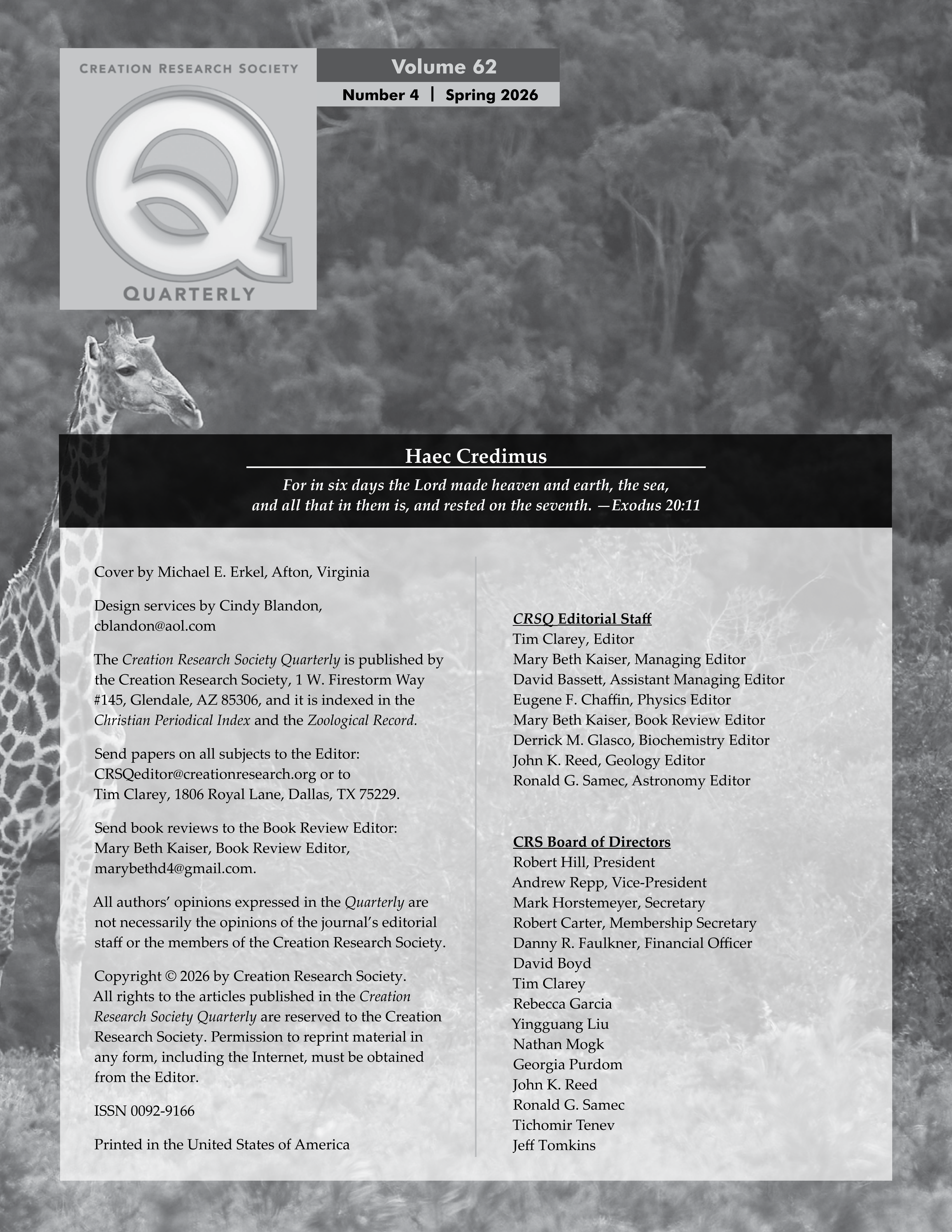
- MITOGENOMIC BARAMINOLOGY ANALYSIS CLASS MAMMALIA
- MOLLUSCAN METHUSELAHS: FOSSIL BIVALVES SHOW EXTREME LONGEVITY
- CREATIONEERING®: A SYSTEMATIC SCIENCE-ENGINEERING-BUSINESS PARADIGM AND EDUCATIONAL PROGRAM
- CELLS ARE INTEGRATED MULTIPROCESSING ANALOG COMPUTING DEVICES — PART 1 AND PART 2
- UNSHAKEN FOUNDATIONS: SCIENTIFIC EVIDENCE SUPPORTING A YOUNG EARTH TIMELINE

CREATION RESEARCH SOCIETY
QUARTERLY
Volume 62
Number 4 | Spring 2026

Articles

Departments

Photo on Table of Contents page by Wolfgang Hasselmann on Unsplash



CREATION RESEARCH SOCIETY
QUARTERLY
Volume 62
Number 4 | Spring 2026

Haec Credimus

*For in six days the Lord made heaven and earth, the sea,
and all that in them is, and rested on the seventh. —Exodus 20:11*

Cover by Michael E. Erkel, Afton, Virginia

Design services by Cindy Blandon,
cblandon@aol.com

The *Creation Research Society Quarterly* is published by the Creation Research Society, 1 W. Firestorm Way #145, Glendale, AZ 85306, and it is indexed in the *Christian Periodical Index* and the *Zoological Record.*

Send papers on all subjects to the Editor:
CRSQeditor@creationresearch.org or to
Tim Clarey, 1806 Royal Lane, Dallas, TX 75229.

Send book reviews to the Book Review Editor:
Mary Beth Kaiser, Book Review Editor,
marybethd4@gmail.com.

ISSN 0092-9166

Printed in the United States of America

Creation Research Society Quarterly 2026 62:276–284

Mitogenomic Baraminology Analysis and the Search for the Baraminic Demarcation Values Among Class Mammalia

Matthew Cserhati

Key Words: boundary of kind mitochondrial genome, molecular baraminology, sequence similarity, taxonomy

Accepted for publication February 25, 2026

Abstract

Molecular baraminology is a subdiscipline within the science of baraminology. Baraminology in general deals with how to classify organisms into different kinds, or baramins. Molecular baraminology uses a sequence similarity cutoff value to either join two species into the same baramin or separate them into two different baramins. Many mitochondrial and chloroplast genome baraminology studies have been performed, but a specific cutoff value has not been determined. To define this cutoff value, one can measure the range of sequence similarity values among species within the same kind across a large dataset.

In this study, the mitochondrial genomes of 1,005 mammalian species were compared to one another and stored in an online database. For any kind, the lowest sequence similarity value was taken as a possible cutoff value. The distribution of all such minimum sequence similarity values was analyzed over various kinds at the taxonomic level of the genus, family, or order.

For all three taxonomic levels the distribution of minimum sequence similarity values was normal, without showing multimodality. The correlation between the minimum sequence similarity and the number of genera/species in the family or the genus was weakly negative. The correlation between the minimum sequence similarity and the number of species in the order was strong and negative. Since the level of the kind rarely reaches that of the order, only genera and families were examined in more detail. The lowest minimum sequence similarity values for genera and families were 83.2% and 75%, respectively. Since the level of the kind for the mammal species used in the database was between the genus and the family, the sequence similarity cutoff value whereby two species can be classified into either the same or different baramins is within the range of 75–83.2%.

Also, the distribution of mtDNA sequence similarity values for several hybrid mammals was analyzed to help determine the sequence similarity cutoff value. Hybridization is a strong indication that two species belong to the same kind. The minimum sequence similarity found in this analysis was 86.6%.

Furthermore, a cumulative proportion function curve was plotted to depict the proportion of mtDNA sequence similarity values over series of sequence similarity values. Two inflection points between the values of 75–85% indicate that this might be the cutoff range that determines whether two species belong to the same or different kinds.

Lastly, an online app called the Mitogenome Database was developed that allows users to perform their own mitochondrial DNA-based baraminology studies.

Simple Summary

This research explores molecular baraminology, a field that uses genetic data to classify organisms into their original "created kinds" based on Biblical interpretation. By analyzing the mitochondrial genomes of over 1,000 mammalian species, the study seeks a specific sequence similarity cutoff to distinguish between kinds. Data from various taxonomic levels and hybridization cases suggest that species within the same kind typically share a genetic similarity between 75% and 83.2%. The author concludes that the "kind" usually aligns with the biological rank of genus or family rather than the broader category of order. Additionally, the study introduces an online database and analysis tool designed to help other researchers perform similar mitochondrial DNA comparisons. These findings aim to provide a standardized, empirical framework for identifying the boundaries of biological diversity.

Introduction

Baraminology is the study of taxonomy based on a Biblical, literal interpretation of the book of Genesis. In Genesis 1:21, we read: "So God created great sea creatures and every living thing that moves, with which the waters abounded, *according to their kind*, and every winged bird according to its kind. And God saw that it was good." A kind is a group of species that are continuous with one another and discontinuous with all other species. To use a technical term, a kind is also called a 'baramin.' Baraminology is the study of these created kinds, and the goal of baraminology is to determine the membership of these kinds.

Baraminology has come quite a long way in developing algorithms, methods, and software to determine the species membership of the kind. Such studies include the Gene Content (GC) method (O'Micks, 2017), the Whole Genome K-mer Signature (WGKS) method (Cserhati, 2020), and mitochondrial and chloroplast genome-based studies (Robinson, 1997; O'Micks, 2018; Cserhati, 2023a, 2023b, 2023c, 2023d, 2024a, 2024b; Di Martino et al., 2024). Morphology-based baraminology tools include the online BARaminology and Cluster AnalYsis (BARCLAY) software (Wood, 2021). However, a specific critical cutoff value remains ever elusive for mitogenome and chloroplast genome studies. This minimum sequence similarity cutoff value predicts that two species belong to the same holobaramin (a group that includes all species in a kind) if their sequence similarity (SS) value is above this limit. Species with an SS value below this cutoff value belong to separate holobaramins.

The reason this cutoff value has not been discovered is likely due to several reasons. In prokaryotes, for example, the gene structure and content lower the shared gene content of two prokaryotic organisms, despite the possibility that they may belong to the same kind. In addition, gene pleiotropy (a single gene influencing multiple distinct traits) may make two organisms look very dissimilar, despite their high common genetic content. God could also have created several externally similar-looking kinds, but which have different genetics (Cserhati and Carter, 2020).

The purpose of the present analysis is to calculate the minimum sequence similarity (MSS) value for mammalian groups having mitochondrial DNA (mtDNA) in the National Center for Biotechnology Database (NCBI). The analysis was performed over the ranks of genus, family, and order since the level of the kind is somewhere within these limits. The MSS value over all mammalian genera, families, and orders should be a good empirical calculation of the baraminic cutoff value for the kind because it is a highly diverse class of animals.

Hybridization is the strongest evidence of two animals belonging to the same kind. In light of this, several mammalian hybrids were analyzed to see how similar they are based on their mitogenome sequences.

Materials and Methods

The mtDNA sequences for a total of 1,005 mammalian species were downloaded from the NCBI database. Using a shell script, each of the complete 1,005 mammalian mtDNA sequences was compared to one another using the bl2seq program. These values were uploaded into a SQLite3 table. The NCBI taxonomy data (including NCBI taxonomy ID, species, genus, family, order, class, phylum, kingdom, and domain information) for all 1,005 mammals were downloaded from https://ftp.ncbi.nih.gov/pub/taxonomy/new_taxdump/new_taxdump.tar.gz. Taxonomic data was extracted from the file rankedlineage.dmp. This data was then uploaded into a SQLite table called taxa. Various SQLite3 queries were run on these tables to calculate results.

Table I. General statistics describing the distribution of minimum sequence similarity values over 57 mammalian families.

Taxonomic Rank	Min SS	Mean SS	Median SS	Max SS
Genus	83.2%	91.2%	91.7%	98.6%
Family	75%	84.4%	84.7%	95.5%
Order	72.5%	78.7%	78.4%	88.3%

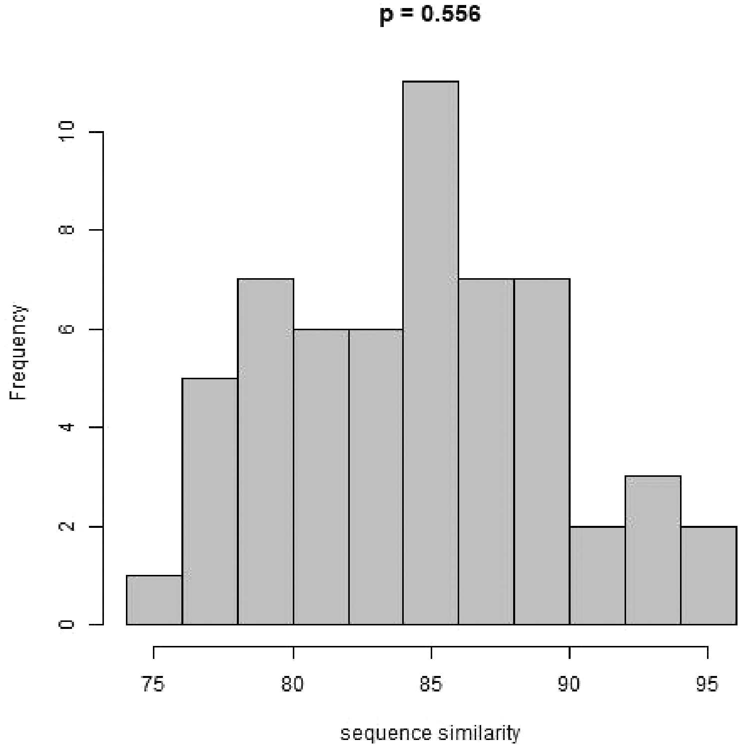


Figure 1. Histogram of all MSS values calculated at the family level.

Only genera, families, and orders with at least three species members were included in the analysis. The Shapiro test was run on the set of minimum sequence similarity values and displayed in a histogram and a linear regression plot. The hist and the plot commands were used in R (version 4.3.1) to depict the histogram and the linear regression plot. The diptest method from the diptest package was used to test sequence similarity values for multimodality.

Supplementary files are available on Zenodo at https://zenodo.org/records/13431371. The Mitogenome Database was programmed in R as part of a shiny app for the online Molecular Baraminology Analysis Tool (MBAT) app at https://molbar.shinyapps.io/molbar.

Results and Discussion

Minimum sequence similarity values across families

In Table I, the MSS values broken down across 57 mammalian families range from 75% to 95.5%. Therefore, the minimum MSS value is 75% for families, which, according to this study, would be the empiric cutoff value that decides whether two species belong to the same or different holobaramins (if the kind is equivalent to the family). Figure 1 depicts a histogram of all MSS values at the family level. The p-value of the Shapiro test is 0.556, which indicates that the distribution is close to normal. However, the histogram does appear to be slightly trimodal, with peaks at MSS values of 79%, 85%, and 93%. However, the Hartigan dip test had a D-value of 0.035, and a p-value of 0.902, which indicates multimodality is likely an artifact.

A question of interest was are the number of species or genera in a family and the MSS values correlated? The correlation value for number of species in a family is -0.343, which indicates a moderate negative effect (see Figure 2A). In general, a larger number of species per family corresponds to lower MSS values and increases the range of MSS values. The correlation value for the number of genera in a family is –0.36, (Figure 2B) where more genera per family also produces lower MSS values and increases the range of MSS values.

In cats (Felidae), the MSS value is 87.1% which includes 15 species in 8 genera (*Acinonyx*, *Catopuma*, *Felis*, *Lynx*, *Otocolobus*, *Prionailurus*, *Neofelis*, *Panthera*), all belonging to the cat kind. In dogs (Canidae), the MSS value is 84.9%, covering 9 species from 5 genera (*Canis*, *Nyctereutes*, *Otocyon*, *Urocyon*, *Vulpes*). In horses (Equidae), the MSS value is 92.9%, encompassing 9 species from a single genus (*Equus*).

Cserhati (2021) studied the molecular and morphological baraminology

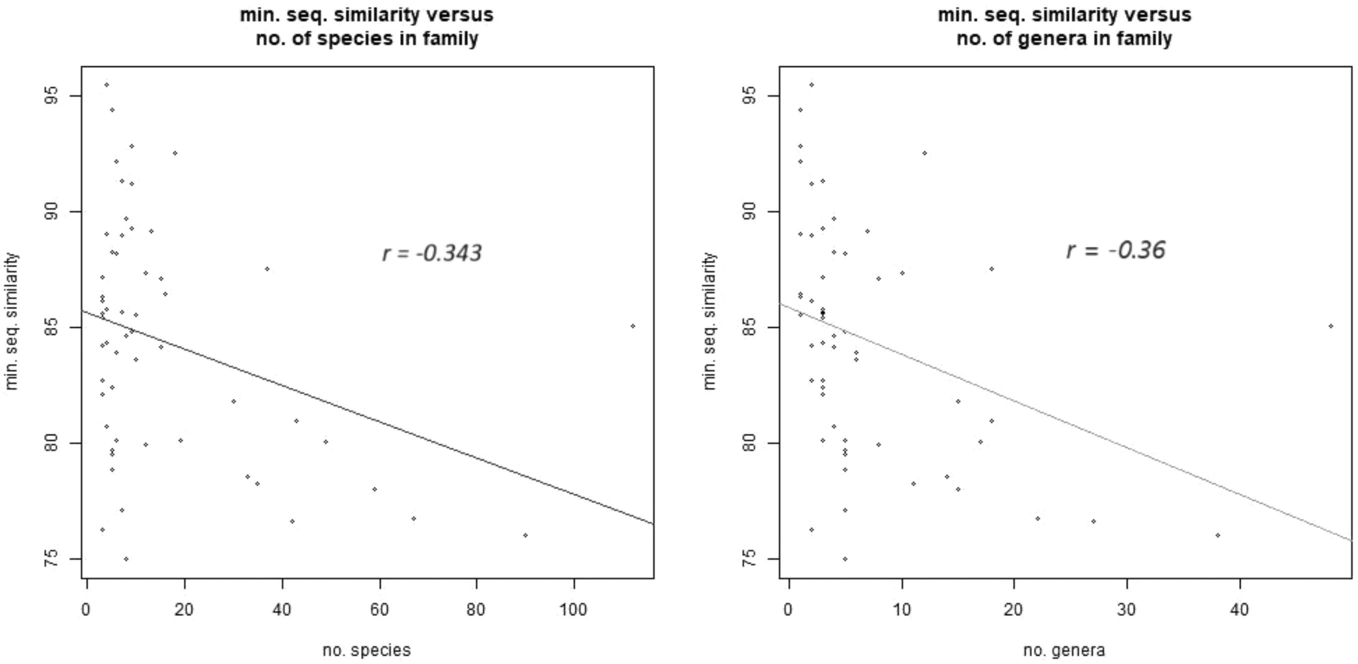


Figure 2. A. MSS according to the number of species in a family. B. MSS according to the number of genera in a family.

Table II. MSS values from several well-known and studied mammal families.

Family	No. species	No. genera	MSS value
Canidae	9	5	84.9%
Equidae	9	1	92.9%
Felidae	15	8	87.1%
Hominidae	8	4	84.7%
Pteropodidae	43	18	81.0%
Rhinolophidae	16	1	86.5%
Vespertilionidae	59	15	78.1%

of bats and found four different kinds. Of these, Pteropodidae (megabats), Rhinolophidae (horseshoe bats), and Vespertilionidae (vesper, or nosed bats) (Table II) had data in the Mitogenome Database. These families had a MSS value of 81%, 86.5%, and 78.1%, respectively. From Table II the lowest MSS value is 78.1%, which is greater than the 75% calculated for all mammalian families in the database. Table II lists the number of species and genera for seven well-known mammalian holobaramins. For statistics for all 117 families in the Mitogenome Database, see Supplementary File 4.

Genus level

At the genus level, the range of MSS values was somewhat higher, between 83.2% and 98.6%. The spread of MSS values is bimodal, with a Shapiro's p-value of 0.066, which is barely above the 5% cutoff limit (Figure 3). According to the dip test, the D-value is 0.035, with a p-value of 0.573, which is not bimodal. This suggests the genus is not equivalent to the kind. However, some genera do coincide with the kind, such as the genus *Homo*, including modern and archaic humans, such as Neanderthals, Denisovans, and *Homo heidelbergensis* (Lightner and Cserhati, 2019; Cserhati, 2023b). Based on this and previous baraminological analyses (Lightner and Cserhati, 2019), the great ape kind should be designated as the family Pongidae, and the human kind should be designated as Hominidae. The correlation between the number of species within a genus and the MSS value is -0.374 (Figure 4), where lower MSS values coincide with greater genus diversity.

Order level

Things are slightly different at the level of the order. Out of 25 orders, only 15 had more than two species so the

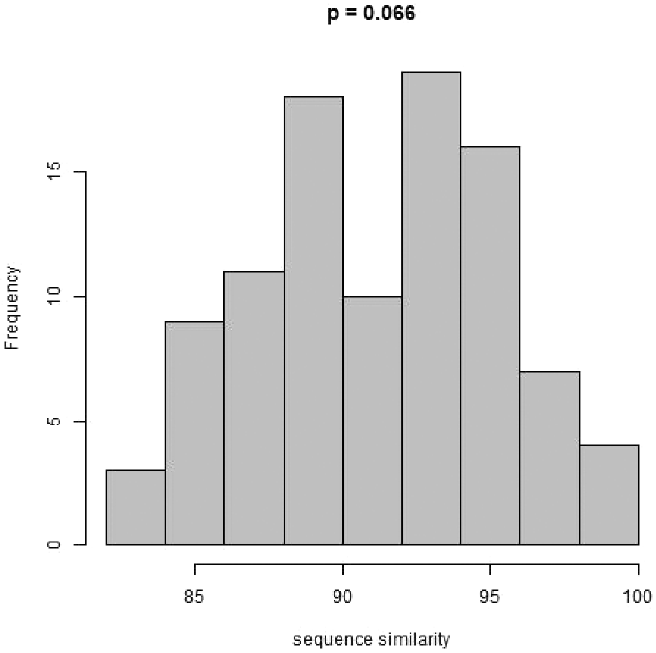


Figure 3. Histogram of all MSS values calculated at the genus level.

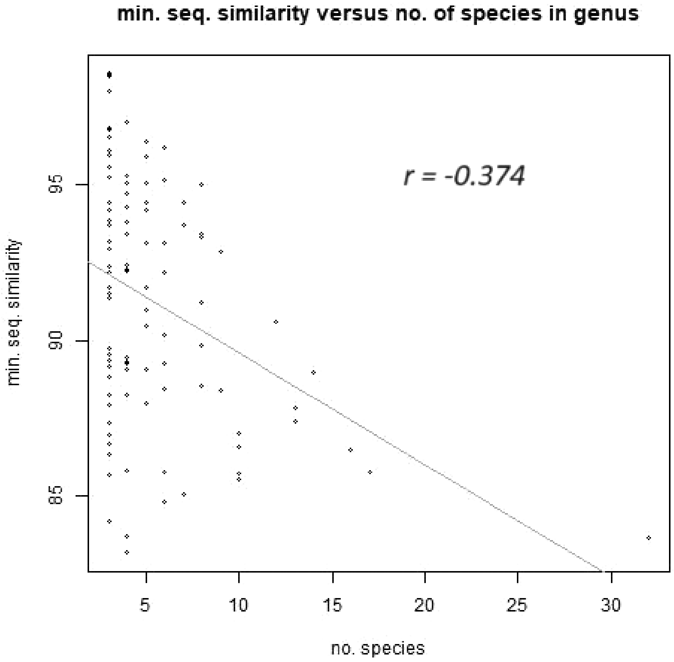


Figure 4. MSS according to the number of species in a genus.

Table III. General statistics for SS values according to genus, family, and order.

Taxonomic rank	Number of taxa	Number of taxa with > 2 species	Shapiro p-value	Correlation
Genus	491	97	0.066	-0.374
Family	117	57	0.556	-0.343
Order	25	15	0.358	-0.634

results from the analysis of the order do not have enough statistical power. The MSS value range is 72.5% to 88.3%. The distribution of SS values is normal, with a Shapiro's p-value of 0.358 (Figure 5). The D-value of the dip test is 0.107, with a p-value of 0.13 (indicating that the data is not multimodal). However, the correlation between the number of species in an order and the MSS value is -0.634, which is a strong correlation (Figure 6) where an order with a large species diversity will possess a lower MSS value.

Mitogenome Analysis Tool app

The mtDNA sequence similarity values have been made available in an online R Shiny app for other researchers to analyze. The Molecular Baraminology Analysis Tools (MBAT) app has a new section on Mitogenome Analysis. This section has two tools: a Taxonomy Database and a Heatmap Generation tool. The app is available at https://molbar.shinyapps.io/molbar.

The user can browse the Taxonomy Database to see what kinds of organisms are available in the app. A total of 6,336 vertebrates have their taxonomic information listed in the database. Table IV lays out the number of species from various tetrapod groups with sequence similarity data in the database. Taxonomic information includes the organism's full taxonomic classification, including species, genus, family, order, class, phylum, kingdom, and domain, as well as its NCBI taxonomy ID. The user can organize the data based on any of the eight taxonomic levels or locate specific data utilizing a search tool (Supplementary Figure 1). The heatmap tool allows the user to select a set of species to generate a heatmap, a sequence similarity matrix, and an SS value histogram (Supplementary Figures 2A–C).

The user has two options to select a species. The first option is to select a species from the drop-down list and then select an MSS value cutoff between 0 and 1. The app will then search for all other species that have an MSS value with the selected species that are greater than or equal to the

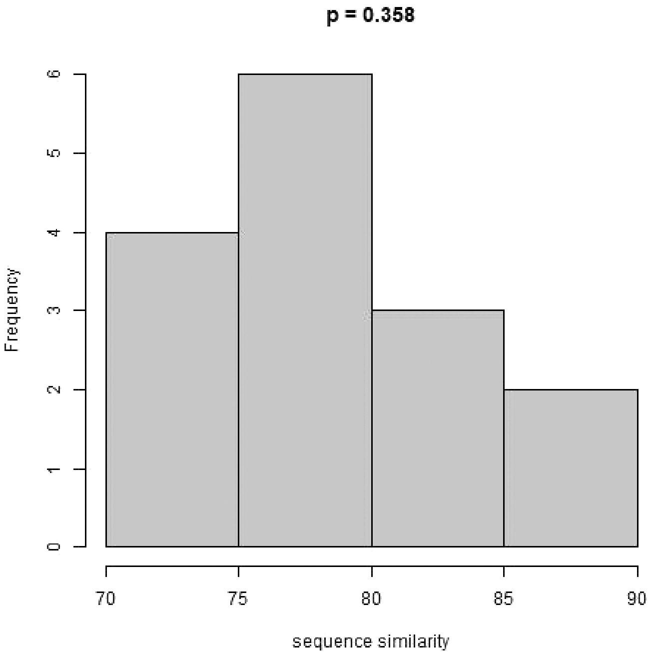


Figure 5. Histogram of all MSS values calculated at the order level.

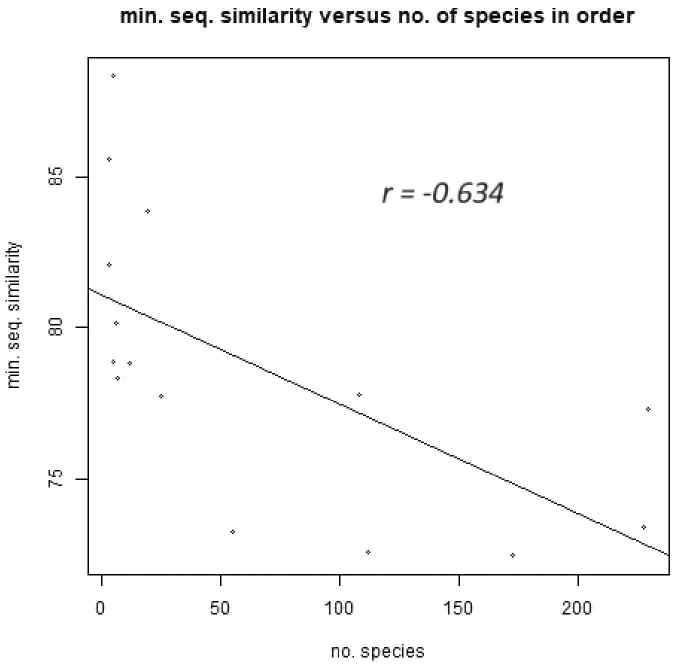


Figure 6. MSS according to the number of species in an order.

Table IV. The number of species with data in the Mitogenome Database from various tetrapod groups.

Group	Number of species	Number of genera
Mammalia	1005	491
Aves	663	371
Lepidosauria	311	166
Amphibia	216	96

cutoff. The second option is to list all species the user wants to examine, and the SS values will be downloaded from the database. The app then creates an SS value matrix for all selected species pairs (Supplementary Figure 2B). The matrix is represented as a heatmap (Supplementary Figure 2A).

A histogram will also show the SS values for all selected species (Supplementary Figure 2C). The Shapiro t-test is performed on the SS matrix, and the p-value will be displayed. P-values above 5% indicate that the SS value distribution is normal. Otherwise, the SS values depart from the normal distribution. This is because if the SS values are from two different kinds, there will be two types of SS values. First, SS values will describe sequence similarity between species of the same kind. These SS values will be high. In contrast, SS values between the two kinds will be low because of the dissimilarity between the two kinds. A bimodal histogram may depict such a dual distribution of SS values, indicating the presence of more than one kind in the data. The SS values depicted in the heat map are also shown at the bottom of the result screen (Supplementary Figure 2C).

MSS of various hybrid animals

Hybridization provides the strongest evidence that two animals belong to the same kind. Therefore, the parental species of several well-known hybrid species were analyzed to see how similar their mtDNA sequences are. This can also be used to measure the MSS value that separates from non-kind. However, this cutoff value is not absolute, since certain species that may be able to hybridize are unable to do so because of various biological factors. These include chromosome mismatching, or incompatibility of reproductive cells due to mutations in their surface receptors, making it impossible for them to fuse. Examples include the mule, which is a hybrid of *E. caballus* and *E. asinus*. An example of gamete incompatibility is when receptor proteins on the surface of egg cells in the

Table V. Mitochondrial SS between 18 mammalian hybrids.

Hybrid	Parental species 1	Parental species 2	Sequence similarity
cama	*Camelus dromedarius*	*Lama glama*	86.55
coywolf	*Canis latrans*	*Canis lupus*	95.61
geep	*Capra hircus*	*Ovis aries*	91.71
huarizo	*Vicugna pacos*	*Lama glama*	98.29
jagger	*Panthera onca*	*Panthera tigris*	91.42
jugapard	*Panthera onca*	*Panthera pardus*	92.52
kunga	*Equus hemionus*	*Equus asinus*	94.98
liger	*Panthera leo*	*Panthera tigris*	91.15
liguar	*Panthera leo*	*Panthera onca*	92.75
lipard	*Panthera leo*	*Panthera pardus*	94
mule	*Equus asinus*	*Equus caballus*	93.56
pizzly bear	*Ursus maritimus*	*Ursus arctos*	94.08
seal hybrid	*Phoca vitulina*	*Halichoerus grypus*	96.18
snow lion	*Panthera uncia*	*Panthera leo*	93.05
snow tiger	*Panthera uncia*	*Panthera tigris*	91
tigard	*Panthera tigris*	*Panthera pardus*	91.01
yakalo	*Bos grunniens*	*Bison bonasus*	94.01
yakalo	*Bos grunniens*	*Bison bison*	97.41

sea urchin genus *Echinometra* allow only conspecific sperm cells to bind via their binding protein (Palumbi, 2009). This means that the real SS cutoff may be lower due to these false negative cases.

These hybrids, their parental species, and their mtDNA SS are listed in Table V. The lowest SS is 86.6%, which corresponds to the hybrid 'cama,' a hybrid between the dromedary camel (*Camelus dromedarius*) and the llama (*Lama glama*).

Cumulative Distribution Function Plot

As a third approach, all mtDNA SS values calculated between all possible mammalian species pairs was visualized in a cumulative distribution function (CDF) plot (see Figure 7). To create the CDF plot, all SS values are ranked from lowest to highest. The x-axis shows the SS value, from 70% to 100%. The y-axis shows the proportion of all SS values that are less than or equal to the corresponding x-axis value (an SS value). No SS values are less than or equal to 70%, whereas all SS values are less than or equal to 100%. Since the SS value (the x-axis) gradually increases, so does the CDF value (the y-axis). The CDF curve strictly monotonically increases. It is interesting to note in Figure 7 that the CDF curve has two inflection points. There is a larger one between 75 and 80%, corresponding to a cumulative proportion of around 50%. Another, smaller inflection point is close to 85%, with a cumulative proportion of around 97.5%. This could indicate that the SS cutoff lies between this SS range (75–85%).

Conclusion

After all these considerations, can anything definite be said about an empirical cutoff value to differentiate species into baramins? As we saw from the example of the family Hominidae, families may contain more than one baramin. This would suggest that we look at the genus, which is one taxonomic level lower than the family. This way, the cutoff SS value would be 83.2%, the lowest MSS value among all genera in this study.

On the other hand, an individual kind may comprise more than one genus. This would mean we should take the lower bound of the MSS value range for families. This value is 75%. While some baramins correspond to the level of the order, such as Crocodylia (Cserhati, 2023c), this is generally not the case.

As a reference, the list of baraminology studies from Wood (2016) was analyzed, and the number of holobaramins corresponding to various taxonomical levels predicted by these studies, ranging from the genus to the superorder, was tallied. The result can be seen in Table VI. In this list, if a holobaramin was made up of more than one family, it was designated as a superfamily. If it contained more groups than a single order, it was considered a superorder. The list of holobaramins from the Wood study can be seen in Supplementary File 4. Overall, the low statistical support for the MSS value of 72.5% for order implies that for mammals, the kind is either at the family or genus level.

When actual animal hybrids are examined (which we can assume to be from the same kind), the MSS is 86.6%, which is above the cutoff limit range that was calculated by looking at groups of genera and families. Only 18

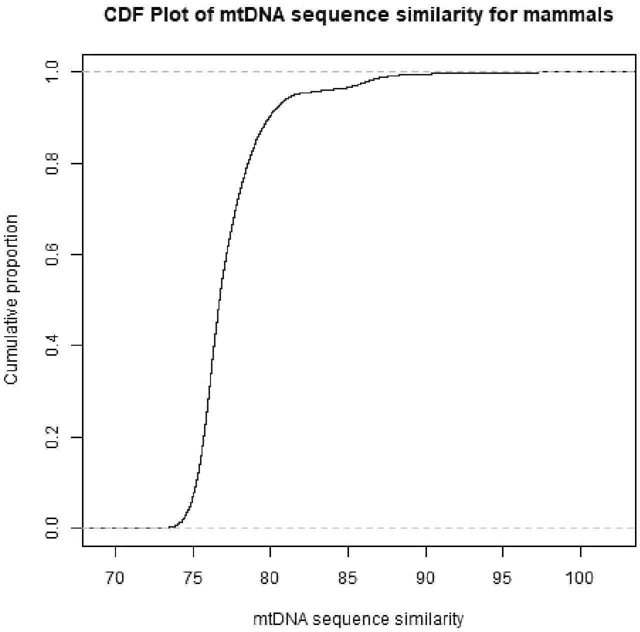


Figure 7. Cumulative Distribution Function Plot of all calculated sequence similarity values in the study.

Table VI. The number of holobaramins found in various baraminology studies listed in Wood (2016).

Taxonomic level	Number of holobaramins
Tribe	1
Genus	1
Subfamily	8
Family	46
Superfamily	9
Suborder	3
Order	1
Superorder	1

hybrids were examined, so with more species, this number might change. Based on the cumulative sequence similarity proportion plot, this range lies between 75–85%.

The result of this study indicates that the SS cutoff value for mtDNA studies is between 75–83.2% for mammals. While the MSS of various genera or families might be greater than these limits, these values were determined by taking the minimum MSS (the MMSS) value over all groups at a specific taxonomic level (genus and order). Any pair of species that are at least this similar based on their mitogenome sequence similarity may be considered to belong to the same baramin. Conversely, two species that are less similar than this may be considered to belong to separate baramins. This value could change with the inclusion of more data into the Mitogenome Database.

While this data is for mammals only, it would be interesting to study SS values for more animal groups, chloroplast SS from plants, and genome similarity for prokaryotes. Prokaryotic reproduction is very different from that of eukaryotes, so the results from this study might be valid only for eukaryotes, or even only for animals. Separate estimates might have to be made for non-animal groups.

The Mitogenome Database will serve as a useful tool for future molecular baraminology studies. The user can select from 6,336 tetrapod species for mitogenome studies from the app's Taxonomy Database. The user can also use the Heatmap Generation tool to run analysis on a selection of species. This includes all species from a selected genus or family. The user can also select a single species and retrieve all species pairs with an SS value above a selected limit. The user can then generate the SS-based heatmap, depict the resulting SS distribution on a heatmap, and depict the SS matrix with the selected species. The heatmap, the histogram, and the SS matrix can all be downloaded. Other baraminologists are encouraged to use this resource.

References

Cserhati, M. 2020. A new baraminology method based on Whole Genome K-mer Signature analysis and its application to insect classification. *Journal of Creation* 34(1): 86–95.

Cserhati, M. 2021. Molecular and morphological analysis predict four bat baramins. *Journal of Creation* 35(1): 117–127.

Cserhati, M. 2023a. Chloroplast genome-based baraminology study of Liliales. *Creation Research Society Quarterly* 60(2): 84–96.

Cserhati, M. 2023b. Baraminic placement of *Homo heidelbergensis* based on molecular data. *Creation Research Society Quarterly* 59(3): 151–159.

Cserhati, M. 2023c. Baraminic analysis of Crocodylia based on mitochondrial DNA similarity. *Answers Research Journal* 16: 259–263.

Cserhati, M. 2023d. Molecular baraminology of marine and freshwater fish. In J.H. Whitmore (editor), *Proceedings of the Ninth International Conference on Creationism*, pp. 181–205. Cedarville University International Conference on Creationism, Cedarville, OH.

Cserhati, M. 2024a. Baraminology of Cucurbitaceae based on chloroplast genome analysis. *Answers Research Journal* 17: 613–619.

Cserhati, M. 2024b. Chloroplast genome-based molecular baraminology analysis of Proteales. *Creation Research Society Quarterly* 60(2): 84–96.

Cserhati, M., and Carter, R. 2020. Hierarchical clustering complicates baraminological analysis. *Journal of Creation* 34(3): 64–73.

Di Martino, O., McGehee, G., and Cserhati, M. 2024. Chloroplast Genome-Based Baraminology of the Order Myrtales. *Answers Research Journal* 17: 637–645.

Lightner, J.K., and Cserhati, M. 2019. The uniqueness of humans is clearly demonstrated by the Gene-Content Statistical Baraminology Method. *Creation Research Society Quarterly* 55(3): 132–141.

O'Micks, J. 2017. Baraminology classification based on gene content similarity measurement. *Creation Research Society Quarterly* 54(1): 27–37.

O'Micks, J. 2018. A preliminary cephalopod baraminology study based on the analysis of mitochondrial genomes and morphological characteristics. *Answers Research Journal* 11: 193–204.

Palumbi, S.R. 2009. Speciation and the evolution of gamete recognition genes: Pattern and process. *Heredity* 102(1): 66–76.

Robinson, D.A. 1997. A mitochondrial DNA analysis of the testudine apobaramin. *Creation Research Society Quarterly* 33(4): 262–272.

Wood, T. 2016. A list and bibliography of baraminology studies. *Journal of Creation Theology and Science Series B: Life Sciences* 6: 91–101.

Wood, T. 2021. Baraminology by cluster analysis: A response to Reeves. *Answers Research Journal* 14: 283–302.

Creation Research Society Quarterly 2026 62:285–297

Molluscan Methuselahs: Extinct Fossil Bivalves that Show Evidence of Extreme Longevity

Jake Hebert and Richard Overman

Key Words: bivalves, *Cucullaea*, fossils, giantism, growth curves, *Lithiotis*, longevity, *Platyceramus*, rudists

Accepted for publication November 30, 2025

Abstract

A previous paper presented strong evidence that fossil *Crassostrea* oysters lived much longer than their modern-day descendants. This paper presents direct and indirect fossil evidence that other (now extinct) bivalves also experienced great longevity. Ontogenetic growth curves constructed for four genera of Cretaceous and Eocene bivalves from Seymour Island, Antarctica, demonstrate that they exhibited longevity described by mainstream paleontologists as “extreme.” This longevity is difficult to explain in a uniformitarian framework, but whether it is a strong argument for pre-Flood longevity hinges on whether the pre-Flood Antarctic climate was warm or cold. Likewise, studies of extant animals have revealed a positive correlation between greater longevity and greater adult body size, as well as a positive correlation between greater longevity and greater ages at sexual or skeletal maturity. Some fossil bivalves, such as the genus *Platyceramus*, the rudists (order *Hippuritida*), and Lithiotid bivalves, were large, slow-growing, and apparently long-lived. However, since these particular bivalves are now extinct, it is not possible to know if their lifespans would have been shortened had they survived to the present day. In light of the Bible’s claim that humans in the pre-Flood world had centuries-long lifespans, this information should be of great interest to creation researchers, since whatever genetic or environmental factors were enabling extreme human pre-Flood longevity were likely also operating in the animal kingdom. These data may add to a growing body of evidence that at least some fossil creatures experienced great longevity.

Simple Summary

J. Hebert and R. Overman review growth band counts in fossilized bivalve shells, such as Cretaceous and Eocene clams from Antarctica, which indicate that fossil clams and oysters achieved extreme longevity, far exceeding nearly all modern bivalves. Extinct bivalves, including the massive *Platyceramus* and rudists, were characterized by prolonged maturation periods often lasting over a century. Unlike today’s long-lived bivalves that typically require cold, deep-water environments, these fossil creatures thrived in shallow, temperate-to-tropical waters. In a creationist framework, these bivalves were killed and buried in the worldwide Noachian Flood (Genesis 6–8). Whatever genetic or environmental factors enabled extreme human pre-Flood longevity (Genesis 5) would likely have also affected the animal kingdom. Thus, the remarkable lifespans seen in these fossil creatures are indirect confirmation of the Bible’s testimony regarding extreme human lifespans in the pre-Flood world.

Introduction and Background

Hebert (2023) suggested that fossils could provide evidence of past extreme longevity in animal forms. A follow-up paper (Hebert, Overman, and Sherwin, 2024) presented evidence that fossil *Crassostrea* (and likely *Magallana*) oysters experienced considerably greater longevity than their modern-day descendants. Hebert (2026) also presented evidence that fossil versions of the bivalves *Glycymeris americana*, *Dosinia japonica*, the bivalve genus *Tridacna*, and possibly some *Mercenaria* bivalves also likely experienced greater longevity than their modern-day descendants. Studies of longevity and aging have repeatedly shown positive correlations between (1) greater longevity and larger adult body sizes and between (2) greater longevity and longer maturation intervals (de Magalhães, Costa, and Church, 2007; Ricklefs, 2010a, 2010b; Ridgway, Richardson, and Austad, 2011; and Moss et al., 2016). In short, the larger an organism's adult body size and the longer its time to reach adulthood, the greater the longevity it is expected to have.

Many animals exhibit asymptotic growth; that is, their length L asymptotically approaches a maximum value that we designate as L_∞ (Figure 1). This asymptotic growth can be described mathematically by the von Bertalanffy (1938) growth curve equation:

$$L(t) = L_\infty \left(1 - e^{-k(t-t_0)}\right) \qquad (1)$$

Here t is the time since spawning (measured in years) and k is a parameter (units of years^{-1}) that indicates the relative speed with which an organism becomes mature. Although k is not a growth rate *per se*, it is a proxy for growth rate.

The value t_0 is the (theoretical) time at which the organism's length is zero. If the animal has zero size at birth, t_0 will be zero. If the creature has a positive, non-zero size at birth, t_0 will be a negative number, indicating that the creature had zero size at the beginning of its gestation, $-t_0$ years before birth.

Equation (1) is usually obtained from a population of organisms. L_∞ thus represents the average adult body length for the population, obtained by fitting of a growth curve to the population's size versus age data. Some adult body sizes in the population will be greater than L_∞, and some will be smaller. A growth curve obtained from a single fossil specimen may be somewhat "herky-jerky" in appear-

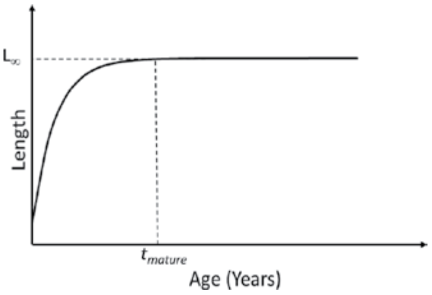


Figure 1. The von Bertalanffy growth curve showing the increase of an organism's length or height as a function of time since birth or hatching. Growth effectively, if not completely, stops when the organism reaches skeletal maturity at time t_{mature}.

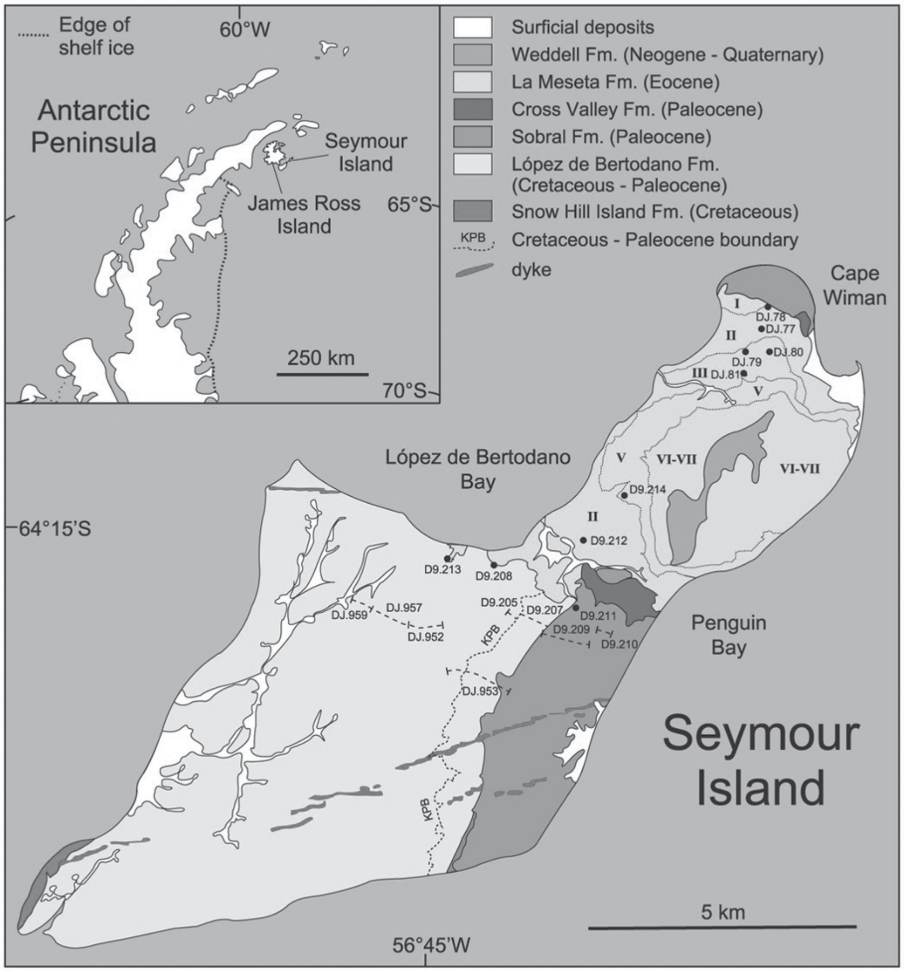


Figure 2. Map of Seymour Island at the tip of the Antarctic Peninsula. The large light-shaded region at the southwestern portion of the island is the López de Bertodano Formation. Image credit: Figure 1 from Crame et al. (2014). CC-BY-SA 4.0 International License. https://creativecommons.org/licenses/by-sa/4.0/.

ance, and not like the smooth function depicted in Figure 2. This is due to uncertainties from the use of allometric equations to estimate body size; see Figure 10 in Hebert (2023) for examples. However, bivalves are somewhat exceptional in that nice, smooth growth curves *can* be obtained from a single fossil or recently-deceased specimen. This is because the growth bands in a bivalve shell give not just body length at time of death, but all the successive cumulative body lengths as a function of age, which enable the construction of a smooth ontogenetic growth curve.

Theoretically, Equation (1) describes indeterminate (never-ceasing) growth, since for any finite time t, the organism's growth never quite stops. As a practical matter, however, Equation (1) is often used to model both indeterminate and determinate growth, since one can treat the age at skeletal maturity t_{mature} as the time at which the slope of the function becomes arbitrarily small. However, Day and Taylor (1997) have criticized this practice, arguing that two separate equations should be used to model growth, one prior to sexual maturity, and one after. Admittedly, von Bertalanffy growth equations sometimes do a poor job of fitting size-versus-age data shortly after birth or spawning. However, in this analysis, we are far more concerned with the behavior of the growth function at ages far after birth or spawning, and so we here ignore this complication, as do many researchers in this field.

Note that t_{mature} is not necessarily the same as the age t_{sex} at sexual maturity, as some animals reach sexual maturity before reaching skeletal maturity. Nevertheless, one might reasonably expect higher ages t_{mature} at skeletal maturity to also imply higher ages of sexual maturity t_{sex}.

Bivalves are excellent choices for longevity comparisons between fossil and modern forms within a taxon. This is because bivalves are extraordinarily numerous in the fossil record, as are other marine invertebrates (Morris and Sherwin, 2011). Also, some extant bivalves are among the longest-lived noncolonial organisms on Earth (Palmer et al., 2021). In Hebert, Overman, and Sherwin (2024), we began a comparison of size and ontogeny data for fossil and modern *Crassostrea* and *Magallana* oysters. The fossil oysters showed evidence of larger adult body sizes, delayed maturation, and greater longevity compared to the extant specimens. Hence, we might expect to see evidence of great longevity in other fossil bivalves. Here, we review fossils of now extinct bivalves showing possible direct and indirect evidence for great longevity. Because these bivalves are extinct, it is not possible to ascertain what their longevities would have been had they survived to the present day.

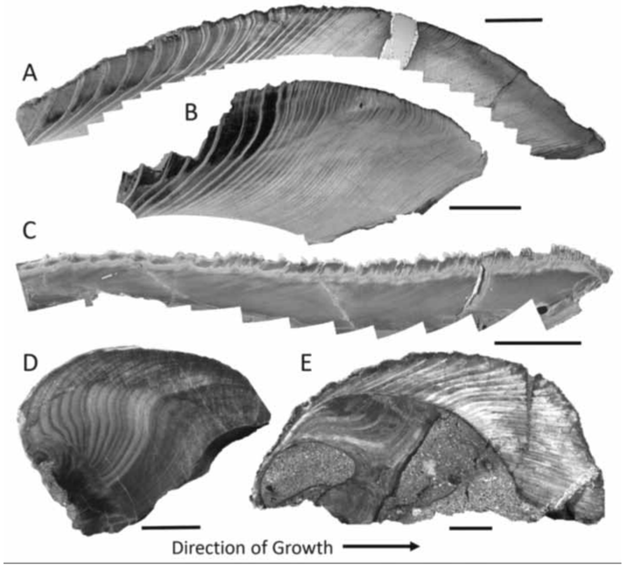


Figure 3. Middle and outer annual growth bands (A-C) in the long-lived Eocene bivalves *Cucullaea raea* and *Retrotapes antarcticus* from Seymour Island, Antarctica. Middle and outer layers of *C. raea* shown in A, with the growth margin shown in B. Middle and outer growth bands of *R. antarcticus* are shown in (C). Also shown (D) are the umbonal (most prominent) region of the *Eurydesma cordatum* valve and the complete shell (E) of *Myonia corrugata*, both from the Permian of South Sydney Basin, Australia. Scale bars: 0.5 cm (A-C) and 1 cm (D-E). Figure 6 from the Open Access Moss, Ivany, and Jones (2021) *Paleobiology* article. CC-BY 4.0 International. (http://creativecommmons.org/licenses/by/4.0/).

Bivalves from Seymour Island, Antarctica

Two studies of fossil marine bivalves from Seymour Island, Antarctica, provide evidence of great fossil bivalve longevity. Seymour Island is a small island located at the tip of the Antarctic Peninsula (Figure 2). It is an especially important high-latitude paleontological site, so much so that it was once dubbed the "'Rosetta Stone' of Southern Hemisphere paleobiology" (Reguero, 2019, p. 328). Buick and Ivany (2004) counted growth rings in twelve *Cucullaea raea* fossils taken from the La Meseta Formation, an Eocene shallow-marine succession of strata located toward the northeast corner of the island (Crame et al., 2014; Moss et al., 2017). *Cucullaea raea* growth bands are shown in Figure 3A-B.

Buick and Ivany estimated that the youngest of these twelve bivalves was 56 years old when it died, and the oldest was 127 years old. Six of the bivalves were more than 90 years old, and five were more than 100 years old. The average age of the sample was 90 years, with a standard deviation of 26 years. Despite the small sample size, Buick and Ivany (2004, p. 922) concluded, "These are some of the longest-lived clams ever documented from the modern or ancient world." They pointed out (p. 922) that these twelve fossil specimens were *not* exceptional, either in size or number of visible bands. Rather, Buick and Ivany selected those particular twelve specimens because their growth bands were particularly visible and, hence, easy to count.

Moss et al. (2017) studied eleven species of fossil bivalves from the Late Cretaceous López de Bertodano Formation on the southwest part of the island, as well as the Eocene La Meseta Formation mentioned previously (Figure 2). As noted earlier, the La Meseta Formation is thought to represent a shallow-marine environment. The López de Bertodano Formation is thought to represent a shallow-water delta/estuary environment, as well as middle-to-outer-shelf deposits (Moss et al., 2017, p. 366). The four Cretaceous species were *Cucullaea ellioti*, *Cucullaea antarctica*, *Nodenskjoldia nodenskjoldia*, and *Lahillia larseni*. The seven Eocene bivalves were *Cucullaea* sp., *Cucullaea raea*, *Cucullaea donaldi*, *Retrotapes antarcticus*, *Retrotapes newtoni*, *Retrotapes robusta*, and *Lahillia wilckensi*. Moss et al. (2017) chose these particular specimens because their internal growth bands are well-preserved and because they are common in previous studies and archival research collections.

They reported (Moss et al., 2017, p. 365), "Despite significant sampling limitations, we find that all 11 species examined are both slow growing and long-lived, especially when compared with modern bivalves in similar temperature settings." Eight of the eleven species had at least one specimen with a lifespan in excess of 50 years, and the *C. raea*, *C. antarctica*, and *N. nodenskjoldia* species had specimens with maximum lifespans of 121, 101, and 131 years, respectively. Moss et al. (2017, pp. 373–374) elaborated:

> While a number of modern taxa can attain life spans in excess of 50 years, the modal [most common, J.H. and R.O.] value of maximum reported life span for bivalve species today is 3 years (Moss et al., 2016). The shortest-lived species measured from Seymour Island reached life spans of at least 22 years. The longevity of bivalves in this assemblage, even as established from such a restricted sample, is impressive. In addition, modern bivalves have [von Bertalanffy] *k* values that range as high as 3, while the sectioned Seymour specimens all revealed *k* values less than 0.25 (Fig. 5A), on the lowest end of the modern distribution and representing extremely slow growth. Within this sample of slow-growing, long-lived fossil individuals, the relationship between *k* and life span seen in modern populations is also apparent: *those exhibiting slower growth tend to have lived longer lives*.... (emphasis added)

Even so, they stated that these should be considered minimum estimates of maximum possible lifespans (pp. 369–370), given that some collectors were not willing to give permission to the researchers to section the specimens in their collections. Hence, the shells Moss et al. examined typically did not include the largest individuals of a given species: at least one specimen was only a little more than half (53%) the known maximum size of the taxon! Even so, Moss et al. (2017) described these longevities as "extreme." They also noted that even older bivalve specimens of these eleven species are likely to exist (p. 371):

> …the likelihood of finding a longer-lived individual than what is observed (here, 131 years) will increase significantly with more intensive sampling. In each respect, it is highly likely that individuals older than those reported are present in existing collections, and virtually certain that they are present in the field waiting to be discovered.

In summary of these two studies, the fitted von Bertalanffy growth curves for the Eocene bivalves are shown in Figure 4, and their fitted von Bertalanffy curves for the Cretaceous bivalves are shown in Figure 5. Both the Eocene and Cretaceous bivalves show maximum body sizes of ~85 mm and maximum lifespans of ~120 to 130 years.

It is important to note that long-lived, slow-growing bivalves are not necessarily unusual in cold climates. A study (Moss et al., 2016) of 140,000 individual living marine bivalves, consisting of 1,148 local populations, showed that bivalves living in high latitudes grow more slowly and live longer than bivalves living at lower latitudes. The longevity of high-latitude bivalves is generally attributed to a combination of cold temperatures and caloric restriction. Montero-Serra et al. (2018) also demonstrated a positive correlation between greater bivalve longevity and greater habitat depth, although the correlation was stronger for corals, macroalgae, and sponges. Thus, bivalves living in colder and/or deeper waters are expected to exhibit greater longevity than those living in warmer and shallower waters.

The Pre-Flood Antarctic: Warm or Cold?

What is truly remarkable about these reported Seymour Island bivalve longevities is that evolutionists believe these bivalves were living in relatively warm waters, despite their belief that the latitude of Seymour Island (64°

S) has changed very little in the last supposed 100 million years (Moss et al., 2017, p. 374). Based on measured oxygen isotope ($\delta^{18}O$) values within the shells, Buick and Ivany (2004) estimated that their Eocene *C. raea* clams lived in relatively warm shallow seas at a temperature of about 14° C (57° F). Moss et al. (2017) estimated that their Cretaceous and Eocene specimens experienced average annual temperatures between 8 and 17° C (between 46 and 63° F). Moreover, as Moss et al. (2017) point out, uniformitarians think the high latitudes were largely ice-free until about 34 million years ago, at the Eocene-Oligocene transition. Buick and Ivany (2004, p. 922) noted, "Despite living at the Antarctic Circle, these Eocene *Cucullaea* grew in temperate waters, and in a less seasonal regime than might be expected from conditions on modern Earth."

Much fossil material suggestive of warmer past temperatures has been recovered from Antarctica (Oard, 2008, 2014). Within a creationist framework, these could either be fossils buried *in situ*, or material that was rafted in from lower latitudes during the Flood. Oard (2014, p. 17) acknowledges both possibilities but has noted the apparent difficulty in explaining how pre-Flood Antarctica could have been warm:

> It is easier to envision the Arctic being warm but not Antarctica because there is an ocean at the North Pole rather than a high-relief land mass. A warm Arctic Ocean would warm the surrounding high latitudes, but Antarctica should have been relatively cool because of its high latitude. High-latitude continents cool off considerably at night and in winter, especially with four to six months of total darkness. In addition, without the weight of today's ice sheets applying isostatic downward pressure, Antarctica would presumably have been at a higher altitude before glaciation,

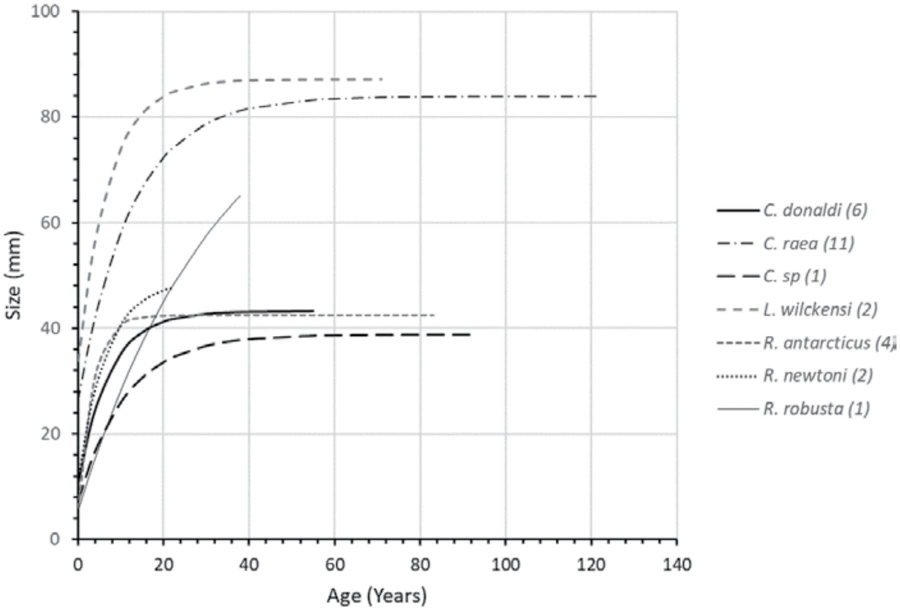


Figure 4. Ontogenetic growth curves for the Eocene *Cucullaea*, *Lahillia*, and *Retrotapes* bivalves from Seymour Island, Antarctica. Numbers in parentheses are the number of specimens in each assemblage. Constructed from data in Table I in Moss et al. (2017). Note that some specimens were living for many decades after achieving skeletal maturity.

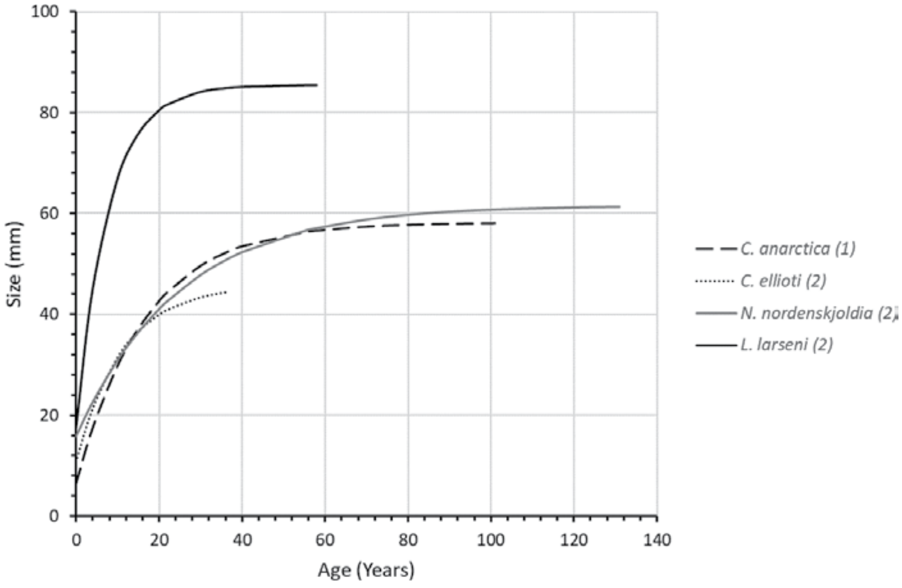


Figure 5. Ontogenetic growth curves for the Cretaceous *Cucullaea*, *Nodenskjoldia*, and *Lahillia* bivalves from Seymour Island, Antarctica. Numbers in parentheses are the number of specimens in each assemblage. Constructed from data in Table I in Moss et al. (2017).

> thereby enhancing the effects of cooling.

It is interesting that, despite this apparent difficulty, uniformitarian scientists still think it plausible that Antarctica could have been much warmer in the past, perhaps because of a greater concentration of atmospheric greenhouse gases. Some creationists have long suggested the pre-Flood climate was much warmer (Whitcomb and Morris, 1991), and Humphreys (2009) suggested this could have been due to a greater concentration of atmospheric carbon dioxide in the pre-Flood atmosphere, for which there is some evidence (Yapp and Poths, 1992).

Genesis 1:29 may give us a very important clue regarding the pre-Flood climate. Here, God told Adam and Eve, "Behold, I have given you every herb bearing seed, which is upon the face of *all* the earth, and every tree, in the which is the fruit of a tree yielding seed; to you it shall be for meat" (emphasis added). The word *all* may imply that vegetation was present everywhere on the pre-Flood Earth, which would seem to rule out ice sheets.

Moreover, based on a detailed study of thousands of well logs from around the world, Clarey (2020, p. 178) has suggested that pre-Flood Antarctica was at a lower paleolatitude than assumed by uniformitarian geologists, which would have resulted in a warmer pre-Flood Antarctic climate.

For this reason, Moss et al. (2017, p. 366) recognized that cold temperatures could not be the cause of these bivalves' extreme longevity. They attributed it to the seasonal availability of food resulting from extended seasons of darkness at high latitudes. Obviously, this explanation does not work if pre-Flood Antarctica was at a lower paleolatitude, as suggested by Clarey. Moreover, we have already seen (Hebert, Overman, and Sherwin, 2024) that *Crassostrea* oysters at mid-latitudes (without long periods of winter darkness) also once experienced much greater sizes and longevities, and grew faster, in absolute terms, than their modern-day descendants living in comparable temperatures and/or latitudes (Hebert, Overman, and Sherwin, 2024). In such cases, this longevity does not seem to be the result of caloric restriction, which creationists probably wouldn't expect in the pre-Flood world, anyway. This doesn't necessarily disprove Moss et al.'s (2017) hypothesis, but it does suggest that there could be another cause for this longevity.

Rudist Bivalves: Large Sizes and Delayed Maturation

The now-extinct rudists (order *Hippuritida*) were a group of Upper Jurassic to Upper Cretaceous marine bivalves that lived in warm, shallow, low-latitude seas (Johnson, 2002; Sha, Cestari, and Fabbi, 2020; Gao et al., 2025). Their fossils are often found in limestone rocks. In the Americas, their Cretaceous fossils extend from Mexico to northern South America and are also found throughout Europe (Figure 6), from central to southern Asia, and in northern Africa (Johnson, 2002; Anonymous a., n.d.).

Figure 6. An Upper Cretaceous fossil rudist bivalve from France. Image by Wilson44691 (Wikimedia Commons, public domain).

They were characterized by box-like, ringed, and tube-shaped valves, some of which were of "exceptionally large shell size" (Skelton, 2018, p. 18). For instance, *Titanosarcolites giganteus*, whose crescent-shaped shell resembled two rams horns with bases fused together, could be two meters long (Vermeij, 2016, p. 5) As in the case of other large extinct and extant bivalves, some have speculated (Benini, 1985) that the large shell sizes were the result of a symbiotic relationship between the rudists and algae. The algae would recycle the bivalve's wastes, including the waste CO_2, which would improve the bivalve's respiratory function, resulting in an increased rate of calcification that would enable the bivalve shells to grow thicker and longer. However, others disagree with this hypothesis. One problem with the hypothesis is that some extant bivalves, which are known to have a symbiotic relationship with algae, do not grow to large sizes (Benini, 1985, p. 24).

As described by Skelton (2018, p. 18),

> …while shell size in most bivalves tends to be limited by decelerated adult growth following relatively rapid juvenile size increase, rudists were able to produce elongated tubular valves *simply by maintaining juvenile-like, relatively high rates of incrementation over many years as adults* (Fig. 17.1–17.2), similarly to the large Liassic bivalves of the *Lithiotis* Gümbel, 1871 facies…. (emphasis ours)

Of course, if rudists maintained "juvenile-like" growth rates for many years, this is simply another way of saying they took a long time to attain maturity. Hence, both the large shell sizes of some specimens and these

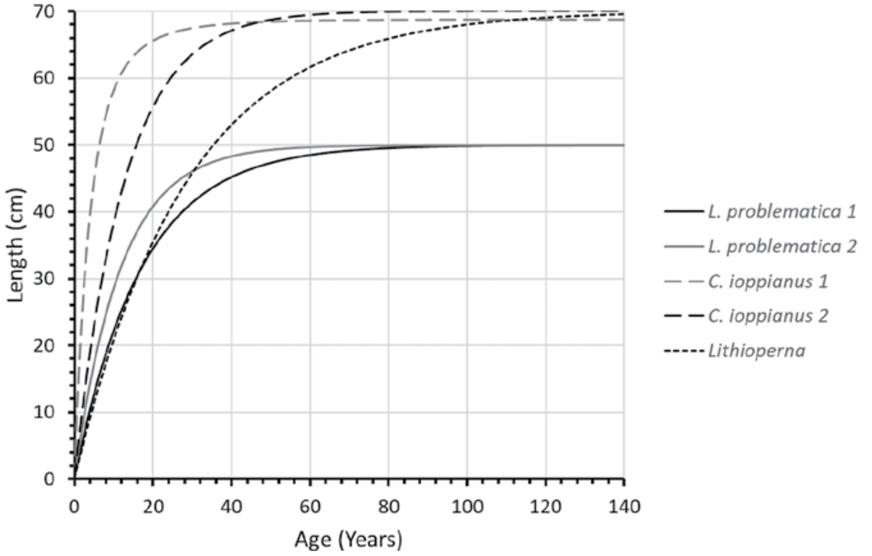


Figure 7. Killam's (2018) implied growth curves for two *L. problematica*, two *C. loppianus*, and one *Lithioperna* lithiotid Jurassic bivalve specimens with postulated values of L_∞ set equal to the known maximum lengths for each taxon. However, these curves are somewhat uncertain, as they were obtained with limited ontological data.

greater ages at maturity are consistent with greater longevity. Because they lived in warm shallow seas, such longevity could not have been the result of cold temperatures or deep water.

Upper Jurassic Lithiotid Bivalves

The above quote by Skelton alluded to large Liassic (Early or Lower Jurassic) *Lithiotis* bivalves. These were large "ubiquitous" bivalves that are thought to have lived in tropical, shallow near-shore tropical marine waters (Fraser, Bottjer, and Fischer, 2004; Posenato et al., 2018, 2022, 2024). As described by Killam (2018, pp. 41, 43), some Early Jurassic lithiotid bivalves reached lengths of 50–70 centimeters (1.6 - 2.3 feet). He noted (p. 43) that these sizes are larger than the largest extant mound-building oyster, *Crassostrea gigas*, which can attain 40 cm (1.3 feet) in length "in exceptional circumstances."

Killam studied three monospecific lithiotid genera from Northern Italy: *Lithiotis problematica*, *Cochlearites loppianus*, and *Lithioperna scutata*. In order to estimate *k* values for these Jurassic bivalves, he inserted into the von Bertalanffy equation a known specimen length $L(t')$ and corresponding ontogenetic age t' for that specimen, obtained either by band counting or from the technical literature. Although he did not say so explicitly, it seems he took the larval size at spawning to be zero, implying $t_0 = 0$. This is a reasonable assumption since even the eggs of the giant clam *Tridacna gigas* are only 100 μm across and are only 160 μm across, even two days after hatching (Ellis, 2003). Killam used known maximum valve sizes for L_∞ in Equation (1) to estimate values of the growth parameter *k*:

$$k = -\frac{1}{t'}\ln\left(1-\frac{L(t')}{L_\infty}\right) \qquad (2)$$

He also obtained an average growth rate (in some cases, the growth rate may have been provided in the literature, in which case the ontogenetic age was inferred). Since the reported lengths for the specimens fell on the linear part of the von Bertalanffy growth equation (see Figure 1), the (juvenile) growth rate could be approximated as

$$\text{Growth Rate} \approx \frac{L(t')}{t'} \qquad (3)$$

Killam obtained *k* values of 0.03 to 0.08 (Killam, 2018, his Table 2, pp. 81–82) for these Jurassic lithiotid bivalves, indicating a prolonged growth interval (by comparison, today's common *Crassostrea virginica* oysters have *k* values of about 0.67 to 0.90). His ontogenetic data for these Jurassic bivalves are summarized in Table I, and the implied growth curves for these species are shown in Figure 7. However, it must be acknowledged that there is some uncertainty in these *k* values, since they were obtained with postulated asymptotic lengths and actual ontogenetic data from only the linear portion of the von Bertalanffy growth curve. Nevertheless, it is generally accepted that these large Jurassic bivalves did take a long time to reach adulthood (Skelton, 2018, p. 18). Again, longer maturation times and larger adult body sizes are generally associated with greater longevity. Killam (2018) rejected the hypothesis that the large sizes of Liassic bivalves were due to accelerated calcification resulting from a photosymbiotic relationship with algae. C. A. Benini (1985, p. 30) also rejected this hypothesis, saying:

> To make a comparison, *Tridacna* [which does have a photosymbiotic relationship with algae]…grows annually 16 times faster than oysters; in just 6 years, *Tridacna* reaches a length of 55 cm. *Lithiotis* and *Cochlearites* grow [sic] to such a length in a time span of more than 20 years.

Benini (1985, p. 30) went on to say:

> Studies based on the growth pattern and periodicity of the Liassic bivalves of the *Lithiotis* facies showed that there is a considerable difference in the growth rate of the intertidal and subtidal taxa (large pelecypods); the large size of the latter is not the result of an accelerated Ca^{2+} mechanism, due to the photosymbiotic action of unicellular algae, *but is just evidence of a long life with constant and "normal" growth under environmental conditions which were apparently very stable.* [emphasis added]

Intertidal organisms are those that live on the part of the seashore that is covered at high tide but uncovered at low tide. Subtidal organisms live below the low-tide mark but still close to shore. So, at least the subtidal *Lithiotis* bivalves seem to have been characterized by relatively long lives.

Figure 8. ***Sphenoceramus/Inoceramus steenstrupi*** **from Greenland on exhibit in the Zoological Museum of Copenhagen, maximum length 1.87 m (6.1 ft); image credit: Mike Beauregard (Wikimedia Commons; Creative Commons Attribution 2.0 Generic license). https://creativecommons.org/licenses/by/2.0/deed.en.**

Truly Enormous Bivalves: The Inoceramidae

This section provides additional examples of extremely large bivalves in the fossil record, considering both geographic and geologic location. It is of specific interest that large bivalves have been found far inland from the coast, at high elevations, and throughout the geologic column. This is a testament to the global Flood described in the Bible. Much fossil information may be gleaned from the online Digital Atlas of Ancient Life (digitalatlasofancientlife.org). This, along with the other mentioned references, is the source for the information below.

Here we focus on two genera of the fossil family Inoceramidae, some members of which were truly enormous. Fossil clams in the genus *Inoceramus* are found in Jurassic to Cretaceous rocks, with the Cretaceous specimens being especially widespread (Rodriguez et al., 2017). Cretaceous specimens have an essentially worldwide distribution. Relatively large, 15.5 cm (6.1 inch) *Inoceramus* bivalve shells have been found in the Pierre Shale of South Dakota. Inoceramids from western Kansas are six feet (183 centimeters) in diameter. However, the record holder is a specimen 187 centimeters in diameter (over six feet) in the Geological Museum of Copenhagen (Figure 8).

Giant *Platyceramus* fossil clams strewn throughout the Green River formation in Utah at 4,000 feet (1,219 meters) above sea level were discovered by Kenneth Carpenter, director of Utah State University's Eastern Prehistoric Museum, and one of his university colleagues. Some researchers classify *Platyceramus* as a subgenus of *Inoceramus*, rather than as a separate genus. The press release (Anonymous b., 2013) describing the Utah find stated:

> "Stumbling upon these giant three- and four-foot clams was a real surprise," Carpenter said. "In places, they were so thick we could literally walk from clam to clam…." These giant clams look like large dinner plates, hence the scientific name *Platyceramus* means "flat clam." Today, giant clams are nowhere near the giant four-foot clams in size. The modern pipsqueaks are only two feet or so across and are native to the shallow coral reefs of the South Pacific and Indian Oceans….The giant clam [prepared for exhibition] is 44 by 48 inches, but in life might have weighed 50 pounds. Their

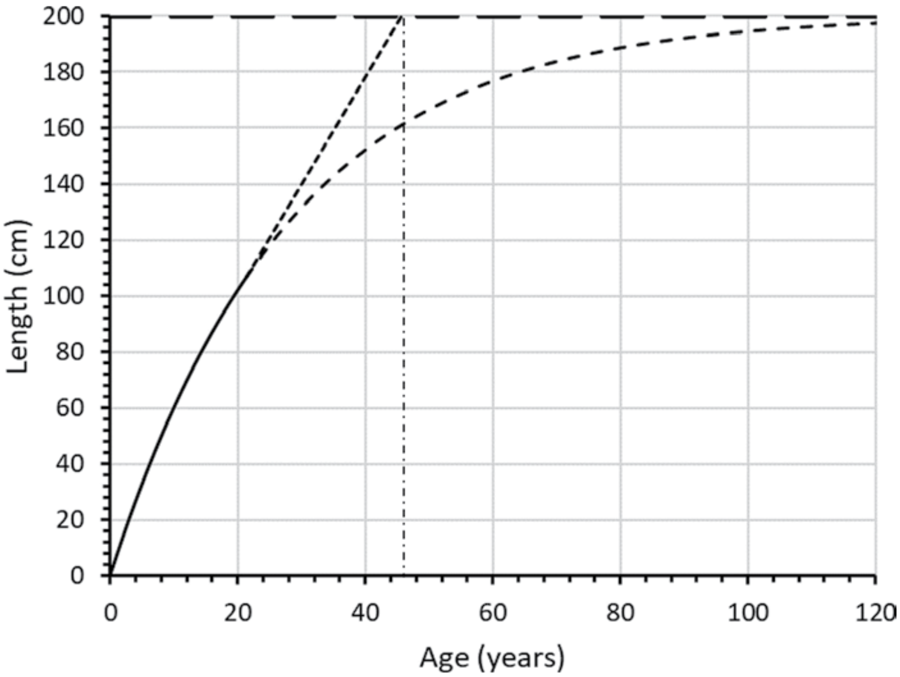


Figure 9. Growth curve (curved dashed line) obtained using Killam's procedure described in the text, for a *P. platinus* bivalve with an assumed (very conservative) asymptotic length of 200 cm. However, this curve is somewhat uncertain, as it was obtained from a limited amount of ontogenetic data, indicated by the solid black curve. Even so, linear extrapolation from the growth trajectory at 21 years implies an age at maturity of nearly 46 years.

> average life span might have been 100 years or more.

Platyceramus platinus clams in Late Cretaceous Kansas chalk grew to giant sizes of 4 feet (1.2 meters) or more. Likewise, specimens from the Niobara of Colorado are nearly 9 feet (2.74 meters) in length, with a width of 3–4 feet, or 0.91 to 1.22 meters (Everhart, 2011). Cretaceous *Platyceramus* Seitz shells were often one meter (3.3 feet) long, with some occasionally growing to lengths exceeding 2–3 meters (6.6–9.8 feet) (Kauffman et. al., 2007).

Killam used the same procedure described in the previous section to estimate *k* for *P. platinus*. For a known length of 107 cm at t = 21.4 years, an assumed spawning length of zero, and a (conservative) value of 200 cm for L_∞; the implied value of *k* is 0.035781. Using these data to construct an ontogenetic growth curve for *P. platinus* implies that the bivalve would have taken more than a century to reach maturity (Figure 9). Admittedly, the curve is somewhat uncertain, as it was obtained using only a postulated value of L_∞ and the data indicated by the solid black line in Figure 9. However, even if we extrapolate the known data, this *P. platinus* would have still taken nearly 46 years to reach maturity. Obviously, one would obtain even greater ages at maturity if one took $L_\infty = 300$ cm.

Conclusion and Discussion

A previous paper (Hebert, Overman, and Sherwin, 2024) presented evidence that fossil *Crassostrea* (and probably *Magallana*) bivalves experienced much greater longevity than their extant counterparts. This paper demonstrated that a number of extinct bivalve species also experienced great longevity, with some having lifespans of a century or more. It is striking that all these fossil bivalves, with the possible exception of some of the Cretaceous Seymour

Table I. Killam's (2018, his Table 2, p. 81) reported lengths, juvenile growth rates, and *k* values for five large lithiotid Jurassic bivalve specimens (representing three species), as well as their postulated asymptotic lengths and implied ontogenetic ages.

Species	Height (cm)	Growth Rate (cm/year)	Approx. Age (yrs)	Postulated L_∞ (cm)	*k* (year^{-1})
Lithiotis problematica	41.3	2.0	21	50	0.084683
	28.0	2.0	14	50	0.058641
Cochlearites loppianus	52.1	3.0	17	70	0.078524
	35.0	4.0	8.8	70	0.079217
Lithioperna scutata	25.0	2.0	13	70	0.035347

Table II. Ages, locations, and depths listed by Moss, Ivany, and Jones (2021) for the ten extant bivalve species with at least one specimen having a reported maximum lifespan of a century or more. Depth and locations were obtained from the listed references. In the case of *Crenomytilus grayanus*, I could not find the original reference cited by Moss (2016), which apparently listed the maximum lifespan as 150 years, rather than 126 years. Also, Moss seems to have mistaken *C. kurriana* for *C. siliqua*. Likewise, the maximum lifespan of *P. generosa* has increased to 179 years since 2016. Also included is the recently discovered deep-sea oyster *Neopycnodonte zibrowii*, which can live for up to 500 years. In some cases, maximum species lengths were obtained from the online *SeaLifeBase* database.

Species	Location	Depth (m)	Age	Max. Species Length (cm)	References
Arctica islandica	N Icelandic Shelf	80	507	13.0	Sample (2007); Butler et al. (2013)
Astarte borealis	Off Ellesmere Island	13.4–14.3	150	3.55	Torres et al. (2011); Moss et al. (2021)
Bathymodiolus childressi	Gulf of Mexico	650	100	12.4	Smith et al. (2000)
Crenomytilus grayanus	Northern Sea of Japan	3–32	126	16.0	Selin and Dulenina (2012); Anisimova et al. (2023)
Cyrtodaria siliqua	Artic & Sub-Arctic	50–500	105	11.0	Símonarson (1974); Kilada et al. (2009)
Glycymeris glycymeris	NW Scotland	25–55	192	6.5	Reynolds et al. (2013)
Hiatella arctica	NE Greenland	10–80	126	5.0	Sejr et al. (2002)
Mercenaria mercenaria	Cape Cod, MA	15	106	13.0	Ridgway et al. (2011)
Neopycnodonte zibrowii	NE Atlantic	420–500+	507	30	Wisshak et al. (2009)
Panopera generosa	British Columbia, CA	10	179	100 (including siphon)	Edge (2021); Wang et al (2023)
Tindaria callistiformis	N Atlantic	3800	100	0.84	Turekian et al. (1975)

Island bivalves, were living in shallow marine environments, and they were all living in temperate to tropical waters. This is a dramatic contrast to long-lived extant bivalves in today's world. Moss, Ivany, and Jones listed 32 bivalve species (their Table I, p. 9) having maximum reported lifespans of fifty years or more. Of these, ten species had maximum reported lifespans of a century or greater. Interestingly, the giant clam *Tridacna gigas* did not make their list. Although some think *T. gigas* can live for more than a century in the wild, this has apparently never been confirmed, as Moss, Ivany, and Jones listed the maximum reported lifespan for *T. gigas* as 60 years. Except for the *M. mercenaria* specimen from Buzzards Bay, Cape Cod (41° N latitude), these extant centenarian specimens were all retrieved from high latitudes (at least 50° N or S latitude) and/or deep (and presumably cold) water (Table II). In the case of the *Bathymodiolus* n. sp., one might wonder if the water temperature at a depth of 650 meters in the Gulf of Mexico would be warm or cold. The *Bathymodiolus* specimens were found at the GC233 brine pool at a depth of 650 meters. Depending upon the precise depth of the mussels in the pool, they could have been living in water as cool as (Joyce et al., 2005) 6° and 8° C (between 43° and 46° F) or as warm as 17° C (63° F).

In contrast, these fossil bivalves were generally exhibiting great longevity in shallow, temperate, or tropical waters, which means that this great longevity had to have a cause other than cold/deep water. And given the lushness of the pre-Flood world, caloric restriction does not seem to be a viable explanation, either.

Bible-believing Christians should be encouraged by this research, as this adds to a growing body of evidence

(Hebert, 2024a, 2024b, 2025a, 2025b, 2026) that animals in the pre-Flood world were experiencing much greater longevity, just as humans were.

References

Anisimova, A.A., M.N. Diagileva, A.V. Sinenko, and I.A. Dmitrieva. 2023. Age-related and seasonal dynamics of the hemocyte population in the mussel *Crenomytilus grayanus* (Dunker, 1853). *Russian Journal of Marine Biology* 49(2): 106–118.

Anonymous a. The Rudists. University Museum of Paleontology. University of California, Berkeley. https://ucmp.berkeley.edu/taxa/inverts/mollusca/rudists.php. (accessed May 6, 2025).

Anonymous b. Big Find: Giant Utah Clams Discovered. *Utah State Today* (Utah State University). https://www.usu.edu/today/story/big-find-giant-utah-clams-discovered. (accessed January 25, 2024).

Anonymous c. Inoceramus. *Geology Page*. 2023. https://www.geologypage.com/2015/02/inoceramus.html. (accessed November 18, 2023).

Benini, C. Accorsi. 1985. The large Liassic bivalves: Symbiosis or longevity. *Palaeogeography, Palaeoclimatology, Palaeoecology* 52(1–2): 21–33.

Buick, D.P., and L.C. Ivany. 2004. 100 years in the dark: Extreme longevity of Eocene bivalves from Antarctica. *Geology* 32(10): 921–924.

Butler, P.G., A.D. Wanamaker, Jr., J.D. Scourse, C.A. Richardson, and D.J. Reynolds. 2013. Variability of marine climate on the North Icelandic Shelf in a 1357-year proxy archive based on growth increments in the bivalve *Arctica islandica*. *Palaeogeography, Palaeoclimatology, Palaeoecology* 373: 141–151.

Clarey, T. 2020. *Carved in Stone: Geological Evidence of the Worldwide Flood*. Institute for Creation Research, Dallas, TX.

Crame, J.A., A.G. Beu, J.R. Ineson, J.E. Francis, R.J. Whittle, and V.C. Bowman. 2014. The early origin of the Antarctic marine fauna and its evolutionary implications. *PLoS ONE* 9(12): e114743.

Day, T., and P.D. Taylor. 1997. von Bertalanffy's growth equation should not be used to model age and size at maturity. *The American Naturalist* 149(2): 381–393.

de Magalhães, J.P., J. Costa, and G.M. Church. 2007. An analysis of the relationship between metabolism, developmental schedules, and longevity using phylogenetic independent contrasts. *The Journals of Gerontology: Series A* 66(2): 149–160.

Digital Atlas of Ancient Life. Paleontological Research Institution, Ithaca, NY. https://www.digitalatlasofancientlife.org/learn/mollusca/bivalvia/evolutionary-history/. (accessed November 18, 2023).

Edge, D.C., D.J. Reynolds, A.D. Wanamaker, D. Griffin, D. Bureau, C. Outridge, B.C. Stevick, R. Weng, and B.A. Black. 2021. A multicentennial proxy record of northeast Pacific sea surface temperatures from the annual growth increments of *Panopea generosa*. *Paleoceanography and Paleoclimatology* 36 (9): e2021PA004291.

Ellis, S. 2003. Spawning and Early Larval Rearing of Giant Clams (Bivalvia: Tridacnidae). Center for Tropical and Subtropical Aquaculture, *Publication No. 130*. https://www.ctsa.org/files/publications/CTSA_1306316728608730954 04.pdf. (accessed May 5, 2025).

Everhart, M. 2011. Inoceramids: Giant clams of the Cretaceous. *Oceans of Kansas*. oceansofkansas.com/Inoceramids/html. Accessed directly from link at www.geologypage.com. (posted November 28, 2011, accessed November 18, 2023).

Fraser, N.M., D.J. Bottjer, and A.G. Fischer. 2004. Dissecting "*Lithiotis*" bivalves: Implications for the Early Jurassic reef eclipse. *PALAIOS* 19(1): 51–67.

Gao, B., Q. Zhang, X. Rao, and L. Ding. 2025. Persistence of a shallow-marine environment in the western Kunlun area (northwestern Tibet) until the early Maastrichtian: Evidence from radiolitid rudist bivalves. *Cretaceous Research* 167: 106035.

Hebert III, L.(J.). 2023. Allometric and metabolic scaling: Arguments for design… and clues to explaining pre-Flood longevity? *Proceedings of the International Conference on Creationism*: Vol. 9, Article 18. https://cedarville.tind.io/record/21181?ln=en&v=pdf (accessed April 17, 2026).

Hebert, J. 2024a. Giantism and delayed maturation in fossil sharks: Evidence for extreme longevity? *Creation Research Society Quarterly* 60(4): 267–283.

Hebert, J. 2024b. Late Pleistocene body size reduction: Evidence of a post-Flood decline in longevity? *Journal of Creation* 38(1): 60–66.

Hebert, J. 2025a. Fossil crocodilians grew larger and longer, and lived longer than extant crocodilians. *Creation Research Society Quarterly* 61(3): 172–188.

Hebert, J. 2025b. Fossil teeth reveal Methuselah-like longevity and delayed maturation in tiny pre-Flood (Jurassic) mammals. *Journal of Creation* 39(1): 1–9.

Hebert, J. 2026. Fossil and modern lifespan comparisons of extant bivalve genera. *Journal of Creation* 40(1): 74–84.

Hebert, J., R. Overman, and F.J. Sherwin. 2024. *Crassostrea* oyster fossils show evidence of extreme longevity. *Creation Research Society Quarterly* 60(3): 171–190.

Humphreys, R. 2009. God's global warming worked just fine: Evidence from the pre-Flood world suggests that we need not fear global warming from carbon dioxide. https://creation.com/global-warming-facts-and-myths. (accessed May 9, 2025).

Johnson, C.C. The rise and fall of rudist reefs. *American Scientist* 90(2): 148–153.

Joye, S.B., I.R. MacDonald, J.P. Montoya, and M. Peccini. 2005. Geophysical and geochemical signatures of Gulf of Mexico seafloor brines. *Biogeosciences* 2: 295–309.

Kauffman, E.G., P.J. Harries, C. Meyer, T. Villamil, C. Arango, and G. Jaecks. 2007. Paleoecology of giant Inoceramidae (*Platyceramus*) on a Santonian (Cretaceous) seafloor in Colorado. *Journal of Paleontology* 81(1): 64–81.

Kilada, R.W., S.E. Campana, and D. Roddick. 2009. Growth and sexual maturity of the northern propellerclam (*Cyrtodaria siliqua*) in Eastern Canada, with bomb radiocarbon age validation. *Marine Biology* 156: 1029–1037.

Killam, D. 2018. The When, How, and Why of Bivalve Shell Growth: Sclerochronology as a Tool to Understand Physiology in Jurassic and Future Oceans. Ph.D. Dissertation. University of California, Santa Cruz.

Montero-Serra, I., C. Linares, D.F. Doak, J.B. Ledoux, and J. Garrabou. 2018. Strong linkages between depth, longevity, and demographic stability across marine sessile species. *Proceedings of the Royal Society B* 285: 20172688.

Morris, J.D., and F.J. Sherwin. 2011. *The Fossil Record* (3rd printing). Institute for Creation Research, Dallas, TX.

Moss, D.K. 2016. The evolution of extreme longevity in modern and fossil bivalves. Ph.D. Dissertation. Syracuse University, Syracuse, NY. https://surface.syr.edu/etd/662/.

Moss, D.K., L.C. Ivany, and D.S. Jones. 2021. Fossil bivalves and the sclerochronological awakening. Open access review published by Cambridge University Press and The Paleontological Society. *Paleobiology*: 1–23. DOI: 10.1017/pab.2021.16.

Moss, D.K., L.C. Ivany, E.J. Judd, P.W. Cummings, C.E. Bearden, W.-J. Kim, E.G. Artruc, and J.R. Driscoll. 2016. Lifespan, growth rate, and body size across latitude in marine Bivalvia, with implications for Phanerozoic evolution. *Proceedings of the Royal Society B* 283: 20161364.

Moss, D.K., L.C. Ivany, R.B. Silver, J. Schue, and E.G. Artruc. 2017. High-latitude settings promote extreme longevity in fossil marine bivalves. *Paleobiology* 43(3): 365–382.

Moss, D.K., D. Surge, M.L. Zettler, I.J. Orland, A. Burnette, and A. Fancher. 2021. Age and growth of *Astarte borealis* (Bivalvia) from the southwestern Baltic Sea using secondary ion mass spectrometry. *Marine Biology* 168: 133.

Oard, M.J. 2008. The paradox of warm-climate vegetation in Antarctica. *Journal of Creation* 22(2): 8–10.

Oard, M.J. 2014. Warm early Eocene Antarctica. *Journal of Creation* 28(3): 17–18.

Palmer, K.L., D.K. Moss, D. Surge, and S. Turek. 2021. Life history patterns of modern and fossil *Mercenaria* spp. from warm vs. cold climates. *Palaeogeography, Palaeoclimatology, Palaeoecology* 566, 110227: 1–13.

Posenato, R., D. Bassi, A. Trecalli, and M. Parente. 2018. Taphonomy and evolution of Lower Jurassic lithiotid bivalve accumulations in the Apennine Carbonate Platform (southern Italy). *Palaeogeography, Palaeoclimatology, Palaeoecology* 489: 261–271.

Posenato, R., G. Crippa, N.J. de Winter, G. Frijia, and P. Kaskes. 2022. Microstructures and sclerochronology of exquisitely preserved Lower Jurassic lithiotid bivalves: Paleobiological and paleoclimatic significance. *Palaeogeography, Palaeoclimatology, Palaeoecology* 602: 1111462.

Posenato, R., G. Crippa, N.J. de Winter, P. Claeys, S. Goderis, G. Frijia, and V. Brombin. 2024. Microstructures and sclerochronology of the *Lithiotis* Facies bivalves (Lower Jurassic): Paleobiological and paleoclimatic significance and their resilience to the early Toarcian extinction. *Palaeogeography, Palaeoclimatology, Palaeoecology* 649: 112329.

Reguero, M.A. 2019. Antarctic Paleontological Heritage: Late Cretaceous-Paleogene vertebrates from Seymour (Marambio) Island, Antarctic Peninsula. *Advances in Polar Science* 30(3): 328–355.

Reynolds, D.J., P.G. Butler, S.M. Williams, J.D. Scourse, C.A. Richardson, A.D. Wanamaker, Jr., W.E.N. Austin, A.G. Cage, and M.D.J. Sayer. 2013. A multiproxy reconstruction of Hebridean (NW Scotland) spring sea surface temperatures between AD 1805 and 2010. *Palaeogeography, Palaeoclimatology, Palaeoecology* 386: 275–285.

Ricklefs, R.E. 2010a. Life-history connections to rates of aging in terrestrial vertebrates. *PNAS* 107(22): 10,314–10,319.

Ricklefs, R.E. 2010b. Embryo growth rates in birds and mammals. *Functional Ecology* 24(3): 588–596.

Ridgway, I.D., C.A. Richardson, and S.N. Austad. 2011. Maximum shell size, growth rate, and maturation age correlate with longevity in bivalve molluscs. *The Journals of Gerontology: Series A* 66A(2): 183–190.

Ridgway, I.D., C.A. Richardson, E. Enos, Z. Unvaried, S.N. Austad, E.E.R. Philipp, and A. Csiszar. 2011. New species longevity record for the Northern Quahog (= Hard Clam), *Mercenaria mercenaria*. *Journal of Shellfish Research* 30(1): 35–38.

Rodriguez, E., G. Young, R. Pallardy, and the editors of *Encyclopaedia Britannica*. 2017. Inoceramus. *Britannica.com*. https://www.britannica.com/animal/Inoceramus/. (posted July 20, 1998, last updated September 4, 2017, accessed December 5, 2023).

Sample, I. 2007. Clam claims oldest animal record. *The Guardian*. https://www.theguardian.com/science/2007/oct/29/clam#:~:text=The%20Arctica%20islandica%20clam%20was%20plucked%20from,marine%20environment%20has%20changed%20in%20recent%20centuries. (accessed May 6, 2025).

Sejr, M.K., M.K. Sand, K.T. Jensen, J.K. Petersen, P.B. Christensen, and S. Rysgaard. 2002. Growth and production of *Hiatella arctica* (Bivalvia) in a high-Arctic fjord (Young Sound, Northeast Greenland). *Marine Ecology Progress Series* 244: 163–169.

Selin, N.I., and P.A. Dulenina. 2012. The growth and lifespan of the mussel *Crenomytilus grayanus* (Bivalvia: Mytilidae) in the Tatar Strait (Sea of Japan) in connection with the conditions of life at the northern border of the species range. *Russian Journal of Marine Biology* 38: 318–324.

Sha, J., R. Cestari, and S. Fabbi. 2020. Paleobiogeographic distribution of rudist bivalves (Hippuritida) in the Oxfordian-early Aptian (Late Jurassic-Early Cretaceous). *Cretaceous Research* 108: 104289.

Símonarson, L.A. 1974. Recent *Cyrtodaria* and its fossil occurrence in Greenland. *Bulletin of the Geological Society of Denmark* 23: 65–75.

Skelton, P.W. 2018. Treatise Online (Number 104). Part N, Revised, Volume 1, Chapter 26A: Introduction to the Hippuritida (Rudists): Shell Structure, Anatomy, and Evolution. Paleontological Institute, University of Kansas. https://journals.ku.edu/treatiseonline/article/view/7414/6753. (accessed May 9, 2025).

Smith, E.B., K.M. Scott, E.R. Nix, C. Korte, and C.R. Fisher. 2000. Growth and condition of Seep Mussels (*Bathymodiolus childressi*) at a Gulf of Mexico brine pool. *Ecology* 81(9): 2392–3403.

Torres, M.E., D. Zima, K.F. Falkner, R.W. MacDonald, M. O'Brien, B.R. Schöne, and T. Siferd. 2011. Hydrographic changes in Nares Strait (Canadian Arctic Archipelago) in recent decades based on δ^{18}O profiles of bivalve shells. *Arctic* 64(1): 45–58.

Turekian, K.K., J.K. Cochran, D.P. Kharkar, R.M. Cerrato, J.R. Vaišnys, H.L. Sanders, J.F. Grassle, and J.A. Allen. 1975. Slow growth rate of a deep-sea clam determined by ^{228}Ra chronology. *PNAS* 72(7): 2829–2832.

Vermeij, G.J. 2016. Gigantism and its implications for the history of life. *PLoS ONE* 11(1): e0146092.

von Bertalanffy, L. 1938. A quantitative theory of organic growth (inquiries on growth laws II). *Human Biology* 10: 181–213.

Wang, J., Q. Xu, M. Chen, Y. Chen, C. Wang, and N. Chen. 2023. Chromosome-level genome assembly of the Pacific geoduck *Panopea generosa* reveals major inter- and intrachromosomal rearrangements and substantial expansion of the copine gene family. *GigaScience* 12: 1–13.

Whitcomb, J. C., and H.M. Morris. 1991. *The Genesis Flood: The Biblical Record and Its Scientific Implications*. 35th printing. Presbyterian and Reformed Publishing Company, Phillipsburg, NJ.

Wisshak, M., M.L. Correa, S. Gofas, C. Salas, M. Taviani, J. Jakobsen, and A. Freiwald. 2009. Shell architecture, element composition, and stable isotope signature of the giant deep-sea oyster *Neopycnodonte zibrowii* sp. n. from the NE Atlantic. *Deep Sea Research Part I: Oceanographic Research Papers* 56(3): 374–407.

Yapp, C.J., and H. Poths. 1992. Ancient atmospheric CO$_2$ pressures inferred from natural goethites. *Nature* 355(6367): 342–344.

Creation Research Society Quarterly 2026 62:298–314

Creationeering®: A Systematic, Integrated Science-Engineering-Business Paradigm and Educational Program

M.F. Horstemeyer

Key Words: design, engineering, entrepreneurship, science, STEM

Accepted for publication December 1, 2025

Abstract

The creationeering® paradigm offers a suggested path for an individual to progress from scientific inquiry through engineering development to a final product, and this paper introduces the associated K–PhD educational framework. This systematic approach is motivated by the Dominion Mandate in Genesis 1:26–28, whereby God calls mankind to rule and reign over the Earth. Our current K–12, undergraduate, and graduate-level learning environments are not integrated for engineering, causing a lack of knowledge in our culture of people who do not fully understand the engineering process. The systems engineering steps are defined by the following: design, analysis/synthesis, procurement/making, logistics, assembly, performance/function, sustainability, and death/recycling. The business aspects include the following: human personnel, finances, legal, sales/marketing, and management. The scientific method is employed for prototyping within the engineering "analysis/synthesis" step. The K–12 creationeering educational program is broken down into four units for K–2, 3–6, 7–9, and 10–12 grades. An example of engineering a car crash is used to illustrate the points. The undergraduate creationeering curriculum maps each course with each engineering step to provide the student understanding of each class fitting into the degree plan. The Liberty University undergraduate ABET-accredited Mechanical Engineering Degree Program is used to illustrate the point. The graduate creationeering focus is on developing analysis/synthesis tools for prototyping. Although pieces of this holistic paradigm have been used in educational engineering programs, particularly at Liberty University, a comprehensive K–PhD program like the creationeering paradigm proposed herein has not. In essence, creationeering states: Create the prototype using the scientific method! Create the engineered product! Create the Intellectual Property! Create the business! Then we can serve mankind with the business to meet humankind's needs.

Simple Summary

Creationeering® is a comprehensive educational and professional framework that merges systems engineering with entrepreneurial business principles. Rooted in a Biblical worldview, the paradigm seeks to bridge the gap between scientific discovery and the delivery of finished products to consumers. The author outlines an integrated K–PhD curriculum that teaches students how to navigate eight specific engineering stages (design, analysis, procurement, logistics, assembly, performance, sustainability, and death/recycling) alongside five core business functions (finance, marketing, management, personnel, and legal). Using the automotive industry as a primary case study, Horstemeyer explains how this model prepares individuals to create intellectual property and manage technical corporations from a Biblical paradigm. Ultimately, the educational engineering program aims to provide a holistic perspective currently missing from traditional STEM education by emphasizing the practical "creation" of the world.

Introduction

Science, design, engineering, and entrepreneurship are often considered separate disciplines. We have programs at universities that train students in these different areas where Bachelor's, Master's, and even Doctoral degrees can be earned, developed in response to industry needs. The focused training of students in each of the distinct disciplines of science, design, engineering, and entrepreneurship leads to an individual's narrow paradigm when considering aspects of the other disciplines. Currently, there is no holistic perspective that integrates these notions, although the Kern Entrepreneurial Engineering Network (KEEN) (2023) has been making progress to that end since 2005.

Since there is also confusion about what engineering is in our society, it is worth staging the history for the reader regarding the topic at hand. Although engineering of wheels, levers, and pulleys occurred in ancient times along with other engineering "products," the definition of engineering has been elusive to most people in society. Maybe because when educators say STEM (Science-Technology-Engineering-Math), they give examples of physics (which is science) or math. In society today, we teach mathematics in the first grade, and we teach science or physics typically in the fourth or fifth grade. When do we teach engineering in elementary education? "Never" is the common response. There does not exist a K–12 engineering curriculum in the U.S. that is commonly used. Outreach programs have become prevalent (Jeffers et al., 2004), but they are limited in scope and time. K12 Engineers Academy (2025) has just six levels, providing a certificate, and mainly focuses on software. K12 Engineering and Technology Pathway (2025) focuses more on mechanical engineering, and in particular robotics, and hosts six classes with no grade orientation. Project Lead The Way (PLTW) (2025) is probably the closest to the full K12 engineering curriculum, where they separate ages in the following three categories: 1) PreK–5th grade, 2) 6th–8th grade, and 3) high school engineering. However, PLTW's board is filled with people with business degrees and not engineering degrees, so they do not have a coherent K–12 paradigm as proposed herein. Finally, Feder et al. (2009), upon encouragement from the National Academy of Engineering, argued for the full commitment of the Kindergarten through High School Program that has yet to be realized based on the continued growing need for engineers in the U.S. The National Academy of Engineering (2010) followed this report with another one that helped define the standards for a K–12 engineering curriculum.

Why do we have "Technology" in STEM if people knew what engineers do? There may be other reasons why society does not understand what engineering is. Theodore von Karman, an aerospace engineer and the first National Medal of Science recipient given by President John F. Kennedy in 1963, helped to clarify engineering by stating the following: "Scientists discover the world that exists; engineers create the world that never was." Hence, science focuses on discovering phenomena in nature using the scientific method, but engineering produces technical innovations, "things," and processes. Based on von Karman's definition (2023), we can differentiate between science and engineering in a clear, distinct way. Even in PLTW, the focus on STEM with science and mathematics illustrates that it is not just engineering and the technologies developed by engineers that are the real focus. Finally, the National Academy of Engineering (2010) admitted that STEM was mostly focused on mathematics and science, and some of the technologies, but really not much on engineering.

Now, how did the word "engineering" arise? Contrary to Google's answer (2023), "derived from the Latin *ingenium* meaning clever or ingenious," it comes from those overseeing the "engines" of war, like catapults (Soedel and Foley, 1979; Rihill, 2007). Hence, those specialists were first called "engineers" in 1390 (Oxford, 2023). Later, Robert Fulton invented the steam engine in 1807 (Knox, 1887). The conclusion was that engineers worked on engines. Today, how many engineers worldwide work on engines? Approximately 2% in the USA (BLS, 2023), so not too many. Hence, the word engineer is a misnomer today; it should be 'creationeer' based on von Karman's definition.

In terms of educational processes, Rensselaer Polytechnic Institute was the first university to award a formal engineering degree in 1835 with a Bachelor of Science in Civil Engineering (ASCE, 2023). However, it was not until Schlager (1956) and Hall (1962) described Bell Telephone Laboratories that we garnered the term "systems engineering" during the 1940's, which encapsulated Bell Labs teaming environment to capture the different phases of design (conceptual, preliminary, and final) before ordering parts and assembling the products. The "systems engineering" paradigm was then transferred in the late 1940s and early 1950s (Fitts, 1951) to airplanes, helicopters, and missile defense systems (Goode and Machol, 1957). The first systems engineering degree started at the University of Arizona in 1961 (University of Arizona, 2023). However, it was not until 1990 that a group of systems engineers created a professional society for systems engineering, the National Council on Systems Engineering (NCOSE), which was changed in 1995 to the International Council on Systems Engineering (INCOSE, 2023). One can see that formalizing systems engineering thinking has been a fairly recent phenomenon when compared to other disciplines like physics, mathematics, etc.

In terms of bringing entrepreneurship and engineering together, probably the first to do so was Frank Turman, Dean of Engineering at Stanford University in 1951, for what we now call "Silicon Valley" (Foster, 1984, pp. 26–37). Turman changed farmland into the electronics industry, starting with Hewlett-Packard. Many other engineering corporations started from Stanford's engineering college, thus creating the computer industry as we know it today. From there, other institutions like MIT, the North Carolina Research Triangle, *etc.* developed technical corporations that arose from the local academic institutions, mainly from their engineering programs. However, it was not until 2005 that a formal academic networking group started for engineering entrepreneurship (KEEN, 2023).

To date, the full integration of a systems engineering approach joined with entrepreneurship in an educational curriculum has not been fully implemented in which each course taken is clearly defined in system so when a freshman starts in engineering, they know why each class is designed for their engineering degree and how they fit together as an engineering system with the opportunity to have entrepreneurship in their curriculum as a minor. Creationeering offers that unified approach, which integrates engineering and entrepreneurship at the undergraduate level. Beyond this, creationeering offers more than just an undergraduate engineering education.

The creationeering paradigm is proposed under the Dominion Mandate given by God in Genesis 1:26–28. Although an education program is not mentioned herein, it can be implied.

> Genesis 1:26–28 (NKJV)—Then God said, "Let Us make man in Our image, according to Our likeness; let them have dominion over the fish of the sea, over the birds of the air, and over the cattle, over all the earth and over every creeping thing that creeps on the earth." So God created man in His *own* image; in the image of God He created him; male and female He created them. Then God blessed them, and God said to them, "Be fruitful and multiply; fill the earth and subdue it; have dominion over the fish of the sea, over the birds of the air, and over every living thing that moves on the earth."

In the following sections, we discuss in order the systems engineering aspects in Section 2, the entrepreneurship aspects in Section 3, and the educational aspects in Section 4, including differentiating between K–5th grade, 6th-8th grades, high school, university undergraduate level, and university graduate school levels. In each section, to help exemplify the abstraction of creationeering, we use one of mankind's greatest engineering inventions in the twentieth century, an automobile, in the context of crashworthiness. The leading cause of death in the U.S. from ages 4–34 is vehicular crash (Ross et al., 2006). Figure 1 shows an example of four different length scales represented as a system, the subsystems, the modules, and the components (Woo, 2017). The automobile typically comprises approximately over 25,000 components made of different materials that have gone through different manufacturing processes.

Engineering Constituent of Creationeering

Creationeering provides a holistic systems perspective that integrates science, design, engineering, and entrepreneurship with a multiscale perspective on the design/control/energy volume from kindergarten to doctoral students. The engineering constituent of creationeering includes the following fundamental, independent, necessary, and sufficient eight required

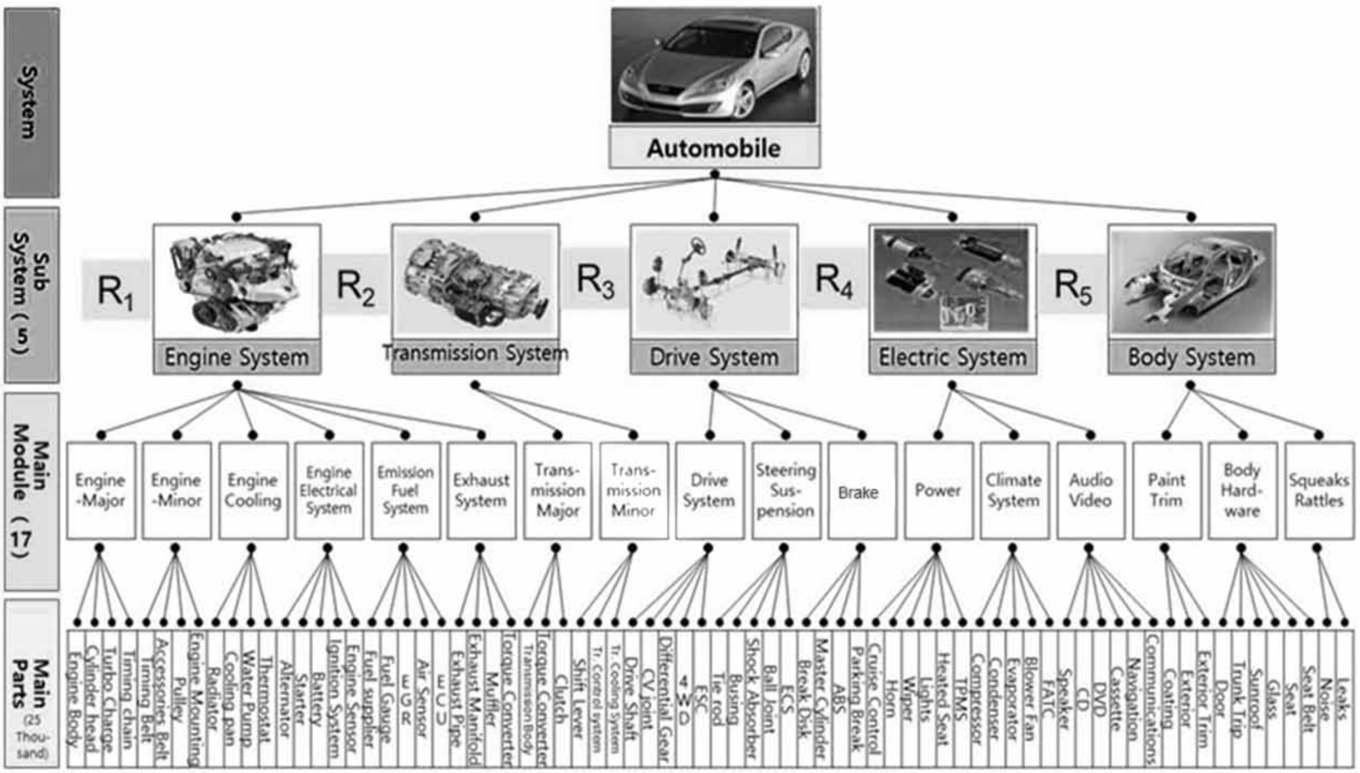


Figure 1. Systems engineering of an automobile that has a design life for 10 years, showing the four length scales of design: the top-level system, the five typical subsystems, 17 main modules, and the 25,000 parts. (Woo, 2017)

steps in any engineering system (see Figure 2):

1. *Design:* a thinking process that defines the engineering problem, includes ideation of solutions, and creates prototypes related to a product, process, software, or system. In defining the engineering problem, the objectives, constraints, and variables are specified and used to determine the possible solutions.
2. *Analysis/Synthesis:* computational and/or experimental evaluation of the designed prototype(s) by applying scientific analytic principles, processes, and tools to reveal the properties and state of a product, process, software, or system.

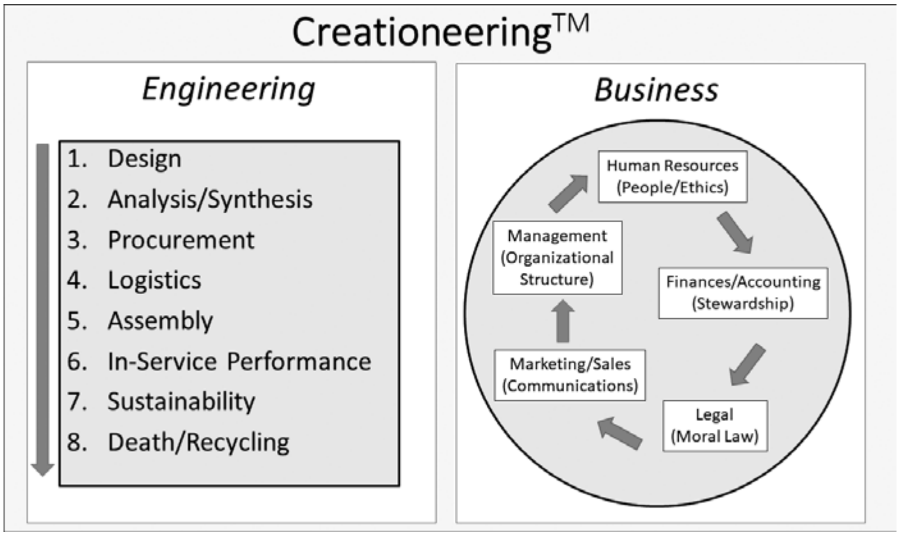


Figure 2. The engineering steps and independent features of a business that are required for an entrepreneur to start a technical business (Horstemeyer et al., 2022).

3. *Procurement or Materials Processing:* the "making" of the products as the final "thing" or for the process or system, also including the exchange of funds for the products and/or "things." The key aspect of making the products is the process-structure-property-performance sequence of a material in terms of the information passage to assure that the design is realized within the tolerances (uncertainties associated with the processes of making the products and/or "things.")
4. *Logistics:* the synchronization process of the distribution, transportation, and warehousing of the products and/or "things" where reliability, maintainability, and availability are dynamically changing before the products and/or "things" can be assembled.
5. *Assembly:* the process of putting components together to make a subsystem and putting subsystems together to make a system.
6. *Performance:* requirements for the life cycle of the product to properly function, considering normal and abnormal environments.
7. *Sustainability:* the operation of an engineering system that employs resources to remain after the process and product are completed. Reliability to continue the operation is oftentimes categorized in sustainability.
8. *Death/Recycling:* operation of performance afterlife in which it will be decided that the product will either be thrown away or returned as a new product after undergoing a new materials processing method.

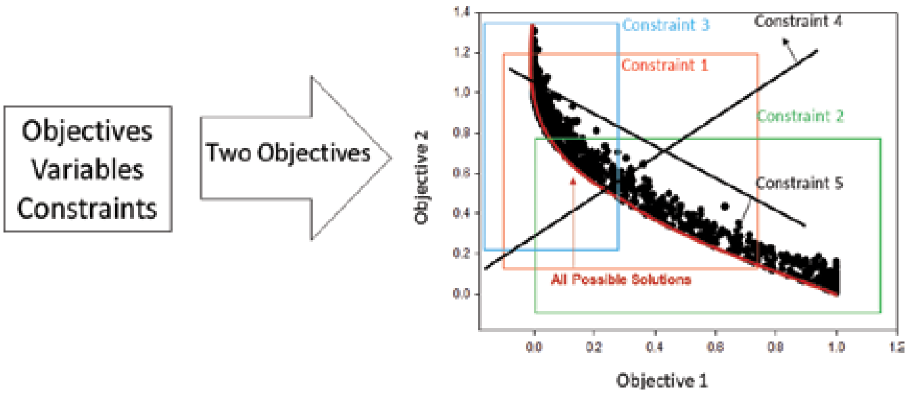


Figure 3. Schematic showing a Pareto (1920) frontier with associated constraints in a multi-objective optimization setup. Two objectives are illustrated.

Creationeering Step 1: Design

Design in engineering is a thought process of devising a component, subsystem, system, or process to meet desired objectives while considering the constraints and feasible variables. Design is typically an iterative process at each length scale and certainly between length scales.

The design process includes objectives, constraints, and variables that are interrelated in a mathematical equation(s) with metrics that are optimized (c.f., Fang et al., 2005a,b; Johnson et al., 2016). There is a continuum from *strong* to *weak* sensitivities of the variables and constraints on the objective(s), which gives rise to uncertainties related to the solution (Coleman and Steele, 1999). How large the uncertainties are is related to the reliability of the solution (Pidong et al., 2017).

In a mathematical sense, an *objective* can be a numerical value or a function that can increase or decrease. For example, a designer may wish to maximize profit or minimize weight. Many mathematical equations can work with single objectives. As Figure 3 illustrates, a simple calculus differentiation can allow a gradient model to easily capture the minimum in the equation, which signifies the optimal solution. When using simple mathematical gradient methods, the designer normally weights the various objectives and sums them to form a single objective. However, Figure 3 also illustrates that a designer can have two or more objectives, which mathematically will introduce what is called a "Pareto Frontier" or sometimes "Pareto Front" (Pareto, 1920). The Pareto Front is the maroon line in Figure 3, illustrating that multiple solutions can satisfy the minimization, meaning there are multiple solutions. However, Figure 3 also illustrates that different constraints can come into and limit the solution space.

From a mathematical perspective, a *constraint* is a condition that must be satisfied for the design to be feasible. Examples include physical laws, limited human capital, funds, user requirements, or bounds on the validity of the mathematical models. Constraints in the mathematical equations can be used directly or can be incorporated into the objective using Lagrange multipliers (Lagrange, 1764, 1811; Rockafellar, 1993) to garner the optimal solution. The different constraints illustrated in Figure 3 limit the solution space and eliminate other possible solutions in the Pareto frontier. Constraints complicate the mathematical equations and decrease the number of possible solutions. Some constraints may be very limiting, and others may not.

A design *variable* is a parameter that is controllable by the designer but could vary depending on the constraints, and minimizing (or maximizing) the solution with respect to the mathematical equations (*e.g.,* thickness or a material type), and is often bounded by maximum and minimum values. In Figure 3, the possible solutions that are admissible after considering the constraints are still many. As such, the solution is typically decided by an engineer in practice. When only one objective is employed in the design analysis, then convergence on a single solution is possible, and an engineer is not necessarily required, because the mathematical equation will decide on the optimal solution. However, when more than one objective is included, then, by definition, since multiple answers are possible, it takes intelligence outside of the engineered system to make the decision on the design, so, hence, an engineer is required. This is consistent at any and every length scale.

Mathematics is the language by which to describe a design. The designer must choose a mathematical equation or set of equations to relate the constraints and objectives to the design variables. They may include complicated finite element analysis (cf., Fang et al., 2005b) and/or reduced order metamodels (cf., Fang et al., 2004, p. 4487). In the context of engineering or creationeering, a design is not the "thing" but only a logical and hopefully mathematical representation of the "thing," while making the "thing" occurs later in the creationeering process after the design is completed.

Design for Procurement

Materials Selection

Picking a material for a particular component requires a decision based on the objectives, constraints, and variables of how it could be made in an upscale manufacturing environment. Third Generation High Strength Steel Alloys can be made in the laboratory, but they cannot be mass-produced. Hence, when a designer is contemplating choosing a material or designing a material for a performance environment (s), one must also consider the material's processing method and the associated objectives, constraints, and variables. Probably the best materials database is from Granta (ANSYS) (Ashby, 2016), which offers a wide range of materials information for different applications. The objectives are related to the properties that are desired, given the constraints of the manufacturing method. Most times, cost is proportional to the volume of the material and is either a hard upper constraint or an objective to be minimized.

Manufacturing Method

Different manufacturing methods exist in order to create the material in the designed shape that is required to meet the engineering objectives. Some of the broad categories include the following: additive manufacturing, casting, forming, heat treatments, joining, machining, molding, and painting. The objectives are to maximize repeatability, minimize the out-of-tolerance requirements for the manufacturing method, and minimize production time. The main constraint is cost. The variables include the machinery, materials, and methods to optimize the objectives. "Concurrent Engineering" (Eppinger, 1991; Sohlenius, 1992) has historically been used to optimize the "performance" and "procurement" at multiple levels, within themselves and then together at the same time.

Design for Logistics

The objectives of designing for logistics are related to minimizing the time difference between assembly steps as the parts are shipped from Tier 1 or Tier 2 vendors. Because different part suppliers (Tier 1 and Tier 2 companies) are possible in a vehicle, different locations need to be assessed in terms of optimizing the "just-in-time" model. Another objective is to maximize the long-term relationship with suppliers for the logistical flow to be reliable. Constraints include product volume constraints, costs, timing, and distance. Some of the variables include transportation mode, costs, timing, and distance.

Design for Assembly

When one thinks of the massive changes that Ford (1913; Brinkley, 2003, p. xxii) introduced to upscale the automobile industry, one needs to go directly to his design for the assembly of such a historical achievement. El Wakil (1998) summarized the status and issues of designing for the assembly almost 100 years later. El Wakil (1998) compared and contrasted the human manual assembly method versus a robotic-automated assembly method, showing the differences in time, costs, and reliability. The objectives are basically to maximize the alignment and location of certain features for the process of assembly, minimize the number of different components in an assembly, minimize fastening screws (expensive and time-consuming), and minimize non-standard components/materials (risk goes up for new components/materials). The constraints include the following: (1) use the largest, rigid part of the assembly as a base or fixture to build upon; (2) avoid components from tangling or nesting during feeding; (3) avoid abrasive, fragile, and flexible components so that they do not retard feeding; (4) avoid re-orienting the assembly as it might require more machinery to support the assembly package. The variables include the machinery type, orientation angle, handling method, and feeding method of the components into the assembly.

Design for Life-Cycle Performance

Typically, when one thinks of designing something, they first think of designing for the "life cycle performance" environment, e.g., winning a race with a race car. The objectives for a car or van on the road has several objectives: (1) minimize damage to the people in the vehicle in a crash, (2) optimize to a certain sound (amplitude and frequency) for the brand of the vehicle (think Harley Davidson), (3) minimize temperature deviations from 70° F (Martinho et al., 2004) inside of the vehicle since that is the human body comfort, (4) minimize humidity deviations from 20% in the car cabin for maximum human body comfort, (5) maximize visual area of driver to keep vehicle safe, (6) minimize outside sounds to the people inside, and (7) minimize displacements of people inside vehicle upon various road conditions (pothole strike, panic brake, railroad strike, etc.). The constraints include the following: (1) keep the resonant frequencies away from 4–10 Hz at least for the driver since the human body parts in the torso region have a 4–10 Hz resonance and it could make the people sick in the vehicle; (2) the structural components should last 100,000 miles; (3) make seats comfortable for the driver and passenger to have customers want to stay in the vehicle; and (4) keep the car cabin noise below 8 dB (Olson, 1972) to keep the car quieter for better driver concentration.

Design for Sustainability

Sustainability can be thought of as sustaining the individual vehicle or sustaining the whole transportation industry. When considering the vehicle, let us consider a Chevrolet Corvette, since it has experienced eight generations in its existence. Each new generation tried to upgrade the vehicle and keep it modernized with the updated environment. In other words, the objectives and constraints changed thus modifying the design and actual vehicle. For example, the E-ray is a hybrid version of the Corvette, where the objective was to minimize carbon emissions from gasoline. When considering all of the transportation vehicles, one might try to minimize the carbon emissions to sustain our environment, so then the objective for transportation would be to minimize the carbon footprint. Thus, the fairly recent trend towards hybrid and electric vehicles arose.

Design for Death/Recycling

Typically, a vehicle's end-of-life is designed for 100,000 miles or ten years, so these would be constraints that would affect the mechanical design of the structural components based upon cyclic fatigue, creep, and crashworthiness. The question herein is what is the objective of the vehicle once it reaches death? Should the materials be recycled? Should the parts still useful be sent to other vehicles for replacement? The objective is typically to maximize profit from the materials once the car is considered "scrapped." Currently, most cars are sent to a scrapyard, where they are stripped of valuable parts, crushed, and recycled into scrap metal or plastic, and the nonrecyclable parts are sent to a landfill (Dean and Sterner, 1969; Adams, 1972).

Creationeering Step 2: Analysis/Synthesis of the Design

Analysis of information or synthesis of complex disparate information within a design includes the application of scientific principles and methods to assess the feasibility of the design. This includes analyzing the properties and state of the component, subsystem, or system. Careful evaluation and deliberation are fundamental to the analysis and/or synthesis of any design. Once a completed design is made into a prototype, then simulations and/or experiments can be used to validate the design (working hypothesis in the scientific method). Most vehicles like cars can be both simulated and experimentally validated (or rejected). However, some large structures like airplanes or submarines can only be tested in smaller scales whereas the larger scales are simulated. Hence, the modern analysis methods can be complex. We should also note that when analyzing the objectives of the design, the engineer must not only meet the technical objectives but also the appropriate aesthetics as well (Burgess, 2001). Getting the right balance of form and function is an art as well as a science.

Now that the overall car "system" has been conceptualized, analysis of the whole system, subsystems, and components is undertaken by a group of engineers in "normal" environments. Normal environments reflect the car functioning in its normal operations. Each engineering team will have different roles and responsibilities related to the engineering requirements "downscaled" from the whole system to the subsystems to the components. The second Design Phase, sometimes called the Preliminary Design or Detailed Design, is accomplished by the engineers based on their analysis. Each engineering team will consider the design for manufacturability (procurement), logistics, the assembly of the components and subsystems, its function/performance environments, sustainability of the car, and death/recycling.

Once this Detailed Design phase is finalized, then the cars will be designed for "abnormal" environments. Abnormal environments reflect the scenarios that can occur by accidents. For the car, the worst abnormal environment is a crash. As such, the most important focus in the final design phase is studying the crashworthiness of a vehicle. Once the final design has been experimentally validated, then the components are ready for procurement for the prototype that in turn will be analyzed by computational or experimental methods.

Creationeering Step 3: Procurement of the Materials for the Design

Procurement is the process of obtaining and the making of materials along with getting the equipment to make a component, subsystem, or system. Detailed knowledge of the definitions of the materials and the materials processing method are required. For example, components can be made from metals through wrought processes (stamping, forming, forging, etc.), casting, and additive manufacturing processes. Different metal chemistries that make up the metal alloys can be used in almost any of the materials-processing methods, which admits now multiple billions of variations of materials. Because there are approximately 25,000–30,000 components in a car, the Original Equipment Manager (OEM), like Ford Motor Company, General Motors Company, etc., having Tier 1, 2, and 3 suppliers is particularly important. Hence, each component is made in a different way.

Creationeering Step 4: Logistics of the Various Components and Subsystems

After something is designed and analyzed and ready to be made, then logistics is required to piece together all of the different personnel and materials to "systemize" the finalized design. Logistics can be defined as the selective application of scientific and engineering efforts undertaken during the acquisition process. The objectives of the design, not only of the product for the performance environment, but also for logistics, can be time efficiency, so that each step is coordinated together in time.

Related to logistics, the automotive supply chain for an Original Equipment Manager (OEM), for example, Ford Motor Company, includes the following: dealerships, manufacturers, Tier 1 suppliers, Tier 2 suppliers, and Tier 3 suppliers. Hence, the 25,000–30,000 components come from these companies, so organizing the scheduling of these components through different corporate bureaucracies is an effort. Logistical scheduling of the supply chain products is complex.

Creationeering Step 5: Assembly of the Various Components and Subsystems

Once the finalized designed parts are ready at hand, then they are ready to be assembled. Assembly refers to a number of parts or subassemblies or any combination thereof joined together to perform a specific function, and subject to disassembly without degradation of any of the parts (Hanifan, 2014, p. 23). Simply, it is putting parts together.

Mass production assembly is what made Henry Ford (1913) famous. Cars existed when Carl Benz (1879) in Germany created the first three-wheeled motor vehicle. However, Ford's first venture into automobile assembly with the Model A involved setting up assembly stands on which the whole vehicle was built, usually by a single assembler who fit an entire section of the car together in one place. This person performed the same activity over and over at his stationary assembly stand. To provide for more efficiency, Ford had parts delivered as needed to each workstation. In this way, each assembly fitter took about 8.5 hours to complete his assembly task. By the time the Model T was being developed, Ford had decided to use multiple assembly stands with assemblers moving from stand to stand, each performing a specific function. This process reduced the assembly time for each fitter from 8.5 hours to a mere 2.5 minutes by rendering each worker completely familiar with a specific task.

Creationeering Step 6: Function or In-Service Life Performance of the Engineered System

Once the validated designed "thing" is put together, then it is ready to perform its designed-for function. This entails the real-life performance of the "thing" so that it fulfills its objectives for which it was designed.

Engineers are not only interested in getting a product to market, but in determining how effectively that product accomplishes the goal for which it was created and how it survives through its routine use.

The reason that different Ford vehicles exist is that their performance or function is different. For example, the Ford Escort's performance objectives are related to increased gas mileage and lower vehicle cost, in contrast to the Ford F-150 truck's performance objectives, which are reliability, ability to pull heavy weights, off-road stability, and lower costs. These different objectives clearly have motivated the completely different designs of these vehicles.

Creationeering Step 7: Sustainability of the Engineered System

Sustainability means how the engineered component, subsystem, or system continues on to the next generation. Sustainability can be thought of as the ability of current generations to use resources so as not compromise the environment or deplete the materials for future generations. To enable all people throughout the world to satisfy their basic needs and enjoy a better quality of life, without compromising the quality of life, affects future generations.

Each engineering team for each car provides minor adjustments to the next year's version to continuously improve the car's usage. Reports from consumers come back to the design team, who then start the creationeering process over for the next-generation vehicle.

Creationeering Step 8: Death/Recycling of the Engineered System

The final stage that an engineer must consider is what to do with the materials once the designed performance of the product is over. Recycling is converting an already existing product or material into a new product. One could consider a system of materials circulation when a materials first objective is over, that there can be a secondary objective of the used product. At this point, the secondary product might need to go through reprocessing to reach its objectives.

Each vehicle is designed for a particular lifetime. For example, a Ford F-150 truck will typically meet an objective of 150,000 miles, while some will reach a stretch objective of 300,000 miles. However, a Ford Escort can last between 100,000 and 200,000 miles. Because the environmental conditions and road usage are different, the 'death' of the vehicle will occur at different times.

Vehicle recycling comprises the dismantling of vehicles into separate parts, some for reuse and others for different reprocessing. Approximately 12–15 million vehicles reach the end of their useful life each year in just the United States alone. The vehicles are shredded, and the metals, polymers, and glass are recovered for recycling, while in many areas, the rest is further sorted by machine for recycling of additional materials. The remainder, known as automotive shredder residue, is put into a landfill. The shredder residue of the vehicles that is not recovered for metal contains many other recyclable materials, including 30% of it as polymers, and 5–10% of it as residual metals. Modern vehicle recycling attempts to be as cost-effective as possible in recycling those residual materials. Currently, 75% of the materials can be recycled, with the remaining 25% ending up as landfill. As the most recycled consumer product, end-of-life vehicles provide the steel industry with more than 14 million tons of steel. A car crusher is often used to reduce the size of the scrapped vehicle for transportation to a steel mill.

Entrepreneurship Constituent of Creationeering

The five fundamental, independent features of a business enterprise or entrepreneurship required to start a business, as shown in Figure 2, are the following:

1. *Human Resources*: the hiring, administration, and training of personnel with ethical standards. The basic ethical basis to undergird human relationships is service-to-one-another as a team, then science, engineering, and entrepreneurship (business) will not be self-centered and oriented towards the team. Tommy Lasorda, former Los Angeles Dodgers baseball coach, always told his players to play for the name on the front of their jersey (the team) and not for the name on the back of the jersey (their own self).
2. *Finances*: management, accounting, and stewardship of money as a commodity to achieve the goals of the business. Herein, one must first make strategic (long-term) goals, from which arise tactical goals (short-term) that can be met with certain finances. The finances are then used to hire people, facilities, equipment, etc., to meet the goals. If finances are the only objective, to maximize profit without any other objectives or constraints, then the engineering system will fail. One can recall 1 Timothy 6:10a (KJV): the love of money is the root of all evil. It is not bad to have an increasing profit; it is just bad to have it without other objectives and constraints to bring that objective into balance for the whole system to thrive.
3. *Legal* an entity requires compliance with laws related to intellectual property, litigation, investigations, and acquisitions. Furthermore, one could place ethics into this category to help the value system of the new technology corporation.
4. *Marketing/Sales*: the action of communicating and connecting the products with the consumers with the Professional Engineering ethics basis of truth, honesty, and meeting genuine client needs.
5. *Management*: an organizational structure to admit the rules, roles, and responsibilities for individuals to operate.

Human Resources Used in the Creationeered System

The term "Human Resources" for a business is to recruit, train, develop, compensate, team-build, conduct performance appraisal, communicate worker health and safety issues, and identify methods for selecting staff for the business system.

Along with managers, the auto industry requires different sets of requirements for the working team. Related to the engineering process, the auto industry requires designers, analysts, materials producers, logistics operators, assemblers, and recyclers. There are different roles and responsibilities for the Original Equipment Manufacturers (OEMs), Tier 1, Tier 2, and Tier 3 corporations throughout the whole supply chain.

Finances/Accounting Used in the Creationeered System

Our Creator has expressed his concern through Jesus in humans being good stewards of the resources that the Creator has supplied for us. Finance and accounting can be defined as the management, allocation, and exchange of resources for the business system.

The largest market in the world is the automotive industry, so different jobs related to money are typical of almost any industry. The following positions are needed: accountants, insurance agents, financial planners, ethics and auditors, etc.

Legal Aspect of the Creationeered System

Most humans have the tendency to believe in moral obligations and responsibilities. Almost everyone (with a few exceptions) believes that it is right to show kindness and wrong to inflict pain on another person.

Legal issues arise from governmental laws and certification boards. Automotive companies have lawyers who address intellectual property, personnel employment issues, insurance, corporate policies, and immigration.

Sales/Marketing Related to the Creationeered System

Sales and marketing are communications of information from the business system to those outside of the system. In other words, interpersonal communications are key to sales and marketing. The sales and marketing personnel's objectives are to maximize clarity of the needs of those outside the business system with those inside the company.

As mentioned, the largest market in the world is the automotive industry, so marketing and selling to the different nations/cultures is a key job. For example, crossover vehicles represent the largest market in the USA [https://www.statista.com/statistics/276506/change-in-us-car-demand-by-vehicle-type/]. The Volkswagen Golf was the number one car sold in Europe in 2019 [https://www.best-selling-cars.com/europe/2019-full-year-europe-best-selling-car-models/], and the number one 2017 vehicle sold in China was the Wuling Hongguang [https://www.goodwood.com/grr/road/news/2018/4/axons-automotive-anorak-chinas-best-selling-cars/].

Management of the Creationeered System

Management is an organizational structure of the business system. The Creator ordered from the very beginning an ordered, organizational structure that started with the family unit, where the father was the accountable entity of the family unit. A good management structure is therefore key to the success of any system.

Ford Motor Company has a fairly low number of management levels, as they believe that it provides a faster, more efficient, and integrated approach to customer service (Moynihan and Titley, 2000). Their structure is outlined as follows: Chairman, President, Executive Vice-President, and Functional Heads. The functional heads have a direct relationship with the workers in each of the categories of the personnel structure. Each company is different based on its ethics and human personnel strategy.

Creationeering K–12 Education

The K–12 educational aspects for creationeering can be focused on the engineering aspect of the paradigm and not so much on the business side. Various instructional methods are used to reinforce the engineering process steps. In particular, the early focus is on the "design" and "analysis" steps of the engineering process in which the NRS (1996) is used. In particular, three areas are considered: (1) Physical Science Content Standard B—"As a result of their activities in grades 9–12 all students should develop an understanding of motion and forces" (NRS, 1996, p. 149); (2) Science Education Program Standard B—"The program of study in science for all students should be developmentally appropriate, interesting, and relevant to students' lives: emphasize student understanding through inquiry: and be connected with other school subjects" (NRC, 1996, p. 212); and (3) Science Education Program Standard C—"The science program should be coordinated with the mathematics program to enhance student use and understanding of mathematics in the study of science and to improve student understanding of mathematics" (NRS, 1996, p. 214).

Hands-on experiments for the "assembly," "performance," and "sustainability" steps of the engineering process are used to demonstrate the crashworthiness concepts for automotive design. Since children can identify with an automobile and safety, this example is excellent for learning. Experiments with simple examples of the eight steps, associated discussions, and open-ended questions are key for K–5 learning. For Grades 6–12, along with the experiments and associated discussions and open-ended questions, additional design complexities and analysis with math and physics are included. The crashworthiness example can include physics principles in car crashes, teacher explanations of the physics applications, a list of materials for each lesson, and vocabulary words and definitions.

Another instructional piece is related to vehicular safety. Some of the topics include the following: discussion of highway safety statistics, collisions and effect on the vehicle and passengers with and without seat belts and air bags, and physics lessons associated with the safety features on vehicles.

The instructional goals include the following: (1) to create an interest in engineering for students in grades K–12, (2) to promote safe driving practices to decrease deaths and injuries in car crashes, and (3) to enhance the level of understanding of science and engineering in grades K–12 by providing detailed hands-on science activities for K–12 teachers.

K–12 Experimental, Lessons, and Activities

Based upon NRS (1996) standards, different levels of understanding scientific concepts have been defined and used in the development of the "analysis" of the "designs" for the car crash scenarios. The following science topics are considered in the engineering design of the crashworthiness vehicles:

1. *Energy*: For grades K–5 students, study potential and kinetic energy in a qualitative sense using the examples of a car rolling from rest down an inclined plane. Energy transformation and conservation of energy are discussed. For Grades 6–12 students, study conservation of energy from both a qualitative and quantitative perspective. Students solve age-appropriate conservation of energy problems associated with the motion of objects. Emphasis is placed on the transformation of kinetic energy to other forms during inelastic collisions. The deformation of various types of materials is discussed in terms of conservation of energy.
2. *Velocity and Acceleration*: In Grades K–5, students study velocity and acceleration from a qualitative perspective. This activity involves students stepping onto a series of evenly spaced lines on the floor at one-second intervals. The distance between the evenly spaced lines is increased to demonstrate increased velocity. To demonstrate acceleration, the distance between the lines is not evenly spaced but increases with each successive line. For Grades 6–12, students study velocity and acceleration from both a qualitative and quantitative perspective. Students solve age-appropriate velocity and acceleration problems and determine velocity and acceleration from displacement-versus-time and velocity-versus-time graphs. Students distinguish between vectors and scalars. Students also conduct the velocity and acceleration activity using timed intervals for uniformly spaced and non-uniformly spaced taped lines.
3. *Conservation of Momentum Demonstration and Newton's Laws*: In Grades K–5, students are introduced to the concepts of conservation of momentum and the relationship between impulse and change in momentum using balloons, Newton's cradles, Hot Wheels cars, happy/unhappy balls, and modeling clay. They also relate the concepts of conservation of momentum and Newton's Laws to car safety and collisions. Emphasis is placed on the relationship between the time it takes to stop an object and the magnitude of the force required to stop the object. The effect of deformation of various types of materials upon the time to bring the occupants in a vehicle to a complete stop is also discussed. For Grades 6–12, students study conservation of momentum and Newton's laws from both a qualitative and quantitative perspective. Students solve conservation of momentum and impulse-change in momentum problems. They also relate the concepts of conservation of momentum and Newton's Laws to car safety and collisions. Emphasis is placed on the relationship between the time it takes to stop and object and the magnitude of the force required to stop the object. The effect of deformation of various types of materials upon the time to bring the occupants in a vehicle to a complete stop is also discussed.
4. *Stop That Egg Activity*: The purpose of this activity is to reinforce the relationship between impulse and change in momentum in a qualitative sense. This activity is the same for students in grades K–5 and 6–12. Students are first asked to throw an egg into a bed sheet held vertically and perpendicular to the ground by two other students. The students are told to throw the egg as fast as they can in an attempt to break it. Because of the deformation of the sheet, it is virtually impossible to break the egg due to the increased time to stop it. Students also relate this activity to the functioning of an airbag in vehicles.
5. *Egg Toss Activity*: Students are then to play egg toss with a partner at ever-increasing distances. This activity is the same for students in Grades K–5 and 6–12. Students quickly learn that they must "give" with the egg and therefore increase the time to stop the egg to prevent it from breaking. This activity may also be implemented as a student competition. This activity also reinforces the relationship between impulse and change in momentum.
6. *Passenger Restraint Systems Activity*: The purpose of this activity is to have students design, analyze, and procure the materials for a passenger restraint system for a passenger (raw egg) that is aboard a wooden car. This activity is the same for students in Grades K–5 and 6–12. Hence, the performance environment is the car rolling down an inclined plane and colliding with a vertical wall. Using the scientific method, students prepare a hypothesis as to which type of restraint system would best protect the egg in a collision. Students then select their material and test it by allowing the car to roll down the ramp and collide with a stationary barrier at the end. Success is measured by whether or not the passen-

ger (egg) is damaged. The students can then redesign the restraint in a sustainable sense. The broken eggs are thrown away upon their "death." The scientific concepts of conservation of momentum and conservation of energy provide the basis for their analysis.

7. *Safety and the Collision Effects upon Passengers*: This phase includes analysis of reaction times, safe following distances, and the forces on passengers in collisions involving various types of restraint systems. Conservation of energy, crumple zones, and vehicle deformation are also included in this chapter. Age-appropriate activities and problem computations are provided for K–12 students.

K–12 Student Competitions

Along with experiments for learning, the authors encourage "competitions" between student groups to help learn the engineering process. The first competition is called "Mission Eggscellence," which demonstrates the application of the eight engineering steps to a bumper on a small car in which an uncooked egg is used as a passenger. The goal is not to allow the egg to crack in the crash. The second competition is called an "Automotive Challenge," which demonstrates the engineering step of procuring a restraint system (seat belt) for the egg in a crash, where the egg represents a passenger. Again, the egg should not crack upon impact. Different impact velocities are achieved by raising the board height, which acts as a track, on which the vehicle rides. It impacts another board at the bottom of the track. The egg should be placed in a sealed paper "baggie" before placing it into the vehicle. The competition includes guidelines for logistics related to pre-competition planning, "day of" competition planning, competition setup, and organizational instructions.

Figure 4. Three middle school students are getting ready to release the vehicle with the egg in it for the Mission Eggscellence competition.

Mission Eggcellence Challenge

In the Mission Eggcellence Challenge, the students are given a previously constructed car which consists of a 12-inch-long, 2-by-4-foot board with skate wheels attached. Students (see Figure 4) design a bumper for a wooden car that will keep a passenger (raw egg) safe. The bumpers, constructed within stated parameters, are attached to the cars using Velcro strips. The egg is restrained by two Velcro strips so the design of the restraint system is not part of the competition. Students use the concepts of impulse and change of momentum, as well as energy dissipation in the deformation of materials, as analysis tools in designing their bumpers. The car's performance objective is to minimize damage to the egg as it rolls down an eight-foot-long inclined ramp and impacts a vertical barrier. Students are eliminated from the competition if the egg breaks during the collision. The angle of inclination of the ramp is increased after each successful run until a winner emerges. In a tie, the winner is the car that uses the bumper with the smallest mass. The Mission Eggcellence Challenge is conducted in the same manner for students in Grades K–5 and 6–12.

Automotive Engineering Challenge

The Automotive Engineering Challenge is based on vehicle safety. The K–2 and 3–5 students use K'nex (or comparable plastic construction kit) components to design, analyze, and assemble a car that will house a raw egg. This car and passenger (raw egg) travel down an eight-foot ramp to impact a barrier (see Figure 5). Emphasis in this competition is placed upon both the design of the front end of the vehicle and the type of restraint system used to hold the egg during impact. The competitions are conducted in the same manner as the Mission Eggcel-

Figure 5. (a) Three middle school students are getting ready to release the vehicle with the egg in it for the Automotive Engineering Challenge competition. (b) Note the K'nex vehicle design for this particular student team.

lence Challenge, in which the winner is determined by the vehicle in which the egg survives the highest angle of inclination without breaking. In case of a tie, the winner is determined to be the car with the smallest mass.

For Grades 6–8 and 9–12, students must design and construct their car from balsa wood and glue. Since the platform for each car is a rectangular piece of balsa wood with a square front end, the emphasis for students in Grades 6–12 is entirely on the construction of the passenger restraint system. This car and passenger (raw egg) also travel down an eight-foot-long inclined ramp to impact a barrier. The wheels for the car consist of compact discs with a plastic hub insert, which has a ¼ inch hole for an axle. The rules for competition are the same for Grades K–5 and 6–12.

Undergraduate Engineering Education

The creationeering paradigm can be applied directly to each and every major engineering program/discipline [ABET, 2012] with a technological entrepreneurship minor. We show, herein, in Table I, the ABET-accredited mechanical engineering program employed at Liberty University. The example of mechanical engineering with an emphasis on automotive engineering illustrated in this paper can be extended to any other engineering discipline. Also, the thinking processes of organization, analysis, and prioritization that are typical of undergraduate engineering curricula are present here in the creationeering paradigm.

Etzkowitz et al. (2000) argued that the future of STEM education will need a stronger emphasis on entrepreneurship. The argument arises from internal university "push" and external industry "pull" on academic structures to develop new "knowledge-based" innovations. Table II summarizes the courses needed for a Technological Entrepreneurship program that Liberty University School of Engineering has developed.

Graduate School Engineering Education

The creationeering paradigm can be applied to any graduate program, albeit the emphasis is usually on the "analysis/synthesis" tools development of the engineering process, although one could argue that there have been many different PhD theses that have addressed design, materials processing, logistics, assembly, sustainability, and recycling as well. We note that some engineering schools are creative in innovating with new corporations based on the graduate-level research. Roach et al. (2019, pp. 207–228) surveyed students from 40 different USA universities and showed that between 16–26% of the graduate students were interested in developing a start-up company from their research. Recently, Colombelli et al. (2021) analyzed a group of PhD students, of which 50% were involved with entrepreneurship. The quantified evidence revealed a positive effect of the entrepreneurial education program on the academic and business outcomes. In other words,

Table I. Example of curriculum for the Mechanical Engineering major, illustrating how each course fits into the creationeering paradigm (Year 1 = YR1; Year 2 = YR2; Year 3 = YR3, Year 4 = YR4).

Course Number	Course Name	Design	Analysis	Procurement/ Making Things	Logistics	Assembly	Life-Cycle Performance	Sustainability	Death/ Recycling
ENGR102	Engineering Intro	YR1							
ENGR110	Engineering Problem Solving Intro	YR1	YR1						
ENGR 125	Visualization Tools		YR2						
ENGR 133	MATLAB		YR1						
Math131	Calc 1		YR1						
Math 132	Calc 2		YR1						
Math 231	Calc 3		YR2						
Math 334	Diff Eq		YR2						
Chem 121	Chemistry		YR2						
Physics 231	Physics 1		YR1						
Physics 232	Physics 2		YR2						
Physics 320	Thermo 1		YR2						
ENGR 210	Statistics	YR2	YR2		YR2	YR2	YR2	YR2	YR2
ENGR 235	Statics						YR2		
ENGR 240	Dynamics			YR2			YR2		
ENGM 310	Materials			YR2			YR2	YR2	YR2
ENGR 313	Mechatronics						YR4	YR4	
ENGR 315	Fluid Dynamics		YR3	YR3			YR3		YR3
ENGR 330	Strength of Materials		YR3	YR3			YR3	YR3	YR3
ENGM 350	Computer Aided Engrg	YR3	YR3				YR3		
ENGR 360	Heat Transfer			YR3			YR3		YR3
ENGM 375	Thermal Fluids Lab			YR3			YR3		
ENGR 381	Engrg Design Intro	YR3	YR3						
ENGR 385	Thermo II						YR3	YR3	
ENGR405	Dynamic Systems Modeling		YR4				YR4	YR4	
ENGR 415	Machine Design	YR4					YR4	YR4	
ENGR 445	Manufacturing Processes			YR4					
ENGR 481	Engring Design 1	YR4	YR4						
ENGR 482	Engring Design 2	YR4	YR4	YR4					
ENGR 200	Comp Teams	YR1–YR4	YR1–YR4	YR1–YR4	YR1–YR4	YR1–YR4	YR1–YR4	YR1–YR4	YR1–YR4

Table II. Example of the Technology Entrepreneurship minor for science, technology, engineering, and mathematics (STEM) undergraduate students illustrating how each course fits into the ereationeering paradigm.

Course Number	Course Name	Human Personnel	Finance	Legal	Sales/ Marketing	Management
ENGR 202	Creationeering Intro	X	X			
ENGI 220	Engineering Economy		X			
Busi 336	Entrepreneurship Intro	X	X	X	X	X
Busi 338	Developing Entrepreneurial Opportunities	X	X	X	X	X
ENGR 470	Technology and Business Practicum 1	X	X	X	X	X
ENGR 475	Technology and Business Practicum 2	X	X	X	X	X

if no industry "pull" exists, then the knowledge "push" from the scientific research will not necessarily move into the space that is helpful for industry. When the knowledge "push" is constrained with the industry "pull," then new domains for new corporations are created. Thus, the creationeering paradigm can create new businesses to help create wealth.

Discussion

The following quote from St. Hill et al. (2013) provides a nice parable for creationeering. "'Give a man a fish; you have fed him for a day. Teach a man to fish, and you have fed him for a lifetime'—Lao Tsu, Chinese philosopher. Revised saying, 'Give a man a fish; you have fed him for today. Teach a man to fish, and you have fed him for a lifetime. Teach a man how to establish a fishing business, and you not only feed him for a lifetime but bring benefits to his family and the community.'" As a creationeer, one can realize the connection from scientific research through the engineering process into the entrepreneurial corporations to genuinely affect the economic, social, environmental, and spiritual transformation of a culture.

These five "business" aspects comprise a system of independent, necessary, and sufficient characteristics that lay the foundation for any corporation. Each of the eight engineering and five business features is independent and necessary to each other in the mathematical and logical sense when thinking about first principles. The ethics statement from the National Society of Professional Engineers (NSPE) lays out seven canons that undergird the whole creationeering system:

1. "Hold paramount the safety, health, and welfare of the public.
2. Perform services only in areas of their competence.
3. Issue public statements only in an objective and truthful manner.
4. Act for each employer or client as faithful agents or trustees.
5. Avoid deceptive acts.
6. Conduct themselves honorably, responsibly, ethically, and lawfully so as to enhance the honor, reputation, and usefulness of the profession."

Summary

Creationeering can be thought of as the following: Create the prototype using the scientific method! Create the engineered product! Create the Intellectual Property! Create the business! From an educational perspective, we need to educate our children with this paradigm, such that when the engineering process and business/entrepreneurship process combine, a modern industrial revolution can arise. If we can train our students with the creationeering paradigm, we are encouraging a clear opportunity for them to rule and reign on the Earth to serve mankind and fulfill God's Dominion Mandate.

References

ABET (Accreditation Board for Engineering and Technology). 2012. *ABET Constitution.* Archived from March 28, 2012. Retrieved January 31, 2012. (March 2025 Bylaws, Constitution, and Rules of Procedure at https://www.abet.org/about-abet/governance/bylaws-constitution-and-rules-of-procedure/.)

Acar, E., and K. Solanki. 2009. System reliability-based vehicle design for crashworthiness and effects of various uncertainty reduction measures. *Structural and Multidisciplinary Optimization* 39:311–325.

Adams, R.L. 1972. An economic analysis

of the junk automobile problem. University of Illinois, Urbana-Champaign, IL.

ASCE Library. 2023. https://ascelibrary.org/doi/10.1061/40594%28265%2941#:~:text=Rensselaer%20Polytechnic%20Institute%2C%20founded%20in,in%20Civil%20Engineering%20in%201834, (accessed January 11, 2023).

Ashby, M. 2016. Material property data for engineering materials. *Engineering Department and Granta Design* 27. (See https://www.ansys.com/content/dam/amp/2021/august/webpage-requests/education-resources-dam-upload-batch-2/material-property-data-for-eng-materials-BOKENGEN21.pdf for October 2021, 5th edition.)

Benz, C. 1879. *Mercedes-Benz Group*. https://group.mercedes-benz.com/company/tradition/company-history/1885–1886.html (accessed/cited February 13, 2025).

BLS, Bureau of Labor Statistics, USA. 2023. https://www.bls.gov/oes/current/oes534011.htm and https://www.bls.gov/oes/current/oes_nat.htm#17–0000 (accessed/cited on January 11, 2023).

Brinkley, D.G. 2003. *Wheels for the World: Henry Ford, His Company, and a Century of Progress, 1903–2003*. Viking Press, New York, NY.

Burgess, S.C. 2001. *Hallmarks of Design*: *Evidence of Purposeful Design and Beauty in Nature*. Day One Publications, Carlisle, PA.

Coleman, H.W., and W.G. Steele. 1999. *Experimentation and Uncertainty Analysis for Engineers*. John Wiley & Sons, New York, NY.

Colombelli, A., A. Panelli, and E. Paolucci. 2021. The implications of entrepreneurship education on the careers of PhDs: Evidence from the challenge-based learning approach. *CERN IdeaSquare Journal of Experimental Innovation* 5(1): 49–55.

Dean, K.C., and J.W. Sterner. 1969. Dismantling a typical junk automobile to produce quality scrap, Volume 7350. U.S. Department of Interior, Bureau of Mines, Washington, D.C.

El Wakil, S.D. 2019. *Processes and Design for Manufacturing*. CRC Press, Boca Raton, FL.

Eppinger, S.D. 1991. Model-based approaches to managing concurrent engineering. *Journal of Engineering Design* 2(4): 283–290.

Etzkowitz, H., A. Webster, C. Gebhardt, and B.R.C. Terra. 2000. The future of the university and the university of the future: Evolution of ivory tower to entrepreneurial paradigm. *Research policy* 29(2): 313–330.

Fang, H., M. Rais-Rohani, and M. Horstemeyer, M. 2004. Multiobjective crashworthiness optimization with radial basis functions. In *10th AIAA/ISSMO Multidisciplinary Analysis and Optimization Conference* (Albany, NY). https://doi.org/10.2514/6.2004–4487.

Fang, H., M. Rais-Rohani, Z. Liu, and M.F. Horstemeyer. 2005. A comparative study of metamodeling methods for multiobjective crashworthiness optimization. *Computers & Structures* 83(25–26): 2121–2136.

Fang, H., K. Solanki, and M.F. Horstemeyer. 2005. Numerical simulations of multiple vehicle crashes and multidisciplinary crashworthiness optimization. *International Journal of Crashworthiness* 10(2): 161–172.

Feder, M., G. Pearson, and L. Katehi (editors). 2009. *Engineering in K–12 Education: Understanding the Status and Improving the Prospects*. National Academies Press, Washington, D.C.

Fitts, P.M. 1951. Human engineering for an effective air-navigation and traffic-control system. *APA PsycNet*. https://psycnet.apa.org/record/1952–01751–000.

Ford, H. 1913. 2023. The moving assembly line and the five dollar workday, https://corporate.ford.com/articles/history/moving-assembly-line.html (accessed/cited on January 11, 2023).

Foster, K. 1984. Encouraging new technology links between industrial and teaching institutions: Aston Science Park. In Arthur, P. 1984. *CADCAM in Education and Training: Proceedings of the CAD ED 83 Conference*. Springer, Boston, MA.

Google. 2023. Where did the word 'engineering' come from? https://www.google.com/search?q=where+did+the+word+engineering+come+from&rlz=1C1GCEB_enUS830US830&oq=where+did+the+word+engineering+come+from&aqs=chrome.0.0i512j0i22i30l5j0i15i22i30l3j0i22i30.6824j1j15&sourceid=chrome&ie=UTF-8, (accessed/cited on January 11, 2023).

Hall, A.D. 1962. *A Methodology for Systems Engineering*. Van Nostrand Reinhold, New York, NY. ISBN 978–0-442–03046–9.

Horstemeyer, M.F., A. Adebayo, M. Jantomaso, J.L. Long, S. Burgess, and A. McIntosh. 2022. Creationeering™: An integrated engineering-business paradigm for technological entrepreneurship from a Biblical basis. *Creation Research Society Quarterly* 58(4): 238–261.

International Council on Systems Engineering (INCOSE). 2023. INCOSE: The Trusted Authority in Systems Engineering. https://www.incose.org/, (accessed/cited on January 11, 2023).

Jeffers, A.T., A.G. Safferman, S.I. Safferman. 2004. Understanding K–12 engineering outreach programs. *Journal of Professional Issues in Engineering Education and Practice* 130(2): 95–108.

Johnson, K.L., S. Chowdhury, W.B. Lawrimore, Y. Mao, A. Mehmani, R. Prabhu, R.,…and M.F. Horstemeyer. 2016. Constrained topological optimization of a football helmet facemask based on brain response. *Materials & Design* 111: 108–118.

K12. 2025. Engineering and technology pathway. https://www.k12.com/career-and-college-prep/career-prep/career-fields/engineering-and-manufacturing/engineering-technology-pathway/.

K12Engineers Academy. 2025. https://www.k12engineers.com/

KEEN. 2023. https://engineeringunleashed.com/about, (accessed/cited on January 11, 2023).

Knox, T.W. 1886. *The Life of Robert Fulton and* *a History of Steam Navigation*. Putnam, New York, NY.

Lagrange, J.L. 1764. *Mécanique Analytique, memoir to the Academy of Paris. Prix de l'Académie royale des sciences de Paris.* In *Œuvres complètes de Lagrange, Tome VI*, pp. 5–61. sites.mathdoc.fr.

Lagrange, J.L. 1811. *Mécanique Analytique*. Paris, France: Ve Courcier (reissued by Cambridge University Press, 2009). ISBN 978–1-108–00174–8. https://archive.org/details/mcaniqueanalyt02lagr?utm_source=copilot.com

National Research Council, & Committee on Standards for K–12 Engineering Education. 2010. *Standards for K–12 engineering education?* National Academies Press, Washington, D.C.

NRS (The National Committee on Science Standards and Assessment). 1996. *National Science Education Standards*. National Academies Press, Washington, D.C.

NSPE (National Society of Professional Engineers). 2023. NSPE Code of Ethics for Engineers. https://www.nspe.org/resources/ethics/code ethics?gclid=EAIaIQobChMIy-fDtq-PA_AIVUsvICh28EwheEAAYASAA-EgKKnvD_BwE, (accessed/cited on January 11, 2023).

Olson, N. 1972. Survey of motor vehicle noise. *The Journal of the Acoustical Society of America* 52(5A): 1291–1306.

Oxford Dictionary. 2023. https://www.oed.com/view/Entry/62225?rskey=zaItca&result=1&isAdvanced=false#eid, (accessed/cited January 11, 2023).

Pareto, W. 1920. *Compendio di Sociologia Generale* (in Italian). (Gaspero) Barbèra: Florence, Italy.

Pidong, W.A.N.G., J. Zhang, Z.H.A.I. Hao, and Q.I.U. Jiwei, Q. I. U. 2017. A new structural reliability index based on uncertainty theory. *Chinese Journal of Aeronautics* (4): 1451–1458.

Project Lead The Way (PLTW). 2025. Engineering curriculum. https://www.pltw.org/curriculum/pltwengineering.

Rihill, T.E. 2007. *The Catapult: A history*. Westholme Publishing, Yardley, PA.

Roach, M., H. Sauermann, and J. Skrentny. 2019. Are foreign STEM PhDs more entrepreneurial? Entrepreneurial characteristics, preferences, and employment outcomes of native and foreign science and engineering PhD students. In *The Roles of Immigrants and Foreign Students in US Science, Innovation, and Entrepreneurship*. University of Chicago Press, Chicago, IL.

Rockafellar, R.T. 1993. Lagrange multipliers and optimality. *SIAM Review* 35(2): 183–238.

Ross, M., D. Patel, and T. Wenzel. 2006. Vehicle design and the physics of traffic safety. *Physics Today* 59(1): 49–54.

Schlager, K.J. 1956. Systems engineering-key to modern development. *IRE Transactions on Engineering Management* EM-3(3): 64–66.

Soedel, W., and V. Foley. 1979. Ancient catapults. *Scientific American* 240(3): 150–161.

Sohlenius, G.1992. Concurrent engineering. *CIRP Annals* 41(2): 645–655.

von Kármán, T. 2023. https://en.wikiquote.org/wiki/Theodore_von_K%C3%A1rm%C3%A1n (cited January 11, 2023).

Woo, S. 2017. *Reliability Design of Mechanical Systems: A Guide for Mechanical and Civil Engineers*. Springer Publishing, New York, NY. DOI 10.1007/978–3-319–50829–0.

***Positionality Statement**: My frame-of-reference comes from my experiences in Mechanical Engineering Education, earning a BS from West Virginia University, an MS from Ohio State University, and a PhD from Georgia Tech. I also taught Mechanical Engineering classes, both undergraduate and graduate, at Mississippi State University and Liberty University. Also, working at Owen Corning Fiberglas and Sandia National Laboratories, I was heavily involved in the science and engineering methodologies. Regarding entrepreneurship, I have started three different companies, so these experiences have biased my position. Finally, I have spoken at many primary and secondary schools (private and public) about science, engineering, and mathematics, and have found that most teachers and students do not really know the process of engineering.*

***Artificial Intelligence**: None of this work used any form of artificial intelligence. By submitting this manuscript, I confirm that I have adhered to appropriate ethical guidelines or approvals for the human subjects research conducted in this study, including taking into consideration any federal requirements and institutional guidelines concerning the use of AI in human subjects research.*

Creation Research Society Quarterly 2026 62:315–330

Cells Are Integrated Multiprocessing Analog Computing Devices—Part 1

Royal Truman[1]*,
Amit Singh[2], and
Peter Borger[3]

Key Words: Analog computing, biological information, biological sensors, cellular processes, concentration gradients

[1] University of Konstanz, Konstanz, Germany
[2] Institute for Biomechanics, ETH Zurich, Switzerland
[3] peter.borger@wort-und-wissen.de
* Correspondence: royal.truman@uni-konstanz.de

Accepted for publication August 21, 2025

Abstract

A computational model of biological cells is presented, conceptualizing them as networks of thousands of coordinated *analog* computing programs, orchestrated by sensors responsive to environmental cues, particularly chemical concentration gradients. These cellular sensors function as dynamic biological variables, performing decision-making to modulate biochemical processes across a continuum of states. By interpreting cells as information-processing systems, this model elucidates their core behaviors, overcoming the formidable complexity of underlying physicochemical interactions.

Simple Summary

This research paper argues that biological cells are best understood as sophisticated analog computing devices rather than just a collection of chemical reactions. The authors propose a top-down framework, where thousands of cellular sensors act as programming variables, detecting concentration gradients to make logical decisions. Unlike digital systems, these analog processes use continuous physical quantities to regulate essential functions like growth, repair, and reproduction. By interpreting biochemical interactions as logic-processing events, the study provides a unifying model for the complex engineering found in nature. This approach highlights how cells integrate hardware and software to achieve autonomous, purposeful behavior across generations.

Introduction

Cells are the fundamental unit of life, capable of autonomous reproduction, energy production, growth, adaptation, self-protection, self-repair, and recycling. Despite the vast amount of research on how individual cells function and are assembled into organisms, a comprehensive, holistic understanding seems more elusive than ever (Minelli, 2021; Mukherjee, 2022; Ball, 2023; Martinez, 2023).

The origin-of-life (OoL) community insists that only material processes must explain everything. The consequence is that allegedly prebiotic self-sustaining chemical reactions must have eventually led to cellular life (Eigen and Schuster, 1979). However, speculating about a multitude of fictitious abiotic individual chemical reactions ignores the fundamental essence of cells, which is what needs explaining. They are capable of autonomous growth, adaptation, self-protection, self-repair, recycling, and producing both their own chemical components and usable energy. Cells coordinate all these processes as recognizable, holistic entities, and reproduce with their individual processes and components in a continuously functional state, reliably for countless generations.

Cells possess the special ability to regulate biochemical processes, as discussed in Appendix 1. But a collection of chemical reactions will not bootstrap into a functional cell.

In this 3-part series, we offer an overarching interpretation of cells as self-contained information processors. Understanding the logic-processing aspects provides a top-down, unifying systems approach, relegating the endless chemical details as 'merely' implementation details.

Various computational models have been applied to describe how cells interact and organize their processing activities internally. For example, concepts from distributed computing and communication mechanisms between the processors have been used to design distributed cellular network models (Goñi-Moreno et al., 2013; Moškon et al., 2021). In addition, various agent-based models (ABMs) have been used to model interactions between cells, organoids, tissues, and bacterial communities, helping to identify emergent system behavior (Pleyer and Fleck, 2023).

These views provide valuable insights into the design and architecture of cellular computing, but we believe a key insight needs to be established. In a nutshell, we believe cells consist of thousands of kinds of analog computing devices, designed to solve distinct problems while collaborating to achieve higher-level goals. Fundamentally, decisions are computed at sensors that are then implemented by recruiting and assembling the necessary *molecular machine* 'hardware' on-demand. Cells disassemble the hardware once they are no longer needed. Through careful regulation, the copies of analog processors can range from none to millions, working in parallel.

Our goal in this 3-part series is to provide a top-down conceptual framework to make sense out of the tens of thousands of cellular processes found throughout nature.

What Are Analog Computing Devices

We offer the following definition of a human-designed analog computing device.

> "Analog computing devices model problems by using continuously changeable physical quantities, like electrical, mechanical, or hydraulic properties, to represent corresponding continuous values. Unlike digital computers that use discrete numerical values, the physical construction of analog computers allows changes in a variable X to directly and continuously produce the intended corresponding function of that variable, $f(X)$."

Ancient examples include sundials, water clocks, candle clocks, the Antikythera mechanism, and astrolabes (Ulmann, 2022). For centuries, slide rules were state-of-the-art computational devices. Current examples include mechanical watches and industrial automated control devices. Future technologies being developed include quantum analog computers using quantum states as continuous variables, neuromorphic computing, and optical analog computers based on intensity, phase, and polarization of light as variables.

The concept of analog computing devices is illustrated by the examples shown in Figure 1.

Real-time analog computing can perform abstract calculations and can control processes.

Cellular Processes Are Regulated by Concentration Gradients

The continuous, analog nature of cellular logic is observed in most, if not all, regulated processes. Some examples are provided in Table I, where concentration gradients produce a rheology-like output. By *signals*, we mean any stimulus interpreted by cellular sensors, such as photons, pressure, temperature, protons, electrons, and so on.

Complex multistep cellular processes are up- and down-regulated using dedicated sensors, as illustrated in the examples in Table II.

Key Role Played by Sensors

An important insight revealed by the examples in Figure 1 is that there is a sensing element, i.e., a precisely crafted interface able to recognize input values and connect them to the rest of the processing system. Human technologies use many kinds of sensors, such as those mentioned in Table III, to regulate equipment. Part of the sensors serve as housings to contain or organize the sensing core element, ensuring that they function effectively. This detail will help clarify how cellular sensors function.

Figure 2 illustrates the key concept of analog computing: a physical-mechanical process transforms a continuous input into an informative continuous output.

Calibrated Interplay of Sensors and Concentration Gradients

Researchers often study how chemical interactions occur, for example, at cell surface binding sites, nuclear receptors, and enzyme active sites to *understand how a cell works*. The assumption is that cellular processes are fundamentally mere chemistry. We view these interactions as engineering details to achieve cellular purposes. Focusing on the fine details instead of the architectural system is unlikely to elucidate very much about how cells function.

The interaction of signals with the relevant sensor is ensured through judicious combinations of biochemicals such as nucleotides and amino acids, plus often ligand attachments

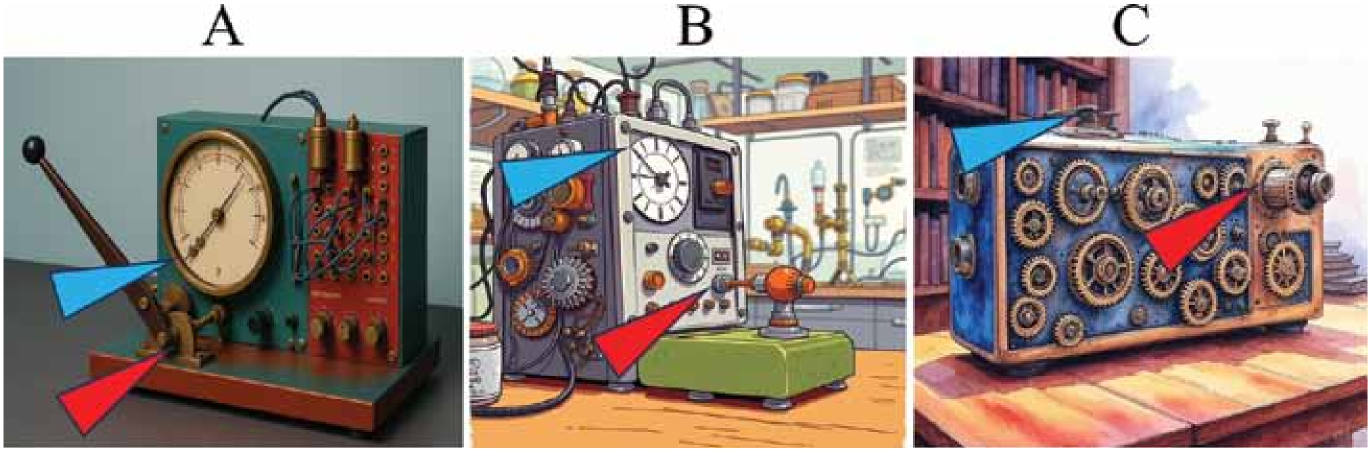


Figure 1. Analog computers convert continuous input values into a corresponding output function using carefully engineered mechanical components. The red arrows point to where input values (signals) are sensed and where conversion to the output function is initiated. The blue arrows point to where the continuous outcome occurs or is displayed. Conceptual images generated by AI.

to produce distinctive 3-dimensional recognition features. Chemical modifications are often used for this purpose. In fact, about 137 kinds of enzymatic chemical modifications have been identified on human RNAs alone, regulated according to cell type and other conditions (Modomics, 2024). Errors in these modifications cause serious problems, generally resulting in diseases (Li and Mason, 2014). For instance, around 27 kinds of chemical

Table I. Signaling gradients produce a continuum of outcomes.

Signaling effector	Description	References
Transcription factors	Control the rate at which a Preinitiation complex (PIC) is formed at promoters.	Petrenko et al., 2019; Farnung and Vos, 2022; Naqvi et al., 2023; Portillo-Ledesma et al., 2024
Transcription factors	Control the rate of polymerase assembly at enhancers.	Martinez-Ara et al., 2023; Domingo et al., 2024; Zhang et al., 2024
Glucose	Control the rates of cellular metabolism or growth.	Carey et al., 2013; Han et al., 2016;
Oxygen	Control the activity of hypoxia-inducible factors (HIFs). (Specific genes are activated).	Ziello et al., 2007; Nguyen et al., 2013
cAMP	Control the rate of activation of several genes.	Walia et al., 2016; Chakraborty et al., 2022
Ca^{2+}	Control the activity of Calcium-dependent enzymes in neurons, such as CaMKs.	Rosenberg and Spitzer, 2011; Mohanan et al., 2022; Virdi et al., 2022
miRNA	Inhibit mRNA translation.	Biasini et al., 2021; Kilikevicius et al., 2022; Ning et al., 2023
Splicing factors	Control selection of alternative splicing (leading to different isoforms).	Li et al., 2021; Ding, 2022; Snyman and Sen, 2023
RNA-binding proteins	Stabilize or destabilize mRNAs, influencing their half-life.	Modic et al., 2024; Komori et al., 2025
Mechanical forces	Sensed by integrins and other mechanosensors, translating into biochemical signals.	Di et al., 2023
Mechanical strain	Regulates nuclear localization of YAP/TAZ proteins.	Koushki et al., 2023; Kim et al., 2024

Table II. Cellular processes respond along a continuum of values.

Process	Processing steps	References
Signal Transduction Pathways	***Protein Kinase Cascades*** Kinases like MAPK (Mitogen-Activated Protein Kinase) are activated in a graded manner depending on the strength and duration of the signal.	MacKeigan et al., 2005; Yoe and López, 2020
	G-Protein Coupled Receptors (GPCRs) Ligand binding to GPCRs leads to a graded activation of downstream effectors, such as adenylate cyclase or phospholipase C.	Powers et al., 2024; Seger, 2024
	Calcium Signaling Intracellular calcium levels regulate various processes, including muscle contraction and neurotransmitter release, in an analog fashion.	Nanou et al., 2016; Kolodkin-Gal et al., 2023; Oh, 2023
Metabolic Pathways	***Enzyme Substrate Interactions*** Enzymes catalyze reactions at rates proportional to substrate concentration until saturation is reached.	Choi et al., 2017; Yu et al., 2023; Olmeda and Rulands, 2024
	Feedback Inhibition Metabolic pathways often involve feedback loops where high concentrations of end products inhibit upstream enzymes, modulating pathway activity continuously.	Liu and Birsoy, 2023; Wang et al., 2024
	Allosteric Regulation Allosteric effectors can modulate enzyme activity in a graded manner by changing their conformation.	Anderson et al., 2024; Tee and Lim, 2024
Cell Cycle Control	***Cyclin-Dependent Kinases (CDKs)*** CDK activity is regulated by the concentration of cyclins, which rise and fall during different phases of the cell cycle.	Ford et al., 2023; Pellarin et al., 2025
	Checkpoints Cell cycle checkpoints respond to varying levels of damage signals, allowing for variable delays depending on the severity of the insult.	Solier et al., 2012; Li et al., 2023
Protein Degradation	***Ubiquitin-Proteasome System*** The rate of protein degradation depends on the concentration of ubiquitin ligases and substrates.	Wang et al., 2023; Soh et al., 2024
	Autophagy Autophagic flux is modulated by nutrient availability and stress signals in a graded manner.	Chimenti et al., 2022; Perucho-Jaimes et al., 2024
Membrane Potential and Ion Channels	***Voltage-Gated Ion Channels*** Membrane potential changes influence ion channel opening probabilities in a continuous fashion.	Chang et al., 2023; Sakellakis et al., 2024;
	Action Potentials While action potentials themselves are digital, the underlying ion flow through channels is an analog process influenced by voltage gradients.	Brunner and Szabadics, 2016; Sakellakis et al., 2024

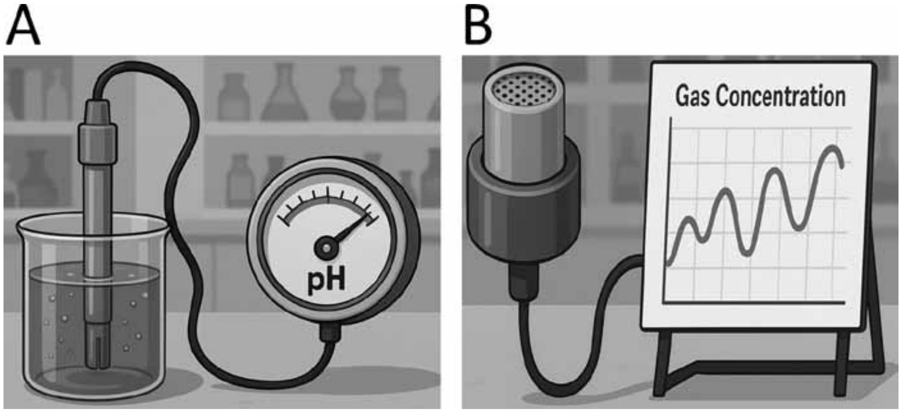


Figure 2 *(left)*. In analog computing, a physical-mechanical process transforms a continuous input into a continuous informative output. A. A sensor identifies the concentration of a substance in a liquid, such as protons, and communicates this along a continuous response. B. Here, the concentration of a gas is mechanically determined and transformed along a continuous scale. Illustrative examples only, generated by AI.

Table II *(continued)*. Cellular processes respond along a continuum of values.

Process	Processing steps	References
Synaptic Transmission	***Neurotransmitter Release*** The amount of neurotransmitter released depends on the frequency and intensity of presynaptic action potentials.	Zbili et al., 2016; Ralowicz et al., 2024
	Receptor Desensitization Receptors can become desensitized in a concentration-dependent manner, affecting synaptic strength.	Field et al., 2021; Stockwell et al., 2024
Chromatin Dynamics	***Histone Modification*** The degree of histone acetylation, methylation, or phosphorylation influences chromatin accessibility and gene expression in a graded manner.	Liu et al., 2023; Bu et al., 2025
	DNA Methylation Levels of DNA methylation can vary across regions, influencing transcriptional activity in a graded manner.	Jin and Robertson, 2011; Héberlé and Bardet, 2019
Oscillatory Systems	***Circadian Rhythms*** Circadian clocks rely on continuous oscillations of protein levels and activities that are modulated by environmental cues.	Liu et al., 2024; Nishio et al., 2024
	p53-Mdm2 Oscillations The p53 tumor suppressor protein exhibits oscillatory behavior in response to DNA damage, with amplitude and frequency reflecting the severity of damage.	Geva-Zatorsky et al., 2006; Proctor and Gray, 2008
Stress Response Pathways	***Heat Shock Proteins (HSPs)*** HSP induction occurs in response to temperature increases, with higher temperatures leading to greater induction.	Tomanek, 2010; Lewis et al., 2016
	Unfolded Protein Response (UPR) UPR signaling adjusts according to the level of unfolded proteins in the ER, enabling graded responses to stress.	Chen et al., 2024; He et al., 2024
Developmental Gradients	***Morphogen Gradients*** Morphogens like Sonic Hedgehog (Shh) or BMPs establish concentration gradients that specify cell fates in a position-dependent manner.	Greenfeld et al., 2021; Simsek and Özbudak, 2022
	Wnt Signaling Wnt ligands induce graded responses that determine tissue patterning during development.	Green et al., 2020; Pond et al., 2020
Immune System Responses	***Cytokine Signaling*** Cytokine concentrations dictate the strength and type of immune response, allowing for fine-tuned regulation.	Altan-Bonnet and Mukherjee, 2019; Cui et al., 2024
	T-Cell Activation T-cell receptor engagement triggers analog-like responses based on the affinity and duration of interaction with antigens.	Zhong et al., 2013; Wu et al., 2023

modifications are necessary for tRNAs to be recognized by mRNA codons (Kirchner, 2015; Lorenz, 2017; Agris et al., 2018; Cappannini et al., 2024).

When considering sensors, it is useful to distinguish between the core sensing element and the housing used to ensure proper functioning. Some chemical details in cellular sensors can be defined as the sensing and logic processing part, whereas other parts are only supportive infrastructure. The latter can often be neglected in order to understand the logic processing being carried out.

Only Portions of Cellular Sensors Specify Intended Binding Partners

Cellular sensors recognize three-dimensional features. For example, codon-anticodon interactions involve primarily only two or three H-bonds from each nucleotide binding partner. Most of the tRNA molecule and ribosome 'merely' fine-tune the microenvironment to optimize the bonding geometry. Each codon defines adjacent sensors on the mRNA strand, thereby specifying where each is located. These precise engineering details are necessary to avoid interacting with the far more numerous identical but incorrect nucleotide triplets distributed among all RNA, as discussed in Appendix 2.

Binding locations can be fine-tuned to regulate their responsiveness. These refinements are accomplished by

Table III. Examples of human-designed sensors.

Sensor	Input → output	Description of technology
Photometer	Light intensity → electrical signal	Intensity of light transmitted through a solution responds gradually to the concentration of a dissolved substance. This allows the concentration of substances to be calculated using the Beer-Lambert law.
pH Meter	Electrical potential → analog pH value	Electrical potential difference across a glass electrode responds gradually with proton concentration, enabling a pH value to be computed.
Thermometer	Temperature → volume change	Volume changes in mercury allow temperatures to be measured.
Pressure meter	Mechanical deformation → electrical signal	Deformation caused in a membrane is detected to determine the pressure of gases.
Flow meter	Pressure difference or velocity → flow rate	Changes in pressure, velocity, or other parameters are detected to determine volume or mass flow rates.
Optical meter	Light presence, reflection, or interruption → electrical signal	Light rays are converted into electrical signals to detect the presence or absence of objects or of their movement.
Electrochemical meter	Redox reaction current or voltage → current/voltage proportional to concentration	Oxidation-reduction reactions are used to measure, for example, gas concentrations.
Wind meter	Wind force → electrical signal	Propeller rotation or ultrasonic time differences are detected to determine wind speed and direction.
Hydrometer	Buoyancy force / sinking depth → density reading (via calibrated scale)	The depth a hydrometer sinks allows a liquid's density to be determined.
Oscilloscope	Voltage over time → visual display (graph on screen)	Voltage changes over time are visualized, allowing users to interpret signals from sensors in medical, automotive, and electronic diagnostics. This is achieved by continuously performing analog mathematical operations, such as addition and subtraction of input signals.

modifying the surrounding region by attaching specific ligands, by using double-strand base-pairing along parts of RNA, by using cysteine-cysteine bonding in proteins, and by other techniques. Sometimes binding interactions represent the normal operation of a sensor, and other times, these only play a supportive role.

- Histone proteins are modified by enzymes that add methyl groups to specific lysine residues, such as H3K4 or H3K27, to regulate gene transcription. For example, trimethylation of H3K4 (H3K4me3) promotes transcription, while trimethylation of H3K27 (H3K27me3) represses it (Ruthenburg et al., 2007). The lysine residues and their surrounding regions act as sensors (recognition sites) for methyltransferases, enabling precise targeting of these modifications.
- Glycosylation modifies proteins for various purposes. For example, O-linked glycosylation at serine or threonine residues can serve as a signal for sorting proteins to specific cellular compartments, such as the lysosome or Golgi apparatus (González, Brito, and González, 2012). Additionally, glycosylation, particularly N-linked, enhances protein solubility and promotes proper folding in the endoplasmic reticulum. Here, specific serine and threonine residues with their surrounding regions act as sensors.
- Phosphorylation often occurs in signal transduction, where serine, threonine, or tyrosine residues and their surrounding region act as sensors. These trigger kinases (called 'writers') to add phosphate groups, while phosphatases (called 'erasers') remove these groups (Han et al., 2017).
- Small regions of transcription factors (TFs) bind to DNA cis-regulatory elements, which act like sensors. Chemical modifications, such as TF phosphorylation or DNA methylation, can alter the affinity or specificity of these binding events (Glasgow, 2021).

It is noteworthy that cellular sensors are assembled when and where needed, in the proper copy number.

Some cellular sensors are designed to interact with different signal mol-

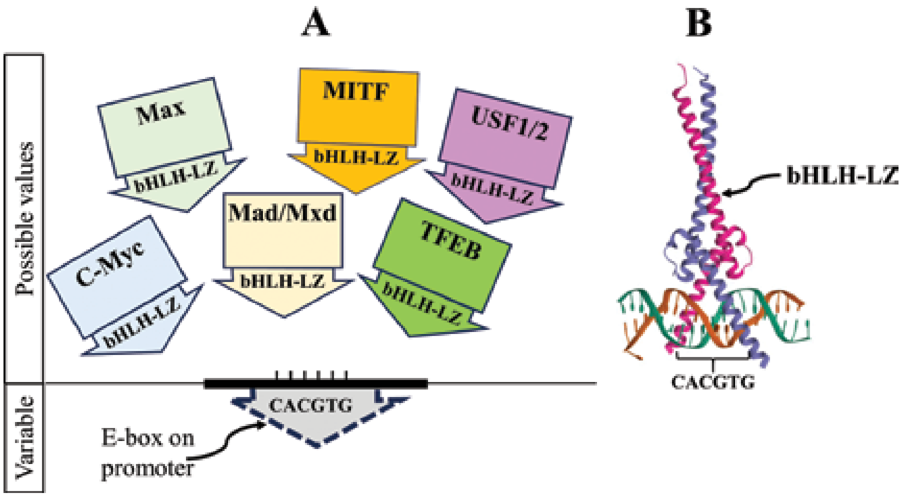


Figure 3. Six different transcription factors can bind to part of the human TERT promoter to regulate the telomerase reverse transcriptase gene (Khattar and Tergaonkar, 2017). A: The E-box (enhancer box) variable can be assigned any of 6 value types through binding to c-Myc, Max, Mad/Mxd complex, MITF, USF1/2, or TFEB using the distinctive bHLH-LZ protein domain. B: Chemical representation of the basic helix-loop-helix leucine zipper (bHLH-LZ) domain recognized by the sensing core part of the E-Box's consensus sequence 'CACGTG.' Source: Protein Data Bank, https://www.rcsb.org/structure/1nkp.

ecules. As an example, transcriptional activators and repressors can compete at the same binding locations, dynamically regulating gene expression by adjusting the relative proportions of the activators and repressors (Jacobs et al., 2023). Also, different combinations of enhancers (DNA sensors) can collaborate to produce a continuum response (Davidson, 2001; Jacobs et al., 2023).

Cellular Sensors Are Programming Variables

The above discussion was intended to clarify why cells should be viewed as information processors, more specifically, analog logic devices.

Variables are fundamental to communicating intention. In digital computers they are specific locations in the memory where values can be placed or extracted. Similarly, in biological cells, sensors are located at special locations to scan for signals (i.e., the values they are designed to recognize). We call these locations variables since logical operations will be performed there. In Part 2, several tables are provided with many examples of variables (sensors) physically located on DNA, RNA, and protein, along with the processes they regulate.

In human language and digital programming, rules specify how values are to be represented. For example, '10' is a valid integer, but '01' and 'X1' are not. In cells, however, values (i.e., the signals) must possess physical features to specify their validity for a sensor. An example is shown in Figure 3, which illustrates how only some TFs must bind to a class of DNA cis-elements, which act as sensors (Khattar and Tergaonkar, 2017). The rate of binding is stochastic and is defined by the concentration gradient of TF.

In digital computing, instructions are communicated explicitly as source and compiled code, whereas in analog computing, there are no instructions separate from the processing equipment. For cells to function autonomously, the variables and their values interact physically, which is true of all analog computing.

Variables Are Used to Express an Intended Outcome

We stated above that variables are fundamental to communication. Since our computational model of cells is intended to clarify the essential nature of thousands of processes, it seems worthwhile to review what variables are all about.

Once a variable has been assigned a value, decisions can be made. The sensor alone or a signal alone accomplishes nothing useful, as recognized by others (Farnsworth et al., 2013):

> "When two or more such configurations are brought into association, there is a combined arrangement, which if persistent, also instantiates information: that of both components plus that of their association."

For example, the Nuclear Localization Signal on proteins are sensors but alone does nothing until bound by importin-α and importin-β. Only jointly can RanGTP and other components be recruited, initiating a process that guides the protein through a Nuclear Pore Complex (Oka and Yoneda, 2018).

Indeed, many researchers use the vocabulary of information to interpret cellular processes, which will be reviewed in Part 3 of this series.

Although variables are implemented physically in analog computers and brains, they have properties that distinguish them from simple material interactions, as summarized in Table IV. The first property mentioned is specificity. To illustrate, cellular sensors must be clearly recognized by the kinase enzymes that are to phosphory-

Table IV. Characteristics of variables that distinguish them from unintentional physical interactions.

Property	Relevant to digital programming and human language	Cellular examples
They must be unambiguous.	Rules specify what variables are and distinguish them from each other.	Codons on mRNA must be recognized as different from the same triplets on random RNA.
They are abstract representations of objects or concepts.	'Best_option' 'Dog' 'Quantity'	Abundance_of_nutrient_x.
Operations can be performed with them.	Cost <= Price × Quantity	Accelerate or slow down the recruitment of proteins and assembly of complexes.
They are used to communicate an intention.	If Pressure > 500 Then Open_Valve.	If the receptor is bound to signal molecule X, then recruit protein Y.
Their purposes do not derive from their physical properties.	The physical structure of the string 'Set_price' is independent of its meaning and purpose(s) to be communicated.	The physical properties of a sensor specify what it will bind to, but are independent of the resulting process to be accomplished.
They can iteratively represent collections of other variables.	Animal = [Cat, Bear, Dog, Horse, Cattle] Dog = [Bulldog, Beagle, Poodle, Collie] Bulldog = {Rocky | Buster | George}	Binding site = [DNA, RNA, protein, sugar, etc.] DNA = [Enhancer, Promoter, Silencer, ori, etc.] Enhancer = [MyoD, Sox2, NF-κB, p53, AP-1, etc.]

late at that position. This explains why humans have >500 kinds of specialized kinases used in signaling networks. The number of targets for each kinase ranges from very few to hundreds, but importantly, each protein kinase must *avoid thousands of off-target phosphorylation sites* (Laub, 2016; Miller and Turk, 2018).

The last entry in Table IV notes that variables can be assigned other variables as their values. This helps to understand cellular processing by recognizing recurring generic patterns. For instance, the notion of a *binding site* applies to thousands of cases. In DNA alone, there are many kinds, such as enhancers and silencers. In addition, there are many variants of enhancers, depending on what they are designed to interact with.

Digital vs. Analog Programming

In modern digital computer programming, software is abstracted from the hardware. Programmers develop source code without considering its physical implementation, trusting that the instructions they program will be carried out.

This has led some to question whether cells are truly computers, since they do not recognize the kind of software coding they are familiar with. Furthermore, in cells, the physical processes can usually be described. For instance, an aminoacyl-tRNA synthetase can link an activated amino acid to a specific nucleotide at the 3′ end of the correct tRNA. As another example, the exact interactions of a codon with its cognate anti-codon can be described physically. These observations have led some to believe that cellular processes are merely chemical processes.

However, in principle, a materialist could "explain" all outcomes of computer programs by laboriously observing the physical processes occurring in the hardware, such as the flow of electrical signals through conductive pathways, the switching of transistors, and the alteration of charges in capacitors, which collectively execute the program's instructions. Clearly, such an approach would neglect the decisions made by humans that change the starting parameters, and, therefore, predictions cannot be made in advance about what a parametrized program will do.

Clearly, the fact that physical processes are involved does not demonstrate that cells are not information processors. In cellular analog programs, sensors serve as the initiating and regulating end of processes that assemble complex hardware to produce biologically important outcomes. This is clarified in Part 2 of this series, using the concept of immediate and major goals of cellular variables. To illustrate, the attachment of a hormone to the correct membrane receptor (the immediate goal) is only the initial step. It triggers a signaling cascade that ultimately regulates protein synthesis—either increasing or decreasing the production of specific proteins that change specific cellular function (the major goal).

In cells, hardware and software are integrated for each process, creating individual *programs*. In contrast, digital variables and values are defined by combining symbols from a binary alphabet {0, 1}, using conversion rules. Thus, the decimal value ‘20’ is represented in the ASCII code by the binary digit ‘10100.’ Analog variables and values are also defined in cells by combining members of an alphabet of amino acids, nucleotides, lipids, sugars, and so on, but only portions of these molecules are directly (i.e., physically) involved in defining the distinguishing property of the variable.

Digital computational models discretize data, whereas analog computing leverages the natural properties of materials or systems, such as electrical voltage, fluid pressure, mechanical motion, or electromagnetic wave amplitude, phase, frequency, or polarization to perform their computations automatically (Gregersen, 2025). A feature of many modern analog computers is the patch panel, which allows users to physically connect different components to specify the configuration needed for a particular problem. The physical wiring defines the “program” that the analog computer will execute (Ulmann, 2022; Balci, 2023). Analogous to cells, once the “wiring” is set up, no source code is necessary.

Key details distinguish analog from digital computing processors (Roquet and Lu, 2014; Sarpeshkar, 2014; Munsky and Neuert, 2015; Grozinger et al., 2019; Waqas et al., 2020):

1. *Physical properties specify the outcome*. Analog decision-making relies on continuous *inherent* physical properties.
2. *Continuous outcomes are achieved*. Regulation of the rate of outcomes can be guided through continuous changes in the input.
3. *Direct response*. The magnitude of effect results automatically and is rarely linear.
4. *Signal integration specifies the outcome*. Multiple causal factors can be collectively integrated. For example, concentration gradients in cells can be modified by multiple factors that lead to an instant collective concentration. Therefore, the concentration of biochemicals has been called a *carrying signal* (Mogas-Díez et al., 2021). Also, cellular programs must often produce multiple effects that require tradeoffs (for example, the level of expression of multiple genes). The tradeoff logic can be rapidly calculated to adjust the informative signal (for example, concentration of TFs).

The analog nature of cellular processes explains why their continuous variables are often modelled using differential equations. In fact, historically, analog computers were designed to solve ordinary differential equations, revealing the conceptual link.

Given the physical nature of cellular sensors or variables, environmental factors like temperature, salinity, and pH can modify their responsiveness to binding partners. Therefore, these factors can also be deliberately adjusted in cells, leading to a far richer notion of variables than available to discrete variables. To exemplify, in a programming language like python

```
set_new_price = 100                (1)
```

expresses an invariant value unless the quantity 100 is changed. In the analog variable concept, a variable like set_new_price itself could assume different nuances, such that even the same value ‘100’ would produce a different effect. Specifically, the responsiveness of sensors can be adjusted.

The notion of cellular variable inexactness might superficially remind one of *Fuzzy logic* (introduced by Zadesh, http://zadeh.cs.berkeley.edu/) used in discrete programming, but as elaborated on in Appendix 3, this is a different concept.

Variable inexactness or fine-tuning might also remind one of the concept of pattern matching used in digital programming, such as:

```
if current_ codon like ‘CU%’    (2)

and is_bound_to_a_suitable_
anticodon

then

next_amino_acid = ‘Leu’
```

This expresses that codons CUU, CUA, CUC, and CUG that satisfy the pattern ‘CU%’ should all be recognized as synonymous. In pattern matching, the alternatives that are satisfied act as synonymous, whereas the distinct structure of a cellular sensor interacting with a signal produces differences that affect the resulting outcomes.

Further Evidence of the Analog Nature of Cellular Programming

Further evidence of the analog nature of biochemical processing has been provided by the facile design of synthetic gene circuits able to detect specific cell states and perform state-specific control of desired protein expression (Prochazka et al., 2022). Especially relevant is the success of cytomorphic circuits technology, discussed in Appendix 4.

Cell membranes can be viewed as an interface for multiple external inputs using specialized receptors (Wurtz, 2021). The signals are encoded into an intracellular language that produces a signaling network able to summarize and coordinate all the incoming signals. The analog nature of signaling networks is emphasized by the cell's ability to enhance the signal strength by enzymatically activating second messengers. The way intracellular signaling networks organize multiple inputs to regulate genes has been referred to as the biological equivalent of a computer's motherboard (Wurtz, 2021).

Research at the University of Edinburgh has revealed that living cells are physically wired in a manner analogous to computer chips, utilizing direct signals to instruct cellular functions (Duan et al., 2019). These insights have inspired the creation of synthetic biological computing devices using DNA, RNA, and proteins, using the same biochemicals and binding interactions found in cells (Benenson, 2012). Shared features include the use of sensors to interact with the exterior, hardware to process logic operations, and actuators to implement the logic output.

So far, we have shown that cellular sensors respond to stimuli in a continuous analog fashion. In Part 2, this will also be shown to apply to the subsequent assembly of the machinery to implement the intended processes. This is true because the biochemicals assembled produce their own new kinds of sensors.

A continuous range of each kind of outcome for cells is also achieved by using multiple receptor copies that are activated over a range of time periods.

Further Computational Insights from Cells

Cells have inspired some new computational models. The observation of template-guided splicing and recombination of DNA sequences (including deletions) to generate new or modified computational instructions inspired genetic algorithms (Daley and McQuillan, 2005; Finck and Beyer, 2009). A variant approach includes the use of pointers to combine fragments of programming code, inspired by how ciliates create their somatic genomes by rearranging genes in their compact germline genome (Rogojin, 2010; Nowacki et al., 2011).

Another concept is based on the use of physical compartments within cells to enable efficient processing. Within cells, there are membrane-enclosed compartments (organelles) that concentrate and constrain the proteins and RNA used in those locations. There are also dedicated regions that are not enclosed in membranes, such as cristae on mitochondria, Cajal bodies, PML Nuclear Bodies, Nuclear Speckles, Transcription Factories, Replication Factories, Chromosome Territories, Plasma Membrane Lipid Rafts, Synaptic Vesicles, Stress Granules, P-bodies, Adherens Junctions, Tight Junctions, Gap Junctions, and Nuclear Pore Complexes. This inspired membrane computing, also called P systems (Păun, 2000; Păun et al., 2009).

Summary and Conclusions

Cells display many features not found in human computing devices. They are technologies that manufacture their own hardware; adapt to changes in the environment; self-repair; recycle parts; and most significantly, reproduce themselves. Especially significant is a cell's ability to make adjustments along a continuum of values. This can be explained by their use of thousands of special sensors that can respond to continuous signals, especially concentration gradients. The sensing part of sensors acts as variables to which continuous values can be assigned. These values regulate cascades of processes that produce the changes required by cells.

Remarkably, cells can also manufacture the sensors themselves, modifying the copy number according to cell requirements. Interpreting cells as computing devices instead of a collection of chemical reactions provides a more productive interpretative framework. Researchers can begin their analysis by focusing on the logic being executed instead of the overwhelming amount of chemical detail.

The emphasis of Part 2 will be on the series of processes that are initiated by and regulated through the binding of signals to their receptors.

The intention of this 3-part series is to provide a new way to interpret what cells are. This is also a necessary foundation for our current research on how metaprogramming occurs in cells (Gudzyk, 2024). In computer science, metaprogramming is an established concept in digital programming whereby compact software instructions generate a broader executable code. Clearly, this occurs in cells. For example, a single gene can produce many copies of different protein variants (after mRNA splicing). The realization that analog sensors and programs are generated by cells will be addressed in the future. It offers a new paradigm in computer science, namely, that of metaprogramming being applied to analog computing.

References

Agris, P.F., E.R. Eruysal, A. Narendran, V.Y.P. Väre, S. Vangaveti, and S.V. Ranganathan. 2018. Celebrating wobble decoding: Half a century and still much is new. *RNA Biology* 15:537–553.

Altan-Bonnet, G., and R. Mukherjee. 2019. Cytokine-mediated communication: A quantitative appraisal of immune complexity. *Nature Reviews Immunology* 19: 205–217.

Anderson, J.W., D. Vaisar, D.N. Jones, L.M. Pegram, G.P. Vigers, H. Chen, J.G. Moffat, and N.G. Ahn. 2024. Conformation selection by ATP-competitive inhibitors and allosteric communication in ERK2. *eLife* 12: RP91507.

Balci, M. 2023. THe Analog Thing. https://metebalci.com/blog/the-analog-thing/.

Ball, P. 2023. *How Life Works: A User's Guide to the New Biology*. The University of Chicago Press, Chicago, IL.

Barciszewska, M.Z., P.M. Perrigue, and J. Barciszewski. 2016. tRNA—the golden standard in molecular biology. *Molecular BioSystems* 12: 12–17.

Benenson, Y. 2012. Biomolecular computing systems: Principles, progress, and potential. *Nature Reviews Genetics* 13: 455–468.

Biasini, A., B. Abdulkarim, S.D. Pretis, J.Y. Tan, R. Arora, H. Wischnewski, R. Dreos, M. Pelizzola, C. Ciaudo, and A.C. Marques. 2021. Translation is required for miRNA-dependent decay of endogenous transcripts. *The EMBO Journal* 40: e104569.

Brunner, J., and J. Szabadics. 2016. Analogue modulation of back-propagating action potentials enables dendritic hybrid signalling. *Nature Communications* 7: 13033.

Bu, S., T. Ye, H. Gao, H. Song, and Y. Zhu. 2025. Histone methylation and acetylation in cancer: Mechanism, progression, and targets. *Oncologie* 27: 29–43.

Cappannini, A., A. Ray, E. Purta, S. Mukherjee, P. Boccaletto, S.N. Moafinejad, A. Lechner, et al. 2024. MODOMICS: A database of RNA modifications and related information. 2023 Update. *Nucleic Acids Research* 52: D239–244.

Carey, M., S. Kehlenbrink, and M. Hawkins. 2013. Evidence for central regulation of glucose metabolism. *Journal of Biological Chemistry* 288: 34981–34988.

Chakraborty, S., P. Singh, and A.S.N. Seshasayee. 2022. Understanding the genome-wide transcription response to various cAMP levels in bacteria using phenomenological models. Edited by Richard A. Notebaart. *mSystems* 7(6): e00900–22.

Chang, S.-Y.S., P.M. Dijkman, S.A. Wiessing, and M. Kudryashev. 2023. Determining the structure of the bacterial voltage-gated sodium channel NaChBac embedded in liposomes by cryo electron tomography and subtomogram averaging. *Scientific Reports* 13: 11523.

Chen, Q., C. Li, W. Wei, J. Li, F. Liu, Y. Fu, L. Tang, and F. Han. 2024. Endoplasmic reticulum stress response pathway-mediated cell death in ovarian cancer. *Frontiers in Oncology* 14: 1446552.

Chimenti, I., V. Picchio, F. Pagano, L. Schirone, S. Schiavon, L. D'Ambrosio, V. Valenti, et al. 2022. The impact of autophagy modulation on phenotype and survival of cardiac stromal cells under metabolic stress. *Cell Death Discovery* 8: 149.

Choi, B., G.A. Rempala, and J.K. Kim. 2017. Beyond the michaelis-menten equation: Accurate and efficient estimation of enzyme kinetic parameters. *Scientific Reports* 7: 17018.

Cui, A., T. Huang, S. Li, A. Ma, J.L. Pérez, C. Sander, D.B. Keskin, C.J. Wu, E. Fraenkel, and N. Hacohen. 2024. Dictionary of immune responses to cytokines at single-cell resolution. *Nature* 625: 377–384.

Daley, M., and I. McQuillan. 2005. Formal modelling of viral gene compression. *International Journal of Foundations of Computer Science* 16: 453–469.

D'Angelo, L., E. Astro, M.D. Luise, I. Kurelac, N. Umesh-Ganesh, S. Ding, I.M. Fearnley, et al. 2021. NDUFS3 Depletion permits complex I maturation and reveals TMEM126A/OPA7 as an assembly factor binding the ND4-module intermediate. *Cell Reports* 35: 109002.

Davidson, E.H. 2001. *Genomic Regulatory Systems: Development and Evolution*. Academic Press, San Diego, CA.

Di, X., X. Gao, L. Peng, J. Ai, X. Jin, S. Qi, H. Li, K. Wang, and D. Luo. 2023. Cellular mechanotransduction in health and diseases: From molecular mechanism to therapeutic targets. *Signal Transduction and Targeted Therapy* 8: 282.

Ding, F., C.J. Su, K.K. Edmonds, G. Liang, and M.B. Elowitz. 2022. Dynamics and functional roles of splicing factor autoregulation. *Cell Reports* 39: 110985.

Domingo, J., M. Minaeva, J.A. Morris, M. Ziosi, N.E. Sanjana, and T. Lappalainen. 2024. Non-linear transcriptional responses to gradual modulation of transcription factor dosage. *eLife* 13: RP100555

Du, Z., and C.M. Lovly. 2018. Mechanisms of receptor tyrosine kinase activation in cancer. *Molecular Cancer* 17(1): 58.

Duan, D., N. Goemans, S. Takeda, E. Mercuri, and A. Aartsma-Rus. 2021. Duchenne muscular dystrophy. *Nature Reviews Disease Primers* 7:13.

Eigen, M. 1979. *The Hypercycle: A principle of natural self-organization*. Springer Berlin / Heidelberg, Berlin/Heidelberg, Germany.

Farnsworth, K.D., J. Nelson, and C. Gershenson. 2013. Living is information processing: From molecules to global systems. *Acta Biotheoretica* 61: 203–222.

Farnung, L., and S.M. Vos. 2022. Assembly of RNA polymerase II transcription initiation complexes. *Current Opinion in Structural Biology* 73: 102335.

Field, M., V. Dorovykh, P. Thomas, and T.G. Smart. 2021. Physiological role for GABAA receptor desensitization in the induction of long-term potentiation at inhibitory synapses. *Nature Communications* 12: 2112.

Finck, S., and H.-G. Beyer. 2009. Weighted recombination evolution strategy on a class of PDQF's. In *Proceedings of the Tenth ACM SIGEVO Workshop on Foundations of Genetic Algorithms*, 1–12. ACM, Orlando, FL.

Ford, K., B.P. Munson, S.H. Fong, R. Panwala, W.K. Chu, J. Rainaldi, N. Plongthongkum, et al. 2023. Multimodal perturbation analyses of cyclin-dependent kinases reveal a network of synthetic lethalities associated with cell-cycle regulation and transcriptional regulation. *Scientific Reports* 13: 7678.

Geva-Zatorsky, N., N. Rosenfeld, S. Itzkovitz, R. Milo, A. Sigal, E. Dekel, T. Yarnitzky, et al. 2006. Oscillations and variability in the p53 system. *Molecular Systems Biology* 2: 2006.0033.

Glasgow, A., H.T. Hobbs, Z.R. Perry, M.L. Wells, S. Marqusee, and T. Kortemme. 2023. Ligand-specific changes in conformational flexibility mediate long-range allostery in the lac repressor. *Nature Communications* 14: 1179.

Goñi-Moreno, A., M. Amos, and F.D.L. Cruz. 2013. Multicellular computing using conjugation for wiring. Edited by Mark Isalan. *PLoS ONE* 8: e65986.

González, M., N. Brito, and C. González. 2012. High abundance of serine/threonine-rich regions predicted to be hyper-O-glycosylated in the secretory proteins coded by eight fungal genomes. *BMC Microbiology* 12: 213.

Green, D.G., A.E. Whitener, S. Mohanty, B. Mistretta, P. Gunaratne, A.T. Yeh, and A.C. Lekven. 2020. Wnt signaling regulates neural plate patterning in distinct temporal phases with dynamic transcriptional outputs. *Developmental Biology* 462(2): 152–164.

Greenfeld, H., J. Lin, and M.C. Mullins. 2021. The BMP signaling gradient is interpreted through concentration thresholds in dorsal–ventral axial patterning. Edited by Sally Lowell. *PLOS Biology* 19(1): e3001059.

Gregersen, E. 2025. Analog computer (*Encyclopedia Britannica).* https://www.britannica.com/technology/analog-computer (accessed March 4, 2025)

Grozinger, L., M. Amos, T.E. Gorochowski, P. Carbonell, D.A. Oyarzún, R. Stoof, H. Fellermann, P. Zuliani, H. Tas, and A. Goñi-Moreno. 2019. Pathways to cellular supremacy in biocomputing. *Nature Communications* 10: 5250.

Gudzyk, I. 2024. What is metaprogramming. https://codefinity.com/blog/What-is-Metaprogramming.

Han, H.-S., G. Kang, J.S. Kim, B.H. Choi, and S.-H. Koo. 2016. Regulation of glucose metabolism from a liver-centric perspective. *Experimental & Molecular Medicine* 48: e218–e218.

Han, W., J. Zhu, S. Wang, and D. Xu. 2017. Understanding the phosphorylation mechanism by using quantum chemical calculations and molecular dynamics simulations. *The Journal of Physical Chemistry B* 121: 3565–3573.

He, J., Y. Zhou, and L. Sun. 2024. Emerging mechanisms of the unfolded protein response in therapeutic resistance: From chemotherapy to immunotherapy. *Cell Communication and Signaling* 22: 89.

Héberlé, É., and A.F. Bardet. 2019. Sensitivity of transcription factors to DNA methylation. Edited by Marnie Blewitt. *Essays in Biochemistry* 63: 727–741.

Jacobs, J., M. Pagani, C. Wenzl, and A. Stark. 2023. Widespread regulatory specificities between transcriptional corepressors and enhancers in *Drosophila*. *Science* 381(6654): 198–204.

Jin, B., Y. Li, and K.D. Robertson. 2011. DNA methylation: Superior or subordinate in the epigenetic hierarchy? *Genes & Cancer* 2: 607–617.

Khattar, E., and V. Tergaonkar. 2017. Transcriptional regulation of telomerase reverse transcriptase (tert) by myc. *Frontiers in Cell and Developmental Biology* 5: 1.

Kilikevicius, A., G. Meister, and D.R. Corey. 2022. Reexamining assumptions about miRNA-guided gene silencing. *Nucleic Acids Research* 50: 617–634.

Kim, E., B.D. Riehl, T. Bouzid, R. Yang, B. Duan, H.J. Donahue, and J.Y. Lim. 2024. YAP mechanotransduction under cyclic mechanical stretch loading for mesenchymal stem cell osteogenesis is regulated by ROCK. *Frontiers in Bioengineering and Biotechnology* 11: 1306002.

Kirchner, S., and Z. Ignatova. 2015. Emerging Roles of tRNA in adaptive translation, signalling dynamics and disease. *Nature Reviews Genetics* 16: 98–112.

Kolodkin-Gal, I., M.R. Parsek, and M.A. Patrauchan. 2023. The roles of calcium signaling and calcium deposition in microbial multicellularity. *Trends in Microbiology* 31: 1225–1237.

Komori, H., G. Rastogi, J.P. Bugay, H. Luo, S. Lin, S. Angers, C.A. Smibert, H.D. Lipshitz, and C.-Y. Lee. 2025. mRNA decay pre-complex assembly drives timely cell-state transitions during differentiation. *Cell Reports* 44: 115138.

Koushki, N., A. Ghagre, L.K. Srivastava, C. Molter, and A.J. Ehrlicher. 2023. Nuclear compression regulates YAP spatiotemporal fluctuations in living cells. *Proceedings of the National Academy of Sciences* 120(28): e2301285120.

Laub, M.T. 2016. Keeping signals straight: How cells process information and make decisions. *PLOS Biology* 14: e1002519.

Lewis, M., M. Götting, K. Anttila, M. Kanerva, J.M. Prokkola, E. Seppänen, I. Kolari, and M. Nikinmaa. 2016. Different relationship between *hsp70* mRNA and hsp70 levels in the heat shock response of two salmonids with dissimilar temperature preference. *Frontiers in Physiology* 7: 511.

Li, J., Z. Yuan, and Z. Zhang. 2010. The cellular robustness by genetic redundancy in budding yeast. Edited by Jianzhi Zhang. *PLoS Genetics* 6: e1001187.

Li, Q., W. Qian, Y. Zhang, L. Hu, S. Chen, and Y. Xia. 2023. A new wave of innovations within the DNA damage response. *Signal Transduction and Targeted Therapy* 8: 338.

Li, S., and C.E. Mason. 2014. The pivotal regulatory landscape of RNA modifications. *Annual Review of Genomics and Human Genetics* 15: 127–150.

Li, Y., D. Wang, H. Wang, X. Huang, Y. Wen, B. Wang, C. Xu, et al. 2021. A splicing factor switch controls hematopoietic lineage specification of pluripotent stem cells. *EMBO Reports* 22(1): e50535.

Liu, R., J. Wu, H. Guo, W. Yao, S. Li, Y. Lu, Y. Jia, X. Liang, J. Tang, and H. Zhang. 2023. Post-translational modifications of histones: Mechanisms, Biological Functions, and Therapeutic Targets. *MedComm* 4: e292.

Liu, X.-L., Z. Duan, M. Yu, and X. Liu. 2024. Epigenetic control of circadian clocks by environmental signals. *Trends in Cell Biology* 34: 992–1006.

Liu, Y., and K. Birsoy. 2023. Metabolic sensing and control in mitochondria. *Molecular Cell* 83: 877–889.

Lorenz, C., C. Lünse, and M. Mörl. 2017. tRNA modifications: impact on structure and thermal adaptation. *Biomolecules* 7: 35.

Mackeigan, J.P., L.O. Murphy, C.A. Dimitri, and J. Blenis. 2005. Graded mitogen-activated protein kinase activity precedes switch-like c-fos induction in mammalian cells. *Molecular and Cellular Biology* 25: 4676–4682.

Martinez Arias, A. 2023. *The Master Builder: How the New Science of the Cell is Rewriting the Story of Life*, First edition. Basic Books, New York, NY.

Martinez-Ara, M., F. Comoglio, and B.V. Steensel. 2024. Large-scale analysis of the integration of enhancer-enhancer signals by promoters. *eLife* 12: RP91994.

Miller, C.J., and B.E. Turk. 2018. Homing in: Mechanisms of substrate targeting by protein kinases. *Trends in Biochemical Sciences* 43: 380–394.

Minelli, A. 2021. *Understanding Development*. Cambridge University Press, Cambridge, UK.

Modic, M., K. Kuret, S. Steinhauser, R. Faraway, E.V. Genderen, I.R.D.L. Mozos, J. Novljan, et al. 2024. Poised PABP–RNA hubs implement signal-dependent mRNA decay in development. *Nature Structural & Molecular Biology* 31: 1439–1447.

MODOMICS: 2025. MODOMICS: A database of RNA modifications and related information. https://genesilico.pl/modomics/.

Mogas-Díez, S., E. Gonzalez-Flo, and J. Macía. 2021. 2D printed multicellular devices performing digital and analogue computation. *Nature Communications* 12: 1679.

Mohanan, A.G., S. Gunasekaran, R.S. Jacob, and R.V. Omkumar. 2022. Role of Ca2+/calmodulin-dependent protein kinase type II in mediating function and dysfunction at glutamatergic synapses. *Frontiers in Molecular Neuroscience* 15: 855752.

Moškon, M., R. Komac, N. Zimic, and M. Mraz. 2021. Distributed biological computation: from oscillators, logic gates, and switches to a multicellular processor and neural computing applications. *Neural Computing and Applications* 33: 8923–8938.

Mukherjee, S. 2023. *The Song of the Cell: An Exploration of Medicine and the New Human*. First Scribner trade paperback edition. Scribner Books, New York, NY.

Munsky, B., and G. Neuert. 2015. From analog to digital models of gene regulation. *Physical Biology* 12: 045004.

Nanou, E., J. Yan, N.P. Whitehead, M.J. Kim, S.C. Froehner, T. Scheuer, and W.A. Catterall. 2016. Altered short-term synaptic plasticity and reduced muscle strength in mice with impaired regulation of presynaptic CaV 2.1 Ca^{2+} channels. *Proceedings of the National Academy of Sciences* 113: 1068–1073.

Naqvi, S., S. Kim, H. Hoskens, H.S. Matthews, R.A. Spritz, O.D. Klein, B. Hallgrímsson, et al. 2023. Precise modulation of transcription factor levels identifies features underlying dosage sensitivity. *Nature Genetics* 55: 841–851.

Nguyen, L.K., M.A.S. Cavadas, C.C. Scholz, S.F. Fitzpatrick, U. Bruning, E.P. Cummins, M.M. Tambuwala, et al. 2013. A dynamic model of the hypoxia-inducible factor 1-alpha (HIF-1α) network. *Journal of Cell Science* 126: 1454–14563.

Ning, H., G. Liu, L. Li, Q. Liu, H. Huang, and Z. Xie. 2023. Rational design of microRNA-responsive switch for programmable translational control in mammalian cells. *Nature Communications* 14: 7193.

Nishio, H., D.L. Cano-Ramirez, T. Muranaka, L.L.D.B. Dantas, M.N. Honjo, J. Sugisaka, H. Kudoh, and A.N. Dodd. 2024. Circadian and environmental signal integration in a natural population of *Arabidopsis*. *Proceedings of the National Academy of Sciences* 121(35): e2402697121.

Nowacki, M., K. Shetty, and L.F. Landweber. 2011. RNA-mediated epigenetic programming of genome rearrangements. *Annual Review of Genomics and Human Genetics* 12: 367–389.

Oh, B.-C. 2023. Phosphoinositides and intracellular calcium signaling: novel insights into phosphoinositides and calcium coupling as negative regulators of cellular signaling. *Experimental & Molecular Medicine* 55: 1702–1712.

Oka, M., and Y. Yoneda. 2018. Importin α: Functions as a nuclear transport factor and beyond. *Proceedings of the Japan Academy, Series B* 94: 259–274.

Olmeda, F., and S. Rulands. 2024. Field theory of enzyme-substrate systems with restricted long-range interactions. *Physical Review E* 110: 024404.

Păun, G. 2000. Computing with membranes. *Journal of Computer and System Sciences* 61: 108–143.

Păun, G., G. Rozenberg, and A. Salomaa. 2009. *The Oxford Handbook of Membrane Computing*. Oxford University Press, New York, NY.

Pellarin, I., A. Dall'Acqua, A. Favero, I. Segatto, V. Rossi, N. Crestan, J. Karimbayli, B. Belletti, and G. Baldassarre. 2025. Cyclin-dependent protein kinases and cell cycle regulation in biology and disease. *Signal Transduction and Targeted Therapy* 10: 11.

Perucho-Jaimes, L., J. Do, A.V. Elgort, and K.B. Kaplan. 2024. Septins modulate the autophagy response after nutrient starvation. Edited by Amy Gladfelter. *Molecular Biology of the Cell* 35: ar4.

Petrenko, N., Y. Jin, L. Dong, K.H. Wong, and K. Struhl. 2019. Requirements for RNA polymerase II preinitiation complex formation in vivo. *eLife* 8: e43654.

Pleyer, J., and C. Fleck. 2023. Agent-based models in cellular systems. *Frontiers in Physics* 10: 968409.

Pond, K.W., K. Doubrovinski, and C.A. Thorne. 2020. Wnt/β-catenin signaling in tissue self-organization. *Genes* 11: 939.

Portillo-Ledesma, S., S. Chung, J. Hoffman, and T. Schlick. 2024. Regulation of chromatin architecture by transcription factor binding. *eLife* 12: RP91320.

Powers, A.S., A. Khan, J.M. Paggi, N.R. Latorraca, S. Souza, J.D. Salvo, J. Lu, et al. 2024. A non-canonical mechanism of GPCR activation. *Nature Communications* 15: 9938.

Prochazka, L., Y.S. Michaels, C. Lau, R.D. Jones, M. Siu, T. Yin, D. Wu, et al. 2022. Synthetic gene circuits for cell state detection and protein tuning in human pluripotent stem cells. *Molecular Systems Biology* 18: e10886.

Proctor, C.J., and D.A. Gray. 2008. Explaining oscillations and variability in the p53-Mdm2 system. *BMC Systems Biology* 2: 75.

Ralowicz, A.J., S. Hokeness, and M.B. Hoppa. 2024. Frequency of spontaneous neurotransmission at individual boutons corresponds to the size of the readily releasable pool of vesicles. *The Journal of Neuroscience* 44(18): e1253232024.

Rogojin, V. 2010. On computational properties of gene assembly in ciliates. *Computer Science Journal of Moldova* 2(53): 171–209.

Roquet, N., and T.K. Lu. 2014. Digital and analog gene circuits for biotechnology. *Biotechnology Journal* 9: 597–608.

Rosenberg, S.S., and N.C. Spitzer. 2011. Calcium signaling in neuronal development. *Cold Spring Harbor Perspectives in Biology* 3(10): a004259–a004259.

Ruthenburg, A.J., H. Li, D.J. Patel, and C.D. Allis. 2007. Multivalent engagement of chromatin modifications by linked binding modules. *Nature Reviews Molecular Cell Biology* 8: 983–994.

Sakellakis, M., S.M. Yoon, J. Reet, and A. Chalkias. 2024. Novel insights into voltage-gated ion channels: Translational breakthroughs in medical oncology. *Channels* 18(1): 2297605.

Sarpeshkar, R. 2010. *Ultra Low Power Bioelectronics: Fundamentals, Biomedical Applications, and Bio-Inspired Systems*. Cambridge University Press, Cambridge, UK, and New York, NY.

Seger, R. 2024. Special issue: MAPK signaling cascades in human health and diseases. *International Journal of Molecular Sciences* 25(20):11226.

Simsek, M.F., and E.M. Özbudak. 2022. Patterning principles of morphogen gradients. *Open Biology* 12: 220224.

Snyman, M., and S. Xu. 2023. The effects of mutations on gene expression and alternative splicing. *Proceedings of the Royal Society B: Biological Sciences* 290: 20230565.

Soh, W.T., H.P. Roetschke, J.A. Cormican, B.F. Teo, N.C. Chiam, M. Raabe, R. Pflanz, et al. 2024. Protein degradation by human 20S proteasomes elucidates the interplay between peptide hydrolysis and splicing. *Nature Communications* 15: 1147.

Solier, S., Y.W. Zhang, A. Ballestrero, Y. Pommier, and G. Zoppoli. 2012. DNA Damage response pathways and cell cycle checkpoints in colorectal cancer: Current concepts and future perspectives for targeted treatment. *Current Cancer Drug Targets* 12: 356–371.

Stockwell, I., J.F. Watson, and I.H. Greger. 2024. Tuning synaptic strength by regulation of AMPA glutamate receptor localization. *BioEssays* 46(7): 2400006.

Tee, W.-V., S.J.M. Lim, and I.N. Berezovsky. 2024. Toward the design of allosteric effectors: Gaining comprehensive control of drug properties and actions. *Journal of Medicinal Chemistry* 67:17191–17206.

Tomanek, L. 2010. Variation in the heat shock response and its implication for predicting the effect of global climate change on species' biogeographical distribution ranges and metabolic costs. *Journal of Experimental Biology* 213: 971–979.

Ulmann, B. 2022. *Analog computing* (De Gruyter textbook, Second extended edition). De Gruyter Oldenbourg, Munich, Germany. https://doi.org/10.1515/9783110787740.

Virdi, G.S., M.L. Choi, J.R. Evans, Z. Yao, D. Athauda, S. Strohbuecker, R.S. Nirujogi, et al. 2022. Protein aggregation and calcium dysregulation are hallmarks of familial Parkinson's disease in midbrain dopaminergic neurons. *Npj Parkinson's Disease* 8(1): 162.

Walia, M.K., P.M. Ho, S. Taylor, A.J. Ng, A. Gupte, A.M. Chalk, A.C. Zannettino, T.J. Martin, and C.R. Walkley. 2016. Activation of PTHrP-cAMP-CREB1 signaling following p53 loss is essential for osteosarcoma initiation and maintenance. *eLife* 5: e13446.

Wang, J., Y. Xiang, M. Fan, S. Fang, and Q. Hua. 2023. The ubiquitin–proteasome system in tumor metabolism. *Cancers* 15: 2385.

Wang, X., Q. Liu, H.-T. Yu, J.-Z. Xie, J.-N. Zhao, Z.-T. Fang, M. Qu, Y. Zhang, Y. Yang, and J.-Z. Wang. 2024. A positive feedback inhibition of isocitrate dehydrogenase 3β on paired-box gene 6 promotes Alzheimer-like pathology. *Signal Transduction and Targeted Therapy* 9(1): 105.

Waqas, M., M. Khurram, and S.M.R. Hasan. 2020. Analog electronic circuits to model cooperativity in Hill process. *Mehran University Research Journal of Engineering and Technology* 39(4): 678–685.

Wu, L., R. Balyan, J. Brzostek, X. Zhao, and N.R.J. Gascoigne. 2023. Time required for commitment to T cell proliferation depends on TCR affinity and cytokine response. *EMBO Reports* 24: e54969.

Wurtz, T. 2021. Nested information processing in the living world. *Annals of the New York Academy of Sciences* 1500: 5–16.

Yu, H., H. Deng, J. He, J.D. Keasling, and X. Luo. 2023. UniKP: A unified framework for the prediction of enzyme kinetic parameters. *Nature Communications* 14: 8211.

Yue, J., and J.M. López. 2020. Understanding MAPK signaling pathways in apoptosis. *International Journal of Molecular Sciences* 21(7): 2346.

Zbili, M., S. Rama, and D. Debanne. 2016. Dynamic control of neurotransmitter release by presynaptic potential. *Frontiers in Cellular Neuroscience* 10: 278.

Zhang, J., Q. Wang, J. Liu, Y. Duan, Z. Liu, Z. Zhang, and C. Li. 2024. Active enhancers: Recent research advances and insights into disease. *Biology Direct* 19: 112.

Zhong, S., K. Malecek, L.A. Johnson, Z. Yu, E.V.-S.D. Miera, F. Darvishian, K. McGary, et al. 2013. T-cell receptor affinity and avidity defines antitumor response and autoimmunity in T-cell immunotherapy. *Proceedings of the National Academy of Sciences* 110: 6973–6978.

Ziello, J.E., I.S. Jovin, and Y. Huang. 2007. Hypoxia-inducible factor (HIF)-1 regulatory pathway and its potential for therapeutic intervention in malignancy and ischemia. *The Yale Journal of Biology and Medicine* 80(2): 51–60.

Appendix 1. Regulated cellular biochemistry does not resemble abiotic chemical behavior

Precisely regulated cellular biochemical processes are fundamentally different from familiar chemical processes, including designed laboratory oscillators, in many ways.

- *Specificity*: Changes caused by biochemical concentration gradients are site-specific (e.g., enzyme-substrate binding), unlike the generalized, non-specific reaction kinetics in non-cellular chemical systems.
- *Complexity and regulation*: Cellular oscillations involve intricate networks of genes, proteins, and feedback loops (e.g., transcription, translation, post-translational modifications), whereas chemical oscillators rely on very few simple molecules.
- *Precision and robustness*: Cellular systems maintain precise and robust control over concentration changes through mechanisms like redundancy and adaptive feedback. Simple oscillatory reactions are very sensitive to initial conditions and external perturbations.
- *Autonomy*: Once improper stoichiometric ratios develop over time, chemical oscillations terminate. In cells, the initiation and termination of such biochemical processes are regulated to satisfy whole-cell needs.
- *Adaptability*: Cellular systems adjust oscillation patterns in response to environmental cues or signaling, while chemical oscillators follow fixed, deterministic dynamics based on static chemical trajectories.
- *Stochasticity*: Cellular processes incorporate noise and stochastic events (e.g., gene expression variability), while chemical oscillators are deterministic and lack such randomness.
- *Single-purpose reaction pathways*: Chemical oscillators follow fixed reaction pathways without the multifunctionality of cellular systems.
- *Timescale*: Cellular oscillations (e.g., circadian rhythms, cell cycle) occur over minutes to days, regulated by molecular clocks, whereas chemical oscillators operate on much shorter, less flexible timescales (seconds to minutes).
- *Energy dependence*: Cellular oscillations are ATP-driven and tightly coupled to metabolism, whereas chemical oscillators are fueled by spontaneous redox reactions without biological energy currencies.
- *Purposeful output*: Cellular oscillations serve functional roles (e.g., homeostasis, division), whereas chemical oscillators are emergent phenomena without biological intent.
- *Multiple oscillating systems*: In cells, hundreds or thousands of processes occur in the same region for independent purposes, often with cross-talk between them.
- *Integration of multiple functions*: In cells, oscillations are often integrated with other processes (such as cell cycle progression or circadian rhythms) to coordinate broader cellular functions.
- *Replication in toto*: In cells, a multitude of biochemical processes are passed on in a functioning state to the daughter cell.

None of the chemical oscillations developed, conceived, or proposed by OoL chemists as precursors for ancient cells resembles the biochemical components or processes used in cells. Cellular biochemical processes must provide the metabolic and energy needs of the integrated and autonomous system as a whole. These rely on sensors to interact and adapt to the environment; enable mobility; interact with other cells; and reproduce.

Appendix 2. Codons must distinguish between identical but incorrect triplets

One way to distinguish cellular variables (i.e., sensors) from purposeless, random interactions is to examine the microenvironment where they interact with the target signals, as illustrated in Figure 4. One might incorrectly suspect that identical triplets located anywhere on mRNA and other RNA molecules could base pair at many locations on any tRNA. Instead, translation occurs rapidly and reliably, one triplet codon after the other. False interactions are avoided with the help of the surrounding regions. This illustrates how cellular sensors must be specially engineered to avoid meaningless interactions.

Reliable codon-anticodon interactions require precise engineering involving scores of enzymes (Sharp et al., 1985; Hopper et al., 2010; Hopper, 2013; Raina and Ibba, 2014; Hopper and Nostramo, 2019; Yu et al., 2019; Truman, 2020b, 2021). This is an example of how the signaling molecule and sensor must also be tailored. Human tRNAs contain, on average, 13 chemically modified nucleotides to ensure proper shapes and to prevent incorrect folds. The anticodon region of each tRNA is shaped into a niche that optimizes H-bonding with the codon triplets, despite each codon nucleotide having the cognate hydrogens in different locations (Yarian et al., 2002; Deutsch et al., 2012; Wang and He, 2014; Barciszewska et al., 2016; Pan, 2018; Roy et al., 2018; Huber et al., 2019; Krutyhołowa et al., 2019; Nguyen et al., 2020). Other modifications enhance proximate interactions with the ribosome to anchor the tRNA in place and prevent reading frame slippage (Hoffer et al., 2020).

Appendix 3. Fuzzy logic programming in digital technologies

In digital programming, techniques exist to process values in a more nuanced fashion than simple true/false decisions. For example, a variable 'Sick' could be assigned a Boolean value true or false. However, there are degrees of sickness, and this might need to be taken into account. In fuzzy logic, categories such as *very_sick*, *moderately_sick*, or *slightly_sick* could be defined to represent degrees or probability of sickness, each covering ranges of values based on some criteria. Programming logic would then be expressed for each of the possible categories.

In practice, continuous (analog) values are often divided into narrow discrete ranges so that digital programs can process them.

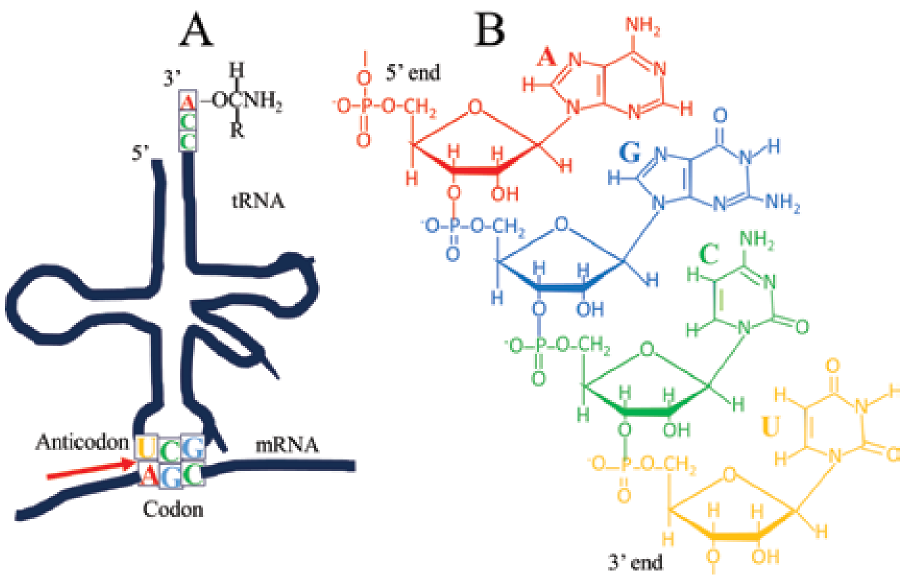


Figure 4. Codon triplets must not base-pair indiscriminately if they are to function as cellular variables. A: The red arrow points to the microenvironment where codons recognize the correct anticodons. B: Chemical structure of the nucleotides.

Appendix 4. Cytomorphic circuits

Cellular biochemical reactions have energy barriers that follow Boltzmann exponential laws that are also found in electronic flow when below the threshold voltage in transistors (Sarpeshkar, 2010, 2012, 2014; Daniel et al., 2013). This mathematical similarity has led to the development of analog electronic "cytomorphic circuits" that are used to mimic cellular processes. Voltages represent molecular concentrations, and currents represent reaction rates (Daniel et al., 2013; Sarpeshkar, 2014; Hanna et al., 2020).

The core architecture of cytomorphic systems typically comprises specialized analog circuit modules called 'Protein Chips' (Beahm et al., 2021) that can model zeroth-, first-, and second-order reactions, including nonlinearities and interactions. By connecting multiple transistor circuits, researchers can faithfully reproduce cascades, loops, fan-in, fan-out, dimerization, and other biochemical network patterns (Beahm et al., 2021; Waqa et al., 2022). Unlike digital simulations that discretize continuous biological processes and solve them iteratively, analog cytomorphic circuits can instantly integrate all the inputs just like cells can (Coldewey, 2016; Woo et al., 2018; Beahm et al., 2021). Acceleration and conceptual simplification of the modelling effort are necessary since gene-protein networks involve tens of thousands of state variables that interact through elaborate feedback loops (Sarpeshkar, 2014; Beahm et al., 2021).

Analog Neuromorphic Circuits

Another technology used to mimic biological analog processing is neuromorphic circuits. These are a type of electronic circuitry using Complementary Metal-Oxide-Semiconductor (CMOS) circuits designed to imitate how brain neurons and synapses are thought to function (Indiveri et al., 2011; Hazan and Tsur, 2021; Chen et al., 2023; Xiao et al., 2024; Yoon et al., 2024). They perform analog parallel processing very effectively, closely mimicking brain neurons and consuming far less energy than conventional computers.

Creation Research Society Quarterly 2026 62:331–344

Cells Are Integrated Multiprocessing Analog Computing Devices—Part 2

Royal Truman[1]*,
Amit Singh[2], and
Peter Borger[3]

Key Words: Adaptor molecules, analog computing, biological information, biological sensors, cellular processes, concentration gradients

[1] University of Konstanz, Konstanz, Germany
[2] Institute for Biomechanics, ETH Zurich, Switzerland
[3] peter.borger@wort-und-wissen.de
* Correspondence: royal.truman@uni-konstanz.de

Accepted for publication February 10, 2026

Abstract

Cells comprise thousands of intricately designed analog computing units that execute complex biochemical processes. Precisely positioned sensors—implemented in DNA, RNA, proteins, lipids, and other biomolecules—respond to continuous signal gradients and generate localized microenvironments that recruit, assemble, and regulate molecular machinery essential for cellular function. These sensor–signal interactions initiate stepwise processes that distinguish an immediate physical recognition goal from a downstream major functional goal, enabling fine-tuned control of rates, timing, and outcomes. Cross-communication among concurrently operating processes supports coordinated adaptation, repair, recycling of obsolete components, and system-wide reproduction while maintaining uninterrupted operation. Cellular logic is implemented through physical interactions, adaptor molecules, and dynamically assembled complexes that realize flexible ‘if–then’ relationships. Unlike conventional digital computers, cells do not separate software from hardware; instead, both are inseparably embodied in adaptive molecular structures whose sensitivities can be modified during execution. This analog computing paradigm provides robustness, scalability, and efficiency that differ fundamentally from digital computation and from purely chemical descriptions. Viewing cells as integrated multiprocessing analog computing devices offers a unifying framework for understanding cellular regulation, autonomy, and biological information processing.

Simple Summary

Biological systems function as integrated analog computing devices rather than following the rigid binary logic of modern digital computers. Instead of separating software from hardware, cells utilize adaptive molecular structures where physical sensors directly interact with continuous environmental signals to regulate growth and repair. These interactions facilitate a stepwise logic processing method, utilizing adaptor molecules and dynamically assembled complexes to achieve complex functional goals. By viewing cellular regulation through this analog computing paradigm, researchers can better understand the robustness and scalability of biological information. This framework highlights how cellular sensors and signals can be physically modified during execution, allowing for a level of fine-tuning and flexibility unattainable by conventional technology. Ultimately, the sources propose that metaprogramming principles enable cells to autonomously self-regulate and reproduce through these sophisticated, non-digital mechanisms.

Introduction

Bacterial and eukaryotic cells are far more than a collection of complex chemical reactions contained in a membrane. Cells autonomously organize and regulate their own growth, adaptation, protection, repair, and recycling, reproducing generation after generation in a constantly functional state. These processes require cells to manufacture both their own chemical components and usable energy.

In Part 1 of this series, we proposed viewing cells as an integrated series of analog computing devices. Thousands of bacterial and eukaryotic sensors interact with concentration gradients and other continuous signals. These sensors function as programming variants that initiate and regulate the biochemical processes necessary to fulfil the necessary functions mentioned above. Focusing on the logic processing provides a unifying overview that allows many chemical details to be neglected to focus on the essential.

Cells Do Not Function Like Familiar Digital Computers

A point emphasized in Part 1 is that cells do not have software that is separate from the hardware, unlike modern digital computers.

Digital computing depends on infrastructure capable of existing in only two distinct states. These binary units, or bits, are combined to encode variables, values, and logical operations, governed by formal rules and structured programming languages. The two distinct states are defined by magnetic polarity, light pulses, range of voltage, and other physical methods. Engineering specifications define an error tolerance so that only distinct states are used.

Before the codon → amino acid mapping used by the genetic code was understood, scientists already assumed that protein sequences were stipulated through some kind of code (Hayes, 1998). Once the genetic code was elucidated, it became common practice to assign the single letters A, C, G, and T to DNA nucleotides and one or three-letter abbreviations to amino acids (e.g., A, C, D or Ala, Cys, Asp). This created a mental association with known technical codes like the Morse and ASCII codes and computer programming languages. Furthermore, Shannon's *information* theory was developed before the genetic code was deciphered, which deals with the transmission of strings of symbols. Consequently, *information* and sequences of letters became linked in the minds of molecular biologists. Decoding mRNA messages seemed to resemble computer programming:

If current_codon = x then amino_acid = y (1)

For example,

If codon = CUA then amino_acid = Leu
If codon = GUC then amino_acid = Val (2)

where Leu is the abbreviation for leucine, and Val for valine.

Although nobody doubts that DNA specifies protein sequences, doubts are expressed about whether DNA represents a computer-like program. Where is the source code? Is the genetic code the only true code found in cells (Lesne, 2023)? (Cellular codes are discussed in Part 3 of this series.) Where do the instructions come from to assemble entire body parts and organisms? Some even insist that cellular processes can be reduced strictly to physical and chemical principles (Sarkar, 2005; Rosenberg, 2006; Bickle, 2010) and that comparisons with computers are only an anthropomorphism or a weak analogy (Nicholson, 2019).

An understandable mistake has been to associate cell processing too strongly with familiar digital computing. In Part 1, we identified sensors as variables, emphasizing that the sensing element directly interacts with a continuous gradient signal. This permits the response to a signal to be adjusted through physical modifications to a small microenvironment. Clearly, this is not how digital variables function. An assignment statement like *new_price = 100* cannot be programmed to produce a different meaning than 100 by modifying characteristics of the composing symbols (e.g., *n*, *e*, *w*, *p*…) that compose the variable '*new_price*.' But as discussed in Part 1, this is how cellular programming is fine-tuned. Reflecting on synonymous codons helps to clarify this distinction. In some cases, only the first two nucleotides uniquely specify the amino acid, and the third 'wobble' position modifies the probability that the codon will be translated correctly. Many overlook that only a small portion of the nucleotides is responsible for anticodon identification, namely, specific H-bonds.

To illustrate, in *E. coli,* the codon *AGA* is usually translated to arginine, but *AGA* is sometimes mistranslated to the similar amino acid lysine due to the similarity at the binding location and the low concentration of the anticodon for AGA that translates to Arg, tRNA^{Arg}(UCU). Consequently, the AGA codon sometimes recognizes a tRNA^{Lys}(UUU) (Sun and Zhang, 2022). This is not a feature of digital programming, whereby variables and values in the same programming instruction have a unique meaning.

Analog Computing Technologies

Analog computing was discussed in Part 1. It uses technologies having a direct physical connection between changes in an input variable (such as a concentration gradient, temperature, pressure, and light flux) and an outcome. We believe that all or virtually all cellular programs are implemented using analog computing principles. Some processes, like chromosome replication, are executed only during the lifespan of a cell, whereas others are replicated and passed in a running state to daughter cells (Handy et al., 2011). Some process details can be inherited by future generations by modifying DNA sequences or using epigenetic tags (Powledge, 2011; Fitz-James and Cavalli, 2022; Tollefsbol, 2022).

The analysis in Part 1 emphasized the key role of sensors, which act as analog variables. Sensor values correspond to the setting along the X-axis of the example shown in Figure 1. Physical adjustments to a sensor result in different response sensitivities, changing binding strengths or rates. But such physical-chemical effects are only the initiating and regulating part of the cellular processes executed. We introduce now the concept of an immediate physical goal to be met by analog variables vs. the implied major goal to be achieved.

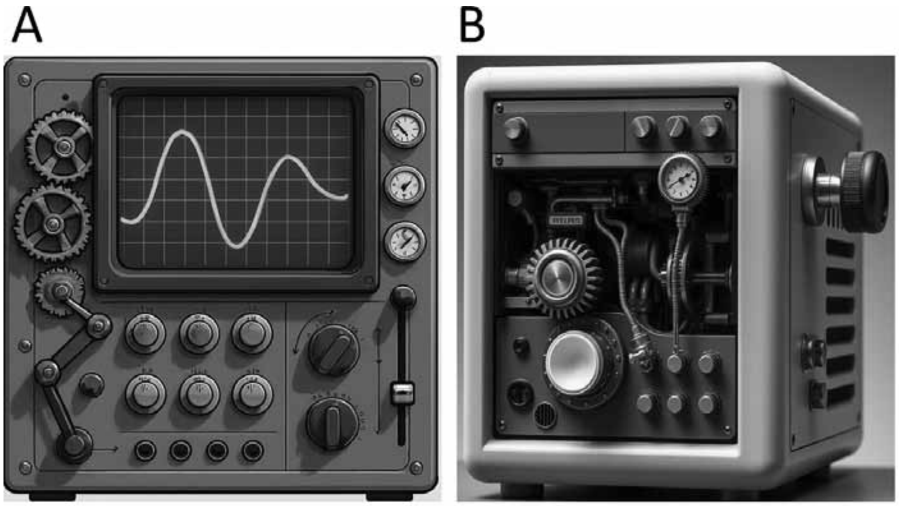


Figure 1. Fictitious analog computers illustrate how continuous physical or mechanical changes in an input variable produce continuous changes in the response. (Image generated by AI).

Immediate Goal of a Cellular Variable ('Step 1')

The immediate task of a sensor is to recognize changes in the signal. In Figure 1, the sensor must be engineered to immediately sense changes in lever position, or dial rotation, or whatever is used to define a continuous input value. For instance, the first goal a codon must satisfy is to identify the intended anticodon on a tRNA defined primarily by ~5 – 9 suitably positioned hydrogen bonds[1], plus stabilizing contributions from portions of neighboring nucleotides in both the tRNA anticodon stem loop and the mRNA (Gorochowski et al., 2015; Nedialkova and Leidel, 2015; Mala and Saraogi, 2022). Post-transcriptional modifications in the anticodon region also contribute to the accuracy and speed of this interaction (Mala and Saraogi, 2022). This physical dependency explains why the composition and abundance of the tRNA pool (which vary in cell- and tissue-dependent manners) are used to regulate mRNA translation velocity (Nedialkova and Leidel, 2015; Davyt et al., 2023).

The general principle is that the effectiveness of the association between cellular variables with values is determined by the geometrical and electrostatic characteristics at the micro-location where the identifying interaction occurs. These sensor locations are strategically located on DNA, RNA, protein, sugar, phospholipid bilayer, etc. For example, a portion of a receptor tyrosine kinases (RTKs) on the outer cell membrane must recognize the defining portion of an extracellular signaling molecule (Laub, 2016). Many studies have helped elucidate the physical basis of sensor interactions that specify the *immediate goal,* but it is important to realize that this is only a means to an end, namely, the conversion of an input informative signal into a downstream process, discussed next.

Major Goal of a Cellular Variable ('Step 2')

Once a sensor has bound to a gradient signal, the next cellular processes can be initiated and regulated. For example, only after the stable codon to anticodon interaction has been established will the next steps occur to carry out the translation.[2] Changes in total bind-

---

[1] Pairing between nucleotides C and G uses 3 H-bonds and pairing between A and U uses 2 H-bonds. However, in the wobble position of tRNA, Inosine (I) arises from the deamination of A by the enzyme ADAR. A with I pairing uses only 1 H-bond (sometimes with a weak contribution from a second H-bond). Therefore, the codon AUA when paired with the IAU anticodon uses only 5 H-bonds. When three C with G interactions are involved then 9 H-bonds are used.

[2] After codon-anticodon pairing, a peptide bond forms between the amino

ing strength and the concentration of tRNA regulate the rate at which these subsequent steps will be initiated, ensuring the correct concentration of protein will be formed. Individual codon translation rates also regulate the process so that sufficient time is available at key protein locations to permit proper folding (Fluman et al., 2014; Faure et al., 2017).

As another example, binding of a signal molecule to a sensor kinase ('Step 1') is followed by autophosphorylation of a histidine amino acid, transfer of the phosphate to another response regulator protein, and then several more steps to modify the expression of several genes (Laub, 2016). The latter constitute 'Step 2,' i.e., the major goal.

Cells possess a distinguishing characteristic that differentiates them from natural chemical processes and all human technologies to date. The processes initiated and controlled by sensors cause a pre-planned assembly of the requisite processing equipment (e.g., molecular machines). Astonishingly, these processes produce new microenvironments that become new sensors that bind to new partners. This permits cellular goals to be regulated along the whole execution chain.

Flexible Programming of Step 1 and Step 2

Programming requires intentions to be expressed using logical operations. Cellular 'reasoning' is implemented by adding, removing, and modifying details during process execution. A sensor provides the 'If' part of a program, namely, if the signal is sensed long enough to begin the processes to achieve the intended outcome. Recall that the sensitivity of the variable (sensor) can be modified in many ways (e.g., using ligand attachments, chemical modifications, cofactors, different pH and temperature, etc.), and influences from different kinds of sensors can be integrated to fine-tune control.

The sequence of activities along the chain leading towards the major goal also has the character of If…Then. When the sensor plus signal microenvironment recruits the first biochemical(s), a new sensor is generated (or was already incorporated into the recruited partner) at a precise location. This self-assembly cascade thereby produces a new, just-in-time cellular process. Throughout all these activities, Boolean AND, OR, and NOT logic can be implemented using physical interactions.

Implementing If…Then logic in cells often relies on the concept of adaptor molecules or adaptor complexes.

Adaptor Molecules and Complexes in Cellular Processing

Recognition of a signal by a sensor is used as the 'if' part of cellular decision-making, and the decision must be physically transmitted to have any merit.

Two examples are shown in Figure 2, involving the concept of adaptor molecules or adaptor assemblies. In Figure 2-A, one end of the tRNA adaptor molecules is recognized by a codon during Step 1. Since the other end of that tRNA has already been charged with the correct amino acid, the next step can be implemented. The reasoning is, for example,

> If a tRNA having anticodon 5′-UCG-3′ binds to an mRNA codon, then add amino acid serine to the growing polypeptide chain.

This flexible design strategy permits different correspondences between *n* codons and 1 amino acid to be implemented by using different sets of tRNAs.

Figure 2-B shows how a cascade of If…Then logic is often found in cells to assemble and execute the machinery stepwise that implements cellular processes. Initiating RNA transcription is an example. To initiate the process, the ~ 8-nucleotide (~8 nt) sequence TATA box sensor binds to part of a TATA-binding protein (TBP). Once TBP is bound to the TATA box, a series of proteins are recruited stepwise by generating a recognition region for the partner it should interact with. Eventually, the preinitiation complex (PIC) is formed. Part of this PIC then interacts with the RNA polymerase complex to position it correctly so that it can begin transcription. The TIP acts like an adaptor complex linking the TATA-box with its activating signal to the processes involved in transcription.

The diagram in Figure 2-B illustrates how, sometimes, it can be somewhat arbitrary which partner is assigned the role of sensor vs. signal. What matters is that the binding interaction is what specifies what is to result. Generally, if the concentration of one variable fluctuates rapidly and considerably, causing a continuous change in output, then that partner is best viewed as the signal. Ambiguity can still result, since cells also often regulate the number of sensors according to need to become more responsive to changes.

These examples answer the concern that to be codes or programs, a correspondence must be changeable (Lesne, 2023). We have just shown that in cells they are indeed. For instance, in the *N*-end *ubiquitin code,* the first position

---

acid in the A site and the polypeptide chain on the P-site tRNA, transferring the chain to the A-site tRNA. During translocation, the ribosome shifts one codon, moving the empty P-site tRNA to the E site and the A-site tRNA (now with the polypeptide) to the P site. This opens the A site for the next aminoacyl-tRNA.

of a protein communicates the half-life of a protein (Varshavsky, 1997), ranging from arginine $t_{1/2}$ ~2 minutes up to methionine $t_{1/2}$ >20 hours (Sriram et al., 2011). This code could have been designed in many ways, since the choice of what each residue should specify is arbitrary. Implementing any of the possible codes could then be engineered by ensuring correct interactions with the protein degradation enzymes.

However, as discussed later in Part 3, the ambiguous term *code* often leads to misunderstandings, since the term has several meanings in the literature.

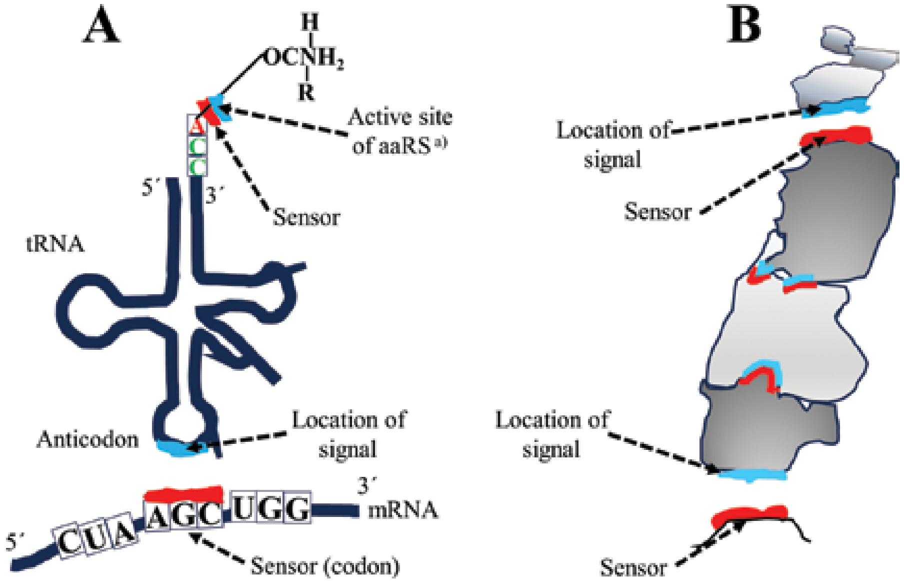


Figure 2. Adaptor molecules are a key strategy used in cells to implement processes flexibly. A: A single adaptor molecule connects a specific sensor to a specific process. The example shows a tRNA. (Other portions of the t-RNA adaptor molecule also interact with parts of the ribosome to ensure correct processing.) B: An alternative design more frequently used in cells links multiple components (proteins and / or RNAs) with each component possessing both a sensor to identify its partner and a recognition portion elsewhere for the sensor of a different component. This stipulates how the machinery is to be assembled and processed stepwise. Red lines indicate sensors and blue lines the recognition signals. a) aaRS = aminoacyl-tRNA synthetases

Sensors Defined Using DNA

Cellular sensors can be engineered using DNA, RNA, proteins, carbohydrates, or lipids as the medium. Some examples of variables located on DNA that are used to regulate important cellular processes are provided in Table I. Only enough examples were provided to exemplify the principle.

The first column documents the cellular process being referred to. The second column mentions what the sensor is, namely, the analog variable used to initiate and regulate the entire process. In column 3, the distinctive sensing feature within the sensor is identified to distinguish it from the surrounding housing (i.e., the casing or enclosure). The housing ensures proper functioning of the sensing feature and helps distinguish it from false sensors. For example, anticodons must not bind to random nucleotide triplets. The fourth column identifies the informational signal the sensor was designed to recognize. It is restricted to only the relevant distinguishing feature, since very often they are also enclosed in an optimizing housing. For example, on average, a protein like a transcription factor (TF) could bind at >3,500 locations with a relevant-size DNA counterpart (Tompa and Rose, 2011). False interactions must be avoided by ensuring a precise fit between the binding partners.

In the fifth column, refining components and activities are documented that serve a quality control function, ensuring the sensor is interacting with a legitimate signal. Often, cofactors, ligands, and other biomolecules are also involved to strengthen the binding interaction. Column six documents some of the biochemicals and complexes that are assembled at the microenvironment where the sensor is interacting with its signal. These execute the useful cellular functions intended by the sensor.

How far a researcher wishes to document the intended outcome depends on what is being studied. For example, the major goal (‘Step 2’) for eukaryotes could be identified as the generation of primary RNAs if one wishes. Others may continue to describe how RNAs are then used to code for proteins or regulatory functions, and so on, even until specific biological outcomes are achieved. Our model is recursive. Sensors are created dynamically and used by cells in linked chains of processes.

The last column is not intended to be an exhaustive list of the references we used to reach our conclusions.

The processes mentioned in Table I will not be discussed in detail to avoid excessive side-tracking details.

A nuance of DNA-based sensors involves regulating DNA expression and replication by binding to an RNA copy.

Table I. Examples of cellular variables located on DNA and the bio-components involved.

Cellular process	Sensor	Sensing feature	Signal recognized by the sensor	Quality control (QC) and stabilization (Stab) of the sensor with signal	Complexes recruited during subsequent processes	References
Initiation of DNA replication in *E. coli*	DnaA boxes within the origin of replication site (ori)	Consensus 5′-TT(T/A)TNCACA-3′ pattern	Helix-turn-helix domain of DnaA	QC: A threshold of multiple DnaA molecules must bind cooperatively. Also, catalytic hydrolysis of ATP on DnaA leads to an ADP-bound form that prevents reuse of the ori. Stab: IHF, Fis, and DiaA.	DnaC binds; DnaB helicase is loaded onto single-stranded DNA; DnaC is released; DnaG associates with DnaB, forms the primosome.	Wegrzyn and Konieczny, 2024
Elongation of DNA in *E. coli*	Individual nucleotide positions on the template strand	Individual A, C, G, and T nucleotides.	Complementary dNTPs positioned in the alpha subunit of Pol III.	QC: Pol III performs proofreading via an induced-fit and 3′–5′ exonuclease activity. Stab: Using a Pol III structuring pocket and Mg^{2+} to coordinate the phosphate groups.	After phosphodiester bond formation, the sliding clamp ensures processive movement of Pol III along the template.	Łazowski and Woodgate, 2024
Initiation of transcription in eukaryotes	TATA box within the promoter region	6-8 nt pattern resembling TATAAA	Part of the TATA-binding protein (TBP)	QC: General transcription factors, including TFIIA and TFIIB. Stab: Activator proteins bound to enhancers	Additional TFs to form the preinitiation complex that positions RNA polymerase II.	Haberle and Stark, 2018
Transcription in eukaryotes	Nucleotide position on the template DNA	Individual nucleotides (A, C, G, and T)	Complementary rNTP in the active site of the RPB1 subunit of Pol II	QC: Pol II with TFIIS execute proofreading. Stab: Using TFIIB, TFIID, Mediator complex, ATP-dependent chromatin remodeling complexes, histone modifications, and various coactivators.	Several elongation factors associated with Pol II to ensure its processive movement.	Svetlov and Nudler, 2013; Su and Vos, 2024
Base excision repair (BER) in most organisms	Damaged nucleobase on a nucleotide	Nucleobase shape after oxidation, alkylation, deamination, etc.	Structurally complementary active site of DNA glycosylases	QC: Glycosylases flip the nucleotide into their active site pocket to check shape complementarity. Stab: Mg^{2+}, XRCC1 and APE1, phosphorylation and acetylation of glycosylases, histone modifications, and chromatin remodeling factors.	Repair complex including an AP endonuclease, DNA polymerase, and DNA ligase.	Chen et al., 2024
Global genome nucleotide excision repair in humans	Location of bulky DNA lesions that distort the DNA helix	Cyclobutane pyrimidine dimers, chemical attachments, etc.	A beta-hairpin motif in a DNA-binding domain of the XPC protein	QC: XPA acts as a damage verification factor; also, the XPB and XPD helicases. Stab: Using RAD23B, Centrin-2, TFIIH complex, and RPA. Also, ubiquitination and sumoylation modifications of XPC.	XPG and XPF-ERCC1 endonucleases, DNA polymerase, and DNA ligase.	Scharer, 2013; Chen et al., 2024
Mismatch excision repair (MMR) in humans	Locations of DNA base mispairing	Wrong base-paired shape after insertions and deletions	Complementary domains in MSH6 subunit of MutSα, and MSH3 of MutSβ	QC: MutLα complex to verify the mispairing. Stab: PCNA and RFC; and also RPA.	Exonuclease 1 (EXO1), DNA polymerase δ or ε, and DNA ligase.	Chen et al., 2024
Remove IES in Paramecium micronucleus	Regions at boundaries of MDSs and IESs	Short pointer sequences	Part of the PiggyMac (Pgm) protein	Both quality-control and stabilization rely on small RNAs and their Argonaute partners as well as chromatin markers.	PgmL, Ku70/Ku80 heterodimers, IV and XRCC4 proteins, nucleases, DNA processing enzymes, and NHEJ.	Rogojin, 2010; Bétermier et al., 2023

We view the sensor as being located on the DNA, with the copy number of RNAs serving as a concentration gradient (signal). Some examples include:

- R-loops form in a controlled manner to regulate transcription, DNA replication, and repair. They typically recruit protein factors that mediate downstream effects.
- Promoter-associated RNAs work in many cases together with protein complexes to fine-tune transcription initiation.
- Long non-coding RNA Xist, which is expressed from and coats one X chromosome in female mammals. Xist recruits protein complexes to ensure transcriptional silencing.

In some cases, binding interaction between RNA and DNA is designed to deactivate processes that would otherwise occur and don't require proteins:

- Triplex structures form Hoogsteen or reverse Hoogsteen base pairing that affect transcription by physically blocking TFs or RNA polymerase from binding.
- G-quadruplex structures form at G-rich DNA regions to influence gene expression by restricting DNA accessibility.

Sensors Defined Using RNA

Thousands of RNA locations need to be precisely targeted for chemical modification, especially on rRNA and tRNA molecules (Liu et al, 2025). Sensors are located at these regions that identify complementary patterns called guide sequences ~10–20 nt (nucleotides) that are found within snoRNAs ~60–300 nt long. In Box C/D snoRNAs, the guide sequences are usually located near the 5′ end, whereas in Box H/ACA snoRNAs, the guide sequences are generally located near the 3′ end. Once bound to the target RNA, another region of the snoRNA recruits enzymes that modify a specific nucleotide, performing 2′-O-methylation or pseudouridylation. There are about 1,740 sno genes (SKI-related proto-oncogenes involved in regulating gene expression, cell growth, and signaling pathways) in the human genome, grouped into 226 families (Zhang et al., 2016).

As a second example, mRNAs must often be downregulated and contain a sensor ~6–8 nt long located in their 3′ untranslated region (3′ UTR). These variables recognize complementary 'seed regions' usually located at the 5′ end of the miRNA that are RNA molecules ~22 nt long. Once the sensor and signal are bound, other complexes are assembled, typically leading to translational repression or mRNA degradation. There are approximately 2,300 human miRNAs (Alles et al., 2019) and many thousands of mRNA targets (Chen, 2025).

Some examples of variables implemented on RNA are provided in Table II, analogous to Table I. Reminiscent of codon to anticodon binding discussed above, it is the concentration gradient of the signal that specifies the rate and degree of the resulting outcome in these examples.

Nucleotide Pairing as a Principle Used by Some Sensors

Given the precision of nucleotide A-T and C-G pairing, nucleotide sequences are an effective design strategy for sensors to identify various concentration gradients. The specificity of the interaction ensures that the *immediate goal* of the cellular variable is fulfilled unambiguously more efficiently and compactly than usually possible from hybrid protein-nucleotide interactions.[3] Illustrative examples include:

- Identification of anticodons of tRNAs by codons (Kim et al., 2024).
- Identification of the correct region of U1 snRNA by the GU pattern at the start position of an intron during mRNA splicing. The branch site nucleotide recognizes the correct nucleotide of the U2 snRNA. But remarkably, the end position of the intron, defined by an AG pattern, identifies a region of the U2AF *protein* instead of an RNA molecule (Karijolich and Yu, 2010; Tholen, 2024).[4]
- The *miRNA recognition element* on an mRNA recognizes the seed region of the correct miRNA that is to regulate it (O'Brien et al., 2018; Prochazka et al., 2022; Bofill-De Ros and Ørom, 2024; Diener et al., 2024).

Reversal of the Role of Sensor and Signal

Generally, we consider the sensor to be the more stationary member of the physical interaction, and the copy number of the signal is what changes. However, the number of cellular sensors is usually also regulated. For example, the copy number of mRNAs and complementary tRNAs is both regulated. Alternatively, the number of TF copies is carefully regulated, whereas the target DNA-binding sites remain fixed in a cell (although some could be silenced).

To which binding partner the sensor and signal are assigned does not affect the analog nature of cellular computing, since it is the *change in concentration of bound states* that specifies the rates of the resulting processes.

Sometimes sensors appear to be rather passive and respond to signals if and when they arrive. In other cases, the sensors seem to play a more active

---

[3] The use of RNA molecules in cellular processes, especially ribosomes, has been used as evidence for the RNA World hypothesis (Michael and Joyce, 2012). This overlooks that using RNA as an adaptor molecule makes sense as a design strategy.

Table II. Examples of cellular variables located on RNA and the bio-components involved.

Cellular process	Sensor	Sensing feature	Signal recognized by sensor	Quality control (QC) and stabilization (Stab) of sensor with signal	Complexes recruited during subsequent processes	References
Remove introns from pre-mRNA	5′ splice site 3′ splice site Branch point	GURAG consensus AG and polypyrimidine tract yUnAy (y = pyrimidine, A = adenosine, n = any nucleotide)	U1 snRNP U2AF heterodimer SF1	QC: G +1 position of intron; Suppression of Splicing (SOS) Stab: Other complementary nucleotides. QC: Distance to Branch Point Stab: Splicing factor FUBP1 QC: Competition between SF1 and QKI Stab: U2 snRNP.	Scores of proteins and RNA which form the E, A, B, B^{act}, B*, C, C*, P and ILS complexes.	Shi, 2017
mRNA regulation by miRNA	miRNA recognition element on mRNA	miRNA seed complementary sequence	6 to 8 nucleotide Seed Region of miRNA and Argonaute protein	QC: kinetic proofreading steps. Selective sorting of specific miRNAs into different AGO proteins Stab: GO protein.	RNA-induced silencing complex (RISC).	Jameel, 2023
Translation of mRNA	Position of codon on mRNA	Codon sequence	tRNA anticodon	QC: Multi-step kinetic ribosomal proofreading. Stab: Proteins and rRNA at the A site.	Proteins and rRNA involved in the elongation cycle and termination processes	Ramakrishnan, 2002; Schmeing and Ramakrishnan, 2009
Chemical editing of tRNAs. ~27 kinds in humans	Location where editing should occur	Specific nucleotide and surrounding structure on the tRNA	tRNA-recognizing active site of editing enzymes	QC: 3D recognition elements on the tRNA are recognized by the enzyme. Stab: Auxiliary protein factors and cofactors.	27 different enzymes / complexes.	Kirchner and Ignatova, 2015; Lorenz et al., 2017; Agris et al., 2018; Modomics, 2025
Chemical editing of mRNA. ~11 kinds in humans	Locations where editing should occur	Specific nucleotide and surrounding structure on the mRNA	mRNA-recognizing active site of enzymes	QC: 3D recognition elements on the mRNA are recognized by the enzyme. Stab: Auxiliary protein and cofactors.	Proteins involved in transcription, localization, translation, degradation, cell death, differentiation, etc.	Eisenberg and Levanon, 2018; Wilkinson et al., 2022; Modomics, 2025

role, searching for their partners. In the latter case, sensor concentrations are regulated and scan their environment (for example, in immune system responses to protect the cell). In both scenarios, the design principles remain the same. Distinctive sensing features are located in sensors; precise signals are recognized that avoid false bindings; quality control measures are used; and stabilizing co-factors are involved. Most importantly, initial recognition and binding are followed by the recruitment and assembly of the machinery needed to perform the intended processes (e.g., destroy all the invading viral DNA). Some examples include:

- Bacteria and archaea store snippets of viral DNA in their CRISPR loci. These become part of a sensor placed on small guide RNAs (gRNAs). These gRNAs target and associate with Cas9 protein (or a similar Cas enzyme) to form a ribonucleoprotein complex. The complex surveys 4–8 bp (base pairs), typically palindromic unmethylated sequences of invading viral DNA, and binds when a complementary sequence is found. Cas9 then cuts the viral DNA at the targeted site (Loenen et al., 2014).

- Small interfering RNAs (siRNAs) primarily target mRNA for degradation or inhibit translation. But in some cases, siRNAs are used as sensors that guide methylation enzymes to DNA to suppress all transposons (Mahfouz, 2010; Xie and Yu, 2015).
- In animal germline cells, piRNAs target complementary transposon sequences (Ozata et al., 2019). This binding then recruits Piwi proteins and assembles the Post-transcriptional Gene Silencing (PTGS) complex. Potentially dangerous transposons are silenced through mechanisms including histone modifications, DNA methylation, and post-transcriptional degradation of transposon transcripts.

A distinguishing feature seems to be that the sensor gradient is now always regulated to be high enough to eliminate *all* the damaging effects, instead of the cell having to produce a *fluctuating* optimal amount of 'Step 2' processes.

Sensors Defined Using Protein Sequences

Portions of proteins are also used as sensors, as illustrated in Table III.

These are only a handful of the thousands of examples present in cells. For example, there are far more kinds of receptors on the cell surface than shown in Table III. Humans have >800 different kinds of G-protein coupled receptors (GPCRs; Casadó and Casadó-Anguera, 2023) that are involved in metabolic regulation and many other physiological processes (Vidad et al., 2021). Humans also have about 58 kinds of receptor tyrosine kinases (RTK) (Cattaneo et al., 2014; Kumar and Hassan, 2023, pp. 245–276), 30–40 cytokine receptors (Brooks, 2017, pp. 1–29), and many other kinds of receptors. Tragically, improperly regulated intracellular signaling pathways often lead to cancer (Du and Lovly, 2018).

Programming Advantages of Using Analog Processes in Cells

Regulating cellular processes by variables able to respond to continuous gradients offers several advantages.

1) *Fine-tuning of effects*. It is advantageous to respond optimally to changing requirements. Changes can be ramped up or down as needed, avoiding waste. For example, the grade of DNA methylation in a gene's promoter—defined as the mean fraction of methylated CpG—defines distinct levels of gene expression and is inversely correlated with gene expression level (Palacios et al., 2024). DNA methylation patterns can also be inherited, creating a form of analog memory.

Quantitative transcriptional regulation can also arise in an analog fashion through multiple histone modifications around the local chromatin environment of a gene (Antoniou-Kourounioti et al., 2023).

Eukaryotic genes can have hundreds of enhancers to which TFs can attach. This provides a strategy to rapidly incorporate a variety of signals to compute an optimal decision. As another example, in the splicing code, multiple enhancers and silencers can be used to specify the probability of incorporating or skipping various exons into the mRNA, producing different ratios of alternative protein variants (Wang et al., 2006; Barash et al., 2010).

2) *Simplification of logic programming*. In principle, a digital form of programming could be used to interpret concentration gradients by dividing into discrete ranges and using digital-style logic for each interval. Since the necessary outcome need not be a linear function of the gradient, this would be a very complex and resource-intensive design. Instead, the molecular machinery attached to cellular sensors is engineered to physically automatically respond appropriately.

3) *Robustness to mutations or misinterpretation*. Cellular sensors and the downstream processes could malfunction for various reasons, such as due to mutations. Such errors could have a significant impact if only true/false digital outcomes were allowed. However, binding interactions typically rely on multiple small contributions, so individual errors would have a small effect. Furthermore, it seems that extra robustness has sometimes been designed into the binding interactions as a buffer against future mutations while avoiding interactions being so strong that they are irreversible (Payne and Wagner, 2015; Aguilar-Rodríguez and Wagner, 2017).

4) *Permits use of simpler, dedicated processing machines*. Digital computers use general-purpose, very complex hardware. There are several reasons why using a variety of simpler, dedicated molecular machines makes more sense in the case of cells. These machines are involved in defining sensors, ensuring reliable interactions with signals, and implementing the downstream processes initiated by sensors.

- The variety of sensors and concentration gradients are built using unrelated media such as DNA, RNA, proteins, lipids, sugars, etc. A monolithic server that integrates all these components would be excessively complex.
- The copy number of dedicated molecular machines (e.g., amino-acyl-tRNA synthetases, ribosomes, spliceosomes, etc.) can be rapidly assembled just in time when needed and dismantled when no longer

Table III. Examples of cellular variables located on proteins and the bio-components involved.

Cellular process	Sensor	Sensing feature	Signal recognized by sensor	Quality control (QC) and stabilization (Stab) of sensor with signal	Complexes recruited during subsequent processes	References
Translocation of proteins in humans	Location of Signal peptide	~25–30 residue pattern at the N-terminal of proteins	Signal recognition particle (SRP), a ribonucleoprotein complex	QC: Proofreading by enhanced stimulation of GTP activity upon correct binding of signal peptide, SRP, and the SRP receptor (SR). Stab: Collaborative binding of Signal peptide, SRP, and SR.	Translocon complex; signal peptidase; several complexes to guide to the endoplasmic reticulum (ER), Golgi apparatus, lysosomes, or out of the cell.	Owji et al., 2018
MAPK/ERK signaling pathway	Extracellular ligand-binding location	Ig-like and EGF-like domains, fibronectin type III repeats, and cysteine-rich regions	Growth factors and mitogen ligands	QC: Ligand to receptor interactions include H-bonds, hydrophobic interactions, electrostatic forces, and van der Waals forces. Stab: Initial ligand binding usually promotes dimerization of receptor monomers. Also, co-receptors are often involved.	Adapter proteins (SOS and GRB2) are recruited, producing a cascade that changes gene expression.	Park et al., 2000; Cordover and Minden, 2020; Kumar and Hassan, 2023
Adenylyl cyclase signaling pathway	Location of extracellular G protein-coupled receptor (GPCR)	3 extracellular loops have distinctive amino acid sequences and shapes. Many GPCRs are glycosylated to provide unique features.	Regions of hormones, neurotransmitters, and odorants; photons	Stab: H-bonds, hydrophobic interactions, van der Waals forces, and ionic bonds.	Heterotrimeric G-protein, and adenylyl cyclase that produces cAMP (a second messenger), which activates protein kinase A, etc. leading to changes in gene expression, metabolism, and cell proliferation.	Dunn et al., 2019; Vidad et al., 2021
Immune defense against pathogens	Location of Complementarity Determining Region (CDR) on the antibody	Complementary sequence for antigen	Regions of antigen recognized	Stab: Non-covalent interactions, including hydrogen bonds, ionic bonds, van der Waals forces, and hydrophobic interactions between CDR and antigen.	A variety of complexes are then assembled that depend on the type of antibody	Osajima et al., 2014; Qu et al., 2021; Ghai et al., 2022
Gene regulation via the Histone Code	Location on H3, H4, H2A, and H2B	Pattern on lysine and arginine recognized by enzymes	The active site of enzymatic writers like HATs, HMTs, E3 ligases, kinases, Sumoylases, ARTs and PARPs	QC: Aberrant modifications could be removed by an eraser enzyme; kinetic proofreading. Stab: Cofactors; presence or absence of other modifications; targeting subunits that recognize specific features.	Recruitment of proteins containing “reader” domains, followed by assembly of Effector Complexes.	Turner, 2000; Arnold et al., 2011; DesJarlais and Tummino, 2016; Wagner et al., 2016

needed, recovering amino acids and nucleotides that can be used for other purposes. To clarify, up to ten million copies of ribosomes translate mRNA strands concurrently in human liver cells vs. none in red blood cells (Shore and Albert, 2022); up to 100,000–200,000 spliceosomes are active in many cell types concurrently (Garcia-Blanco, 2003); and ~75,000 polymerase II/III are active in many cell types

(Jackson et al., 1998). Capacity is adjusted taking into account cell type, stage in the cell cycle, and current cellular needs.

- Cells often use different versions of molecular machines for special purposes, such as those done by different spliceosomes (Mabin et al., 2021) and ribosomes (Chen et al., 2020). The proportion of these can be adjusted rapidly as needed.
- Using fewer components decreases the possible points of system failure.
- Defective parts can be easily replaced or repaired, for example, a damaged protein or RNA (Swovick et al., 2018; Yoon-Mo et al., 2023).
- Multiple copies of redundant critical components –including gene copies (Li et al., 2010) can be used, including preformed subassemblies for rapid ramp-up (D'Angelo et al., 2021) and to enhance overall cell robustness.
- Assembling complex monolithic cellular computing devices would not only be error-prone but also time-intensive. However, frequent disassembly of small processors and assembling new ones decreases the chance of wear and tear accumulating (e.g., through oxidation or misfolding of proteins, etc.).

Summary and Conclusions

We have emphasized that thousands of cellular sensors can respond to continuous changes in informative signals. The resulting sensor and signal interaction produces a microenvironment that recruits the necessary biochemicals in a series of regulated steps to provide useful processes. The assembly steps usually also generate new sensors, allowing optimal output to be regulated at several levels and to integrate many relevant factors about the current needs of a cell. This is an entirely different perspective than the chemistry-based notion that proteins and other biomolecules randomly happen to interact properly, perhaps after a few rounds of natural selection.

Cellular logic rarely displays the nature of digital programming. In cells, changes in the sensor's physical properties and signals modify the sensitivity of response, which is not how digital computing works. For example, in these assignment statements in digital programming

```
current_object = 'x'
kurrent_object = 'x'                (4)
```

there is no difference in the probability of being assigned the value of 'x.' Also, one cannot assume that physically more similar variables would lead to more similar outcomes.

In digital computing, the symbols are freely assignable and abstract. In cellular variables, distinct physical binding must occur. This might suggest that analog variables do not possess the key property of abstractness, that is, to be arbitrarily assignable to mean whatever a programmer wishes. Given the requirement of physical binding, might cellular processes be deterministic machines instead of computing devices? The answer is no, as explained by the concept of adaptors. A membrane receptor (sensor) must indeed recognize when a specific hormone has attached, but the abstract intention is revealed by the set of proteins thereby produced several steps later.

The abstract logic is not expressed in a separate source code, but is engineered into how the downstream activities will be judiciously assembled. Traced back to the sensor, small physical changes in the sensor properties will inevitably correlate with the processing outcome. Stated in another way, the abstract character of cellular variables is their ability to achieve useful goals that are unrelated to the physical binding properties used.

The intention of this 3-part series is to prepare the path to continue retro-engineering how cells function, in particular their ability to adapt, self-regulate, and reproduce autonomously.

An important intuition championed by creationist computer science professor Uwe Assmann in Germany is the concept of cellular metaprogramming. In computer science, this refers to the technique of simpler code being used to generate more complex executable code. This is relevant for our work, since clearly sensors on, for example, proteins were not present in the DNA genome, but were implicit and generated. Other examples of metaprogramming include sensors present on RNA (i.e., not on the DNA from which RNA arose) involved in chemical editing, intron-exon splicing, translation, gene regulation, RNA localization, RNA degradation rates, translation initiation strength, etc.

This series will prepare the groundwork for the concept of analog metaprogramming, whereby the necessary hardware and logic processing machinery are assembled by cells as needed.

Thousands of different programs execute concurrently in cells, usually with many copies of each. Through carefully engineered physical interfaces, these processes can execute autonomously as analog computing devices with little resemblance to digital computers and even less to natural chemical processes.

References

Aguilar-Rodríguez, J., J.L. Payne, and A. Wagner. 2017. A thousand empirical adaptive landscapes and their navigability. *Nature Ecology & Evolution* 1: 0045.

Alles, J., T. Fehlmann, U. Fischer, C. Backes, V. Galata, M. Minet, M. Hart, et al. 2019. An estimate of the total number of true human miRNAs. *Nucleic Acids Research*

47: 3353–3364.

Antoniou-Kourounioti, R.L., A. Meschichi, S. Reeck, S. Berry, G. Menon, Y. Zhao, J. Fozard, et al. 2023. Integrating analog and digital modes of gene expression at *Arabidopsis* FLC. *eLife* 12: e79743.

Arnold, K.M., S. Lee, and J.M. Denu. 2011. Processing mechanism and substrate selectivity of the core NuA4 histone acetyltransferase complex. *Biochemistry* 50(5):727–737.

Barash, Y., J.A. Calarco, W. Gao, Q. Pan, X. Wang, O. Shai, B.J. Blencowe, and B.J. Frey. 2010. Deciphering the splicing code. *Nature* 465: 53–59.

Bétermier, M., L.A. Klobutcher, and E. Orias. 2023. Programmed chromosome fragmentation in ciliated protozoa: Multiple means to chromosome ends. Edited by Melissa Bruckner Lodoen. *Microbiology and Molecular Biology Reviews* 87: e00184–22.

Bickle, J. 2010. *Philosophy and Neuroscience: A Ruthlessly Reductive Account*. Nachdr. (Studies in Brain and Mind, Volume 2.) Kluwer Academic Publishers, Dordrecht, Holland.

Bofill-De Ros, X., and U.A.V. Ørom. 2024. Recent progress in miRNA biogenesis and decay. *RNA Biology* 21: 36–43.

Brooks, A.J., F. Dehkhoda, and B.B. Kragelund. 2017. Cytokine receptors. In *Diabetes Epidemiology, Genetics, Pathogenesis, Diagnosis, Prevention, and Treatment*, edited by Enzo Bonora and Ralph DeFronzo. "Endocrinology," pp. 1–29. Springer International Publishing, Cham, Switzerland.

Casadó, V., and V. Casadó-Anguera. 2023. What are the current trends in G protein-coupled receptor targeted drug discovery? *Expert Opinion on Drug Discovery* 18: 815–820.

Cattaneo, F., G. Guerra, M. Parisi, M.D. Marinis, D. Tafuri, M. Cinelli, and R. Ammendola. 2014. Cell-surface receptors transactivation mediated by G protein-coupled receptors. *International Journal of Molecular Sciences* 15: 19700–19728.

Chen, B. 2025. miRTarDS: high-accuracy refining protein-level microRNA target interactions from prediction databases using sentence-BERT. *bioRxiv*. https://www.biorxiv.org/content/10.1101/2024.05.17.594604v10.

Chen, J., R. Potlapalli, H. Quan, L. Chen, Y. Xie, S. Pouriyeh, N. Sakib, L. Liu, and Y. Xie. 2024. Exploring DNA damage and repair mechanisms: A review with computational insights. *BioTech* 13: 3.

Chen, Y.-X., Z.-Y. Xu, X. Ge, J.-Y. Hong, S. Sanyal, Z.J. Lu, and B. Javid. 2020. Selective translation by alternative bacterial ribosomes. *Proceedings of the National Academy of Sciences* 117: 19487–19496.

Cordover, E., and A. Minden. 2020. Signaling pathways downstream to receptor tyrosine kinases: Targets for cancer treatment. *Journal of Cancer Metastasis and Treatment* 6:45.

D'Angelo, L., E. Astro, M.D. Luise, I. Kurelac, N. Umesh-Ganesh, S. Ding, I.M. Fearnley, et al. 2021. NDUFS3 depletion permits complex I maturation and reveals TMEM126A/OPA7 as an assembly factor binding the ND4-module intermediate. *Cell Reports* 35: 109002.

Davyt, M., N. Bharti, and Z. Ignatova. 2023. Effect of mRNA/tRNA mutations on translation speed: Implications for human diseases. *Journal of Biological Chemistry* 299: 105089.

DesJarlais, R., and P.J. Tummino. 2016. Role of histone-modifying enzymes and their complexes in regulation of chromatin biology. *Biochemistry* 55: 1584–1599.

Diener, C., A. Keller, and E. Meese. 2024. The miRNA–target interactions: an underestimated intricacy. *Nucleic Acids Research* 52: 1544–1557.

Du, Z., and C.M. Lovly. 2018. Mechanisms of receptor tyrosine kinase activation in cancer. *Molecular Cancer* 17: 58.

Dunn, H.A., C. Orlandi, and K.A. Martemyanov. 2019. Beyond the ligand: Extracellular and transcellular G protein–coupled receptor complexes in physiology and pharmacology. *Pharmacological Reviews* 71: 503–519.

Eisenberg, E., and E.Y. Levanon. 2018. A-to-I RNA editing — immune protector and transcriptome diversifier. *Nature Reviews Genetics* 19: 473–490.

Faure, G., A.Y. Ogurtsov, S.A. Shabalina, and E.V. Koonin. 2017. Adaptation of mRNA structure to control protein folding. *RNA Biology* 14: 1649–1654.

Fica, S.M., N. Tuttle, T. Novak, N.-S. Li, J. Lu, P. Koodathingal, Q. Dai, J.P. Staley, and J.A. Piccirilli. 2013. RNA catalyses nuclear pre-mRNA splicing. *Nature* 503: 229–234.

Fitz-James, M.H., and G. Cavalli. 2022. Molecular mechanisms of transgenerational epigenetic inheritance. *Nature Reviews Genetics* 23: 325–341.

Fluman, N., S. Navon, E. Bibi, and Y. Pilpel. 2014. mRNA-programmed translation pauses in the targeting of *E. coli* membrane proteins. *eLife* 3: e03440.

Garcia-Blanco, M.A. 2003. Messenger RNA reprogramming by spliceosome-mediated RNA trans-splicing. *Journal of Clinical Investigation* 112: 474–480.

Ghai, T., A. Das, and R. Patel. 2022. The investigation of the effect of antibody recruiting molecules on various antigenic markers (cancer, bacteria, viruses): a literature review. *Undergraduate Research in Natural and Clinical Science and Technology (URNCST) Journal* 6: 1–7.

Gorochowski, T.E., Z. Ignatova, R.A.L. Bovenberg, and J.A. Roubos. 2015. Trade-offs between tRNA abundance and mRNA secondary structure support smoothing of translation elongation rate. *Nucleic Acids Research* 43: 3022–3032.

Haberle, V., and A. Stark. 2018. Eukaryotic core promoters and the functional basis of transcription initiation. *Nature Reviews Molecular Cell Biology* 19: 621–637.

Handy, D.E., R. Castro, and J. Loscalzo. 2011. Epigenetic modifications: Basic mechanisms and role in cardiovascular disease. *Circulation* 123: 2145–2156.

Hayes, B. 1998. The invention of the genetic code. *American Scientist* 86: 8–14.

Jackson, D.A., F.J. Iborra, E.M.M. Manders, and P.R. Cook. 1998. Numbers and organization of RNA polymerases, nascent transcripts, and transcription units in HeLa nuclei. *Molecular Biology of the Cell* 9: 1523–1536.

Jacobs, J., M. Pagani, C. Wenzl, and A. Stark. 2023. Widespread regulatory specificities between transcriptional corepressors and enhancers in *Drosophila*. *Science* 381: 198–204.

Jameel, Z.I. 2023. MicroRNA biogenesis, mechanisms of function, circulation, and application role in human diseases. *International Journal of Scientific Research in Biological Sciences* 10: 71–80.

Karijolich, J., and Y.-T. Yu. 2010. Spliceosomal snRNA modifications and their function. *RNA Biology* 7: 192–204.

Kim, Y., S. Cho, J.-C. Kim, and H.-S. Park. 2024. tRNA engineering strategies for genetic code expansion. *Frontiers in Genetics* 15: 1373250.

Kirchner, S., and Z. Ignatova. 2015. Emerging roles of tRNA in adaptive translation, signalling dynamics and disease. *Nature Reviews Genetics* 16: 98–112.

Kumar, D., and M.I. Hassan. 2023. Regulation of receptor tyrosine kinase gene expression. In Mansour, H.M. et al, *Receptor Tyrosine Kinases in Neurodegenerative and Psychiatric Disorders*. Elsevier, Amsterdam, Netherlands.

Laub, M.T. 2016. Keeping signals straight: How cells process information and make decisions. *PLOS Biology* 14: e1002519.

Łazowski, K., R. Woodgate, and I.J. Fijalkowska. 2024. *Escherichia coli* DNA replication: The old model organism still holds many surprises. *FEMS Microbiology Reviews* 48(4): fuae018.

Lesne, A. 2023. Molecular codes in biology: The genetic code and beyond. *HAL Open Science*. https://hal.science/hal-04085620/.

Li, J., Z. Yuan, and Z. Zhang. 2010. The cellular robustness by genetic redundancy in budding yeast. Edited by Jianzhi Zhang. *PLoS Genetics* 6: e1001187.

Liu, B., T. Wu, B.A. Miao, F. Ji, S. Liu, P. Wang, Y. Zhao, et al. 2025. snoRNA-facilitated protein secretion revealed by transcriptome-wide snoRNA target identification. *Cell* 188(2): 465–483.e22.

Loenen, W.A.M., D.T.F. Dryden, E.A. Raleigh, G.G. Wilson, and N.E. Murray. 2014. Highlights of the DNA cutters: A short history of the restriction enzymes. *Nucleic Acids Research* 42: 3–19.

Lorenz, C., C. Lünse, and M. Mörl. 2017. tRNA modifications: impact on structure and thermal adaptation. *Biomolecules* 7: 35.

Mabin, J.W., P.W. Lewis, D.A. Brow, and H. Dvinge. 2021. Human spliceosomal snRNA sequence variants generate variant spliceosomes. *RNA* 27: 1186–1203.

Mahfouz, M.M. 2010. RNA-directed DNA methylation: Mechanisms and functions. *Plant Signaling & Behavior* 5: 806–816.

Mala, P., and I. Saraogi. 2022. Enhanced codon-anticodon interaction at in-frame UAG stop codon improves the efficiency of non-natural amino acid mutagenesis. *ACS Chem Biol.* 17: 1051–1060.

MODOMICS: 2025. MODOMICS: A database of RNA modifications and related information. *Nucleic Acids Research* 52(D1): D239-D244. https://pubmed.ncbi.nlm.nih.gov/38015436/.

Nedialkova, D.D., and S.A. Leidel. 2015. Optimization of codon translation rates via tRNA modifications maintains proteome integrity. *Cell* 161: 1606–1618.

Nicholson, D.J. 2019. Is the cell really a machine? *Journal of Theoretical Biology* 477: 108–126.

O'Brien, J., H. Hayder, Y. Zayed, and C. Peng. 2018. Overview of microRNA biogenesis, mechanisms of actions, and circulation. *Frontiers in Endocrinology* 9: 402.

Osajima, T., M. Suzuki, S. Neya, and T. Hoshino. 2014. Computational and statistical study on the molecular interaction between antigen and antibody. *Journal of Molecular Graphics and Modelling* 53: 128–139.

Owji, H., N. Nezafat, M. Negahdaripour, A. Hajiebrahimi, and Y. Ghasemi. 2018. A comprehensive review of signal peptides: structure, roles, and applications. *European Journal of Cell Biology* 97: 422–441.

Ozata, D.M., I. Gainetdinov, A. Zoch, D. O'Carroll, and P.D. Zamore. 2019. PIWI-interacting RNAs: Small RNAs with big functions. *Nature Reviews Genetics* 20: 89–108.

Palacios, S., et al. 2025. Analog epigenetic memory revealed by targeted chromatin editing. *Cell Genomics* 11: 100985.

Park, P.W., O. Reizes, and M. Bernfield. 2000. Cell surface heparan sulfate proteoglycans: selective regulators of ligand-receptor encounters. *Journal of Biological Chemistry* 275: 29923–29926.

Payne, J.L., and A. Wagner. 2015. Mechanisms of mutational robustness in transcriptional regulation. *Frontiers in Genetics* 6: 322.

Powledge, T.M. 2011. Behavioral epigenetics: How nurture shapes nature. *BioScience* 61(8): 588–592.

Prochazka, L., Y.S. Michaels, C. Lau, R.D. Jones, M. Siu, T. Yin, D. Wu, et al. 2022. Synthetic gene circuits for cell state detection and protein tuning in human pluripotent stem cells. *Molecular Systems Biology* 18: e10886.

Qu, L., X. Qiao, F. Qi, N. Nishida, and T. Hoshino. 2021. Analysis of binding modes of antigen–antibody complexes by molecular mechanics calculation. *Journal of Chemical Information and Modeling* 61: 2396–2406.

Ramakrishnan, V. 2002. Ribosome structure and the mechanism of translation. *Cell* 108: 557–572.

Robertson, M.P., and G.F. Joyce. 2012. The origins of the RNA world. *Cold Spring Harbor Perspectives in Biology* 4: a003608–a003608.

Rogojin, V. 2010. On computational properties of gene assembly in ciliates. *Computer Science Journal of Moldova* 18, no.2(53): 171–209.

Rosenberg, A. 2006. *Darwinian Reductionism, or, How to Stop Worrying and Love Molecular Biology*. University of Chicago Press, Chicago, IL.

Sarkar, S. 2005. *Molecular Models of Life: Philosophical Papers on Molecular Biology*.

(Life and Mind: Philosophical Issues in Biology and Psychology.) MIT Press, Cambridge, MA.

Scharer, O.D. 2013. Nucleotide excision repair in eukaryotes. *Cold Spring Harbor Perspectives in Biology* 5: a012609–a012609.

Schmeing, T.M., and V. Ramakrishnan. 2009. What recent ribosome structures have revealed about the mechanism of translation. *Nature* 461: 1234–1242.

Shi, Y. 2017. Mechanistic insights into precursor messenger RNA splicing by the spliceosome. *Nature Reviews Molecular Cell Biology* 18: 655–670.

Shore, D., and B. Albert. 2022. Ribosome biogenesis and the cellular energy economy. *Current Biology* 32(12): R611–R617.

Sriram, S.M., B.Y. Kim, and Y.T. Kwon. 2011. The N-end rule pathway: emerging functions and molecular principles of substrate recognition. *Nature Reviews Molecular Cell Biology* 12: 735–747.

Su, B.G., and S.M. Vos. 2024. Distinct negative elongation factor conformations regulate RNA polymerase II promoter-proximal pausing. *Molecular Cell* 84: 1243–1256.e5.

Sun, M., and J. Zhang. 2022. Preferred synonymous codons are translated more accurately: proteomic evidence, among-species variation, and mechanistic basis. *Science Advances* 8: eabl9812.

Svetlov, V., and E. Nudler. 2013. Basic mechanism of transcription by RNA polymerase II. *Biochimica et Biophysica Acta (BBA)—Gene Regulatory Mechanisms* 1829(1): 20–28.

Swovick, K., K.A. Welle, J.R. Hryhorenko, A. Seluanov, V. Gorbunova, and S. Ghaemmaghami. 2018. Cross-species comparison of proteome turnover kinetics. *Molecular & Cellular Proteomics* 17(4): 580–591.

Tholen, J. 2024. Branch site recognition by the spliceosome. *RNA* 30(11): 1397–1407.

Tollefsbol, T.O. (editor). 2023. *Handbook of Epigenetics: The New Molecular and Medical Genetics*, Third edition. Elsevier, San Diego, CA; Cambridge, MA; London, UK; Oxford, UK, and Academic Press. Inc., New York, NY.

Tompa, P., and G.D. Rose. 2011. The Levinthal paradox of the interactome. *Protein Science* 20(12): 2074–2079.

Turner, B.M. 2000. Histone acetylation and an epigenetic code. *BioEssays* 22: 836–845.

Varshavsky, A. 1997. The N-end rule pathway of protein degradation. *Genes Cells* 2: 13–28.

Vidad, A.R., S. Macaspac, and H.L. Ng. 2021. Locating ligand binding sites in G-protein coupled receptors using combined information from docking and sequence conservation. *PeerJ* 9: e12219.

Wang, Z., X. Xiao, E.V. Nostrand, and C.B. Burge. 2006. General and specific functions of exonic splicing silencers in splicing control. *Molecular Cell* 23(1): 61–70.

Wegrzyn, K., and I. Konieczny. 2024. Toward an understanding of the DNA replication initiation in bacteria. *Frontiers in Microbiology* 14: 1328842.

Wilkinson, E., Y.-H. Cui, and Y.-Y. He. 2022. Roles of RNA modifications in diverse cellular functions. *Frontiers in Cell and Developmental Biology* 10: 828683.

Xie, M., and B. Yu. 2015. siRNA-directed DNA methylation in plants. *Current Genomics* 16: 23–31.

Yoon, S.J., J.T. Park, and Y.K. Lee. 2024. The neuromorphic computing for biointegrated electronics. *Soft Science* 4(3): 30.

Zhang, B., D. Han, Y. Korostelev, Z. Yan, N. Shao, E. Khrameeva, B.M. Velichkovsky, Y.-P.P. Chen, M.S. Gelfand, and P. Khaitovich. 2016. Changes in snoRNA and snRNA abundance in the human, chimpanzee, macaque, and mouse brain. *Genome Biology and Evolution* 8(3): 840–850. doi: 10.1093/gbe/evw038.

Creation Research Society Quarterly 2026 62:345–358

Unshaken Foundations: Reclaiming Earth's History Through Scripture, Science, and the Coherence of Faith—

Paper 2: Scientific Evidence Supporting a Young-Earth Timeline

Jonathan K. Corrado*

Key Words: Biblical genealogies, Creation days, doctrinal integrity, Scriptural authority, young-Earth chronology

* Jonathan K. Corrado, PhD, ThM, PE, Corresponding author, Cincinnati, OH, Jcorrado2@liberty.edu

Accepted for publication July 18, 2025

Abstract

The second paper in this series delves into the scientific evidence underpinning young-Earth creationism (YEC), challenging deep-time paradigms through empirical observations. It highlights key phenomena, including rapid geological processes, such as those observed at Mount St. Helens, the presence of soft tissues in fossils, carbon-14 in supposedly ancient materials, and ice core layering patterns. These findings support a young-Earth timeline and question assumptions foundational to conventional old-Earth models. Further exploration is given to fossil records, polystrate fossils, and genetic entropy, all of which align with YEC interpretations. This paper systematically integrates scientific discoveries with the theological framework established in the first paper (*CRSQ* Vol 62, no. 3), emphasizing the compatibility of scientific inquiry with Scripture. This work advances the series by presenting a cohesive, empirical case for a young Earth.

Simple Summary

This paper by Jonathan K. Corrado presents a scientific defense of young-Earth creationism (YEC) by challenging standard deep-time geological and biological paradigms. The author argues that empirical observations, such as the discovery of soft tissues in dinosaur fossils and measurable carbon-14 in ancient diamonds, align better with a 6,000-year timeline than with evolutionary models. Central to this perspective is the global Flood, which is credited with rapidly forming the fossil record, stratified rock layers, and even mountain ranges through catastrophic processes. Additionally, the text addresses complex issues like distant starlight and genetic entropy, suggesting that these phenomena support a recent creation when viewed through a Biblical lens. Ultimately, the work seeks to harmonize scientific inquiry with Scriptural authority, proposing that Earth's history is best understood as a series of rapid, catastrophic events.

Setting the Scientific Stage

The age of the Earth has long been a subject of intrigue and debate, bridging the realms of science, theology, and philosophy. While the first paper in this series established the theological foundations of young-Earth creationism (YEC), this second installment ventures into the scientific evidence that supports a young-Earth timeline. Against the backdrop of widespread acceptance of deep-time paradigms and evolutionary theory, a growing body of scientific discoveries challenges these conventions, shedding new light on Earth's history. This paper examines key scientific findings, highlighting evidence from geology, paleontology, and radiometric analyses that align with the Biblical narrative of an Earth approximately 6,000 years old.

One of the driving purposes of this series is to provide a critical synthesis of YEC arguments, consolidating them into a cohesive and accessible resource. Supporting evidence for the young-Earth perspective often remains scattered across numerous texts, papers, and articles. By unifying these arguments into an interconnected discussion, this paper aims to create a scripture-centered defense that is both coherent and readily available. This effort also serves to resist the pressure to conform to secular paradigms, reinforcing the authority of Scripture and the Biblical account of Creation as the foundation for interpreting Earth's history.

The goal that scientific inquiry can, and should, harmonize with theological convictions is not new. As Johannes Kepler, the father of modern astronomy, once stated, "Science is thinking God's thoughts after Him" (Kepler, 1619). This sentiment underscores the perspective of YEC proponents, who argue that empirical observations, when viewed through a Biblical lens, consistently point to the intentional design and recent formation of the Earth and life on the Earth.

This paper explores critical phenomena, including the rapid formation of geological structures, the discovery of soft tissues in fossils, and anomalies in radiometric dating, all of which undermine traditional long-age assumptions. It further examines alternative interpretations of ice core data and fossil records, emphasizing how catastrophic events, such as the global Flood, provide coherent explanations for these findings. By bridging theological convictions with empirical evidence, this study demonstrates how the YEC model offers a scientifically informed and scripturally consistent account of Earth's history.

Building on the theological foundation laid in the first paper (*CRSQ* Vol 62, no. 3), this segment explores the scientific evidence that reinforces the YEC framework. At the heart of this exploration is the pivotal event of the global Flood, as described in Genesis, which offers a cohesive explanation for Earth's geological and fossil records. This study demonstrates how empirical observations align with a scripturally consistent young-Earth timeline, setting the stage for deeper scientific discussions.

The Global Flood: A Literal and Universal Catastrophe

Building upon the debate over the poetic versus historical nature of Genesis (found in paper 1), the scope and scale of the Flood described in Genesis 6–9 offer another profound point of examination. Just as the literary structure of Genesis 1 reinforces a literal reading of the creation account, the detailed narrative of the Flood provides compelling evidence for a global event, further supporting the historical reliability of Genesis (Barrick, 2008).

Noah's Ark and the Extent of the Flood

The Bible's Flood narrative repeatedly uses the phrase "all flesh," emphasizing the complete destruction of all land-dwelling life. This language unequivocally points to a worldwide catastrophe since a localized Flood would not have necessitated Noah's Ark. If the Flood had been regional, Noah and his family could have simply relocated to a safer area. Furthermore, the Ark's massive dimensions and its purpose of housing pairs of every animal kind underscore the conclusion that the Flood was global in scale, capable of impacting all land-dwelling creatures (Snelling, 2014).

The size of Noah's Ark itself affirms the universality of the Flood. Measuring 300 cubits long, 50 cubits wide, and 30 cubits high, the Ark was an enormous structure far exceeding the requirements for a regional Flood. In a localized scenario, smaller animals could have migrated to unaffected areas while birds could have flown to safety. Yet the extensive design and capacity of the Ark were essential for preserving animal life during a global deluge (Woodmorappe, 1996).

Additionally, the Flood narrative describes the breaking up of the "fountains of the deep" and the opening of the "windows of heaven" (Genesis 7:11), leading to waters that prevailed above even the highest mountains. Such descriptions confirm the impossibility of the Flood being geographically contained, as water exceeding the height of all mountains would naturally inundate the entire planet. The literary structure of the Genesis Flood account further supports its global scope, with the narrative emphasizing the universality of the judgment and the comprehensive renewal of creation following the Flood (Shea, 2018).

Further evidence for the global nature of the Flood comes from cultural and historical records, which provide anthropological support for the YEC framework. Ancient Flood legends from diverse civilizations often recount catastrophic events that closely parallel the Biblical description. These accounts, preserved through oral traditions, myths, and written records, commonly include strikingly similar elements: a massive, destructive deluge; the survival of humanity through the preservation of select individuals and animals; and the Flood as a judgment or act of divine intervention. These recurring motifs suggest a shared human memory of a significant, worldwide event. Sarfati (2015) notes that more than 200 Flood traditions exist worldwide, many featuring details improbable to coincide by chance, such as the sending of birds and the grounding of an ark on a mountain.

For instance, the Mesopotamian *Epic of Gilgamesh,* one of the oldest surviving literary works, includes a Flood narrative with uncanny similarities to the Genesis account. In the story, Utnapishtim is warned by the gods of an impending Flood and instructed to construct a large boat to save his family and pairs of animals. This account mirrors key details in the Noahic Flood, including the warning, the construction of an Ark, and the preservation of life (Woodmorappe, 1996).

Similarly, Native American tribes, such as the Hopi and the Algonquian peoples, recount legends of a great Flood that reshaped the Earth and destroyed a corrupt civilization. In these stories, survivors are often depicted as being divinely chosen to repopulate the world. Ancient cultures across Asia, including India and China, also preserve strikingly similar narratives, emphasizing the universality of the Flood legend. The Indian *Manu Flood Legend,* for example, describes a man who was warned by a divine being to build a boat and save life from the destruction caused by the waters (Barrick, 2008). Whitcomb and Morris (1961) argue that the global distribution of these legends—with shared core elements despite cultural isolation—strongly points to a single historical event remembered by humanity's early descendants after dispersing from Babel.

These Flood accounts, though varying in detail, consistently point to a catastrophic global Flood as a central event in early human history. Young-Earth creationists interpret this remarkable consistency across geographically and culturally distinct civilizations as corroboration of the historical reality of the Genesis Flood. They argue that these stories reflect a common origin—a shared collective memory passed down from survivors of a real, global Flood event, but distorted with time.

Furthermore, YEC proponents emphasize that the widespread presence of Flood narratives cannot be adequately explained by localized flooding events. The global distribution of such stories and their shared themes suggests a deeper historical connection rather than isolated or coincidental occurrences (Snelling, 2014). By weaving these cultural records into the fabric of historical understanding, YEC perspectives highlight the Flood's profound impact on shaping early human history and its alignment with the Biblical account.

Post-Flood Distribution of Animal Species

The post-Flood distribution of animal species also presents evidence consistent with a worldwide Flood. YEC proponents argue that the dispersal of animals from Mount Ararat, where the Ark is said to have rested, explains modern species biogeography. They suggest that animals migrated to their present locations over time, potentially aided by natural land bridges via Flood tectonics (Oard, 2024). Oard further emphasizes that changing post-Flood climates, driven by a single Ice Age event, created corridors of habitability that allowed rapid animal movement. Timothy Clarey (2020) highlights how such post-Flood mechanisms align with the diversity and distribution of modern species, reinforcing the Flood narrative as the foundation for current biogeographical patterns.

The Duration and Covenant Significance of the Flood

The Flood's duration further highlights its universal scope. Noah and his family remained on the Ark for about a year, emphasizing the scale and severity of the event. Following the Flood, God established His covenant with Noah, marking it with a rainbow as a sign of His promise never again to destroy the Earth with a Flood. If the Flood had been a localized event, this divine promise would lose most of its significance because localized Floods have occurred throughout history. Such an interpretation would imply a breach of God's covenant, contradicting the Biblical teaching that God is faithful and cannot lie (Faulkner, 2016).

Scientific Challenges Addressed by YEC

Geology and Stratified Rock Layers

Geology is among the first disciplines exploited to challenge the YEC timeline. However, geology provides robust evidence supporting the YEC timeline, offering a compelling case that the Earth's geological features are the result of catastrophic events rather than gradual processes over millions of years. The stratified rock layers, fossil records, and monumental features such as the Grand Canyon are best explained as the outcomes of Noah's Flood, a catastrophic event of unparalleled scale described in the Bible. According to YEC, this global deluge rapidly deposited vast amounts of sediment, formed rock layers, and created fossils in a matter of months. What mainstream science interprets as evidence of deep time is more accurately understood within the YEC framework as the aftermath of a global Flood (Austin, 1994; Clarey, 2020).

In addition, YEC highlights rapid stalactite and stalagmite formation as strong evidence challenging the conventional long-age interpretation of geological processes. Observations show that stalactites and stalagmites can form within decades in environments such as mines and tunnels, where mineral-rich water replicates natural cave conditions. This demonstrates that these formations do not require tens of thousands of years to develop. Oard (2020a) expands this point by showing that even the excavation of large cave systems need not require vast timescales. In Part 1 of his study, he documents that powerful post-Flood groundwater flow—driven by high hydraulic gradients—could have rapidly dissolved carbonate rock and opened extensive cave networks in a relatively short period.

YEC suggests that the post-Flood period provided the unique climatic and geological conditions required for rapid mineral deposition. Oard's Part 2 analysis demonstrates that speleothem growth rates vary dramatically depending on temperature, water chemistry, and CO_2 degassing—all of which would have been intensified in the immediate post-Flood world. Elevated CO_2 levels, warmer cave temperatures, and abundant mineral-saturated water would have accelerated calcite precipitation far beyond modern rates (Oard, 2020b). The elevated precipitation and mineral-saturated water following the Flood would have significantly accelerated the development of such formations (Vardiman, 1996). Further, in Part 3, Oard argues that Ice Age conditions produced by warm post-Flood oceans would have sustained high rainfall and rapid groundwater movement, maximizing both cave excavation and speleothem growth. These combined Flood and Ice Age variables create an environment ideally suited for the rapid formation of caves and cave deposits, removing the need for long-age interpretations (Oard, 2020c).

Furthermore, YEC proponents point to turbidites—sedimentary layers formed by underwater landslides—as additional evidence supporting the Flood model. Turbidites, with their characteristic graded bedding, can form extensive sedimentary layers in a short amount of time. YEC argues that the catastrophic processes of Noah's Flood, including underwater landslides triggered by tectonic upheavals and massive water displacement, could have produced widespread turbidite deposits. This interpretation provides a more plausible explanation than the conventional view requiring millions of years. The rapid deposition of turbidites perfectly aligns with the YEC perspective that the Earth's geological features were shaped by the intense and dynamic conditions of the Flood (Austin, 1994).

The Geological and Paleontological Implications of the Flood

From a YEC perspective, the global Flood is a central and defining event that seamlessly aligns with a young-Earth framework, profoundly shaping the Earth's geological and fossil records. Within this view, the Flood serves as a pivotal explanation for key features of the natural world within a timeline of approximately 6,000–10,000 years. Several key points reinforce this perspective:

1. **Geological Features:** YEC proponents assert that many of Earth's geological formations—such as sedimentary rock layers, canyons, and fossil deposits—are direct results of the catastrophic effects of the Flood. The rapid burial of plants and animals during the event is seen as the primary mechanism for fossilization, challenging the uniformitarian principles that suggest such processes require vast periods (Austin, 1994; Clarey, 2020).
2. **Fossil Record:** According to YEC, the fossil record reflects the massive and rapid burial of organisms during the Flood. Variables like habitat, mobility, and density during the event are viewed as the determinants for the order in which fossils appear in sedimentary layers, contradicting the conventional interpretation that these layers represent evolutionary progression of millions of years (Snelling, 2014).
3. **Mass Extinction Events:** YEC proponents argue that the mass extinction events evidenced in the fossil record are best explained by the global Flood rather than by gradual processes or isolated catastrophes over millions of years. The Flood's unmatched scale and intensity are believed to have caused the simultaneous and rapid destruction of numerous species. The resulting fossilized remains, found in sedimentary deposits worldwide, are interpreted as evidence of a single, global catastrophe rather than multiple, localized extinctions over deep time (Whitcomb and Morris, 1961; Clarey, 2020).
4. **Plate Tectonics and Mountains:** YEC theories propose "catastrophic plate tectonics" as the explanation for the rapid formation of mountain ranges, ocean trenches, and other large-scale geological features. These are suggested to have developed swiftly during and after the Flood, in contrast to the mainstream view requiring millions of years (Austin, 1994; Clarey, 2020).
5. **Magnetic Reversals in Rocks:** The geomagnetic reversals recorded in rock strata, commonly interpreted as evidence of a lengthy geological timeline, are reexamined within the YEC framework. YEC proponents contend that these reversals occurred rapidly during the Flood due to catastrophic plate tectonics and massive geological upheaval. This interpretation aligns magnetic anomalies with the short timescale of a global Flood rather than millions of years of slow changes (Humphreys, 1994).
6. **Radiometric Dating:** YEC challenges the reliability of radiometric dating methods, which support an ancient Earth. Instead, it is posited

that processes during the Flood may have altered isotopic ratios, leading to inaccurate dating of rocks and fossils (Snelling, 2014).[1]

7. **Uniformitarian Assumptions Challenged:** The Flood narrative fundamentally opposes the principle of uniformitarianism in geology, replacing it with catastrophism. Within YEC, the widespread sedimentary layers and geological upheaval observed today are interpreted as evidence of the Flood, aligning seamlessly with a young-Earth timeline (Barrick, 2008; Clarey, 2020).

Reinterpreting Scientific Evidence

Building on the reinterpretation of scientific evidence through a YEC lens, the geological and paleontological implications of the global Flood underscore its centrality within this framework. By examining the Flood's transformative effects on Earth's physical features, including sedimentary rock formations, fossil deposits, and even magnetic reversals, proponents argue for a cohesive explanation that aligns with a literal Biblical timeline. These considerations not only challenge conventional perspectives on Earth's history but also set the stage for further exploration of how such a catastrophic event shaped the natural world.

Scientific Challenges to Deep Time: The Problem of Soft Tissue in Fossils

Among the most compelling scientific phenomena that challenge the conventional old-Earth timeline is the discovery of soft tissues, such as collagen, blood vessels, and even proteins, in dinosaur fossils. These findings, widely reported in the 1990s and early 2000s [and continuing today], have sparked significant debate within the scientific community. Under standard old-Earth timelines, these fossils are believed to be tens of millions of years old. However, such materials should degrade entirely within a much shorter time frame—thousands of years rather than millions—according to known biochemical decay rates (Collins et al., 1995; Schweitzer et al., 2005).

Pioneering research by paleontologist Dr. Mary Schweitzer revealed soft tissues were preserved in a *Tyrannosaurus rex* femur, initially dated to 68 million years ago. Subsequent studies have identified similar materials in other fossils, creating an enigma for conventional scientific theories. Collagen, a structural protein found in connective tissue, has an upper limit of preservation in optimal conditions, typically estimated at tens of thousands of years. The survival of these tissues over purportedly millions of years defies current understanding of molecular decay (Nielsen-Marsh and Hedges, 2000; Schweitzer et al., 2005; Snelling, 2014; Anderson, 2016).

Proponents of an ancient Earth have suggested exceptional preservation mechanisms or unknown chemical processes to explain these findings (Schweitzer et al., 2005; Schweitzer et al., 2007). However, such hypotheses remain speculative and lack direct experimental validation outside of controlled laboratory conditions. Anderson (2016) notes that even proposed stabilization mechanisms cannot prevent the predictable breakdown of proteins over deep time, and that soft-tissue finds are accumulating faster than explanations can account for them. By contrast, the YEC perspective offers a straightforward explanation: these fossils could not be as old as commonly believed. Within a Biblical timeline of approximately 6,000 years, the preservation of soft tissues aligns seamlessly with the expected timescale (Barrick, 2008; Thomas, 2013; Snelling, 2014; Anderson, 2016). Young-Earth researchers have documented numerous cases of soft-tissue preservation and have demonstrated that biochemical decay kinetics place strong constraints on deep-time models (Anderson, 2016).

Moreover, the YEC model ties the preservation of soft tissue in fossils directly to the events of the Genesis global Flood. Proponents argue that the Flood provided the catastrophic conditions necessary for the rapid burial of organisms, shielding them from decay and fostering exceptional preservation (Austin, 1994; Clarey, 2020). The deluge's immense geological upheaval would have created sedimentary environments with low oxygen and high pressure, perfect for slowing down the biochemical processes that lead to the breakdown of soft tissues (Snelling, 2014).

This link to the Flood reinforces the broader argument for a young Earth, suggesting that these fossils were buried not millions of years ago but rather during a single, global catastrophe. By embedding these findings within the framework of the Flood, YEC adherents offer an integrative explanation that unites the fossil evidence with a literal interpretation of Biblical history. Armitage (2014) further demonstrated soft fibrillar collagen in a Triceratops horn, supporting the view that soft-tissue preservation is widespread—not an isolated anomaly—and consistent with recent deposition. This perspective underscores the significance of the Flood as a pivotal historical event, shaping the fossil record and challenging deep-time assumptions (Barrick, 2008; Morris, 2012; Armitage, 2014; Anderson, 2016).

Ice Core Sampling and Rapid Layer Formation

Ice core sampling provides compelling evidence supporting the YEC frame-

---

[1] Also see Oard, M.J. 2019. *The Deep Time Deception: Examining the Case for Millions of Years.* Creation Book Publishers, Powder Springs, GA.

work because it challenges conventional interpretations of Earth's history. In polar regions, scientists have extracted cores from deep ice sheets containing layers of snowfall accumulation, traditionally interpreted as annual cycles stretching back hundreds of thousands of years. However, YEC proponents argue that these layers do not necessarily represent annual snowfall. Instead, they suggest that rapid and extreme weather events—such as storms or dramatic seasonal fluctuations—could have formed multiple layers in a single year, aligning with the YEC timeline (Oard, 1990). Oard's extensive analysis in *The Frozen Record* (2005) demonstrates that ice-core "annual" layers become increasingly ambiguous with depth, often merging, thinning, or disappearing altogether—making long-age interpretations highly uncertain. He shows that counting methods rely heavily on uniformitarian assumptions rather than direct observation, and that post-Flood Ice Age conditions would have produced dramatically higher snowfall rates, generating many layers per year rather than one.

Furthermore, Oard's more recent work, *The Frozen Paradox* (2025), argues that the deepest portions of the Greenland and Antarctic ice cores are inconsistent with slow, linear accumulation. He notes that volcanic activity during and after the Flood, combined with warm oceans and elevated atmospheric moisture, would have produced intense, repeated snowstorms capable of depositing dozens of layers in a single season. These conditions would naturally generate the apparent "annual" layering invoked by long-age models, but within the far shorter timescale of a post-Flood Ice Age.

The discovery of the "Lost Squadron" provides a striking example supporting this perspective. In 1942, a group of World War II planes was abandoned on the Greenland ice sheet. When rediscovered decades later, the planes were buried under approximately 80 meters (262 feet) of ice, far exceeding the depth expected based on conventional ice accumulation rates. This rapid burial demonstrates that significant ice accumulation can occur in a much shorter timeframe under certain conditions. YEC proponents use this example to argue that rapid and extreme climatic events, such as those following the global Flood described in Genesis, could similarly account for the multi-layering observed in ice cores (Hayes, 1994).

Furthermore, YEC proponents attribute the rapid formation of ice layers to the aftermath of the global Flood. They posit that the Flood triggered massive climatic upheavals, dramatically altering weather patterns and resulting in extreme snowfall and ice accumulation. This period of intense post-Flood instability, often referred to as the YEC Ice Age, could have led to the rapid formation of ice sheets and the layering observed in ice cores. Catastrophic atmospheric events occurring during and immediately following the Flood, such as violent storms and rapid temperature shifts, would have created the conditions necessary for the accumulation of multiple layers in a very short timeframe (Oard, 1990, 2004, 2024; Barrick, 2008).

This perspective reinterprets ice core evidence through the lens of the Flood, directly challenging conventional interpretations of annual cycles and emphasizing the significant role of the Flood in shaping Earth's physical history. By aligning ice core data with the Flood narrative, YEC adherents provide further support for a young Earth and a literal, global deluge (Snelling, 2014; Clarey, 2020).

Fossil Record and Catastrophic Burial

The fossil record provides compelling evidence for the YEC perspective, offering insights into Earth's history and the catastrophic global Flood described in Genesis. Conventional science often interprets the fossil record as documenting gradual evolutionary changes over billions of years, suggesting a progression from simple organisms to more complex life forms. However, YEC proponents reject macroevolution—the concept of large-scale changes between species—in favor of microevolution, which refers to limited adaptive changes within "kinds" of organisms. According to YEC, God created organism kinds with inherent genetic variability, enabling the diversity of life observed today to develop over a much shorter timeframe (Austin, 1994).

From the YEC viewpoint, the fossil record reflects the order of burial during the catastrophic global Flood, rather than evolutionary transitions. This perspective posits that factors such as an organism's habitat, mobility, and density during the Flood determined its placement within sedimentary layers. Marine organisms, being closest to the point of origin, would have been buried first, followed by less mobile land animals and, finally, highly mobile creatures. This burial sequence mirrors the observed arrangement of fossils, offering an alternative explanation to evolutionary interpretations (Morris, 2012).

Further supporting this view, YEC advocates highlight polystrate fossils—such as upright tree trunks spanning multiple sedimentary layers—as evidence of rapid burial during the Flood. These fossils challenge the assumption that each layer represents millions of years of deposition. Instead, YEC proponents argue that polystrate fossils could only form through sudden and catastrophic sedimentation processes, consistent with the intense geological activity described in the Flood narrative (Austin, 1994; Morris, 2012).

Additionally, evidence of exceptional fossil preservation, such as fish discovered mid-predation and soft tissues found in dinosaur remains, strongly supports the rapid burial conditions required for fossilization. Under long-age models, such soft tissues—including proteins and blood vessels—could not have persisted for millions of years. Yet their survival aligns with YEC explanations of the Flood's unique fossilization conditions. The rapid burial and geological upheaval associated with the Flood would have shielded organisms from decay, facilitating their extraordinary preservation (Schweitzer et al., 2005; Snelling, 2014).

The Cambrian Explosion offers further evidence consistent with YEC interpretations. Characterized by the sudden appearance of fully formed and diverse organisms, this event lacks transitional forms, directly challenging evolutionary theory. Instead, YEC proponents argue that the abrupt emergence of complex life is indicative of the catastrophic processes and burial patterns during the Flood (Meyer, 2013).

Fossil graveyards also provide compelling support for the YEC model. These sites, where the remains of diverse plants and animals are chaotically intermingled, suggest a single, global catastrophe involving widespread flooding and sediment transport. For instance, the presence of marine fossils atop mountain ranges, such as the Himalayas, points to large-scale hydrological upheaval consistent with the Genesis Flood (Snelling, 2014).

YEC perspectives emphasize that the scarcity of transitional fossils further undermines evolutionary narratives, reinforcing the idea that organisms were created fully formed as described in Genesis. Instead of depicting evolutionary progress, the fossil record is interpreted as a snapshot of ecological zones and burial patterns shaped by the Flood's catastrophic events (Morris, 2012; Meyer, 2013).

By integrating the order of fossil burial, polystrate formations, exceptional preservation, and the Cambrian Explosion, YEC proponents present a cohesive explanation rooted in the Flood narrative. This interpretation challenges long-age models and highlights the fossil record as a testament to the rapid and catastrophic processes described in Genesis, affirming the historical and geological validity of a young-Earth framework.

Theological and Scientific Implications

Critics have suggested the possibility of a "tranquil Flood" that covered the globe without leaving significant evidence. However, this concept is inherently inconsistent with the destructive nature of flooding. Modern examples such as the 2005 Indonesian tsunami vividly demonstrate the catastrophic impact of such events. They dramatically altered landscapes within mere hours. The notion that a global Flood could rise and recede without leaving any trace defies logic and observable reality. Instead, the widespread destruction evident in sedimentary deposits and geological upheaval serves as compelling evidence of the Flood's magnitude (Clarey and Werner, 2023).

The global Flood not only reaffirms the Bible's historical reliability but also serves as a central explanation for Earth's geological and fossil evidence within the YEC framework. By understanding the Flood as a literal, worldwide catastrophe, its significance within the Genesis narrative is clear—providing a foundational event that shaped the physical world and underscoring the accuracy of the Biblical account. Furthermore, YEC perspectives extend their lens beyond the Flood to address broader scientific questions, offering alternative interpretations of phenomena in astronomy, biology, and geology that challenge conventional paradigms and reaffirm a Scriptural worldview.

Expanding Scientific Perspectives in YEC

YEC offers a comprehensive framework rooted in Biblical chronology, presenting a cohesive perspective that confirms the Earth and universe are young, challenging mainstream scientific assumptions about their age. By building on the geological and paleontological implications of the Flood narrative, YEC proponents provide scientifically informed, faith-driven interpretations of phenomena spanning astronomy, biology, and geology. From distant starlight to mutation accumulation, fossil preservation, and radioactive decay, YEC advocates address these topics through a lens that prioritizes catastrophic events and Biblical timelines. Their interpretations challenge conventional models and highlight the alignment of scientific evidence with the Biblical account of Earth's history. These perspectives invite a reassessment of evidence and emphasize the interpretive nature of scientific inquiry.

Transitioning from this overarching framework, we delve deeper into specific domains of science where YEC perspectives provide alternative viewpoints. Starting with astronomy, the study of distant starlight offers fascinating debates about the age and expanse of the universe.

Astronomy and Distant Starlight

Conventional astronomy presents a unique challenge to YEC, particularly with the visibility of stars and galaxies located billions of light-years away. Mainstream science interprets this as evidence for a universe billions of years old, since light traveling at a constant speed would require such vast timeframes to reach Earth. However, YEC proponents highlight several key assumptions underlying this interpretation, such as the constancy of the speed of light over time and the uniformity of cosmic conditions (Humphreys, 1994; Lisle, 2010b; Faulkner, 2017).

Faulkner (2017) further observes that assumptions such as homogeneity, isotropy, and constant light-speed may not apply to the early universe. He proposes what he calls the *Dasha theory*, drawing on the Biblical description of God creating fully mature plants on Day 3. By analogy, God could have created astronomical objects and the intervening light simultaneously, ensuring their immediate visibility from Earth without requiring billions of years for the light to arrive. This model differs from both the ASC (Anisotropic Synchrony Convention) approach of Jason Lisle and D. Russell Humphreys' gravitational time-dilation model, both discussed below, by appealing to the theological principle of mature creation.

Faulkner (2013; 2016) emphasizes that deep-time cosmology rests on underlying philosophical assumptions—especially the belief that present cosmic conditions have always operated in the same way. He argues that much of modern cosmology relies on theoretical constructs that extend beyond direct observation. While dark matter has significant empirical support (Faulkner, 2017), inflationary models and dark energy are more model-dependent constructs introduced to address tensions within the standard Big Bang framework. Faulkner further notes that the distant-starlight issue is not unique to YEC; standard cosmology faces unresolved light-travel challenges such as the horizon problem, demonstrating that all cosmological models must contend with explanatory gaps (Hartnett, 2007).

One key area of contention is that the light emitted by these distant stars and galaxies is visible from Earth. In mainstream science, the time required for this light to traverse such immense distances strongly supports an ancient universe. However, YEC advocates question the reliability of this assumption, presenting alternative models that align with the Biblical timeline of 6,000–10,000 years. Some also critique the philosophical assumptions underlying standard cosmology, noting how Big Bang cosmology builds upon naturalistic presuppositions (Psarris, 2006; 2012).

Dr. Russell Humphreys has proposed a solution through his gravitational time dilation model, which is rooted in Einstein's general theory of relativity. Humphreys suggests that during the Creation Week described in Genesis, gravitational forces caused time to flow at different rates in various parts of the universe. Specifically, he posits that Earth was located in a gravitational well, where time moved more slowly relative to the outer regions of the cosmos. This model allows for the light from distant stars to reach Earth within the Biblical timeframe, while billions of years elapsed in the outer universe (Humphreys, 1994;). Humphreys' model provides a scientifically grounded mechanism for reconciling distant starlight with a young-Earth timeline.[2]

Another perspective comes from Dr. Jason Lisle, who has developed the Anisotropic Synchrony Convention (ASC). This model challenges the assumption that light travels at the same speed in all directions. Lisle argues that light traveling toward an observer could effectively reach Earth instantaneously, while light traveling away would take longer. This perspective, though unconventional, offers an alternative explanation for the visibility of distant starlight within a young universe (Lisle, 2010a; 2010b).[3]

Critics of these models often point to gaps in empirical evidence. However, YEC proponents contend that conventional science itself does not have all the answers when it comes to the origins of the universe. For instance, the Big Bang theory, while widely accepted, still faces major unresolved questions regarding the initial singularity, the cause of the universe's rapid expansion, and the precise mechanisms behind the formation of large-scale cosmic structures (Psarris, 2006; Ham, 2012; Faulkner, 2013). These gaps indicate that all interpretations of astronomical evidence—whether YEC or conventional—are, to some extent, based on assumptions and incomplete knowledge.

From the YEC perspective, the study of distant starlight highlights the interpretive nature of science, particularly in areas where direct observation and experimentation are impossible. While mainstream science leans on long-age models to interpret cosmic phenomena, YEC maintains that the universe's design reflects the intentionality of a Creator. This view challenges the prevailing narrative and underscores the need for openness to alternative perspectives in the quest to understand our universe. Faulkner and Psarris both emphasize that astronomy is among the most assumption-laden sciences, making cosmology especially prone to worldview influence.

Genetic Entropy and Biological Observations

The concept of genetic entropy, introduced by Dr. John Sanford, describes the gradual accumulation of harm-

---

[2] While influential and widely discussed, this proposal is not universally accepted within YEC astronomy, and several creationist physicists have raised questions about its assumptions and implications.

[3] Like Humphreys' proposal, the ASC model remains a subject of internal debate among YEC researchers, who differ on its physical plausibility and hermeneutical implications.

ful mutations in the genome over time. This process directly challenges the viability of macroevolutionary mechanisms, which require vast timescales to produce complex biological innovations. Instead, genetic entropy demonstrates a net loss of genetic functionality over generations, a notion fundamentally inconsistent with the idea of evolutionary progress. YEC proponents interpret this steady decline in genomic fitness as evidence for a young-Earth timeline, suggesting that life began in a state of genetic perfection—as described in Genesis—and has since deteriorated due to the consequences of sin and the Fall.

Sanford's research highlights that most mutations are neutral or deleterious, and natural selection is largely ineffective at removing these errors. This observation results in a continual degradation of genome integrity over time, which YEC advocates interpret as a reflection of the degenerative effects of mutations within a recent creation paradigm. Mutation rates observed in human populations further support this perspective, with genomic timelines calculated to be consistent with thousands, rather than millions, of years. These timelines align closely with Biblical genealogical records, reinforcing the YEC framework (Sanford, 2008).

YEC proponents also connect genetic entropy to the concept of "created kinds," which emphasizes significant genetic variation within distinct groups without requiring extended evolutionary timescales. This perspective posits that God endowed each created kind with inherent genetic variability, enabling the diversity of life observed today to arise rapidly after creation and following events like the global Flood. For example, genetic bottlenecks associated with Noah's Flood are seen as consistent with Biblical history. YEC proponents argue that genetic entropy highlights the challenges posed by mutation accumulation to long-term genome stability and underscores the young-Earth timeline (Carter, Sanford, and Hardy, 2008; Jeanson, 2017).

While old-Earth models suggest genetic evidence supporting common ancestry over tens of thousands of years, YEC advocates reinterpret this data through a Biblical lens. The concept of genetic entropy complements YEC claims by highlighting the limitations of macroevolutionary mechanisms and reinforcing the viability of a young-Earth model. Furthermore, the phenomenon of "mutational meltdown," widely acknowledged in population genetics, where harmful mutations accumulate faster than natural selection can eliminate them, aligns with Sanford's observations and offers additional insight into the constraints of evolutionary explanations for long-term species survival.

By integrating the principles of genetic entropy with the broader discussion of created kinds and mutation rates, YEC perspectives present a cohesive framework that challenges traditional evolutionary narratives and underscores the reliability of the Biblical account of creation and human history.

Carbon-14 in "Ancient" Materials and Rapid Geological Processes

Radiometric dating remains a cornerstone of modern science, routinely employed to estimate the ages of rocks and fossils through methods such as carbon dating and uranium-lead dating. These techniques consistently support an Earth age of approximately 4.5 billion years, utilizing predictable decay rates of radioactive isotopes. While this evidence poses a significant challenge to the YEC timeline, proponents argue that these methods rest on several major assumptions—such as initial conditions, constant decay rates, and the absence of contamination—that could potentially distort results. As previously discussed, events like Noah's Flood may have altered isotopic ratios, undermining the reliability of radiometric dating as portrayed by mainstream science. By challenging these assumptions, YEC proponents maintain that such dating results are not necessarily irreconcilable with a young-Earth framework (Vardiman, 2005; Clarey, 2020).

Furthermore, the detection of measurable carbon-14 (C-14) in materials traditionally considered millions or billions of years old—including coal, diamonds, and fossilized organic matter—adds complexity to conventional interpretations of deep time. Since C-14 has a short half-life of roughly 5,730 years, it should decay entirely within 50,000–100,000 years, becoming undetectable in samples presumed to be millions of years old (Manov and Curtiss, 1951). Yet measurable levels of C-14 have been repeatedly identified in such materials. YEC advocates interpret these findings as evidence of a relatively recent burial and formation—likely during Noah's Flood—challenging deep-time models and supporting a young-Earth timeline (Baumgardner, 2003, 2005; Snelling, 2014).

Critics attribute detectable C-14 in ancient samples to contamination, but YEC researchers counter that advanced radiocarbon analysis techniques significantly minimize this possibility. They argue that the presence of C-14 bolsters the case for a young Earth while highlighting methodological limitations in radiometric dating, which depends on assumptions about initial conditions and decay constants, including assumptions about initial C-14 levels, closed-system behavior, and constant decay rates. Interestingly, some secular scientists have acknowledged trace C-14 in ancient samples, attributing it to contamination or unexplained chemical processes. While mainstream interpretations vary, the persistent detection of C-14 remains an active topic of scientific debate and provides an opportunity for YEC perspectives to challenge conventional models (Baumgardner, 2003).

The reliability of radiometric dating methods is further questioned when considered alongside illustrative examples of rapid geological processes, such as the 1980 eruption of Mount St. Helens. This eruption triggered dramatic landscape transformations, including rapid sediment deposition, canyon formation, and stratified rock layers—features that are traditionally regarded as requiring millions of years to develop under uniformitarian principles. Within mere hours, pyroclastic flows generated finely layered deposits resembling ancient geological formations. YEC proponents contend that such rapid processes exemplify how catastrophic events, including Noah's Flood, could account for much of Earth's geological record within a young timeline (Austin, 1986; Snelling, 2014).

Additionally, observations from post-eruption ecological recovery at Mount St. Helens reveal instances of accelerated soil formation and environmental stabilization—challenging long-age models that assume extended timescales are required for these processes. For YEC advocates, Mount St. Helens serves as a natural laboratory, illustrating the plausibility of catastrophic frameworks that align with a young-Earth model (Austin, 1986; Clarey, 2020).

By integrating evidence of carbon-14 in ancient materials with examples of rapid geological processes, YEC proponents highlight the limitations of conventional long-age models. Together, these phenomena underscore the interpretive nature of radiometric dating and offer robust support for a young-Earth perspective grounded in both scientific observations and the Biblical narrative.

Polonium Halos in Rocks

Polonium halos—tiny, spherical zones of discoloration in biotite caused by the radioactive decay of short-lived polonium isotopes—serve as compelling evidence for rapid rock formation. Polonium-214, for example, has a half-life of only 0.0001643 seconds (164.3 microseconds), meaning its decay products could not produce visible halos unless the host rock solidified almost instantaneously.

Dr. Robert Gentry extensively documented the presence of these halos in granitic biotite, arguing that they are a "fingerprint of creation." Because conventional models require granites to cool slowly over millions of years, Gentry maintained that the existence of polonium halos indicates rapid formation of Earth's basement rocks during the creation week (Gentry, 1974; 1986).

While Gentry's pioneering work brought radiohalos to prominence within creationist research, later studies—especially those conducted under the Radioisotopes and the Age of the Earth (RATE) project—have expanded and in many respects superseded his interpretation. Snelling and other RATE researchers demonstrated that episodes of accelerated nuclear decay during the Flood, combined with rapid cooling of granitic plutons and hydrothermal fluid transport of polonium, can produce the observed distribution and clarity of halos within a short period (Snelling, 2005a; 2005b). This model retains the evidential force of Gentry's observations while embedding them within a broader and experimentally supported Flood-geology framework.

Although some skeptics propose secondary geological processes to explain polonium halos, YEC researchers argue that such models fail to account for the halos' pristine textures, clustered distribution patterns, and association with uranium-rich zones. These features continue to pose challenges for conventional geochronology and are frequently cited within YEC literature as evidence supporting a young Earth and the rapid geological processes described in Genesis.

Mainstream geologists do not accept the creationist interpretation; however, several secular studies acknowledge that the precise origin and formation mechanisms of polonium halos remain unresolved, indicating these structures present unanswered questions within standard geological models (Gentry, 1986).

Earth's Magnetic Field Decay

The Earth's magnetic field is steadily decreasing in strength, a phenomenon that YEC proponents often cite as evidence for a young Earth. Historical measurements since the early 19th century show that the magnetic field has weakened by approximately 10 percent, a trend that cannot be sustained over billions of years without the field's total collapse.

Prior to Humphreys' Dynamic Decay Model, creationist physicist Dr. Thomas G. Barnes proposed a "Free Decay Model" of the geomagnetic field, arguing that the field has been steadily weakening since creation (Barnes, 1973). Building on Barnes' foundational work, Dr. Russell Humphreys developed a more comprehensive model within a young-Earth framework, incorporating geomagnetic reversals associated with Flood-related processes (Humphreys,1990; 1994). Humphreys' model accounts for the observed trend of rapid decay within a timeline of thousands of years. Furthermore, his predictions regarding the magnetic field strengths of Uranus and Neptune were later confirmed by spacecraft observations, lending additional credibility to his approach (Humphreys and DeSpain, 2016).

In contrast, mainstream science relies on the geodynamo theory, which posits that Earth's magnetic field is generated, and sustained, by convective currents in the liquid outer core. However, this model faces unresolved challenges, including the origin of the magnetic field and the energy dissipation rate, both of which align more consistently with a young-Earth perspective. Humphreys and DeSpain (2016) point out that the geodynamo requires extremely fine-tuned starting conditions and ongoing energy inputs that are difficult to reconcile with a system supposedly billions of years old. Furthermore, the theory struggles to explain how a stable, self-sustaining magnetic field could have originated in the first place, since dynamo models require an already-existing seed field of significant strength.

Secular geophysicists recognize the current decay of Earth's magnetic field and have expressed concerns about the long-term sustainability of the Earth's geodynamo. This observed decay rate, when extrapolated backward, suggests a magnetic field strength inconsistent with billions of years of Earth history (Humphreys and DeSpain, 2016). Humphreys notes that the field's exponential decay rate implies a much younger age for the Earth—the field would have been impossibly strong and physically destructive if it had been decaying for even a fraction of the claimed deep-time timescale. Additionally, rapid magnetic reversals documented in the rock record—occurring in hours or days rather than millennia—fit well with Humphreys' Flood-related model but pose serious difficulties for conventional slow-acting dynamo assumptions (Merrill, McElhinny, and McFadden, 2003; Humphreys and DeSpain, 2016).

Heat Problems in Plate Tectonics

Conventional plate tectonics operates over millions of years, allowing ample time for heat generated by slow crustal movement to dissipate into the surrounding mantle. However, when YEC researchers propose Catastrophic Plate Tectonics (CPT)—a rapid, runaway subduction event during the Genesis Flood—the timescale is dramatically compressed from millions of years to months. This accelerated scenario introduces significant heat-dissipation challenges that uniformitarian plate tectonics does not face. In a CPT framework, the friction, deformation, and rapid subduction of tectonic plates would produce immense thermal energy that must be removed quickly to avoid overheating the oceans and destabilizing the crust. Creationist geophysicists argue that mechanisms such as enhanced mantle convection and rapid heat transport are required to make such accelerated tectonic activity physically viable (Baumgardner, 1994; Snelling, 2014).

YEC theorists address the plate tectonics issue with the concept of catastrophic plate tectonics, which posits that much of the tectonic activity occurred rapidly during Noah's Flood. This accelerated motion, termed "runaway subduction," would have resulted in rapid geological changes while avoiding the prolonged heat buildup associated with gradualist models. The rapid sinking of cold oceanic plates into the mantle would have driven the formation of modern geological features, such as mountain ranges and ocean trenches, within a Biblical timeframe.

YEC proponents acknowledge that CPT would generate immense heat during the Flood year—far more rapidly than conventional plate-tectonic models assume over millions of years. While several mechanisms have been proposed to help dissipate this heat—such as enhanced mantle convection, rapid hydrothermal circulation through the crust, increased radiation of heat from newly formed oceanic crust, and post-Flood ocean-driven climatic changes—none fully resolve the thermal challenge within current scientific modeling. Creationist geophysicists such as Baumgardner, Snelling, and Humphreys note that each proposed mechanism may remove part of the heat, but no combination has yet been demonstrated—through numerical simulation or laboratory calibration—to dissipate the total thermal load predicted during runaway subduction. Baumgardner's own modeling (1994) acknowledges that reduced mantle viscosity would accelerate plate sinking but also dramatically increase heat generation. Snelling (2014) observes that rapid mineral phase changes and dehydration reactions would release additional latent heat, while Humphreys and DeSpain (2016) argue that rapid geomagnetic reversals require intense convection that would itself contribute to heating. Because these sources and sinks of heat have not been quantitatively reconciled within a unified model, CPT researchers acknowledge that the heat problem remains an unresolved aspect of the theory—one that may require physical mechanisms not yet discovered or a degree of God's providential involvement. Even so, CPT continues to provide a coherent explanatory framework for the rapid formation of ocean basins, mountain uplift, and global geological restructuring consistent with a young-Earth timescale.

Secular geologists acknowledge the challenges associated with heat generation and dissipation in plate tectonics, often describing it as the "thermal catastrophe" problem. While mainstream models continue to explore solutions, the recognition of this issue lends indirect support to the plausibility of rapid tectonic activity during a shorter timescale (Austin and Snelling, 1994).

Building on the insights from astronomy, biology, geology, and anthropology, the evidence explored here demonstrates the comprehensive and multifaceted nature of YEC interpretations. YEC proponents provide scientifically informed frameworks that prioritize catastrophic events, such as the global Flood, and align closely with Biblical chronology. These alternative approaches challenge long-held assumptions of deep time within mainstream science, offering innovative explanations for phenomena like genetic entropy, the persistence of carbon-14 in ancient materials, polonium halos in rocks, magnetic field decay, and heat dissipation in geological processes.

While secular science often interprets these findings within the context of long-age models, shared observations—such as the limits of natural selection, unresolved challenges in radiometric dating, and anomalies in fossil preservation—reveal areas where the data itself prompts further inquiry. YEC perspectives not only highlight the interpretive nature of science but also provide a cohesive and logical worldview rooted in both empirical evidence and theological convictions. By weaving together insights from multiple disciplines, YEC offers a compelling vision of Earth's history that reaffirms the reliability of Scripture and encourages a continued search to understand reality within the framework of creation.

Concluding Insights: A Scientific and Scriptural Synthesis

The scientific evidence explored in this paper underscores the compatibility of empirical inquiry with the YEC timeline. Through a critical analysis of geological formations, fossil preservation, radiometric dating anomalies, and the extraordinary discoveries of soft tissues in fossils, a compelling case emerges for a young Earth. These phenomena challenge conventional deep-time paradigms, offering alternative explanations that align seamlessly with the Biblical account of a catastrophic global Flood and a recent creation.

The global Flood described in Genesis is central to the YEC framework. It provides a coherent explanation for the rapid geological processes and fossilization patterns observed today. From the dramatic sedimentation at Mount St. Helens to the remarkable preservation of carbon-14 in ancient materials, the evidence invites us to reevaluate long-held assumptions about Earth's history. Furthermore, the rapid layering of ice cores, the presence of polystrate fossils, and magnetic field decay collectively support a model that prioritizes catastrophic processes over uniformitarian interpretations.

These findings not only reflect a profound harmony between scientific inquiry and Biblical revelation, but also directly challenge the foundational assumptions of old-Earth perspectives. For instance, the persistence of soft tissues in fossils and the detection of carbon-14 in supposedly ancient materials pose significant problems related to the validity of multi-million-year timelines. The coherence of YEC explanations, grounded in both empirical evidence and scripture, calls into question whether old-Earth models adequately address these anomalies without resorting to speculative mechanisms.

As part of this series, this review builds upon the theological foundation laid in the first installment, bridging the authority of Scripture with empirical evidence. By doing so, it affirms that the YEC model offers not only theological coherence but also scientific credibility. This foundation sets the stage for the next exploration into the philosophical and interdisciplinary implications of the YEC worldview, highlighting its relevance in the broader dialogue between faith and science.

Ultimately, this study affirms that Scripture provides not just spiritual truth but also a consistent lens through which we can understand the physical world. It challenges us to approach scientific inquiry with humility, recognizing that human theories are fallible, but God's Word remains unchanging and reliable. Grounded in these truths, the YEC perspective offers both intellectual depth and spiritual assurance, inspiring believers to trust in the Creator who designed both the universe and the very processes through which it operates. Furthermore, it invites readers to critically evaluate prevailing deep-time paradigms, urging a reconsideration of whether old-Earth models can truly reconcile with the evidence presented and the Scriptural testimony of a young Earth.

References

Anderson, K. 2016. *Echoes of the Jurassic: Discoveries of Dinosaur Soft Tissue*. Creation Research Society Books, Chino Valley, AZ.

Armitage, M.H., and K. Anderson. 2014. Soft sheets of fibrillar collagen found in fossilized *Triceratops* horn. *Acta Histochemica* 116(6): 603–608.

Austin, S.A. 1986. Rapid burial and fossilization. In *Proceedings of the First International Conference on Creationism*, edited by Robert E. Walsh, pp. 187–200. Creation Science Fellowship, Pittsburgh, PA.

———. 1994. *Grand Canyon: Monument to Catastrophe.* Institute for Creation Research, Santee, CA.

———. 2012. *Footprints in the Ash: The Explosive Story of Mount St. Helens*. Master Books, Green Forest, AR.

Austin, S.A., and A.A. Snelling. 1994. Tectonics of the Flood. In *Proceedings of the Third International Conference on Creationism*. Creation Science Fellowship, Pittsburgh, PA.

Barnes, T.G. 1973. *Origin and Destiny of the Earth's Magnetic Field.* Institute for Creation Research, San Diego, CA.

Barrick, W.D. 2008. A Biblical model for the origin and history of the Earth's geologic processes. In *Coming to Grips with Genesis*, edited by Terry Mortenson and Thane H. Ury, pp. 423–452. Master Books, Green Forest, AR.

———. 2008. Biblical chronology: Genesis 5 and 11. *The Master's Seminary Journal* 19(2): 127–143.

Baumgardner, J.R. 2003. Carbon-14 evidence for a recent global flood and a young Earth. In *Proceedings of the Fifth International Conference on Creationism*, edited by R.L. Ivey, Jr., pp. 127–142. Creation Science Fellowship, Pittsburgh, PA.

———. 2005. ^{14}C Evidence for a Recent Global Flood and a Young Earth. In *Radioisotopes and the Age of the Earth: Results of a Young-Earth Creationist Research Initiative*, edited by L. Vardiman, A.A. Snelling, and E.F. Chaffin, pp. 587–630. Institute for Creation Research, Dallas, TX, and Creation Research Society, Chino Valley, AZ.

Carter, R.W., J.C. Sanford, and W.H. Brewer. 2008. Mitochondrial Diversity within Modern Human Populations. In *Proceedings of the Sixth International Conference on Creationism*, edited by A.A. Snelling, pp. 111–116. Creation Science Fellowship, Pittsburgh, PA.

Clarey, T. 2020. *Carved in Stone: Geologic Evidence of the Worldwide Flood*. Institute for Creation Research, Dallas, TX.

Clarey, T.L., and D.J. Werner. 2023. A Progressive Global Flood Model Confirmed by Rock Data Across Five Continents. *Proceedings of the International Conference on Creationism:* Vol. 9, Article 23.

Collins, M.J., C.M. Nielsen-Marsh, J. Hiller, E.E. Smith, P. Roberts, R.C. Prigodich, T.A. Wess, et al. 1995. The survival of organic matter in bone: A review. *Journal of Archaeological Science* 22(2): 175–183.

Faulkner, D.R. 2013. A Biblical creationist astronomy. *Journal of Creation* 27(1): 56–64.

———. 2013. A proposal for a new solution to the light travel time problem. *Answers Research Journal* 6: 279–284.

———. 2013. *Starlight and Time*: Is it a problem for Biblical creation? *Answers Research Journal* 6: 27–41.

———. 2016. *The Created Cosmos: What the Bible Reveals About Astronomy*. Master Books, Green Forest, AR.

———. 2016. *The Expanse of Heaven: Where Creation and Astronomy Intersect.* Master Books, Green Forest, AR.

———. 2017. The Case for Dark Matter. *Answers Research Journal* 10: 89–101.

———. 2019. *Falling Flat: A Refutation of Flat Earth Claims*. Master Books, Green Forest, AR.

Gentry, R.V. 1974. Radiohalos in a radiochronological and cosmological perspective. *Science* 184(4132): 62–66.

———. 1986. *Creation's Tiny Mystery*, 2nd edition. Earth Science Associates, Knoxville, TN.

Ham, K. 2012. 10 best evidences that confirm a young Earth. *Answers Magazine*. Answers in Genesis, Petersburg, KY.

Hartnett, J.W. 2007. *Starlight, Time and the New Physics*. Creation Book Publishers, Powder Springs, GA.

Hayes, D. 1994. *The Lost Squadron: A Fleet of Warplanes Locked in Ice for Fifty Years*. Hyperion Press, New York, NY.

Humphreys, D.R. 1990. The Earth's magnetic field Is young. *Creation Research Society Quarterly* 27(1): 15–20.

———. 1994. *Starlight and Time: Solving the Puzzle of Distant Starlight in a Young Universe.* Master Books, Green Forest, AR.

Humphreys, D.R., and M.J. DeSpain. 2016. *Earth's Mysterious Magnetism and That of Other Celestial Orbs*. Creation Research Society, Glendale, AZ.

Jeanson, N.T. 2017. *Replacing Darwin: The New Origin of Species*. Master Books, Green Forest, AR.

Kepler, J. 1619. *The Harmony of the World* (*Harmonice Mundi*) Georgius Tampachius and Johannes Plancus (Tampach and Plank), Linz, Austria.

Lisle, J. 2010a. *The Physics of Einstein: The Theory of Relativity Made Simple*. Master Books, Green Forest, AR.

———. 2010b. Anisotropic Synchrony Convention—A solution to the distant starlight problem. *Answers Research Journal* 3: 191–207.

Manov, G.G., and L.F. Curtiss. 1951. The half-life of carbon 14. *Journal of Research of the National Bureau of Standards* 46(4): 310–316.

Merrill, R.T., M.W. McElhinny, and P.L. McFadden. 2003. *The Magnetic Field of the Earth: Paleomagnetism, the Core, and the Deep Mantle*. Academic Press, London, UK.

Meyer, S.C. 2013. *Darwin's Doubt: The Explosive Origin of Animal Life and the Case for Intelligent Design*. HarperOne, New York, NY.

Morris, H.M. 2012. *The Young Earth*. Revised and expanded. Master Books, Green Forest, AR.

Morris, J.D. 2012. *The Global Flood: Unlocking Earth's Geologic History*. Institute for Creation Research, Dallas, TX.

Nielsen-Marsh, C.M., and R.E.M. Hedges. 2000. Patterns of diagenesis in bone I: The effects of site environments. *Journal of Archaeological Science* 27(12): 1139–1150.

Oard, M.J. 1990. *An Ice Age Caused by the Genesis Flood*. Institute for Creation Research, El Cajon, CA.

———. 2004. *Frozen in Time: Woolly Mammoths, the Ice Age, and the Biblical Key to Their Secrets*. Master Books, Green Forest, AR.

———. 2005. *The Frozen Record: Examining the Ice Core History of the Greenland and Antarctic Ice Sheets*. Institute for Creation Research, Dallas, TX.

———. 2020a. Rapid growth of caves and speleothems: Part 1—The excavation of the cave. *Journal of Creation* 34(1): 71–78.

———. 2020b. Rapid growth of caves and speleothems: Part 2—Growth rate variables." *Journal of Creation* 34(2): 90–97.

———. 2020c. Rapid growth of caves and speleothems: Part 3—Flood and Ice Age variables." *Journal of Creation* 34(2): 99–104.

———. 2024. *How Noah's Flood Caused a Single Ice Age*. Creation Book Publishers, Powder Springs, GA.

———. 2025. *The Frozen Paradox: Ice Cores vs. Deep Time—What Ice Cores Reveal About*

Earth's History. Creation Book Publishers, Powder Springs, GA.

Psarris, S. 2006. *What You Aren't Being Told About Astronomy, Volume I: Our Created Solar System*. DVD. Creation Astronomy Media. https://www.creationastronomy.com/product/volume-i-our-created-solar-system-dvd/.

———. 2012. *What You Aren't Being Told About Astronomy, Volume II: Our Created Stars and Galaxies*. DVD. Creation Astronomy Media. https://www.creationastronomy.com/product/volume-ii-our-created-stars-and-galaxies-dvd/.

Sanford, J.C. 2008. *Genetic Entropy and the Mystery of the Genome*. Lima, NY: Elim Publishing, Lima, NY.

Sarfati, J. 2015. *The Genesis Account: A Theological, Historical, and Scientific Commentary on Genesis 1–11*. Creation Book Publishers, Powder Springs, GA.

Shea, W.H. 2018. The structure of the Genesis Flood narrative and its implications. *Origins* 6(1): 8–38.

Schweitzer, M.H., J.L. Wittmeyer, J. Horner, and J.K. Toporski. 2005. Soft-tissue vessels and cellular preservation in *Tyrannosaurus rex*. *Science* 307(5717): 1952–1955.

Schweitzer, M.H., W. Zheng, T.P. Cleland, M. Bern, and J.Horner. 2007. Analyses of soft tissue from *Tyrannosaurus rex* suggest the presence of protein. *Science* 316(5822): 277–280.

Snelling, A.A. 2005a. Radiohalos: A tale of three granitic plutons. In *Radioisotopes and the Age of the Earth: Results of a Young-Earth Creationist Research Initiative*, edited by L. Vardiman, A.A. Snelling, and E.F. Chaffin, pp. 381–468. Institute for Creation Research, Dallas, TX, and Creation Research Society, Chino Valley, AZ.

———. 2005b. Radioisotopes and the age of the Earth: A young-Earth creationist research initiative—Overview. In *Radioisotopes and the Age of the Earth: Results of a Young-Earth Creationist Research Initiative*, pp. 1–28. Institute for Creation Research, Dallas, TX, and Creation Research Society, Chino Valley, AZ.

———. 2014. *Earth's Catastrophic Past: Geology, Creation, and the Flood*, Volumes I & II. Dallas, TX: Institute for Creation Research, Dallas, TX.

Thomas, B. 2013. *Dinosaurs and the Bible*. Institute for Creation Research, Dallas, TX.

Whitcomb, J.C., and H.M. Morris. 1961. *The Genesis Flood: The Biblical Record and Its Scientific Implications*. Presbyterian and Reformed Publishing, Phillipsburg, NJ.

Woodmorappe, J. 1996. *Noah's Ark: A Feasibility Study*. Institute for Creation Research, Santee, CA.

Letters to the Editor

The policy of the editorial staff of CRSQ *is to allow letters to the editor to express a variety of views. As such, the content of all letters is solely the opinion of the author, and does not necessarily reflect the opinion of the* CRSQ *editorial staff or the Creation Research Society.*

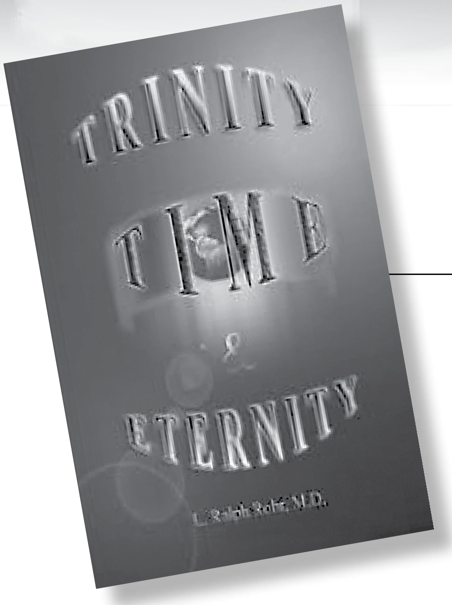
LXX Corruptions in Messianic Prophecy

Dear Editor:

Tompkins, et al. wrote a persuasive article about corruptions in messianic prophecy scriptures in the LXX (Volume 62:136–149). The ancient Dead Sea Scrolls give support to their conclusions and offer no support to the LXX translation. The Dead Sea Scrolls are essentially the same as the MT in Isaiah 4.2, Isaiah 9:6, and Isaiah 53:2. The following passages dealt with in the article are missing in the Dead Sea Scrolls: Genesis 3:15, Numbers 24:17, Psalm 2:12, Proverbs 30:4, Hosea 11:1, and Zechariah 13:7. In Isaiah 52:15, the LXX uses the verb "wonder" and the MT uses the verb "sprinkle"; but the Dead Sea Scrolls uses "startle" and in a footnote states "Or, sprinkle." Finally, in Zechariah 12:10, the LXX uses the verb "mocked" and the MT uses the verb "pierced"; but the Dead Sea Scrolls uses "[have pierced," indicating that the part in brackets was lost due to damage. So, three of these passages are the same in the MT as in the Dead Sea Scrolls, six are not in the Dead Sea Scrolls, the other two may be said to weakly favor the MT, and none of these that are in the Dead Sea Scrolls may be said to be supportive of the LXX. In addition, the Dead Sea Scrolls do not include the verses in Genesis 5 that relate to Methuselah and the timing of his death relative to the Flood.

Arthur Manning
Vineland, NJ
rntc@juno.com

Media Reviews



Trinity, Time & Eternity

by L. Ralph Rohr, M.D.

Confessor Press, Salt Lake City, UT, 2002, 310 pages.

Having recently and enthusiastically read assorted books on the Christian doctrine of the Trinity, I approached L. Ralph Rohr's treatise, *Trinity, Time & Eternity*, eagerly anticipating yet another perspective on this intriguing topic. By the time I finished the reading, I had experienced both delight and disappointment, clarity and concern, wonder and warning. The author's presentation begins with a sound summary of the nature of science and the nature of God, yet ends Chapter II by leaving the reader believing that he accepts the Big Bang cosmogony as scientific fact.

Rohr's Trinity Analogy: The Electromagnetic Spectrum

Though some may judge his Chapter III trinitarian example to be simply a triad (where all three components are needed to complete the whole), Rohr's discussion of the Holy Trinity, unlike others who commit the error of tritheism (Deity presented as *three separate* but coequal *gods*) or modalism (*one God* manifesting Himself *in different forms at different times*), was most enlightening and worthy of further consideration.

His amazingly consistent analogy of the Trinity involves the idea that God can be compared to light. In fact, Rohr's 'God is (like) light' simile makes use of the triune electromagnetic (E-M) spectrum. The electromagnetic spectrum—the "light" of Genesis 1:3—is of one fundamental essence (E-M wave energy) exhibited as a continuum of three differentiated displays. *God the Father* is likened to high-energy [high-frequency/short-wavelength (10^{-14} millionths of a meter)] electromagnetic radiation—gamma rays, X-rays, ultraviolet (UV) rays—that are powerful, creative and destructive (Exod. 33:20, 22 / 1 Tim. 6:16). *God the Son*, the Lord Jesus Christ, represents all visible light [violet to red (3.80–7.40) x 10^2 millionths of a meter)]; light that is also touchable, beautiful, and instructive (Lk. 12:49–50/ Jn. 1:18; 14:9/ Col. 1:15/ 1 Jn. 1–3). Proceeding seamlessly from this central, confined, visible-light region of the E-M spectrum—which, in turn, emanated directly from the high-energy section of the spectrum—is the myriad of low-energy [low-frequency/ long-wavelength (10^4 meters)] waves [infrared (IR) waves, microwaves, radio/ TV waves], similar in nature to the warm, gentle and comforting, communicative Holy Spirit (Jn. 14:16–21).

With one chapter devoted to each divine member of the Godhead (Chapters IV-VI), this 'God is light' model of the Holy Trinity is not only Biblical (1 Jn. 1:5), but it also places no limits on God as each end of the electromagnetic spectrum is boundless. It is a rather simple, yet effective, way to compare the complexity of three Persons being one God to the three portions of the E-M spectrum's (i.e., light's) single essential essence—electromagnetic energy.

Rohr's Critique of Young-Earth Creationists

Besides the seeming endorsement of the Big Bang scenario, the author set off other personal alarms in his contrasting of time with eternity by his over-emphasis on disproved special relativity postulates, his uncritical acceptance of unproved quantum mechanics paradoxes, and his stern criticism of approved creation-science principles (Chapters VII & VIII and Appendix B). Regarding young-Earth creationists (YECs), such as myself, Rohr issues the following rebuke:

> "They place their credence in origins and mechanisms of the [E]arth entirely upon supernatural explanations as recounted in Genesis, according to their own inflexible interpretations of those chapters. They advocate their interpretations strongly, despite what some other Bible believers perceive as rational internal Biblical contradictions and conflicts with mainstream science. They tend to view the debate in theological terms of satanic forces utilizing secular science to corrupt young minds and society…. A purely supernatural conclusion of the debate seems alien to the realities of life on this crowded physical planet." (pp. 156, 158)
>
> "Nevertheless, the geological revolution [17th–19th centuries AD], following on the heels of the scientific revolution [16th–17th centuries AD (Appendix A features Galileo Galilei (1564–1642), one of its founding fathers], shook the substrata of the medieval church's comfortable worldview. No longer the small green orb of a humanly comprehensible few thousand years age, our world became the inscrutable product of unimaginable eons of internally heated explosive upheavals and endless wearing away and settling of massive landforms. The [E]arth, which had traditionally been viewed as the product of a massive supernatural set of human hands which worked in terms of human comprehension, became more mysterious than ever before. The geological revolution seemed to thwart an anthropocentric reading of the Genesis account of creation." (Appendix B-p. 24; henceforth abbreviated as B-24)
>
> "The medieval worldview ran hard aground on scientific dogma and Biblical faith suffered a grievous wound, which festers today. Today many people cling to the medieval young [E]arth as if their faith in God depended upon the validity of that primitive perspective. They are shaken in their faith if God operated over a greater time period than the short, limited chronology that limited human intellect can grasp. As seen in Chapters VII and VIII, a limited time perspective, comfortable to human notions, is not essential to a Biblical worldview, and may even confuse clearly expressed Biblical sense in some cases…." (B-24–B-25)
>
> "To accept that the [E]arth we inhabit is older than a few thousand years is not to surrender the field of debate to materialistic geologists. Nor need it relinquish in the least the veracity of a simple and straightforward reading of the Genesis account." (B-25)

Rohr's Tolerance of Theistic Evolution and Rejection of Atheistic Darwinism

Though a believer in a Big Bang origin of the universe and an advocate for an old Earth, the author would not consider himself to be an accommodationist when it comes to interpreting the Genesis account of creation. "Middle-ground scientists who are Christians," according to

Rohr (a retired Christian medical doctor), "strike a balance between secularist and creationist extremes" (p. 157). He says that though they are

> "From a wide variety of Christian backgrounds, they are theologically less restrictive than the scientific creationists. They do not compromise for the sake of compromise, but seek legitimate common ground between science and the Bible…. Though they believe scientific evidence favors an ancient [E]arth, they individually accept a broad span of propositions about how life on the [E]arth arose, including the concept of theistic evolution (God-initiated or God-directed evolution)." (p. 157)

Lest you accept, at this point, that Dr. Rohr is a Christian Darwinist because he has not totally embraced theistic evolution and has referred to YEC thinking as 'inflexible," "purely supernatural" [only religious?], "alien," "anthropocentric," "medieval," "primitive," and "restrictive," he makes it very clear that he, in no way, accepts gradual evolution in the slightest. In fact, in his 'Appendix B,' he refers to gradual evolution as "philosophic materialism" and defines it as "an irrational assumption, a form of faith which denies existence of the supernatural Creator because such a One has not been discovered by natural means" (B-14, 15). In his 'Appendix C,' entitled "The Demise of Darwinian Evolution," the author labels this faith in gradualism as "atheistic materialism…a choice not compelled by objective evidence so much as by philosophic inclination" (C-72). In Rohr's 'Appendix C,' naturalistic evolution is also called "the transmutation hypothesis" (C-45) with its philosophical foundation clearly identified: "the fundamental assumption of materialistic faith—no supernatural, no God, no miracles—by definition" (C-73). The author even attacks "the master presumption of Darwinism" (C-79)—natural selection—in saying that it is a "well-known fact of contemporary science that there was no positive evidence to support the hypothesis of the transmutation of one species [more correctly *baramin* (created 'kind')] into another via the mechanism of natural selection" (C-78).

Darwin Develops Darwinism by Reinterpreting Research…*of Creationists!*

Despite the lack of positive, objective evidence to support his speculations, Charles Darwin managed to appropriate, redefine, and incorporate the published observations of creationists as the elemental components that formed the framework for his materialistic faith. These so-called "biological facts of Darwinian dogma" (C-44) would be "1. Linnaean taxonomy" [of Swedish botanist Carolus Linnaeus (1707–1778)], "2. Variation of structure and function" [courtesy of English zoologist Edward Blyth (1810–1873)], and "3. The struggle for survival" [from English economist Thomas Malthus' (1766–1834) *An Essay on the Principle of Population*] (C-44).

According to Linnaeus, the Father of Taxonomy, "The first step of science is to know one thing from another" (C-59). Indeed, evolutionist Loren Eiseley has said "An orderly and classified arrangement of life was an absolute necessity before the investigation of evolution, or even its recognition, could take place" (C-61). Edward Blyth had determined in 1835, twenty-four years before Darwin's *Origin*, that natural selection was solely a conservative process, the preservative of the Genesis kinds. Even so, Darwin repackaged the concept, promoting it as a creative causative agent for biological variation and the plausible mechanism for his evolutionary hypothesis. Rohr correctly admits that "Darwin never mentioned the very articulate views of Edward Blyth who anticipated and clearly defined the mechanism of natural selection so important to Darwin's intellectual revolution" (C-65). For the "final component of the Darwinian formula…. Darwin claimed inspiration from Thomas Malthus, economist and Anglican clergyman, who first published his *Essay on Population* anonymously in 1798," though he later republished it under his name in 1803. This work, which documented the notion of competition for limited resources, was read by Darwin in October 1838. He afterward said of Malthus' thesis, "Here, then, I had at last got a theory by which to work" (C-63). "Darwin's Bulldog," Thomas Henry Huxley, would later remark, "The facts of variability, of the struggle for existence, of adaptation to conditions, were notorious enough; but none of us had suspected that the road to the heart of the species problem *lay through them*,…." (C-73; italics added).

Rohr masterfully documents that despite "Darwin's hope that his own published views would be better grounded in demonstrable fact and empirical observation" than earlier evolutionists, like Jean-Baptiste Lamarck (1744–1829) and his own grandfather, Erasmus Darwin (1731–1802), "…Darwin's postulates have been disabled by over a century of exploration, and today Darwin's materialistic claims are more speculative than when he first synthesized them, despite popular teaching to the contrary" (C-52). It is important to note that these plagiarized postulations, before they were misinterpreted by materialistic musings, were viewed as settled scientific "facts" (C-44). Even evolutionist Loren Eiseley, as quoted once again by the author, admits that

> "The leading tenets of Darwin's work—the struggle for existence, variation, natural selection and sexual selection—are all fully expressed in Blyth's paper of 1835 [An Attempt to Classify the "Varieties" of Animals,…]." (C-66)

In agreement with Dr. Rohr, it is indeed a travesty of history that "*most of the world is ignorant that Darwin extracted out of its creationist context the key mechanism for his evolutionist hypothesis* [i.e., natural selection] *from a good scientist to whom* *he never gave due credit*" (C-47; italics in original), not to mention the other basic concepts from others he doctored and distorted!

Deciphering Rohr's Worldview: If Not This or That, Then What?

This leads us to finally contemplate the author's personal interpretative framework of origins. I believe the following text admissions of L. Ralph Rohr, M.D., will more than suffice:

> "…the appearance of evolution of life of differing forms of life (change through time) is more rationally explained by a series of specific creations out of eternity reaching into long eons of time." (p. 169)
>
> "…concerning the evolution of life on planet [E]arth, the observed facts best fit a scenario of sequential intelligent creation over vast expanses of time." (p. 171)
>
> "For Darwin, the evolution by large jumps or macromutations clearly required miraculous intervention, in other words, the operation of a supernatural agency…. If gradual changes leading to transmutation of species cannot be documented, then…its only alternative is the 'realms of miracle' or supernatural creation, according to Darwin!…In other words, there is no forthcoming rational materialistic explanation for evolution by jumps. It should be obvious, however, that such a picture of developmental life history is exactly what one would expect to see over long periods of time as each new specifically adapted living creation was created and inserted into its predetermined ecological niche by its Creator. In other words, the concept of evolution by jumps, or saltation, cannot be differentiated from supernatural intelligent creation—such a picture is exactly what one would expect to see if God created!" (C-84, 85)
>
> "For Darwin, to accept evolution by sudden jumps, with nothing but gaps in the rocky record of life, would be to reject naturalistic scientific explanation in favor of miraculous supernatural explanation. Yet this is precisely what many contemporary evolutionists have done…. What research reveals is what evolutionists are in rebellion against…. The rocky record of life is entirely consistent with divine creation…. What evolutionists must postulate as naturalistic evolution by 'jumps' is more rationally explained by Intellect,…. But if current proposals of evolution by jumps suggest the 'miraculous' or a 'creationist' point of view, as Darwin stated, then perhaps we need to re-examine such a view in a more 'scientific' fashion." (C-89, 90, 92)

In the final analysis, indeed within the closing pages of the last appendix of the book, the author lets it be known to his readers that he holds to "a variant of [the] Darwinian mechanism, which Darwin himself considered and rejected" (C-80), notably 'punctuated equilibrium' or, simply, 'punctuationism,' albeit with a theistic cause but still within an old-Earth framework; in other words, a hybrid of *progressive creationism*! Though the author never identifies his origins model with any of these terms, his own words pigeonhole him into this creation-compromise category…but with a twist. Rohr attempts to sidestep the theological dilemma of animal and plant death before Adam by (1) associating the first two chapters of Genesis, like the last two chapters of Revelation, with the realm of "eternity" (pp. 151, 154, 172, 182, 202), rather than this temporal world, (2) defining the Curse of Genesis, Chapter 3, as being time itself (pp. 151, 154, 161, 162, 165), experienced in this reality as entropy, regress, decay, degeneration, and death, and (3) "theologically restrict[ing] the Biblical sense of death only to human spiritual death" (p. 164).

Concluding Remarks

If, as the author quoted, "the concept of evolution by jumps, or saltation, cannot be differentiated from supernatural intelligent creation" (C-85), then why integrate the former into your worldview at all? The only reason would be the firm acceptance of the eons timescale of Big-Bang astronomy and uniformitarian geology instead of the Bible's straightforward chronology of six-to-seven millennia. This adoption of deep time violates the linguistic meaning of the time words and the order of events as recorded in Genesis 1, dissociates man's sin (documented in Genesis 3) as the reason for organism death and creature extinction, and dismisses entirely the global Flood of Genesis 7 & 8 as the principal cause of the geologic column and its fossil record.

Doesn't it just make sense to believe that God, the supernatural intelligent Creator, meant a literal Creation Week when He compared it to our calendar week of seven solar days in the Fourth Commandment (Exod. 20:8–11) which He directly wrote (Exod. 31:18/ Deut. 9:10)? After all, He defined and delineated each of those days as consisting of exactly one evening and one morning (Gen. 1:5, 8, 13, 19, 23, 31), rather than being "six perfect days *of eternity*" (Chapter IX, p. 202; italics added) as advocated by Rohr. Such a literal week would preclude both evolution by spurts *and* the deep time of "atheistic materialism." The young-Earth scenario of Biblical creationists honors the ancient Hebrew rendering of both the Genesis creation and Flood accounts, is supported by proper interpretation of true scientific investigation, and gives glory to the one and only triune God—the God Who clothes Himself in light (Ps. 104:2), is said to be light (Jn. 1:7–9; 8:12/ 1 Jn. 1:5/ Rev. 21:23; 22:5), and the One Who actually formed light (Gen. 1:3/ Isa. 45:7), the triune light of the electromagnetic spectrum.

David V. Bassett, M.S.

Instructions to Authors

Submission

Electronic submissions of all manuscripts and graphics are preferred and should be sent to the editor of the *Creation Research Society Quarterly* in Word, WordPerfect, or Star-Office/Open Office (see the inside front cover for address). Printed copies also are accepted. If submitting a printed copy, an original plus two copies of each manuscript should be sent to the editor. The manuscript and copies will not be returned to authors unless a stamped, self-addressed envelope accompanies submission. If submitting a manuscript electronically, a printed copy is not necessary unless specifically requested by the *Quarterly* editor. Manuscripts containing more than 35 pages (double-spaced and including references, tables, and figure legends) are discouraged. An author who determines that the topic cannot be adequately covered within this number of pages is encouraged to submit separate papers that can be serialized.

All submitted manuscripts will be reviewed by two or more technical referees. However, each section editor of the *Quarterly* has final authority regarding the acceptance of a manuscript for publication. While some manuscripts may be accepted with little or no modification, typically editors will seek specific revisions of the manuscript before acceptance. Authors will then be asked to submit revisions based upon comments made by the referees. In these instances, authors are encouraged to submit a detailed letter explaining changes made in the revision, and, if necessary, give reasons for not incorporating specific changes suggested by the editor or reviewer. If an author believes the rejection of a manuscript was not justified, an appeal may be made to the *Quarterly* editor (details of appeal process at the Society's web site, www.creationresearch.org).

Authors who are unsure of proper English usage should have their manuscripts checked by someone proficient in the English language. Also, authors should endeavor to make certain the manuscript (particularly the references) conforms to the style and format of the *Quarterly*. Manuscripts may be rejected on the basis of poor English or lack of conformity to the proper format.

The *Quarterly* is a journal of original writings, and only under unusual circumstances will previously published material be reprinted. Questions regarding this should be submitted to the Editor (CRSQeditor@creationresearch.org) prior to submitting any previously published material. In addition, manuscripts submitted to the *Quarterly* should not be concurrently submitted to another journal. Violation of this will result in immediate rejection of the submitted manuscript. Also, if an author uses copyrighted photographs or other material, a release from the copyright holder should be submitted.

Appearance

Manuscripts shall be computer-printed or neatly typed. Lines should be double-spaced, including figure legends, table footnotes, and references. All pages should be sequentially numbered. Upon acceptance of the manuscript for publication, an electronic version is requested (Word, WordPerfect, or Star-Office/Open Office), with the graphics in separate electronic files. However, if submission of an electronic final version is not possible for the author, then a cleanly printed or typed copy is acceptable.

Submitted manuscripts should have the following organizational format:

1. Title page. This page should contain the title of the manuscript, the author's name, and all relevant contact information (including mailing address, telephone number, fax number, and e-mail address). If the manuscript is submitted by multiple authors, one author should serve as the corresponding author, and this should be noted on the title page.

2. Abstract page. This is page 1 of the manuscript, and should contain the article title at the top, followed by the abstract for the article. Abstracts should be between 100 and 250 words in length and present an overview of the material discussed in the article, including all major conclusions. Use of abbreviations and references in the abstract should be avoided. This page should also contain at least five key words appropriate for identifying this article via a computer search.

3. Introduction. The introduction should provide sufficient background information to allow the reader to understand the relevance and significance of the article for creation science.

4. Body of the text. Two types of headings are typically used by the *CRSQ*. A major heading consists of a large font bold print that is centered in column, and is used for each major change of focus or topic. A minor heading consists of a regular font bold print that is flush to the left margin, and is used following a major heading and helps to organize points within each major topic. Do not split words with hyphens, or use all capital letters for any words. Also, do not use bold type, except for headings (italics can be occasionally used to draw distinction to specific words). Italics should not be used for foreign words in common usage, e.g., "et al.", "ibid.", "ca." and "ad infinitum." Previously published literature should be cited using the author's last name(s) and the year of publication (ex. Smith, 2003; Smith and Jones, 2003). If the citation has more than two authors, only the first author's name should appear (ex. Smith et al., 2003). Contributing authors should examine this issue of the *CRSQ* or consult the Society's web site for specific examples as well as a more detailed explanation of manuscript preparation.

Frequently-used terms can be abbreviated by placing abbreviations in parentheses following the first usage of the term in the text, for example, polyacrylamide gel electrophoresis (PAGE) or catastrophic plate tectonics (CPT). Only the abbreviation need be used afterward. If numerous abbreviations are used, authors should consider providing a list of abbreviations. Also, because of the variable usage of the terms "microevolution" and "macroevolution," authors should clearly define how they are specifically using these terms. Use of the term "creationism" should be avoided. All figures and tables should be cited in the body of the text, and be numbered in the sequential order that they appear in the text (figures and tables are numbered separately with Arabic and Roman numerals, respectively).

5. Summary. A summary paragraph(s) is often useful for readers. The summary should provide the reader an overview of the material just presented, and often helps the reader to summarize the salient points and conclusions the author has made throughout the text.

6. References. Authors should take extra measures to be certain that all references cited within the text are documented in the reference section. These references should be formatted in the current *CRSQ* style. (When the *Quarterly* appears in the references multiple times, then an abbreviation to *CRSQ* is acceptable.) The examples below cover the most common types of references:

Robinson, D.A., and D.P. Cavanaugh. 1998. A quantitative approach to baraminology with examples from the catarrhine primates. *CRSQ* 34:196–208.

Lipman, E.A., B. Schuler, O. Bakajin, and W.A. Eaton. 2003. Single-molecule measurement of protein folding kinetics. *Science* 301:1233–1235.

Margulis, L. 1971a. The origin of plant and animal cells. *American Scientific* 59:230–235.

Margulis, L. 1971b. *Origin of Eukaryotic Cells*. Yale University Press, New Haven, CT.

Hitchcock, A.S. 1971. *Manual of Grasses of the United States*. Dover Publications, New York, NY.

Walker, T.B. 1994. A biblical geologic model. In Walsh, R.E. (editor), *Proceedings of the Third International Conference on Creationism* (technical symposium sessions), pp. 581–592. Creation Science Fellowship, Pittsburgh, PA.

7. Tables. All tables cited in the text should be individually placed in numerical order following the reference section, and not embedded in the text. Each table should have a header statement that serves as a title for that table (see a current issue of the *Quarterly* for specific examples). Use tabs, rather than multiple spaces, in aligning columns within a table. Tables should be composed with *14-point type* to insure proper appearance in the columns of the *CRSQ*.

8. Figures. All figures cited in the text should be individually placed in numerical order, and placed after the tables. Do not embed figures in the text. Each figure should contain a legend that provides sufficient description to enable the reader to understand the basic concepts of the figure without needing to refer to the text. Legends should be on a separate page from the figure. All figures and drawings should be of high quality (hand-drawn illustrations and lettering should be professionally done). Images are to be a minimum resolution of 300 dpi at 100% size. Patterns, not shading, should be used to distinguish areas within graphs or other figures. Unacceptable illustrations will result in rejection of the manuscript. Authors are also strongly encouraged to submit an electronic version (.cdr, .cpt, .gif, .jpg, and .tif formats) of all figures in individual files that are separate from the electronic file containing the text and tables.

Special Sections

Letters to the Editor:

Submission of letters regarding topics relevant to the Society or creation science is encouraged. Submission of letters commenting upon articles published in the *Quarterly* will be published two issues after the article's original publication date. Authors will be given an opportunity for a concurrent response. No further letters referring to a specific *Quarterly* article will be published.

Editor's Forum:

Occasionally, the editor will invite individuals to submit differing opinions on specific topics relevant to the *Quarterly*. Each author will have opportunity to present a position paper (2000 words), and one response (1000 words) to the differing position paper. In all matters, the editor will have final and complete editorial control. Topics for these forums will be solely at the editor's discretion, but suggestions of topics are welcome.

Book Reviews:

All book reviews should be submitted to the book review editor, who will determine the acceptability of each submitted review. Book reviews should be limited to 1000 words. Following the style of reviews printed in this issue, all book reviews should contain the following information: book title, author, publisher, publication date, number of pages, and retail cost. Reviews should endeavor to present the salient points of the book that are relevant to the issues of creation/evolution. Typically, such points are accompanied by the reviewer's analysis of the book's content, clarity, and relevance to the creation issue.

Author Copies:

CRSQ policy is that authors get 10 free copies of the issue containing their article, regardless of the number of co-authors. These free copies must be pre-ordered before the issue goes to press.

Creation Research Society
Membership/Subscription Application and Renewal Form

The membership/subscription categories are defined below:

1. **Voting Member** ....Those having at least an earned master's degree in a recognized area of science.
2. **Sustaining Member** ....Those without an advanced degree in science, but who are interested in and support the work of the Society.
3. **Student Member** ....Those who are enrolled full time in high schools, undergraduate colleges, or postgraduate science programs (e.g., MS, PhD, MD, and DVM). Those holding post-doctoral positions are not eligible. A graduate student with a MS degree may request voting member status while enrolled as a student member.
4. **Senior Member** ....Voting or sustaining members who are age 65 or older.
5. **Life Member** ....A special category for voting and sustaining members, entitling them to a lifetime membership in the Society.
6. **Subscriber** ....Libraries, churches, schools, etc., and individuals who do not subscribe to the Statement of Belief.

All members (categories 1–5 above) must subscribe to the Statement of Belief as defined on the next page.

Please complete the lower portion of this form and mail it with payment to CRS Membership Secretary, 1 W. Firestorm Way #145, Glendale, AZ 85306, or fax for credit card payment to (928) 636-1153. Applications may also be completed online at creationresearch.org.

This is a ☐ new ☐ renewal application for the subscription year beginning Summer 20_____. *(Please type or print legibly.)*

Name ______________________________ Address ______________________________

City ____________________ State ______ Postal/Zip code _______ Country ______________

Phone (optional) ______________________ Email______________________________

Degree____________________________ Field________________________________

Year granted______________ Institution ____

Presently associated with

I have read and subscribe to the CRS Statement of Belief. Signature

For foreign orders, including Canadian, payment must be made in U.S. dollars by a check drawn on a U.S. bank, international money order, or credit card. *Please do not send cash.*

Indicate applicable category ⬇	*Indicate payment* ⬇			
	Paper**			
☐ Voting ☐ Sustaining	USA	Canada/ Mexico	Other countries	**Paper-less‡**
☐ Regular [per year]	☐ $60	☐ $80	☐ $100	☐ $40
☐ Senior (65+) [per year]	☐ $50	☐ $70	☐ $90	☐ $35
☐ Life member	☐ $800	☐ $800	☐ $800	☐ $800
☐ Student* [per year]	☐ $50	☐ $70	☐ $90	☐ $0
☐ Subscriber [per year]	☐ $63	☐ $83	☐ $103	☐ $42

* Student members are required to complete the bottom portion of this form.
NOTE: Student members may qualify for the *Future Leaders Sponsorship* program.
See the CRS website at www.creationresearch.org for details.
** Rates for the paper option include postage for First Class Mail International

‡ **PAPERLESS option:** You may opt out of receiving paper copies of the CRS periodicals (*CRS Quarterly* and *Creation Matters*). By choosing this option you may register for access to the Premium Area of the website, where you may view or download electronic (PDF) versions of these publications. Of course, regular members and subscribers may also have access to the Premium Area. Only members, however, will have access to the Members Exclusive Area of the website.

Member/Subscriber $_____ per year
x ______ years
SUBTOTAL $__________
Optional contribution + $__________
Life membership + $__________
TOTAL $__________

☐ Visa ☐ MasterCard ☐ Discover
☐ American Express ☐ Check/money order
Card number ________________________
Expiration date (mo/yr) ________________
Phone number (______) ________________
Signature __________________________

***Student Members* are required to complete the following:**

School or institution now attending____________________
____

Your current student status: ☐ high school; ☐ undergraduate;
graduate program ☐ MS ☐ PhD; ☐ other ______________

Year you expect to graduate or complete your degree__________

Major, if college or graduate student ____________________

Signature __________________________________

Order Blank for Past Issues

Cost of complete volumes (per volume): .... members (all categories) – $18.00 + S/H
nonmembers and subscribers (libraries, schools, churches, etc.) – $25.00 + S/H

Cost of single issues (per issue): .... members (all categories) – $5.00 + S/H
nonmembers and subscribers (libraries, schools, churches, etc.) – $7.00 + S/H

	Number			
Volume	**1**	**2**	**3**	**4**
24	☐	☐	☐	☐
25	☐	☐	☐	☐
26	☐	☐	☐	☐
27	☐	☐	☐	☐
28	☐	☐	☐	☐
29	☐	☐	☐	☐
30	☐	☐	☐	☐
31	☐	☐	☐	☐
32	☐	☐	☐	☐
33	☐	☐	☐	☐
34	☐	☐	☐	☐
35	☐	☐	☐	☐
36	☐	☐	☐	☐

	Number			
Volume	**1**	**2**	**3**	**4**
37	☐	☐	☐	☐
38	☐	☐	☐	☐
39	☐	☐	☐	☐
40	☐	☐	☐	☐
41	☐	☐	☐	☐
42	☐	☐	☐	☐
43	☐	☐	☐	☐
44	☐	☐	☐	☐
45	☐	☐	☐	☐
46	☐	☐	☐	☐
47	☐	☐	☐	☐
48	☐	☐	☐	☐
49	☐	☐	☐	☐

	Number			
Volume	**1**	**2**	**3**	**4**
50	☐	☐	☐	☐
51	☐	☐	☐	☐
52	☐	☐	☐	☐
53	☐	☐	☐	☐
54	☐	☐	☐	☐
55	☐	☐	☐	☐
56	☐	☐	☐	☐
57	☐	☐	☐	☐
58	☐	☐	☐	☐
59	☐	☐	☐	☐
60	☐	☐	☐	☐
61	☐	☐	☐	☐
62	☐	☐	☐	☐

Add 20% for postage (**for U.S. orders:** min. $6, max. $18; **for Canadian orders:** min. $10, no max.; **for other foreign orders:** min. $15, no max.)

Total enclosed: $_______________

Make check or money order payable to Creation Research Society. Please do not send cash. For foreign orders, including Canadian, please use a check in U.S. funds drawn on a U.S. bank, an international money order, or a credit card.

(Please type or print legibly)

Name ______________________________ Address ____

City ______________________________ State ________ Zip _______________ Country ________________________

☐ Visa ☐ MasterCard ☐ Discover ☐ American Express Card number ______________________________________

Expiration date (mo/yr) _____________ Signature ____

Mail to: Creation Research Society, 1 W. Firestorm Way #145, Glendale, AZ 85306, USA

Creation Research Society

History—The Creation Research Society was organized in 1963, with Dr. Walter E. Lammerts as first president and editor of a quarterly publication. Initially started as an informal committee of 10 scientists, it has grown rapidly, evidently filling a need for an association devoted to research and publication in the field of scientific creation, with a current membership of over 600 voting members (graduate degrees in science) and about 1000 non-voting members. The *Creation Research Society Quarterly* is a peer-reviewed technical journal. It has been gradually enlarged and modified, and is currently recognized as one of the outstanding publications in the field. In 1996 the *CRSQ* was joined by the newsletter *Creation Matters* as a source of information of interest to creationists.

Activities—The Society is a research and publication society, and also engages in various meetings and promotional activities. There is no affiliation with any other scientific or religious organizations. Its members conduct research on problems related to its purposes, and a research fund and research center are maintained to assist in such projects. Contributions to the research fund for these purposes are tax deductible. As part of its vigorous research and field study programs, the Society operates the Van Andel Creation Research Center in Glendale, Arizona.

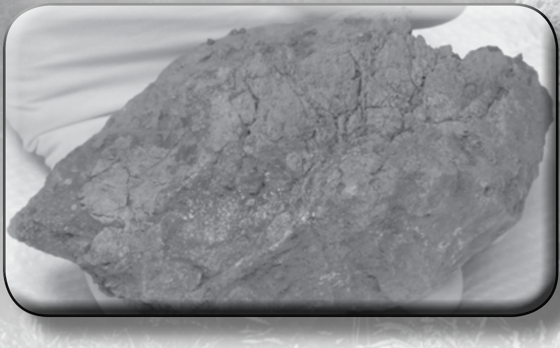
Membership—Voting membership is limited to scientists who have at least an earned graduate degree in a natural or applied science and subscribe to the Statement of Belief. Sustaining membership is available for those who do not meet the academic criterion for voting membership, but do subscribe to the Statement of Belief.

Statement of Belief—Members of the Creation Research Society, which include research scientists representing various fields of scientific inquiry, are committed to full belief in the biblical record of creation and early history, and thus to a concept of dynamic special creation (as opposed to evolution) both of the universe and the earth with its complexity of living forms. We propose to re-evaluate science from this viewpoint, and since 1964 have published a quarterly of research articles in this field. *All members of the Society subscribe to the following statement of belief:*

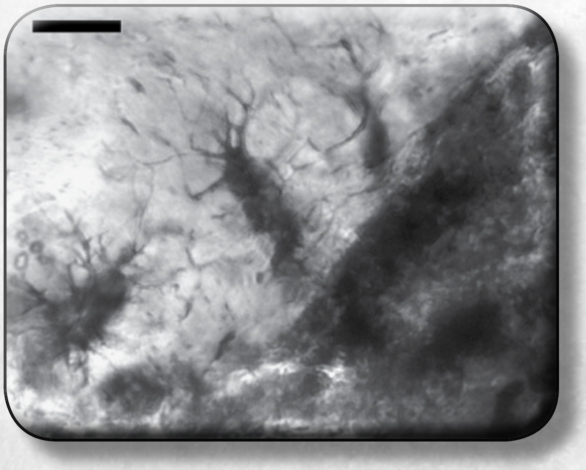
1. The Bible is the written Word of God, and because it is inspired throughout, all its assertions are historically and scientifically true in all the original autographs. To the student of nature this means that the account of origins in Genesis is a factual presentation of simple historical truths.
2. All basic types of living things, including humans, were made by direct creative acts of God during the Creation Week described in Genesis. Whatever biological changes have occurred since Creation Week have accomplished only changes within the original created kinds.
3. The Great Flood described in Genesis, commonly referred to as the Noachian Flood, was a historical event worldwide in its extent and effect.
4. We are an organization of Christian men and women of science who accept Jesus Christ as our Lord and Savior. The act of the special creation of Adam and Eve as one man and woman and their subsequent fall into sin is the basis for our belief in the necessity of a Savior for all people. Therefore, salvation can come only through accepting Jesus Christ as our Savior.

iDINO II

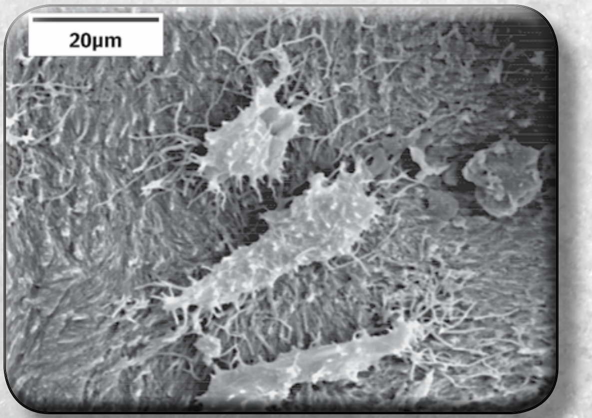
Investigation of Dinosaur Intact Natural Osteo-tissue



A fragment of the *Triceratops* brow horn. Fragments, such as this one, still contain tissue and cells.



Microscopic examination of tissue extracted from a *Triceratops* horn reveals bone cells still present.



Electron microscope picture of intact bone cells still in tissue extracted from a *Triceratops* horn.

How can pliable, stretchable tissue survive inside dinosaur fossils for over 65 million years?

How can this tissue still contain intact cells and even dinosaur proteins?

How can this fragile biological material survive for so long?

The answer to these questions directly challenges the current, evolutionary-biased, geologic timescale.

The Creation Research Society began its iDINO research initiative for the purpose of studying soft tissue in dinosaur fossils. The first phase of the project detected pliable, unfossilized tissue in a brow horn of a *Triceratops*. Within this tissue were intact osteocytes (bone cells). Some results from the iDINO project have been published in a technical microscopy journal and presented at an international microscopy conference. The Spring 2015 issue of the *Creation Research Society Quarterly* also features a special report of the iDINO project. Plus, to further spread the important information about soft tissue, the Society is developing a video (Echoes of the Jurassic).

The **second phase** of the project (iDINO II) will look more extensively at the process of tissue preservation. Evolutionists have offered various theories of how this tissue could survive for millions of years. iDINO II will methodically investigate these preservation claims, assessing their plausibility.

The iDINO results have already provided a strong challenge to the evolutionary worldview. More extensive and detailed examination may provide even stronger evidence that the age of dinosaur fossils is far less than 65 million years. To this end, the Society continues to seek those willing to fund this project with either one-time gifts or monthly donations.

For more information contact us at (928) 636-1153 or crsvarc@crsvarc.com.

Also visit http://tinyurl.com/nphm2c4 for project updates and details.

V62N4